2020

The effects of photosymbiosis on gene expression in the facultatively symbiotic coral Astrangia poculata, with a focus on NF-kappaB signaling and antioxidant enzymes

https://hdl.handle.net/2144/41678
Boston University

BOSTON UNIVERSITY

GRADUATE SCHOOL OF ARTS AND SCIENCES

Dissertation

THE EFFECTS OF PHOTOSYMBIOSIS ON GENE EXPRESSION IN THE FACULTATIVELY SYMBIOTIC CORAL ASTRANGIA POCULATA, WITH A FOCUS ON NF-kappaB SIGNALING AND ANTIOXIDANT ENZYMES

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Submitted in partial fulfillment of the

requirements for the degree of

Doctor of Philosophy

2020

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For the first teacher I ever had, my mom. I love you!

ACKNOWLEDGEMENTS

My dissertation research is the culmination of collaborative efforts between me and my many scientist colleagues and mentors. Without their guidance, support, and wisdom, this dissertation would not have been possible. My utmost gratitude goes to my advisors, particularly John Finnerty, one of the most amiable, funny (and tall!) people I have ever met. Thank you for always having my best interests at heart, for entertaining my crazy ideas (be it for my research or teaching the two iterations of Marine Genomics) and for nurturing my growth as a scientist. I would also like to thank my committee members for their support and advice in all things science and life — Les Kaufman for reminding me to see the forest beyond the trees (and to know their scientific names), Chip Celenza for his insightful discussions on genetics and RNA-seq, Sean Mullen for his foundational help in phylogenies and genomics, and Kim McCall for always being there to address my scientific concerns.

Thank you to my lab mates — Karina Lord for her optimism and teaching me the finer points of marine species identification, dive master Katey Lesneski for getting me confident enough to dive into the Belizean waters during my first field season, Joanna Lee for bringing her hard work, her Hawaiian vibes, love of *Mola molas* and Bobaface into the lab, Brian Granger and Tristan Lubinski for their invaluable help with coding and bioinformatics, Derek Stefanik for helpful discussions on genomics and encouragement, and Liz Burmester and Lauren Friedman for laying the groundwork for my *Astrangia poculata* and *Nematostella vectensis* projects. I would also like to thank Tiffany Dill for being a true friend throughout my graduate career and for helping me craft my

departmental talks. I could not have done it without your camaraderie, enthusiasm, and constructive feedback.

I am also deeply appreciative of my former undergrads — Erika Lee for being the most incredible LA for BI 108 anyone could ask for, killing it by producing 3 new LAs from that section, going on to join the Finnerty lab, and now pursuing a nursing career. Thank you to Joanna Lee for her hard work as an undergrad in the lab, done with humor and determination. Many of my happiest memories of grad school are of working with you both.

I would also like to thank Kathryn Spilios for being a great teaching mentor over the course of three BI 108 semesters as a TF and twice as a Teaching Fellow Mentor for first-year grad students. Her belief in me and her support as I updated the BI 108 curriculum with Small World Initiative's interactive labs to promote scientific thinking in undergraduate labs made an indelible impact on me as an instructor. From pedagogy to handling student concerns to designing new curricula, thank you so much for your advice and dedication to students. Many of my greatest joys in grad school came from teaching and inspiring young minds because they remind us why we love science.

Finally, I would like to thank my family and friends for their support throughout these years. To my younger sister for her relentless sass and laughs, I wish you all the happiness and successes on your journey to become a Doctor of Physical Therapy. To my mom for instilling in me her love of science, medicine, and for her kindness, wisdom, generosity, and love as I undertook my own scientific journey. Thank you.

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ABSTRACT

Corals are critical to marine biodiversity and human welfare. Coral reefs cover <1% of the seafloor but support ~1/3 of all marine species. Approximately 1.5 billion people live within 100 km of coral reefs, relying upon them for food, income from tourism, and protection from storms. Their economic value has been estimated at $375 billion annually.

The foundation of coral reefs is the intracellular symbiosis between corals and photosynthetic dinoflagellates of the family Symbiodiniaceae. Tropical corals satisfy up to 95% of their nutritional requirements through photosynthesis, and their ability to construct reefs is biochemically coupled to photosynthesis.

While permitting corals to thrive, photosymbiosis also increases their exposure to environmental stressors and vulnerability to climate change. Reliance on photosynthesis restricts reef-building corals to shallow, clear, tropical waters, where they experience higher temperatures and UV exposure. The generation of reactive oxygen species by the symbiont also exposes corals to greater oxidative stress. The symbiosis is particularly sensitive to climate change: all of the mass coral bleaching events have occurred since 1982, driven by elevated ocean temperatures.

Molecular cross-talk between host and symbiont impacts resilience of the coral holobiont and resistance to bleaching. Unfortunately, we know little about how photosymbiosis impacts expression or activity of coral genes. Tropical corals engage in an obligate symbiosis with Symbiodiniaceae, so we cannot study their gene expression in a stable aposymbiotic state. However, the northern star coral, *Astrangia poculata,* engages in a facultative symbiosis with Symbiodiniaceae.

I used RNA sequencing to investigate how symbiosis impacts gene expression in *A. poculata*, focusing on genes implicated in photosymbiosis: antioxidant enzymes (specifically superoxide dismutases) and the NF-κB signaling pathway. From an improved transcriptome assembly, I recovered core elements of a primitively simple NF-κB signaling pathway and a rich complement of SOD proteins. 273 coral transcripts— many associated with protein metabolism and vesicle-mediated transport— were differentially expressed in symbiotic versus aposymbiotic corals. Unlike in the facultatively symbiotic sea anemone *Exaiptasia*, symbiosis was not associated with depressed NF-κB transcript levels. IKKε, a potential positive regulator of NF-κB activity, was strongly up-regulated, as was one particular superoxide dismutase.

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LIST OF ABBREVIATIONS

ANK	Ankyrin repeat domain
ANOVA	Analysis of variance
ASW	Artificial seawater
ATP	Adenosine triphosphate
BLAST	Basic local alignment search tool
BUSCO	Benchmarking universal single-copy ortholog
CCS	Copper chaperone for superoxide dismutase
CO_2	Carbon dioxide
COI	Cytochrome oxidase subunit I
Cu	Copper
DF	Degrees of freedom
DNA	Deoxyribonucleic acid
ELISA	Enzyme-linked immunosorbent assay
ETC	Electron transport chain
FDR	False discovery rate
Fe	Iron
gb	Gigabases
GB	Gigabytes
GO	Gene ontology
GRR	Glycine-rich region
GTP	Guanosine triphosphate
H_2O_2	Hydrogen peroxide
HAT	Histone acetyltransferase
IκB	Inhibitor of kappa B
IKK	Inhibitor of kappa B kinase
IL	Interleukin
iNOS	Inducible nitric oxide synthase
IPT	Immunoglobulin-like, plexin, transcription factors
IRF	Interferon regulatory factors
Log_2 FC	Log_2 fold change
miRNA	Micro ribonucleic acid

MS	Mean square
MUSCLE	Multiple sequence comparison by Log-expectation
NEMO	Nuclear factor-kappa-B essential modulator
NF-κB	Nuclear factor-kappa light-chain-enhancer of activated beta cells
NIK	Nuclear factor inducing kinase
NLS	Nuclear localization signal
NO	Nitric oxide
Nv	*Nematostella vectensis*
O_2^-	Superoxide
OH•	Hydroxide radical
PAR	Photosynthetically active radiation
PCA	Principal component analysis
PE	Paired end
RHD	Rel homology domain
RNA	Ribonucleic acid
ROS	Reactive oxygen species
RPKM	Reads per kilobase of transcript per million mapped reads
RT-qPCR	Real time – quantitative polymerase chain reaction
SDD	Scaffold dimerization domain
SE	Single end
SOD	Superoxide dismutase
STKc	Serine-threonine kinase catalytic domain
TAB1	TAK1 binding protein 1
TACC	Texas advanced computing cluster
TAD	Transactivation domain
TAK1	TGF-β activated kinase 1
TBK	Tank-binding kinase
TGF-β	Transforming growth factor-beta
TLR	Toll-like receptor
TNF	Tumor necrosis factor
TNFR	Tumor necrosis factor receptor
UV	Ultraviolet
Zn	Zinc

CHAPTER 1: EFFECTS OF PHOTOSYMBIOSIS ON CORAL GENE EXPRESSION – ONE KEY TO UNDERSTANDING REEF RESILIENCE IN A CHANGING WORLD

1.1 Introduction

The loss of keystone species, such as reef-building corals, due to climate change has negative consequences for biodiversity and to humans in particular because corals provide the extensive framework for entire marine ecosystems. Complex calcium carbonate coral reefs cover less than 1% of the seafloor (Burke, 2012) in nutrient-deficient oligotrophic waters, yet support approximately a third of all known marine species (Costanza et al., 1997). Humans rely heavily upon reef-dwelling species for food—fishing of these species is a $375 billion dollar industry, representing 25% of all fishing activity in developing countries (Costanza et al., 1997, Burke, 2012).

The ability of corals to survive and construct reefs in oligotrophic tropical waters depends upon their symbiosis with photosynthetic dinoflagellates of the family Symbiodiniaceae (formerly *Symbiodinium* sp.). Corals provide shelter, carbon, nitrogen, oxygen, and phosphorus to these micro-algal endosymbionts, while the Symbiodiniaceae provide photosynthates that supply up to 95% of the host's energetic requirements (Muscatine & Porter, 1977). Photosynthesis and skeletogenesis are inherently coupled, although the precise mechanisms linking the two processes are not well understood (Davy et al. 2012). As a corollary, non-photosynthetic aposymbiotic cnidarians do not build calcium carbonate skeletons. Thus, the existence and foundation of coral reef structures is dependent on the mutually beneficial coral-algal symbiosis.

While the photosymbiosis with Symbiodiniaceae permits corals to thrive in oligotrophic tropical waters, it also increases their exposure to certain environmental stressors. Photosymbiosis constrains corals to live in relatively shallow, clear waters, exposing them to warmer temperatures and higher ultraviolet (UV) light levels (Frankowiak et al., 2016). Photosymbiosis also exposes corals to greater endogenous sources of oxidative stress (Falkowski et al., 1984). The symbiont can satisfy most of the coral's energetic requirements via photosynthesis, but during daylight hours, it infuses the coral's cells with oxygen and reactive oxygen species (ROS) such as hydrogen peroxide (H_2O_2; Weis, 2008). As a result, intracellular symbiosis exposes corals to increased oxidative stress relative to strictly heterotrophic cnidarians.

The coral-algal photosymbiosis is acutely sensitive to environmental stress, including those related to climate change. Breakdown of the symbiotic relationship results in bleaching, the common name for the color change that occurs when corals expel their photosynthetic symbionts, revealing the white calcium carbonate skeleton underneath. In this process, the host coral cells harboring symbionts may expel them, or undergo apoptosis, or autophagy (Weis, 2008). Bleaching can be triggered by a range of environmental stressors including thermal stress (Lesser et al., 1990, Brown, 1996), excessive UV radiation (Lesser et al., 1990), pollution (Douglas, 2003), oxidative stress (Weis, 2008, Hoegh-Guldberg & Bruno, 2010), and malnutrition (Rosset et al., 2017). Bleaching is reversible if environmental conditions improve (Lasker et al., 1984), but prolonged bleaching eventually leads to the death of the coral colony, and widespread bleaching can lead to the collapse of the coral reef ecosystem (Ainsworth et al., 2016).

The connection between high sea surface temperatures and coral bleaching is clear e.g., all of the significant thermally induced coral bleaching events have been documented since 1980, including 1983, 1987, 1992, 1998, 2005, 2016, and 2017 (Eakin, 2018, National Oceanic and Atmospheric Administration, 2018). As a general pattern, bleaching has occurred when El Niño events superimpose rapid temperature spikes on an already increasing baseline temperature. In rapid succession, the El Niño in March 2015, El Niño in 2016, and La Niña in early 2017, plus the gradual increase in baseline thermal stress that corals were already facing prior to 2015, led to 51% of coral reefs globally being under thermal stress (Eakin, 2018). Currently, 75% of the world's coral reefs are considered "threatened" by increasing water temperatures caused by global warming and other anthropogenic factors (Burke, 2012).

While rising ocean temperatures are the critical environmental driver of mass coral bleaching, thermal stress is associated with a myriad of other stressors in corals. Therefore, a coral's resilience in the face of thermal stress may depend in part on its response to these associated stressors. For example, the coral-algal symbiosis links elevated temperatures to oxidative stress (Figure 1-1). If not counteracted by antioxidant defense mechanisms, reactive oxygen species generated as a byproduct of photosynthesis can accumulate in the host and symbiont (Asada, 1987), damaging DNA, proteins, and lipids, including the enzymes and cofactors involved in photosynthesis (e.g., quinone binding protein of photosystem II, photosystem I). Indeed, it has been hypothesized that oxidative stress mediates symbiont expulsion in corals (Lesser, 1989), and the administration of exogenous anti-oxidants has been shown to increase the temperature

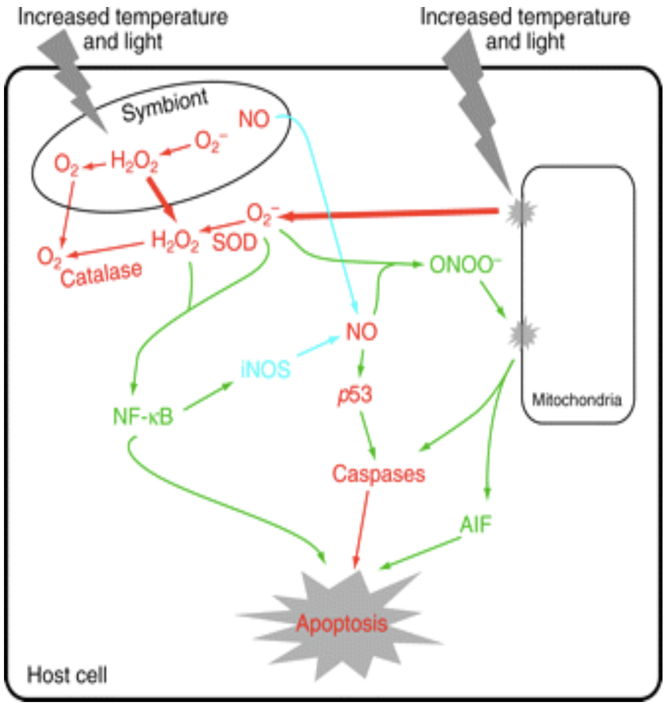


Figure 1-1. Linkage of Heat Stress to Oxidative Stress in Coral-Algal Symbiosis Photosynthesis by the symbiont generates O_2^- and H_2O_2. The latter can escape the symbiont and move into the host cell. Thermal and UV stress also damage the host's mitochondrial membranes, contributing to the accumulation of superoxide and H_2O_2 in the host cell. Multiple molecular pathways may be mobilized in response to the elevated ROS. The pathways depicted in red are supported by direct empirical evidence in cnidarian-dinoflagellate symbiosis, while those in blue are supported by indirect evidence, and those in green are known from other photosymbiotic relationship involving metazoan hosts. Figure reproduced from Weis (2008).

threshold for bleaching (Lesser, 1997).

Given the causal relationship between photosymbiosis and increased intracellular levels of reactive oxygen species, it is perhaps not surprising that a number of studies comparing symbiotic and aposymbiotic cnidarians have identified changes in the expression of antioxidant genes. For example, in a study on sea anemones, the symbiotic species *Anemonia viridis* exhibited greater diversity of SOD expression (1 CuZnSOD, 4 MnSODs, and 2 FeSODs) and activity than the aposymbiotic *Actinia schmidti* (4

CuZnSODs and 1 MnSOD) using gel electrophoresis (Richier et al., 2005; see Chapter 3 for further discussion). Interestingly, the symbiotic *A. viridis* was also more resilient to experimental elevation of oxygen levels and temperature (hyperoxia 100% O_2 and +7°C), exhibiting no change in gel electrophoresis banding pattern and activity relative to control conditions. In contrast, aposymbiotic *A. schmidti* was highly sensitive to the increased O_2 partial pressure and heat, showing biomarkers for cellular damage (Richier et al., 2005). The authors also found that exposure to high O_2 partial pressure may precondition symbiotic animal cells to oxidative stress (Richier et al., 2005). Another more recent study compared freshwater hydras that differ in their association with the green alga *Chlorella*. *Hydra viridissima* engages in a stable photosymbiosis with *Chlorella*, while *Hydra vulgaris*, engages in an unstable photosymbiosis with the same alga (Ishikawa et al., 2016). *H. viridissima* was found to exhibit greater resistance to oxidative stress and starvation than *H. vulgaris*. Expression of the ROS scavenger ascorbate peroxidase was higher in the symbiotic *H. viridissima* (Ishikawa et al., 2016). These are consistent with the hypothesis that the evolution of photosymbiosis in animals was preceded by the evolution of a greater capacity to resist oxidative stress (Ishikawa et al., 2016, Ishikawa et al., 2016, Melo Clavijo et al., 2018).

In addition to antioxidant enzymes such as SOD, the cellular response to elevated ROS in corals is also hypothesized to involve increased activity of the transcription factor NF-κB (see Figure 1-1). However, contrary to expectations based on NF-κB's role in regulating the oxidative stress response, a recent study on the sea anemone *Exaiptasia pallida* found that NF-κB RNA and protein levels were decreased in symbiotic relative to aposymbiotic (Mansfield et al., 2017). These authors hypothesized that the symbiont specifically suppresses NF-κB expression as a means of altering the anemone's immune response. This hypothesis emphasizes NF-κB's role as a regulator of the innate immune system over its role as a regulator of the oxidative stress response. In another result compatible with the notion that symbiosis requires suppression of the host immune response, targeted depletion of transforming growth factor-beta (TGF-β) in larvae of the coral *Fungia scutaria* was associated with both an increased immune response and a reduction in the percentage of larvae colonized by symbionts, suggesting that photosymbiosis causes immunosuppression in the host (Berthelier et al., 2017). The TGF-β receptor was also targeted by micro ribonucleic acid (miRNA) in *Aiptasia* during the onset and maintenance of symbiosis (Baumgarten et al., 2018).

As the above studies show, the molecular cross-talk between host and symbiont during cnidarian photosymbiosis can be studied by comparing gene expression in symbiotic versus aposymbiotic cnidarians. Unfortunately, how photosymbiosis impacts the expression or activity genes in corals is largely unknown. Studying the impact of photosymbiosis on gene expression is not experimentally tractable in most tropical corals because they engage in an obligate symbiosis with Symbiodiniaceae, making it impossible to establish the baseline pattern of gene expression in an unstressed aposymbiotic host. Bleached coral is always in a state of nutritional stress.

In my research, I have investigated gene expression associated with photosymbiosis using the northern star coral, *Astrangia poculata*. *A. poculata* is a wide-ranging temperate coral that engages in a facultative symbiosis with Symbiodiniaceae, (Peters et al., 1988). *A. poculata* can derive up to 70% of its energy from its photosynthetic symbiont *Breviolum psygmophilum* (formerly, *Symbiodinium psygmophilum* clade B2), but unlike tropical corals, it can also live stably in an aposymbiotic state for long periods. This means that it can exist in nature as symbiotic colonies (which appear brown), aposymbiotic colonies (which appear white), or mixed colonies (in which the polyps may be white or brown or "mottled"; Figure 1-2). This unique ability of *A. poculata* to have two stable symbiotic states lends itself to research aimed at disentangling the effects of symbiotic state on genes involved in the oxidative stress response in the absence of a stressor.


Credit: J. Dimond

Figure 1-2. Aposymbiotic and Symbiotic *A. poculata* Colonies
A. poculata in an aposymbiotic state (white, left) and a symbiotic state (brown, right). In both of these colonies, the polyps and tentacles are extended.

As described above, two particular aspects of host gene expression that have received particular attention in the literature are genes involved in responding to oxidative stress and the NF-κB signaling pathway. Below, I describe the potential importance of these pathways for regulating or maintaining photosymbiosis.

H_2O_2 is the most abundant ROS in marine environments; it can be produced in multiple ways and it has a relatively long half-life. It is photochemically formed in naturally occurring surface and ground waters exposed to sunlight (Cooper & Zika, 1983) and is generated via metabolic activity in marine organisms (Lesser, 2006) and their photosynthetic counterparts. In open waters, any accumulation of H_2O_2 is attenuated by ocean currents and vertical mixing. By contrast, high levels of ROS from UV exposure, photochemical degradation, and anthropogenic sources can accumulate in shallow water environments. Symbiotic cnidarians such as corals can encounter high photon fluctuations and UV radiation that are able to penetrate >20 meters into their natural habitats (Jerlov, 1950, Jokiel, 1980). H_2O_2 concentrations vary widely: from 10-420 nM in ocean surface waters (Yuan & Shiller, 2001, Yuan & Shiller, 2005) to 0.5-3.5 μM in shallow tidal pools (Abele-Oeschger et al., 1997). In shallow coastal habitats, high concentrations of H_2O_2 can accumulate from anthropogenic sources, such as industrial runoff, and through natural processes such as atmospheric wet deposition. Precipitation over continental landmasses can markedly increase surface water concentrations of H_2O_2, as rainwater contains as much as 0.1-247 μM H_2O_2 (Sakugawa et al., 1990, Vione et al., 2003), while oceanic precipitation has 3.5-82 μM H_2O_2 (Cooper & Lean, 1989, Yuan & Shiller, 2000).

There are a number of reasons why H_2O_2 is a particularly relevant form of ROS in marine organisms, and in corals in particular. H_2O_2 is uncharged and small, so it readily permeates cell membranes and, at high levels, causes significant damage to biological macromolecules (Lesser, 2006). H_2O_2 can also degrade into more highly reactive ROS, O_2^- anions and OH• radicals (Schreck et al., 1991). In photosynthetic cnidarians, the photosystem II of the micro-algal endosymbionts generates ROS in the form of O_2^- (Figure 1-1), which is reduced to H_2O_2 by the antioxidant SOD. H_2O_2 can then be reduced to O_2 by ascorbate peroxidase (Lesser, 2006). Photosystem I can reduce O_2 to O_2^- via the Mehler reaction, which constitutes the highest chloroplast source of O_2^- (Asada, 1987). H_2O_2 can also react with ferrous iron to form an excited and very reactive OH• through a Fenton reaction. To counter Fenton reactions, organisms have developed metal ion sequestration mechanisms (e.g., transferrin, lactoferrin, and ferritin; siderophores in bacteria), which reduce the bioavailability of iron and thus the reduction of H_2O_2 to OH•. Of the ROS generated by photosynthetic activity of the symbiont, only uncharged H_2O_2 and O_2 can diffuse across cellular membranes to accumulate in host coral cells (Weis, 2008). Host animal cells contain organelles that generate ROS through normal metabolic activity. For example, within the mitochondrial electron transport chain, NADH dehydrogenase (complex I) and the activity between ubiquinone and complex III generates O_2^- that is transformed by SOD into H_2O_2 and O_2. Cytochromes, which are found in the animal, plant, and bacteria endoplasmic reticulum, can also generate O_2^- (Halliwell & Gutteridge, 1999).

Taken together, there are many naturally occurring sources of ROS in the host, micro-algal symbiont, and environment that the coral must counteract to mitigate oxidative damage. Because marine organisms are exposed to varying levels of ROS depending on their environment (e.g., depth and turbidity determine the amount of light that reaches the organisms) and endogenous metabolic activities, the oxidative stress response to protect against ROS-induced damage is also varied (Ross & Van Alstyne 2007, Friedman et al., 2018).

1.2 Differential Gene Expression Associated With Photosymbiosis and Reactive Oxygen Species Exposure

A number of candidate genes and pathways exhibit altered expression in response to both oxidative stress and photosymbiosis. Innate immune pathways have been implicated in the breakdown of symbiosis; however, there are conflicting reports on its transcriptomic regulation in cnidarians. Genes involved in the nuclear factor-kappa B (NF-κB) signaling pathway in particular show altered expression in response to oxidative stress and with a shift from aposymbiotic to symbiotic states. There is evidence that NF-κB regulation is altered by photosymbiosis in *Exaiptasia* (= *Aiptasia*) (Mansfield et al., 2017) and the sea sponge *Cliona varians* (Riesgo et al., 2014). Mansfield et al. determined that NF-κB mRNA, protein, and activity increase with the loss of symbionts in *Exaiptasia* and that introducing symbiotic algae (family Symbiodiniaceae) into *Exaiptasia* larvae reduces NF-κB protein levels (Mansfield et al., 2017). In symbiotic vs. aposymbiotic *C. varians*, differences in multiple gene ontology terms associated with NF-κB were noted; for example, aposymbiotic *C. varians* had increased expression of genes involved in “positive regulation of NF-κB transcription factor activity,” and decreased expression of genes involved in “NF-κB inducing kinase activity,” “aerobic respiration," and "oxidation-reduction processes." Upon reinfection of aposymbiotic *C. varians* with symbiotic algae (family Symbiodiniaceae), there was a decrease in expression of genes related to "NF-κB transcription factor activity" and "inhibitor of κB kinase (IKK)/NF-κB cascade." Additionally, there was a decrease in expression of genes involved in "cell growth" and the "Wnt receptor signaling pathway" (Riesgo et al., 2014). In our differential expression analysis of symbiotic and aposymbiotic corals treated with H_2O_2 or untreated (controls), we found significantly increased expression of an innate immunity pathway IRF3/IRF7 member, IKKε (refer to Chapter 4). Burmester found changes in expression of two innate immunity genes: neurogenic locus Notch-like increased in expression and olfactomedin 2A decreased in expression in symbiotic corals compared to aposymbiotic corals (false discovery rate [FDR] $p < 0.003$; 2017). Together, these studies suggest a role for NF-κB and innate immunity in the acquisition or loss of the symbiotic state in corals, and that it may be involved in modulating the organismal response to ROS exposure.

Using *A. poculata* as a model system, I tested the following hypothesis:

1. Photosymbiosis elicits predictable changes in gene expression in *Astrangia poculata*. Specifically,
    - a. Symbiotic colonies exhibit greater expression of antioxidant genes and pathways, as observed in a number of cnidarian systems.
    - b. Symbiotic colonies exhibit reduced expression of NF-κB as recently reported in *Exaiptasia pallida*, a facultatively symbiotic sea anemone (Mansfield et al., 2017).

To test this hypothesis, I pursued the following specific aims.

Aim 1. In order to determine how symbiotic state impacts gene expression in *A. poculata*, we assembled and annotated a new and improved reference transcriptome for *A. poculata*. The new *A. poculata* transcriptome incorporated 39.4 billion base pairs of sequence generated by Liz Burmester of the Finnerty lab as well as 10.5 gigabases (gb) out of 96.4 gb of RNA sequence data that I generated. The rationale for generating a new transcriptome as well as the process of sequence generation, assembly, and annotation using RNA sequencing of both symbiotic and aposymbiotic corals, under control conditions and with H_2O_2 exposure is described in Chapter 2.

Aim 2. In order to evaluate the completeness of the *A. poculata* transcriptome and to determine if I could recover full-length versions of key candidate genes, I reconstructed the motif architecture and molecular evolution of the SOD gene family and the NF-κB signaling pathway. This work is described in Chapter 3.

Aim 3. The rationale for the differential expression analyses of the new *A. poculata* transcriptome (Chapter 2) using RNA sequencing of both symbiotic and aposymbiotic corals, under control conditions and with H_2O_2 exposure, is described in Chapter 4.

CHAPTER 2: DEVELOPMENT AND EVALUATION OF REFERENCE TRANSCRIPTOMES FOR ASTRANGIA POCULATA: HOST AND SYMBIODINIAECEAE

2.1 Introduction

The symbiosis between hermatypic corals and photosynthetic dinoflagellates of the family Symbiodiniaceae (LaJeneusse et al., 2018) forms the metabolic foundation of coral reef ecosystems (Dubinsky & Achituv, 1990). As reviewed in Chapter 1, this symbiosis is currently under threat from climate change and a host of additional environmental challenges (Hughes et al., 2003, Hoegh-Guldberg et al., 2007). There is an urgent interest in better understanding (1) how this symbiosis is regulated at the cellular level (Weis 2008), (2) how the coral host and the symbiont might contribute to cellular stress responses (Lesser 1996, Weis 2008), and (3) why some coral holobionts exhibit greater stress resistance than others (Bellantuono et al., 2012, Palumbi et al., 2014).

While the photosymbiosis with Symbiodiniaceae permits corals to thrive in oligotrophic tropical waters, it also increases their exposure to certain environmental stressors. Photosymbiosis constrains corals to live in relatively shallow, clear waters, exposing them to warmer temperatures and higher ultraviolet (UV) light levels (Frankowiak et al., 2016). Photosymbiosis also exposes corals to greater oxidative stress (Falkowski et al., 1984). The symbiont can supply up to 95% of the coral's energetic requirements via photosynthesis, but during daylight hours, it infuses the coral's cells with oxygen and reactive oxygen species (ROS) such as hydrogen peroxide (Weis, 2008).

Indeed, the formation of a long and stable photosymbiosis may require the evolution of greater oxidative stress tolerance (Ishikawa et al., 2016).

Given their facultatively symbiotic state (Figure 2-1) and the range of depths over which they occur, colonies of *A. poculata* are presumably exposed to a natural gradient of ROS (Figure 2-2). Symbiotic colonies living in warm, shallow, intertidal pools would be exposed to the highest levels of ROS. In addition to endogenous ROS generated by active photosynthesis as described above, corals in shallow pools accumulate high levels of ROS from exogenous sources such as photo-decay of organic matter and atmospheric deposition (Abele et al., 1999). Conversely, aposymbiotic colonies living in deeper, cooler waters may experience relatively lower levels of ROS. Aposymbiotic colonies in shallow pools and symbiotic colonies in deeper waters would be exposed to an intermediate level of oxidative stress.

As adaptive responses to cellular stress often involve changes in gene expression (Murray et al., 2004, de Nadal et al., 2011), we were interested in how the presence of the symbiont impacts gene expression of the host, how ROS impacts gene expression, and how the symbiotic state might impact the reaction to ROS. These questions are not experimentally tractable in most tropical corals because they engage in an obligate symbiosis with Symbiodiniaceae, making it impossible to establish the baseline pattern of gene expression in an unstressed aposymbiotic host. Bleached coral is always in a state of nutritional stress. Because *A. poculata* engages in a facultative symbiosis with Symbiodiniaceae, specifically *Breviolum psygmophilum*, we were able to directly compare gene expression in the symbiotic and aposymbiotic state in the presence or absence of 0.00025% H_2O_2.

Figure 2-1. Aposymbiotic and Symbiotic *A. poculata*
Aposymbiotic (white, left) and symbiotic (brown, right) *A. poculata* colonies living side-by-side off the coast of Fort Wetherill, Rhode Island. Photo by J. Dimond.

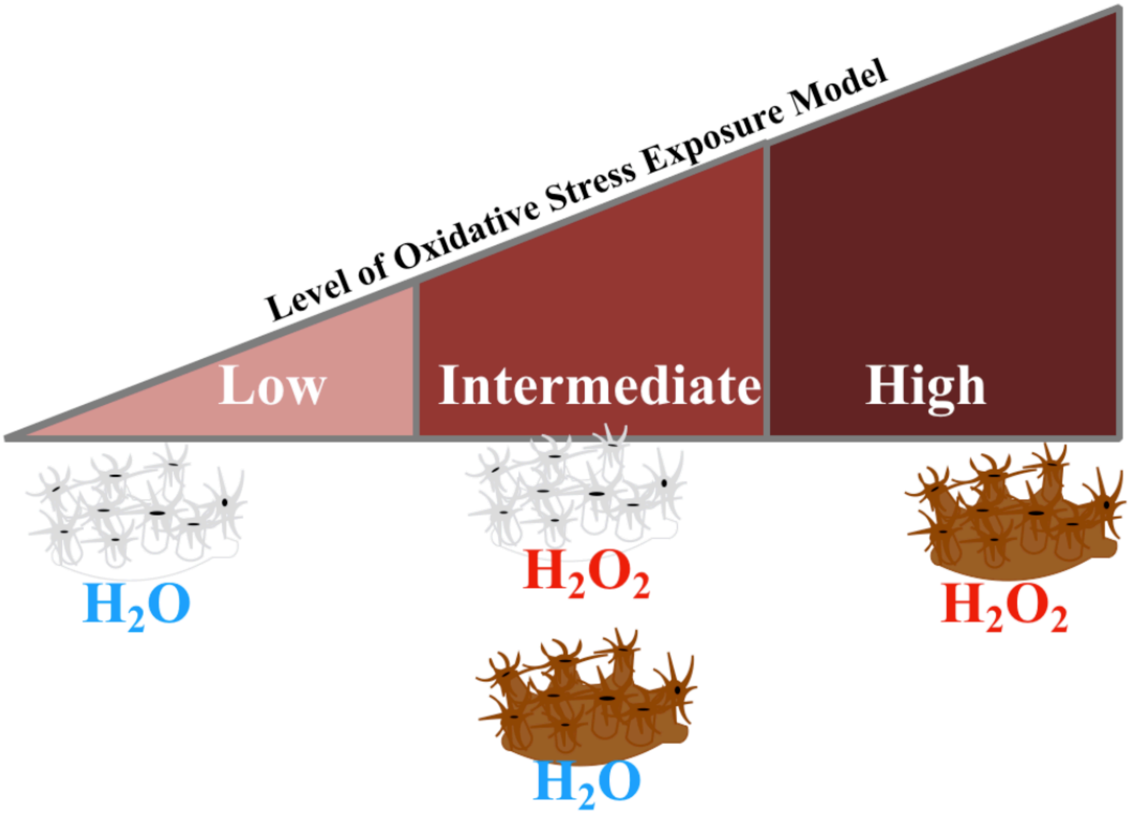


Figure 2-2. Experimental Exposure to a Range of ROS
A. poculata colonies are exposed to a range of oxidative stress by exposing symbiotic (brown) colonies and aposymbiotic (white) colonies to control conditions or 0.00025% H_2O_2. As a result, we can compare three levels of ROS exposure: low (aposymbiotic corals under control conditions), intermediate (aposymbiotic corals treated with H_2O_2 and symbiotic corals under control conditions [which are exposed to photosynthetically produced ROS]), or high (symbiotic corals treated with H_2O_2).

Given the additional endogenous production of ROS in symbiotic corals, we expect symbiotic and aposymbiotic *A. poculata* to respond differently to exogenous ROS exposure (i.e., H_2O_2): symbiotic *A. poculata* that is exposed to endogenous ROS from abundant *B. psygmophilum* will elicit a more robust transcriptomic response to exogenous ROS than aposymbiotic *A. poculata*, which is not be exposed to the same magnitude of ROS from *B. psygmophilum*. In a study of sea anemones *Anemonia viridis* (symbiotic) and *Actinia schmidti* (aposymbiotic), Richier et al. discovered that symbiotic *A. viridis* exhibited greater diversity of superoxide dismutase (SOD) expression and activity (2005). Symbiotic *A. viridis* was also more resilient to artificial perturbations (hyperoxia 100% O_2 and +7°C) and was no different from its control. In contrast, aposymbiotic *A. schmidti* was highly sensitive to the increased oxygen (O_2) partial pressure and heat, showing biomarkers for cellular damage (Richier et al., 2005). The authors also found that exposure to high O_2 partial pressure may precondition symbiotic animal cells to oxidative stress (Richier et al., 2005). A recent study compared gene expression profiles in *Hydra viridissima,* which engages in a stable photosymbiosis with the green alga *Chlorella*, and *Hydra vulgaris*, which engages in an unstable photosymbiosis with the same alga (Ishikawa et al., 2016). *H. viridissima* exhibited greater resistance to oxidative stress and starvation than *H. vulgaris*. In symbiotic *H. viridissima,* genes related to the mitochondria and electron transport chain (ETC) showed decreased expression compared to *H. vulgaris*. Decreased expression of these genes suggests decreased endogenous production of ROS by the mitochondrial ETC. Expression of the ROS scavenger ascorbate peroxidase was high in both species, but higher in *H. viridissima* (Ishikawa et al., 2016). Similarly, in a study comparing gene expression by quantitative real time - polymerase chain reaction (qRT-PCR) in symbiotic and aposymbiotic states of the coral *Acropora tenuis*, expression of the antioxidant Na-dependent ascorbic acid as well the anti-apoptotic protein ubiquitin carboxy terminal hydrolase were higher in symbiotic corals (Yuyama et al., 2011).

To determine how the symbiotic state of *A. poculata* impacts the transcriptional response to H_2O_2 exposure, we first had to assemble a comprehensive reference transcriptome that was representative of conditions that would be used in our differential expression experiments. Burmester used RNA-sequenced 100 bp paired-end data from four symbiotic control colonies, two aposymbiotic control colonies, and a mottled colony to assemble her *A. poculata* transcriptome with CLC Genomics WorkBench (2017). However, attempts to recover full-length *A. poculata* NF-κB transcripts with that transcriptome were unsuccessful. In order to capture full-length transcripts of innate immunity genes that are implicated in photosymbiosis and H_2O_2 exposure, I generated more sequencing data (symbiotic and aposymbiotic corals exposed to H_2O_2 and control), at a deeper level (24 libraries underwent 150 bp paired-end RNA-sequencing on a single flow cell), to assemble with Velvet-Oases at various k-mers. Finally, I conducted quality control measures to show the generated transcriptome is representative.

2.2 Experimental Design

2.2.1 *A. poculata* Collection and H_2O_2 Exposure

Colonies of *A. poculata* in two symbiotic states were collected at Fort Wetherill

State Park in Jamestown, RI, in 2015 by Elizabeth Burmester, Kathryn Lesneski, and Karina Scavo Lord. Using SCUBA, four symbiotic and four aposymbiotic colonies were harvested by chiseling the colonies away from rocky substrates at depths between 2 and 4 meters, fully within the range enabling photosynthesis. Colonies were returned to the New England Aquarium and housed in a flow-through artificial seawater system. Seawater was filtered using a protein skimmer and the abundance of suspended microorganisms in the system was controlled by UV light treatment. Tanks were illuminated for 10 h d^{-1} using T5 HO fluorescent lighting fixtures (Hamilton Technology, Aruba Sun T5-V Series). Photosynthetically active radiation (PAR) was kept constant at an average of 37.5 ± 10.1 µmol m^{-2} s^{-1}. Corals were fed daily with frozen copepods directed to all polyps within each colony using a turkey baster (Burmester, 2017). The corals were housed for a period of three months before experimentation to acclimate to laboratory conditions.

Prior to RNA isolation, four symbiotic and four aposymbiotic colonies collected in Fort Wetherill, RI, in fall 2015 were split in half and exposed to control conditions or 0.00025% H_2O_2 for 18 hours. This is the same level of H_2O_2 that was used in a previous study to reliably induce a significant change in the expression of hundreds of genes, including known or suspected oxidative stress response genes, in seven genets of the starlet sea anemone, *N. vectensis* (Friedman et al., 2018). A 14-day exposure to twice this level of H_2O_2 (0.0005%) was survivable by at least some genets of *A. poculata*, but consistently caused a reduction in tentacle extension relative to control conditions (Figure 2-3; Delacruz, Finnerty & Finnerty, unpublished results).

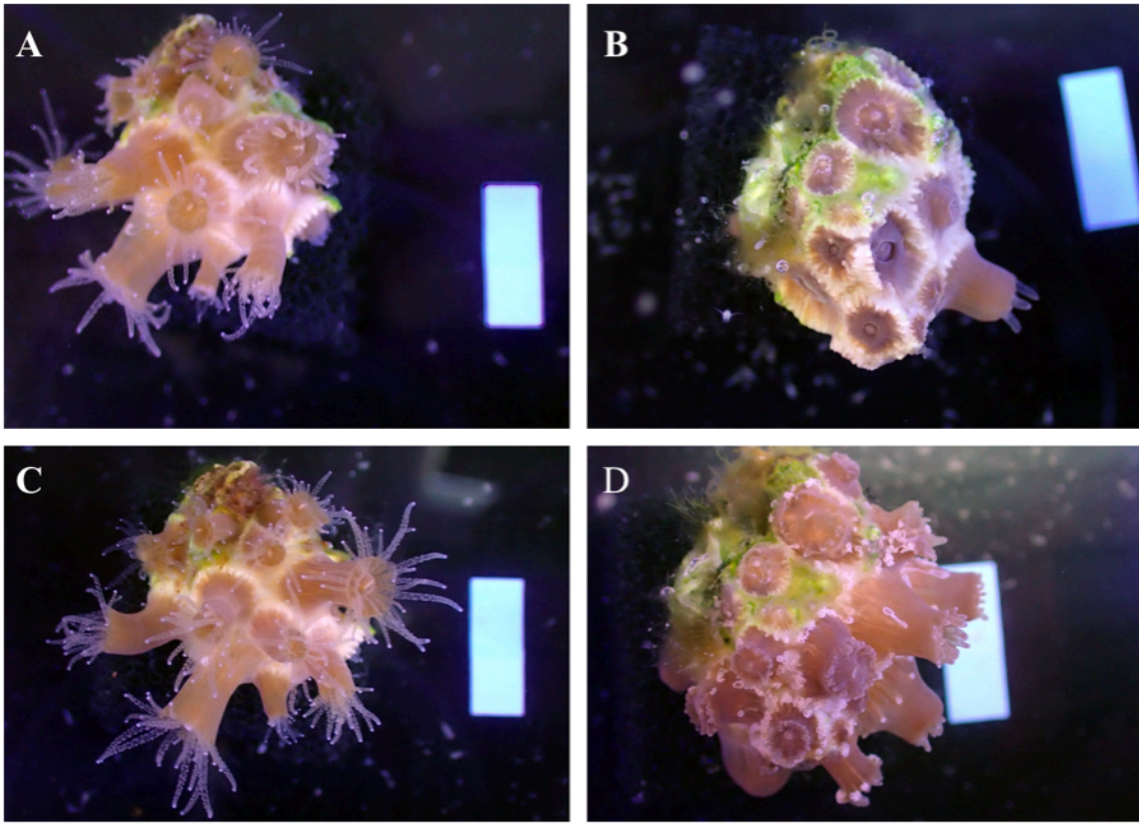


Figure 2-3. Symbiotic *A. poculata* Exposed to H_2O_2
A single symbiotic *A. poculata* colony from Fort Wetherill was split approximately in half, and each half was exposed to either unadulterated artificial seawater (ASW) (A, C) or ASW + 0.0005% H_2O_2 (B, D). The colony fragments are shown after 3 days (A, B) or 14 days (C, D) exposure, with the respective solutions replaced daily with freshly made media. Tentacle extension was consistently greater under control conditions (A, C) than under H_2O_2 exposure (B, D), although tentacle tips remained visible in the H_2O_2-exposed colonies. Photos by Roger Finnerty.

2.2.2 RNA Isolation, Library Preparation, and Sequencing

To prepare each coral library for RNA sequencing (see Figure 2-4 for Fort Wetherill samples), we isolated total RNA from a single symbiotic or aposymbiotic polyp using TRIzol according to the manufacturer's protocol (Life Technologies Thermo Fisher Scientific). Single polyps were sampled from all 15 colonies. For the single mottled colony collected in Fort Wetherill, two polyps were sampled, one symbiotic and the other aposymbiotic. The sampled polyps, including the surrounding skeleton, were removed from their respective colonies using bone-cutting scissors. Excised polyps were frozen in liquid nitrogen and then pulverized with mortar and pestle. Pulverized polyps were combined with approximately 1.0 ml TRIzol, and the resulting slurry was homogenized using ground glass tissue grinders. The resulting pellet was resuspended in nuclease-free water and nucleotide concentration and purity were determined using a NanoDrop 2000 (Thermo Fisher Scientific).

cDNA libraries were prepared for each RNA sample using the Illumina TruSeq RNA Sample Prep Kit v2. Each library was prepared with uniquely indexed primer-adaptors. Prior to sequencing, the size range of the library inserts was determined on a Bioanalyzer 2100 (Agilent). Multiple libraries were multiplexed and sequenced over two lanes of a flow cell (12 libraries/lane) on an Illumina HiSeq 2000 at the Harvard Bauer Core Facility, generating 150-bp paired-end reads (Table 2-1). This data pipeline yielded 8 sequenced libraries from symbiotic polyps (n=4 from control polyps and n=4 from H_2O_2-treated polyps) and 16 sequenced libraries from aposymbiotic polyps (n=8 from control polyps and n=8 from H_2O_2-treated polyps).

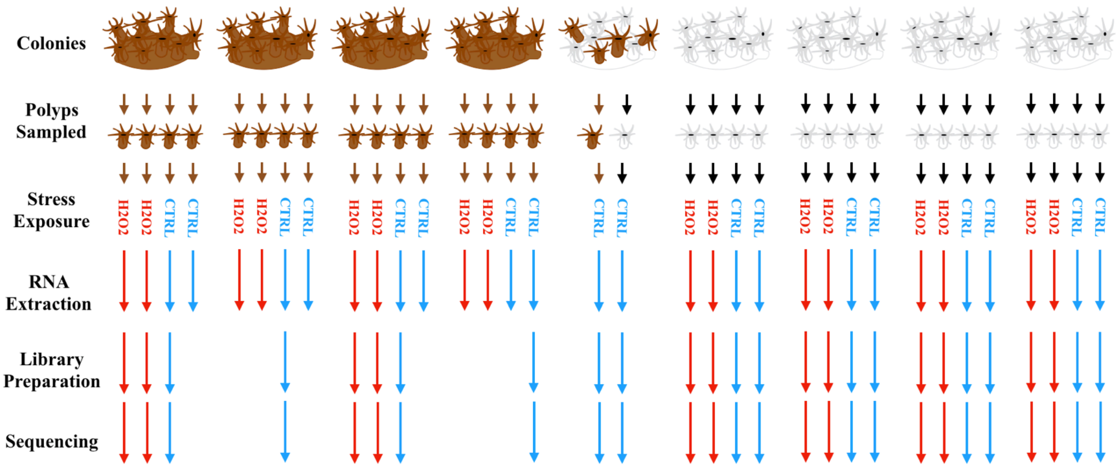


Figure 2-4. Fort Wetherill Samples in Library Sequencing Pipeline
Samples were collected from Fort Wetherill, RI, in 2012 and 2015. After acclimation to laboratory conditions (at least 3 months), the corals were subjected to either 0.00025% H_2O_2 or control conditions before extraction of RNA from polyps and preparation of cDNA libraries. The arrows indicate the number of samples at each step and the color of the arrows represents H_2O_2 (red) or control (blue) treatment.

2.2.3 Sequence Processing and Transcriptome Assembly for *A. poculata*

A reference transcriptome was assembled using 17.4 gigabases (gb) of data generated in this study (described above) and 39.5 gb of data generated previously from colonies collected at Fort Wetherill, RI, and Woods Hole, MA, in 2012. Details of the collection, RNA isolation, library preparation, and sequencing of these 2012 samples are described above and elsewhere (Burmester, 2017). The assembly was conducted as follows. First, separate population-specific assemblies were generated using 17.4 gb of data generated from colonies collected at Fort Wetherill in 2015 and 39.5 gb of data generated from colonies collected at Fort Wetherill and Woods Hole in 2012 (Table 2-1). Each of the assemblies was produced using a multi-kmer approach with the Velvet-Oases pipeline (Zerbino & Birney, 2008, Schulz et al., 2012). Nine single-kmer assemblies were produced using kmers ranging from 65-145 bp in increments of 10 bp. After these nine assemblies were produced, they were merged at a kmer of 75 bp. Following assembly of the Fort Wetherill and Woods Hole holobiont assemblies, the two transcriptomes were separately clustered at decreasing levels of sequence-identity (0.95, 0.90, 0.85) using CD-HIT-EST (Li et al., 2006, Fu et al., 2012) to remove nearly identical sequences. To confirm that distinct genes were not lost in the clustering process, the clustered assemblies were evaluated using BUSCO (Li et al., 2006, Fu et al., 2012) to determine whether full-length versions of 978 conserved metazoan orthologs could be recovered. Clustering at 0.90 sequence identity reduced the number of contigs by approximately 75% in both the Fort Wetherill and Woods Hole holobiont assemblies, while retaining complete versions of conserved metazoan orthologs at frequencies of 96.4% (Fort Wetherill) and 97.3% (Woods Hole). The Fort Wetherill and Woods Hole assemblies that had been clustered at 0.90 were then concatenated and subjected to another round of clustering. The combined holobiont transcriptome, clustered at 0.90, reduced the complexity of the original holobiont transcriptomes without sacrificing recovery of conserved orthologs. This transcriptome was then parsed into three taxonomically distinct collections as described below. The unclustered, population-specific transcriptomes were retained to facilitate studies on intraspecific genetic variation.

Table 2-1. ***A. poculata*** **Libraries Sequenced**

Library	**Symbiotic State**	**Stress Exposure**	**Read Length (nt)**	**Seq. Reads (millions)**	**Seq. Yield (gigabases)**	**In Assembly**
Apo-1a-H2O2	Aposymbiotic	H_2O_2	150	18.4	2.8	**Yes**
Apo-1b-H2O2	Aposymbiotic	H_2O_2	150	13.3	2.0	n/a
Apo-1a-Ctrl	Aposymbiotic	none	150	15.2	2.3	n/a
Apo-1b-Ctrl	Aposymbiotic	none	150	16.1	2.4	n/a
Apo-2a-H2O2	Aposymbiotic	H_2O_2	150	16.8	2.5	n/a
Apo-2b-H2O2	Aposymbiotic	H_2O_2	150	14.1	2.1	n/a
Apo-2a-Ctrl	Aposymbiotic	none	150	20.4	3.1	n/a
Apo-2b-Ctrl	Aposymbiotic	none	150	16.4	2.5	n/a
Apo-3a-H2O2	Aposymbiotic	H_2O_2	150	18.1	2.7	n/a
Apo-3b-H2O2	Aposymbiotic	H_2O_2	150	9.4	1.4	n/a
Apo-3a-Ctrl	Aposymbiotic	none	150	23.3	3.5	n/a
Apo-3b-Ctrl	Aposymbiotic	none	150	13.0	2.0	**Yes**
Apo-4a-H2O2	Aposymbiotic	H_2O_2	150	19.1	2.9	n/a
Apo-4b-H2O2	Aposymbiotic	H_2O_2	150	19.2	2.9	n/a
Apo-4a-Ctrl	Aposymbiotic	none	150	14.0	2.1	n/a
Apo-4b-Ctrl	Aposymbiotic	none	150	14.6	2.2	n/a
Sym-1a-H2O2	Symbiotic	H_2O_2	150	19.9	3.0	**Yes**
Sym-1b-Ctrl	Symbiotic	none	150	15.6	2.3	n/a
Sym-1b-H2O2	Symbiotic	H_2O_2	150	19.4	2.9	n/a
Sym-2a-Ctrl	Symbiotic	none	150	17.0	2.6	n/a
Sym-3a-Ctrl	Symbiotic	none	150	16.2	2.4	n/a
Sym-3a-H2O2	Symbiotic	H_2O_2	150	20.4	3.1	n/a
Sym-3b-H2O2	Symbiotic	H_2O_2	150	18.7	2.8	n/a
Sym-4b-Ctrl	Symbiotic	none	150	19.1	2.9	**Yes**
AS_Sym	Symbiotic	none	100	124	12.4	**Yes**
AS_Apo	Aposymbiotic	none	100	151	15.1	**Yes**
WH-sym1	Symbiotic	none	100	24.5	2.5	**Yes**
WH-sym2	Symbiotic	none	100	21.3	2.1	**Yes**
WH-sym3	Symbiotic	none	100	17.6	1.8	**Yes**
WH-apo1	Aposymbiotic	none	100	25.4	2.5	**Yes**
WH-sym4	Symbiotic	none	100	16.2	1.6	**Yes**
WH-apo2	Aposymbiotic	none	100	15.3	1.5	**Yes**
		Total Assembly		**465.7**	**50.0**	

2.2.4 Parsing of Coral and *Symbiont* Transcripts

To discriminate coral transcripts from *Breviolum psygmophilum* transcripts in our *A. poculata* holobiont transcriptome, we used a published pipeline (Davies et al., 2016). BLASTx was used to compare contigs in the *A. poculata* assembly against four sequence databases: (1) sequences derived from 14 Symbiodiniaceae-free cnidarian transcriptomes and genomes; (2) putative coral sequences derived from 23 Symbiodiniaceae-associated coral transcriptomes and genomes; (3) sequences derived from 6 transcriptomes and genomes of cultured Symbiodiniaceae (presumably free of coral sequences); and (4) putative Symbiodiniaceae sequences derived from the 15 transcriptomes and genomes of coral holobionts. *A. poculata* sequences with significant BLAST hits (defined as E-value < 1E-5) to databases (1) and (2) but not (3) or (4) were sorted into a coral transcriptome, while contigs with significant BLAST hits to databases (3) and (4) but not (1) or (2) were sorted into a *Breviolum* transcriptome. If queries produced significant hits to both coral and Symbiodiniaceae, they were parsed into a third transcriptome designated "other" (Figure 2-5). Parsing was performed on the Texas Advanced Computing Cluster (TACC) at The University of Texas at Austin. Transcriptome statistics are presented in Table 2-2 along with comparable data from other recently generated cnidarian transcriptomes.

In addition to taxonomic affiliation, annotations were derived from BLAST results using Blast2GO Pro (Conesa et al., 2005; Gotz et al., 2008). Gene names were extracted from the top BLAST hit, and Gene Ontology (GO) categories were assigned. Contigs that did not produce significant BLAST hits were not annotated.

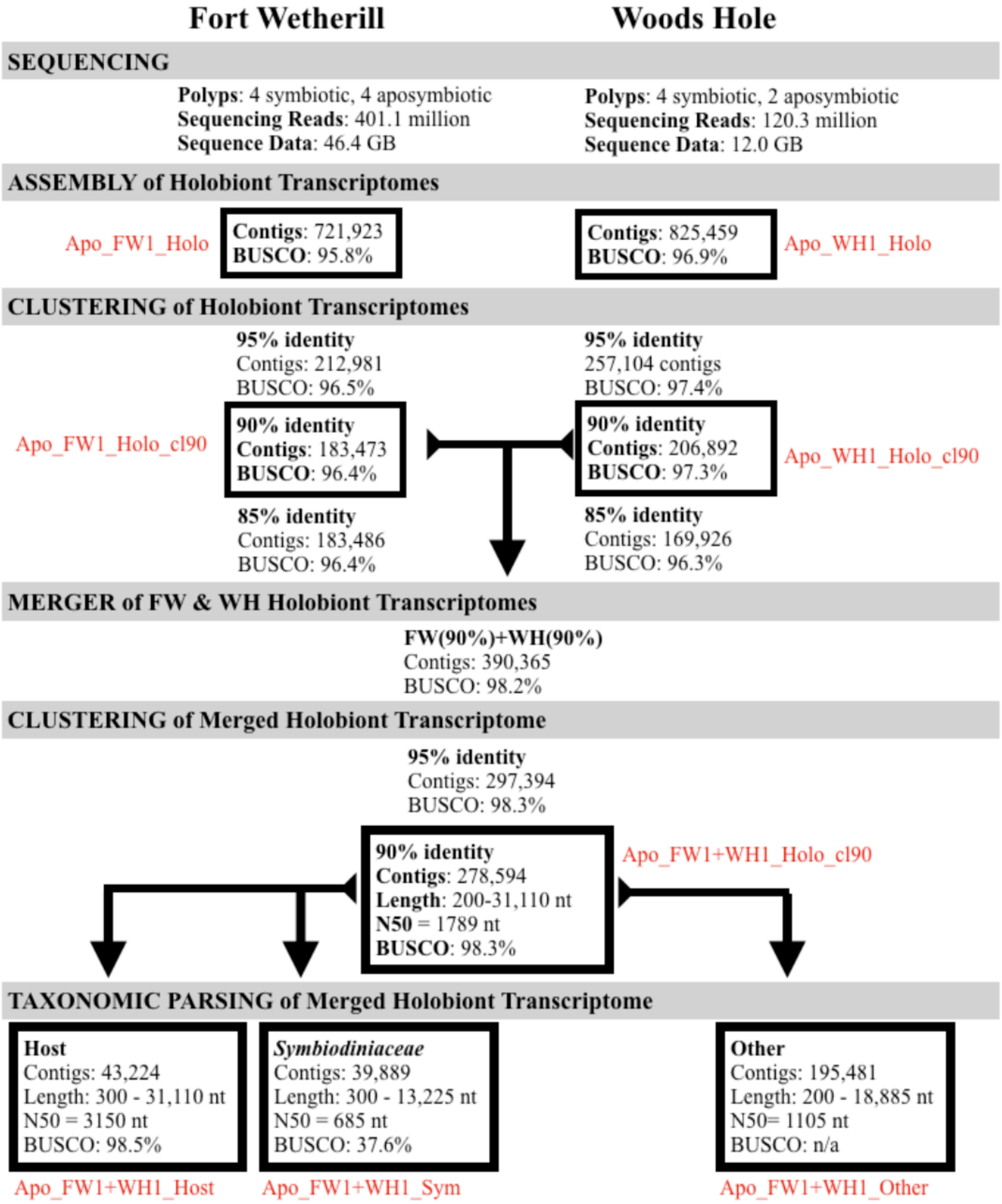


Figure 2-5. Assembly Pipeline of the *A. poculata* Transcriptome
Red text designates names of various transcriptome versions after the sequencing, assembly, clustering, merging, and clustering steps. The *A. poculata* merged transcriptome is composed of Apo_FW+WH1_Host and Apo_FW+WH1_Sym. There was one mottled colony from Fort Wetherill sequenced.

Table 2-2. Recently Published Cnidarian Transcriptomes

Species	**Sequencing Yield** (nt x 10^6)	**N50**	**Contigs**	**Coral Contigs**	**Symbiodiniaceae Contigs**	**Reference**
Astrangia poculata	511.1 PE (100-150 bp)	1789	278,594	43,224 (16%)	39,889 (14%)	this study
Edwardsiella lineata	188.1 PE (40 bp)	1036	90,440	—	—	Stefanik et al., 2014
Porites austaliensis	71 PE (100 bp)	2037	74,997	26,658 (35%)	26,627 (35%)	Shinzato et al. 2013
Orbicella faveolata	387 PE (75 bp)	1551	442,294	178,943 (40%)	130,217 (29%)	Pinzón et al. 2015
Acropora millepora	2 SE (>400 bp) > 400 SE > 125 PE	2023	56,260	—-	—-	Moya et al. 2012
Stylophora pistillata	—	2088	470,497	—	—	Maor-Landaw et al. 2017
Balanophyllia europea	—	1246	961,667	—	—	Maor-Landaw et al. 2017
Platygyra carnosus	59.6 PE (90 bp)	811	162,468	47,732 (29%)	—	Sun et al. 2013
Millepora alcicornis	76.5 PE (150 bp)	749	479,982	26%	—-	Ortiz-González et al. 2017
Pocillopora damicornis	115 SE (150 bp)	1104	135,265	—	—	Mass et al. 2017
Porites astreoides	594 PE (150 bp)	763	867,255	129,718 (15%)	186,177 (21%)	Mansour et al. 2016

2.2.5 Recovery of Conserved Orthologs from the *A. poculata* Transcriptome

To assess the recovery of full-length transcripts from genes that are widely conserved across the animal kingdom, we used BUSCO (Waterhouse et al., 2017) to compare all contigs in the *A. poculata* assembly to a set of 978 "universal single-copy conserved orthologs." Each ortholog was scored as "complete," "fragmented," or "missing." Results obtained for the *A. poculata* transcriptome were compared to a previously generated BUSCO analysis of 20 publicly available cnidarian and scleractinian transcriptomes (Burmester 2017; Figure 2-6).

To assess the recovery of single-copy orthologs that are widely conserved among alveolates, we used BUSCO (Waterhouse et al., 2017) to compare all contigs in the Symbiodiniaceae assemblies to a set of 234 single-copy orthologs from alveolates. Again, each ortholog was scored as "complete," "fragmented," or "missing." For comparison, the same analysis was performed on five publicly available Symbiodiniaceae transcriptomes (Figure 2-6; data obtained from www.comparative.reefgenomics.org).

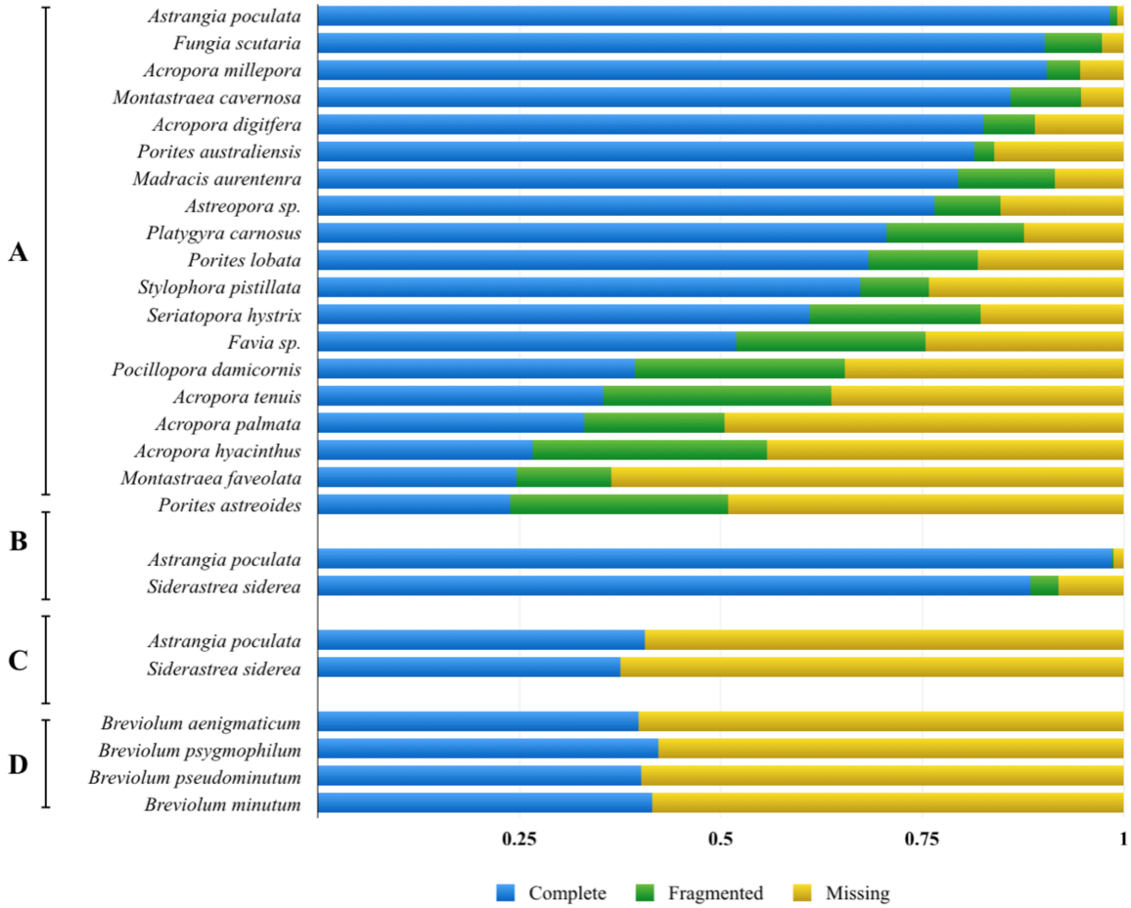


Figure 2-6. Recovery of Universal, Single-Copy Orthologs From Cnidarian Transcriptomes. (A) Transcriptomes generated from coral holobionts. (B) Collections of putative coral transcripts parsed from coral holobiont transcriptomes in (A). (C) Collections of putative Symbiodiniaceae transcripts parsed from coral holobiont transcriptomes in (A). (D) Transcriptomes generated from Symbiodiniaceae.

2.2.6 Phylogenetic Affinity of Coral Transcripts in the *A. poculata* Transcriptome

To confirm the species identity of our coral transcriptome, we produced a molecular phylogeny based on the mitochondrial cytochrome oxidase subunit I (COI; Figure 2-7; modified by Joanna Lee from Burmester, 2017). We searched NCBI to obtain COI sequences for *A. poculata* (Podar et al. 2001; AY039209.1) and 41 other hermatypic corals (Kim 2008, Kitahara et al., 2010, Arrigoni et al., 2012, Kayal et al., 2013, Kitahara et al., 2014, Addamo et al., 2016, Burmester 2017). Nucleotide sequences from all taxa were converted into amino acid format using the translate tool on ExPASy (https://web.expasy.org/translate/). We evaluated the completeness of the COI protein sequences from all species by testing whether all conserved motifs were present using MEME (Bailey et al., 2009). A phylogenetic tree was produced using the Phylogeny Analysis tool on the Phylogeny.fr website via a four-step process: (1) sequences were aligned using MUSCLE (Multiple Sequence Comparison by Log-Expectation; settings: maximum 16 iterations with diagonals; Edgar 2004); (2) poorly aligned regions were removed from the alignment using Gblocks (default setting; Dereeper et al., 2008); (3) a maximum-likelihood phylogeny was generated using PhyML (Dereeper et al., 2008); and (4) the resulting phylogeny was rendered using TreeDyn (Dereeper et al., 2008).

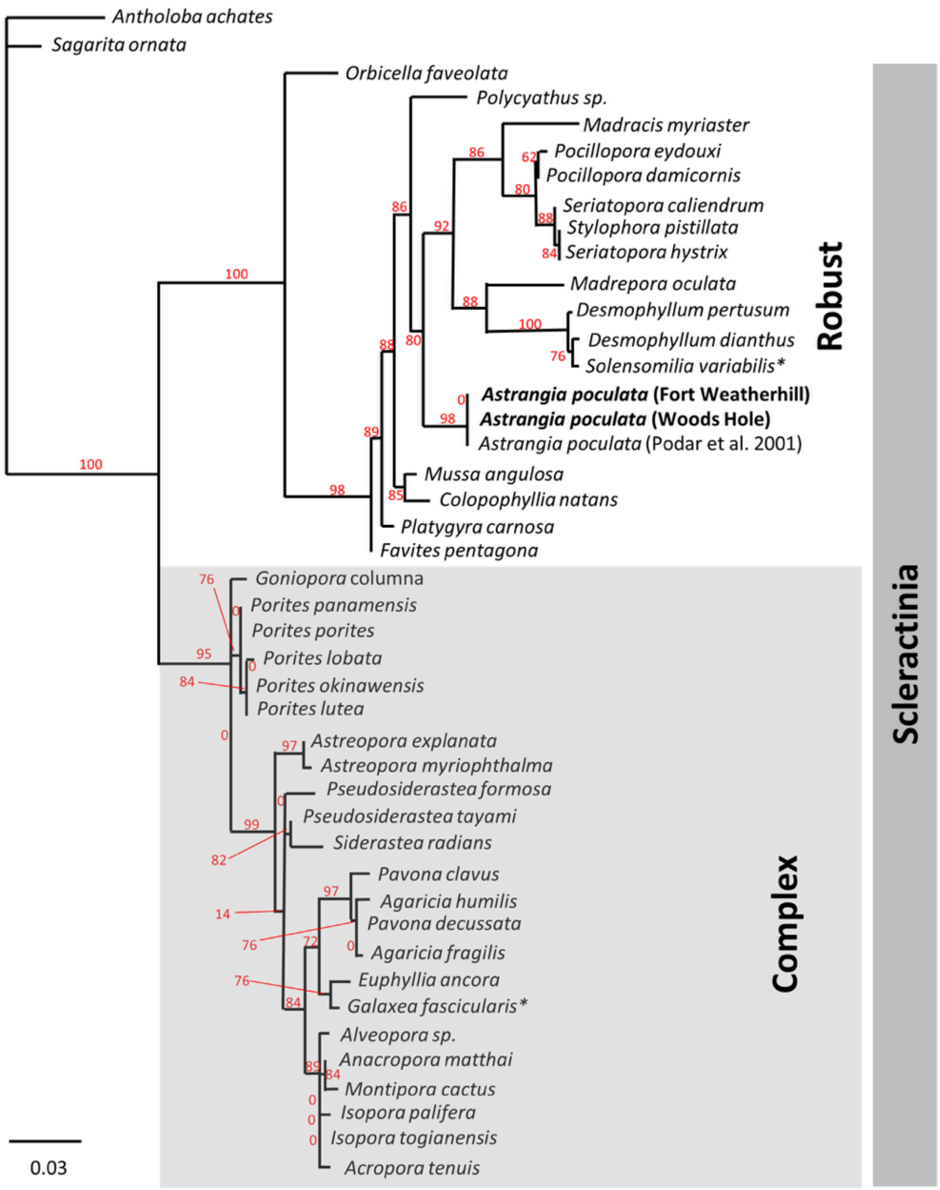


Figure 2-7. Coral Phylogeny Based on Cytochrome Oxidase Subunit I
This maximum likelihood phylogeny was created with 44 anthozoan cytochrome oxidase I amino acid sequences. Bootstrap values are represented in red. Two species of Actinaria were used as an outgroup. Branch lengths in the horizontal axis are proportionate to the number of amino acid substitutions per 100 residues (scale at lower left). The two Scleractinian clades in the tree correspond to the widely supported Robust and Complex coral lineages, with the exception of the taxa indicated by asterisks. Modified from Burmester (2017).

2.3 Results

2.3.1 *A. poculata* Sequencing Yield

Sequencing yielded a total of 642.9 million 150-bp paired-end reads from 24 polyps: 4 H_2O_2-treated symbiotic polyps, 4 control symbiotic polyps, 8 H_2O_2-treated aposymbiotic polyps, and 8 control aposymbiotic polyps (Table 2-1). The yield from individual specimens ranged from 2.5 to 4.9 gb nucleotides, with a total of 96.4 gb of data. Following quality trimming, we obtained a total of 61.2 gb of nucleotide data, 1.4 to 3.5 gb per specimen.

2.3.2 Transcriptome Statistics

A total of 50.0 gb of sequence data was used to generate the assembly: 10.5 gb from the current study, plus 27.5 gb of additional sequence data from Fort Wetherill *A. poculata* and 12.0 gb from Woods Hole *A. poculata* sequences generated previously (Table 2-1). Initially, separate assemblies were produced for Fort Wetherill and Woods Hole (Figure 2-5). This initial Fort Wetherill assembly consisted of more than 721,000 contigs, and we were able to identify complete sequences for 95.8% of 978 universally conserved metazoan orthologs using BUSCO (Waterhouse et al., 2017). The initial Woods Hole assembly consisted of more than 825,000 contigs, with 96.9% recovery of complete metazoan orthologs. These two assemblies were then clustered at 90% using CD-HIT (Li & Godzik 2006, Fu et al., 2012), which reduced the number of contigs by approximately 75% in each case with no reduction in the recovery of complete metazoan orthologs. The clustered transcriptomes were then combined, and clustered again at 90%.

This combined Fort Wetherill / Woods Hole holobiont transcriptome encompassed 278,598 contigs ranging in size from 200 to 31,111 nucleotides, with an n50 of 1789 nucleotides. The recovery of complete metazoan orthologs was 98.3%. This recovery was higher than that reported for any recently published cnidarian transcriptomes (Figure 2-6).

Using a published taxonomic sorting pipeline for cnidarian transcriptomes (Davies et al., 2016), 43,224 of the 278,594 contigs were parsed into a host-enriched transcriptome and 39,889 were parsed into a *B. psygmophilum*-enriched transcriptome (Figure 2-5). Contigs that could not be unambiguously assigned to host or *B. psygmophilum* were parsed into a third transcriptome of 195,481 contigs. For the coral-enriched transcriptome, we recovered complete sequences for 98.5% of conserved metazoan orthologs. We recovered complete sequences for just 95 of 234 single-copy orthologs that are widely conserved in alveolates within the *B. psygmophilum*-enriched transcriptome; this recovery rate (37.6%) was comparable to that for other published Symbiodiniaceae transcriptomes (Figure 2-6).

2.3.3 Coral-Enriched Transcriptome Annotation

Almost all of the coral-enriched contigs were annotated with Blast2GO Pro (Conesa et al., 2005; Gotz et al., 2008), with 42,777 contigs retrieving BLAST hits and only 447 queries failing to retrieve BLAST hits from NCBI at an expected value of 1E-05 or lower (Figure 2-8). Of the 99% of contigs that did produce BLAST hits, most were mapped and assigned GO annotations (28,213 contigs or 66% of contigs with BLAST hits), while 14,564 contigs produced BLAST hits but were not assigned GO annotations (34%).

Next, we looked at the top GO categories (Biological Process, Molecular Function, and Cellular Compartment) assigned to the annotated coral-enriched contigs (Figure 2-9). The most common GO terms under Biological Processes were “cellular protein metabolic process” and “gene expression.” Under Molecular Function, the most common GO terms were “purine nucleotide binding” and “purine ribonucleotide binding.” Under Cellular Compartment, the most common GO terms were “nucleus” and “cytosol.”

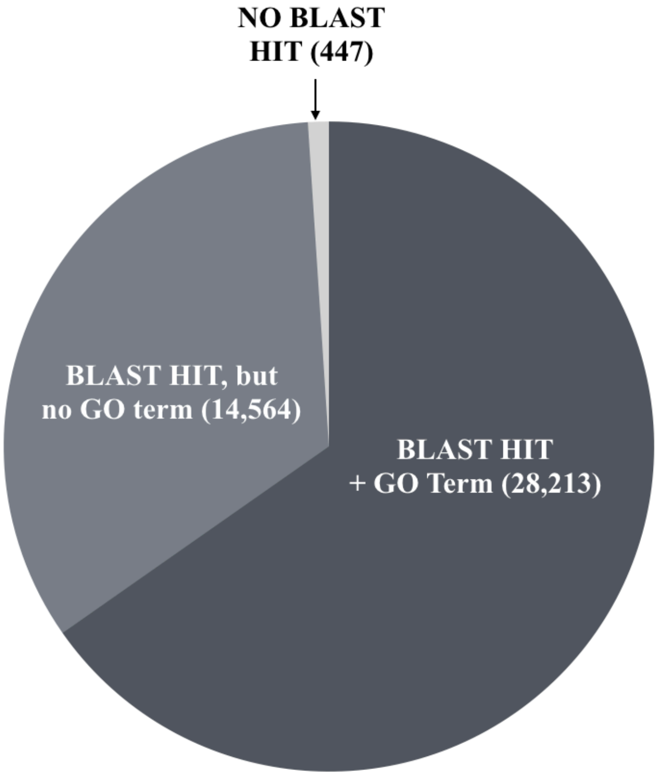


Figure 2-8. Coral-Enriched Contigs Producing BLAST Hits

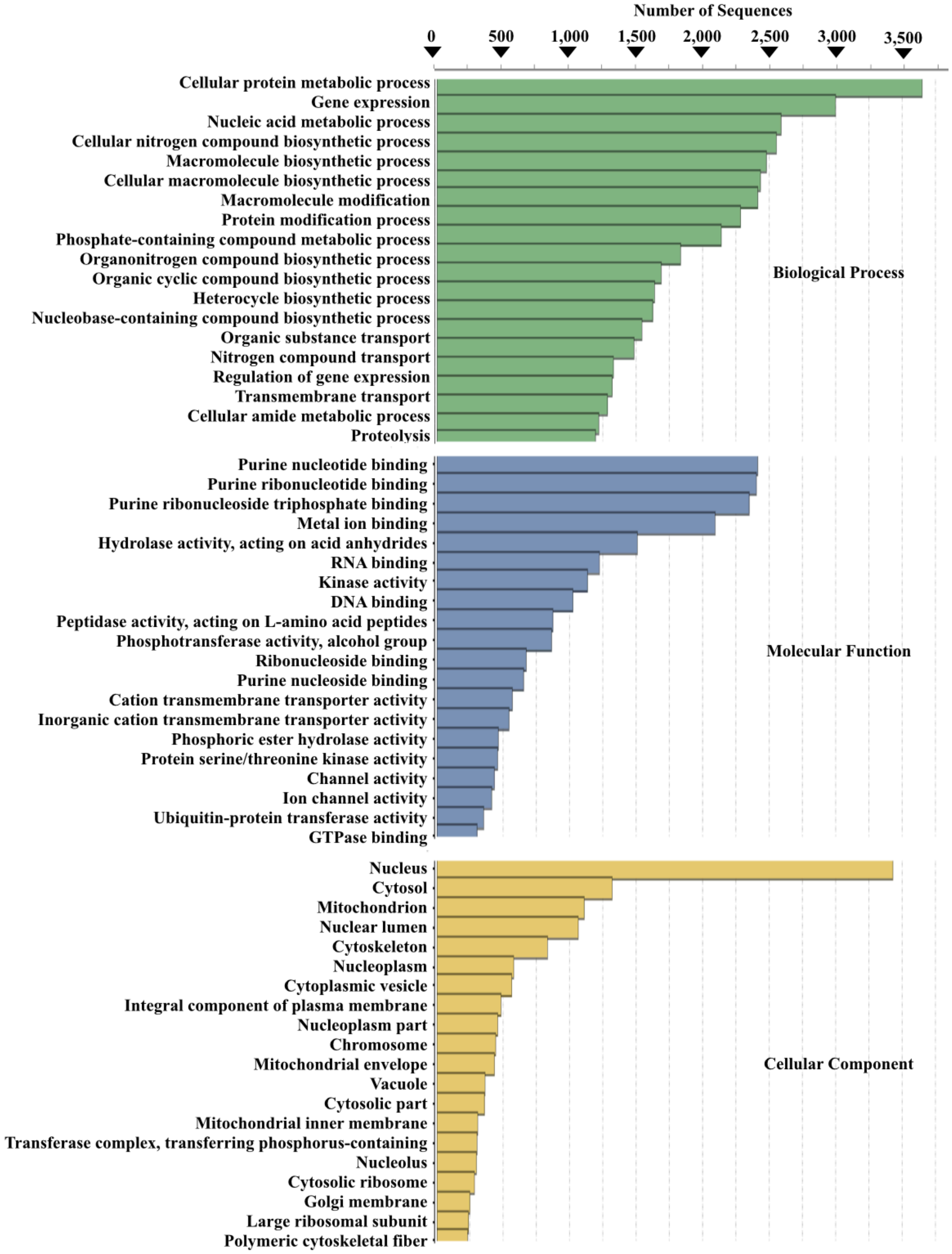


Figure 2-9. Top GO Categories of the Coral-Enriched Transcriptome
The top GO categories of biological processes, molecular functions, and cellular components of the coral-enriched transcriptome are depicted here.

2.3.4 *B. psygmophilum*-Enriched Transcriptome Annotation

Of the 39,889 transcripts parsed into the *B. psygmophilum*-enriched transcriptome, 35,260 (88.4%) retrieved BLAST hits from NCBI at an E-value threshold of 1E-05 or lower (Figure 2-10). Of the contigs that did produce BLAST hits, 83% were assigned GO annotations. The top GO categories (Biological Process, Molecular Function, and Cellular Compartment) assigned to the annotated symbiont-enriched contigs are found in Figure 2-11. The most common GO terms under Biological Processes were “cellular protein metabolic process” and “phosphate-containing compound metabolic process.” Under Molecular Function, the most common GO terms were “metal ion binding” and “purine nucleotide binding.” Under Cellular Compartment, the most common GO terms were “nucleus” and “plastid.”

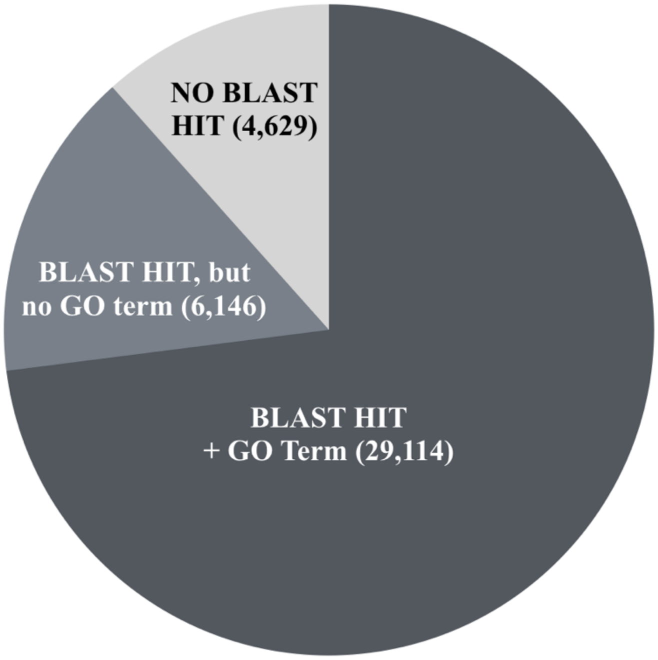


Figure 2-10. ***B. psygmophilum*-Enriched Contigs Producing BLAST Hits**

2.3.5 Taxonomic Affinity of Coral-Enriched and *B. psygmophilum*-Enriched Transcriptome Sequences

To confirm the taxonomic affinity of the sequences in the coral-enriched and *B. psygmophilum*-enriched transcriptomes, we examined the top species hits of the contigs retrieved in the Blast2GO annotation pipeline (Conesa et al., 2014; Gotz et al., 2005). Of the 42,777 coral-enriched contigs that produced BLAST hits, the large majority matched sequences from the phylum Cnidaria (39,628 contigs or 93% of contigs with BLAST hits). These contigs with cnidarian top species hits were further broken down to three orders: Scleractinia (26,893 contigs; *Acropora digitfera, Acropora millepora, Acropora palmata, Astrangia sp., Euphyllia ancora, Galaxea astreata, Galaxea fascicularis, Montastrea (Orbicella) franksi, Pocillopora damicornis,* and *Stylophora pistillata*); Actinaria (12,623 contigs; *Actinia equina, Exaiptasia pulchella, Anemonia viridis, Anthopleura elegantissima, Exaiptasia pallida,* and *Nematostella vectensis*); and Hydra (112 contigs; *Hydra vulgaris*). Six contigs with BLAST top hits to Symbiodiniaceae were not considered further as they may be contaminating species.

Of the 35,260 *B. psygmophilum*-enriched contigs that produced BLAST hits, the large majority matched sequences from the family Symbiodiniaceae (29,242 contigs or 83% of contigs with BLAST hits). There were also 157 contigs (0.45% of contigs with BLAST hits) with top species hits to cnidarians: 125 Scleractinia (species: *A. digitifera, M. (O.) faveolata, S. pistillata,* and *Suberites domuncula*); 27 Actinaria (species: *E. pallida* and *N. vectensis*); and 5 Hydra (species: *H. vulgaris*) contigs. As these 157 sequences were possibly from contaminating coral species and not Symbiodiniaceae, we did not consider them further.

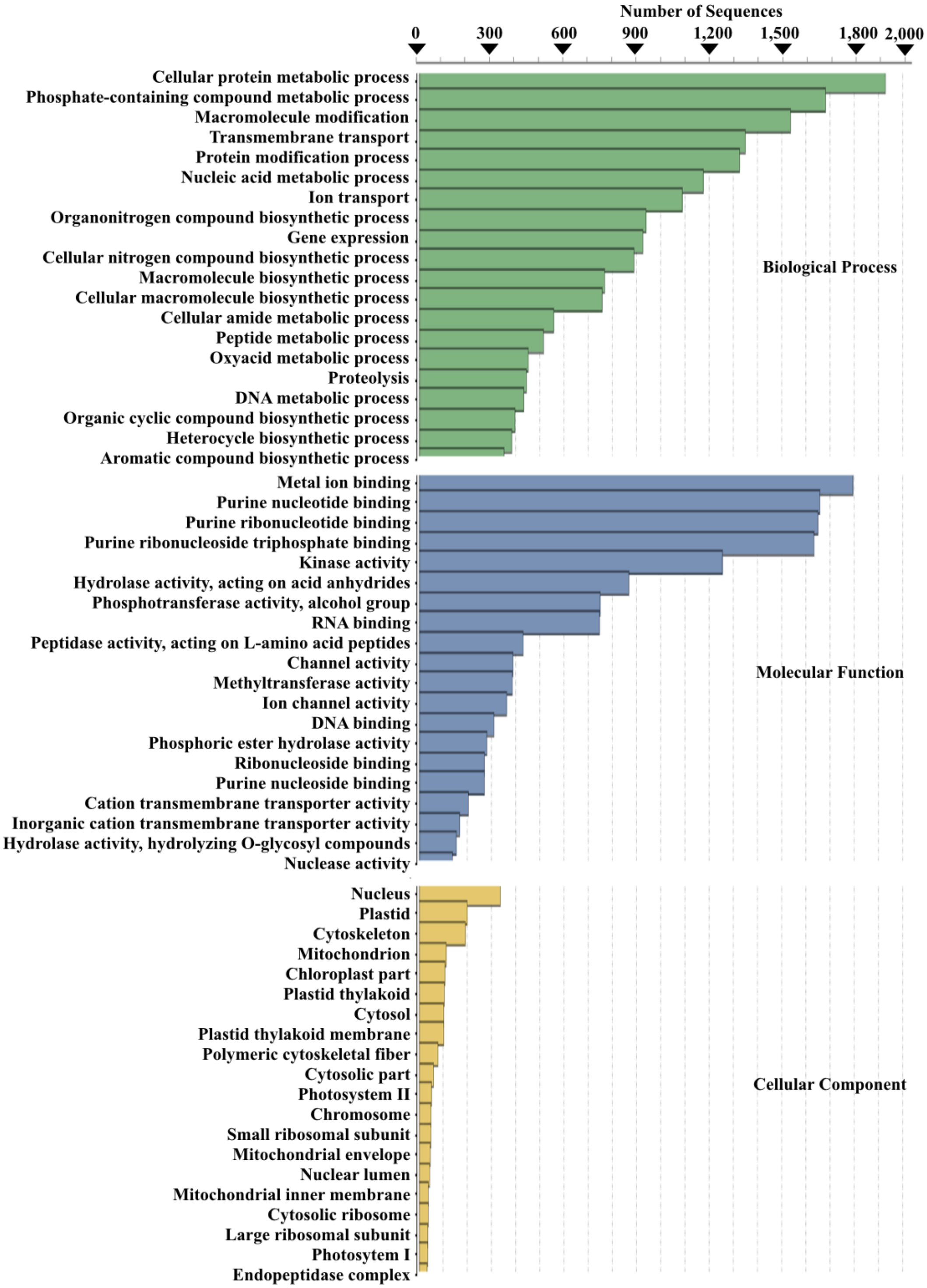


Figure 2-11. Top GO Categories of the *B. psygmophilum*-Enriched Transcriptome
The top GO categories of biological processes, molecular functions, and cellular components of the *B. psygmophilum*-enriched transcriptome are depicted here.

2.3.5.1 Recovery of COI Sequences From the Coral-Enriched Transcriptome

To further confirm the taxonomic affinity of the coral sequences in the Fort Wetherill and Woods Hole transcriptomes, we used BLAST to identify all candidate COI sequences with greatest resemblance to published coral COI sequences. We then generated a maximum likelihood tree of 42 coral COI amino acid sequences, including the putative *A. poculata* sequences we recovered from the Fort Wetherill and Woods Hole transcriptomes (Figure 2-7; modified from Burmester, 2017). The Fort Wetherill and Woods Hole COI sequences clustered together with a published *A. poculata* sequence (Podar et al., 2001) at a bootstrap proportion of 0.98. This *A. poculata* branch was nested within the robust coral clade, as expected.

2.4 Discussion

2.4.1 Evidence That the *A. poculata* Transcriptome is Representative

The present study describes a transcriptome assembly for *A. poculata* based on roughly 50.0 gb of RNA sequencing. This is one of the largest transcriptomic datasets currently available for any cnidarian (Traylor-Knowles et al., 2011, Stefanik et al., 2014, Mansour et al., 2016) and the first transcriptome of a facultatively symbiotic coral. To ensure that we captured transcripts expressed throughout *A. poculata's* complex symbioses with *B. psygmophilum*, we generated cDNA libraries from both symbiotic and aposymbiotic states. Evidence that the transcriptome assembly is representative of the expressed gene repertoire of a coral included the comparable recovery of metazoan orthologs to other cnidarian transcriptomes (Figure 2-6). Taken together, these data suggest that our sequencing effort was sufficient to produce a representative transcriptome that captures a large fraction of the transcript variety encoded by the *A. poculata* transcriptome.

Our BLAST analysis revealed that >70.2% of the *A. poculata* holobiont transcripts retrieved results from the NCBI nr database at an expected value of 1E-05 or lower compared to 40.1% of transcripts that retrieved results from the nr database with an expected value of 1E-03 or lower in the Burmester assembly (2017). The increase in the recovery of BLAST hits is likely due to differences in the assembly that generated a higher fraction of apparently full-length transcripts as well as updates in the NCBI database that resulted in better representation of coral sequences.

Judging by the BUSCO analysis, we obtained a greater fraction of complete versions of "universal," single-copy metazoan orthologs in our coral-enriched transcriptome than any other published cnidarian transcriptome, including that of Burmester, which had lower recovery of complete (86.9%), fragmented (10.7%), and missing orthologs (2.3%, 2017). The recovery of full-length alveolate orthologs in the *B. psygmophilum*-enriched transcriptomes was not nearly as high (95 out of 234; Figure 2-6). However, the collection of species sampled for the Alveolata database in BUSCO is biased towards parasitic species associated with human diseases, and does not include any members of the Symbiodiniaceae. Of note, we obtained a complete sequence for the 95 proteins for which we did recover an ortholog. This suggests that we had saturated coverage of all the genes in that dataset for which an ortholog could be found in the Symbiodiniaceae.

2.5 Conclusion

The *Astrangia* transcriptomes described here are both representative and replete with full-length transcripts. They therefore should prove useful in a range of future studies, including *in silico* cloning studies to elucidate the evolution of gene families (see Chapter 3) and as a reference for read mapping in differential gene expression studies (see Chapter 4).

2.6 Acknowledgements

This work could not have been completed without the contributions of the entire Finnerty Lab, Andie Chan of the Baum Lab and the Davies Lab. The *Astrangia* colonies used in this chapter were purchased from Woods Hole (2012) and collected from Fort Wetherill (2012, collected by Andie Chan; 2015, collected by Liz Burmester, Katey Lesneski and Karina Scavo Lord). Liz Burmester extracted RNA from the 2012 coral samples, prepared them into cDNA libraries, sent them off for sequencing, and assembled her *Astrangia* transcriptome with CLC Genomics Workbench (Burmester, 2017). The Fort Wetherill samples collected in 2015 had their RNA extracted by Liz Burmester and interns from the New England Aquarium. I performed the quality control steps, prepared the RNA into cDNA libraries, and sent them to be sequenced at the Harvard Bauer Core. Then, I performed trimming of the reads and assembled multiple initial versions of the *Astrangia* transcriptome using a multi-kmer approach. The final version of the transcriptome used here was assembled by John Finnerty using a multi-kmer script I modified from Zerbino et al. for the previous assemblages (2008). Joanna Lee then parsed the transcriptome using a published pipeline (Davies et al., 2016) into symbiont-enriched and coral-enriched and “other” transcriptomes. Joanna Lee and I performed the transcriptome annotation using BLAST2GO. Joanna Lee modified the coral phylogeny based on COI sequences that Liz Burmester initially generated (2017) to include COI sequences from both Fort Wetherill and Woods Hole *A. poculata*. A heartfelt thank you to all those who’ve contributed their scientific expertise and knowledge — I’m deeply grateful for your help in the making of this *Astrangia* transcriptome into a reality.

CHAPTER 3: COMPUTATIONAL IDENTIFICATION AND EVOLUTIONARY ANALYSIS OF THE NF-κB SIGNALING PATHWAY AND THE SUPEROXIDE DISMUTASE FAMILY

3.1 Introduction

A principal aim of this dissertation research was to understand how photosymbiosis impacts gene expression in cnidarians. While our approach was to compare global gene expression patterns using RNA sequencing (Wang et al., 2009), we paid particular attention to the expression of genes known to be altered during photosymbiosis in other model systems. Examination of these candidate genes could help to determine if exogenous ROS and photosymbiosis affect gene expression similarly in other taxa, especially other cnidarians. We focused on the superoxide dismutase (SOD) gene family, antioxidant enzymes that are central to the oxidative stress response in a wide range of taxa (Das et al., 1995, Alscher et al., 2002, Djavaheri-Mergny et al., 2004, Higuchi et al., 2009), and the NF-κB signaling pathway, which is implicated in the response to oxidative stress (Benov & Fridovich 1995, Richier et al., 2003, Rojo et al., 2004, Xu et al., 2007) and the regulation of metazoan-algal photosymbioses (Mansfield et al., 2017).

To determine whether similar alterations in candidate gene expression occur in two or more organisms, it is critically important to distinguish orthologs from paralogs; this requires a detailed phylogenetic analysis of protein sequence and structure. In this chapter, I describe our reconstruction of the molecular evolution of the core components of the NF-κB signaling pathway and the SOD gene family in cnidarians, incorporating transcripts recovered from our *A. poculata* transcriptome. We were able to recover full-length transcripts for all of the core components of the NF-κB signaling pathway as well as six SOD family members. Within each of these predicted proteins, we identified numerous conserved motifs and residues of known functional significance that support the functional conservation of these genes. By extending these comparisons to other metazoan phyla and closely related outgroups, we were able to infer where critical pathway functions first appeared in evolution and discriminate primitive from derived traits in our model systems.

To place my studies in context, I first provide detailed background on the NF-κB signaling pathway and SOD gene family. I then describe how we recovered pathway members and evaluated their primary structure and evolution in metazoans and representatives of closely related outgroups (Fliasteria; Choanoflagellata).

3.2 The NF-κB Family of Transcription Factors

NF-κB is a transcription factor that was first identified as a regulator of immunoglobulin genes in mouse and human B lymphocytes (Singh et al., 1986). Since its discovery, the NF-κB signaling pathway has been shown to participate in a wide range of cellular processes and in response to a correspondingly wide range of upstream inducers. For example, gene targets of NF-κB are involved in innate immunity (Karin & Delhase 2000, Sun, 2017), development (Wolenski et al., 2013), cell survival (Piva et al., 2006), and the oxidative stress response (Ikeda et al., 2002, Fang, 2004, Gilmore, 2006).

Upstream activators of the NF-κB pathway in insects and vertebrates include pathogens (DiDonato et al., 1997), chemicals (Schreck et al., 1992, Chen & Shi 2002), ultraviolet (UV) light (Legrand-Poels et al., 1998), oxidative stress (Schreck et al., 1992, Schreck et al., 1992, Ikeda et al., 2002, Michiels et al., 2002, Takada et al., 2003, Gloire et al., 2006, Oliveira-Marques et al., 2009, Morgan & Liu 2011), and thermal stress (Riesgo et al., 2014).

NF-κB proteins have been found in phylogenetically diverse animal lineages including vertebrates, echinoderms, arthropods, annelids, molluscs, cnidarians, and sponges, and NF-κB–related proteins have been recovered in closely related animal outgroups including filastereans and choanoflagellates; however, NF-κB proteins are notably absent in nematodes and ctenophores (Finnerty & Gilmore, 2015). The number of NF-κB proteins varies across taxa. In filastereans, choanoflagellates, and diploblastic animals, only single NF-κB proteins have been recovered, whereas all triploblastic animals have multiple distinct NF-κB genes (reviewed in Finnerty and Gilmore, 2015). For example, *Drosophila* has three NF-κB proteins (Relish, Dorsal, and Dif) and mammals have five: NF-κB1, NF-κB2, RelA, RelB, and c-Rel (Gilmore, 2006).

All NF-κB proteins contain an N-terminal Rel homology domain (RHD) involved in DNA binding, dimerization, and nuclear localization (Gilmore, 2006, Sullivan et al., 2007). Members of one class of NF-κB proteins (e.g., human NF-κB1 and NF-κB2, *Drosophila* Relish) contain an inhibitory C-terminal ankyrin-repeat (ANK) domain, which masks the nuclear localization sequence (NLS) to prevent nuclear localization (reviewed in Wan and Lenardo, 2009). Induced proteolysis of the C-terminal ANK domain yields an active NF-κB protein that is capable of nuclear translocation and DNA binding. The full-length form of NF-κB1 is also known as p105, while the cleaved form lacking an ANK region is known as p50. Full-length and cleaved NF-κB2 are known as p100 and p52, respectively. Other NF-κB family members (e.g., human RelA, RelB, and c-Rel), contain a C-terminal activation domain but lack the C-terminal ANK domain. This difference in the C-terminus defines the two distinct subclasses of the NF-κB proteins, sometimes called class I and class II or the NF-κB and Rel subclasses, respectively (Gilmore, 2006). Members of each class are closely related to one another in terms of their amino acid sequences within the RHD (Sullivan et al., 2007).

Members of both the NF-κB and Rel subclasses bind to cis-regulatory sequences near target genes as homodimers or heterodimers (Gilmore, 2006). NF-κB dimers bind a consensus target site known as a κB-site, generally within the consensus sequence 5′-GGGRNYYYCC-3′ (reviewed in Wan and Lenardo, 2009). Different homo- and heterodimers exhibit various binding specificities, which can be modulated by associating with non–NF-κB proteins. One such protein is ribosomal protein S3, which interacts with the NF-κB p65/p50 complex (reviewed in Wan and Lenardo, 2009) to enhance NF-κB binding and promote transcription of its target genes. Ribosomal protein S3 activation occurs when inhibitor of nuclear factor kappa B kinase β (IKKβ) phosphorylates it at serine (Ser)209 to induce its nuclear translocation (Wan et al., 2011).

3.3 NF-κB Signaling Pathways

Based primarily on studies in mammals, two principal NF-κB signaling pathways have been described: the canonical pathway and non-canonical pathway (Figure 3-1). “Alternative” pathways have also been described. These pathways differ with respect to their upstream inducers, kinase cascades, inhibitor of kappa B (IκB) proteins, NF-κB proteins, and target genes. Activation of the canonical, non-canonical, or alternative NF-κB pathway results in translocation of an NF-κB dimer from the cytoplasm to the nucleus. Translocation of NF-κB dimers requires degradation of an inhibitory IκB protein, which masks the NF-κB NLS, thereby sequestering the NF-κB dimer in the cytoplasm (described in more detail in 3.3.1). Thus, NF-κB is a latent cytoplasmic protein complex that is induced and activated at the post-translational level to translocate into the nucleus and modify target gene transcription.

3.3.1 The Canonical NF-κB Pathway

The canonical NF-κB signaling pathway is activated when upstream receptors bind lipopolysaccharides (LPS), interleukin-1 (IL-1), proinflammatory cytokines, and tumor necrosis factor alpha (TNF-α), among others. The signal is transduced through various proteins including transforming growth factor beta-activated kinase 1 (TAK1/MAP3K7), which phosphorylates IKKβ. In many cells, IKKβ exists as a dimer with IKKα, and the IKK complex is held together by a scaffold protein called IKKγ or NEMO (nuclear factor κB essential modulator; Jin and Jeang, 1999). Once the IKK complex is activated, IKKβ phosphorylates two serine residues near the N-terminus of IκB, targeting it for ubiquitination and degradation. IκB typically sequesters NF-κB (p105-RelA) in the cytoplasm; phosphorylation and subsequent degradation of IκB reveals the NF-κB NLS, permitting NF-κB (p50-RelA) to translocate into the nucleus and regulate target genes by binding κB DNA-binding sites (Gilmore, 2006).

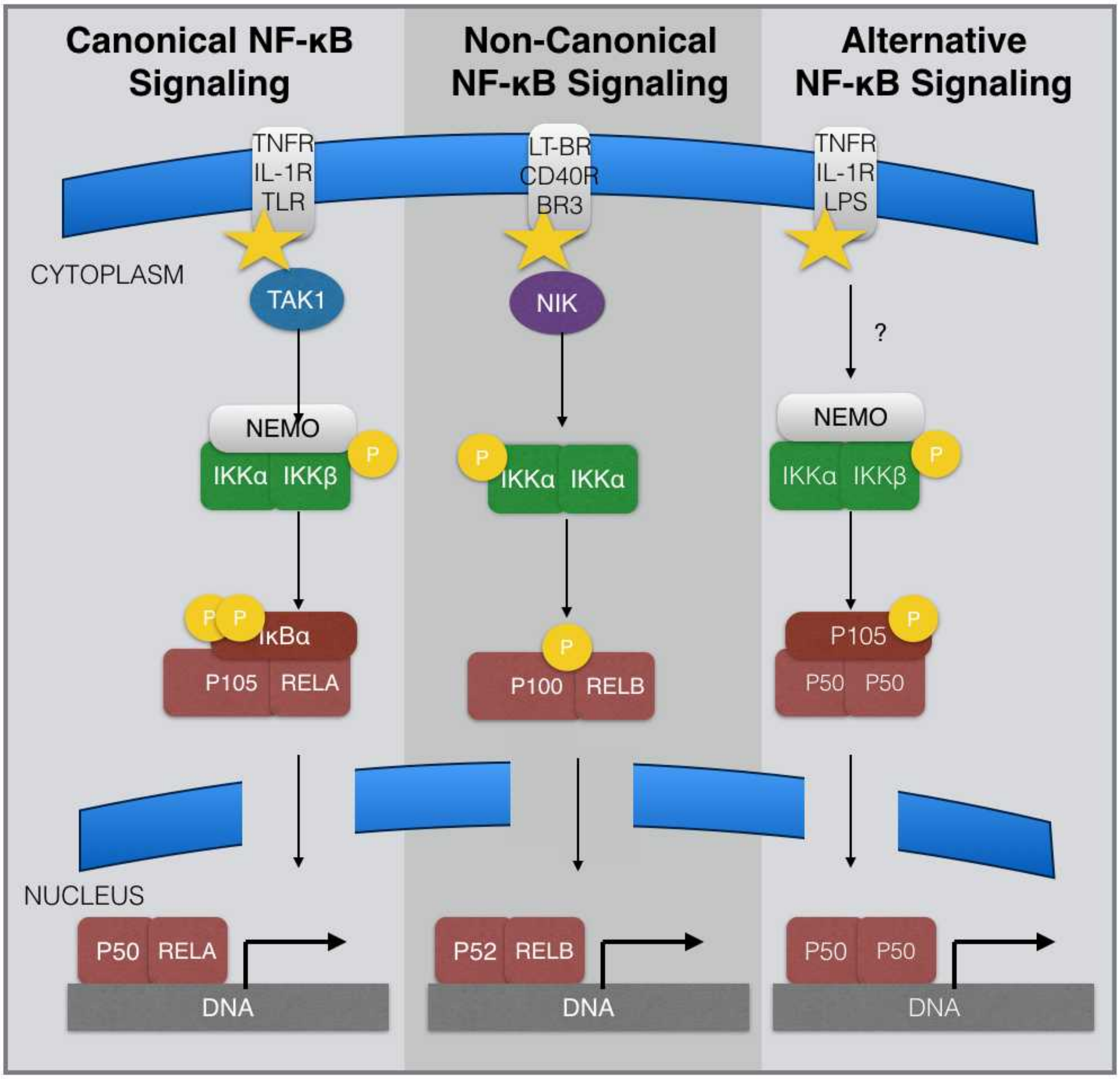


Figure 3-1. NF-κB Signaling Pathways in Mammals
Three alternative NF-κB signaling pathways have been described, based largely on data from mammals. They differ with respect to the upstream inducers, kinases, IκB proteins, and NF-κB proteins involved. Modified from Oeckinghaus (2011) and Beinke and Ley (2004). Abbreviations are as follows: tumor necrosis factor receptor (TNFR), interleukin – 1 receptor (IL-1R), Toll-like receptor (TLR), nuclear factor – kappa B essential modulator (NEMO), inhibitor of kappa B kinase (IKK), nuclear factor kappa B inducing kinase (NIK), inhibitor of kappa B (IκB), lymphotoxin – beta receptor (LT-BR), cluster of differentiation 40 receptor (CD40R), beta receptor 3 (BR3), and lipopolysaccharide (LPS).

3.3.2 The Non-Canonical NF-κB Pathway

In the non-canonical pathway, a p100-RelB heterodimer is sequestered in the cytoplasm via the C-terminal IκB-like ANK domain of p100. Specific activators of the non-canonical NF-κB pathway include lymphotoxin-beta (LT-β), cluster of differentiation 40 (CD40), and B-cell activating factor (BAFF or BR3). When receptors for these factors bind their ligands, signals are transduced to NF-κB–inducing kinase (NIK). NIK, also called MAP3K14, is a serine-threonine protein kinase that phosphorylates and activates IKKα homodimers. Activated IKKα in turn phosphorylates p100 at two serine residues (S866 and S870) in the ANK-region leading to ubiquitination and degradation of the C-terminal inhibitory ANK domain by the 26S proteasome (Fong & Sun, 2002). Removal of the ANK domain from p100 yields the active p52 protein. The p52-RelB complex is able to translocate into the nucleus, where it binds DNA-binding sites (called κB sites) and regulates the transcription of target genes (Gilmore 2006).

3.3.3 An Alternative NF-κB Pathway

While both the canonical and non-canonical pathways involve an NF-κB heterodimer (a member of the NF-κB subfamily, p100/p52 or p105/p50, complexed with a member of the Rel subfamily, e.g., RelA or RelB), alternative pathways exist that involve NF-κB homodimers (Gilmore, 2006, Sun & Ley, 2018). In one pathway, a p50 homodimer enters the nucleus, and, in concert with Bcl-3 or I*κ*Bζ, regulates the transcription of target genes (Gilmore, 2006). Prior to induction of this pathway, p50 is retained in the cytoplasm in a complex with p105. In complexes of p150 with a p50 homodimer as shown in Figure 3-1, or possibly a single p50 protein (Beinke & Ley, 2004), the ANK region of p105 blocks the NLS of p50, preventing its translocation into the nucleus. Proteolytic degradation of p105 is triggered by the phosphorylation of two serine residues at the C-terminus of the protein by IKKα and IKKβ, which may or may not be held together in complex by scaffold protein NEMO (Beinke and Ley, 2004). IKKα and IKKβ, in turn, may be activated through phosphorylation by TAK1, though this has not yet been demonstrated conclusively (Sun & Ley, 2018).

3.3.4 Evolution of NF-κB Signaling in Basal Animal Model Lineages

The sea anemone *Nematostella vectensis* was the first diploblastic animal in which NF-κB and its signaling pathway components were identified, initiating research into the early evolution of NF-κB signaling (Sullivan et al., 2007). Sullivan and co-workers mined the newly sequenced *N. vectensis* genome and identified NF-κB and several putative NF-κB signaling components, including homologs of IκB, IKK, Toll-like receptor (TLR), and tumor necrosis factor receptor (TNFR; Sullivan et al., 2007). Below, I summarize what was known about each of these core NF-κB signaling components in *N. vectensis*, other cnidarians, sponges, and non-metazoans, and then describe the bioinformatic and phylogenetic analyses that we conducted to address gaps in our knowledge of the early evolution of NF-κB signaling in *A. poculata*.

3.3.4.1 Evolution of NF-κB and IκB

N. vectensis has a single NF-κB locus. The predicted 440 amino acid *N. vectensis*

NF-κB (Nv-NF-κB) protein includes an N-terminal RHD with a clearly recognizable DNA-binding loop, dimerization domain, and NLS (Sullivan et al., 2007). Based on overall sequence similarity and a phylogenetic analysis of the RHD sequence, Nv-NF-κB is more similar to members of the NF-κB subfamily than to members of the Rel subfamily (Sullivan et al., 2007). However, unlike the vertebrate members of the subfamily, the Nv-NF-κB protein lacks a C-terminal ANK domain (Sullivan et al., 2007)

Functional studies of Nv-NF-κB suggest that it behaves similarly to other NF-κB proteins; that is, the Nv-NF-κB protein binds to κB DNA-binding sites and upregulates transcription of target genes (Wolenski et al., 2011). Furthermore, because Nv-NF-κB lacks the C-terminal ANK domain that masks the NLS and causes it to be sequestered in the cytoplasm, Nv-NF-κB localizes to the nucleus when expressed in vertebrate cell culture (Wolenski et al., 2011).

Although there is no C-terminal inhibitory ANK domain in Nv-NF-κB, *N. vectensis* does express an ANK-repeat protein that has a high degree of sequence similarity to the ANK domains of NF-κB1 and NF-κB2 proteins. This predicted ANK domain protein (Nv-IκB) is encoded at a separate locus in the *N. vectensis* genome (Sullivan et al., 2007). When co-expressed in chicken fibroblast cells, Nv-IκB interacts directly with Nv-NF-κB and sequesters it in the cytoplasm (Wolenski et al., 2011).

The presence of a C-terminal ANK domain varies among the NF-κB proteins in triploblastic animals (Huguet et al., 1997). For this reason, cnidarians could provide clues about NF-κB proteins in the diploblast-triploblast ancestor. The presence of a single NF-κB protein lacking an ANK repeat domain in *N. vectensis* raised the possibility that the addition of an ANK domain occurred with the evolution of triploblastic animals (Sullivan et al., 2007). However, subsequent studies of a closely related anemone, *E. lineata*, identified a single NF-κB protein that contains both an RHD and an ANK-repeat region (Stefanik et al., 2014). Single NF-κB proteins possessing ANK repeats were also found in the sea anemone *E. pallida*, the corals *Acropora millepora* and *Platygyra carnosus*, and a representative corallimorph (Finnerty & Gilmore. 2015). Moreover, the sponge *Amphimedon queenslandica* encodes an NF-κB protein that includes an N-terminal RHD and a C-terminal ANK-repeat region (Gauthier & Degnan, 2008). Together, these observations suggest that the ancestral NF-κB protein in anthozoan cnidarians contained an ANK-repeat region (Finnerty & Gilmore, 2015). Interestingly, the single NF-κB protein of *Hydra* lacks an ANK-repeat region; thus, in cnidarians, the ANK-repeat region appears to have been lost independently in multiple lineages.

3.3.4.2 Evolution of IκB Kinases

A key regulatory node in the activation of the NF-κB pathway is the upstream IκB kinase (IKK). Mammals have four IKK-like proteins, which can be subdivided into two classes: one class comprises IKKα and IKKβ, while a second class comprises IKKε and TANK-1 binding kinase (TBK; Hacker & Karin, 2006). In mammals, canonical NF-κB signaling is controlled primarily by IKKβ, which phosphorylates N-terminal serine residues in independent IκBs (e.g., IκBα, IκBβ), whereas non-canonical signaling is regulated by an IKKα homodimer (Huguet et al., 1997, Sun, 2011, Sun, 2017), which phosphorylates C-terminal residues in NF-κB p100. Generally, IKKε and TBK are not thought to directly regulate either canonical or non-canonical NF-κB signaling (Fitzgerald et al., 2003, Hacker & Karin, 2006, Chau et al., 2008). IKKε has been shown to indirectly interact with p52 via RelA (p65; Wietek et al., 2008), crossing both canonical and non-canonical NF-κB signaling pathways. In fact, NF-κB and interferon regulatory factor (IRF) signal transduction may exhibit crosstalk through IKKε and TBK as these two kinases are indirectly involved in NF-κB signaling (Tojima et al., 2000) and directly involved in IRF signaling (Fitzgerald et al., 2003, Chau et al., 2008).

A number of studies suggest a possible role for IKKε and TBK in NF-κB signaling. For example, TBK can phosphorylate IKKβ, which in turn phosphorylates IκB, leading to NF-κB activation (Tojima et al., 2000). Both IKKε and TBK have also been shown to phosphorylate IκB directly, in vertebrate cell lines (Pomerantz & Baltimore, 1999, Shimada et al., 1999) and insect cell lines (Tojima et al., 2000). Specifically, TBK1 phosphorylates IκB at one of two serines, leading to proteolysis of IκB (Tojima et al., 2000). Similarly, Wolenski et al. demonstrated that Nv-IKKε can phosphorylate one of two serine residues of the independent IκB protein in the sea anemone *N. vectensis* (S47; 2011). Furthermore, p65/RelA could be phosphorylated at S536 by IKKε and TBK (McWhirter and Maniatis, unpublished but reported in Fitzgerald et al., 2003). Another paper showed that IKKε mediates the phosphorylation of p65/RelA in cells induced by TNF-α (Wietek et al., 2006). Since RelA activation is dependent on IKKβ catalytic activity, it is possible that NF-κB activity can be increased through TBK phosphorylation of IKKβ (Fujita et al., 2003, Hacker & Karin, 2006).

IKKε and TBK appear to be more directly involved in another innate immune pathway, the IRF3/IRF7 pathway, which is induced by TLR in response to viral infections (Fitzgerald et al., 2003). Both IKKε and TBK have been shown to phosphorylate functionally important serines on IRF3 (McWhirter et al., 2004). IKKε and TBK can bind to scaffold proteins NF-κB activator (TANK), NF-κB-activating kinase associated protein (NAP1), or TBK1 adaptor (SINTBAD) to phosphorylate IRF3, which then translocates into the nucleus to regulate target genes (Chau et al., 2008). NF-κB signaling protein NEMO (IKK-γ,) was found to be required for the activation of IRF3 and IRF7 in response to viral infections (Zhao et al., 2007). Further evidence of crosstalk in NF-κB and IRF signal transduction comes from IRF3-p65 associations required for response to LPS stimulation (Zhao et al., 2007, Chau et al., 2008).

Among non-bilaterian animals, two IKK proteins have been recovered from the cnidarians *N. vectensis* and *Exaiptasia pallida*, while single IKK proteins have been recovered from sponges and ctenophores (Sullivan et al., 2007, Wolenski et al., 2011, Mansfield et al., 2017). As my research helped to reveal, one of the cnidarian proteins is most closely related to vertebrate IKKα and IKKβ, and the other is most closely related to vertebrate IKKε/TBK. These findings have been published in a multi-author study (Mansfield et al., 2017), but as they derived from my dissertation research, they are described below.

3.3.4.3 Evolution of Superoxide Dismutases (SODs)

SODs represent one of the primary cellular defenses against oxidative stress in a taxonomically wide range of organisms (Zelko et al., 2002). SODs catalyze the conversion of superoxide (O_2^-) into diffusible H_2O_2 in the reaction $2O_2^- \rightarrow O_2 + H_2O_2$ (McCord & Fridovich, 1969). Catalase then breaks down H_2O_2 into H_2O and O_2. Without the activity of SODs and other antioxidants, ROS would accumulate in cells and cause lipid oxidation, protein denaturation, and DNA damage (Zelko et al., 2002).

SODs are metalloproteins that differ in the metals they bond, which may be copper (Cu), zinc (Zn), iron (Fe), or manganese (Mn) (Case, 2017). Some SODs can bind either Fe or Mn, and, at the amino acid level, the sequence identity between FeSODs and MnSODs approaches 50%. All FeSODs and MnSODs exhibit the same basic structure comprising seven α helices and two β pleated sheets (Fink & Scandalios, 2002). These similarities imply a common ancestor of the FeSOD and MnSOD families (Case, 2017).

The CuZnSOD family shares little sequence similarity with the FeMnSOD family; 25% of amino acids are shared between human CuZnSOD (SOD1) and MnSOD (SOD2), with much of the resemblance restricted to a particular region of the respective proteins: positions 36-63 of SOD1 and 142-169 of SOD2. CuZnSODs have eight β pleated sheets that form a "Greek key" pattern comprising eight loops: two loops to bind to copper and zinc, another loop to bind O_2^-, and five additional loops (Bordo et al., 1994). The significant structural differences between the CuZnSOD and FeMnSOD families suggest that the families may have undergone convergent evolution (Fink & Scandalios, 2002).

Based upon their broader phylogenetic distribution, the FeMnSODs appear to be more ancient than the CuZnSODs, and more specifically, the FeSODs appear to be the most ancient. FeSODs have been identified in aerobic and anaerobic bacteria (Yost &

Fridovich, 1973, Hatchikian & Henry, 1977), Archaea (Kirby et al., 1981), protists (Dufernez et al., 2006), and plants (Alscher et al., 2002). MnSODs have been identified in Archaea and Eukarya. CuZnSODs have been identified in plants and animals, but not in Archaea or protists (Fink & Scandalios, 2002, Banci et al., 2005, Wilkinson et al., 2006).

Many eukaryotic organisms have multiple SODs from both the CuZnSOD and FeMnSOD families. For example, *Arabidopsis thaliana* possesses seven SOD isoforms: three CuZnSODs, three FeSODs, and one MnSOD (Alscher et al., 2002). Vertebrates commonly have three SOD isoforms: two CuZnSODs and one FeMnSOD (Halliwell & Gutteridge, 1999). In humans, the three SODs are designated SOD1, SOD2, and SOD3, and they differ in their quaternary structure and subcellular localization. SOD1 is a CuZnSOD that functions as a dimer and is found in the cytoplasm. SOD2 is a FeMnSOD that functions as a tetramer and is found in the mitochondria. SOD3 is a CuZnSOD tetrameric protein found in the extracellular space. A related protein, copper chaperone for superoxide dismutase (CCS), is involved in transferring Cu to SOD1.

Five putative SOD proteins have been identified in *N. vectensis* (Tarrant et al., 2014). Nv-SOD1 had no reported cnidarian ortholog prior to the work described by Tarrant et al. (2014), while a second SOD gene in *N. vectensis* appears to be most similar to *A. viridis* SODb (Plantivaux et al., 2004). Nv-SOD3 is most similar to human SOD3 (Tarrant et al., 2014). Nv-MnSOD1 appears orthologous to a putative SOD from *Acropora digitifera* (Tarrant et al., 2014) and Nv-MnSOD2 appears orthologous to MnSOD2 from *Strongylocentrotus purpuratus* and *Capitella teleta*. No functional studies have characterized the activity of SOD proteins in *N. vectensis*.

SOD genes are known to be downstream targets for NF-κB transcription factor activity in some vertebrate cell lines (Morgan & Liu, 2011), including MnSOD in lung carcinoma cells (Das et al., 1995, Jones et al., 1997, Djavaheri-Mergny et al., 2004, Kairisalo et al., 2007) and CuZnSOD in PC12 pheochromocytoma cell lines (Rojo et al., 2004). In these examples, the SODs that are upregulated by NF-κB are thought to confer protection from excessive levels of oxidative stress. It has also been shown that organisms lacking either MnSOD or CuZnSOD exhibit reduced resistance to oxidative stress. MnSOD-/- mice exhibit neonatal mortality upon exposure to atmospheric levels of oxygen that triggers unchecked oxidative stress (Li et al., 1995). CuZnSOD-/- mice have shorter life spans than their wildtype littermates and some develop carcinomas due to oxidative stress (Elchuri et al., 2005).

3.4 Methods

We reconstructed the evolution of the NF-κB signaling pathway and SOD gene family in Cnidaria through phylogenetic and bioinformatics analyses of existing genomic and transcriptomic resources, as well as new transcriptomes we developed for *N. vectensis* and *A. poculata*, the latter of which is described in Chapter 4. We utilized the following published transcriptomes and/or genomes for cnidarians: *Hydra vulgaris* (Siebert et al., 2011), *Exaiptasia* (Baumgarten et al., 2015), *Corallium rubrum* (Pratlong et al., 2015), *A. digitifera* (Shinzato et al., 2011), *Pocillopora damicornis* (Traylor-Knowles et al., 2011), *E. lineata* (Stefanik et al., 2014), and *N. vectensis* (Putnam et al., 2007).

3.4.1 Recovery of NF-κB Signaling Proteins from Metazoans and Outgroups

Genes that encode core elements of NF-κB signaling pathways (NF-κB, IκB, IKKα, IKKβ, IKKε, TBK, TAK1, and NIK) and SODs proteins were identified using tBLASTn with human NF-κB signaling proteins as query sequences. Representatives of major metazoan lineages and closely related outgroups (Deuterostomia, Ecdysozoa, Cnidaria, Ctenophora, Porifera, Choanoflagellata, Placozoa, and Filasterea) were queried. Reciprocal BLAST searches were performed to verify that the top hits included the original query sequences. Amino acid sequences designated with the suffix "-like" were identified as the top hit in the initial BLAST search, but did not return the original query sequence in a reciprocal blast (e.g., NIK-like from *Trichoplax adhaerens* was the top BLAST hit among *Trichoplax* sequences to human NIK, but it did not return human NIK as the top hit in a reciprocal BLAST). For each gene family, the entire amino acid sequence available for each protein was included in a text file in FASTA format (Lipman & Pearson, 1985). These sequence files are available in Appendices A.1-A.5.

3.4.2 Identification of Conserved Motifs

We used MEME (versions 4.10.2, 4.11.2, 4.11.3, and 4.11.4; Bailey et al., 2009) to identify evolutionarily conserved "motifs" in SOD proteins and core proteins of the NF-κB signaling pathway. MEME discovers "recurring, fixed-length patterns" of conserved amino acids using an approach known expectation maximization (Bailey et al., 2009). Separate “training sets” were assembled for (1) NF-κB + IκB , (2) IKK, (3) NIK, (4) TAK1, and (5) SODs. Where possible, each training set contained at least one representative from all of the major metazoan lineages and outgroups listed above. As MEME does not account for phylogenetic divergence between sequences, the training sets were trimmed to remove closely related amino acid sequences; these sequences could confound the identification of deeply conserved domains that have undergone strong stabilizing selection over the course of animal evolution (Finnerty & Gilmore, 2015). The parameters of our MEME analysis were as follows: number of motifs: 20; site distribution: any number of repetitions per sequence (e.g., to allow identification of multiple ANK repeats in IκB proteins); minimum width of motifs: 6 amino acids; and maximum width of motifs: 50 amino acids. After using MEME to identify conserved motifs among the sequences in our training sets, we searched larger sets of protein sequences—which could include closely related protein sequences—for the same conserved motifs using the MAST program (Bailey et al., 2009). The training set for NF-κB + IκB proteins was adapted from Finnerty and Gilmore (2015). Due to their large size, the MEME outputs for NF-κB, IKK, TAK1, NIK, and SODs are located in Appendices A.10-A.14. A user-friendly guide to using the MEME outputs can be found prior to Appendix A.10.

3.4.3 Identification of Functionally Important Residues and Domains

The identification of conserved motifs is based solely on statistically significant patterns of sequence conservation, without reference to protein function. After identifying motifs, we manually searched within or between the motifs for specific residues and domains with known functional significance. For example, we searched NF-κB–like proteins for glycine-rich regions (GRR) and sites of IKK phosphorylation. GRRs were found by visually inspecting sequences just downstream of the C-terminus of the RHD. Putative IKK phosphorylation sites were found by sequence alignment to known IKKα phosphorylation sites using Clustal Omega (Sievers et al., 2011).

3.4.4 Phylogenetic Analysis of NF-κB Signaling Proteins

Phylogenetic analyses were performed to reconstruct the molecular evolution of the IKK, NIK, TAK1, NF-κB, FeMnSOD, and CuZnSOD protein families. In each case, Clustal Omega (Sievers et al., 2011) was used to generate an amino acid sequence alignment (Appendices A.6-A.9). Maximum likelihood trees were then created using PAUP* (Swofford, 2002) with all characters and gaps having equal weight. The support for individual nodes was assessed using 1000 replications of the bootstrap resampling procedure (Felsenstein, 1985). Some sequences suspected of creating long-branch attraction artifacts were removed to examine the effect on tree topology (Philippe et al., 2005).

For each phylogenetic analysis, we aligned amino acids from highly conserved regions of the respective proteins. For the three kinase families (IKK, TAK1, and NIK), we utilized portions of the protein that encompass the most conserved part of the serine-threonine kinase catalytic domain. For IKK, this was the region between motifs 1 and 7 (Mansfield et al., 2017). For TAK1, we aligned the region between motifs 5 and 9. For

NIK, we aligned the region between motifs 1 and 5. For the CuZnSODs, including the CCS subfamily, we aligned the region encompassed by motifs 1-10. For the FeMnSODs, we aligned the region between motifs 11 and 15.

3.5 Results

3.5.1 Evolutionary Conservation of NF-κB and IκB Proteins

Based on an analysis by Finnerty and Gilmore (2015) of 21 NF-κB proteins and 3 independent IκB sequences recovered from 2 representative deuterostomes (*Homo* and *Ciona*), 2 protostomes (*Drosophila* and *Biomphalaria*), 3 anemones (*N. vectensis*, *Edwardsiella*, and *Exaiptasia*), 2 corals (*Acropora* and *Platygyra*), a corallimorph (*Discosoma*), a sponge (*Amphimedon*), and a filasterean (*Capsaspora*), MEME identified 14 conserved motifs (Figure 3-2). We used MAST to search for these same motifs in *A. poculata* NF-κB proteins from the reference transcriptome we generated (Chapter 2). Of note, Finnerty and Gilmore (2015) also included an analysis of the NF-AT family of proteins, another family of RHD-proteins that share a common evolutionary history with NF-κB proteins. The NF-AT proteins were not included in the current analysis.

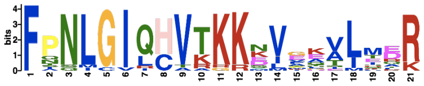
#	E-value	Conserved Domain; Sites	LOGO Representation of Consensus Sequence
1	6.1e-060	No known domain. Unique to anthozoan cnidarians.	
2	1.6e-361	**RHD**; <u>DNA binding</u>: 14,16-17, 19-20, 23-25;	
3	1.5e-236	**RHD**;	
4	5.5e-128	**RHD**;	
5	3.7e-150	**RHD**; <u>DNA binding</u>: 8,10-11;	
6	7.3e-173	**RHD**;	
7	1.7e-121	**RHD**; <u>DNA binding</u>: 17;	
8	1.2e-462	**IPT**; <u>DNA binding</u>: 25,27; <u>ankyrin binding</u>: 2,4-6,8-10;	
9	1.2e-333	**IPT**; <u>DNA binding</u>: 14-15; <u>ankyrin binding</u>: 6-8, 21;	
10	6.0e-079	**IPT**; <u>ankyrin binding</u>: 3;	
11	3.6e-189	**IPT**; <u>ankyrin binding</u>: 6,9,11;	
12	2.7e-116	No known domain	
13	1.1e-280	**ANK**;	
14	1.5e-047	**ANK** like;	

Figure 3-2. Conserved Motifs in NF-κB Proteins Identified by MEME. Motifs are numbered based on their positions in the protein, from amino to C-terminus (see Figure 3-3). Several motifs reside within conserved domains in the Conserved Domain Database (Marchler-Bauer et al., 2017): ANK=ANK repeat (cl26073); IPT=IPT_NF-κB (cd01177); RHD=RHD-n (n-terminal Rel Homology Domain; cd07883). In the LOGO representations, the height of each letter is proportional to the frequency of the amino acid at that position in all sequences in the training set. Residues directly involved in DNA or ankyrin binding are listed. Adapted from Finnerty and Gilmore (2015).

The arrangement of 14 conserved motifs in 24 NF-κB and IκB proteins is depicted in Figure 3-3. NF-κB proteins have not been found in the phylum Nematoda or the phylum Ctenophora—the absence of NF-κB in these lineages thus must be due to secondary loss (Finnerty & Gilmore, 2015). The consensus sequence for each motif is presented in Figure 3-3. All of the identified motifs were highly significant, with an E-value of $1.5e^{-47}$ or less. The relative order of the motifs was consistent across all taxa in the analysis, indicating that the overall architecture of NF-κB proteins is highly conserved, although certain sequences were lacking specific motifs (Figure 3-3).

Multiple motifs were identified within each of the three major conserved functional domains of the NF-κB proteins, including the RHD, the IPT domain (Immunoglobulin-like fold, Plexins, Transcription factors), and the inhibitory (IκB-binding) domain. Six of the motifs were found to reside within the RHD-NF-κB domain (NCBI Conserved Domain Database; cd07935). With the exception of *Hydra*, which was missing motifs 3-5, and human RelB, which was missing motif 3, these six motifs were present in every metazoan NF-κB protein included in the analysis. The DNA-binding loop, which contacts DNA on target genes regulated by NF-κB proteins, was found within motif 2 and was present in all taxa.

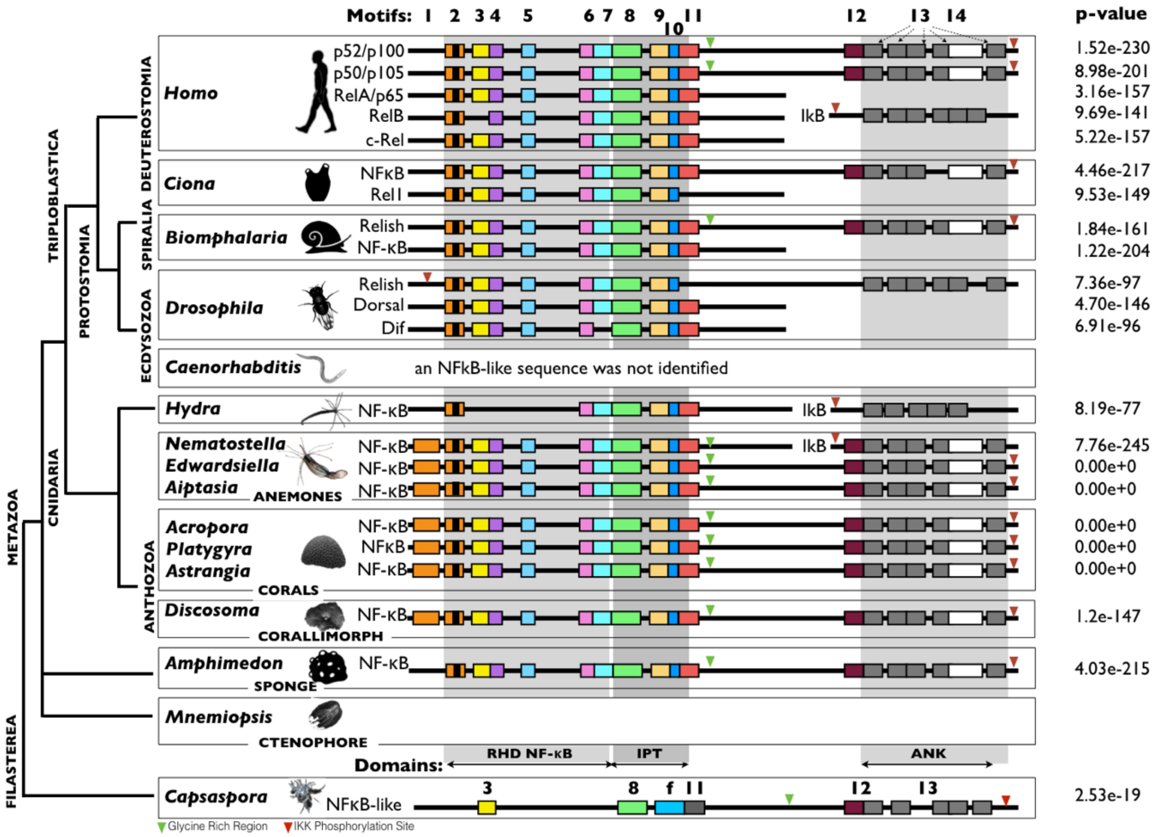


Figure 3-3. Motif Architecture of NF-κB and IκB Across Animal Evolution Conserved motifs identified by MEME are depicted as colored boxes. The width of each box is proportional to the length of the motif in amino acids. To convey the conservation of motif order across proteins, the inter-motif regions (black line segments connecting motifs) are not drawn to scale so that motifs are in register. The vertical black bar within motif 2 depicts the location of the DNA-binding loop. Proteins are grouped by taxon, and the phylogenetic relationships among taxa are shown along the left side of the figure. Motifs 1-14 are shared across multiple NF-κB and IκB proteins. Motif f is shared between the *Capsaspora* NF-κB–like sequence and members of the NF-AT family. Red and green triangles indicate the locations of putative IKK phosphorylation sites and glycine-rich regions, respectively (Table 3-1). This figure was modified from Finnerty and Gilmore (2015) and Mansfield et al. (2017).

Four of the motifs reside within the IPT domain (NCBI Conserved Domain Database; cd001177; Bork et al., 1999), a domain involved in protein folding and DNA binding (Bork et al., 1999, Siponen et al., 2010). All four motifs within this domain were identified in almost all animal NF-κB proteins, with the exception of *Ciona* Rel 1 and *Drosophila* Relish.

The final three motifs (motifs 12-14) were present in NF-κB proteins with a C-terminal inhibitory ANK-repeat region, such as human p100 and p105 and most cnidarian NF-κB proteins. Motifs 13 and 14 corresponded to ANK repeats. Several of the most highly conserved residues common to ANK repeats were found at the N-terminal end of motif 13 (GxTPLHxA; Li et al., 2006). Similarly, motif 14 showed perfect conservation of TPLHxA at the N-terminus, in addition to other residues that were among the most highly conserved positions in ANK repeats (the GA at positions 22-23 of motif 14 corresponds to the conserved GA at positions 25-26 of the consensus ANK repeat; Li et al., 2006). The consistent arrangement of motifs 13 and 14 in the ANK-repeat region of sponge, cnidarian, and vertebrate NF-κB and IκB proteins suggests a common ancestral arrangement of six ANK repeats (motifs 13-13-13-13-14-13), and that this arrangement has been highly conserved in diverse animal lineages over the last ~600 million years. Motif 12 did not show clear resemblance to any ANK repeat, but its consistent position at the N-terminus of the ANK-repeat region suggests that it has also been widely conserved since the common ancestor of filastereans, sponges, cnidarians, and triploblastic animals.

As phosphorylation by IKK is a critical step in the induction of NF-κB signaling (Zandi et al., 1997, Claudio et al., 2002, Coope et al., 2002, Dejardin et al., 2002, Lang et al., 2003), we searched the C-terminal end of the ANK regions for candidate serine residues that could be substrates for IKK. As shown in Table 3-1, we found a highly conserved arrangement of residues flanking a pair of serines at the C-terminal end of nearly all of the cnidarian NF-κB proteins that possess a C-terminal inhibitory region: DSGFGS (the only exception was found in *Astrangia* (DSG**L**GS)). The two cnidarian NF-κB proteins that lacked terminal ANK regions did possess candidate IKK phosphorylation sites at the N-terminus of their IκB proteins: *Nematostella* (DSGFGGS) and *Hydra* (DSGFVS). The consensus cnidarian sequence DSGFGS was highly similar to the sequences found in the *Ciona* NF-κB protein (DSAFGS) and human p100 (DSAYGS). *Amphimedon* had no recognizable IKK phosphorylation sites (Gauthier & Degnan, 2008). These findings suggest that IKK-dependent processing of NF-κB proteins may not be strictly conserved across animal evolution.

Another functionally important feature found in many NF-κB proteins is a glycine-rich region upstream of the ANK region that is involved in arresting proteasomal processing (Lin & Ghosh, 1996). As shown in Table 3-1, cnidarian (Wolenski et al., 2011) and poriferan (Gauthier & Degnan, 2008) NF-κB proteins possess GRRs adjacent to the RHD. In contrast, *Drosophila* Relish does not possess a GRR; it has been shown previously that processing of this protein occurs via a caspase-mediated mechanism rather than via the 26S proteasome; therefore, a GRR is not required to arrest proteasomal processing (Blank et al., 1991, Lin & Ghosh, 1996, Heusch et al., 1999, Karin & Ben-Neriah, 2000, Stoven et al., 2003). These findings suggest that GRR-mediated arrest of proteasomal processing of NF-κB proteins is widely conserved across animal evolution, but that a novel mechanism evolved in the lineage leading to *Drosophila* Relish.

Many of the functionally important sites known to occur in the RHD, IPT, and ANK domains reside within conserved motifs identified by MEME, and these sites are generally highly conserved. For example, we found that the ankyrin-binding residues of the IPT domain all fall within motifs 8-11 (Figure 3-2). Furthermore, the most highly conserved residues present in the motifs often corresponded to known sites of DNA or ankyrin binding. For example, in motif 8, there were seven strictly conserved positions (K2; C4; R5; M6; K8; N9; S10; K25; V27); two of these are involved in DNA binding (K25, V27), whereas five are involved in ankyrin binding (K2, C4, R5, M6, K8, N9, S10). Of note, the other functionally important positions were much more highly variable (14:T/E/D/M; 20:Y/G/F/I/W; 30:D/F/V/N), and we found several strictly conserved positions not associated with a known function (e.g., I3; G11; G15; E18; L21).

Protein (sp)	IKK Phos	Glycine-rich Region
DEUTEROSTOMES		
p52/p100(Hs)	KEDSAYGSQS	PTFSQPFGGGSHMGGGSGGAAGGYGGAGGGGS
p50/p105(Hs)	RDSDSVCDS	PNFSDSFGGGSGAGAGGGGMFGSGGGGGGTGSTG
IκB(Hs)	RHDSGLDS	-
NF-κB (Ci)	QCDSAFGSLP	PDFLDHTGNGSTGGYSFNPQAAILPSSYN
NF-κB (Bg)	-------	QRFLEYWNSTGVADYKRGASGASVRG
Relish (Bg)	RDSGDSPT	PLDGYEFGDGGLGGSDLGGDGGGMSMGHSGGGGMMQGGMGNGGNGGS
METOZOA/Cnidaria		
NF-κB (Hv)	NEDSGFVSLT	PAIPDFDVAQLKYFSPQEQLNQLFSDEQ
NF-κB (Nv)	FYDSGFGGSLE	PHFTDFLSGGSSGATGGGGSS
NF-κB (El)	LGDSGFGSES	PHFSDYFPPGGGGSSGAMGGPGDGGG
NF-κB (Ex)	REDSGFGSQS	PHFSDYYPPGGPPGAAGGGGG
NF-κB (Ad)	GFDSGFGSQS	PHFSDYFKDGSGGGDPPAAGGGGGG
NF-κB (Pc)	GFDSGFGSQS	PHFSDYFGGGGGGGPPGMGGAGGGGGGGFG
NF-κB (Ap)	GFDSGLGSHS	PHFSDYFGSGGGGGPPPSAGGAGGGGFGGFGALGLLG
NF-κB (Di)	VPDSNVSEFNF	-----FGGGGQPGVGGGSGGGTGLGGFG
METOZOA/Porifera		
NF-κB (Aq)	TYDSGI**S**SNP**S**	THFNNFFEGPGGGGGAGGGAGGAGGFFSRDFNYGSGGGYNSGFNFFGGSSGGGGGSGGGS
FILASTERIA		
NF-κB (Co)	FTRSSHGSQD	RHD – 36 AMINO ACIDS -GRGGGGGSSSSKGGDE

Table 3-1. IKK Phosphorylation Sites in IκB and Glycine-Rich Regions (GRRs)
Species abbreviations are: Ad=*Acropora digitifera*; Ap=*Astrangia poculata*; Aq=*Amphimedon queenslandica*; Bg=*Biomphalaria glabrata*; Ci=*Ciona intestinalis*; Co=*Capsaspora owczarzaki*; Di=*Discosoma*; Dm=*Drosophila melanogaster*; El=*Edwardsiella lineata*; Hs=*Homo sapiens*; Hv=*Hydra vulgaris*; Nv=*Nematostella vectensis*; Pc=*Platygyra carnosus.*

3.5.2 Evolutionary Conservation of IKK Proteins

We analyzed 20 protein sequences from bilaterians, non-bilaterians, and metazoan outgroups that produced BLAST hits to human IKKα, IKKβ, IKKε, and/or TBK using MEME (Bailey et al., 2009) to create our training set. Major metazoan lineages were represented, including non-vertebrate deuterostomes (*Ciona*), protostomes (*Drosophila*), Cnidaria (*N. vectensis* and *Exaiptasia*), Porifera (*Amphimedon*), Hydra (*Hydra*), Placozoa (*Trichoplax*), and Ctenophora (*Mnemiopsis* and *Pleurobrachia*). We also obtained a single IKK-like sequence from the filasterean *Capsaspora* and the choanoflagellate *Monosiga*.

Twenty statistically significant motifs were identified, 13 of which were found within the serine-threonine kinase catalytic domain (STKc; NCBI accession number cd14039; 1-10; 15-17; Figure 3-4; Mansfield et al., 2017). Seven of the motifs were located in the C-terminal half of the IKK protein, including motif 14, which corresponds to the NEMO-binding domain. Importantly, the motifs identified can be divided into three groups: (1) those shared by both IKKα/β and IKKε/TBK (motifs 1-7, 10); (2) those that were unique to IKKα/β (motifs 9, 11-14); and (3) those that were unique to IKKε/TBK (motifs 15-20). Functionally important residues found within the motifs are shown in Figure 3-4.

The existence of these paralog-specific motifs allowed us to reconstruct the evolution of the IKK family over the course of animal phylogeny (Figure 3-5; Mansfield et al., 2017; Appendix A.6). Only single IKK-like proteins were found in *Amphimedon*, *Mnemiopsis*, *Pleurobrachia*, and *Capsaspora*. The *Capsaspora* and *Mnemiopsis* sequences lacked motif 10, which was shared by all the IKK paralogs, and with one exception, they lacked any motifs unique to either the IKKα/β subfamily or the TBK/IKKε subfamily (Figure 3-4). The one exception was motif 14 in the *Mnemiopsis* IKK-like gene, which was otherwise restricted to the IKKα/β subfamily and known to encode a NEMO binding domain. For this reason, it is unclear whether the *Capsaspora* and *Mnemiopsis* sequences constitute *bona fide* IKK proteins, and so we designated them “IKK-like.” On the other hand, the sponge and placozoan sequences possessed one or more IKK-specific motifs. *Amphimedon* possessed motif 10, which was shared by all IKK paralogs, as well as motifs 16, 18, and 19, which were unique to the TBK/IKKε subfamily. For this reason, we tentatively designated this protein “TBK/IKKε.” By contrast, the *Trichoplax* sequence possessed two motifs—motifs 8 and 9—unique to the IKKα/β subfamily. This sequence appears to have been truncated at both the N-terminus and the C-terminus, as it is missing conserved motifs at both ends. Based on the presence of motifs 8 and 9, we tentatively designated it as “IKKα/β.” The remaining metazoan taxa possessed two distinct lineages of IKK proteins, one with conserved motifs characteristic of IKKα/β and one with motifs characteristic of TBK/IKKε.

#	E-value	Conserved Domain; Sites	LOGO Representation of Consensus
1	1.9e-093	**STKc;** ATP binding: 7-11, 15, 18, 21; Polypeptide substrate binding: 11	
2	3.4e-095	**STKc;** ATP binding: 13;	
3	2.1e-079	**STKc;** ATP binding: 5-8, 12; Polypeptide substrate binding: 14; SDD: 18, 20, 21;	
4	1.5e-269	**STKc;** ATP binding: 38, 40; Substrate binding: 33, 35, 37; SDD: 3, 6	
5	5.2e-081	**STKc;** ATP binding: 1, 10; Polypeptide substrate binding: 13;	
6	3.1e-100	**STKc;** Polypeptide substrate binding: 10-13;	
7	1.3e-223	**STKc;** Polypeptide substrate binding: 24, 29;	
8	7.7e-008	**STKc;** Polypeptide substrate binding: 27;	
9	2.0e-020	**STKc;** Polypeptide substrate binding: 1, 7-10;	
10	5.2e-063	**STKc;**	
11	1.1e-013	No known domain	
12	4.3e-009	No known domain	
13	3.8e-009	No known domain	
14	4.8e-002	No known domain	
15	8.0e-013	**STKc;**	
16	3.8e-097	**STKc;**	
17	2.1e-021	**STKc;**	
18	7.4e-006	No known domain	
19	1.2e-004	No known domain	
20	3.5e-020	No known domain	

Figure 3-4. Conserved Motifs in IKK Proteins Identified by MEME
Motifs are numbered based on their relative position in the IKK proteins, from the N-terminus to the C-terminus (Figure 3-5). Several motifs reside within the serine-threonine kinase catalytic domain (Conserved Domain Database: STKc; cd14039; Marchler-Bauer et al., 2017). In the LOGO representations, the height of each letter is proportionate to the relative frequency of the given amino acid at that position across all sequences in the training set. Within each motif, the positions of residues directly involved in adenosine triphosphate (ATP) or polypeptide substrate binding are indicated.

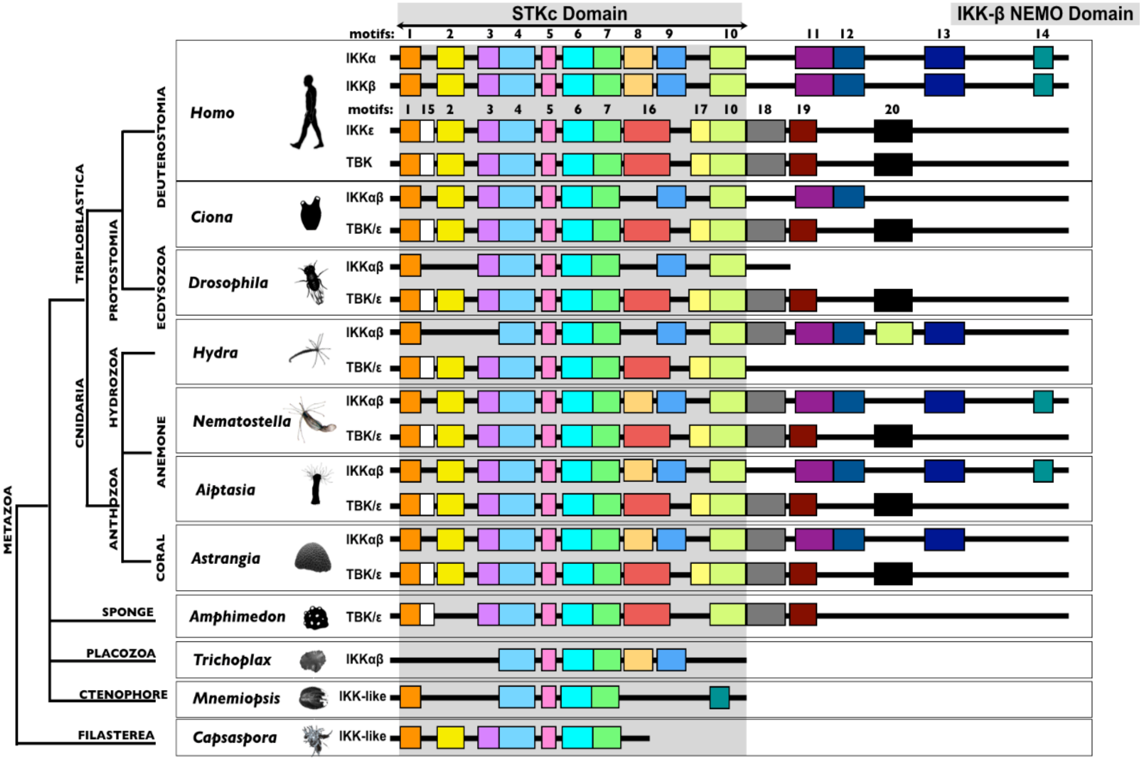


Figure 3-5. Motif Architecture of IKK Proteins Across Animal Evolution
Motifs identified by MEME are depicted as colored boxes. The width of each box is proportional to the length of the motif in amino acids. To convey the conservation of motif order across proteins, the inter-motif regions (black line segments connecting motifs) are not drawn to scale so that motifs are in register. Proteins are grouped by taxon, and the phylogenetic relationships among taxa are shown along the left side of the figure. See Figure 3-4 for motif LOGOs. Modified from Mansfield et al., 2017.

A maximum likelihood phylogeny based on the conserved motifs shared among IKK proteins supports distinct IKKα/β and TBK/IKKε clades, with each cnidarian and bilaterian model system included in the analysis represented by sequences in both clades (Figure 3-6; Mansfield et al., 2017). This result is consistent with the origin of distinct IKKα/β and TBK/IKKε progenitors via gene duplication of an ancestral IKK sequence sometime prior to the divergence of cnidarians and bilaterians.

Functionally important residues within the catalytic (STKc) domain and the alpha helical scaffold dimerization domain (SDD) tend to reside within the evolutionarily conserved motifs identified by MEME, and are typically highly conserved across taxa. For example, we found that the STKc domain spans motifs 1-10 (Figure 3-4), and the most highly conserved residues present in the motifs often corresponded to known sites of ATP or polypeptide substrate binding. For example, in motif 1, there were eight strictly conserved positions (L7; G8; Q9; G10; A11; V15; G18; K21); all of these are involved in ATP binding, while one is involved in both ATP binding and polypeptide substrate binding (A11). Of note, some functionally important positions were much more highly variable (12:F/T/Y; 13:G/A), and we found several strictly conserved positions not associated with a known conserved function (e.g., W1; R5).

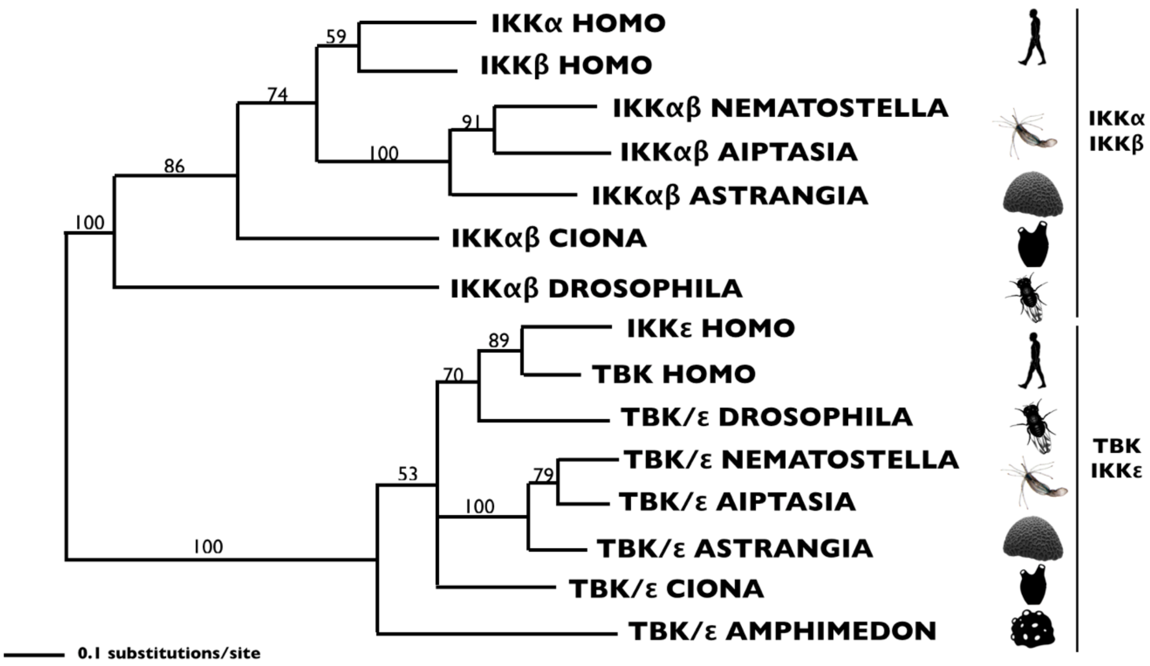


Figure 3-6. Maximum-Likelihood Phylogeny of IKK Proteins
Numbers above branches indicate bootstrap support values. Reproduced from Mansfield et al., 2017.

3.5.3 Evolutionary Conservation of TAK1 Proteins

We analyzed six protein sequences from bilaterians, non-bilaterians, and metazoan outgroups that produced BLAST hits to human TAK1 using MEME (Bailey et al., 2009) to create the training set (Appendix A.12). Major metazoan lineages were represented, including non-vertebrate deuterostomes (*Ciona*), protostomes (*Drosophila*), Cnidaria (*N. vectensis*), Porifera (*Amphimedon*), and Placozoa (*Trichoplax*).

We identified 14 conserved motifs in TAK1 (Figure 3-7) that occupy the same relative position in two or more sequences (Figure 3-8). We used MAST to search for these same motifs in available cnidarian transcriptomes and the reference *A. poculata* transcriptome we generated (Chapter 2). Particularly in the region of the protein corresponding to the serine threonine kinase catalytic domain (STKc), the arrangement of motifs 2-10 was highly conserved among diploblastic and triploblastic animals. There were a few exceptions: both *Capsaspora* and *Trichoplax* were missing motif 10; *Hydra* TAK1 was missing motifs 8 and 10; the *Acropora* sequence was lacking motifs 5-6; and *Drosophila* TAK1 was missing motifs 3, 8, and 9. The most divergent sequence was that from the sponge *Amphimedon*, which lacked motifs 3, 4, 5, 8, and 10. Overall, the pattern of conserved motifs suggests that TAK1 originated near the base of metazoan radiation, and the STKc was largely conserved from *Capsaspora* to *Homo.*

A maximum likelihood-based phylogeny based on the amino acid sequences in the conserved STKc alignment (Appendix A.7) was consistent with the conclusions derived from the motif analysis (Figure 3-9). The TAK1 sequences of the two deuterostomes, *Homo* and *Ciona,* clustered together, while sequences from the four cnidarians *Aiptasia*, *N. vectensis*, *Acropora*, and *A. poculata* formed their own TAK1 clade. The anomalous position of the *Drosophila* TAK1 sequence is probably due to long branch attraction, as this sequence was highly divergent.

Prior functional analyses of TAK1 proteins identified the TAK1 binding protein (TAB1) and activation loop, as well as specific residues involved in ATP binding and/or protein substrate binding. There was a high degree of overlap between these functionally important sites and the evolutionarily conserved motifs identified by MEME. For example, we found that the activation loop resides within motifs 6-7 (Figure 3-7). Furthermore, the most highly conserved residues present in the motifs often corresponded to known sites of ATP or polypeptide substrate binding. For example, in motif 2, there were five strictly conserved positions (G1; R2; G3; S4; V8); all of these are involved in ATP binding, while one is involved in both ATP binding and polypeptide substrate binding (S4). Of note, other functionally important positions were much more highly variable (5:F/Y/G; 7:V/R/A; 9:Y/C/R/H), and we found several strictly conserved positions not associated with a known function (e.g., G6, K10, A11).

#	E-value	Conserved Domain; Sites	LOGO Representation of Consensus
1	1.2e+002	No known domain	
2	6.5e-011	**STKc_TAK1;** ATP binding: 1-4, 8; Polypeptide substrate binding: 4;	
3	5.7e-024	**STKc_TAK1;** ATP binding: 7, 9, 36;	
4	1.2e-040	**STKc_TAK1;** ATP binding: 6-9, 13; Polypeptide substrate binding: 13, 15;	
5	1.2e-040	**STKc_TAK1;**	
6	4.1e-066	**STKc_TAK1;** ATP binding: 4, 6, 8, 9, 11, 23; Polypeptide substrate binding: 4, 6, 8, 26; Activation loop: 22-29	
7	1.6e-104	**STKc_TAK1;** Polypeptide substrate binding: 6-9; Activation loop: 1-9	
8	1.9e+000	**STKc_TAK1;** TAB1 binding site: 5;	
9	9.3e-058	**STKc_TAK1;** TAB1 binding site: 10-22;	
10	6.2e-006	**STKc_TAK1;** TAB1 binding site: 3-6;	
11	3.1e+002	No known domain	
12	9.5e+002	No known domain	
13	6.6e-007	No known domain	
14	3.6e+001	No known domain	

Figure 3-7. Sequence of TAK1 Motifs Identified by MEME
Motifs are numbered based on their relative position in the TAK1 proteins from the N-terminus to the C-terminus (Figure 3-8). Several of the motifs reside within the serine-threonine kinase catalytic domain (Conserved Domain Database: STc_TAK1, cd14058; Marchler-Bauer et al., 2017). In the LOGO representations, the height of each letter is proportionate to the relative frequency of the given amino acid at that position across all sequences in the training set. Within each motif, the positions of residues directly involved in ATP, polypeptide substrate, or TAB1 binding, and the activation loop are indicated.

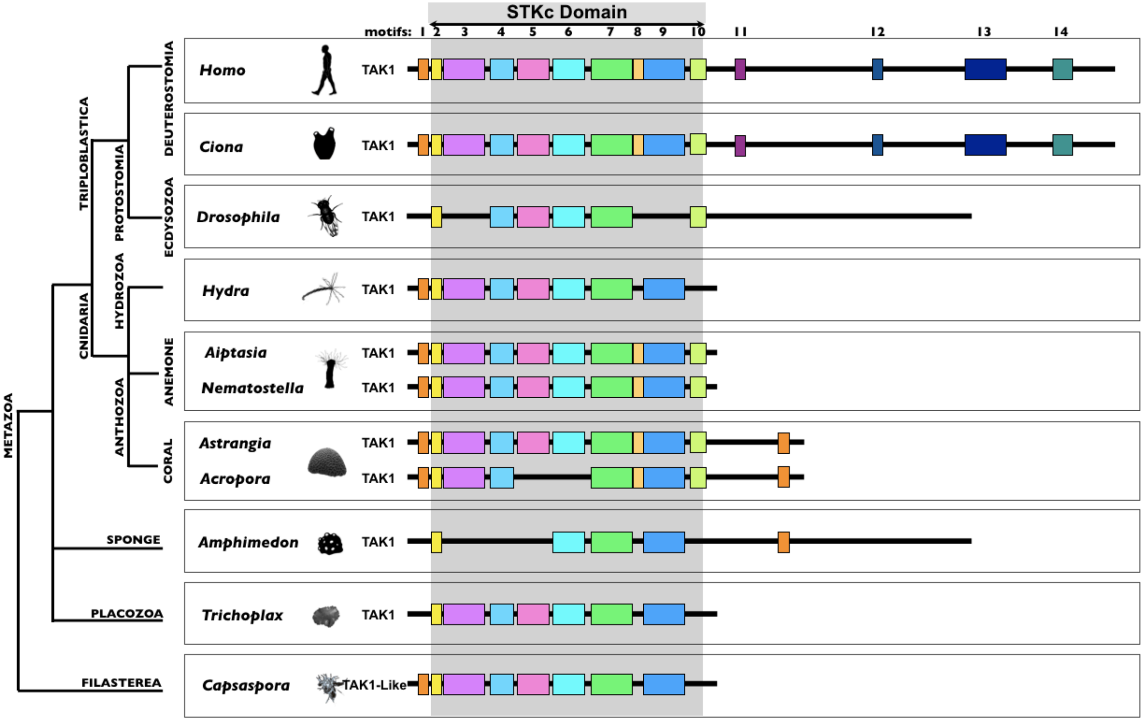


Figure 3-8. Motif Architecture of TAK1 Proteins Across Animal Evolution
Conserved motifs identified by MEME are depicted as colored boxes. The width of each box is proportional to the length of the motif in amino acids. To convey the conservation of motif order across proteins, the inter-motif regions (black line segments connecting motifs) are not drawn to scale so that motifs are in register. Proteins are grouped by taxon, and the phylogenetic relationships among taxa are shown along the left side of the figure. The TAK1-like sequence from *Capsaspora* did not reciprocally BLAST to the original BLAST query.

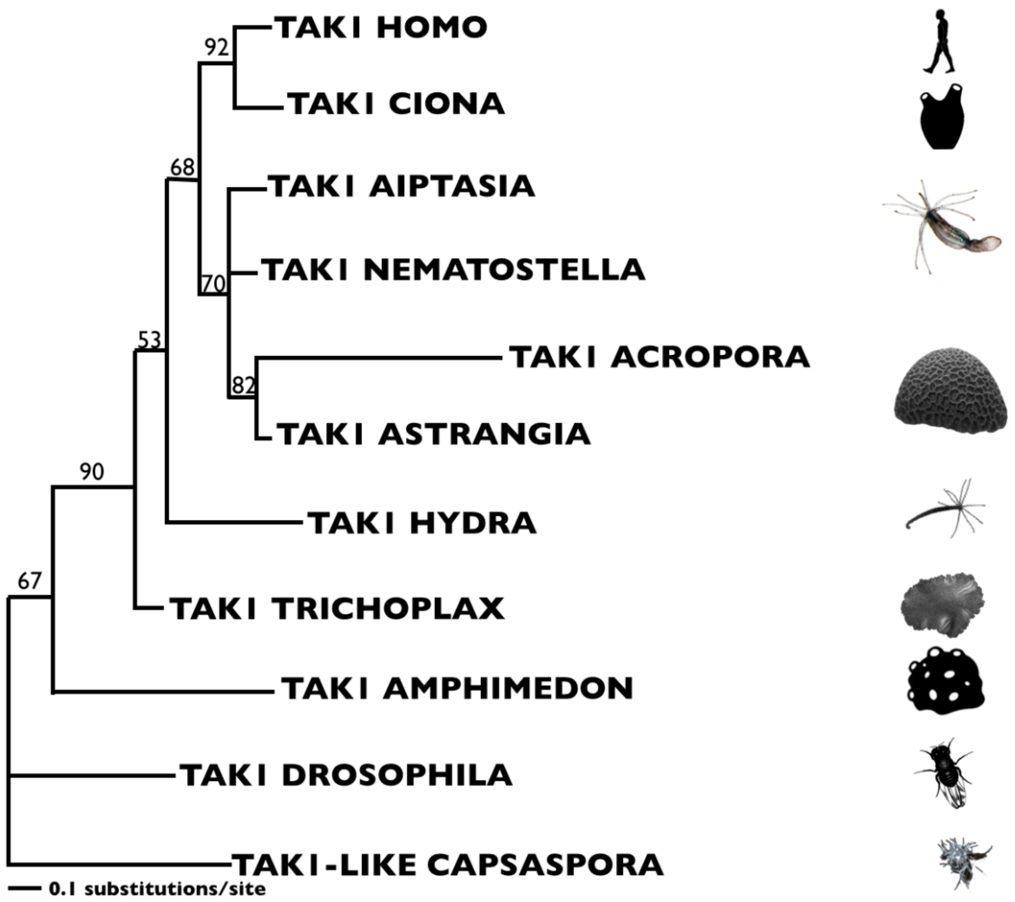


Figure 3-9. Maximum-Likelihood Phylogeny of TAK1 Proteins
Numbers above branches indicate bootstrap support values.

3.5.4 Evolutionary Conservation of NIK Proteins

We analyzed four protein sequences from bilaterians, non-bilaterians, and metazoan outgroups that produced BLAST hits to human NIK using MEME (Bailey et al., 2009) in our training set (Appendix A.13). Major metazoan lineages were represented, including non-vertebrate deuterostomes (*Branchiostoma*), protostomes (*Drosophila*), and Cnidaria (*Exaiptasia*).

Similar to the IKK and TAK1 analyses, MEME (Bailey et al., 2009) revealed a consistent arrangement of conserved motifs within the STKc of NIK proteins (Figure 3-10). Five motifs, ranging in length from 14-49 amino acids, were shared widely across metazoans, all of them located within STKc. We used MAST to search for these same motifs in available cnidarian transcriptomes and the reference *A. poculata* transcriptome we generated. The only exceptions to the conservation of these five motifs were the absence of motif 1 in *Aiptasia*, *Trichoplax*, and *Capsaspora*. The conserved pattern of motifs suggests that (1) the NIK family originated prior to the divergence of filastereans and animals and (2) the STKc of NIK has been largely conserved since its origin (Figure 3-11). A maximum likelihood-based phylogeny shown in Figure 3-12, based on an amino acid alignment of conserved motifs within STKc (Appendix A.8), was consistent with the conclusions derived from the motif analysis. However, there remained some uncertainty as to whether the NIK sequences from all of the diploblastic animals are *bona fide* NIK homologs. These sequences were identified as the top matches in BLAST searches using a human NIK query, but reciprocal BLASTs using the NIK-like genes found in *Drosophila*, *A. poculata*, *Amphimedon*, *Trichoplax*, and *Capsaspora* did not identify human NIK (MAP3K14) as the top match, but rather matched best to other members of the MAP3K family, e.g., MAP3K4, MAP3K2, and MAP3K1. A wider analysis of MAP3K proteins is needed to confirm the specific identity of the proteins from these taxa.

Prior functional analyses of NIK proteins identified the activation binding loop as well as specific residues involved in ATP binding and/or polypeptide substrate binding. There was a high degree of overlap between these functionally important sites and the evolutionarily conserved motifs identified by MEME. For example, we found that the activation binding loop resides within motifs 3 and 4 (Figure 3-10). Furthermore, the most highly conserved residues present in the motifs often corresponded to known sites of ATP or polypeptide substrate binding. For example, in motif 3, there were seven conserved positions involved in ATP binding (D22; K24; A26; N27; F29; D41; S44), four of which are involved in both ATP binding and polypeptide substrate binding (D22, K24, A26, S44). Another 10 conserved positions (G40; D41; F42; G43; S44; A45; V46; T47; L48; Q49) were involved in the activation binding loop. Of note, the other functionally important positions were much more highly variable (e.g., 26:A/E/D; 29:F/M/L; 44:S/M/H), and we found several strictly conserved positions not associated with a known conserved function (e.g., L13; H20; L39).

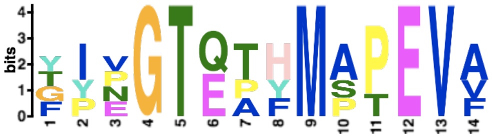
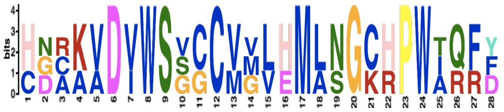
#	E-value	Conserved Domain; Sites	LOGO Representation of Consensus
1	2.7e-001	**STKc_NIK;** ATP binding:10-14; Polypeptide substrate binding: 12	
2	2.8e-007	**STKc_NIK;** ATP binding: 3, 19-20	
3	4.1e-017	**STKc_NIK;** ATP binding: 22, 24, 26, 27, 29, 41, 44; Polypeptide substrate binding: 22, 24, 26, 44; Activation binding loop: 40-49	
4	9.4e-002	**STKc_NIK;** Polypeptide substrate binding: 4-7; Activation binding loop: 1-7	
5	2.6e-014	**No known domain**	

Figure 3-10. Conserved Motifs in NIK Proteins Identified by MEME
The motifs are numbered based on their relative position in the NIK proteins, from the N-terminus to the C-terminus (see Figure 3-11). Several of the motifs reside within conserved domains found in the Conserved Domain Database (Marchler-Bauer et al., 2017); STKc=serine-threonine kinase catalytic domain (cd13991). In the LOGO representations, the height of each letter is proportionate to the relative frequency of the given amino acid at that position across all sequences in the training set. Within each motif, the positions of residues directly involved in ATP or polypeptide substrate binding or the activation loop are indicated.

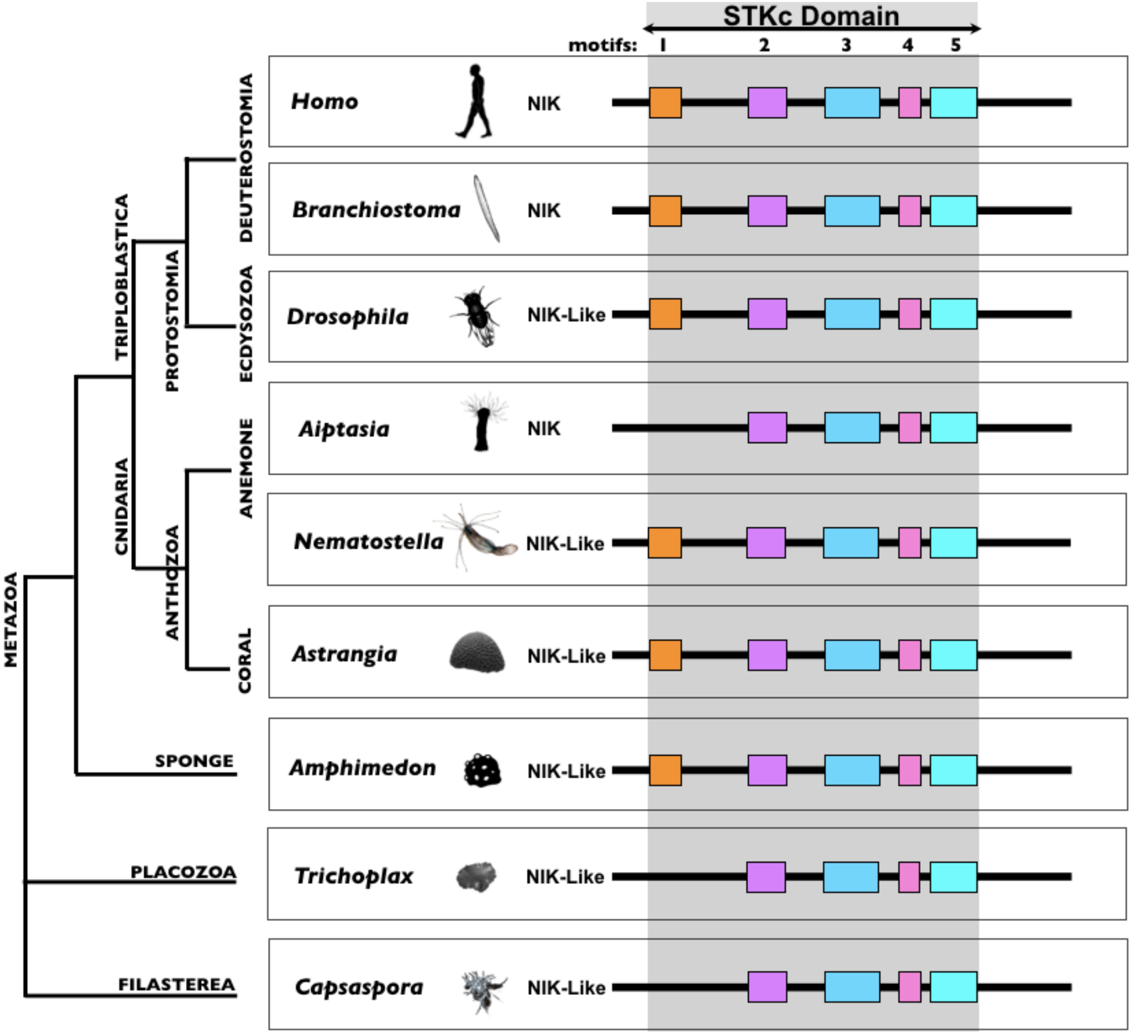


Figure 3-11. Motif Architecture of NIK Proteins Across Animal Evolution
Conserved motifs identified by MEME are depicted as colored boxes. The width of each box is proportional to the length of the motif in amino acids. To convey the conservation of motif order across proteins, the inter-motif regions (black line segments connecting motifs) are not drawn to scale so that motifs are in register. Proteins are grouped by taxon, and the phylogenetic relationships among taxa are shown along the left side of the figure. NIK-like sequences did not reciprocally BLAST to retrieve the original BLAST queries.

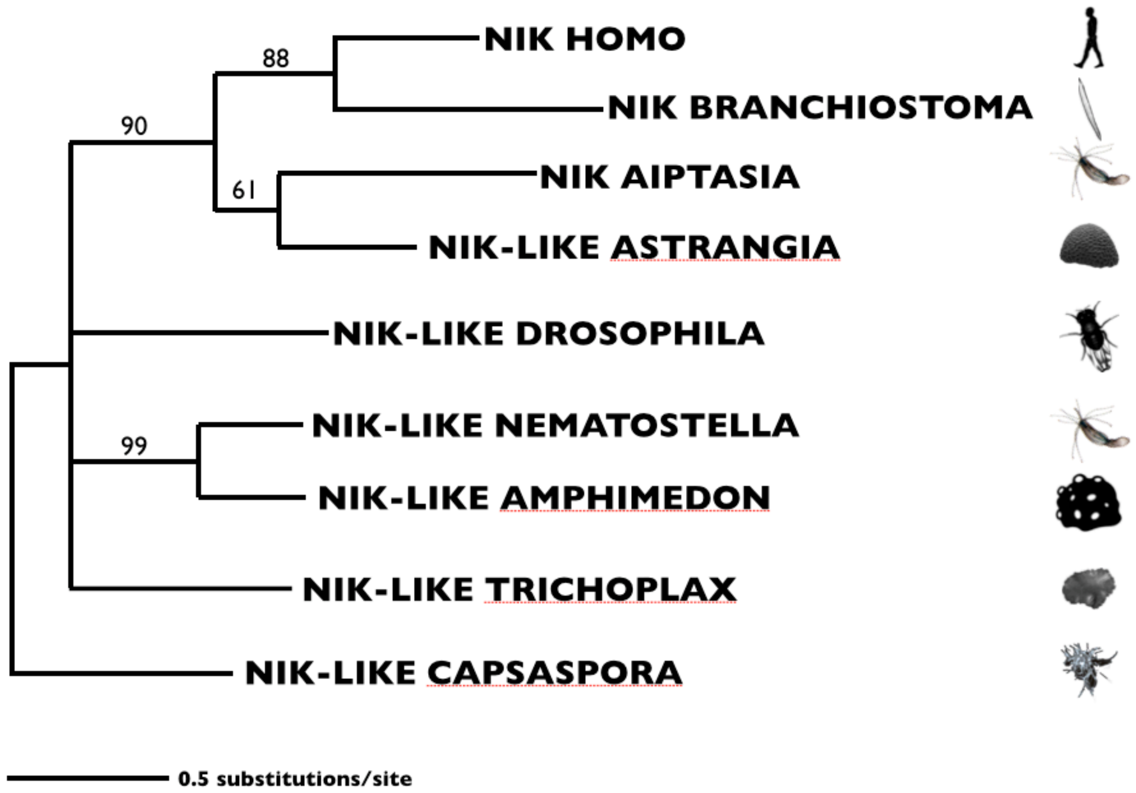


Figure 3-12. Maximum-Likelihood Phylogeny of NIK Proteins
Numbers above branches indicate bootstrap support values.

3.5.5 Evolutionary Conservation of Superoxide Dismutases (SODs)

We analyzed 41 protein sequences from bilaterians, non-bilaterians, and metazoan outgroups that produced BLAST hits to human CCS, CuZnSOD, or MnSOD using MEME (Bailey et al., 2009) to create our training set (Appendix A.14). Major metazoan lineages were represented, including non-vertebrate deuterostomes (*Ciona*), protostomes (*Drosophila*), Nematoda (*Caenorhabditis elegans*), Cnidaria (*N. vectensis* and *Acropora*), Porifera (*Amphimedon*), Hydra (*Hydra*), Mollusca (*Crassostrea*), Placozoa (*Trichoplax*), Ctenophora (*Mnemiopsis* and *Pleurobrachia*), and the filasterean (*Capsaspora)*.

We conducted a joint MEME analysis of CuZnSODs, MnSODs, and CCS proteins to determine if there are conserved motifs within and between subfamilies. As with other gene families, we compiled sequences from diploblastic and triploblastic animals as well as *Capsaspora*. The analysis identified 15 conserved motifs, several of which were highly significant based upon their E-values (Figure 3-13). Five of these motifs (motifs 4, 6-9) were shared between CuZnSODs and CCS proteins. However, only motif 11 was shared among some CuZnSODs and MnSODs (Figure 3-14).

The phylogenetic distribution of SOD proteins and conserved motifs showed that both *A. poculata* and *N. vectensis* possess single CCS proteins that have all 10 conserved motifs found in the single CCS proteins of other metazoans (Figure 3-14). *N. vectensis* and *A. poculata* expressed three distinct CuZnSODs, more than any other taxon that we analyzed. Such a diverse complement of SODs in *N. vectensis* was reported previously (Tarrant et al., 2014). Two of these *N. vectensis* SOD proteins exhibited the same arrangement of six motifs found in most other CuZnSODs. The third, like human

CuZnSOD2, was lacking motif 7. In contrast, the three CuZnSODs in *A. poculata* exhibited the same arrangement of six motifs found in most other CuZnSODs. Two distinct MnSODs were recovered in both *N. vectensis* and *A. poculata.* These MnSODs shared conserved motifs 14-16 at the C-terminus of the protein, except for MnSOD2 in *N. vectensis*, which lacked motif 15. In *A. poculata*, the second MnSOD lacked motif 1. Unfortunately, a molecular phylogenetic approach did little to resolve the evolution of the SOD family. The gene trees shown in Figure 3-15 (see Appendix A.9 for the multiple sequence alignment) were often at odds with underlying organismal relationships, possibly because of difficulty in achieving a reliable alignment of animals and filastereans.

Prior functional analyses of SOD proteins identified the E-class and P-class dimer interfaces as well as specific residues involved in Cu^{2+} binding and/or Zn^{2+} binding. There was a high degree of overlap between these functionally important sites and the evolutionarily conserved motifs identified by MEME. For example, we found that the E-class dimer interface resides within motifs 1, 4, 6, and 8 (Figure 3-13). Furthermore, the most highly conserved residues present in the motifs often corresponded to known sites of Cu^{2+} or Zn^{2+} binding. For example, in motif 6, there were six strictly conserved positions (H9; H11; F13; G14; D15; H26); three of these are involved in Cu^{2+} binding (H9; H11; H26), while one is involved in both Cu^{2+} and Zn^{2+} binding (H26). Of note, the other functionally important positions were much more highly variable (e.g., 3:P/K/E/A/N; 12:E/Q/V/D; 25:P/D/G/A/N), and we found several strictly conserved positions not associated with a known conserved function (e.g., G4; H6; G19, C20; N28;

P29).

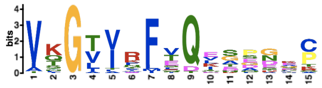
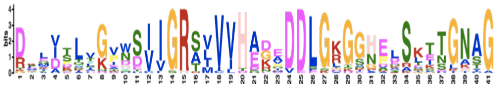
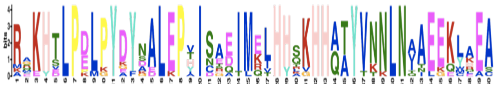
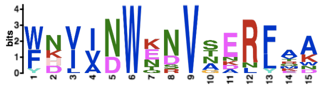
#	E-value	Conserved Domain; Sites	LOGO Representation of Consensus
1	3.3e-57	**Cu-Zn_SOD;** E-class dimer interface:13-15	
2	2.5e-86	**Cu-Zn_SOD;**	
3	5.1e-04	**Cu-Zn_SOD;**	
4	2.8e-61	**Cu-Zn_SOD;** E-class dimer interface: 4, 6	
5	2e-02	**Cu-Zn_SOD;**	
6	3.4e-435	**Cu-Zn_SOD;** Cu^{2+} bind: 9, 11, 26; Zn^{2+} bind: 26; E class dimer interface: 13-15	
7	1.6e-240	**Cu-Zn_SOD;** Cu^{2+} binding: 3; Zn^{2+} binding: 3, 12, 15; P class dimer interface: 20	
8	3.7e-381	**Cu-Zn_SOD;** E-class dimer interface: 13, 14; Cu^{2+} binding: 20	
9	1.5e-82	No known domain	
10	8.8e-64	No known domain	
11	1.7e-09	No known domain	
12	1.6e-370	No known domain	
13	4.8e-154	No known domain	
14	1.3e-294	No known domain	
15	3.7e-31	No known domain	

Figure 3-13. Conserved Motifs in SOD Proteins Identified by MEME
Motifs are numbered from the N-terminus to the C-terminus. Motifs residing in the Cu-Zn_SOD domain (cd00305) are indicated (Marchler-Bauer et al., 2017). In the LOGO representations, the height of each letter is proportionate to the frequency of the given amino acid at that position. Within each motif, residues directly involved in Cu^{2+} or Zn^{2+} binding or E-class or P-class dimer interfaces are indicated.

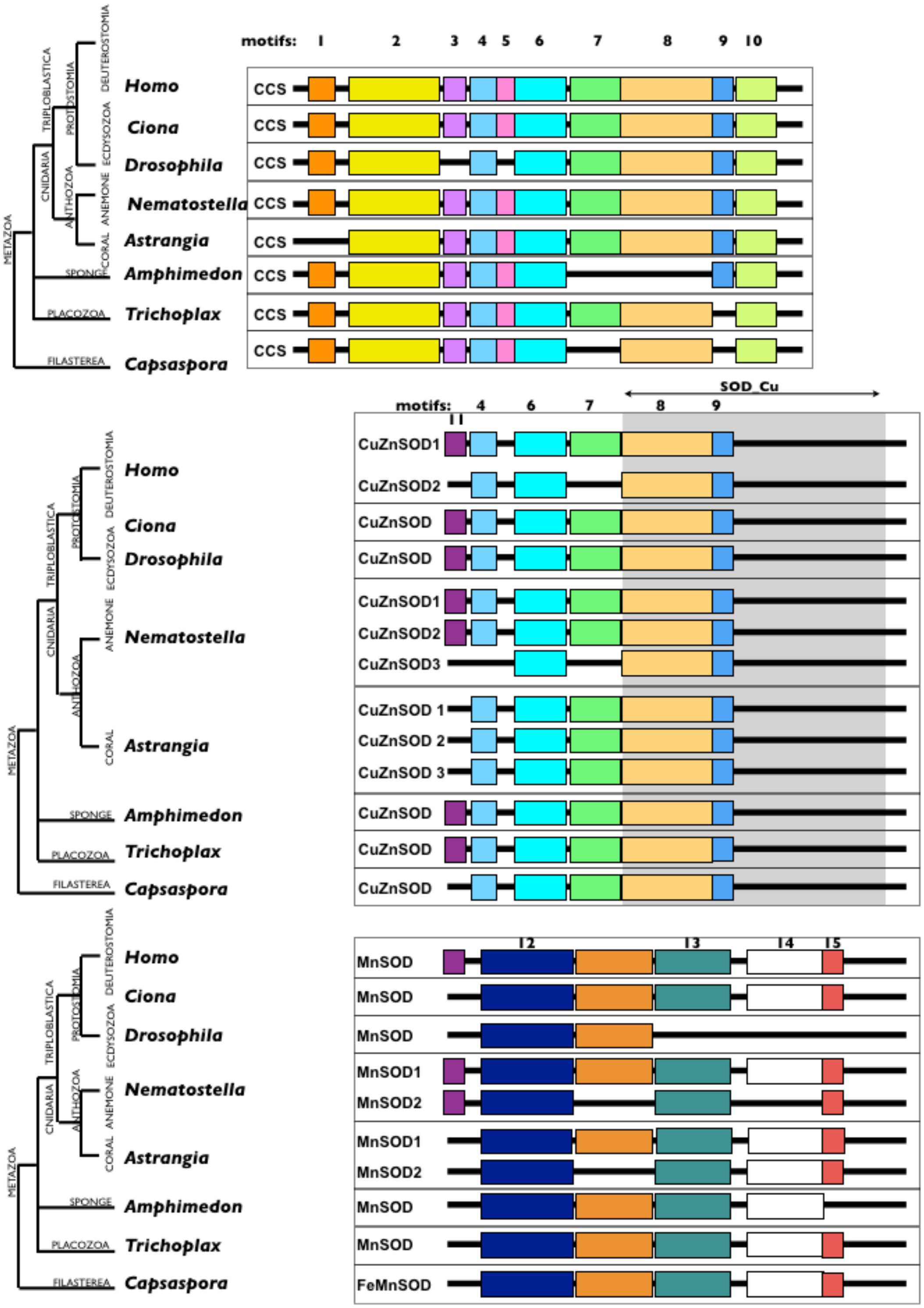


Figure 3-14. Motif Architecture of SOD Proteins Across Animal Evolution
Figure was drawn as described in other diagrams.

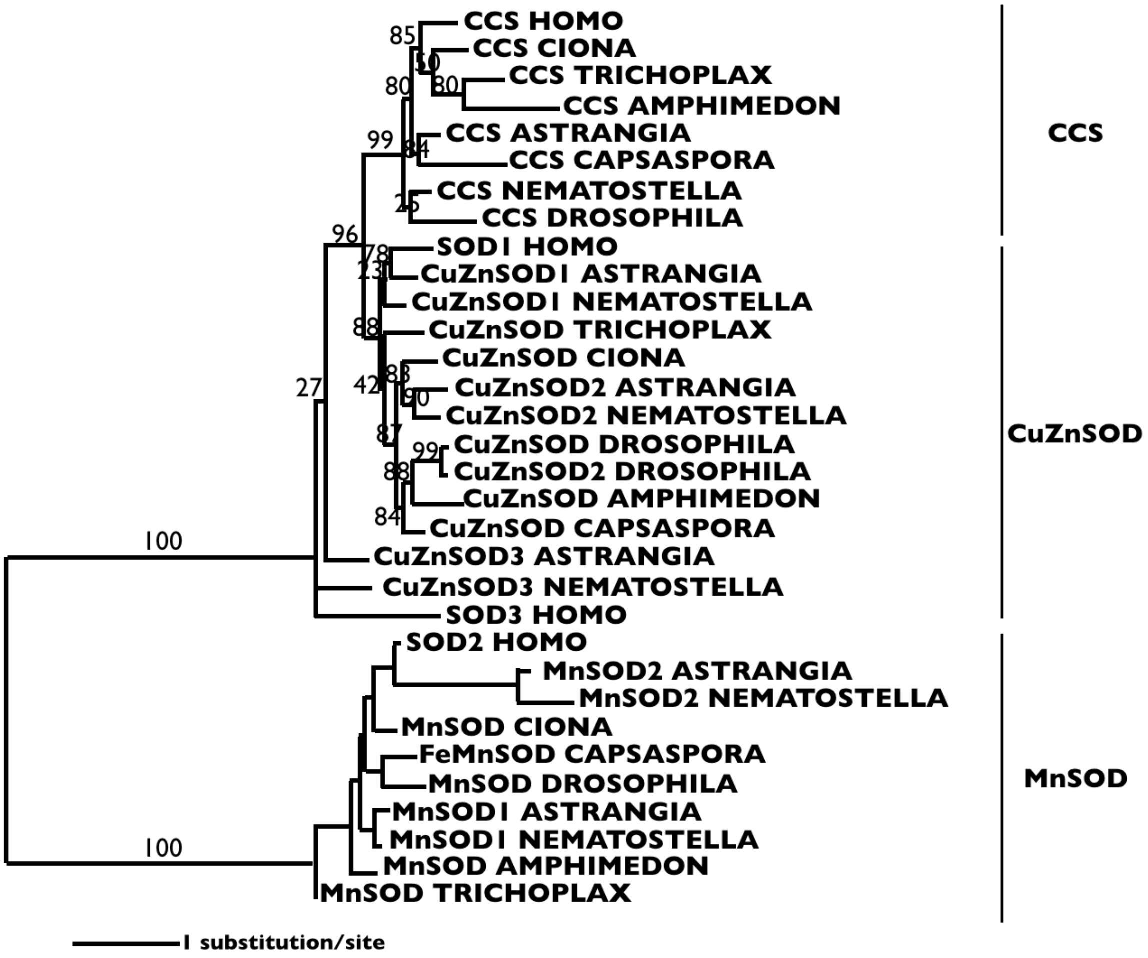


Figure 3-15. Maximum-Likelihood Phylogeny of SOD Proteins
Numbers above branches indicate bootstrap support values.

3.6 Discussion

The data and analyses described in this chapter support three major conclusions. First, “motifs” represent an important level of selection that is intermediate between individual amino acid residues and previously characterized domains. Second, cnidarians possess the core components of an NF-κB signaling pathway that appears primitive and simple relative to that of vertebrates or other bilaterian metazoans. Third, cnidarians possess an expanded complement of SOD proteins compared to vertebrates.

3.6.1 Conservation of Motifs During Protein Evolution

Studies of protein evolution often focus on the level of individual residues or conserved functional domains. However, as this study reveals, a well-established functional domain may be comprised of smaller modules (i.e., motifs) whose length and amino acid composition are tightly constrained by stabilizing selection.

There are multiple benefits to studying protein motifs. First, because motifs can be defined by an explicitly quantitative process, they represent a repeatable and objective unit for comparing protein structure across studies. Second, since motifs often represent the sites of conserved intra- or inter-molecular interactions, they provide information about the “interactional architecture” of proteins (Arthur, 2000). Third, as phylogenetic characters, motifs can be useful for reconstructing the evolution of proteins.

The motifs detected in the current study provide a more complete understanding of NF-κB evolution than would be apparent from considering only the presence or absence of key domains or the identity of particular amino acid residues. Discussions of

NF-κB diversity and evolution in the literature commonly employ a simple diagrammatic representation of the proteins, with a single box at the N-terminus representing the Rel Homology Domain, and, depending upon the protein, multiple boxes at the C-terminus representing ankyrin repeats (e.g., NF-κB1) or a single box representing the activation domain (Figure 3-16A). Such representations fail to capture the diversity of NF-κB proteins in three important ways. First, depicting the RHD as a single visual element overstates the similarity between the RHD regions of NF-κB proteins within and between species. For example, while the NF-κB proteins of both *Astrangia* and *Hydra* possess recognizable Rel Homology Domains (Figure 3-3), the loss of three highly conserved motifs 3-5 from the center of the RHD in *Hydra* suggests that the protein has diverged significantly in function. Similarly, the common depiction of trans-activating domains (TAD) implies evolutionary homology and possible conserved function, a conclusion that is suggested in a recent review (2012; Figure 3-16B). However, neither the MEME analysis presented here, nor the multiple sequence alignments reported in other studies, provide compelling evidence of sequence homology in the TADs of human RelA, RelB, and c-Rel. In the current study, we did not identify a single conserved motif in this region. Finally, illustrations such as the one shown in Figure 3-16 suggest equivalence among ankyrin repeats. In contrast, MEME identified two different types of ankyrin repeat (motifs 13 and 14; Figure 3-3) that occupy a consistent position relative to each other in sponges, cnidarians, and bilaterians, over the approximately 600 million years since these lineages last shared a common ancestor (Figure 3-3; Peterson & Butterfield, 2005). Going forward, more accurate illustrations of NF-κB would include the motifs identified in this study, facilitating a quick visual comparison of protein structure that has an objective and statistically rigorous basis in sequence conservation. Below, I use the conservation of motifs—and residues at key locations within motifs—to reconstruct elements of the NF-κB signaling pathway in the common ancestor of cnidarians and bilaterians.

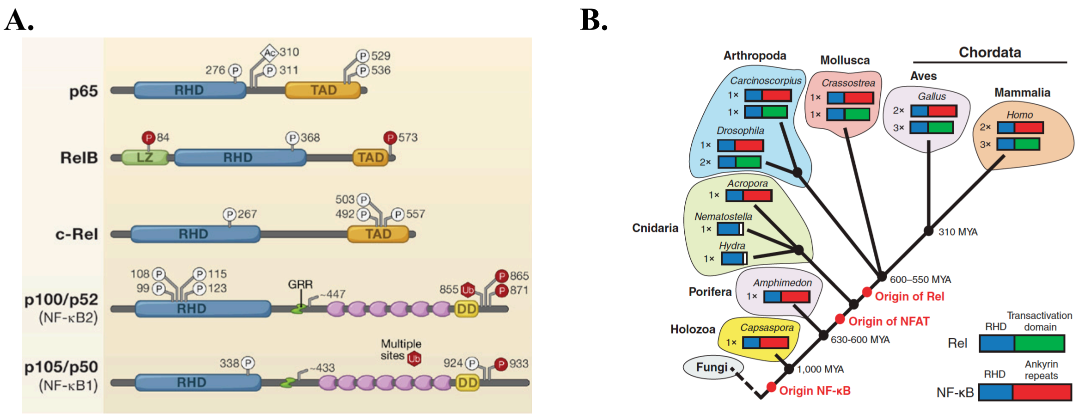


Figure 3-16. Diagrammatic Representation of NF-κB Proteins in the Literature
(A) A diagram of the five human NF-κB proteins reproduced from Hayden and Ghosh (2008). DD=death domain; GRR=glycine rich region; LZ=leucine zipper; P=phosphorylation site; RHD=REL homology domain; TAD=transactivation domain; Ub=ubiquitination site. (B) Proposed evolution of NF-κB proteins, reproduced from Wolenski and Gilmore (2012). The Rel homology domain is depicted as a blue box, the ankyrin repeat region as a red box, and the trans-activating domain as a green box.

3.6.2 A Primitive and Simple NF-κB Signaling Pathway in Cnidaria

Our analysis indicates that cnidarians possess a primitive and simple NF-κB signaling pathway that reflects the condition inferred for the cnidarian-bilaterian ancestor. Based on the NF-κB, IκB, and IKK paralogs that we identified in coral, anemones, and corallimorphs, the cnidarian NF-κB signaling pathway clearly does not correspond to the "non-canonical" pathway of vertebrates, as recently suggested (Mansfield et al., 2017). It also does not correspond to the canonical NF-κB pathway. The distinction between the canonical and non-canonical pathways relies upon the involvement of specific NF-κB, IκB, and IKK paralogs that did not exist when cnidarians diverged from bilaterians. For example, in both canonical and non-canonical pathways, a critical step is the formation of an NF-κB heterodimer, consisting of a Rel subfamily member (e.g., p65) and an NF-κB subfamily member (e.g., p50). However, with respect to NF-κB and IκB, it is clear that cnidarians possess only a single NF-κB protein with a C-terminal region that consists of an IκB-like region.

The single cnidarian NF-κB protein is strikingly similar to the p100 or p105 proteins of vertebrates (Figure 3-17). For example, almost every motif is conserved between *A. poculata* NF-κB and human p105 except for a single anthozoan-specific motif (motif 1). Within these motifs, there is extensive conservation of residues implicated in inter- or intra-molecular interactions: 12/12 of the residues involved in DNA binding, 7/8 of the residues involved in dimerization, 5/11 of the residues involved in ankyrin binding, and 3/3 sites of IKK phosphorylation are strictly conserved (Figure 3-17). Because of the presence of the conserved residues that have been proven necessary for specific molecular interactions in other model systems, including the NLS and GRR, we conclude that the NF-κB protein of *A. poculata,* like vertebrate p100 or p105, is able to form a homo-dimer, bind ankyrin, undergo phosphorylation by IKK, and translocate to the nucleus following the proteolysis of the ankyrin-repeat region.

In many cases, the hypothesized functional conservation that we can infer between human and cnidarian NF-κB proteins based on sequence conservation has been supported by empirical studies. For example, the DNA-binding preferences of NF-κB from the anemones *N. vectensis* and *E. pallida* appear very similar to those of human p50 or p52 (Wolenski et al., 2011, Ryzhakov et al., 2013, Mansfield et al., 2017), and less similar to those of human cRel (Mansfield et al., 2017) or RelA (Ryzhakov et al., 2013, Mansfield et al., 2017). There is also empirical evidence for cnidarian NF-κB possessing similar dimerization properties (Ryzhakov et al., 2013), nuclear localization (Wolenski et al., 2011, Mansfield et al., 2017), and activation by IKKs (Wolenski et al., 2011, Mansfield et al., 2017).

Importantly, as both human p105 and *Astrangia* NK-κB include an integral ANK (IκB-like) region, dimers consisting of these NK-κB proteins would be sequestered in the cytoplasm until the ANK region is proteolytically cleaved. Based on the phylogenetically broad comparison of NF-κB protein structure presented here, the presence of both RHD and ANK-repeat regions was the ancestral condition for NF-κB. More specifically, the presence of both RHD and ANK-repeat regions in the single NF-κB proteins of the sponge *Amphimedon* and most cnidarians, in addition to the NF-κB–like protein of *Capsaspora*, strongly supports the conclusion that the ancestral NF-κB protein possessed both RHD and ANK-repeat domains, as originally suggested by Huguet based only on data from triploblastic animals (1997). The ANK region appears to have been independently lost, or at least genetically separated, from NF-κB proteins in at least three independent lineages: on the line leading to *N. vectensis*, on the line leading to *Hydra*, and within the triploblastic animals, in the common ancestor of the Rel subfamily.

One novel finding of this analysis was the identification of a highly conserved motif in the N-terminal region of anthozoan cnidarians. Motif 1 was found at the N-terminus of NF-κB in corals, anemones, and the one representative corallimorph in the study. Ten positions in this motif, which spans 29 residues, were strictly conserved among the anthozoan cnidarians included in this study. This motif did not appear to correspond to any previously defined protein domain.

In humans, a key event in NF-κB signaling is the phosphorylation of IκB (or the ANK region of a p105-type protein) by an IKKα/IKKβ heterodimer or an IKKα homodimer. It is clear from our analysis that cnidarians possess a single IKKα/β protein, which is likely a direct descendant of the ancestral protein that gave rise to human IKKα and IKKβ. There is very strong conservation between the human and cnidarian proteins descended from this ancestral protein. For example, human IKKα and *Astrangia* IKKα/β share all of the same motifs (Figure 3-18), and within these motifs, there is strong conservation of residues involved in ATP binding (17/19 identical), polypeptide substrate binding (7/10 identical), and scaffold dimerization (9/14 identical). Based on the presence of the elements necessary for molecular interactions, we conclude that the IKK sequences from both taxa encode the ability to bind ATP and polypeptide substrates. Empirical support for conserved functionality of cnidarian and vertebrate IKKα/β comes from a study involving co-expression of an anemone IKKα/β and NF-κB in a human cell line (Mansfield et al., 2017). *Exaiptasia* IKKα/β phosphorylated *Exaiptasia* NF-κB to induce the proteolysis of the ANK region, which was followed by nuclear localization of an activated NF-κB. Wolenski et al. (2011) conducted a similar study on an IKK protein from the sea anemone *N. vectensis*, but in that case the protein under study was not IKKα/β, but rather an IKKε/TBK1 homolog.

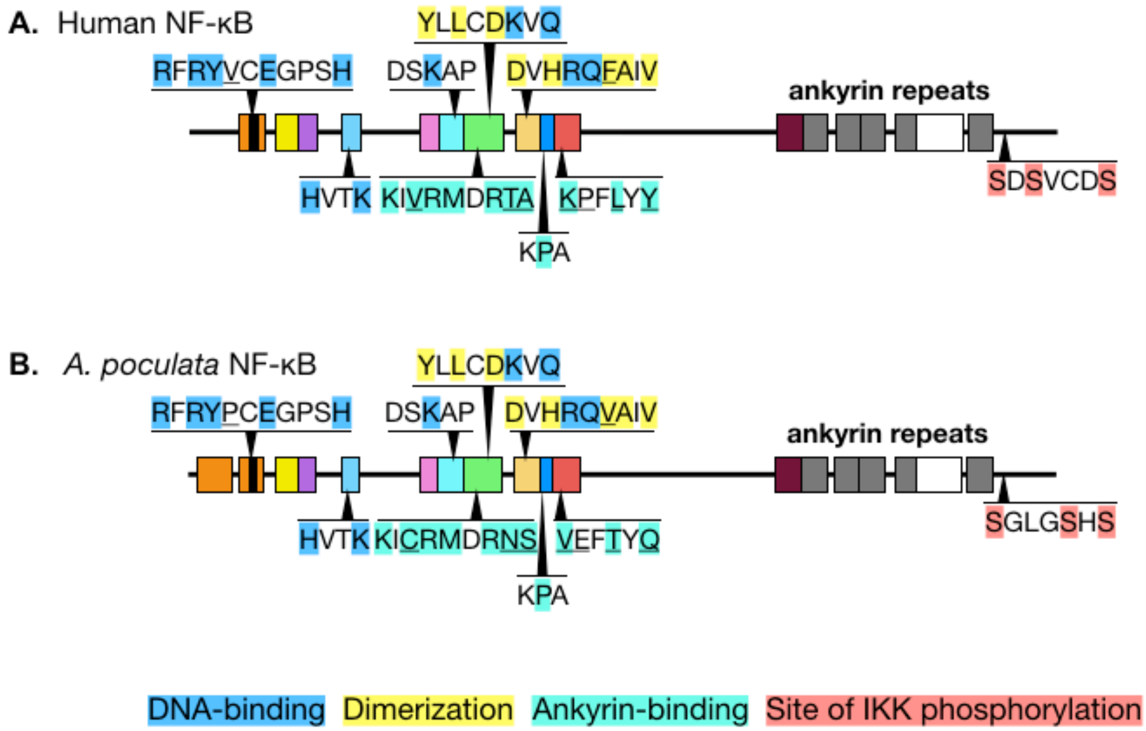


Figure 3-17. Comparison of Human and *A. poculata* NF-κB Motif Residues Conserved motifs identified by MEME are depicted as colored boxes. The width of each box is proportional to the length of the motif in amino acids. To convey the conservation of motif order across proteins, the inter-motif regions (black line segments connecting motifs) are not drawn to scale so that motifs are in register. The vertical black bar within motif 2 depicts the location of the DNA-binding loop. Pertinent sequences related to DNA binding, dimerization, ankyrin binding, and sites of IKK phosphorylation are highlighted in blue, yellow, cyan and burnt orange, respectively. Underlined residues represent differences between the human and *A. poculata* sequences. This figure was modified from Finnerty and Gilmore (2015) and Mansfield et al. (2017). This figure includes data presented in Figure 3-3.

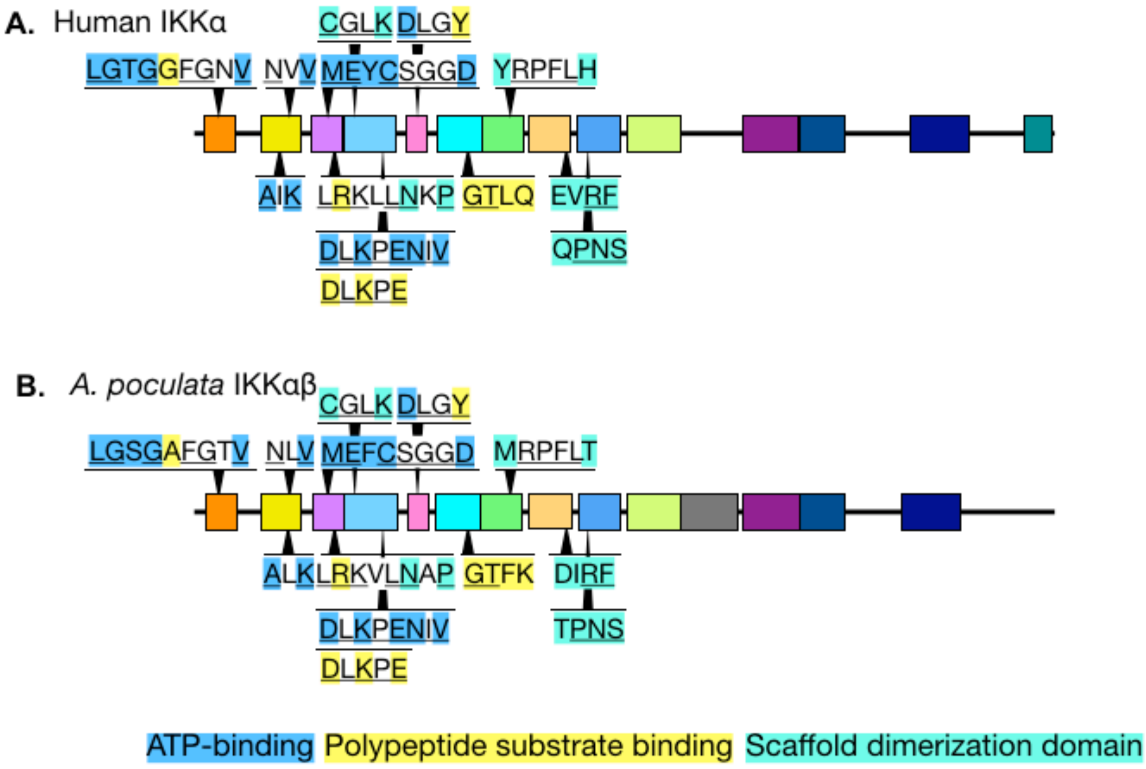


Figure 3-18. Comparison of Human and *A. poculata* IKKα/β Motif Residues
Conserved motifs identified by MEME are depicted as colored boxes. The width of each box is proportional to the length of the motif in amino acids. To convey the conservation of motif order across proteins, the inter-motif regions (black line segments connecting motifs) are not drawn to scale so that motifs are in register. Pertinent sequences related to ATP binding, polypeptide substrate binding, and the scaffold dimerization domain are highlighted in blue, yellow, and cyan, respectively. Underlined residues represent differences between the human and *A. poculata* sequences. This figure includes information presented in Figure 3-5.

In human NF-κB signaling, IKKα/IKKβ heterodimers or IKKα homodimers are activated by an upstream kinase, either NIK or TAK1. In the canonical pathway, TAK1 phosphorylates an IKKα/IKKβ/NEMO complex, while in the non-canonical pathway, NIK phosphorylates IKKα/IKKα (Figure 3-1). Based on our analyses, we conclude that cnidarians possess a clear ortholog of TAK1, but no clear ortholog of NIK except in *Exaiptasia*. *Astrangia* TAK1 reciprocally BLASTed to human TAK1 with an E value of 0. The NIK-like protein of *N. vectensis* failed to recover human NIK in a reciprocal BLAST, but rather recovered MAP3K5, a related serine-threonine kinase in humans. It therefore appears that there may not be a *bona fide* ortholog of NIK in neither *Astrangia* nor *N. vectensis*, but only in *Exaiptasia*.

Therefore, the more logical candidate for *in vivo* activation of IKKα/β in cnidarians is TAK1. TAK1 is known to phosphorylate IKKα/IKKβ/NEMO in humans (Clark et al., 2011). Although interestingly, murine B cells deficient in TAK1 still show the capacity for NF-κB activation (Sato et al., 2005), which could be a consequence of the recruitment of non-canonical signaling or autoactivation of IKK.

Given the diversity of kinases we identified in cnidarians (IKKα/β, TBK/IKKε, TAK1, NIK for *Exaiptasia* and NIK-like protein for *A. poculata* and *N. vectensis*), and the known functional repertoire of these kinases in other organisms, there are a number of other possible mechanisms whereby cnidarian NF-κB signaling could be activated. IKKα and IKKβ are known to participate in both trans- and autophosphorylation (Rothwarf & Karin, 1999, Hacker & Karin, 2006), and both can phosphorylate TBK/IKKε at serine (Ser)172 (Clark et al., 2011). IKKε and IKKα can induce degradation of IκB (by IKKε:

Boehm et al., 2007; Eddy et al., 2005; phosphorylation at Ser32 and Ser36 by IKKα: Senftleben et al., 2001) and drive NF-κB signaling.

Based on the presence of shared core NF-κB signaling elements, we hypothesize a simpler NF-κB signaling pathway in cnidarians that could reflect the situation found in the cnidarian-bilaterian ancestor (Figure 3-19). In this pathway, an NF-κB1–type homodimer is sequestered in the cytoplasm due to the ANK region blocking of the NLS. In this dimer, one of the NF-κB proteins may include the ANK region while the other could have undergone proteolytic removal of the ANK domain, akin to a human p105-p50 dimer, as described in Beinke and Ley (2004) and Gilmore (2006). The pathway would be activated when TAK1 phosphorylates an IKKα/β homodimer, which in turn phosphorylates the ankyrin-repeat region of NF-κB to target it for proteosomal degradation. Finally, the processed NF-κB homodimer, similar to human p50/p50, translocates into the nucleus to regulate transcription of target genes by binding to κB binding sites.

Of course, there may be multiple NF-κB signaling pathways in cnidarians as in other model systems (Oeckinghaus, 2011; Figure 3-1), but the pathway suggested here, unlike the canonical or non-canonical pathway, is consistent with the presence of NF-κB signaling components found in cnidarians and known pathways found in bilaterian model systems. Proving the existence of the proposed pathway will require the demonstration of (1) the presence of pre-processed NF-κB homodimers (p105/p50-type) in the cytoplasm of cnidarian cells (e.g., using “pull-down” assays), and (2) the ability of cnidarian TAK1 to phosphorylate an IKKα/β homodimer, and for this event to trigger the eventual nuclear localization of a processed NF-κB homodimer.

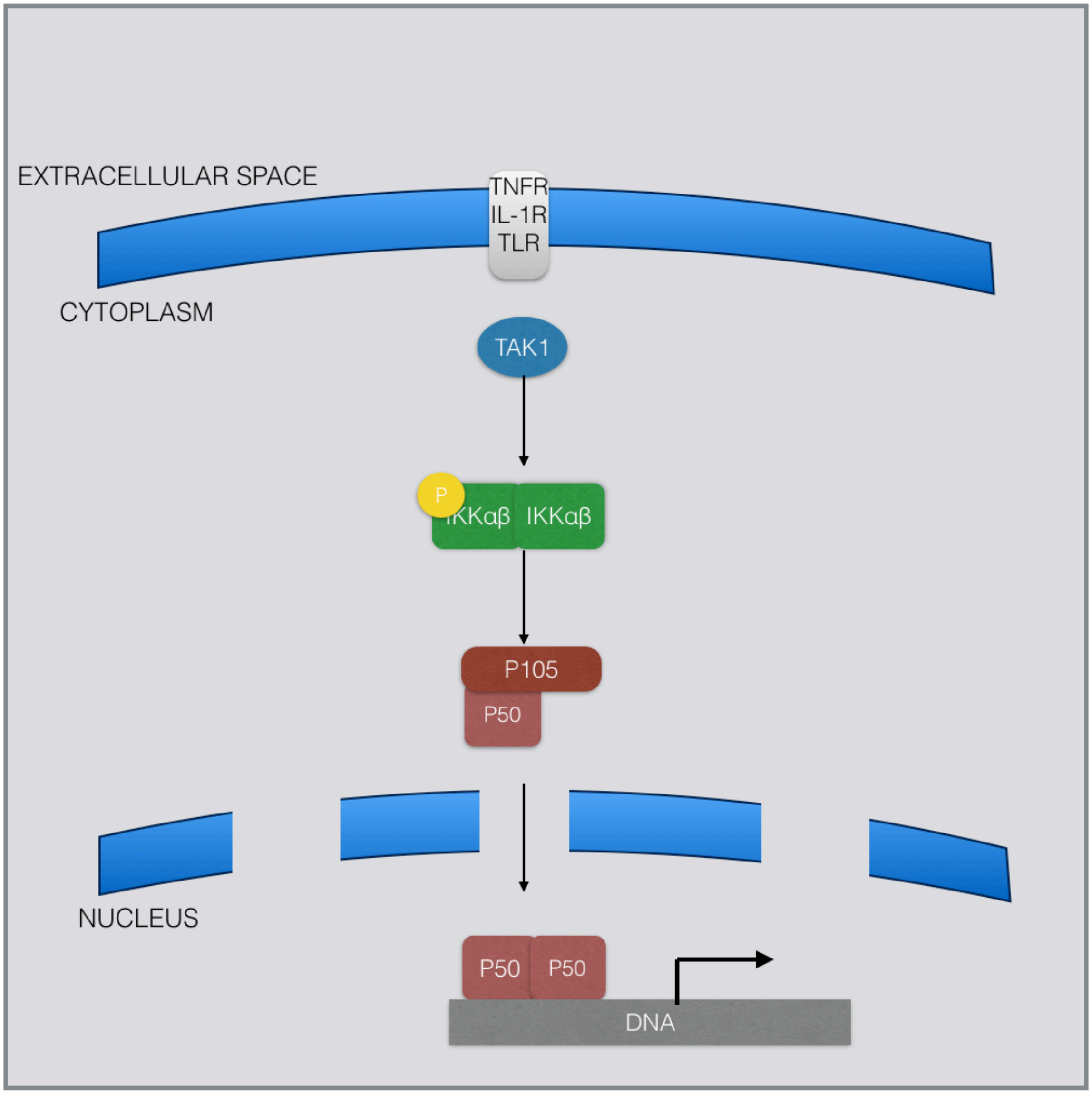


Figure 3-19. Proposed NF-κB Signaling Pathway in Cnidarians
A putative NF-κB signaling pathway is proposed based on data generated from this study. Cnidarians may also employ other variations of the NF-κB signaling pathway as seen in mammals (Oeckinghaus, 2011; Figure 3-1). Abbreviations are as follows: tumor necrosis factor receptor (TNFR), interleukin-1 receptor (IL-1R), Toll-like receptor (TLR), transforming growth factor-beta activating kinase (TAK1), inhibitor of kappa B kinase (IKK), deoxyribonucleic acid (DNA).

3.6.3 The SOD Complement of Anthozoan Cnidarians

The data presented here reveal a relatively rich complement of SOD proteins in cnidarians relative to other animal phyla. For example, while humans possess two CuZnSODs (SOD1 and SOD3) and a single MnSOD (SOD2; reviewed in (Zelko et al., 2002), *A. poculata* and *N. vectensis* each express three CuZnSOD proteins and two MnSODs (This study; Tarrant et al., 2014), more than any other taxon sampled in this study. Based on the phylogeny depicted in Figure 3-15, it appears that the anthozoan CuZnSOD1 and CuZnSOD2 are most closely related to human SOD1, while the anthozoan CuZnSOD3 is most closely related to human SOD3.

In mammals, the diversification of SOD proteins is associated with different subcellular localization of the three SOD paralogs. SOD1 localizes principally to the cytoplasm, but also to the mitochondria (Kawamata & Manfredi, 2008), SOD2 localizes in the mitochondria, and SOD3 localizes in the extracellular space (Zelko et al., 2002). The pattern of subcellular localization has direct consequences for the biological function of a given SOD isoform; for example, in humans, SOD1 may protect against ROS generated by the respiratory chain on the outer side of the inner mitochondrial matrix, whereas SOD2 would be unable to counteract these ROS because of its localization to the mitochondrial matrix (Kawamata & Manfredi, 2008). Assuming that the pattern of subcellular localization was already established in the common ancestor of cnidarians and humans, cnidarians appear to have duplicated a SOD gene expressed principally in the cytoplasm (like human CuZnSOD1) and a SOD gene expressed principally in the mitochondrion (like human MnSOD, also known as SOD2).

Given the differing expression patterns of SOD proteins in other animals, and the impact of subcellular location on function, data on subcellular localization of cnidarian SOD genes may prove critical to understanding the diversification of cnidarian SOD genes. A number of prior studies have shown that the multiple SODs of anthozoan cnidarians can exhibit different subcellular localization and differences in tissue-specific expression. For example, Richier et al. identified seven bands of SOD activity in the photosymbiotic sea anemone *A. viridis* (Richier et al., 2003, Richier et al., 2005). The single CuZnSOD band was localized to the cytoplasm of endodermal and ectodermal cells, but absent from the mitochondria or zooxanthellae. Four separate bands of MnSOD activity were detected, but contrary to expectations, only one of these bands was restricted to the mitochondria (of both endodermal and ectodermal cells). The other three MnSOD bands were localized to non-mitochondrial compartments of the endoderm and to the zooxanthellae. Two FeSODs, presumably encoded by the symbiont, were localized to the zooxanthellae and the endodermal cells. The authors of the Richier et al. studies suggest that greater diversity of SOD classes “may account for the high tolerance of symbiotic cnidarians to hyperoxia and hypoxia/hyperoxia transitions.” However, the pattern of SOD localization observed in the Richier et al. studies and others suggests that the symbiont plays a key role in mitigating the effect of ROS generated by photosynthesis, and not all host-encoded SOD isoforms are well positioned to counteract ROS generated by the symbiont. For example, an immunocytochemical study on *A. viridis*, the same anemone investigated in the Richier et al. study (2003), reported CuZnSOD being particularly pronounced in the cnidae where its function would presumably be unrelated to symbiosis (Hawkridge, 2000).

A more direct test of the role for specific SOD isoforms during photosymbiosis is to compare SOD activity in the symbiotic vs. aposymbiotic states of facultatively symbiotic species. In the sea anemone model, *Anthopleura*, Rodriguez-Lanetty and colleagues found that one particular CuZnSOD was significantly decreased in expression in the symbiotic state compared to the aposymbiotic state (2006). In the symbiotic sea anemone *Anemonia viridis*, CuZnSOD activity was also decreased, but other SODs, e.g., FeSODs and MnSODs, showed increased activity (Richier et al., 2005). These data suggest that SOD expression in response to symbiosis is likely to vary among SOD proteins; this is the pattern we observed in our comparison of gene expression in symbiotic vs. aposymbiotic *A. poculata* (Chapter 4).

3.7 Conclusions and Future Directions

To identify candidate genes that may be involved in symbiosis, we mined the *A. poculata* and *N. vectensis* transcriptomes for components of the NF-κB signaling pathway and members of the SOD gene family. After recovering candidate transcripts for core elements of the NF-κB signaling pathway, we evaluated the predicted proteins for the presence of conserved motifs and residues of known functional significance. Conservation of these motifs and residues support the functional conservation of these genes. By extending the comparisons to other metazoan phyla and closely related outgroups to the animals, we predicted where critical pathway functions first appeared in evolution and discriminated primitive from derived traits in the studied model system (*A.*

poculata). As the NF-κB signaling components of early animals do not conform strictly to either the canonical or non-canonical signaling pathway of mammals, the data presented here suggest that the distinct pathways evolved relatively recently, and within the vertebrate lineage specifically. The ancestral NF-κB pathway was neither the canonical pathway nor the non-canonical pathway. Thus, future studies could explore how to the NF-κB pathway is activated in cnidarians.

In our investigation of the SOD gene family, we determined that the same complement of paralogs was present in the transcriptome of *A. poculata*. We recovered candidate transcripts for all previously identified SODs known to be present in *N. vectensis* and putative orthologs of CCS and SODs in *A. poculata*. We identified SOD gene duplications over the course of animal evolution. The anthozoan cnidarians possess three distinct CuZnSOD proteins and two distinct MnSODs, more than any other taxon sampled in this study.

This body of bioinformatic work provides a foundation for future cellular and molecular studies to characterize the structure and function of the putative NF-κB pathway and SOD proteins. With respect to NF-κB signaling, future studies should investigate the activation and output of the NF-κB signaling pathway in cnidarians, with a focus on the role of particular kinases in signal transduction. In terms of studying the evolutionary association between RHD and ANK domains in NF-κB proteins, cnidarians provide two additional opportunities to study the consequence of splitting the ANK domain from an ancestral NF-κB protein that possessed both RHD and ANK domains, i.e., within the Edwardsiid anemones in the line leading to *Nematostella*, and in freshwater hydrozoan *Hydra*. With respect to the SODs, it will be important to determine how the spatial expression and biological function differs among the three CuZnSOD paralogs and two MnSOD paralogs of cnidarians. Finally, the analyses presented here will aid in investigations of the roles that NF-κB signaling and SOD genes play in the maintenance and regulation of cnidarian photosymbiosis.

3.8 Acknowledgements

The identification of conserved motifs in the NF-κB proteins of metazoans and closely related outgroups was originally performed by John Finnerty (Finnerty and Gilmore, 2015). I located these motifs in a predicted *Astrangia* NF-κB protein based upon an assembled transcript I mined from the *Astrangia* transcriptome. Simplified versions of the NF-κB MEME analysis and of the IKK phylogeny are published in Mansfield et al. (2017).

CHAPTER 4: TRANSCRIPTIONAL DIFFERENCES BETWEEN SYMBIOTIC AND APOSYMBIOTIC ASTRANGIA POCULATA UNDER CONTROL CONDITIONS AND WITH HYDROGEN PEROXIDE EXPOSURE

4.1 Introduction

The molecular cross-talk between host and symbiont during cnidarian photosymbiosis can be studied by comparing gene expression in symbiotic versus aposymbiotic cnidarians. Currently, how photosymbiosis impacts the expression or activity of genes in corals is largely unknown. Studying the impact of photosymbiosis on gene expression is not experimentally tractable in most tropical corals because they engage in an obligate symbiosis with Symbiodiniaceae, making it impossible to establish the baseline pattern of gene expression in an unstressed aposymbiotic host. Bleached corals are always in a state of nutritional stress.

A number of prior studies have explored the effects of hosting Symbiodiniaceae on gene expression or gene activity in cnidarians, but these studies have limited relevance to the question of how symbiosis affects scleractinian corals because (1) they were performed on taxa that are distantly related to corals, (2) photosymbiosis was confounded with other differences between samples, and/or (3) they only examined the expression or activity of a few candidate genes. Below I review these studies to illustrate their limitations, but also to develop expectations for how gene expression might be expected to differ between symbiotic and aposymbiotic *Astrangia poculata*.

Ishikawa et al., studied the effects of stable symbiosis and unstable symbiosis in *Hydra viridissima* and *Hydra vulgaris,* respectively (2016). The stably symbiotic *H. viridissima* had greater expression of the antioxidant ascorbate peroxidase and appeared to be more resistant to both oxidative stress and starvation (Ishikawa et al., 2016). In symbiotic *H. viridissima,* genes related to the mitochondria and electron transport chain (ETC) showed decreased expression compared to *H. vulgaris*. Decreased expression of these genes suggests decreased endogenous production of reactive oxygen species (ROS) by the mitochondrial ETC. However, these findings are of limited relevance to photosymbiosis in corals because (1) the ancestor of *Hydra* (class Hydrozoa) diverged from the ancestor of corals (class Anthozoa) more than 540 million years ago, (2) the photosynthetic symbiont *Chlorella* (phylum Chlorophyta) is also distantly related to the photosynthetic symbiont in corals (phylum Dinoflagellata), and (3) the Ishikawa et al. study compared two different species, so differences in gene expression could be attributable to differences between species and not simply between alternative symbiotic states (2016).

In a comparison of two closely related anemones, symbiotic *Anemonia viridis* expressed a greater diversity of superoxide dismutase (SOD) isoforms (1 CuZnSOD, 4 MnSODs, and 2 FeSODs), higher SOD activity (FeSOD and MnSODs), and appeared to be more resistant to oxidative and thermal stress than aposymbiotic *Actinia (schmidti) mediterranea,* which expressed 4 CuZnSODs and 1 MnSOD isoforms (Richier et al., 2015). However, these findings are of limited relevance to photosymbiotic corals because (1) the ancestor of anemones (order Actinaria) diverged from the ancestor of corals (order

Scleractinia) more than 200 million years ago and (2) though the two species compared are members of the same family (Actinnidae), differences in protein expression could be attributed to differences in host species and not differences in symbiotic state.

In experimentally bleached sea anemones, *Exaiptasia pallida*, Mansfield et al. (2017) found that RNA levels, protein levels, and DNA-binding activity of the transcription factor NF-κB were significantly higher than in symbiotic individuals. Furthermore, introduction of Symbiodiniaceae into naïve *E. pallida* larvae resulted in a decrease in NF-κB expression, which the authors suggest could possibly support a role for innate immunity in regulating photosymbiosis (Mansfield et al., 2017). In the same species, Lehnert et al. (2014) found differential expression of apoptotic genes in symbiotic versus aposymbiotic *E. pallida,* with 5 transcripts expressed at lower levels and 8 transcripts expressed at higher levels in symbiotic individuals. These studies have limited relevance to photosymbiosis in corals because (1) the ancestor of anemones (order Actinaria) diverged from the ancestor of corals (order Scleractinia) more than 200 million years ago and (2) the *E. pallida* in the Mansfield et al. study were experimentally bleached with menthol and heat so a change in symbiotic state may be conflated with the stress from bleaching (2017).

Yuyama and coworkers compared gene expression in *Acropora tenuis* larvae both before and after the acquisition of symbionts. The introduction of Symbiodiniaceae was associated with higher expression of the antioxidant, Na-dependent ascorbic acid and greater expression of anti-apoptotic protein ubiquitin carboxy terminal hydrolase (Yuyama et al., 2011) as measured by high coverage gene expression profiling (HiCEP).

However, because this study focused only on the larval stage, gene expression changes related to symbiotic state are conflated with gene expression changes related to development.

The aforementioned studies all bear indirectly on the question of how photosymbiosis affects gene expression in corals, but none presents an ideal model for addressing this question. Ideally, comparisons would involve a single species of scleractinian coral that exists in naturally symbiotic and aposymbiotic states, where the comparison between symbiotic states is not confounded by differing levels of organismal stress or different developmental states. Additionally, gene expression should be characterized at a transcriptome-wide level.

As described in Chapter 1, the northern star coral *A. poculata* is an ideal model system for studying transcriptional changes in corals because it is a facultatively symbiotic coral and lives stably in either symbiotic or aposymbiotic states i.e. it is unstressed in its aposymbiotic state. It should be noted that *A. poculata's* stably aposymbiotic state is not a good model for bleaching *per se*, because bleaching is a stress response. A prior study compared gene expression in 4 symbiotic and 2 aposymbiotic *A. poculata* using RNA-seq (Burmester, 2017). While a transcriptome-wide comparison of two distinct metabolic strategies might be expected to identify hundreds or thousands of differentially expressed genes, her study identified only two significantly differentially expressed genes (false discovery rate [FDR] $p < 0.003$), both of which can be tenuously implicated in innate immunity based on their sequence similarity to genes that have been functionally annotated in other model systems. The first, a transcript encoding a Notch-like protein, was increased in expression in symbiotic corals compared to aposymbiotic corals; the second, a transcript encoding olfactomedin 2A, was decreased in expression in symbiotic corals compared to aposymbiotic corals.

Due to the fact that only two coral genes were detected in the Burmester study, we suspected that the ability to detect differentially expressed genes could have been compromised by a lack of sufficient replicates (4 symbiotic and 2 aposymbiotic *A. poculata*) and/or limitations of the reference transcriptome that was used to map the sequencing reads (2017; Chapter 2). While the Burmester transcriptome exhibited excellent recovery of universal metazoan genes (86.9% complete orthologs), it comprised relatively short contigs overall, judging by the low n50 (789 nucleotides). This suggests the presence of many partially assembled contigs, which would reduce the power to detect differential gene expression. Of note, the Burmester transcriptome lacked a full-length NF-κB transcript, one of the focal genes in the present study. The new *A. poculata* assembly described in Chapter 2 exhibits improved recovery of universal metazoan genes (98.3% complete orthologs) and a 2.7-fold increase in n50 (1789 vs. 789 nucleotides). The presence of more fully-assembled transcripts would increase the power of differential expression analysis. Importantly, the new *A. poculata* assembly recovered a full-length NF-κB contig (Chapter 3).

Based on the results generated in the Burmester study as well as the other cnidarian systems described above, we can frame hypotheses about the expression of particular genes in symbiotic vs. aposymbiotic corals. Specifically, we would expect: (1) differences in the expression of genes involves in innate immunity, with NF-κB expression being reduced in symbiotic corals; (2) differences in the expression of genes involved in apoptosis; and (3) an increase in the expression of antioxidant enzymes, such as SOD, ascorbate peroxidase, and Na-dependent ascorbic acid, in symbiotic corals.

In addition to the findings from these gene expression studies, Lin et al. (2015) identified genes present in the genomes of both the coral *Acropora digitifera* and the coral symbiont *Symbiondinium kawagutii* "that can potentially be involved in symbiotic material exchange and collaborative combat against stressors." These genes, which were often lacking in the sequenced genomes of the non-symbiotic cnidarians *Nematostella vectensis* and *Hydra magnipapillata*, include amino acid transporter, arsenite methyltransferase, arsenite transporter, bicarbonate transporter, carbonic anhydrase, folate transporter, glucose transporter, glutamate synthase, lipid transporter, metal ion transporter, phosphate transporter, phospholipid transporting ATPase, riboflavin transporter, sugar transporter, sulfate transporter, urease, lectins and nitrite transporter. As these genes are all presumably required for symbiosis in *A. poculata*, we would expect all 18 of these genes to be expressed at higher levels in symbiotic *A. poculata*. However, as they are encoded by both the coral genome and symbiont genome, they could be expressed by either partner or both partners.

As outlined in Chapter 2, to determine how the symbiotic state of *A. poculata* impacts transcription, we isolated RNA from individual polyps, generated libraries for RNA sequencing on the Illumina platform, mapped the trimmed sequencing reads to the reference transcriptome described in Chapter 2, and conducted differential expression analysis. This analysis identified 273 significantly differentially expressed coral genes between symbiotic vs. aposymbiotic corals. Furthermore, the symbiotic state was associated with the increased expression of one particular SOD transcript, as well as IKKε, a potential activator of NF-κB. Our data do not support the hypothesis that NF-κB expression is decreased in symbiotic *A. poculata*.

4.2 Experimental Design

4.2.1 Data Generation

All aspects of data generation, including coral collection, library preparation, sequencing, transcriptome assembly, and transcriptome parsing were described in Chapter 2. For the differential expression study described here, eight *Astrangia* colonies were sampled, all from Fort Wetherill, RI. The colonies sampled included four symbiotic colonies and four aposymbiotic colonies (Figure 2-4; samples corresponding to blue arrows from symbiotic and aposymbiotic colonies were examined). From the symbiotic colonies, a total of eight polyps were sampled (two polyps from each of four different symbiotic colonies). However, high-quality RNA was obtained from only four of these symbiotic polyps, one from each of the four symbiotic colonies. From four aposymbiotic colonies, we sampled a total of eight polyps (two per colony). High-quality RNA was extracted from all 8 of the aposymbiotic polyps.

4.2.2 Read Mapping

All 12 of the sequenced libraries were mapped to the holobiont assembly using (1) default, (2) stringent and (3) very stringent parameters of CLC Genomics WorkBench

7.0.4 (Qiagen Bioinformatics) as described by Lehri et al. (2017). The default parameters were as follows: match score = 1, mismatch cost= 2, insertion cost = 3, deletion cost = 3, length fraction = 0.5, similarity fraction = 0.8, maximum number of hits for a read = 30. The “stringent” and “very stringent” parameters differed from the default parameters with respect to length fraction (0.8 or 0.9, respectively) and similarity fraction (0.9 or 1.0, respectively). After exploring the effects of varying mapping stringency, the differential expression analysis was ultimately conducted using very stringent read mapping parameters.

4.2.3 Differential Expression Analysis

Differential expression analysis was performed using the edgeR package on CLC Genomics WorkBench. edgeR uses a negative-binomial statistical model to estimate dispersion between libraries’ global gene expression; it is optimized for small sample sizes (Robinson et al., 2010). First, the sequencing reads from all eight aposymbiotic and all four symbiotic polyps were mapped to the holobiont transcriptome. I then made the following three comparisons: (1) all four symbiotic polyps vs. all eight aposymbiotic polyps, (2) all four symbiotic polyps vs. seven aposymbiotic polyps (excluding Apo4c, which exhibited much higher expression of symbiont transcripts than the other seven aposymbiotic polyps), and (3) all four symbiotic polyps versus the polyp from each aposymbiotic colony exhibiting lower expression of Symbiondiniaceae transcripts ($n = 4$). Genes were regarded as significantly differentially expressed between treatments if the Log_2 fold change (FC) was ≤ -2.0 or ≥ 2.0 with a false discovery rate (FDR) $p \leq 0.05$.

After identifying differentially expressed genes in each of the three comparisons described above, I subsequently checked the differentially expressed contigs to confirm their taxonomic affinity, *i.e.*, coral host genome or symbiont genome.

To determine if overall differences in host and/or symbiont gene expression could distinguish symbiotic from aposymbiotic polyps, we ran principal components analyses (PCAs) based on the expression levels of all genes (i.e., not just differentially expressed genes) using CLC Genomics Workbench. To determine if the samples cluster based on the expression of differentially expressed genes, we ran a hierarchical clustering of samples using Pearson's correlations and average linkages between contigs' reads per kilobase of transcript per million mapped reads (RPKM) (Babicki et al., 2016). To determine which genes and pathways were differentially expressed, we used BLAST2GO Pro to associate specific Gene Ontology (GO) categories with the differentially expressed contigs. Finally, we examined the expression levels of candidate genes and pathways that were previously shown to be differentially expressed in response to symbiotic state, including genes in the nuclear factor-kappa B (NF-κB) signaling pathway as well as the superoxide dismutase (SOD) gene family.

4.3 Results

4.3.1 Read Mapping

As expected, there was a clear difference between symbiotic and aposymbiotic polyps in the percentage of sequencing reads that mapped to coral versus symbiont contigs (Table 4-1). In the aposymbiotic samples, an average of 23.5-23.6% of reads map to a coral contig in the reference transcriptome (depending on the stringency of read mapping), while 0.7-0.8% of reads map to a symbiont contig. By contrast, in the symbiotic samples, an average of 16.3-17.8% of reads map to a coral contig, while 7.7-10.9% of reads map to a symbiont contig. The average fraction of reads mapping to a symbiont contig differed significantly between aposymbiotic and symbiotic polyps (single-factor analysis of variance, DF = 1, MS = 145.63, f = 5.00, p = 0.049). Varying the mapping stringency had only a slight effect on read mapping, in most cases altering the percentage of reads mapping to coral or symbiont contigs by 0.0-0.3%. Among the aposymbiotic polyps, Apo4c exhibited an unusually high percentage of reads mapping to symbiont contigs (1.9-2.9%), a value greater than the average plus twice the standard deviation under all three stringency levels. This suggests that polyp Apo4c falls along a continuum between the aposymbiotic and symbiotic states. For this reason, in subsequent analyses, I investigated the effects of removing this outlier.

There was a greater number of differentially expressed coral genes as the stringency in read mapping increased from low (default parameters) to high (very stringent parameters; Table 4-2). The differential expression analysis was therefore conducted using very stringent read mapping parameters.

Table 4-1. Read Mapping Statistics for Symbiotic and Aposymbiotic Polyps

		% Map to Coral by Stringency			% Map to Sym. by Stringency		
Colony	Polyp	Low	Medium	High	Low	Medium	High
Apo1	c	19.1	19.2	19.3	0.8	0.8	0.9
	d	20.9	21.1	20.8	0.4	0.4	0.3
Apo2	c	23.3	23.5	24.7	0.7	0.7	0.7
	d	24.3	24.5	25.6	0.4	0.4	0.3
Apo3	c	28.5	28.7	28.6	0.2	0.2	0.2
	d	24.0	24.1	24.3	0.5	0.5	0.5
Apo4	c	17.7	17.6	15.2	1.9	1.9	2.9
	d	29.9	30.2	30.1	0.3	0.3	0.2
	Avg±sd	23.5±4.3	23.6±4.3	23.6±4.9	0.7±0.5	0.7±0.5	0.8±0.9
Sym1	c	11.3	11.6	10.0	5.0	5.1	6.9
Sym2	c	15.2	15.2	12.2	14.9	15.0	21.2
Sym3	c	21.6	21.7	21.5	6.3	6.3	8.7
Sym4	c	22.4	22.5	21.5	4.6	4.6	6.8
	Avg±sd	17.6±5.3	17.8±5.2	16.3±6.1	7.7±4.9	7.8±4.9	10.9±6.9

Table 4-2. Number of Differentially Expressed Coral Genes According to Read Mapping Stringencies (FDR p < 0.05)

Low Stringency	Medium Stringency	High Stringency
277	273	308

4.3.2.1 Clustering of Samples Based on Overall Gene Expression

Based on overall expression of transcripts from the host transcriptomes, a PCA did not clearly discriminate polyps derived from symbiotic colonies vs. polyps derived from aposymbiotic colonies (Figures 4-1A). However, based on the overall expression of transcripts from the symbiont transcriptome, a PCA did clearly discriminate polyps derived from symbiotic colonies vs. polyps derived from aposymbiotic colonies (Figures 4-1B and 4-2B). Pairs of polyps derived from the same aposymbiotic colony tended to cluster together with respect to host gene expression (Figure 4-1A) but not with respect to symbiont gene expression (Figure 4-1B).

Upon removal of sample Apo4c, the same general pattern holds (Figures 4-2). The symbiotic and aposymbiotic polyps cannot be differentiated based upon overall expression of host transcripts (Figure 4-2A), but they can be differentiated based upon overall expression of symbiont transcripts (Figure 4-2B).

4.3.2.2 Quantification of Differentially Expressed Coral Transcripts

The number of significantly differentially expressed coral transcripts changed depending on which of the eight aposymbiotic samples were included in the comparison (Table 4-3). Comparing all symbiotic polyps (n= 4) vs. all aposymbiotic polyps (n = 8) resulted in the identification of 308 significantly differentially expressed coral transcripts. Removal of Apo4c from symbiotic sample resulted in an increased number of differentially expressed genes: 352 vs. 308. I also explored using only four aposymbiotic polyps, one from each aposymbiotic colony. For this comparison, I intentionally selected the member of each pair of aposymbiotic polyps obtained from the same colony that exhibited the lower level of symbiont expression based on the read mapping results shown in Table 4-1. This comparison, which included all four symbiotic polyps and the following four aposymbiotic polyps: Apo1d, Apo2d, Apo3c and Apo4d, resulted in a sharp reduction in the number of differentially expressed genes, from 308 or 352, down to 58 (Table 4-3). All subsequent analyses were based upon the second comparison, using all four symbiotic polyps versus seven of the eight aposymbiotic polyps (excluding sample Apo4c).

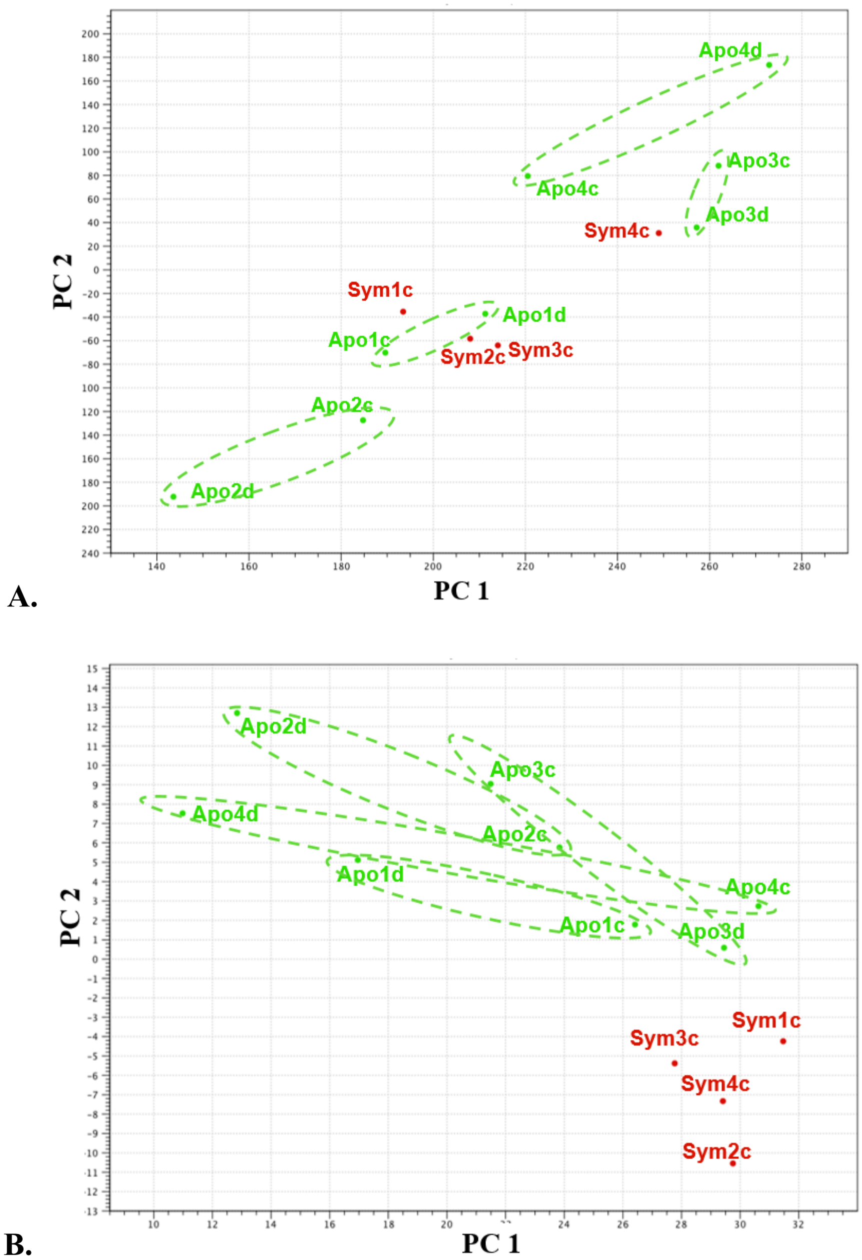


Figure 4-1. Principal Components Analysis (PCA) of Gene Expression Levels in Symbiotic and Aposymbiotic Polyps

PCAs were performed on the expression of (**A**) all 43,224 contigs in the host transcriptome and (**B**) all 39,889 contigs in the symbiont transcriptome. Red indicates symbiotic polyps (n=4) and green indicates aposymbiotic polyps (n=8). Dashed lines encircle polyps derived from the same colony. In (**A**), PC1 accounts for 65% of the variation and PC 2 accounts for 13%. In (**B**), PC 1 accounts for 78% of the variation and PC 2 accounts for 6%.

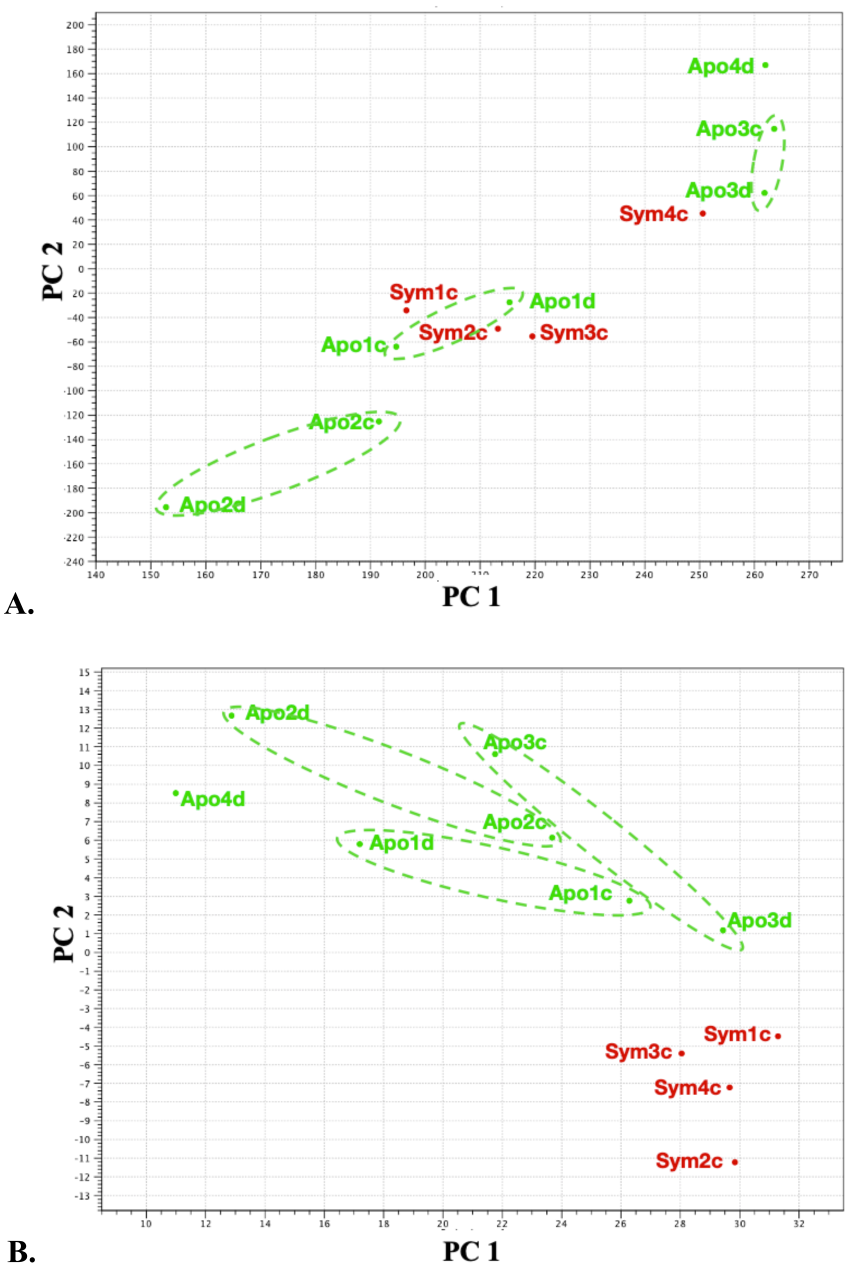


Figure 4-2. PCA of Gene Expression Levels in Symbiotic and Aposymbiotic Polyps Minus Apo4c

PCAs were performed on the expression of (**A**) all 43,224 contigs in the host transcriptome and (**B**) all 39,889 contigs in the symbiont transcriptome. Red indicates symbiotic polyps (n=4) and green indicates aposymbiotic polyps (n=7). Dashed lines encircle polyps derived from the same colony. In (**A**), PC1 accounts for 64% of the variation and PC 2 accounts for 13%. In (**B**), PC 1 accounts for 77% of the variation and PC 2 accounts for 8%.

Table 4-3. Number of Differentially Expressed Coral Genes

Symbiotic (n = 4) vs. Aposymbiotic (n = 8)	Symbiotic (n = 4) vs. Aposymbiotic (n = 7)	Very Symbiotic (n = 4) vs. Very Aposymbiotic (n= 4)
308	352	58

4.3.3 Effects of Symbiosis on Gene Expression

When the sequencing reads from four symbiotic and seven aposymbiotic polyps (minus Apo4c) were compared, 352 putative coral transcripts were differentially expressed, and 21,496 putative symbiont contigs were differentially expressed (Log_2 FC ≥ 2.0 or ≤ -2.0; FDR $p \leq 0.05$). With respect the differentially expressed coral transcripts, 244 were expressed at higher levels in symbiotic polyps relative to aposymbiotic polyps, and 108 were expressed at lower levels. With respect to the differentially expressed symbiont transcripts, the large majority were expressed at higher levels in symbiotic polyps relative to aposymbiotic polyps (21,483 vs. 13).

4.3.3.1 Differentially Expressed Features

As described in Chapter 2, we used BLAST2GO to annotate all of the contigs in the assembly (Chapter 2). Of the 352 differentially expressed genes in the coral-enriched transcriptome, 338 (96.0%) had significant BLAST hits. For each of these 338 sequences, we examined the species associated with the top BLAST hits to confirm their identity as coral transcripts (Figure 4-3A). For 251 of these 338 contigs, the top BLAST match was to a sequence from another cnidarian, either another coral (*A. digitifera, A. millepora, Astrangia sp., or Stylophora pistillata*; n=164) or the sea anemones *Nematostella vectensis* or *Exaiptasia pallida* (n=87; Figure 4-3B). Of the remaining 87 differentially expressed contigs that produced BLAST hits, 1 returned a top hit to a sequence from Symbiodiniaceae. The remaining 86 contigs returned top hits to sequences other than Symbiodiniaceae and Cnidaria. As these 87 sequences were possibly from contaminating symbiotic species and not *A. poculata*, we did not consider their gene ontology further. We also identified 22 putative coral genes among the differentially expressed symbiont transcripts that appeared to be *bona fide* coral genes based on the BLASTs we conducted (i.e., the top ~5-30 hits were to sequences from other cnidarians; Figure 4-3 C, D). We considered all 273 of these putative coral contigs' expression and gene ontologies further.

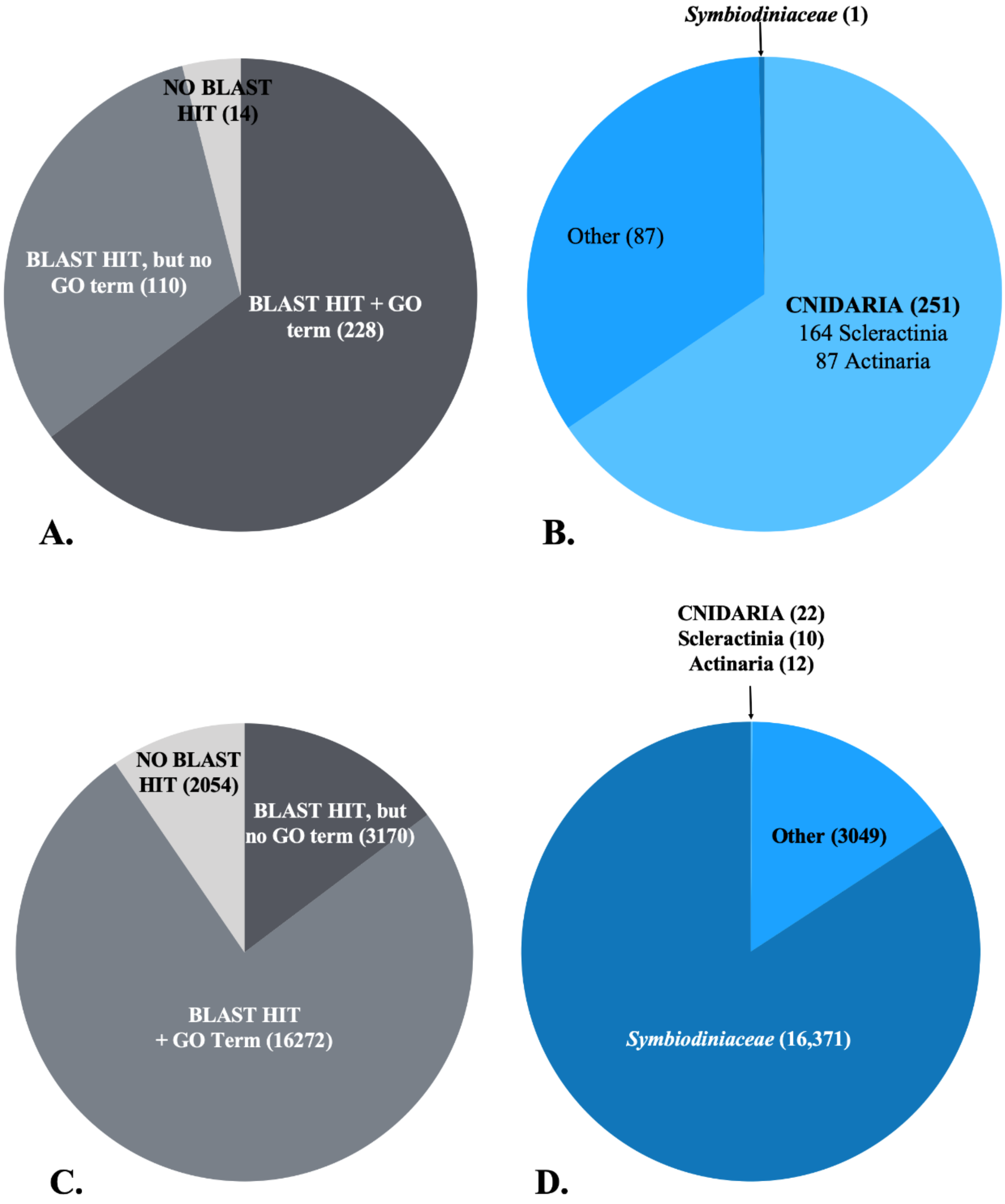


Figure 4-3. Differentially Expressed Contigs Producing BLAST Hits
(**A**) 338 of 352 presumptive coral contigs that are differentially expressed in symbiotic vs. aposymbiotic corals produced BLAST hits, and the taxonomic source of the top BLAST hit is summarized in (**B**). (**C**) 19,442 out of 21,496 presumptive Symbiodiniaceae contigs that are differentially expressed in symbiotic vs. aposymbiotic corals produced BLAST hits, and the taxonomic source of the top BLAST hit is summarized in (**D**).

4.3.3.2 Differential Expression of Genes

In a hierarchical clustering analysis of the 273 differentially expressed coral contigs across all 11 samples, the symbiotic samples (n=4) did not group together to the exclusion of the aposymbiotic samples (n=7; Figure 4-4). The tightest clustering was exhibited by pairs of aposymbiotic polyps derived from the same colony: Apo1c/1d, followed by Apo2c/2d, and finally Apo3c/3d. Aside from the pairs of samples derived from the same source colony, the next tightest clustering of samples involved four of the aposymbiotic samples (Apo1c, 1d, 2c, 2d,) followed by three of the four symbiotic samples (Sym2c, 3c and 4c). Even among the most tightly clustered contigs, the heat-map showed that no single gene consistently exhibits higher than average expression across all four symbiotic colonies or across all seven aposymbiotic colonies (Figure 4-4).

For the 273 differentially expressed contigs with top BLAST hits to Cnidaria, the most highly represented GO terms in the Biological Process category are shown in Figure 4-5. Nearly half of the putative coral contigs (130/273) had GO terms assigned to them and several contigs had multiple GO category designations. The most common GO terms under Biological Processes were “cellular protein metabolic processes” and “gene expression” (Figure 4-5). A more detailed breakdown of the gene ontology of differentially expressed coral genes is presented below.

The top five GO categories with the greatest number of differentially expressed genes are depicted in Figure 4-6: “cellular protein metabolic process”, “gene expression”, “cellular nitrogen compound biosynthetic process”, “cellular macromolecule biosynthetic process” and “macromolecule biosynthetic process”. As it turns out, many of these GO categories share numerous differentially expressed genes in common, including elongation factor Tu, interferon regulatory factor 2, ubiquitin-like protein FUB1, DNA-directed RNA polymerase II subunit RPB4, and seven ribosomal proteins. The fold-change in gene expression for genes in all five GO categories are summarized in Figure 4-6. There was a clear trend for these ribosomal proteins, as 6/7 of them were increased in expression in symbiotic vs. aposymbiotic polyps (Figure 4-6).

Below, I examine the expression of genes that have previously been implicated in photosymbiosis, including core components of the NF-κB signaling pathway and antioxidant enzymes.

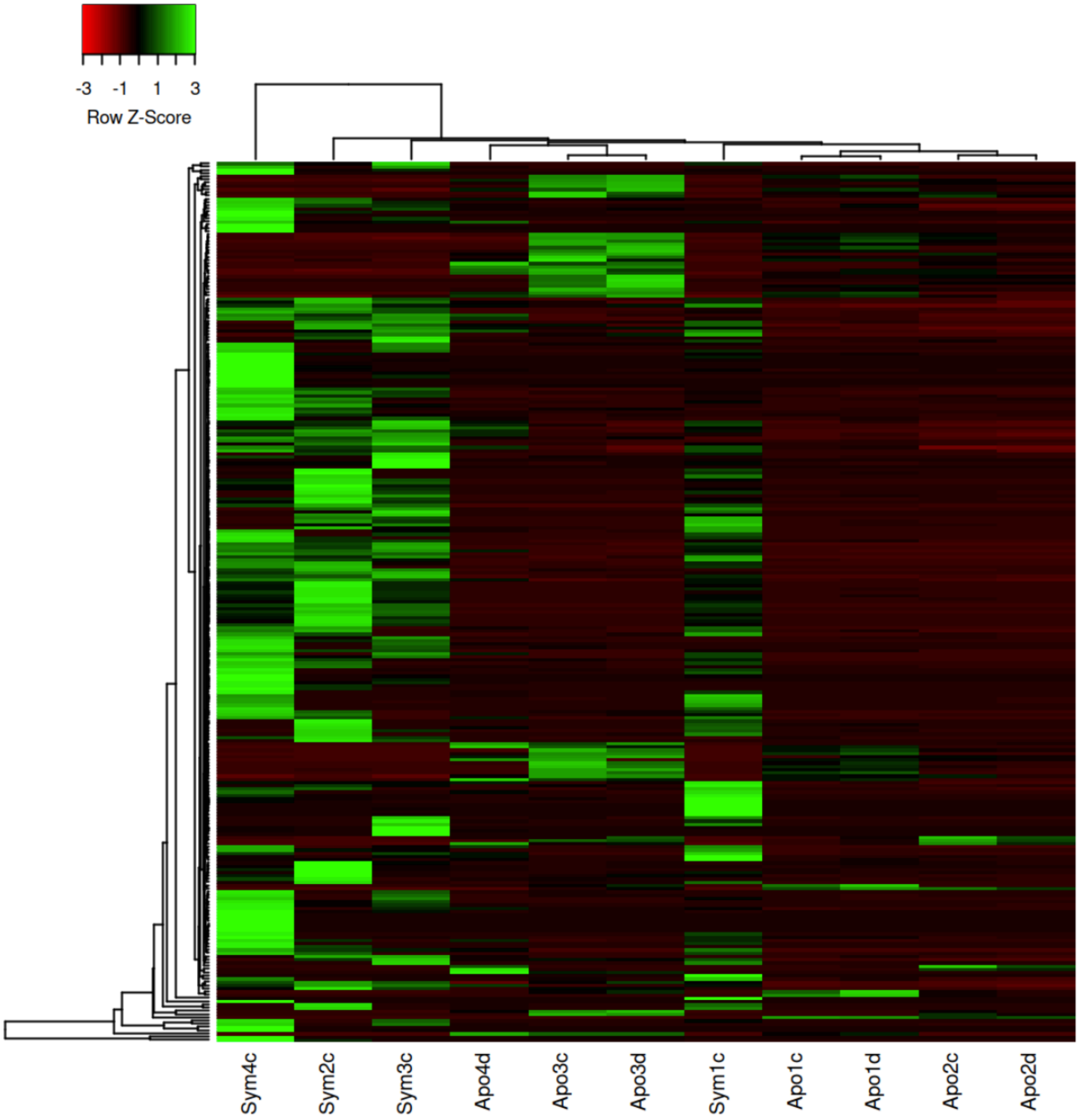


Figure 4-4. Hierarchical Clustering of Samples' Differentially Expressed Coral Genes

The rows correspond to differentially expressed coral contigs (n=273), and the columns correspond to samples (n=11). The color scale indicates the z-score of the genes' RPKM relative to the mean RPKM of each gene across all samples. Genes are hierarchically clustered according to Pearson's correlations.

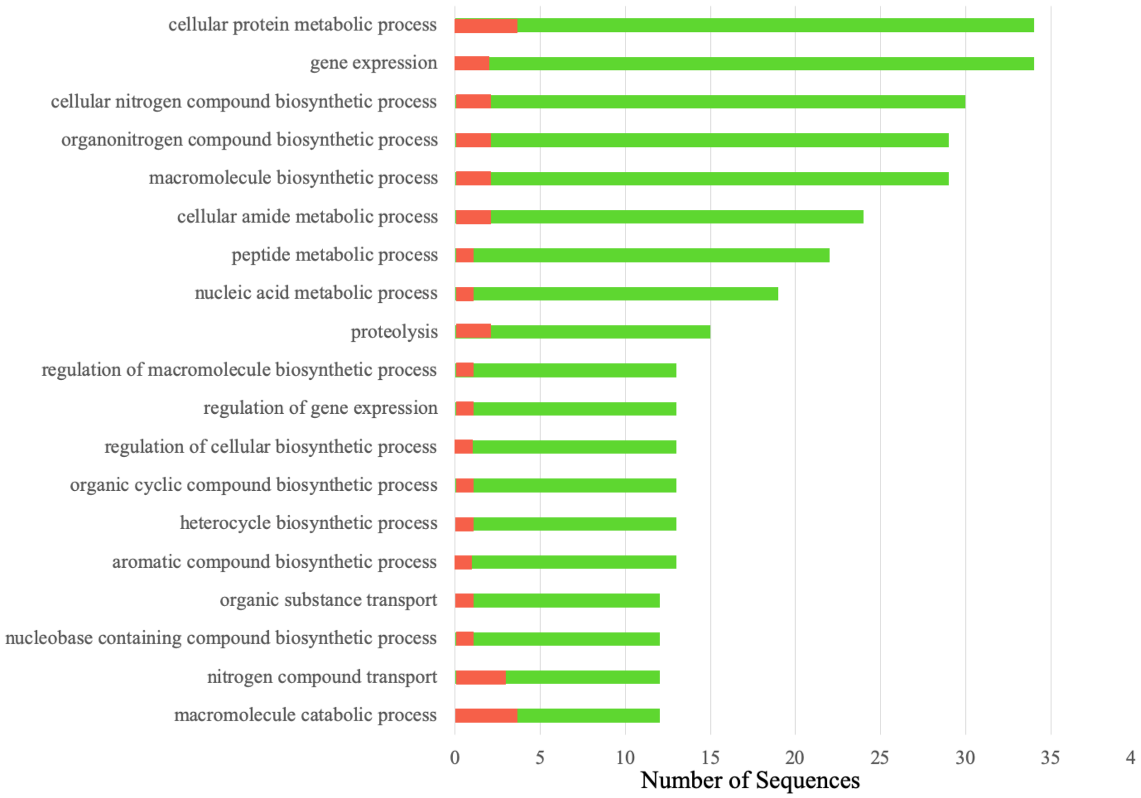


Figure 4-5. Top Biological Processes GO Categories of Coral-enriched Contigs of Symbiotic Control vs. Aposymbiotic Control FDR $p \leq 0.05$

The top GO categories of Biological Processes of symbiotic control vs. aposymbiotic control animals (FDR $p \leq 0.05$) are depicted here.

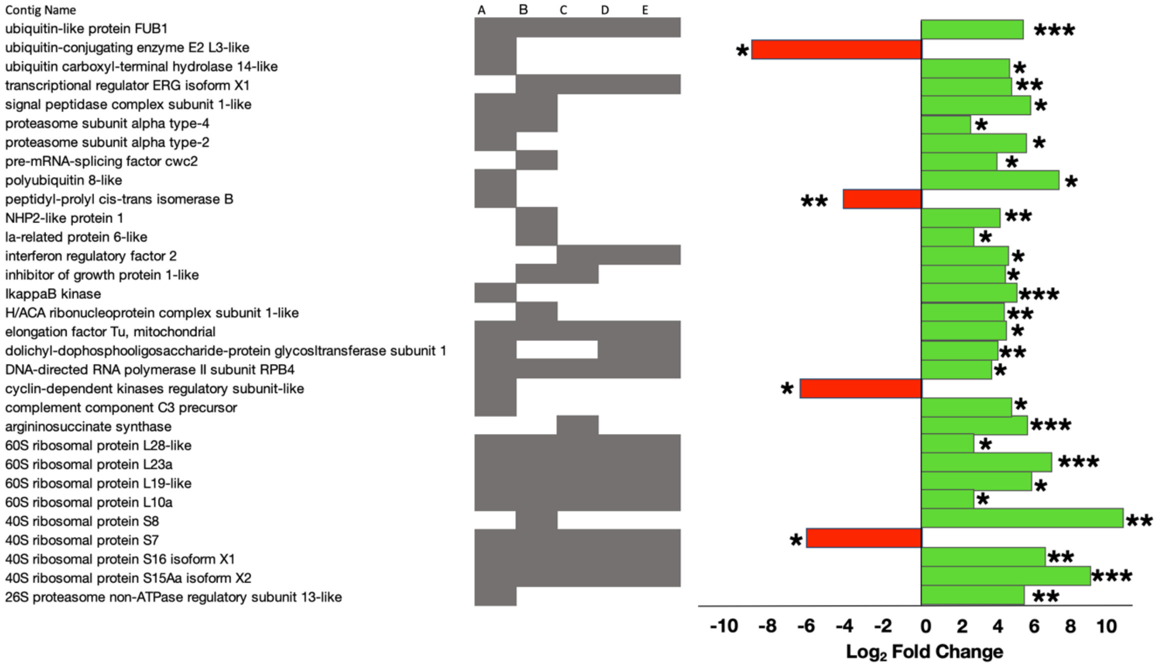


Figure 4-6. Differential Expression of Contigs in the Top Five GO Categories
The gene name for the top BLAST hit associated with each differentially expressed contigs is shown in the left Colum. The GO categories associated with that gene are indicated by gray boxes. A = Cellular Protein Metabolic Process; B = Gene Expression; C = Cellular Nitrogen Compound Metabolic Process; D = Cellular Macromolecule Biosynthetic Process; E = Macromolecule Biosynthetic Process. The fold-change is indicated by green or red bars (for increased or decreased expression in symbiotic polyps, respectively). The number of asterisks corresponds to the FDR p-value.
* = 0.01-0.05; ** = 0.001-0.009; *** = 0.0001-0.0009.

4.3.3.3 Comparison to the Previous Study on *Astrangia*

As described above, Burmester observed increased expression of neurogenic locus Notch-like and decreased expression of olfactomedin 2A in symbiotic *A. poculata* (2017). In general agreement with the Burmester study, we found two neurogenic notch-like genes that exhibited significantly higher expression in symbiotic polyps. One of these transcripts exhibited a top blast hit to "neurogenic locus notch homolog protein1-like isoform X1" (Log_2 FC =5.41, FDR p = 0.03), and the other exhibited a top blast hit to "neurogenic locus notch-like protein 4" (2 contigs; Log_2 FC =3.61, FDR p = 0.05; Log_2 FC =5.45, FDR p = 0.02). However, in contrast to the Burmester study, we identified an olfactomedin 2A-like transcript that was sharply increased in expression in symbiotic polyps: "olfactomedin-like protein 2A isoform X2" (Log_2 FC =5.99, FDR p = 0.038).

4.3.3.4 Expression of NF-κB Pathway Components

To investigate whether nuclear factor kappa B (NF-κB) signaling might be impacted by symbiotic state, we examined the expression of seven genes associated with NF-κB signaling: NF-κB, inhibitor of kappa B (IκB), IKKε, IKKα/β, and transforming growth factor beta activating kinase (TAK1). When we conducted tBLASTn searches at NCBI using the human proteins as query sequences, we identified one putative NF-κB ortholog in the transcriptome (E value = 2.00E-110), one IκB (E value = 7.00E-34), one IKKε (E value = 3.00E-126), one IKKα (E value = 7.00E-149), and one TAK1 (E value =4.00E-127). A detailed analysis of the molecular evolution of these proteins, which serves to corroborate the identities inferred from the BLAST searches, is described in Chapter 3.

In general, NF-κB signaling components, including NF-κB transcription factor itself, were not significantly differentially expressed in symbiotic vs. aposymbiotic corals (Figure 4-10). However, the expression of an IKKε homolog was dramatically and significantly increased in symbiotic relative to aposymbiotic corals (Log_2 FC = 4.67, FDR p = 0.0003; Figure 4-7).

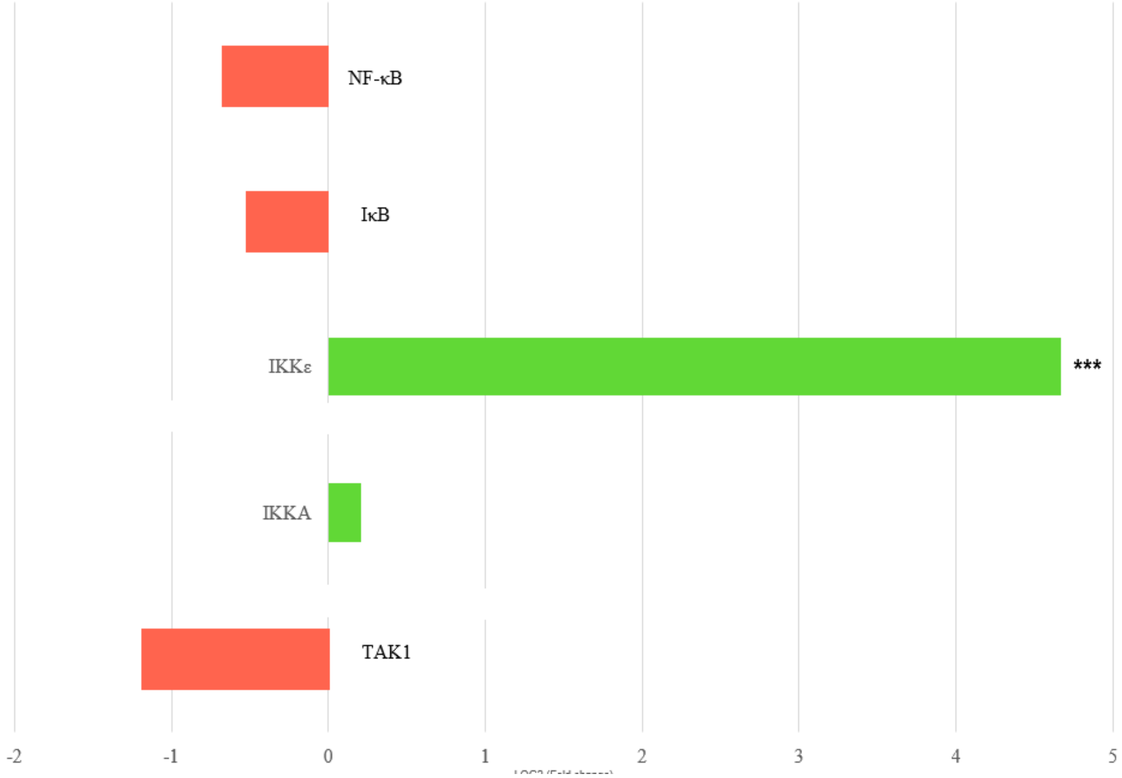


Figure 4-7. Expression of NF-κB Signaling Pathway Members in Symbiotic vs. Aposymbiotic Polyps
Green bars represent increased expression in symbiotic polyps. Red bars represent decreased expression in symbiotic polyps. Only IKKε was significantly differentially expressed. *** designates an FDR p = 0.0001-0.0009.

4.3.3.5 Expression of the SOD Family of Genes

To investigate whether antioxidant defense genes might be impacted by symbiotic state, we examined the expression of genes from the superoxide dismutase (SOD) family. As described in Chapter 2, we identified six SOD family members in the transcriptome, including three CuZnSODs, two MnSODs, and a single copper chaperone of superoxide dismutase (CCS). Five of these contigs showed no significant difference in expression, but an apparent ortholog of the *Nematostella* (Nv) CuZnSOD1 gene exhibited significantly higher expression in symbiotic polyps (Log_2 FC = 4.46, FDR p = 0.014; Figure 4-8).

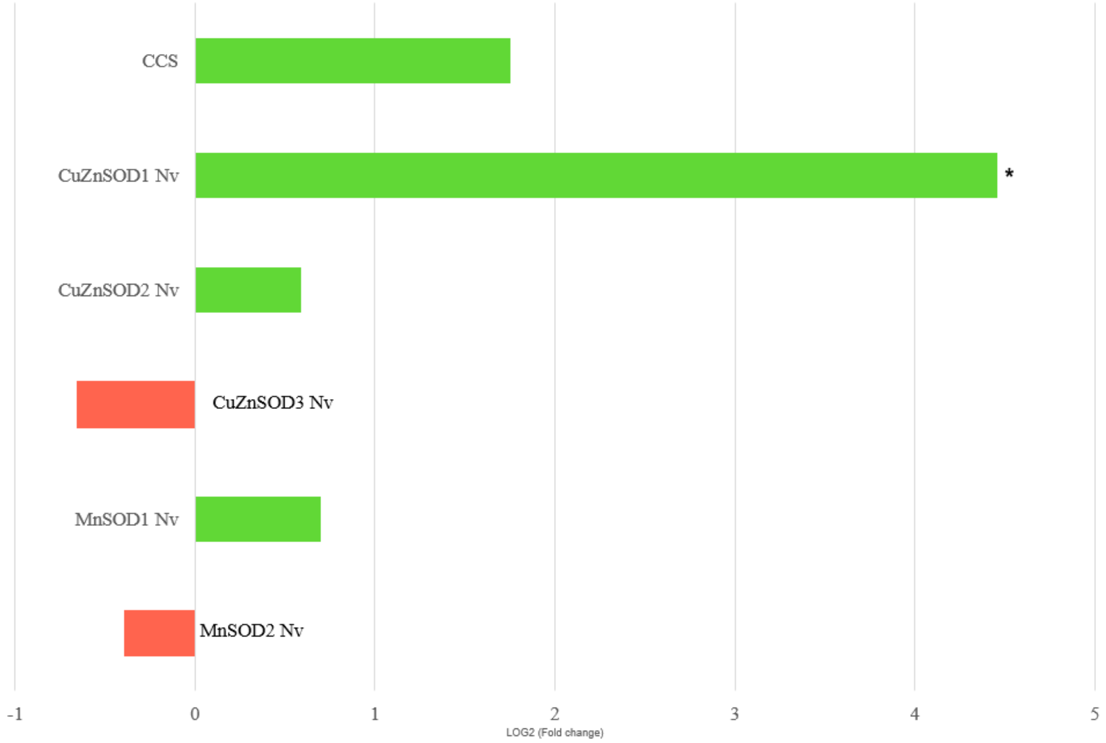


Figure 4-8. Expression of SOD Contigs in Symbiotic vs. Aposymbiotic Polyps
Green bars represent increased expression in symbiotic polyps. Red bars represent decreased expression in symbiotic polyps. * indicates an FDR p = 0.01-0.05

4.3.3.6 Genes Previously Implicated in the Maintenance of Symbiosis

Previous studies identified 18 genes shared by Symbiodiniaceae and corals as important in the maintenance of symbiosis between the coral *Acropora digitifera* and symbiodinaeacean *Fugacium kawagutii* (Table 3 in Lin et al., 2015; Figure 6 in Li et al., 2018). In *A. poculata*, we were able to identify homologs corresponding to 16 the 18 genes found in *A. digitifera*; we failed to identify a lectin or nitrite transporter. None of these 16 *A. poculata* genes were differentially expressed in symbiotic vs. aposymbiotic corals (Figure 4-9).

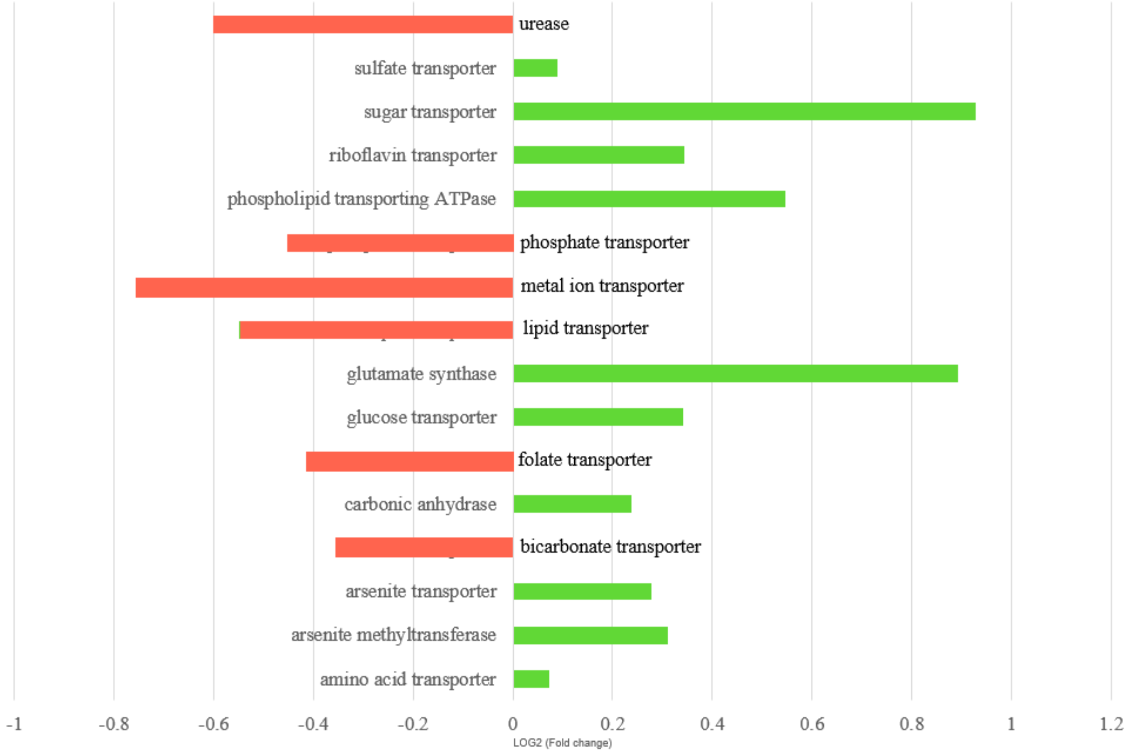


Figure 4-9. Expression of Symbiosis Related Contigs in Symbiotic vs. Aposymbiotic Polyps
None of the observed differences in expression were significant at FDR p≤0.05.

4.4 Discussion

Symbiotic and aposymbiotic *A. poculata* differ from each other in two important ways. First, they differ dramatically in the abundance of an intracellular symbiont whose presence requires the maintenance of a specialized intracellular compartment (the symbiosome) and the extensive exchange of inorganic nutrients and metabolites. Second, they differ dramatically in their primary trophic strategy. The symbiotic corals rely extensively on autotrophy, while the aposymbiotic corals rely exclusively on heterotrophy. Based on these qualitative differences in physiological state, we expected to find pervasive differences in the expression of the host coral's genes depending on whether it was symbiotic or aposymbiotic. This expectation was not borne out. For example, it was not possible to clearly distinguish symbiotic from aposymbiotic corals using either a PCA analysis of overall expression of host genes (Figure 4-2) or hierarchical clustering of differentially expressed host genes (Figure 4-4). However, some specific genes that were found to be differentially expressed in previous studies comparing symbiotic versus non-symbiotic cnidarians were corroborated in this current study.

4.4.1 Comparison to the Prior Study on *A. poculata*

In terms of overall gene expression, our approach identified hundreds of differentially expressed coral genes in symbiotic vs. aposymbiotic *A. poculata*, in contrast to the prior study by Burmester whose approach identified two differentially expressed coral genes (2017). The disparity in the number of significantly differentially expressed coral genes is largely attributable to differing thresholds for declaring statistical significance. To identify significantly differentially expressed genes, we employed a false discovery rate p-value cut-off of $p \leq 0.05$, while Burmester specified $p \leq 0.003$ (2017). At the same FDR $p < 0.003$ utilized by Burmester, 58 differentially expressed coral genes would be identified in this study. Thus, even at the same p-value, the analysis conducted here seems to exhibit greater statistical power. The remaining disparity may be attributed to differences in (1) the number of replicates, (2) the quality of the transcriptome assembly, and (3) the stringency of read mapping. Burmester compared RNA levels in 4 symbiotic polyps vs. 2 aposymbiotic polyps, while we compared 4 symbiotic polyps to 7 aposymbiotic polyps. Additionally, by standard metrics such as BUSCO score and N50, the assembly used here appears to comprise more complete transcripts than that used by Burmester. As a result, sequencing reads derived from the same transcript might map to the same contig in this study, but may have been split among multiple partial contigs in the prior study, reducing the statistical power. Finally, Burmester used the default read mapping parameters of CLC Genomics, whereas I implemented more stringent read mapping parameters. As my comparison of three mapping stringencies shows, increased stringency can increase the number of differentially expressed genes that achieve statistical significance.

Our study did support the differential expression of both genes previously reported to be differentially expressed in *A. poculata* (Burmester 2017). As in the previous study, we found increased expression of neurogenic notch homologs in symbiotic *A. poculata*. However, unlike the previous study, we found increased expression of an olfactomedin-like protein 2A homolog.

4.4.2 Effect of Symbiotic State on NF-κB

Altered expression of NF-κB has been associated with a change in symbiotic state in at least two model systems. Riesgo et al. reported that two NF-κB-related gene ontology categories exhibited altered expression when they compared the boring sponge *Cliona varians* in its native symbiotic state to an experimentally induced aposymbiotic state. Relative to a symbiotic individual, the aposymbiotic individual exhibited lower expression of genes in the GO category "negative regulation of NF-kappaB transcription factor activity." When the aposymbiotic specimen was allowed to re-acquire symbionts, the now "re-infected" individual exhibited lower expression of genes in the GO category "positive regulation of NF-κB transcription factor activity." Both results appear to associate the symbiotic state with lower expression of NF-κB-related genes. However, the study has significant technical flaws including the lack of any replication, i.e., n=1 in both comparisons. Furthermore, the paper does not disclose how the expression of individual genes is affected.

As described above, in the facultatively symbiotic sea anemone, *Exaiptasia pallida*, experimentally induced bleaching led to an increase in NF-κB RNA, protein, and DNA-binding activity. Furthermore, decreased NF-κB expression was observed following introduction of symbionts into *E. pallida* larvae (Mansfield et al., 2017).

While we found that the components of NF-κB signaling are present, only an IKK homolog was significantly differentially expressed when comparing symbiotic corals and aposymbiotic corals, for both control conditions (Figure 4-7). The putative IKK is most like IKKε (reciprocal BLAST e value = 3.00E-126 to human TBK/IKKε), which is more specifically associated with another innate immune pathway, the IRF7 pathway (Chau et al., 2008). However, IKKε has been shown to activate NF-κB reporter genes in cell culture (Shimada et al., 1999) and it can phosphorylate an NF-κB-associated IκB in the sea anemone *Nematostella* (Wolenski et al., 2011), though evidence of a direct role for this kinase in activating NF-κB *in vivo* is lacking. However, there is evidence of crosstalk in NF-κB and IRF signal transduction from IRF3-p65 associations required for response to lipopolysaccharide stimulation (Zhao et al., 2007, Chau et al., 2008). If IKKε activates the NF-κB signaling pathway in symbiotic *A. poculata*, this would be inconsistent with findings in *Exaiptasia* where aposymbiotic *Exaiptasia* exhibited decreased NF-κB levels compared to re-infected symbiotic *Exaiptasia* (Mansfield et al., 2017).

4.4.3 Effect of Symbiotic State on SOD Expression

In our study, symbiotic *A. poculata* exhibited roughly 22-fold greater expression of CuZnSOD1 RNA than aposymbiotic *A. poculata* (Log_2 FC = 4.46, FDR p = 0.01; Figure 4-8). Interestingly though, none of the other SOD genes exhibited a significant increase in expression. In humans, paralogous members of the SOD family differ in their associated metal ions, their quaternary structure, and their subcellular localization. SOD1 is a CuZnSOD that functions as a dimer and is found in the cytoplasm. SOD2 is a FeMnSOD that functions as a tetramer and is found in the mitochondria. SOD3 is a CuZnSOD tetrameric protein found in the extracellular space. Unfortunately, due to gene duplications that appear to have occurred within Cnidaria (described in Chapter 3), there is no one-to-one correspondence between the *Astrangia* and human SODs allowing us to infer the subcellular location of the coral genes under an assumption of evolutionary conservation. *A. poculata* CuZnSOD1 and CuZnSOD2 appear most closely related to the human SOD1 based on molecular phylogenetic analysis (see Figure 3-15). This would suggest a cytoplasmic location for *A. poculata* CuZnSOD1, arguably an ideal location to counteract ROS generated by the symbiont that might leak from the symbiosome into the cytoplasm. Indeed, if the duplication of cnidarian CuZnSOD1 and CuZnSOD2 were associated with a change in subcellular localization, an interesting possibility is that CuZnSOD1 might be targeted specifically to the symbiosome. An homologous pattern of sub-cellular localization might explain also why *A. poculata* CuZnSOD3, whose closest human homolog is expressed in the extracellular space, and *A. poculata* MnSOD1 and MnSOD2, whose closest human homolog is expressed in the mitochondrion, might not be expressed at significantly levels in symbiotic corals; i.e., these proteins would not be best positioned to respond to ROS generated by the symbiont. Symbiotic polyps likely experience higher physiological levels of H_2O_2 in the cytoplasm than in either the mitochondria or extracellular space, thus express greater baseline levels of CuZnSOD1 than aposymbiotic polyps.

The increased expression of CuZnSOD1 in symbiotic vs. aposymbiotic *A. poculata* is at odds with reports from some sea anemones. Significant upregulation of SODs was seen in aposymbiotic anemones, e.g., *Anthopleura elegantissima* (Rodriguez-Lanetty et al., 2006) and *Exaiptasia* sp. (Richier et al., 2005). In the sea anemone model, *Anthopleura*, researchers reported that the antioxidant CuZnSOD was decreased in expression by 1.5 fold in the symbiotic state compared to the aposymbiotic state (Rodriguez-Lanetty et al., 2006). In the symbiotic sea anemone *Anemonia viridis*, a decrease in CuZnSOD activity was reported after symbiosis onset, with increased activity of other SODs, e.g., FeSOD and MnSODs (Richier et al., 2005).

Gene expression studies comparing symbiotic and non-symbiotic marine organisms suggest a connection between harboring a photosynthetic symbiont and the expression of antioxidant genes and pathways. It has been hypothesized that the repeated evolution of photosymbiosis in animals is enabled by the evolution of a greater capacity to resist oxidative stress (Ishikawa et al., 2016, Ishikawa et al., 2016, Melo Clavijo et al., 2018). It has also been shown that host protection from ROS can be attributed to SODs generated by Symbiodiniaceae that reduce the expression of host enzymes (Rodriguez-Lanetty et al., 2006).

4.4.4 Effect of Symbiotic State on Genes Implicated in Symbiosis Maintenance

In terms of the coral genes implicated in the maintenance of coral-algal symbiosis, none of the 16 coral genes that are thought to be necessary for maintaining symbiosis (lectin and nitrite transporter were not found in the *A. poculata* transcriptome; Lin et al., 2015) were differentially expressed in symbiotic vs. aposymbiotic corals (Figure 4-9). This was an unexpected finding because we hypothesized that symbiotic corals would upregulate genes implicated in the maintenance of coral-algal symbiosis. However, as these genes are present in both corals and their symbionts, expression of these genes by the symbiont may be sufficient to maintain symbiosis, such that elevated expression of these genes by the host is not required.

4.4.5 Potentially Confounding Biological Factors

One potential confounding factor when comparing gene expression (or any other aspect of the phenotype) in "symbiotic" and "aposymbiotic" *A. poculata* is that the abundance of zooxanthellae can vary continuously from the most aposymbiotic to the most symbiotic individual. Furthermore, since *A. poculata* colonies may be mottled, a brown symbiotic polyp next to a white aposymbiotic polyp in the same colony would theoretically hold varying concentrations of *B. psygmophilum*. The wide range of reads mapped to the symbiont transcriptome in aposymbiotic colonies (0.29% - 2.87%) supports the notion that even original aposymbiotic colonies carry varying concentrations of Symbiodiniaceae. This could be empirically confirmed by counting Symbiodiniaceae cells prior to experimentation to determine the cell density of Symbiodiniaceae per host cell, thus quantifying the degree to which the polyp is "symbiotic." There is also an established relationship between symbiont abundance and coral color (Scheufen et al., 2017). In the current study, we did not attempt to measure symbiont abundance directly, or to estimate it based on colony color. However, the read mapping results presented in Table 4.1 indicate a clear distinction in the Symbiodiniaceae reads in symbiotic vs. aposymbiotic polyps. This analysis also allowed us to explore the effect of removing an outlier among that aposymbiotic polyps that exhibited an unusually high fraction of reads mapping to symbiont contigs. As expected if we probably discriminated symbiotic polyps from aposymbiotic ones, there was a significant difference between symbiotic and aposymbiotic polyps in the percentage of reads mapping to the coral contigs in the reference transcriptome (single-factor ANOVA, DF = 1, MS = 145.63, f = 5.00, p = 0.049) as well as to symbiont contigs in the reference transcriptome (single-factor ANOVA, DF = 1, MS = 275.03, f = 18.42, p = 0.002). In both cases, the number of reads mapping to coral contigs was higher. This is unsurprising because host coral cells outnumber Symbiodiniaceae cells 100:15 and can be as high as 1000:5 in severely bleached *A. millepora* (Mieog et al., 2009). Furthermore, the percentage of mapped reads to the coral-enriched transcriptome and the symbiont-enriched transcriptomes do not exceed 100% in any of the libraries, suggesting very stringent mapping to a holobiont transcriptome prior to parsing is effective in reducing any heterogeneity in the transcriptome i.e. if the coral-enriched transcriptome only contained cnidarian contigs and the symbiont-enriched transcriptome only contained *B. psygmophilum* contigs, then the percent mapped to both transcriptomes should equal less than 100% (to account for other transcripts that do not fall under either coral or *B. psygmophilum*).

4.4.6 Potential Biological Confounders

Biological effects may have confounded the results from this study. For example, confounding factors like symbiotic state switching or gender could impact gene expression studies of symbiosis. Coral colonies can switch symbiotic states, as they do not inherit symbiotic states for life, and sampled polyps may be transitioning from one symbiotic state to another. This may have led to the lack of significance in genes involved in symbiosis maintenance. Sex of the coral colonies was not factored in during collection processes nor the differential expression analysis and may have confounded results.

4.5 Conclusion and Future Directions

There does not seem to be a significant difference in coral-enriched gene expression between symbiotic vs. aposymbiotic coals. Questions on host-microbe model systems should focus more on Symbiodiniaceae genotype rather than the effect of stress, as gene expression was found to be more consistent among corals harboring Symbiodiniaceae (DeSalvo et al., 2008). We suggest that harboring endosymbionts may confer resilience to environmental challenges by providing the host with nutrition; this may make them better able to withstand stressors (such as oxidative ones) and stochasticity in the environment. *A. poculata* remains a good model system for studying reef-building corals because it allows isolation of symbiotic state as a variable, as reef-building corals cannot survive without Symbiodiniaceae indefinitely. Future exploratory studies may delve into the function of specific transcriptional pathways under different experimental conditions to further elucidate their roles in modulating symbiotic states in corals. Functional biochemical and molecular studies, e.g., qPCR to validate differential expression (or lack thereof) of NF-κB, IKK, and SOD, or adding an IKK inhibitor to examine the effect on ROS exposure, may be done in parallel to confirm bioinformatic findings.

CHAPTER 5: CONCLUSIONS AND FUTURE DIRECTIONS

In order to explain the variation in stress responses that we see in nature, it is important to understand their molecular basis. Here, I will (1) discuss how my work in studying photosymbiosis is a stepping stone for future studies and can be applied to coral restoration practices and (2) merge my analysis of core nuclear factor – kappa B (NF-κB) signaling components in Cnidaria with my observations on the differential gene expression patterns that result. The correlational support of NF-κB playing a role in the reactive oxygen species (ROS) exposure response of corals will be weighed in these analyses. Finally, I will also propose experiments to test the connection directly.

My dissertation research focused on the transcriptomic effects of photosymbiosis in *A. poculata*, and I tested the hypothesis that differences in gene expression underlie a mechanistic connection between symbiotic state in cnidarians. To test this hypothesis, I utilized an anthozoan cnidarian as a model system: the northern star coral, *A. poculata*. *A. poculata* is facultatively symbiotic and is a bridge to tropical reef-building corals because it allows questions to be interrogated in a lab-tractable manner without compromising survival. Future studies would validate our differences in photosymbiosis findings in obligate tropical reef-building corals. However, results from that experiment would have to be interpreted with caution as it would be difficult to parse out whether reef-building corals' differential gene expression is due to the presence of algae (or lack thereof, which accelerates the dying process) or their ability to survive for the duration of the experiment and/or conditions.

Our findings may inform the future direction of coral nursery and restoration activities. First, we will need to confirm our results by conducting western blots, enzyme-linked immunosorbent assays or quantitative polymerase chain reactions for protein/mRNA of copper zinc superoxide dismutase 1 (CuZnSOD1) and inhibitor of kappa B kinase epsilon (IKKε) before, during, and after algal (re)introduction of symbiotic and aposymbiotic *A. poculata*. If the observation holds true that they are indeed important for coral survival, we could implement this as gene therapy into reef-building coral nurseries and other coral restoration projects to augment corals' resilience to exogenous and endogenous ROS. Coral gene therapy could be viewed as a biological supplement for better coral health and wellbeing. For example, a transgene encoding CuZnSOD1 could be inserted into a viral vector. The capsid should be stripped of its immunogenic factors in order to avoid an immune response by the host or Symbiodiniaceae and should contain specific serotypes so that there is viral tropism to the targeted host, endosome, or symbiosome. This would increase the delivery efficacy of the gene therapy into the target. Using RNA gene therapy would allow for a high yield of protein expression, albeit transiently. DNA gene therapy would require translocation of the transgene into the nucleus and DNA integration into the genome for more prolonged protein expression, but at a low yield and a risk for off-target effects. Gene therapy through viral construct delivery may also require immunosuppression, which would dysregulate the already sensitive coral-algal symbiosis. More immunosuppression may lead to higher colony forming units of Symbiodiniaceae and/or increase the risk of viral infection and bacterial colonization. Current clinical practices in alleviating immune responses resulting from gene therapies include prescription of corticosteroids, which may be effective in corals. Further considerations are that viral vector constructs have size limitations as well (adeno-associated viruses allow up to a 4.7 kb transgene and can also use nanoparticles i.e. non-viral vectors for gene therapy delivery) and may not be scalable as they present a significant financial challenge. Once safety, efficacy, stability, and durability of this gene therapy has been demonstrated in reef-building corals in nurseries and restoration habitats, they can be released into the wild.

The proposed model for NF-κB signaling in cnidarians is neither the canonical nor non-canonical pathway, but an ancestral one, consisting of signal transduction through transforming growth factor-beta activated kinase 1 (TAK1), inhibitor of kappa B kinase alpha (IKKα)/β homodimer, p105/p50, to p50/p50 binding of κB binding sites (Figure 3-19).

We found that symbiotic *A. poculata* have higher expression of IKKε than aposymbiotic *A. poculata* (Figure 4-7). The upregulation of IKKε is interesting because it is an essential component of the interferon regulatory factor 3 (IRF3)/IRF7 signaling pathway (Fitzgerald et al., 2003) and gives the impression that IRF3/IRF7 may be involved in mitigating oxidative stress in cnidarians. While there is evidence of cross talk between IRF3-p65 (Zhao et al., 2007; Chau et al., 2008), we did not find a p65 homolog in *N. vectensis* or *A. poculata*.

We note that symbiosis in *A. poculata* should not be seen as an infection to be mediated, as the coral exists in stable states of symbiosis, aposymbiosis, and both within the same colony. Also, we did not identify significantly differentially expressed contigs involved in innate immunity that would indicate detection of pathogenesis or infections, e.g., differential expression of toll-like receptors.

Limitations of our experiment may have impeded our discovery of any significant expression of NF-κB signaling. The transient nature of NF-κB activity, its rapid degradation may have limited capturing significant levels of NF-κB differential expression directly. Earlier RNA extraction time points could be performed in order to capture optimal NF-κB activation and mRNA expression of its target genes.

Our findings open opportunities for further investigation into questions such as: What is the symbiont's contribution to the coral holobiont's photosymbiosis response? How is the cnidarian ancestral NF-κB signaling pathway activated? What is the role of the IRF3/IRF7 signaling pathway and is it activated post–NF-κB signal transduction? Does NF-κB knockdown compromise H_2O_2 resistance in *A. poculata*? The work in this dissertation provides an ample platform for addressing these topics of great biological significance.

In summary, the evolutionary success of corals—and the future health of the world's oceans—depends on their ability to tolerate fluctuating severity and frequency of environmental perturbations. My fundamental transcriptomic discoveries provide insight into coral coping mechanisms that may be mobilized in response to a changing climate and help formulate recommendations to ensure the survival of corals.

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CURRICULUM VITAE

[redacted]

[redacted]

APPENDIX

A.1 NF-κB FASTAS

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>NFkB[Ciona intestinalis] NP_001071772.1

MSDQSLVLHQSTRENMFPEENGEPYLEIIENPKSRGFRFRYTCEGPSHGGIPGGSSDKNKKTFPAVKI
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ERYIAAEMQLSSINDGFPQEVQRNIKDEDRKRIAAKAQSEAKSIDLSVVRLMFIAYLPDSNGAFTIML
KPVISDAIFDSKAPNAATLKICRMDCNAGSASGGDEVYLLCDKVQKDDIQVVFSEEDMQGNNLWEAYG
SFSPTDVHRQFAIVFRTPAYKDTEIKMPVNVQVQLRRKSDNEVSESRPFTYLPNKSDLELIDRKRRKV
MPDFLDHTGNGSTGGYSFNPQAAILPSSYNFSGNTGSGNTAGNGAGKVKEARRPPQKQQNPQKGPVDP
SVLMMLNRIKTEPKSPSPPTTYSNFPPIAYMSPAKSEPSPPAPMSIGGSPAAQVPQEEEYLPGTRIPL
PKNARPHTGLPQMSFQNPIVLSQQQQMQQQQIQQQQQQHLQQIQQQQAYSNYSPMYSTTYGLDNTQHM
VYSTPSPDYGQQIIQQLSPQEVQEYEETVMNELSTVDAGDLVDIMNVDLNHNPMPQTTNSNIINQAYD
QANILTQTNNTYGGGSGSFRGSVVDPIIPQPLSNAPLPILSQQFSQQLLELTEYDLADIESDAGAERK
PKPGNNNDDEQEEDYASAYCEEQDTTDSTAHEAEPKSFSTVQSDCCNVEADAAMLKMEKLSLAPSMPT
KLDSLKPEKKFDSKQVETKTKGPLKRSVTSTTASVTQALEKYAVKTMNRNSSALHDFSVTGDIRMLLV
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VIDLLKVGADPLVLDSYGNHSIHVACRHGNADILNRLLNCKQVYDMEMDTKNFDGLGCFHLAGKASSG
TRQCLGLLREFAFDVNMPDMKSRRTALHMAVEADNIVVAGCLISECDADLEASTYEGYTPLHVAASLD
HCEIATLLLACGADPEASSAPPGREDGMTPLDLATSDQMRDLLNGVFMKNIKEELDNSNYSDEEDLAT
LDPLIRLKLCKLLNLEKSGSDWYALASRLSLDYIVPFIDTTENPTDLLLDNYMFKHGTVAGLRSALMN
IGRHDAVQLLNRAATTTCVDKFDSNATEQCDSAFGSLPNQIDVI
```

```
>rel1[Ciona] NP_001029013.1

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RSAVDVDLNIVRLCFEAFIPDARGKYTQKLEPVVSDPIYDKKATCSSVLKICRVDKTHGSCMGNEEVF
LLCDKVQKEDIQVVFYRDNWEALGDFSSVDVHRQVAIVFRTPPFCNENIQEKVDVQFKLRRPSDMETS
KPLVFTYLPVYHAMLLDR
```

```
>NFkB1_Homo gi|34577122|ref|NP_003989.2|

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QEQKSGRTALHLAVEHDNISLAGCLLLEGDAHVDSTTYDGTTPLHIAAGRGSTRLAALLKAAGADPLV
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>NFkB2_Homo NP_002493 [Homo sapiens]

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FGDFSPTDVHKQYAIVFRTPPYHKMKIERPVTVFLQLKRKRGGDVSDSKQFTYYPLVEDKEEVQRKRR
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PECLDLLVDSGAEVEATERQGGRTALHLATEMEELGLVTHLVTKLRANVNARTFAGNTPLHLAAGLGY
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PPGGLCHGHPQPQVH

>RelA_Homo NP_001230914 p65 isoform 4 [Homo sapiens]

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NNNPFQVPIEEQRGDYDLNAVRLCFQVTVRDPSGRPLRLPPVLSHPIFDNRAPNTAELKICRVNRNSG
SCLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRTPPYADPSLQAPVRVSMQL
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>RelB_Homo NP_006500.2[Homo sapiens]

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>cRel NP_002899.1 proto-oncogene c-Rel [Homo sapiens]

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>NFkBCys_Nev

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>NFkBSer_Nev

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>NFkB_Ed

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>NFkBb_Aiptasia

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>NFkB_Acropora

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>NFkB_Corallimorph

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>NFkB_Hydra

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>NFkB_Astrangia

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>NFkB_Biomphalaria

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>Relish_Biomphalaria

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>Relish_Dmel

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>Dorsal_Dmel

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>Dif_Dmel

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>NFkB_Amphimedon

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>NFkB_Capsaspora

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A.2 IKK FASTAS

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A.3 TAK1 FASTAS

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A.4 NIK FASTAS

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DLSQGWKSAGGIYNPKQMPHGPPSKDGGARRKPGAIGNVASDAQGRATFTLSASQLNVWDIIGHALVV
```

```
HERPDDFGLGNAPRSSENGNVGAGVGAGIIARSAGLLGNAKRVCACDGKTLWSDSNPGALLPNKRVHI
DNNSPPPVARSVSEGKPAIERAMDVTHPFILSSI

>CuZnSOD_Capsaspora
MTKLVAVLKGDGAVKGTVVFTDDGAATKVEGTIEGLAPGKHGFHIHEFGDNTNGCISAGPHFNPAGKT
HGAPEDEERHVGDLGNVEAGADGIAKFTITDNLIQVSGVNSIVGRSVVIHADIDDLGKGGHELSKTTG
NAGGRLACGVIGVAK

>FeMnSOD_Capsaspora
MLQSAALVRSVASRASATAAVAAAVPMRAKHTLPDMPYDYSALEPVISAEIMKIHHSKHHQAYVNNLN
IAEEKYAEATAKNDLSAQIALQSAIKFNGGGHINHSIFWTNLAPASQSGSPSAELNKAINAEFGSFDA
FVEKFNTQTAAVQGSGWGWLGYDKTKGRVVITACANQDPLQALTGHTPLLGIDVWEHAYYLQYKNARP
DYLKAIWKVVNWNNVNERFAAASRK

>CCS_Nematostella
MASMSEVPTETRMEFAVEMTCEKCVNKVKQVLDGVQGVSSYSVDLGEQCVIVDTVLPSGQ
VQEMLEKTELKTILRGHGAGRAGKTAQHLGAAVAMIDCEKVQGLTRFVQVSGDNCIIDGT
IDGLTPGNHGFHIHEFGDFSNGCTSTGAHFNPTNNQHGAREDEERHVGDLGNIIANQNGR
ATFRFEDKTVKVWDIIGRAIVVHADEDDLGRGGHELSKSTGNSGARVGCGIIARSAGLFQ
NTKKYCACDGRTLWEDKPLKASSQL

>CuZnSOD3_Nematostella
MGQATFINVRLRGVPPLTVHGFHIHKSGDIITKGCQSAKGHFNPYGKTHAGPRKRDRHVG
DLGNVWSDYHGNVRTSFFDHMVSLYGPDSVIGRSIVLHAERDDLGRGIGEYRTGSLATGN
AGARLACCVIVHV

>CuZnSOD2_Nematostella
MPIQAVCCMSGTEGVKGTIKFVQEAEGKPCKITGTIEGLKAGNHGFHIHVYGDNTNGCVS
AGPHFNPFKKEHGGPSDENRHVGDLGNVVAGDDGKACIDMTDALVTLVGEHSVVGRSVVV
HADEDDLGRGGHEDSKTTGHAGGRLACGVIGITQAS

>CuZnSOD1_Nematostella
MVIRGVCCLVGDNEVKGVIHFTQQAPDGPCTLRGRITGLTEGKHGFHIHEFGDNTNGCTS
AGAHYNPHGKMHGAPEDKDRHLGDLGNIEADANGIADVSITDCLVSLTGQCSIIGRSLVV
HEGMDDLGAGGHELSLTTGNAGGRVACGVIGIAL

>MnSOD1_Nematostella
MLLARVARLSSRKAVLPVALVRAKHTLPDLPYDYDALEPTINTEIMRLHHSKHHATYVNN
LNIAEEKCLEAQAKGDVATAIALQPAVKFNGGGHLNHSIFWTNLSPNGGGEPTGELMEAI
KRDFGSFENFKERFNAATIAVQGSGWGWLGYDKVNKRLAIATCFNQDPLQPTTGLVPLLG
IDVWEHAYYLQYKNVRPDYVKAIYDVINWTNVAERLQAASS

>MnSOD2_Nematostella
MAAKKGSLLFLVLLFCDVWCSIDGNPYHEIVKYMEEYTLPELPYDYNELEPHIDEATLRV
HHLGHHAAYTKKLNAALKEWRESGKEKDLASKSIVEILRNNEQIPDKWRTDVINNGGGFV
NHALYWATMSPNPKSEPRTPTGKIGDLIDKSHGNFSMFKQWFDEQVNSMFGSGYTWLCQD
VTSGFLTILNMGNQESPVAYRLNPVLVIDLWEHAFYLKHQNKRPGYVHSWWHLVDWERVN
ELLEWWQNQNIHDEL

>CCS_Astrangia
MEFAVQMTCQKCVDAIHNSLDGAEGVKSFTVDLNTEQVIVETTLSTGQVQKLIENSGRMA
```

```
ILRGLGAAGTQPTHLGAAVVEMQSGSILGVTRFVQVSEDLCVIDGTIDGLAPGLHGLNIH
ELGDLSQGCMSTGDHYNPRSCRHGAPEDSERHIGDLGNILADKNGRASFRLEDKDVKVWD
VIGRSLVVHHGEDDLGRGNNELSKITGNSGPGLTCGIIARSAGLFQNTKKFCACDGKILW
EDKPLSAPTSMPSQL

>CuZnSOD1_Astrangia
MARAVCLLAGDVQGSIKFSQEYPGGPCVITGVLQGLTEGHHGIHILEFGDISQGSNSAGA
HYNPLNKTHGGPEDEDRHVGDLGNIEADSQGQADVNITDNVVSLTGEHSVIGRTLAVCEG
VDDLGRGGHELSLRTGNSGACLACGVIGIAKTSENTKISQDDSV

>CuZnSOD2_Astrangia
MASALRLDNLEFTVQNLVSMVSCLFIFHFYVTSPVILHSFPSASCSKWITPNDSSVKGVI
HFEQEAEGKECKITGEVTGLTEGKHGFHVHQFGDGTNGCTSAGPHFNPTGKTHGGPDDEI
RHYGDLGNITADKDGKAKIDMTDKLVSIIGKDSVVGRTIVVHAKVDDLGKGGDEESLKTG
NAGPRWACGVIGITK

>CuZnSOD3_Astrangia
MMLATVAATKISVSEQDEPSEITAFSFITPNSKPPPGTETPVKGTVKLMQGNRQRPPYDH
TIMIVHISGLPPYTPHGFHIHEFGDIVTDGCQSTGGHYNPFNHTHGGPQDQIRHVGDLGN
LVTDQKGVIDAVLEDHVVSLIGDYTVIGRAFVIHQKRDDLGRGTGPARNESLKTGNAGPR
LGCGVIFDAASN

>MnSOD1_Astrangia
MLSRGCGSFCSLKKLFPAVIAGATRAKHTLPDLPYDYNALEPTISAEIMQIHHSKHHATY
VNNLNVAEEKFAEAQAKGDTNAMIALQPALKFNGGGVMNHNIFWTNLSPNGGGEPTGALM
EAIKQDFGSFENFKERFNTASIAVQGSGWGWLGYNKVDKRLVITTCANQDPLQATTGLVP
LLGIDV


>MnSOD2_Astrangia
MASIGLSLFVAIFLRFSSIECATPYEEITQYKEEYSLPDLPYNYDGLEPFIDEATLRVHH
LGHHAAYTKKLNAALKSWRESGKTSELSSKPIATILKNIQLIPYDWRLKIRNNGGGYVNH
ALYWAIMSPNPNNEERKPSGRVAQLIDESFGSYSNFQSIFEKTALEVFGSGYAWLCLDVE
NGGVKIRGSTNQDSPLNQHGLLPILVIDVWEHAYYLQHQNRRAAYVQSFWNVIDWDAVSE
LLEWWPKQTKHDEL
```

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CLUSTAL O(1.2.4) multiple sequence alignment


TBK/E_Amphimedon        WSSKDKLGQGATGQVFAGYSKRSGDKVAIKMFTSPSEY-KAMQ-----SEMQTIKA--LK    52
TBK/E_Astrangia         WNIKDILGQGATGAVYKGRNKKTGDTFAVKISNQLGMM-RPVE-----VRRREFEVLNKL    54
TBK/E_Nematostella      WNLKSVLGQGATGAVYTGRHKKSGDVVAVKTSNHLGMM-RPLE-----VRKREFDVLSKL    54
TBK/E_Aiptasia          WHIKDVLGQGATGAVYKGRDKKTGNEVAIKVTNHLGMM-RPLD-----VRKREFEVLNRL    54
TBK/E_Drosophila        WCTTSVLGKGATGSVFQGVNKITGESVAVKTFNPYSHM-RPAD-----VQMREFEALKKV    54
TBK/E_Ciona             WSTTEILGQGATGFVFKGREKKTGQEYAIKVFNSLNYMARSLE-----ARRREFEVLRKV    55
TBK_Homo                WLLSDILGQGATANVFRGRHKKTGDLFAIKVFNNISFL-RPVD-----VQMREFEVLKKL    54
IKKE_Homo               WHTDDLLGQGATASVYKARNKKSGELVAVKVFNTTSYL-RPRE-----VQVREFEVLRKL    54
IKKAB_Drosophila        WERCRNLGEGGFGLVIHWRNRTTGREIATKHIKEMGALSADQQVKLSERWNKELNWSRQF    60
IKKAB_Ciona             WTLIKILGSGGFGQVSLWKNKQ-DVKLAVKQCKN------QLSRQNERRWRKEVEMMQRL    53
IKKA_Homo               WEMRERLGTGGFGNVCLYQHRELDLKIAIKSCRL------ELSTKNRERWCHEIQIMKKL    54
IKKB_Homo               WEMKERLGTGGFGNVIRWHNQETGEQIAIKQCRQ------ELSPRNRERWCLEIQIMRRL    54
IKKAB_Astrangia         WVEERCLGSGAFGTVLLYENKITKEQIALKRCRM------ELNPHNKKLWHQEVDIMKRL    54
IKKAB_Nematostella      WVEERCVGTGSFGTVTLWENKITKEQIVLKKCRL------DLSPSNRNQWQKEVEIMKGL    54
IKKAB_Aiptasia          WIEERCLGAGGFGTVTLWKHKYNHEYLAIKKCRL------DLSPANRQRWHQEVEILKKL    54
                        *     :* *. . *     :      . *            .          ..

TBK/E_Amphimedon        -THPNIVSFFELNEI--------EKKHQYHIIAMELCNGGSLYEVIDSPQNAYGLDEYQF    103
TBK/E_Astrangia         -NHENIVKLYASET---------ELRSQNEIIVMELCSGGSLFTLLENPANAYGFLEDDF    104
TBK/E_Nematostella      -DHENIVKIFASET---------ELRSQNEIIVMELCSGGSLFTMLEHPSNAYGLSEQDC    104
TBK/E_Aiptasia          -DHENIVRIFASEN---------ELRSQNEIIAMELCSGGSLYTLLEHPSNSYGFSEKDC    104
TBK/E_Drosophila        -NHENIVKLLAIEE---------DQEGRGKVIVMELCTGGSLFNILDDPENSYGLPEHEF    104
TBK/E_Ciona             -DHKNVVRLFSVEE---------ELTTKHDVIIMELCPNGSLYSMLDDPENLYGLPESEF    105
TBK_Homo                -NHKNIVKLFAIEE---------ETTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEF    104
IKKE_Homo               -NHQNIVKLFAVEE---------TGGSRQKVLVMEYCSSGSLLSVLESPENAFGLPEDEF    104
IKKAB_Drosophila        KNFPHIVAGVDIEDPDFLEYLNGMFSAKLPVIVLEYCNGGDVRKRLQSPENANGLTEFEV    120
IKKAB_Ciona             -NHPSIVNFVEV-----PVEIQNAYVDHYVALGMEYCEAGDLRKFLTQPENCCGLPEFQV    107
IKKA_Homo               -NHANVVKACDV-----PEELN-ILIHDVPLLAMEYCSGGDLRKLLNKPENCCGLKESQI    107
IKKB_Homo               -THPNVVAARDV-----PEGMQNLAPNDLPLLAMEYCQGGDLRKYLNQFENCCGLREGAI    108
IKKAB_Astrangia         -EHPNLVSAKDV-----PPPLD-VSDDELPLLAMEFCSGGDLRKVLNAPESCCGLKEKTV    107
IKKAB_Nematostella      -DHPNIVKAIDV-----PAVLD-VREGQLPLLGMEYCEGGDLRKVLNSPDNCAGLKEASV    107
IKKAB_Aiptasia          -DHANIVKAKDV-----PAILD-VSGGEIPLLAMEYCEGGDLRRILNTPENIRGLKESTV    107
                          .  :*                        : :* *  *.:   :    .  *: *

TBK/E_Amphimedon        KSVIFDVASGMRHLRDH-GFVHRDIKPGNIMRCINPDGSFVFKLADFGTARQLDP-NEHF    161
TBK/E_Astrangia         KQVVKDVAAGMKHLREQ-GMVHRDLKPGNIMRVAKVDGSFVYKLTDFGAARELEA-HEGF    162
TBK/E_Nematostella      ITVIRDVVAGMKHLHDN-GIVHRDLKPGNIMRVYRDDGSCVYKLTDFGAARELME-SDQF    162
TBK/E_Aiptasia          KDIIRDVVAGMEHLRKQ-GIVHRDLKPGNIMRVFNDDGTCSYKLTDFGAARELEHSAEQF    163
TBK/E_Drosophila        LLVLEHLCAGMKHLRDN-KLVHRDLKPGNIMKFISEDGQTIYKLTDFGAARELED-NQPF    162
TBK/E_Ciona             HRVLSHITAGMKHLHDK-GIVHRDLKPGNIMRSLDDDGTAVYKLTDFGAARELGD-DEQF    163
TBK_Homo                LIVLRDVVGGMNHLREN-GIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELED-DEQF    162
IKKE_Homo               LVVLRCVVAGMNHLREN-GIVHRDIKPGNIMRLVGEEGQSIYKLTDFGAARELDD-DEKF    162
IKKAB_Drosophila        RQILGALRKALHFLHSQCGICHRDLKPDNIVIQRGVDGKKIYKLTDFGLARGTPD-QTMV    179
IKKAB_Ciona             RNILQDIGSAIEHLHER-QLVHRDLKPENIVMKEKEKNVFQFKIIDLGYAKEINE-NSFG    165
IKKA_Homo               LSLLSDIGSGIRYLHEN-KIIHRDLKPENIVLQDVGGK-IIHKIIDLGYAKDVDQ-GSLC    164
IKKB_Homo               LTLLSDIASALRYLHEN-RIIHRDLKPENIVLQQGEQR-LIHKIIDLGYAKELDQ-GSLC    165
IKKAB_Astrangia         LKITSDVAAAVEFLHGH-RIIHRDLKPENIVISHADNK-VVYKLIDLGYAKELDQ-GSLA    164
IKKAB_Nematostella      LRVITDIANAVQFLHSK-RIIHRDLKPENIVINFTNGN-AVYKLIDLGYAKQLDQ-GSMA    164
IKKAB_Aiptasia          IEVTADVAHAIEFLHSK-RIIHRDLKPENIVIQHTDGK-DIYKLIDLGYAKQLDQ-YSIA    164
                          :   :  .:..*: .  : ***:** **:          .*: *:* *:
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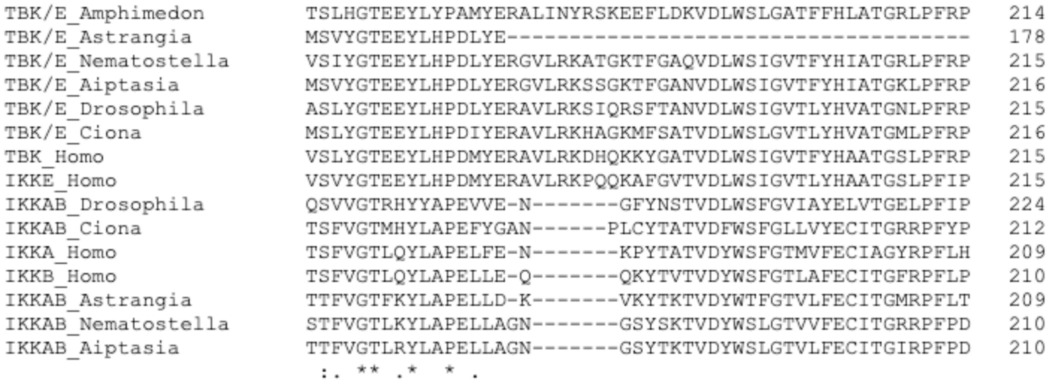
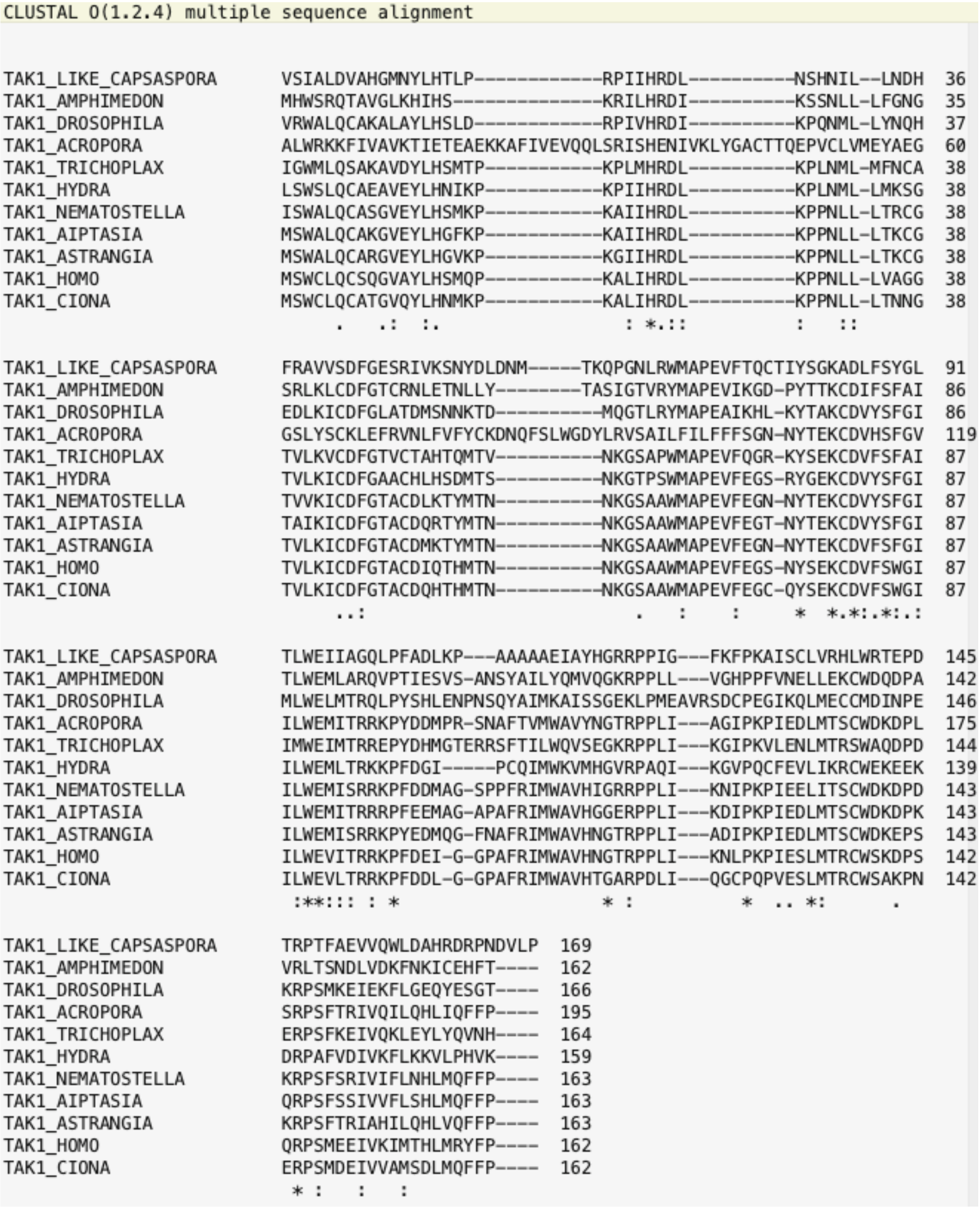


```
TBK/E_Amphimedon        TSLHGTEEYLYPAMYERALINYRSKEEFLDKVDLWSLGATFFHLATGRLPFRP   214
TBK/E_Astrangia         MSVYGTEEYLHPDLYE-------------------------------------   178
TBK/E_Nematostella      VSIYGTEEYLHPDLYERGVLRKATGKTFGAQVDLWSIGVTFYHIATGRLPFRP   215
TBK/E_Aiptasia          MSVYGTEEYLHPDLYERGVLRKSSGKTFGANVDLWSIGVTFYHIATGKLPFRP   216
TBK/E_Drosophila        ASLYGTEEYLHPDLYERAVLRKSIQRSFTANVDLWSIGVTLYHVATGNLPFRP   215
TBK/E_Ciona             MSLYGTEEYLHPDIYERAVLRKHAGKMFSATVDLWSLGVTLYHVATGMLPFRP   216
TBK_Homo                VSLYGTEEYLHPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRP   215
IKKE_Homo               VSVYGTEEYLHPDMYERAVLRKPQQKAFGVTVDLWSIGVTLYHAATGSLPFIP   215
IKKAB_Drosophila        QSVVGTRHYYAPEVVE-N-------GFYNSTVDLWSFGVIAYELVTGELPFIP   224
IKKAB_Ciona             TSFVGTMHYLAPEFYGAN------PLCYTATVDFWSFGLLVYECITGRRPFYP   212
IKKA_Homo               TSFVGTLQYLAPELFE-N-------KPYTATVDYWSFGTMVFECIAGYRPFLH   209
IKKB_Homo               TSFVGTLQYLAPELLE-Q-------QKYTVTVDYWSFGTLAFECITGFRPFLP   210
IKKAB_Astrangia         TTFVGTFKYLAPELLD-K-------VKYTKTVDYWTFGTVLFECITGMRPFLT   209
IKKAB_Nematostella      STFVGTLKYLAPELLAGN-------GSYSKTVDYWSLGTVVFECITGRRPFPD   210
IKKAB_Aiptasia          TTFVGTLRYLAPELLAGN-------GSYTKTVDYWSLGTVLFECITGIRPFPD   210
                        :.  ** .*  *  .
```

A.6 IKK Multiple Sequence Alignment

A multiple sequence alignment of known and putative IKK homologs encoding the STKc domain (motifs 1-7) was performed using CLUSTAL Omega prior to creating the IKK maximum likelihood tree.

* indicate a conserved amino acid; : indicates conservation of very similar amino acids; and . indicates conservation of similar amino acids.



```
CLUSTAL O(1.2.4) multiple sequence alignment


TAK1_LIKE_CAPSASPORA      VSIALDVAHGMNYLHTLP------------RPIIHRDL----------NSHNIL--LNDH  36
TAK1_AMPHIMEDON           MHWSRQTAVGLKHIHS--------------KRILHRDI----------KSSNLL-LFGNG  35
TAK1_DROSOPHILA           VRWALQCAKALAYLHSLD------------RPIVHRDI----------KPQNML-LYNQH  37
TAK1_ACROPORA             ALWRKKFIVAVKTIETEAEKKAFIVEVQQLSRISHENIVKLYGACTTQEPVCLVMEYAEG  60
TAK1_TRICHOPLAX           IGWMLQSAKAVDYLHSMTP-----------KPLMHRDL----------KPLNML-MFNCA  38
TAK1_HYDRA                LSWSLQCAEAVEYLHNIKP-----------KPIIHRDL----------KPLNML-LMKSG  38
TAK1_NEMATOSTELLA         ISWALQCASGVEYLHSMKP-----------KAIIHRDL----------KPPNLL-LTRCG  38
TAK1_AIPTASIA             MSWALQCAKGVEYLHGFKP-----------KAIIHRDL----------KPPNLL-LTKCG  38
TAK1_ASTRANGIA            MSWALQCARGVEYLHGVKP-----------KGIIHRDL----------KPPNLL-LTKCG  38
TAK1_HOMO                 MSWCLQCSQGVAYLHSMQP-----------KALIHRDL----------KPPNLL-LVAGG  38
TAK1_CIONA                MSWCLQCATGVQYLHNMKP-----------KALIHRDL----------KPPNLL-LTNNG  38
                               .   .:  :.                 : *.::          :   ::

TAK1_LIKE_CAPSASPORA      FRAVVSDFGESRIVKSNYDLDNM-----TKQPGNLRWMAPEVFTQCTIYSGKADLFSYGL  91
TAK1_AMPHIMEDON           SRLKLCDFGTCRNLETNLLY--------TASIGTVRYMAPEVIKGD-PYTTKCDIFSFAI  86
TAK1_DROSOPHILA           EDLKICDFGLATDMSNNKTD----------MQGTLRYMAPEAIKHL-KYTAKCDVYSFGI  86
TAK1_ACROPORA             GSLYSCKLEFRVNLFVFYCKDNQFSLWGDYLRVSAILFILFFFSGN-NYTEKCDVHSFGV  119
TAK1_TRICHOPLAX           TVLKVCDFGTVCTAHTQMTV----------NKGSAPWMAPEVFQGR-KYSEKCDVFSFAI  87
TAK1_HYDRA                TVLKICDFGAACHLHSDMTS----------NKGTPSWMAPEVFEGS-RYGEKCDVYSFGI  87
TAK1_NEMATOSTELLA         TVVKICDFGTACDLKTYMTN----------NKGSAAWMAPEVFEGN-NYTEKCDVYSFGI  87
TAK1_AIPTASIA             TAIKICDFGTACDQRTYMTN----------NKGSAAWMAPEVFEGT-NYTEKCDVYSFGI  87
TAK1_ASTRANGIA            TVLKICDFGTACDMKTYMTN----------NKGSAAWMAPEVFEGN-NYTEKCDVFSFGI  87
TAK1_HOMO                 TVLKICDFGTACDIQTHMTN----------NKGSAAWMAPEVFEGS-NYSEKCDVFSWGI  87
TAK1_CIONA                TVLKICDFGTACDQHTHMTN----------NKGSAAWMAPEVFEGC-QYSEKCDVFSWGI  87
                               ..:                         .   :    :     *  *.*:.*:.:

TAK1_LIKE_CAPSASPORA      TLWEIIAGQLPFADLKP---AAAAAEIAYHGRRPPIG---FKFPKAISCLVRHLWRTEPD  145
TAK1_AMPHIMEDON           TLWEMLARQVPTIESVS-ANSYAILYQMVQGKRPPLL---VGHPPFVNELLEKCWDQDPA  142
TAK1_DROSOPHILA           MLWELMTRQLPYSHLENPNSQYAIMKAISSGEKLPMEAVRSDCPEGIKQLMECCMDINPE  146
TAK1_ACROPORA             ILWEMITRRKPYDDMPR-SNAFTVMWAVYNGTRPPLI---AGIPKPIEDLMTSCWDKDPL  175
TAK1_TRICHOPLAX           IMWEIMTRREPYDHMGTERRSFTILWQVSEGKRPPLI---KGIPKVLENLMTRSWAQDPD  144
TAK1_HYDRA                ILWEMLTRKKPFDGI-----PCQIMWKVMHGVRPAQI---KGVPQCFEVLIKRCWEKEEK  139
TAK1_NEMATOSTELLA         ILWEMISRRKPFDDMAG-SPPFRIMWAVHIGRRPPLI---KNIPKPIEELITSCWDKDPD  143
TAK1_AIPTASIA             ILWEMITRRRPFEEMAG-APAFRIMWAVHGGERPPLI---KDIPKPIEDLMTSCWDKDPK  143
TAK1_ASTRANGIA            ILWEMISRRKPYEDMQG-FNAFRIMWAVHNGTRPPLI---ADIPKPIEDLMTSCWDKEPS  143
TAK1_HOMO                 ILWEVITRRKPFDEI-G-GPAFRIMWAVHNGTRPPLI---KNLPKPIESLMTRCWSKDPS  142
TAK1_CIONA                ILWEVLTRRKPFDDL-G-GPAFRIMWAVHTGARPDLI---QGCPQPVESLMTRCWSAKPN  142
                           :**::: : *                   * :          *  .. *:      .

TAK1_LIKE_CAPSASPORA      TRPTFAEVVQWLDAHRDRPNDVLP  169
TAK1_AMPHIMEDON           VRLTSNDLVDKFNKICEHFT----  162
TAK1_DROSOPHILA           KRPSMKEIEKFLGEQYESGT----  166
TAK1_ACROPORA             SRPSFTRIVQILQHLIQFFP----  195
TAK1_TRICHOPLAX           ERPSFKEIVQKLEYLYQVNH----  164
TAK1_HYDRA                DRPAFVDIVKFLKKVLPHVK----  159
TAK1_NEMATOSTELLA         KRPSFSRIVIFLNHLMQFFP----  163
TAK1_AIPTASIA             QRPSFSSIVVFLSHLMQFFP----  163
TAK1_ASTRANGIA            KRPSFTRIAHILQHLVQFFP----  163
TAK1_HOMO                 QRPSMEEIVKIMTHLMRYFP----  162
TAK1_CIONA                ERPSMDEIVVAMSDLMQFFP----  162
                           * :   :   :
```

A.7 TAK1 Multiple Sequence Alignment

A multiple sequence alignment of known and putative TAK1 homologs encoding the STKc domain (motifs 5-9) was performed using CLUSTAL Omega prior to creating the maximum likelihood tree (Figure 3-9). * indicate a conserved amino acid; : indicates conservation of very similar amino acids; and . indicates conservation of similar amino acids.

```
CLUSTAL O(1.2.4) multiple sequence alignment

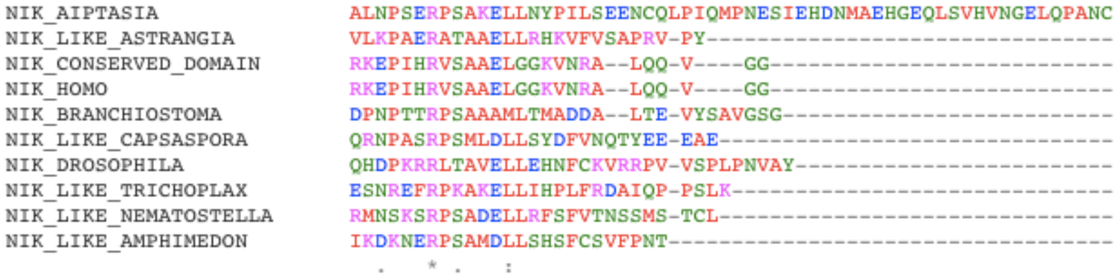

NIK_AIPTASIA               ------------------SSGS---------------------IVKANSGITLPFRKQTN
NIK_LIKE_ASTRANGIA         ----YLEGTHWMS-TRSIGEGFFGSCSL--CTDLHTGFL--------------FAIKKIP
NIK_CONSERVED_DOMAIN       ----YREEVHWATHQLRLGRGSFGEVH--RMEDKQTGFQ--------------CAVKKVR
NIK_HOMO                   ----YREEVHWATHQLRLGRGSFGEVH--RMEDKQTGFQ--------------CAVKKVR
NIK_BRANCHIOSTOMA          ----FRLDQHWWS-IMELGSGRFGTVYLSCLASEEQEFH--------------FAAKKLD
NIK_LIKE_CAPSASPORA        LRSVISLGVAPIK-KGVLGTGAFSTCFM--AAIPLDRMEAGGKAAHQPSRIALVAMKQMT
NIK_DROSOPHILA             ----RSVHFRWHR-GIKIGQGRFGKVYT--AVNNNTGEL--------------MAMKEIA
NIK_LIKE_TRICHOPLAX        ---------QWQK-GKLLGTGAYSTCYA--ARDIKSGTL--------------MAVKQVK
NIK_LIKE_NEMATOSTELLA      -------PNNWRK-GKLLGAGAFGQVYM--CHDLDTGRE--------------LAVKQIE
NIK_LIKE_AMPHIMEDON        ----ITAPARWSK-GRLLGTGAFGQVFL--CTDLDTQMD--------------MAVKVVD
                                             . *                                   *

NIK_AIPTASIA               GDDDEEDDENRNRKR---KLSRIPSRKYDPSELVIWSKLSGQNIRCLDLFGAVQDDQFVT
NIK_LIKE_ASTRANGIA         VE------VFE------------------SNEIEIWGSLSGRHPNILELYGAVKYRQTVI
NIK_CONSERVED_DOMAIN       LE------VFR------------------AEELMACAGLT--SPRIVPLYGAVREGPWVN
NIK_HOMO                   LE------VFR------------------AEELMACAGLT--SPRIVPLYGAVREGPWVN
NIK_BRANCHIOSTOMA          VT------QVR------------------RDELEICCCLD--NPYIAAHFGAVREGRETY
NIK_LIKE_CAPSASPORA        YA------RNT-------HEEEEKVMMQVMQEITILAGLV--HPNVVSFYGTQQDGNHVR
NIK_DROSOPHILA             IQ------PGE-----------TRALKNVAEELKILEGIK--HKNLVRYYGIEVHREELL
NIK_LIKE_TRICHOPLAX        QQ------QVY---------------ESLIKEISLLNRLN--HPNIVRCYGATVQDSHFN
NIK_LIKE_NEMATOSTELLA      TG------QLNS--------STKNEVKALEGEIEFMKAFR--NERIVQYYGIETDDLHIY
NIK_LIKE_AMPHIMEDON        ID------HIENIKPSLDSLKMSKEVRSFETEVQLLKNIH--HERVVGYYGTERREGKLF
                                                          *:     :          :*

NIK_AIPTASIA               IFMEYMEEGSLANLLQHQESGHLDERCCIYILQXVMEAVKFLHSLSVIHCDIKGENVFTN
NIK_LIKE_ASTRANGIA         IFMEYMSGGSVAEY-----AGRMNEFLAVYILGKVISAVEFMHSQQILHRDIKGGNVLLD
NIK_CONSERVED_DOMAIN       IFMELLEGGSLGQLVKE--QGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLS
NIK_HOMO                   IFMELLEGGSLGQLVKE--QGCLPEDRALYYLGQALEGLEYLHSRRILHGDVKADNVLLS
NIK_BRANCHIOSTOMA          IFMEFLEGYTLEKIIDQ--YRTLHQYMALFYLCQVFEGLVYLEEQRIVHSDVKAANMMVS
NIK_LIKE_CAPSASPORA        VIMELMAGGTVTSLLQR--MGKLTDSSAGFLARQLVEGMAYLHSMAVAHRDLKGTNLLLS
NIK_DROSOPHILA             IFMELCSEGTLESLVEL--TGNLPEALTRRFTAQLLSGVSELHKHGIVHRDIKTANIFLV
NIK_LIKE_TRICHOPLAX        IFAEWLAGGSIASMLHN--YGPFQENISNAYCLQILRGLVYLHDRRIVHRDVKGDNILVD
NIK_LIKE_NEMATOSTELLA      IFMEYLPGGSIHEHIKQ--HGALNESLTRKYSRQILEGILYLHTNRIVHRDIKGANILRD
NIK_LIKE_AMPHIMEDON        IFMEYLAGGSIYQHLKN--TGALSEALTRKYTRQILEGVAFLHGMKIVHRDIKGANILRD
                           :: *     :: .         : :          . .:  :.   : * *:*  *::

NIK_AIPTASIA               XTXTXIKLGDYGSAIQLPLGLECI--RLQKTINGTEPFMSPEVATL--------------
NIK_LIKE_ASTRANGIA         DTGQQVKLADFGMSVRCE------NFLQDNAPKGTEVFMAPEVCRS--E-YHSFSADIWS
NIK_CONSERVED_DOMAIN       SDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIPGTETHMAPEVVLG--R-SCDAKVDVWS
NIK_HOMO                   SDGSHAALCDFGHAVCLQPDGLGKSLLTGDYIPGTETHMAPEVVLG--R-SCDAKVDVWS
NIK_BRANCHIOSTOMA          SDGAHLKLIDFGMAHTIPDGADWVEPQRNAFPEGTQTHMPTEVAEC--K-PHNCKVDVWS
NIK_LIKE_CAPSASPORA        DDQMVLKIADFGSAVRVTDPNISH--DELREARGTAAFLAPEVIKGAS--SDCFASDVWS
NIK_DROSOPHILA             DGSNSLKLGDFGSAVKIQAHTTVP-G-ELQGYVGTQAYMAPEVFTKTNSDGHGRAADIWS
NIK_LIKE_TRICHOPLAX        ATGRIVKLADFGSAIQLTATKLTGAGLLQGQMVGTVAFMAPEVLRG--E-NYGRSSDVWS
NIK_LIKE_NEMATOSTELLA      LYGN-VKLADFGASKRLQTIRSK---TGFRSVHGTPYWMAPEVING--E-GYGRKADVWS
NIK_LIKE_AMPHIMEDON        SNGN-VKLADFGASKRLQTIRS-----GIGSVHGTPYWMAPEVIKG--DDPYTFKADIWS
                                  : *:* :                   **   :  **

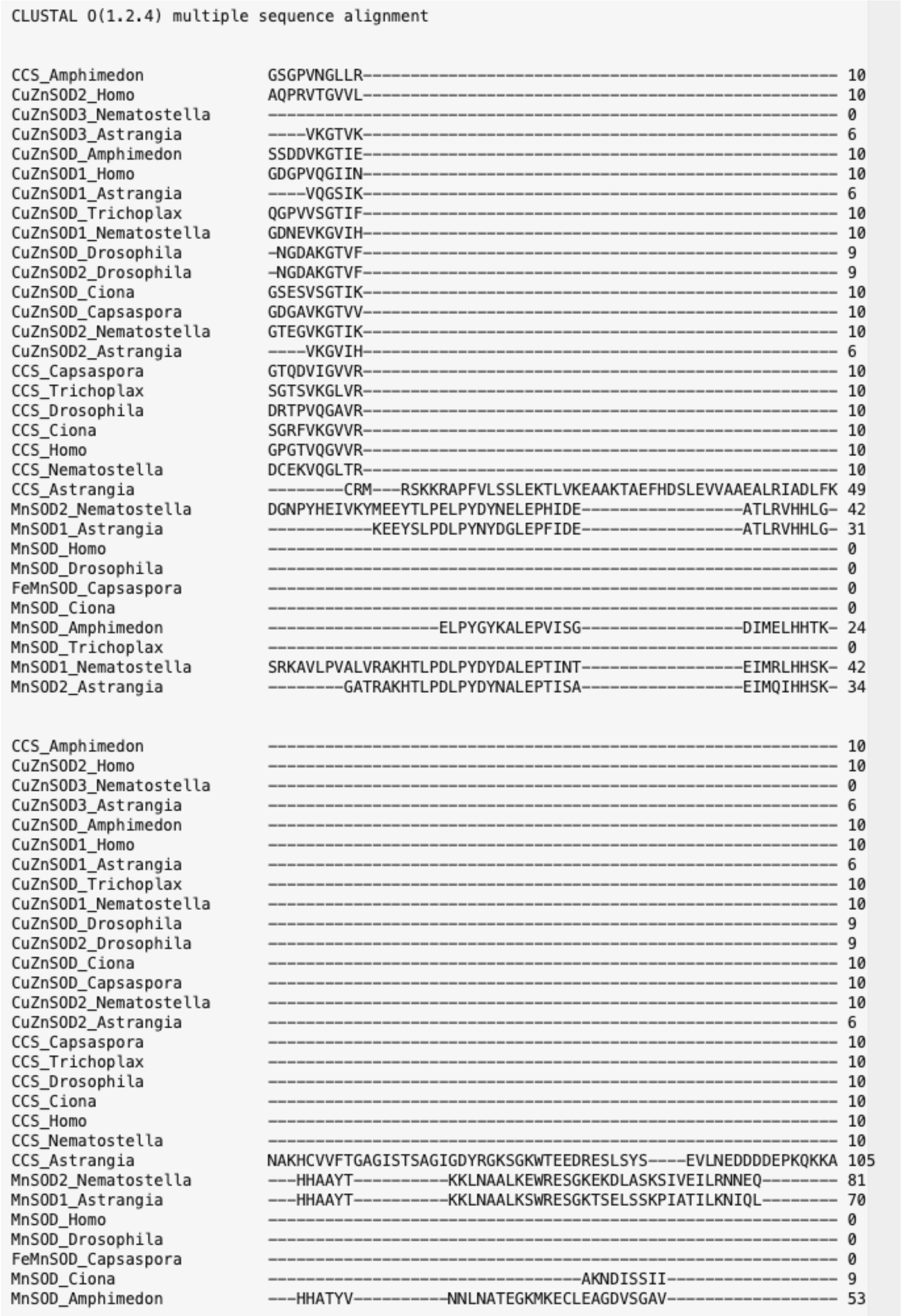
NIK_AIPTASIA               ----------------------------------EQPPP-----LPRCSDGMRAMLTDMF
NIK_LIKE_ASTRANGIA         LMCLLYQMLAGKPPWMEFFP----CAFLFKIGMASEPPP-----SPPCSPEVEDLFSLGF
NIK_CONSERVED_DOMAIN       SCCMMLHMLNGCHPWTQFFR----GPLCLK--IASEPPP-VREIPPSCAPLTAQAIQEGL
NIK_HOMO                   SCCMMLHMLNGCHPWTQFFR----GPLCLK--IASEPPP-VREIPPSCAPLTAQAIQEGL
NIK_BRANCHIOSTOMA          GCCVGLHMLNGCHPWIRRYS----HAATLLLIIVSKAEEIKTEIPSSIHESFQSLLRCGL
NIK_LIKE_CAPSASPORA        VGCCIIEMVSAQSPWTQEFGTDNQFSLMYAIASTEEMP----AWPESCQESTGHFLRSCL
NIK_DROSOPHILA             VGCVVVEMASGKRPWAQ-FDS--NFQIMFKVGM-GEKP----QAPESLSQEGHDFIDHCL
NIK_LIKE_TRICHOPLAX        LGCVMIQMLTGKLPWGA-DNISNHFALIYKIATATETP----SVPEHLRQDTRDFLLRCL
NIK_LIKE_NEMATOSTELLA      VGCTVVEMLTTKPPWAD-FE---PMAALFKIATQPTEP----ELPSDLSVDAVEFVRSTL
NIK_LIKE_AMPHIMEDON        VGATVVEMLKCRPPWSD-FE---PTAAMFKIVMNDTKP----DLPPHCSEQAHNFIELCF
                                                                                  .   :
```



```
NIK_AIPTASIA              ALNPSERPSAKELLNYPILSEENCQLPIQMPNESIEHDNMAEHGEQLSVHVNGELQPANC
NIK_LIKE_ASTRANGIA        VLKPAERATAAELLRHKVFVSAPRV-PY--------------------------------
NIK_CONSERVED_DOMAIN      RKEPIHRVSAAELGGKVNRA--LQQ-V----GG---------------------------
NIK_HOMO                  RKEPIHRVSAAELGGKVNRA--LQQ-V----GG---------------------------
NIK_BRANCHIOSTOMA         DPNPTTRPSAAAMLTMADDA--LTE-VYSAVGSG--------------------------
NIK_LIKE_CAPSASPORA       QRNPASRPSMLDLLSYDFVNQTYEE-EAE-------------------------------
NIK_DROSOPHILA            QHDPKRRLTAVELLEHNFCKVRRPV-VSPLPNVAY-------------------------
NIK_LIKE_TRICHOPLAX       ESNREFRPKAKELLIHPLFRDAIQP-PSLK------------------------------
NIK_LIKE_NEMATOSTELLA     RMNSKSRPSADELLRFSFVTNSSMS-TCL-------------------------------
NIK_LIKE_AMPHIMEDON       IKDKNERPSAMDLLSHSFCSVFPNT-----------------------------------
                            .   * .   :
```

A.8 NIK Multiple Sequence Alignment

A multiple sequence alignment of known and putative NIK homologs encoding the STKc (motifs 1-6 and 8-9) was performed using CLUSTAL Omega prior to creating the maximum likelihood tree (Figure 3-12). * indicates a conserved amino acid; : indicates conservation of very similar amino acids; and . indicates conservation of similar amino acids.

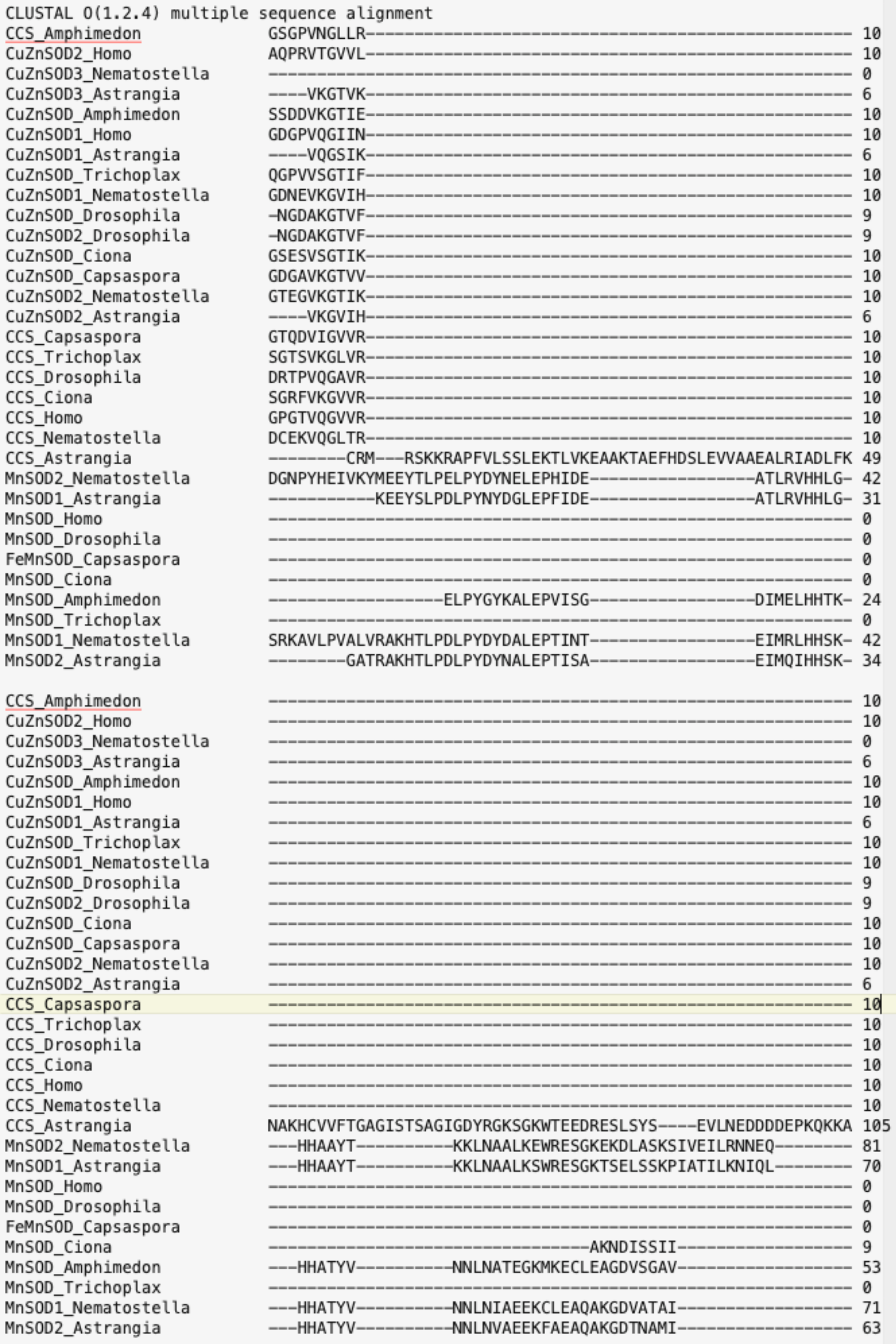


```
CLUSTAL O(1.2.4) multiple sequence alignment


CCS_Amphimedon             GSGPVNGLLR-------------------------------------------------- 10
CuZnSOD2_Homo              AQPRVTGVVL-------------------------------------------------- 10
CuZnSOD3_Nematostella      ------------------------------------------------------------ 0
CuZnSOD3_Astrangia         ----VKGTVK-------------------------------------------------- 6
CuZnSOD_Amphimedon         SSDDVKGTIE-------------------------------------------------- 10
CuZnSOD1_Homo              GDGPVQGIIN-------------------------------------------------- 10
CuZnSOD1_Astrangia         ----VQGSIK-------------------------------------------------- 6
CuZnSOD_Trichoplax         QGPVVSGTIF-------------------------------------------------- 10
CuZnSOD1_Nematostella      GDNEVKGVIH-------------------------------------------------- 10
CuZnSOD_Drosophila         -NGDAKGTVF-------------------------------------------------- 9
CuZnSOD2_Drosophila        -NGDAKGTVF-------------------------------------------------- 9
CuZnSOD_Ciona              GSESVSGTIK-------------------------------------------------- 10
CuZnSOD_Capsaspora         GDGAVKGTVV-------------------------------------------------- 10
CuZnSOD2_Nematostella      GTEGVKGTIK-------------------------------------------------- 10
CuZnSOD2_Astrangia         ----VKGVIH-------------------------------------------------- 6
CCS_Capsaspora             GTQDVIGVVR-------------------------------------------------- 10
CCS_Trichoplax             SGTSVKGLVR-------------------------------------------------- 10
CCS_Drosophila             DRTPVQGAVR-------------------------------------------------- 10
CCS_Ciona                  SGRFVKGVVR-------------------------------------------------- 10
CCS_Homo                   GPGTVQGVVR-------------------------------------------------- 10
CCS_Nematostella           DCEKVQGLTR-------------------------------------------------- 10
CCS_Astrangia              --------CRM---RSKKRAPFVLSSLEKTLVKEAAKTAEFHDSLEVVAAEALRIADLFK 49
MnSOD2_Nematostella        DGNPYHEIVKYMEEYTLPELPYDYNELEPHIDE-----------------ATLRVHHLG- 42
MnSOD1_Astrangia           -----------KEEYSLPDLPYNYDGLEPFIDE-----------------ATLRVHHLG- 31
MnSOD_Homo                 ------------------------------------------------------------ 0
MnSOD_Drosophila           ------------------------------------------------------------ 0
FeMnSOD_Capsaspora         ------------------------------------------------------------ 0
MnSOD_Ciona                ------------------------------------------------------------ 0
MnSOD_Amphimedon           ------------------ELPYGYKALEPVISG-----------------DIMELHHTK- 24
MnSOD_Trichoplax           ------------------------------------------------------------ 0
MnSOD1_Nematostella        SRKAVLPVALVRAKHTLPDLPYDYDALEPTINT-----------------EIMRLHHSK- 42
MnSOD2_Astrangia           --------GATRAKHTLPDLPYDYNALEPTISA-----------------EIMQIHHSK- 34


CCS_Amphimedon             ------------------------------------------------------------ 10
CuZnSOD2_Homo              ------------------------------------------------------------ 10
CuZnSOD3_Nematostella      ------------------------------------------------------------ 0
CuZnSOD3_Astrangia         ------------------------------------------------------------ 6
CuZnSOD_Amphimedon         ------------------------------------------------------------ 10
CuZnSOD1_Homo              ------------------------------------------------------------ 10
CuZnSOD1_Astrangia         ------------------------------------------------------------ 6
CuZnSOD_Trichoplax         ------------------------------------------------------------ 10
CuZnSOD1_Nematostella      ------------------------------------------------------------ 10
CuZnSOD_Drosophila         ------------------------------------------------------------ 9
CuZnSOD2_Drosophila        ------------------------------------------------------------ 9
CuZnSOD_Ciona              ------------------------------------------------------------ 10
CuZnSOD_Capsaspora         ------------------------------------------------------------ 10
CuZnSOD2_Nematostella      ------------------------------------------------------------ 10
CuZnSOD2_Astrangia         ------------------------------------------------------------ 6
CCS_Capsaspora             ------------------------------------------------------------ 10
CCS_Trichoplax             ------------------------------------------------------------ 10
CCS_Drosophila             ------------------------------------------------------------ 10
CCS_Ciona                  ------------------------------------------------------------ 10
CCS_Homo                   ------------------------------------------------------------ 10
CCS_Nematostella           ------------------------------------------------------------ 10
CCS_Astrangia              NAKHCVVFTGAGISTSAGIGDYRGKSGKWTEEDRESLSYS----EVLNEDDDDEPKQKKA 105
MnSOD2_Nematostella        ---HHAAYT----------KKLNAALKEWRESGKEKDLASKSIVEILRNNEQ-------- 81
MnSOD1_Astrangia           ---HHAAYT----------KKLNAALKSWRESGKTSELSSKPIATILKNIQL-------- 70
MnSOD_Homo                 ------------------------------------------------------------ 0
MnSOD_Drosophila           ------------------------------------------------------------ 0
FeMnSOD_Capsaspora         ------------------------------------------------------------ 0
MnSOD_Ciona                ---------------------------------AKNDISSII------------------ 9
MnSOD_Amphimedon           ---HHATYV----------NNLNATEGKMKECLEAGDVSGAV------------------ 53
```

Appendix A.9 SOD Multiple Sequence Alignment Continued on Next Page



```
CLUSTAL O(1.2.4) multiple sequence alignment
CCS_Amphimedon             GSGPVNGLLR-------------------------------------------------- 10
CuZnSOD2_Homo              AQPRVTGVVL-------------------------------------------------- 10
CuZnSOD3_Nematostella      ------------------------------------------------------------ 0
CuZnSOD3_Astrangia         ----VKGTVK-------------------------------------------------- 6
CuZnSOD_Amphimedon         SSDDVKGTIE-------------------------------------------------- 10
CuZnSOD1_Homo              GDGPVQGIIN-------------------------------------------------- 10
CuZnSOD1_Astrangia         ----VQGSIK-------------------------------------------------- 6
CuZnSOD_Trichoplax         QGPVVSGTIF-------------------------------------------------- 10
CuZnSOD1_Nematostella      GDNEVKGVIH-------------------------------------------------- 10
CuZnSOD_Drosophila         -NGDAKGTVF-------------------------------------------------- 9
CuZnSOD2_Drosophila        -NGDAKGTVF-------------------------------------------------- 9
CuZnSOD_Ciona              GSESVSGTIK-------------------------------------------------- 10
CuZnSOD_Capsaspora         GDGAVKGTVV-------------------------------------------------- 10
CuZnSOD2_Nematostella      GTEGVKGTIK-------------------------------------------------- 10
CuZnSOD2_Astrangia         ----VKGVIH-------------------------------------------------- 6
CCS_Capsaspora             GTQDVIGVVR-------------------------------------------------- 10
CCS_Trichoplax             SGTSVKGLVR-------------------------------------------------- 10
CCS_Drosophila             DRTPVQGAVR-------------------------------------------------- 10
CCS_Ciona                  SGRFVKGVVR-------------------------------------------------- 10
CCS_Homo                   GPGTVQGVVR-------------------------------------------------- 10
CCS_Nematostella           DCEKVQGLTR-------------------------------------------------- 10
CCS_Astrangia              --------CRM---RSKKRAPFVLSSLEKTLVKEAAKTAEFHDSLEVVAAEALRIADLFK 49
MnSOD2_Nematostella        DGNPYHEIVKYMEEYTLPELPYDYNELEPHIDE-----------------ATLRVHHLG- 42
MnSOD1_Astrangia           -----------KEEYSLPDLPYNYDGLEPFIDE-----------------ATLRVHHLG- 31
MnSOD_Homo                 ------------------------------------------------------------ 0
MnSOD_Drosophila           ------------------------------------------------------------ 0
FeMnSOD_Capsaspora         ------------------------------------------------------------ 0
MnSOD_Ciona                ------------------------------------------------------------ 0
MnSOD_Amphimedon           ------------------ELPYGYKALEPVISG-----------------DIMELHHTK- 24
MnSOD_Trichoplax           ------------------------------------------------------------ 0
MnSOD1_Nematostella        SRKAVLPVALVRAKHTLPDLPYDYDALEPTINT-----------------EIMRLHHSK- 42
MnSOD2_Astrangia           --------GATRAKHTLPDLPYDYNALEPTISA-----------------EIMQIHHSK- 34

CCS_Amphimedon             ------------------------------------------------------------ 10
CuZnSOD2_Homo              ------------------------------------------------------------ 10
CuZnSOD3_Nematostella      ------------------------------------------------------------ 0
CuZnSOD3_Astrangia         ------------------------------------------------------------ 6
CuZnSOD_Amphimedon         ------------------------------------------------------------ 10
CuZnSOD1_Homo              ------------------------------------------------------------ 10
CuZnSOD1_Astrangia         ------------------------------------------------------------ 6
CuZnSOD_Trichoplax         ------------------------------------------------------------ 10
CuZnSOD1_Nematostella      ------------------------------------------------------------ 10
CuZnSOD_Drosophila         ------------------------------------------------------------ 9
CuZnSOD2_Drosophila        ------------------------------------------------------------ 9
CuZnSOD_Ciona              ------------------------------------------------------------ 10
CuZnSOD_Capsaspora         ------------------------------------------------------------ 10
CuZnSOD2_Nematostella      ------------------------------------------------------------ 10
CuZnSOD2_Astrangia         ------------------------------------------------------------ 6
CCS_Capsaspora             ------------------------------------------------------------ 10
CCS_Trichoplax             ------------------------------------------------------------ 10
CCS_Drosophila             ------------------------------------------------------------ 10
CCS_Ciona                  ------------------------------------------------------------ 10
CCS_Homo                   ------------------------------------------------------------ 10
CCS_Nematostella           ------------------------------------------------------------ 10
CCS_Astrangia              NAKHCVVFTGAGISTSAGIGDYRGKSGKWTEEDRESLSYS----EVLNEDDDDEPKQKKA 105
MnSOD2_Nematostella        ---HHAAYT----------KKLNAALKEWRESGKEKDLASKSIVEILRNNEQ-------- 81
MnSOD1_Astrangia           ---HHAAYT----------KKLNAALKSWRESGKTSELSSKPIATILKNIQL-------- 70
MnSOD_Homo                 ------------------------------------------------------------ 0
MnSOD_Drosophila           ------------------------------------------------------------ 0
FeMnSOD_Capsaspora         ------------------------------------------------------------ 0
MnSOD_Ciona                ---------------------------------AKNDISSII------------------ 9
MnSOD_Amphimedon           ---HHATYV----------NNLNATEGKMKECLEAGDVSGAV------------------ 53
MnSOD_Trichoplax           ------------------------------------------------------------ 0
MnSOD1_Nematostella        ---HHATYV----------NNLNIAEEKCLEAQAKGDVATAI------------------ 71
MnSOD2_Astrangia           ---HHATYV----------NNLNVAEEKFAEAQAKGDTNAMI------------------ 63
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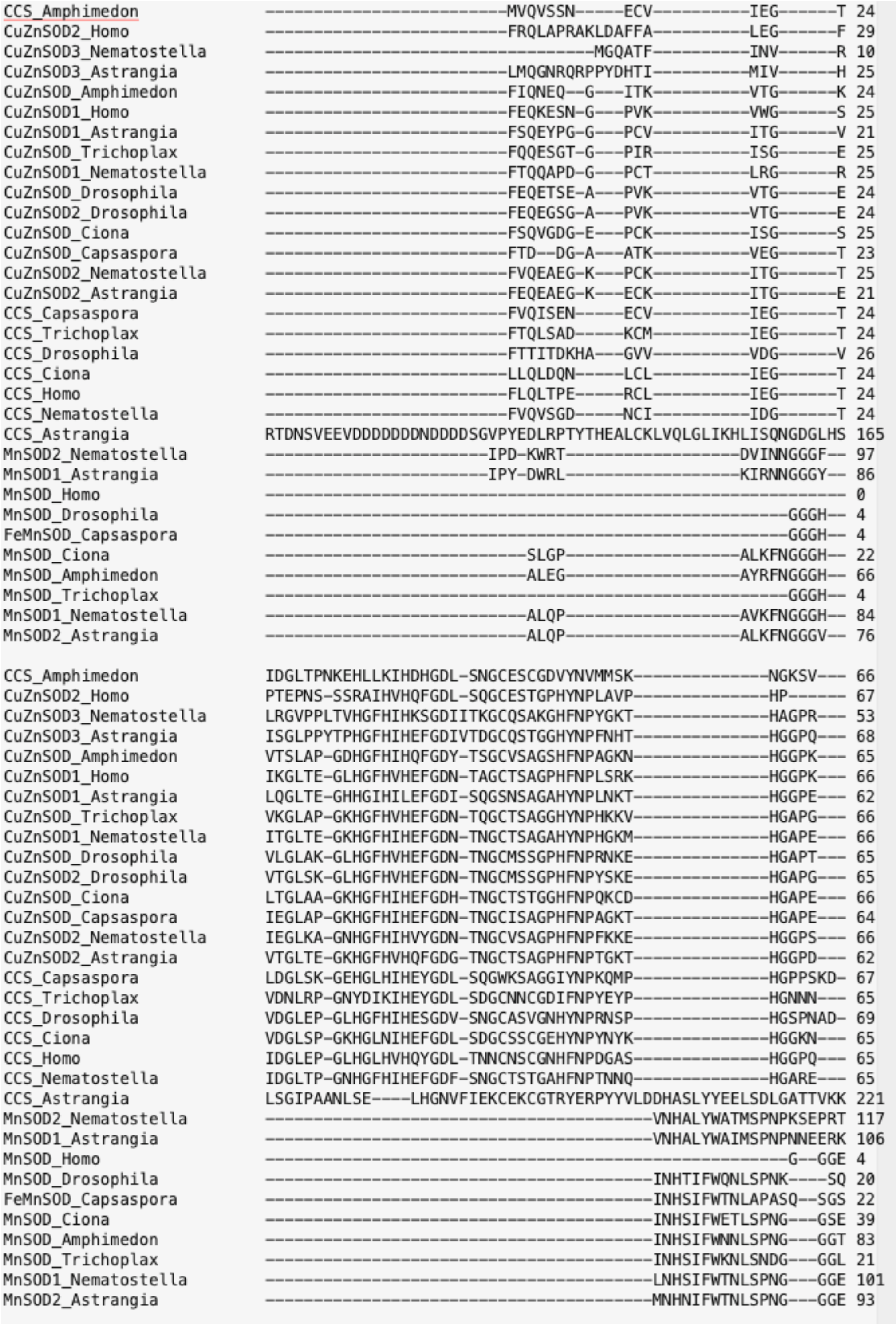
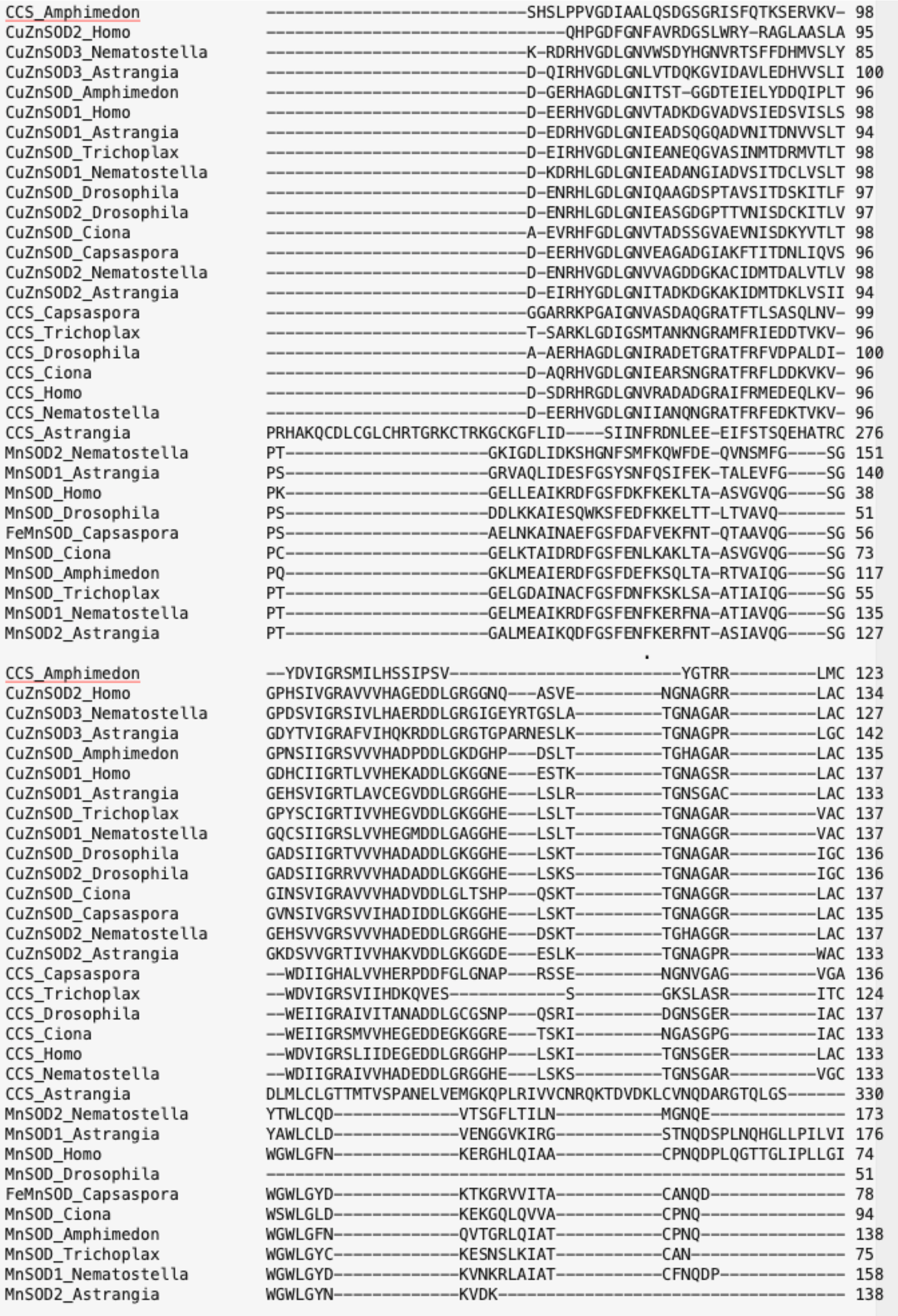
Appendix A.9 SOD Multiple Sequence Alignment Continued on Next Page



```
CCS_Amphimedon            -------------------------MVQVSSN-----ECV----------IEG------T 24
CuZnSOD2_Homo             -------------------------FRQLAPRAKLDAFFA----------LEG------F 29
CuZnSOD3_Nematostella     ----------------------------------MGQATF----------INV------R 10
CuZnSOD3_Astrangia        -------------------------LMQGNRQRPPYDHTI----------MIV------H 25
CuZnSOD_Amphimedon        -------------------------FIQNEQ--G---ITK----------VTG------K 24
CuZnSOD1_Homo             -------------------------FEQKESN-G---PVK----------VWG------S 25
CuZnSOD1_Astrangia        -------------------------FSQEYPG-G---PCV----------ITG------V 21
CuZnSOD_Trichoplax        -------------------------FQQESGT-G---PIR----------ISG------E 25
CuZnSOD1_Nematostella     -------------------------FTQQAPD-G---PCT----------LRG------R 25
CuZnSOD_Drosophila        -------------------------FEQETSE-A---PVK----------VTG------E 24
CuZnSOD2_Drosophila       -------------------------FEQEGSG-A---PVK----------VTG------E 24
CuZnSOD_Ciona             -------------------------FSQVGDG-E---PCK----------ISG------S 25
CuZnSOD_Capsaspora        -------------------------FTD--DG-A---ATK----------VEG------T 23
CuZnSOD2_Nematostella     -------------------------FVQEAEG-K---PCK----------ITG------T 25
CuZnSOD2_Astrangia        -------------------------FEQEAEG-K---ECK----------ITG------E 21
CCS_Capsaspora            -------------------------FVQISEN-----ECV----------IEG------T 24
CCS_Trichoplax            -------------------------FTQLSAD-----KCM----------IEG------T 24
CCS_Drosophila            -------------------------FTTITDKHA---GVV----------VDG------V 26
CCS_Ciona                 -------------------------LLQLDQN-----LCL----------IEG------T 24
CCS_Homo                  -------------------------FLQLTPE-----RCL----------IEG------T 24
CCS_Nematostella          -------------------------FVQVSGD-----NCI----------IDG------T 24
CCS_Astrangia             RTDNSVEEVDDDDDDDNDDDDSGVPYEDLRPTYTHEALCKLVQLGLIKHLISQNGDGLHS 165
MnSOD2_Nematostella       -----------------------IPD-KWRT------------------DVINNGGGF-- 97
MnSOD1_Astrangia          -----------------------IPY-DWRL------------------KIRNNGGGY-- 86
MnSOD_Homo                ------------------------------------------------------------ 0
MnSOD_Drosophila          ------------------------------------------------------GGGH-- 4
FeMnSOD_Capsaspora        ------------------------------------------------------GGGH-- 4
MnSOD_Ciona               ---------------------------SLGP------------------ALKFNGGGH-- 22
MnSOD_Amphimedon          ---------------------------ALEG------------------AYRFNGGGH-- 66
MnSOD_Trichoplax          ------------------------------------------------------GGGH-- 4
MnSOD1_Nematostella       ---------------------------ALQP------------------AVKFNGGGH-- 84
MnSOD2_Astrangia          ---------------------------ALQP------------------ALKFNGGGV-- 76

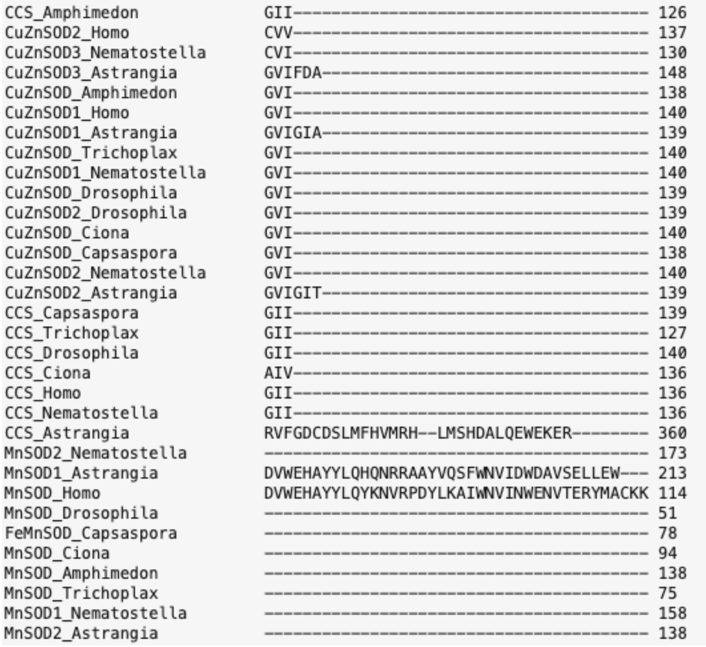
CCS_Amphimedon            IDGLTPNKEHLLKIHDHGDL-SNGCESCGDVYNVMMSK--------------NGKSV--- 66
CuZnSOD2_Homo             PTEPNS-SSRAIHVHQFGDL-SQGCESTGPHYNPLAVP--------------HP------ 67
CuZnSOD3_Nematostella     LRGVPPLTVHGFHIHKSGDIITKGCQSAKGHFNPYGKT--------------HAGPR--- 53
CuZnSOD3_Astrangia        ISGLPPYTPHGFHIHEFGDIVTDGCQSTGGHYNPFNHT--------------HGGPQ--- 68
CuZnSOD_Amphimedon        VTSLAP-GDHGFHIHQFGDY-TSGCVSAGSHFNPAGKN--------------HGGPK--- 65
CuZnSOD1_Homo             IKGLTE-GLHGFHVHEFGDN-TAGCTSAGPHFNPLSRK--------------HGGPK--- 66
CuZnSOD1_Astrangia        LQGLTE-GHHGIHILEFGDI-SQGSNSAGAHYNPLNKT--------------HGGPE--- 62
CuZnSOD_Trichoplax        VKGLAP-GKHGFHVHEFGDN-TQGCTSAGGHYNPHKKV--------------HGAPG--- 66
CuZnSOD1_Nematostella     ITGLTE-GKHGFHIHEFGDN-TNGCTSAGAHYNPHGKM--------------HGAPE--- 66
CuZnSOD_Drosophila        VLGLAK-GLHGFHVHEFGDN-TNGCMSSGPHFNPRNKE--------------HGAPT--- 65
CuZnSOD2_Drosophila       VTGLSK-GLHGFHVHEFGDN-TNGCMSSGPHFNPYSKE--------------HGAPG--- 65
CuZnSOD_Ciona             LTGLAA-GKHGFHIHEFGDH-TNGCTSTGGHFNPQKCD--------------HGAPE--- 66
CuZnSOD_Capsaspora        IEGLAP-GKHGFHIHEFGDN-TNGCISAGPHFNPAGKT--------------HGAPE--- 64
CuZnSOD2_Nematostella     IEGLKA-GNHGFHIHVYGDN-TNGCVSAGPHFNPFKKE--------------HGGPS--- 66
CuZnSOD2_Astrangia        VTGLTE-GKHGFHVHQFGDG-TNGCTSAGPHFNPTGKT--------------HGGPD--- 62
CCS_Capsaspora            LDGLSK-GEHGLHIHEYGDL-SQGWKSAGGIYNPKQMP--------------HGPPSKD- 67
CCS_Trichoplax            VDNLRP-GNYDIKIHEYGDL-SDGCNNCGDIFNPYEYP--------------HGNNN--- 65
CCS_Drosophila            VDGLEP-GLHGFHIHESGDV-SNGCASVGNHYNPRNSP--------------HGSPNAD- 69
CCS_Ciona                 VDGLSP-GKHGLNIHEFGDL-SDGCSSCGEHYNPYNYK--------------HGGKN--- 65
CCS_Homo                  IDGLEP-GLHGLHVHQYGDL-TNNCNSCGNHFNPDGAS--------------HGGPQ--- 65
CCS_Nematostella          IDGLTP-GNHGFHIHEFGDF-SNGCTSTGAHFNPTNNQ--------------HGARE--- 65
CCS_Astrangia             LSGIPAANLSE----LHGNVFIEKCEKCGTRYERPYYVLDDHASLYYEELSDLGATTVKK 221
MnSOD2_Nematostella       ----------------------------------------VNHALYWATMSPNPKSEPRT 117
MnSOD1_Astrangia          ----------------------------------------VNHALYWAIMSPNPNNEERK 106
MnSOD_Homo                ------------------------------------------------------G--GGE 4
MnSOD_Drosophila          ----------------------------------------INHTIFWQNLSPNK----SQ 20
FeMnSOD_Capsaspora        ----------------------------------------INHSIFWTNLAPASQ--SGS 22
MnSOD_Ciona               ----------------------------------------INHSIFWETLSPNG---GSE 39
MnSOD_Amphimedon          ----------------------------------------INHSIFWNNLSPNG---GGT 83
MnSOD_Trichoplax          ----------------------------------------INHSIFWKNLSNDG---GGL 21
MnSOD1_Nematostella       ----------------------------------------LNHSIFWTNLSPNG---GGE 101
MnSOD2_Astrangia          ----------------------------------------MNHNIFWTNLSPNG---GGE 93
```

Appendix A.9 SOD Multiple Sequence Alignment Continued on Next Page



```
CCS_Amphimedon             ---------------------------SHSLPPVGDIAALQSDGSGRISFQTKSERVKV- 98
CuZnSOD2_Homo              -------------------------------QHPGDFGNFAVRDGSLWRY-RAGLAASLA 95
CuZnSOD3_Nematostella      ---------------------------K-RDRHVGDLGNVWSDYHGNVRTSFFDHMVSLY 85
CuZnSOD3_Astrangia         ---------------------------D-QIRHVGDLGNLVTDQKGVIDAVLEDHVVSLI 100
CuZnSOD_Amphimedon         ---------------------------D-GERHAGDLGNITST-GGDTEIELYDDQIPLT 96
CuZnSOD1_Homo              ---------------------------D-EERHVGDLGNVTADKDGVADVSIEDSVISLS 98
CuZnSOD1_Astrangia         ---------------------------D-EDRHVGDLGNIEADSQGQADVNITDNVVSLT 94
CuZnSOD_Trichoplax         ---------------------------D-EIRHVGDLGNIEANEQGVASINMTDRMVTLT 98
CuZnSOD1_Nematostella      ---------------------------D-KDRHLGDLGNIEADANGIADVSITDCLVSLT 98
CuZnSOD_Drosophila         ---------------------------D-ENRHLGDLGNIQAAGDSPTAVSITDSKITLF 97
CuZnSOD2_Drosophila        ---------------------------D-ENRHLGDLGNIEASGDGPTTVNISDCKITLV 97
CuZnSOD_Ciona              ---------------------------A-EVRHFGDLGNVTADSSGVAEVNISDKYVTLT 98
CuZnSOD_Capsaspora         ---------------------------D-EERHVGDLGNVEAGADGIAKFTITDNLIQVS 96
CuZnSOD2_Nematostella      ---------------------------D-ENRHVGDLGNVVAGDDGKACIDMTDALVTLV 98
CuZnSOD2_Astrangia         ---------------------------D-EIRHYGDLGNITADKDGKAKIDMTDKLVSII 94
CCS_Capsaspora             ---------------------------GGARRKPGAIGNVASDAQGRATFTLSASQLNV- 99
CCS_Trichoplax             ---------------------------T-SARKLGDIGSMTANKNGRAMFRIEDDTVKV- 96
CCS_Drosophila             ---------------------------A-AERHAGDLGNIRADETGRATFRFVDPALDI- 100
CCS_Ciona                  ---------------------------D-AQRHVGDLGNIEARSNGRATFRFLDDKVKV- 96
CCS_Homo                   ---------------------------D-SDRHRGDLGNVRADADGRAIFRMEDEQLKV- 96
CCS_Nematostella           ---------------------------D-EERHVGDLGNIIANQNGRATFRFEDKTVKV- 96
CCS_Astrangia              PRHAKQCDLCGLCHRTGRKCTRKGCKGFLID----SIINFRDNLEE-EIFSTSQEHATRC 276
MnSOD2_Nematostella        PT---------------------GKIGDLIDKSHGNFSMFKQWFDE-QVNSMFG----SG 151
MnSOD1_Astrangia           PS---------------------GRVAQLIDESFGSYSNFQSIFEK-TALEVFG----SG 140
MnSOD_Homo                 PK---------------------GELLEAIKRDFGSFDKFKEKLTA-ASVGVQG----SG 38
MnSOD_Drosophila           PS---------------------DDLKKAIESQWKSFEDFKKELTT-LTVAVQ------- 51
FeMnSOD_Capsaspora         PS---------------------AELNKAINAEFGSFDAFVEKFNT-QTAAVQG----SG 56
MnSOD_Ciona                PC---------------------GELKTAIDRDFGSFENLKAKLTA-ASVGVQG----SG 73
MnSOD_Amphimedon           PQ---------------------GKLMEAIERDFGSFDEFKSQLTA-RTVAIQG----SG 117
MnSOD_Trichoplax           PT---------------------GELGDAINACFGSFDNFKSKLSA-ATIAIQG----SG 55
MnSOD1_Nematostella        PT---------------------GELMEAIKRDFGSFENFKERFNA-ATIAVQG----SG 135
MnSOD2_Astrangia           PT---------------------GALMEAIKQDFGSFENFKERFNT-ASIAVQG----SG 127
                                                                  .
CCS_Amphimedon             --YDVIGRSMILHSSIPSV------------------------YGTRR---------LMC 123
CuZnSOD2_Homo              GPHSIVGRAVVVHAGEDDLGRGGNQ---ASVE---------NGNAGRR---------LAC 134
CuZnSOD3_Nematostella      GPDSVIGRSIVLHAERDDLGRGIGEYRTGSLA---------TGNAGAR---------LAC 127
CuZnSOD3_Astrangia         GDYTVIGRAFVIHQKRDDLGRGTGPARNESLK---------TGNAGPR---------LGC 142
CuZnSOD_Amphimedon         GPNSIIGRSVVVHADPDDLGKDGHP---DSLT---------TGHAGAR---------LAC 135
CuZnSOD1_Homo              GDHCIIGRTLVVHEKADDLGKGGNE---ESTK---------TGNAGSR---------LAC 137
CuZnSOD1_Astrangia         GEHSVIGRTLAVCEGVDDLGRGGHE---LSLR---------TGNSGAC---------LAC 133
CuZnSOD_Trichoplax         GPYSCIGRTIVVHEGVDDLGKGGHE---LSLT---------TGNAGAR---------VAC 137
CuZnSOD1_Nematostella      GQCSIIGRSLVVHEGMDDLGAGGHE---LSLT---------TGNAGGR---------VAC 137
CuZnSOD_Drosophila         GADSIIGRTVVVHADADDLGKGGHE---LSKT---------TGNAGAR---------IGC 136
CuZnSOD2_Drosophila        GADSIIGRRVVVHADADDLGKGGHE---LSKS---------TGNAGAR---------IGC 136
CuZnSOD_Ciona              GINSVIGRAVVVHADVDDLGLTSHP---QSKT---------TGNAGGR---------LAC 137
CuZnSOD_Capsaspora         GVNSIVGRSVVIHADIDDLGKGGHE---LSKT---------TGNAGGR---------LAC 135
CuZnSOD2_Nematostella      GEHSVVGRSVVVHADEDDLGRGGHE---DSKT---------TGHAGGR---------LAC 137
CuZnSOD2_Astrangia         GKDSVVGRTIVVHAKVDDLGKGGDE---ESLK---------TGNAGPR---------WAC 133
CCS_Capsaspora             --WDIIGHALVVHERPDDFGLGNAP---RSSE---------NGNVGAG---------VGA 136
CCS_Trichoplax             --WDVIGRSVIIHDKQVES------------S---------GKSLASR---------ITC 124
CCS_Drosophila             --WEIIGRAIVITANADDLGCGSNP---QSRI---------DGNSGER---------IAC 137
CCS_Ciona                  --WEIIGRSMVVHEGEDDEGKGGRE---TSKI---------NGASGPG---------IAC 133
CCS_Homo                   --WDVIGRSLIIDEGEDDLGRGGHP---LSKI---------TGNSGER---------LAC 133
CCS_Nematostella           --WDIIGRAIVVHADEDDLGRGGHE---LSKS---------TGNSGAR---------VGC 133
CCS_Astrangia              DLMLCLGTTMTVSPANELVEMGKQPLRIVVCNRQKTDVDKLCVNQDARGTQLGS------ 330
MnSOD2_Nematostella        YTWLCQD-------------VTSGFLTILN-----------MGNQE-------------- 173
MnSOD1_Astrangia           YAWLCLD-------------VENGGVKIRG-----------STNQDSPLNQHGLLPILVI 176
MnSOD_Homo                 WGWLGFN-------------KERGHLQIAA-----------CPNQDPLQGTTGLIPLLGI 74
MnSOD_Drosophila           ------------------------------------------------------------ 51
FeMnSOD_Capsaspora         WGWLGYD-------------KTKGRVVITA-----------CANQD-------------- 78
MnSOD_Ciona                WSWLGLD-------------KEKGQLQVVA-----------CPNQ--------------- 94
MnSOD_Amphimedon           WGWLGFN-------------QVTGRLQIAT-----------CPNQ--------------- 138
MnSOD_Trichoplax           WGWLGYC-------------KESNSLKIAT-----------CAN---------------- 75
MnSOD1_Nematostella        WGWLGYD-------------KVNKRLAIAT-----------CFNQDP------------- 158
MnSOD2_Astrangia           WGWLGYN-------------KVDK------------------------------------ 138
```

Appendix A.9 SOD Multiple Sequence Alignment Continued on Next Page



```
CCS_Amphimedon             GII------------------------------------- 126
CuZnSOD2_Homo              CVV------------------------------------- 137
CuZnSOD3_Nematostella      CVI------------------------------------- 130
CuZnSOD3_Astrangia         GVIFDA---------------------------------- 148
CuZnSOD_Amphimedon         GVI------------------------------------- 138
CuZnSOD1_Homo              GVI------------------------------------- 140
CuZnSOD1_Astrangia         GVIGIA---------------------------------- 139
CuZnSOD_Trichoplax         GVI------------------------------------- 140
CuZnSOD1_Nematostella      GVI------------------------------------- 140
CuZnSOD_Drosophila         GVI------------------------------------- 139
CuZnSOD2_Drosophila        GVI------------------------------------- 139
CuZnSOD_Ciona              GVI------------------------------------- 140
CuZnSOD_Capsaspora         GVI------------------------------------- 138
CuZnSOD2_Nematostella      GVI------------------------------------- 140
CuZnSOD2_Astrangia         GVIGIT---------------------------------- 139
CCS_Capsaspora             GII------------------------------------- 139
CCS_Trichoplax             GII------------------------------------- 127
CCS_Drosophila             GII------------------------------------- 140
CCS_Ciona                  AIV------------------------------------- 136
CCS_Homo                   GII------------------------------------- 136
CCS_Nematostella           GII------------------------------------- 136
CCS_Astrangia              RVFGDCDSLMFHVMRH--LMSHDALQEWEKER-------- 360
MnSOD2_Nematostella        ---------------------------------------- 173
MnSOD1_Astrangia           DVWEHAYYLQHQNRRAAYVQSFWNVIDWDAVSELLEW--- 213
MnSOD_Homo                 DVWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYMACKK 114
MnSOD_Drosophila           ---------------------------------------- 51
FeMnSOD_Capsaspora         ---------------------------------------- 78
MnSOD_Ciona                ---------------------------------------- 94
MnSOD_Amphimedon           ---------------------------------------- 138
MnSOD_Trichoplax           ---------------------------------------- 75
MnSOD1_Nematostella        ---------------------------------------- 158
MnSOD2_Astrangia           ---------------------------------------- 138
```

A.9 SOD Multiple Sequence Alignment
A multiple sequence alignment of known and putative SOD homologs encoding the catalytic domain (motifs 1-10) was performed using CLUSTAL Omega prior to creating the maximum likelihood tree (Figure 3-15).

MEME Output User Note:
The following MEME outputs can be uploaded as .txt files onto MEME when asked to input motif files. For A.11 IKK MEME output, motifs can be uploaded as a .htm file or typed in fasta format (DNA, RNA or protein). Please see below for further guidance from MEME on inputting motifs.

"Type in motifs

> When this option is available you may directly input multiple motifs by typing them (or using "cut-and-paste"). First select the desired motif alphabet using the menu immediately to the left. If you select the "Custom" option then you must provide an alphabet definition in the file input that immediately follows. Warning: custom alphabets are *case-sensitive*. You may optionally give each motif an identifier and alternate name by inputting a line like `>Identifer Alternate-Name` preceeding the motif. You can then enter each motif as either matrices, sequence sites or regular expressions. You can enter multiple motifs by typing an empty line after each motif. Individual motifs will be shown in square brackets, and errors in your motifs will be highlighted in red while warnings will be highlighted in yellow. Mouse-over individual motifs to display their sequence logos. View the examples for more information on what is possible.

Upload motifs

When this option is available you may upload a file containing motifs in MEME motif format. This includes the outputs generated by MEME and DREME, as well as files you create using the motif conversion scripts or manually following the MEME motif format guidelines.

Databases (select category)

When this option is available you can select the category of motif database desired from the list below it. Then select the motif database from the displayed list. Consult the motif database documentation for descriptions of all the motif databases present on this MEME Suite server.

Submitted motifs

This option is only available when you have invoked the current program by clicking on a button in the output report of a different MEME Suite program. By selecting this option you will input the motifs sent by that program."

(http://meme-suite.org/doc/mast.html)

A.10 NF-κB MEME Output from Finnerty and Gilmore, 2005

```
**********************************************************************
MEME - Motif discovery tool
**********************************************************************
MEME version 4.10.2 (Release date: Thu Sep 03 15:00:54 2015 -0700)

For further information on how to interpret these results or to get
a copy of the MEME software please access http://meme-suite.org .

This file may be used as input to the MAST algorithm for searching
sequence databases for matches to groups of motifs.  MAST is
available
for interactive use and downloading at http://meme-suite.org .
**********************************************************************


**********************************************************************
REFERENCE
**********************************************************************
If you use this program in your research, please cite:

Timothy L. Bailey and Charles Elkan,
"Fitting a mixture model by expectation maximization to discover
motifs in biopolymers", Proceedings of the Second International
Conference on Intelligent Systems for Molecular Biology, pp. 28-36,
AAAI Press, Menlo Park, California, 1994.
**********************************************************************
```

```
********************************************************************
TRAINING SET
********************************************************************
DATAFILE= SFile2_NFkB-NFAT_MEME_input.txt
ALPHABET= ACDEFGHIKLMNPQRSTVWY
Sequence name            Weight Length  Sequence name
Weight Length
-------------            ------ ------  -------------
NFkB[Ciona               1.0000   1200  rel1[Ciona]
1.0000    290
NFat?                    1.0000   1093  NFkB1_Homo
1.0000    969
NFkB2_Homo               1.0000    899  RelA_Homo
1.0000    448
RelB_Homo                1.0000    579  cRel
1.0000    619
NFAT1                    1.0000    905  NFAT2
1.0000    353
NFAT3                    1.0000    832  NFAT4
1.0000   1075
NFAT5                    1.0000   1531  NFkBCys_Nev
1.0000    440
NFkBSer_Nev              1.0000    440  NFAT_Nev
1.0000    921
NFkB_Ed                  1.0000    860  NFAT_Ed
1.0000    460
NFkBb_Aiptasia           1.0000    848  NFAT_Aiptasia
1.0000    678
NFkB_Acropora            1.0000    904  NFAT_Acropora
1.0000    679
NFkB_Corallimorph        1.0000    915  NFAT_Corallimorph
1.0000    538
NFkB_Hydra               1.0000    477  NFAT_Hydra
1.0000   1975
NFkB_Platygyra           1.0000    918  NFATa_Platygyra
1.0000    529
NFATb_Platygyra          1.0000    550  NFkB_Biomphalaria
1.0000    610
NFkB_Sphaeroforma_arctic 1.0000    449  Relish_Biomphalaria
1.0000   1085
Relish_Dmel              1.0000    971  Dorsal_Dmel
1.0000    678
Dif_Dmel                 1.0000    667  NFkB_Amphimedon
1.0000   1095
NFkB_Capsaspora          1.0000   1223  IkB_Nev
1.0000    383
IkB_Hym                  1.0000    304
********************************************************************
```

```
********************************************************************
COMMAND LINE SUMMARY
********************************************************************
This information can also be useful in the event you wish to report
a
problem with the MEME software.

command: meme SFile2_NFkB-NFAT_MEME_input.txt -protein -oc . -
nostatus -time 18000 -maxsize 60000 -mod anr -nmotifs 20 -minw 6 -
maxw 50

model:  mod=           anr    nmotifs=        20    evt=
inf
object function=  E-value of product of p-values
width:  minw=            6    maxw=           50    minic=
0.00
width:  wg=             11    ws=              1    endgaps=
yes
nsites: minsites=        2    maxsites=       50    wnsites=
0.8
theta:  prob=            1    spmap=         pam    spfuzz=
120
global: substring=     yes    branching=      no    wbranch=
no
em:     prior=       megap    b=          151950    maxiter=
50
        distance=    1e-05
data:   n=           30390    N=              39

sample: seed=            0    seqfrac=         1
Dirichlet mixture priors file: prior30.plib
Letter frequencies in dataset:
A 0.069 C 0.018 D 0.054 E 0.059 F 0.034 G 0.070 H 0.026 I 0.044 K
0.049
L 0.085 M 0.023 N 0.051 P 0.072 Q 0.059 R 0.044 S 0.095 T 0.058 V
0.063
W 0.006 Y 0.023
Background letter frequencies (from dataset with add-one prior
applied):
A 0.069 C 0.018 D 0.054 E 0.059 F 0.034 G 0.070 H 0.026 I 0.044 K
0.049
L 0.085 M 0.023 N 0.051 P 0.072 Q 0.059 R 0.044 S 0.095 T 0.058 V
0.063
W 0.006 Y 0.023
********************************************************************
```

```
********************************************************************
MOTIF  1 MEME    width =  31  sites =  30  llr = 1849  E-value =
1.2e-462
********************************************************************
--------------------------------------------------------------------
      Motif 1 Description
--------------------------------------------------------------------
Simplified        A  :::::2:::11:2:::::::::::::1::::
pos.-specific     C  :::5::1:1::32:::::::::7::::::::
probability       D  ::::::5:::::::::6::::::6::::57:
matrix            E  :2:::::::2:::2::29:::::1::::2::
                  F  :::::::::::::::::::2:::::3:::2:
                  G  ::::::::::9:::a8:::2::2:::::2::
                  H  :::::::::::::::::::::::::::::::
                  I  ::a::1:1::::::::::32:2:::1::::7
                  K  :5::1::4:::::1:::::::::29::7::2
                  L  7::::2::::::::::::3:98:::::::::
                  M  :::::4:::::::1::::::1::::::::::
                  N  ::::::1:3::::1:21::::::::::::::
                  P  2::::::::::1::::::::::::::1::::
                  Q  ::::::::::::::::::::::::::7::::
                  R  :1::7::3:::::1::::::::::1:1::::
                  S  ::::::4125:4:1:::::::::1:::2:::
                  T  :::1:1::3::1:3::1::::::::::1::1
                  V  :1:1:1::::::6:::::4::::::7:::1:
                  W  :::22::::::::::::::::::::::::::
                  Y  :::::::::::::::::::3:::::::::::

         bits    7.3
                 6.6
                 5.9
                 5.1
Relative         4.4   * *                 *
Entropy          3.7   ***     *   *  *    * *
(88.9 bits)      2.9 * ***     * * **** ******* * **
                 2.2 ********  *** *****************
                 1.5 *******************************
                 0.7 *******************************
                 0.0 -------------------------------

Multilevel           LKICRMDKNSGSVTGGDEVYLLCDKVQKDDI
consensus            PE WWLSRTE CAE  E IF IGK F  GFK
sequence                               LG


--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 1 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value
Site
-------------             ----- ---------            ---------------
NFkBSer_Nev                 275  5.95e-40 LDSKEPSASQ
LKICRMDKNSGCVTGGDEIYLLCDKVQKDDI EIHFYEMDDI
NFkBCys_Nev                 275  5.95e-40 LDSKAPSASQ
LKICRMDKNSGCVTGGDEIYLLCDKVQKDDI EIHFYEMDDI
NFkB_Platygyra              269  8.92e-40 YDSKAPSASN
LKICRMDRNSGCVTGGDEVYLLCDKVQKDDI EVTFYETEVE
NFkB_Acropora               268  1.73e-37 YDSKAPSAAN
LKICRMDRNSGCVTGNDEVYLLCDKVQKDDI AVVFYEIDEN
NFkBb_Aiptasia              272  1.43e-36 YDSKAPASCQ
LKICRMDKNSGCVTGGDEIYLLCDRVQKDDI EIRFYENNDD
NFkB_Ed                     276  4.22e-36 RDSKAPSASQ
LKICRMDKNSGCVTGGTEIFLLCDKVQKDDI ELRFYEFDDN
NFkB_Corallimorph           273  2.81e-34 YDSKSPAAST
LKICRMDRNSGCVTGGDEVYLLCDRVQRDDI EVHFYEEDES
NFkB1_Homo                  251  3.34e-34 YDSKAPNASN
LKIVRMDRTAGCVTGGEEIYLLCDKVQKDDI QIRFYEEEEN
NFkB[Ciona                  223  3.35e-33 FDSKAPNAAT
LKICRMDCNAGSASGGDEVYLLCDKVQKDDI QVVFSEEDMQ
NFkB2_Homo                  228  1.15e-32 HDSKSPGASN
LKISRMDKTAGSVRGGDEVYLLCDKVQKDDI EVRFYEDDEN
cRel                        186  4.29e-32 YDNRAPNTAE
LRICRVNKNCGSVRGGDEIFLLCDKVQKDDI EVRFVLNDWE
RelA_Homo                   194  7.55e-32 FDNRAPNTAE
LKICRVNRNSGSCLGGDEIFLLCDKVQKEDI EVYFTGPGWE
rel1[Ciona]                 185  3.88e-31 YDKKATCSSV
LKICRVDKTHGSCMGNEEVFLLCDKVQKEDI QVVFYRDNWE
Relish_Biomphalaria         254  6.56e-31 YDSKSPGASA
LKICRMDKYGGCCSGNEEVFLLCEKVQKDDI QVRFVEQNPD
NFkB_Amphimedon             252  4.38e-30 YDSKAPSAGT
LKICRLDRTSGSVKGGDDVFLLCDKVQKNDI EVVFYEDKQE
RelB_Homo                   303  1.47e-29 YDKKSTNTSE
LRICRINKESGPCTGGEELYLLCDKVQKEDI SVVFSRASWE
NFkB_Biomphalaria           290  3.16e-28 PIHDKKSSKD
LVICRVDKSSGKARGGDEVFLLCDKVNKEDI KVRFYEENEQ
NFAT_Corallimorph           487  4.36e-26 QCSSSGPPGN
PEIWWASVTEGSVEGGDELGLIGKKFQSGFK VRFFSEKPSG
NFATb_Platygyra             472  1.03e-25 QCSSSGPPGN
PEIWWASISEGSAEGGDELGLIGKKFQSGFK VRFFSVNPTG
NFATa_Platygyra             451  1.03e-25 QCSSSGPPGN
PEIWWASISEGSAEGGDELGLIGKKFQSGFK VRFFSVNPTG
NFAT_Acropora               448  1.66e-25 QCSSSGPPGN
PEIWWASISEGSANGGDELGLIGKKFQSGFK VRFFSVNASE
NFAT_Nev                    683  1.82e-25 QCSSSGATGN
PEIWWTSRTEGCVEGGEELGLIGKKFPTGFK VRFSANLPSG
```

```
NFAT_Ed                     389  1.63e-24 QCSSSGAAGS
PEIWWASRTEGSVEGGDELGLIGKRFPTGFK VKFSADLPSG
NFAT_Aiptasia               430  3.09e-23 QCSSSGPTGS
PEIWWTSRTEGSVEGKEEMGLIGKKFPSDVK VRFYANLSSG
Dif_Dmel                    255  6.02e-23 SSPIYGKSSE
LTITRLCSCAATANGGDEIIMLCEKIAKDDI EVRFYETDKD
Dorsal_Dmel                 225  5.79e-22 PIFDKKAMSD
LVICRLCSCSATVFGNTQIILLCEKVAKEDI SVRFFEEKNG
NFkB_Hydra                  237  1.60e-21 YDGKNKKGCE
YKILRLSSVSGTPKGGEEVWMLCDKFDKSDV EVRFFDDTPV
Relish_Dmel                 343  1.07e-20 NNRKSAQTGE
LRIVRLSKPTGGVMGNDELILLVEKVSKKNI KVRFFEEDED
NFkB_Capsaspora             397  1.55e-20 AISQPIYNAK
LAITKISHSSGPVTGGNEVIMLCSKIRKGVT GVRMTDPTQW
NFkB_Sphaeroforma_arctic    318  8.97e-19 VVSFPIFNAK
LMINKLSTGFGSCNGQNEVILLCSKVRKATT TVVVSDAAML
--------------------------------------------------------------------


--------------------------------------------------------------------
      Motif 1 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkBSer_Nev                         6e-40  274_[1]_135
NFkBCys_Nev                         6e-40  274_[1]_135
NFkB_Platygyra                    8.9e-40  268_[1]_619
NFkB_Acropora                     1.7e-37  267_[1]_606
NFkBb_Aiptasia                    1.4e-36  271_[1]_546
NFkB_Ed                           4.2e-36  275_[1]_554
NFkB_Corallimorph                 2.8e-34  272_[1]_612
NFkB1_Homo                        3.3e-34  250_[1]_688
NFkB[Ciona                        3.4e-33  222_[1]_947
NFkB2_Homo                        1.1e-32  227_[1]_641
cRel                              4.3e-32  185_[1]_403
RelA_Homo                         7.6e-32  193_[1]_224
rel1[Ciona]                       3.9e-31  184_[1]_75
Relish_Biomphalaria               6.6e-31  253_[1]_801
NFkB_Amphimedon                   4.4e-30  251_[1]_813
RelB_Homo                         1.5e-29  302_[1]_246
NFkB_Biomphalaria                 3.2e-28  289_[1]_290
NFAT_Corallimorph                 4.4e-26  486_[1]_21
NFATb_Platygyra                     1e-25  471_[1]_48
NFATa_Platygyra                     1e-25  450_[1]_48
NFAT_Acropora                     1.7e-25  447_[1]_201
NFAT_Nev                          1.8e-25  682_[1]_208
NFAT_Ed                           1.6e-24  388_[1]_41
NFAT_Aiptasia                     3.1e-23  429_[1]_218
Dif_Dmel                            6e-23  254_[1]_382
Dorsal_Dmel                       5.8e-22  224_[1]_423
NFkB_Hydra                        1.6e-21  236_[1]_210
Relish_Dmel                       1.1e-20  342_[1]_598
```

```
NFkB_Capsaspora                   1.6e-20  396_[1]_796
NFkB_Sphaeroforma_arctic            9e-19  317_[1]_101
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 1 width=31 seqs=30
NFkBSer_Nev              (  275) LKICRMDKNSGCVTGGDEIYLLCDKVQKDDI  1
NFkBCys_Nev              (  275) LKICRMDKNSGCVTGGDEIYLLCDKVQKDDI  1
NFkB_Platygyra           (  269) LKICRMDRNSGCVTGGDEVYLLCDKVQKDDI  1
NFkB_Acropora            (  268) LKICRMDRNSGCVTGNDEVYLLCDKVQKDDI  1
NFkBb_Aiptasia           (  272) LKICRMDKNSGCVTGGDEIYLLCDRVQKDDI  1
NFkB_Ed                  (  276) LKICRMDKNSGCVTGGTEIFLLCDKVQKDDI  1
NFkB_Corallimorph        (  273) LKICRMDRNSGCVTGGDEVYLLCDRVQRDDI  1
NFkB1_Homo               (  251) LKIVRMDRTAGCVTGGEEIYLLCDKVQKDDI  1
NFkB[Ciona               (  223) LKICRMDCNAGSASGGDEVYLLCDKVQKDDI  1
NFkB2_Homo               (  228) LKISRMDKTAGSVRGGDEVYLLCDKVQKDDI  1
cRel                     (  186) LRICRVNKNCGSVRGGDEIFLLCDKVQKDDI  1
RelA_Homo                (  194) LKICRVNRNSGSCLGGDEIFLLCDKVQKEDI  1
rel1[Ciona]              (  185) LKICRVDKTHGSCMGNEEVFLLCDKVQKEDI  1
Relish_Biomphalaria      (  254) LKICRMDKYGGCCSGNEEVFLLCEKVQKDDI  1
NFkB_Amphimedon          (  252) LKICRLDRTSGSVKGGDDVFLLCDKVQKNDI  1
RelB_Homo                (  303) LRICRINKESGPCTGGEELYLLCDKVQKEDI  1
NFkB_Biomphalaria        (  290) LVICRVDKSSGKARGGDEVFLLCDKVNKEDI  1
NFAT_Corallimorph        (  487) PEIWWASVTEGSVEGGDELGLIGKKFQSGFK  1
NFATb_Platygyra          (  472) PEIWWASISEGSAEGGDELGLIGKKFQSGFK  1
NFATa_Platygyra          (  451) PEIWWASISEGSAEGGDELGLIGKKFQSGFK  1
NFAT_Acropora            (  448) PEIWWASISEGSANGGDELGLIGKKFQSGFK  1
NFAT_Nev                 (  683) PEIWWTSRTEGCVEGGEELGLIGKKFPTGFK  1
NFAT_Ed                  (  389) PEIWWASRTEGSVEGGDELGLIGKRFPTGFK  1
NFAT_Aiptasia            (  430) PEIWWTSRTEGSVEGKEEMGLIGKKFPSDVK  1
Dif_Dmel                 (  255) LTITRLCSCAATANGGDEIIMLCEKIAKDDI  1
Dorsal_Dmel              (  225) LVICRLCSCSATVFGNTQIILLCEKVAKEDI  1
NFkB_Hydra               (  237) YKILRLSSVSGTPKGGEEVWMLCDKFDKSDV  1
Relish_Dmel              (  343) LRIVRLSKPTGGVMGNDELILLVEKVSKKNI  1
NFkB_Capsaspora          (  397) LAITKISHSSGPVTGGNEVIMLCSKIRKGVT  1
NFkB_Sphaeroforma_arctic (  318) LMINKLSTGFGSCNGQNEVILLCSKVRKATT  1
//

--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 1 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 31 n= 29220 bayes= 10.6011 E= 1.2e-
462
  -571   -523   -749   -715   -263   -697   -515   -292   -661
309   -250   -679    160   -642   -611   -698   -581   -404   -298
61
   -88   -445   -326    187   -449   -411   -266   -396    324   -
402     44   -292   -473   -240    126   -344    -70     -2   -333
-339
  -691   -626   -786   -851   -642   -720   -754    448   -810   -
567   -588   -816   -800   -858   -769   -839   -700   -430   -611
-680
  -235    472   -507   -435   -237   -405   -367   -139   -384    -
82   -164    -68   -492   -428   -373   -136     20     32    502
-251
  -451   -528   -553   -397   -568   -527   -337   -500     81   -
489   -432   -409   -601   -304    392   -494   -432   -505    508
-417
   117   -280   -551   -473   -250   -471   -405     81   -423
121    384   -454   -535   -466   -412   -420     18    116   -252
-281
  -403    182    304   -337   -582   -340   -324   -647   -355   -
657   -617    109   -547   -420   -435    188   -378   -619   -518
-445
  -307     77   -367   -272   -410   -423     31    104    283   -
367   -303   -311   -488   -256    267      0    -71    -85   -319
-332
  -235    164   -243    -52   -358   -107   -247   -306   -170   -
351   -269    245   -124   -246   -220     69    216    -87   -293
37
    87     73   -270    181    -17   -102     27   -346   -178   -
371   -294   -245   -420   -256   -228    216    -48   -333   -308
-304
   -50   -388   -344   -403   -489    369   -410   -483   -368   -
549   -440   -322   -519   -488   -364   -357   -418   -458   -331
-422
  -230    416   -502   -552   -577    -93   -536   -568    -57   -
603   -519   -435    -17   -562   -525    216     77   -460   -503
-557
   156    318   -659   -646   -557   -390   -616   -393   -640   -
538   -485   -560   -113   -622   -586   -356   -372    320   -512
-580
  -191   -359   -210    162    -19   -313   -195   -312     66   -
127    130     85   -371   -182    109    -41    225   -300   -260
-247
  -512   -598   -571   -637   -682    382   -613   -711   -600   -
742   -675   -561   -703   -705   -585   -603   -648   -693   -519
-622
```

```
  -270   -401   -293   -369   -486    352   -372   -483   -105   -
545   -441    100   -511   -146   -344   -345   -405   -465   -331
-407
  -378   -524    353    186   -555   -385   -343   -535   -329   -
564   -507     38   -532   -351   -418   -376     -3   -517   -467
-442
  -488   -554   -189    403   -578   -531   -472   -501   -526   -
611   -546   -442   -687   -327   -532   -584   -538   -551   -461
-533
  -484   -434   -780   -730   -353   -743   -713    274   -699
164     60   -723   -763   -720   -699   -728   -488    264   -461
-506
  -637   -526   -697   -692    280    167   -329    184   -620   -
479   -478   -565   -727   -603   -563   -645   -613   -547    245
386
  -493   -447   -697   -610   -242   -674   -551   -189   -570
336    201   -642   -643   -550   -523   -641   -491   -301   -325
-402
  -547   -490   -815   -738   -274   -763   -650    235   -700
314   -183   -753   -741   -650   -647   -759   -548   -301   -370
-453
  -256    533   -675   -677   -608    171   -638   -535   -671   -
622   -554   -581   -593   -649   -612   -378   -402    -86   -536
-610
  -365   -634    328    142   -639   -428   -388   -558    215   -
569   -505   -284   -523   -306   -405    -54   -410   -516   -556
-503
  -363   -369   -489   -433   -516   -481   -390   -378    421   -
476   -391   -378   -515   -434     31   -486   -395   -469   -311
-427
  -466   -415   -764   -727    290   -743   -757     88   -702   -
320   -335   -716   -777   -779   -737   -726   -470    336   -550
-516
   -84   -342   -140   -150   -412   -410    -82   -362   -243   -
313   -204   -111    -62    363    -18   -201   -311   -379   -234
-353
  -420   -510   -510   -375   -594   -501   -325   -484    384   -
477   -416   -379   -585   -289     19     69     11   -486   -394
-431
   -99   -536    303    151   -576    165   -327   -593    -44   -
602   -548    -19   -530   -365   -406   -128   -376   -569   -508
-441
  -378   -449    360   -268    228   -361   -324   -441   -364   -
510   -467    -27   -548   -423   -421   -353    -91    -15   -383
-337
  -436   -401   -712   -643   -443   -673   -642    385    217   -
336   -340   -638   -731   -638   -510   -644     15    -20   -533
-521
--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
      Motif 1 position-specific probability matrix
---------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 31 nsites= 30 E= 1.2e-462
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.733333  0.000000  0.000000  0.233333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.033333
 0.033333  0.000000  0.000000  0.233333  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.033333  0.000000  0.000000
0.000000  0.100000  0.000000  0.033333  0.066667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.533333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.033333  0.000000  0.033333  0.000000
0.000000  0.000000  0.033333  0.066667  0.066667  0.233333  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.066667  0.000000  0.000000  0.000000  0.000000
0.000000  0.700000  0.000000  0.000000  0.000000  0.233333  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.066667  0.000000  0.200000  0.366667  0.000000  0.000000
0.000000  0.000000  0.000000  0.066667  0.133333  0.000000  0.000000
 0.000000  0.066667  0.466667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.100000  0.000000
0.000000  0.000000  0.366667  0.000000  0.000000  0.000000  0.000000
 0.000000  0.033333  0.000000  0.000000  0.000000  0.000000
0.033333  0.100000  0.366667  0.000000  0.000000  0.000000  0.000000
0.000000  0.300000  0.100000  0.033333  0.033333  0.000000  0.000000
 0.000000  0.066667  0.000000  0.033333  0.000000  0.033333
0.000000  0.000000  0.000000  0.000000  0.000000  0.333333  0.033333
0.000000  0.000000  0.166667  0.266667  0.033333  0.000000  0.033333
 0.133333  0.033333  0.000000  0.233333  0.033333  0.033333
0.033333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.466667  0.033333  0.000000  0.000000  0.000000
 0.066667  0.000000  0.000000  0.000000  0.000000  0.933333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.333333  0.000000  0.000000  0.000000  0.033333
0.000000  0.000000  0.033333  0.000000  0.000000  0.000000  0.066667
0.000000  0.000000  0.433333  0.100000  0.000000  0.000000  0.000000
 0.200000  0.166667  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.033333
0.000000  0.000000  0.000000  0.000000  0.600000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.200000  0.033333  0.000000
0.000000  0.000000  0.066667  0.033333  0.066667  0.100000  0.000000
0.000000  0.100000  0.066667  0.333333  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.766667
0.000000  0.000000  0.033333  0.000000  0.000000  0.166667  0.000000
0.033333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.633333  0.233333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.066667  0.000000
0.000000  0.000000  0.000000  0.066667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.033333  0.933333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.033333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.300000  0.000000  0.266667  0.033333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.400000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.233333  0.233333
0.000000  0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.033333  0.333333
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.900000  0.100000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.233333  0.000000  0.766667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.733333  0.000000  0.000000  0.000000  0.233333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.033333  0.000000  0.000000
 0.000000  0.000000  0.566667  0.133333  0.000000  0.000000
0.000000  0.000000  0.233333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.066667  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.900000  0.000000  0.000000  0.000000  0.000000
0.000000  0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.266667  0.000000
0.000000  0.066667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
 0.066667  0.000000  0.033333  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.033333  0.100000
0.666667  0.066667  0.033333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.733333  0.000000  0.000000  0.000000  0.000000
0.000000  0.033333  0.166667  0.066667  0.000000  0.000000  0.000000
 0.033333  0.000000  0.466667  0.166667  0.000000  0.233333
0.000000  0.000000  0.033333  0.000000  0.000000  0.033333  0.000000
0.000000  0.000000  0.033333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.666667  0.000000  0.200000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.033333  0.000000
0.000000  0.000000  0.000000  0.033333  0.066667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.666667  0.233333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.066667  0.033333  0.000000  0.000000
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 1 regular expression
--------------------------------------------------------------------
[LP][KE]I[CW][RW][ML][DS][KR][NT][SE]G[SC][VA][TE]GG[DE]E[VIL][YFG]L
[LI][CG][DK]K[VF]QK[DG][DF][IK]
--------------------------------------------------------------------




Time 79.45 secs.

********************************************************************


********************************************************************
MOTIF  2 MEME    width =  29  sites =  20  llr = 1406  E-value =
1.6e-361
********************************************************************
--------------------------------------------------------------------
      Motif 2 Description
--------------------------------------------------------------------
Simplified        A  ::::::::1::1:::::::::::4::::1
pos.-specific     C  ::::::::::::::::::9:::1::::::
probability       D  :::::::::::::::::1:::::::::::
matrix            E  ::7:1a1::::::::::3:a:::::::::
                  F  ::::::::::::6:a::::::::::::::
                  G  :::::::::1:9:::::1::a:::a7::a
                  H  1::::::::::::::::::::::7:::::
                  I  :1:a2::::::11:::::::::::::4::
                  K  ::1:::::711::::::2:::::::::::
                  L  :7::5:::::::1:::::::::::::61:
                  M  :1::::::::::2::::::::::::::::
                  N  ::::::1:::1::::::::::::::::::
                  P  :::::::a:2:::::::4:::6:::::9:
                  Q  ::1:::9:15:::::::::::1:::::1:
                  R  1:1::1::2:9::a:a:::::4:::::::
                  S  :::::::::3::::::::1:::9::4:::
                  T  ::::2:::1::::::::11:::1::::::
                  V  122:2::::::::::::1:::1::::1::
                  W  :::::::::::::::::::::::::::::
                  Y  8:::::::::1:1:::a::::::::::::

         bits    7.3
                 6.6
                 5.9
                 5.1               * * *
Relative         4.4 *  *         **** **
Entropy          3.7 *  * ***  ** **** ***  **   *
(101.4 bits)     2.9 *  * **** ******* ***********
                 2.2 ***************** ***********
```

```
                 1.5 *****************************
                 0.7 *****************************
                 0.0 -----------------------------

Multilevel           YLEILEQPKQRGFRFRYPCEGPSHGGLPG
consensus             V  V    S  M    E   R A SI
sequence                              K


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 2 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value
Site
-------------             ----- ---------            ---------------
NFkB_Corallimorph            45  2.79e-37 ANLTGSYTGP
YLEILEQPKQRGFRFRYPCEGPSHGGLPG EYSEKSKKSY
NFkB_Acropora                44  2.79e-37 QVPTGSYQGP
YLEILEQPKQRGFRFRYPCEGPSHGGLPG EYSEKGKKSY
NFkBb_Aiptasia               44  3.43e-36 VQMEMGYEGP
YLEILEQPKSRGFRFRYPCEGPSHGGLPG EFSDSKNKSY
NFkB_Platygyra               44  6.43e-36 QMPPATYSGP
YMEILEQPKQRGFRFRYPCEGPSHGGLPG QYSEKGKKSY
NFkBCys_Nev                  49  6.43e-36 NAEEPSYTEP
YLEILEQPKPRGFRFRYPCEGPSHGGLPG QFSTSKSKSY
NFkB_Ed                      49  1.67e-34 GASGGVYSGP
YLEILEQPRPRGFRFRYPCEGPSHGGLPG QFSTSKNKSY
NFkB2_Homo                   39  2.80e-34 EPAPETADGP
YLVIVEQPKQRGFRFRYGCEGPSHGGLPG ASSEKGRKTY
NFkB1_Homo                   44  4.12e-34 QMALPTADGP
YLQILEQPKQRGFRFRYVCEGPSHGGLPG ASSEKNKKSY
RelA_Homo                    20  1.81e-33 PAEPAQASGP
YVEIIEQPKQRGMRFRYKCEGRSAGSIPG ERSTDTTKTH
NFkB[Ciona                   25  8.18e-33 NMFPEENGEP
YLEIIENPKSRGFRFRYTCEGPSHGGIPG GSSDKNKKTF
rel1[Ciona]                   6  3.44e-32      MDRIP
VLEIVEQPKQRGMRFRYECEGRSAGSIPG KNTNGDRKTW
cRel                          9  4.28e-32   MASGAYNP
YIEIIEQPRQRGMRFRYKCEGRSAGSIPG EHSTDNNRTY
NFkBSer_Nev                  49  6.55e-32 NAEEPSYTEP
YLEILEQPKPRGFRFRYPSEGPSHGGLPG QFSTSKSKSY
NFkB_Amphimedon              47  1.37e-31 SSPYSSLTQV
RLEIVEQPKSRGFRFRYDCEGQSHGGLPG ENSEKNRRQK
NFkB_Biomphalaria           115  3.11e-31 PHVQTAASTP
YVEILEQPKSRGLRFRYECEGRSAGSVPG ENSTNDHRTY
Relish_Biomphalaria          57  5.14e-31 TIPSSPQAKP
YVVITEQPQQRGFRFRYECEGPSHGGLQG TKSERSRKSY
RelB_Homo                   126  1.13e-30 SPAPGPGPQP
HLVITEQPKQRGMRFRYECEGRSAGSILG ESSTEASKTL
```

```
Dorsal_Dmel                  48  2.16e-26 QSTKNVRKKP
YVKITEQPAGKALRFRYECEGRSAGSIPG VNSTPENKTY
Dif_Dmel                     79  2.54e-24 LPEPSARSGP
HLRIVEEPTSNIIRFRYKCEGRTAGSIPG MNSSSETGKT
NFkB_Hydra                   16  5.96e-22 EIFGISHSGP
YLKIERQPRKYGYRFRYKTEGVCHGGILA DTDGAVNCGS
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 2 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB_Corallimorph                 2.8e-37  44_[2]_842
NFkB_Acropora                     2.8e-37  43_[2]_832
NFkBb_Aiptasia                    3.4e-36  43_[2]_776
NFkB_Platygyra                    6.4e-36  43_[2]_846
NFkBCys_Nev                       6.4e-36  48_[2]_363
NFkB_Ed                           1.7e-34  48_[2]_783
NFkB2_Homo                        2.8e-34  38_[2]_832
NFkB1_Homo                        4.1e-34  43_[2]_897
RelA_Homo                         1.8e-33  19_[2]_400
NFkB[Ciona                        8.2e-33  24_[2]_1147
rel1[Ciona]                       3.4e-32  5_[2]_256
cRel                              4.3e-32  8_[2]_582
NFkBSer_Nev                       6.6e-32  48_[2]_363
NFkB_Amphimedon                   1.4e-31  46_[2]_1020
NFkB_Biomphalaria                 3.1e-31  114_[2]_467
Relish_Biomphalaria               5.1e-31  56_[2]_1000
RelB_Homo                         1.1e-30  125_[2]_425
Dorsal_Dmel                       2.2e-26  47_[2]_602
Dif_Dmel                          2.5e-24  78_[2]_560
NFkB_Hydra                          6e-22  15_[2]_433
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 2 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 2 width=29 seqs=20
NFkB_Corallimorph        (   45) YLEILEQPKQRGFRFRYPCEGPSHGGLPG  1
NFkB_Acropora            (   44) YLEILEQPKQRGFRFRYPCEGPSHGGLPG  1
NFkBb_Aiptasia           (   44) YLEILEQPKSRGFRFRYPCEGPSHGGLPG  1
NFkB_Platygyra           (   44) YMEILEQPKQRGFRFRYPCEGPSHGGLPG  1
NFkBCys_Nev              (   49) YLEILEQPKPRGFRFRYPCEGPSHGGLPG  1
NFkB_Ed                  (   49) YLEILEQPRPRGFRFRYPCEGPSHGGLPG  1
NFkB2_Homo               (   39) YLVIVEQPKQRGFRFRYGCEGPSHGGLPG  1
NFkB1_Homo               (   44) YLQILEQPKQRGFRFRYVCEGPSHGGLPG  1
RelA_Homo                (   20) YVEIIEQPKQRGMRFRYKCEGRSAGSIPG  1
NFkB[Ciona               (   25) YLEIIENPKSRGFRFRYTCEGPSHGGIPG  1
rel1[Ciona]              (    6) VLEIVEQPKQRGMRFRYECEGRSAGSIPG  1
cRel                     (    9) YIEIIEQPRQRGMRFRYKCEGRSAGSIPG  1
```

```
NFkBSer_Nev              (   49) YLEILEQPKPRGFRFRYPSEGPSHGGLPG  1
NFkB_Amphimedon          (   47) RLEIVEQPKSRGFRFRYDCEGQSHGGLPG  1
NFkB_Biomphalaria        (  115) YVEILEQPKSRGLRFRYECEGRSAGSVPG  1
Relish_Biomphalaria      (   57) YVVITEQPQQRGFRFRYECEGPSHGGLQG  1
RelB_Homo                (  126) HLVITEQPKQRGMRFRYECEGRSAGSILG  1
Dorsal_Dmel              (   48) YVKITEQPAGKALRFRYECEGRSAGSIPG  1
Dif_Dmel                 (   79) HLRIVEEPTSNIIRFRYKCEGRTAGSIPG  1
NFkB_Hydra               (   16) YLKIERQPRKYGYRFRYKTEGVCHGGILA  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 2 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 29 n= 29298 bayes= 10.7673 E= 1.6e-
361
  -329   -320   -429   -397     29   -464    172   -315   -348   -
314   -285   -386   -495   -420     -4   -390   -384    -50    -33
497
  -400   -360   -598   -513   -198   -584   -469     33   -473
305    106   -544   -558   -470   -434   -541   -397    133   -271
-339
  -308   -536   -187    334   -549   -435   -312   -442    114   -
445   -378   -333   -476    -10     37   -393   -350    105   -404
-411
  -578   -525   -714   -757   -523   -657   -685    446   -715   -
427   -446   -727   -733   -771   -692   -741   -586   -291   -530
-575
  -263   -250   -524    -41   -226   -451   -388    178   -400
228   -144   -432   -511   -444   -390   -402    119    167   -235
-262
  -485   -551   -220    404   -575   -528   -469   -498   -518   -
608   -543   -439   -682   -422   -310   -580   -534   -549   -458
-530
  -261   -306   -360    -69   -389   -433    -38   -331   -251   -
274   -161   -142   -384    382   -189   -340   -305   -354   -194
-344
  -513   -589   -616   -625   -637   -593   -595   -658   -585   -
646   -653   -650    377   -640   -584   -606   -588   -647   -532
-621
  -137   -391   -474   -370   -517   -464   -325   -387    402   -
445   -371   -353   -514   -109    114   -449   -120   -446   -314
-398
  -257   -386   -209   -217   -443    -47   -249   -422     33   -
429   -358   -175     86    290   -185    126   -277   -401   -349
-334
  -348   -279   -446   -440   -441   -418   -217   -374    -56   -
396   -368   -182   -423   -288    433   -414   -381   -469   -191
-100
```

```
  -100   -356   -298   -358   -447    366   -366   -102   -322   -
507   -397   -277   -479   -445   -319   -320   -384   -418   -287
-378
  -436   -358   -608   -575    419   -600   -478     16   -551
37    275   -574   -595   -563   -532   -535   -469   -284   -191
95
  -448   -376   -534   -540   -528   -499   -319   -477   -215   -
495   -471   -443   -515   -394    444   -513   -480   -567   -287
-453
  -502   -402   -589   -596    483   -581   -506   -384   -576   -
334   -372   -589   -605   -642   -569   -548   -565   -443   -230
-167
  -448   -376   -534   -540   -528   -499   -319   -477   -215   -
495   -471   -443   -515   -394    444   -513   -480   -567   -287
-453
  -719   -611   -711   -772   -316   -656   -490   -665   -711   -
627   -641   -681   -731   -721   -652   -746   -708   -695   -297
542
  -200   -395      8    201   -373    -62   -222   -338    183   -
349   -274   -212    202   -181   -186   -256    -23    -48   -298
-283
  -362    576   -531   -487   -449   -536   -482   -386   -512   -
471   -386   -507   -595   -557   -457   -391   -304   -462   -433
-484
  -496   -553   -228    404   -579   -533   -476   -505   -540   -
615   -551   -447   -692   -433   -537   -590   -544   -557   -461
-535
  -384   -492   -451   -513   -578    380   -505   -592   -477   -
639   -553   -435   -604   -591   -468   -478   -532   -573   -417
-514
  -226   -372   -371   -315   -409   -388   -315   -368   -160   -
372   -349   -358    303    -54    247   -320   -302    -71   -348
-386
  -177     53   -360   -402   -346   -335   -355   -354   -300   -
395   -303   -216   -402   -399   -293    305     79   -382   -277
-309
   233   -417   -609   -652   -557   -454    458   -642   -614   -
655   -604   -558   -619   -642   -585   -438   -460   -546   -482
-491
  -384   -492   -451   -513   -578    380   -505   -592   -477   -
639   -553   -435   -604   -591   -468   -478   -532   -573   -417
-514
  -252   -355   -521   -582   -587    318   -551   -597   -572   -
626   -549   -468   -566   -596   -546    182   -393   -485   -484
-561
  -447   -395   -742   -686   -276   -701   -650    311   -654
263   -184   -684   -709   -651   -639   -690   -450     11   -381
-441
  -197   -353   -349   -319   -380   -373   -337   -351   -280    -
38   -345   -372    349    -76   -304   -298   -287   -340   -351
-392
```

```
   -95   -358   -306   -365   -453    369   -373   -447   -330   -
513   -404   -284   -484   -451   -326   -324   -386   -424   -294
-385
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 2 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 29 nsites= 20 E= 1.6e-361
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.100000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.050000  0.000000  0.000000  0.050000  0.000000  0.800000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.050000  0.000000  0.700000  0.050000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.650000  0.000000  0.000000
0.000000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
0.050000  0.050000  0.000000  0.000000  0.150000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.050000  0.000000  0.000000
0.000000  0.150000  0.000000  0.450000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.150000  0.200000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.950000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.050000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.050000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.050000  0.000000
0.900000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.050000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.700000  0.000000  0.000000  0.000000  0.000000
0.050000  0.150000  0.000000  0.050000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.050000
0.000000  0.000000  0.050000  0.000000  0.000000  0.000000  0.150000
0.500000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.050000  0.000000  0.000000  0.050000  0.000000
0.000000  0.850000  0.000000  0.000000  0.000000  0.000000  0.050000
 0.050000  0.000000  0.000000  0.000000  0.000000  0.900000
0.000000  0.050000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.600000  0.000000
0.000000  0.050000  0.000000  0.100000  0.200000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.050000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.050000  0.250000  0.000000  0.050000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.350000
0.000000  0.000000  0.000000  0.050000  0.050000  0.000000  0.000000
 0.000000  0.900000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.050000  0.050000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.550000
0.050000  0.350000  0.000000  0.000000  0.050000  0.000000  0.000000
 0.000000  0.050000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.900000  0.050000  0.000000  0.000000  0.000000
 0.350000  0.000000  0.000000  0.000000  0.000000  0.000000
0.650000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.650000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.350000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.400000  0.000000  0.550000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.050000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.100000  0.000000  0.000000  0.850000
0.050000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.050000  0.000000  0.000000  0.000000  0.000000  0.950000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
---------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 2 regular expression
--------------------------------------------------------------------
Y[LV]EI[LV]EQPK[QS]RG[FM]RFRY[PEK]CEG[PR]S[HA]G[GS][LI]PG
--------------------------------------------------------------------




Time 155.98 secs.

********************************************************************


********************************************************************
MOTIF  3 MEME    width =  29  sites =  21  llr = 1362  E-value =
1.2e-333
********************************************************************
--------------------------------------------------------------------
      Motif 3 Description
--------------------------------------------------------------------
Simplified        A  ::6:2::2:2::::::a::::::2::::4
pos.-specific     C  :::::::::1:::::::::::::::1:::
probability       D  ::3::3::::a:::::::::::::::2:1
matrix            E  :8::::::::::::::::::::::::::2
                  F  :::1::a::::::::3:::a::::1::::
                  G  ::1:8::1:::::::::::::::::::::
                  H  ::::::::::::a1:::::::::::2:::
                  I  :::::1:::::::::::a:::::::::3:
                  K  :::1:2:::::::1::::::6::::211:
                  L  :::3:::::::::::::::::::::::1:
                  M  :::::::::::::::::::::::::::::
                  N  ::::::::::::::::::::::::::6:1
                  P  ::::::::6:::::::::::::a6:::::
                  Q  :::::::12:::::a:::::1::::::::
                  R  :::1:::::::::7::::::3::1:::::
                  S  :::::1:5:2:::::::::::::::::::
                  T  :::::::::3:::::::::::a:::::2:
                  V  :::::1:::::a:::2::9::::::::1:
                  W  a::::::::::::::::::::::::3:::
                  Y  :::1:::::::::::2::::::::9::::

         bits    7.3 *
                 6.6 *
                 5.9 *
                 5.1 *           *           *
Relative         4.4 *     *   * * *  * * *  *
Entropy          3.7 *     *   *** * ** * ** *
(93.6 bits)      2.9 *** * *   ***** ******* ***
                 2.2 *** * * * *****************
                 1.5 *****************************
```

```
                 0.7 *****************************
                 0.0 -----------------------------

Multilevel           WEALGDFSPTDVHRQFAIVFKTPPYWNIA
consensus              D A          V    R     D
sequence                            Y


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                  Site
-------------             ----- ---------            ---------------
NFkBSer_Nev                 321  8.14e-37 EMDDITGKYT
WEDLGKFSPCDVHRQFAIVFKTPPYWNIA IERPANVLVE
NFkBCys_Nev                 321  8.14e-37 EMDDITGKYT
WEDLGKFSPCDVHRQFAIVFKTPPYWNIA IERPANVLVE
NFkB_Platygyra              315  1.43e-33 ETEVETGKKT
WEAGGVFAPTDVHRQVAIVFKTPPYWNVA TERPVKVQLE
NFkB_Corallimorph           318  2.42e-33 YEEDESGKII
WEDLGVFAPSDVHRQFAIVFKTPPFWNIA TERPVKVHIE
NFkB_Ed                     322  4.03e-33 EFDDNTGKTS
WEDMAVFSPSDVHRQFAIVFKTPPYWNVA IEKPAPVMLE
Relish_Biomphalaria         299  2.39e-32 VEQNPDGSVK
WEAYGNFGPLDVHRQYAIVFKTPAYWNTN IDKAVNVLIM
NFkBb_Aiptasia              317  3.26e-32 YENNDDGKPI
WEDTGKFAPADVHRQFAIVFKTPAYHNIA IERPVEVLLE
NFkB[Ciona                  268  5.16e-32 SEEDMQGNNL
WEAYGSFSPTDVHRQFAIVFRTPAYKDTE IKMPVNVQVQ
NFkB_Acropora               313  8.08e-32 YEIDENGKRS
WEGQGLFAPTDVHRQVAIVFKTPAYWNIA VERPVKVHLE
NFkB1_Homo                  295  8.08e-32 FYEEEENGGV
WEGFGDFSPTDVHRQFAIVFKTPKYKDIN ITKPASVFVQ
NFkB_Biomphalaria           335  1.73e-29 YEENEQGMVV
WEDLGDFGQGDVHRQYAIVFRTPSYHNTE ITRPAEVLMQ
cRel                        225  2.82e-29 DIEVRFVLND
WEAKGIFSQADVHRQVAIVFKTPPYCKAI TEPVTVKMQL
NFkB2_Homo                  270  3.18e-29 VRFYEDDENG
WQAFGDFSPTDVHKQYAIVFRTPPYHKMK IERPVTVFLQ
rel1[Ciona]                 224  1.65e-28 DIQVVFYRDN
WEALGDFSSVDVHRQVAIVFRTPPFCNEN IQEKVDVQFK
RelB_Homo                   342  1.85e-28 DISVVFSRAS
WEGRADFSQADVHRQIAIVFKTPPYEDLE IVEPVTVNVF
RelA_Homo                   233  6.40e-28 DIEVYFTGPG
WEARGSFSQADVHRQVAIVFRTPPYADPS LQAPVRVSMQ
Relish_Dmel                 388  3.56e-26 FEEDEDGETV
WEAYAKFRESDVHHQYAIVCQTPPYKDKD VDREVNVYIE
Dorsal_Dmel                 269  4.82e-26 FFEEKNGQSV
WEAFGDFQHTDVHKQTAITFKTPRYHTLD ITEPAKVFIQ
```

```
NFkB_Amphimedon             302  7.39e-25 ETTGGMQLQP
WMAKGRFGPNDVHHQYAIVFQTPTFYNQA IEHPVQVWIA
Dif_Dmel                    300  7.52e-24 YETDKDGRET
WFANAEFQPTDVFKQMAIAFKTPRYRNTE ITQSVNVELK
NFkB_Hydra                  280  3.69e-20 RFFDDTPVVP
WSALAIVNKSDVHNQNLIIFRTPPYKHKV LDQPVKVKIE
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 3 block diagrams
--------------------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkBSer_Nev                       8.1e-37  320_[3]_91
NFkBCys_Nev                       8.1e-37  320_[3]_91
NFkB_Platygyra                    1.4e-33  314_[3]_575
NFkB_Corallimorph                 2.4e-33  317_[3]_569
NFkB_Ed                             4e-33  321_[3]_510
Relish_Biomphalaria               2.4e-32  298_[3]_758
NFkBb_Aiptasia                    3.3e-32  316_[3]_503
NFkB[Ciona                        5.2e-32  267_[3]_904
NFkB_Acropora                     8.1e-32  312_[3]_563
NFkB1_Homo                        8.1e-32  294_[3]_646
NFkB_Biomphalaria                 1.7e-29  334_[3]_247
cRel                              2.8e-29  224_[3]_366
NFkB2_Homo                        3.2e-29  269_[3]_601
rel1[Ciona]                       1.7e-28  223_[3]_38
RelB_Homo                         1.9e-28  341_[3]_209
RelA_Homo                         6.4e-28  232_[3]_187
Relish_Dmel                       3.6e-26  387_[3]_555
Dorsal_Dmel                       4.8e-26  268_[3]_381
NFkB_Amphimedon                   7.4e-25  301_[3]_765
Dif_Dmel                          7.5e-24  299_[3]_339
NFkB_Hydra                        3.7e-20  279_[3]_169
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 3 in BLOCKS format
--------------------------------------------------------------------------------
BL   MOTIF 3 width=29 seqs=21
NFkBSer_Nev              (  321) WEDLGKFSPCDVHRQFAIVFKTPPYWNIA  1
NFkBCys_Nev              (  321) WEDLGKFSPCDVHRQFAIVFKTPPYWNIA  1
NFkB_Platygyra           (  315) WEAGGVFAPTDVHRQVAIVFKTPPYWNVA  1
NFkB_Corallimorph        (  318) WEDLGVFAPSDVHRQFAIVFKTPPFWNIA  1
NFkB_Ed                  (  322) WEDMAVFSPSDVHRQFAIVFKTPPYWNVA  1
Relish_Biomphalaria      (  299) WEAYGNFGPLDVHRQYAIVFKTPAYWNTN  1
NFkBb_Aiptasia           (  317) WEDTGKFAPADVHRQFAIVFKTPAYHNIA  1
NFkB[Ciona               (  268) WEAYGSFSPTDVHRQFAIVFRTPAYKDTE  1
NFkB_Acropora            (  313) WEGQGLFAPTDVHRQVAIVFKTPAYWNIA  1
NFkB1_Homo               (  295) WEGFGDFSPTDVHRQFAIVFKTPKYKDIN  1
NFkB_Biomphalaria        (  335) WEDLGDFGQGDVHRQYAIVFRTPSYHNTE  1
```

```
cRel                     (  225) WEAKGIFSQADVHRQVAIVFKTPPYCKAI  1
NFkB2_Homo               (  270) WQAFGDFSPTDVHKQYAIVFRTPPYHKMK  1
rel1[Ciona]              (  224) WEALGDFSSVDVHRQVAIVFRTPPFCNEN  1
RelB_Homo                (  342) WEGRADFSQADVHRQIAIVFKTPPYEDLE  1
RelA_Homo                (  233) WEARGSFSQADVHRQVAIVFRTPPYADPS  1
Relish_Dmel              (  388) WEAYAKFRESDVHHQYAIVCQTPPYKDKD  1
Dorsal_Dmel              (  269) WEAFGDFQHTDVHKQTAITFKTPRYHTLD  1
NFkB_Amphimedon          (  302) WMAKGRFGPNDVHHQYAIVFQTPTFYNQA  1
Dif_Dmel                 (  300) WFANAEFQPTDVFKQMAIAFKTPRYRNTE  1
NFkB_Hydra               (  280) WSALAIVNKSDVHNQNLIIFRTPPYKHKV  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 29 n= 29298 bayes= 10.7502 E= 1.2e-
333
  -488   -416   -503   -507   -208   -504   -456   -465   -469   -
351   -381   -495   -586   -507   -427   -548   -495   -453    725
-206
  -427   -549   -203    397   -184   -504   -441   -483   -412   -
567   -128   -414   -615   -214   -467   -307   -482   -512   -452
-498
   299   -316    232   -427   -554    100   -449   -559   -471   -
589   -511   -319   -522   -500   -494   -305   -336   -443   -478
-510
  -161   -278   -202   -131    174    -68   -161   -201     96
139     84     -7   -349    -17     96   -215    -18   -208   -178
241
   152   -334   -431   -480   -524    345   -476   -520   -452   -
571   -474   -395   -525   -533   -436   -334   -373   -444   -392
-481
  -152   -320    205     13   -295   -273   -156     77    180    -
87   -204      2   -331   -143     30     -2   -166     86   -220
-207
  -348   -249   -463   -449    470   -483   -408   -216   -437   -
170   -208   -458   -478   -516   -448   -396   -423   -148    -89
-26
   133   -354   -202   -211   -411     88   -245   -401   -175   -
413   -337     13   -424     61     16    215   -239   -375   -334
-316
  -203   -359   -328    -67   -386   -371     25   -356    -38   -
362   -345   -345    320    105   -280   -122   -286   -344   -350
-386
   118    204   -401   -372   -310    -81   -351   -215   -309    -
91   -218    -30   -460   -364   -322     85    268    -38   -267
-313
```

```
  -486   -509    416   -273   -542   -515   -436   -541   -519   -
586   -541   -279   -639   -555   -513   -531   -536   -550   -425
-476
  -492   -484   -693   -713   -543   -636   -661   -252   -686   -
464   -474   -704   -707   -750   -658   -688   -532    396   -543
-594
  -500   -431   -441   -481     44   -528    508   -496   -502   -
445   -396   -294   -569   -294   -333   -468   -450   -497   -193
-90
  -364   -334   -457   -383   -478   -436     94   -399    101   -
410   -369    -88   -463   -266    413   -420   -375   -458   -238
-371
  -572   -572   -631   -462   -641   -622   -377   -647   -565   -
591   -502   -577   -650    407   -506   -645   -608   -664   -466
-594
  -197   -196   -413   -349    300   -368   -197     43   -308   -
153    100    -36   -425   -359   -296   -309    -27    170   -104
330
   368   -215   -502   -464   -401   -300   -475   -350   -447   -
100   -331   -466   -547   -505   -435   -252   -313   -261   -346
-426
  -592   -538   -725   -771   -539   -665   -694    446   -729   -
446   -465   -740   -741   -783   -703   -755   -601   -309   -541
-590
   -60   -168   -367   -330   -265   -399   -311     54   -320   -
212   -193   -378   -395   -401   -288   -367    -95    362   -274
-355
  -355      3   -469   -456    471   -487   -414   -229   -444   -
180   -218   -464   -484   -523   -454   -402   -430   -290    -97
-33
  -389   -479   -493   -330   -554   -469   -276   -439    358   -
428   -368   -345   -545     68    266   -431   -368   -441   -348
-385
  -574   -569   -682   -747   -673   -618   -652   -656   -678   -
717   -651   -631   -709   -722   -649   -529    408   -644   -543
-644
  -532   -602   -630   -642   -651   -605   -608   -675   -602   -
662   -671   -665    377   -657   -599   -623   -605   -665   -542
-634
    91   -354   -348   -316   -384   -374   -335   -354    -45   -
360   -347   -368    316   -337     49   -124    -70   -342   -353
-393
  -588   -480   -646   -642    216   -636   -281   -466   -572   -
434   -435   -518   -678   -557   -515   -596   -567   -505    -80
516
   -37    211   -238     -4   -347   -327    256   -310    192   -
322   -248   -208   -387   -176     46   -254   -219   -304    539
85
  -374   -470    208   -278   -524   -292     80   -576     89   -
591   -548    339   -495   -359   -365   -286    -29   -570   -454
-387
```

```
   -30   -209   -339    -34   -183   -345   -259    248     79
26    105   -288    -81    -38   -246   -284    148     71   -164
-186
   213   -331     69    155   -308   -280   -165    -12     41   -
295   -216    125   -339   -149   -127    -71   -175    -50   -232
-218
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 29 nsites= 21 E= 1.2e-333
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  0.809524  0.047619  0.000000
0.000000  0.000000  0.000000  0.000000  0.047619  0.000000  0.000000
0.047619  0.000000  0.047619  0.000000  0.000000  0.000000  0.000000
 0.571429  0.000000  0.285714  0.000000  0.000000  0.142857
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.142857  0.047619
0.000000  0.000000  0.095238  0.285714  0.047619  0.047619  0.000000
0.047619  0.095238  0.000000  0.047619  0.000000  0.000000  0.142857
 0.238095  0.000000  0.000000  0.000000  0.000000  0.761905
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.285714  0.047619  0.000000  0.000000
0.000000  0.095238  0.190476  0.047619  0.000000  0.047619  0.000000
0.000000  0.047619  0.095238  0.000000  0.142857  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.952381  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.047619  0.000000  0.000000
 0.190476  0.000000  0.000000  0.000000  0.000000  0.142857
0.000000  0.000000  0.000000  0.000000  0.000000  0.047619  0.000000
0.095238  0.047619  0.476190  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.047619  0.000000  0.000000
0.047619  0.000000  0.047619  0.000000  0.000000  0.000000  0.619048
0.190476  0.000000  0.047619  0.000000  0.000000  0.000000  0.000000
 0.190476  0.095238  0.000000  0.000000  0.000000  0.047619
0.000000  0.000000  0.000000  0.047619  0.000000  0.047619  0.000000
0.000000  0.000000  0.190476  0.333333  0.047619  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.047619  0.000000
0.952381  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.095238  0.000000  0.142857  0.000000  0.000000  0.047619  0.000000
0.000000  0.714286  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.333333  0.000000
0.000000  0.047619  0.000000  0.000000  0.047619  0.047619  0.000000
0.000000  0.000000  0.000000  0.047619  0.238095  0.000000  0.238095
 0.952381  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.047619  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.047619  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.047619  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.047619  0.857143  0.000000  0.000000
 0.000000  0.047619  0.000000  0.000000  0.952381  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.619048  0.000000  0.000000  0.000000  0.000000
0.095238  0.285714  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.190476  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.047619  0.000000  0.000000  0.000000  0.571429
0.000000  0.095238  0.047619  0.047619  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.142857  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.857143
 0.047619  0.095238  0.000000  0.047619  0.000000  0.000000
0.190476  0.000000  0.190476  0.000000  0.000000  0.000000  0.000000
0.000000  0.047619  0.000000  0.000000  0.000000  0.333333  0.047619
 0.000000  0.000000  0.238095  0.000000  0.000000  0.000000
0.047619  0.000000  0.095238  0.000000  0.000000  0.571429  0.000000
0.000000  0.000000  0.000000  0.047619  0.000000  0.000000  0.000000
 0.047619  0.000000  0.000000  0.047619  0.000000  0.000000
0.000000  0.285714  0.095238  0.095238  0.047619  0.000000  0.047619
0.047619  0.000000  0.000000  0.190476  0.095238  0.000000  0.000000
 0.380952  0.000000  0.095238  0.190476  0.000000  0.000000
0.000000  0.047619  0.047619  0.000000  0.000000  0.142857  0.000000
0.000000  0.000000  0.047619  0.000000  0.047619  0.000000  0.000000
--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
      Motif 3 regular expression
---------------------------------------------------------------------
WE[AD]L[GA]DFSPTDVHRQ[FVY]AIVF[KR]TPPYW[ND]IA
---------------------------------------------------------------------




Time 229.80 secs.

*********************************************************************


*********************************************************************
MOTIF  4 MEME    width =  21  sites =  50  llr = 1467  E-value =
1.1e-280
*********************************************************************
---------------------------------------------------------------------
      Motif 4 Description
---------------------------------------------------------------------
Simplified        A  :::3:::a21:::111211::
pos.-specific     C  ::::::::2::1:::2::1::
probability       D  :2:::::::::21:2::::::
matrix            E  ::::::::21:::2::1::::
                  F  ::::::::::::::::::1::
                  G  9:::::::::::4::1::1::
                  H  :::::a1:::2:1::::::::
                  I  ::::::1:13:::1:22:112
                  K  :1:::::::1:1:1:::1:::
                  L  :1::8:5::11::2:12:295
                  M  :::::::::::::::::::::
                  N  :3:::::::112:::::::::
                  P  :::6:::::::::1:::::::
                  Q  :1:::::::2:211::1::::
                  R  11:::::::1:::1::1::::
                  S  ::1:::::::::1:1::11::
                  T  ::8:::::::1::11:1::::
                  V  :::11:1:5::::1:33:1:2
                  W  :::::::::::::::::::::
                  Y  ::::::::::::::::::1::

         bits    7.3
                 6.6
                 5.9
                 5.1      *
Relative         4.4      *
Entropy          3.7      * *
(42.3 bits)      2.9 * * ** *           *
                 2.2 * *******          **
                 1.5 *************  **  **
```

```
                 0.7 *********************
                 0.0 ---------------------

Multilevel           GNTPLHLAVIxGNLxVVxLLL
consensus             D A        Q   L   I
sequence                             A


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                    Site
-------------             ----- ---------            ---------------
NFkB_Corallimorph           507  1.06e-19 RHLTAVQDDN
GDTALHLAVINCQQEVIQCLL EVMASVPDSN
NFkB_Platygyra              513  7.66e-18 RHLTAVQDDS
GDTALHLAVINSQQEVVQCLL DIMAGLPESY
NFkB1_Homo                  686  2.92e-17 ADVNAQEQKS
GRTALHLAVEHDNISLAGCLL LEGDAHVDST
NFkB_Platygyra              654  7.13e-17 ANMSAQDGTS
GKTPLHHAVEQDNLAVAGFLI LEANCDVDAT
NFkB_Corallimorph           648  1.01e-16 ADMSIQDGTS
GRTPLHHAVEQDNLAVAGFLI LEANCDVNAV
NFkB_Acropora               504  1.01e-16 RHLTAVQDDN
GDTALHLAVINSQQEVIHCLV DVMAGLPESF
NFkBb_Aiptasia              618  1.96e-16 FPELHWQNYD
GYTPLHLAVIKGNREIIQILL SEGANVEAKD
NFkB_Amphimedon             689  4.34e-16 RSLTAVQNQE
GDTALHLAIIHNHQDVVLQLL DVLPQLPPTE
IkB_Nev                     294  5.07e-16 ADINVPDCGS
GKTALHHAVETNNLRLVSYLL FQCNACVDAE
NFkB2_Homo                  527  5.07e-16 LGVVNLTNHL
HQTPLHLAVITGQTSVVSFLL RVGADPALLD
NFkB2_Homo                  488  7.99e-16 RHLLTAQDEN
GDTPLHLAIIHGQTSVIEQIV YVIHHAQDLG
NFkBb_Aiptasia              652  9.28e-16 ANVEAKDGTC
GRSPLHLAIEHDNLAIAGYLI LEARCDVDSL
NFkBb_Aiptasia              506  2.20e-15 RQITAVQNDD
GDTALHIAVINCQFTAIEGLV SVMKDLQGDF
NFkB_Amphimedon             874  2.54e-15 ETNIECTDFS
GNTPLHCAAALGNVAIVSLLI AAGANLVCQN
NFkB_Platygyra              584  2.91e-15 SANVRLRDRH
GNTAVHIACMHGDAVCLKALL NFNVSKTVLN
NFkBb_Aiptasia              577  2.91e-15 NADATLRDRH
GNTPVHTACAQGDVHCLRVLL DTKLRKEKDG
NFkB_Ed                     582  2.91e-15 KADPTLRDRH
GNTPVHIACVQGDVTCLQVLL NPHLRQVDGT
NFkB_Ed                     657  3.83e-15 ADMEARDGTC
GRSPLHHAVETNNLAIAGYLI LEVKCDVNVT
```

```
NFkB1_Homo                  583  3.83e-15 DDIINMRNDL
YQTPLHLAVITKQEDVVEDLL RAGADLSLLD
NFkB_Ed                     511  5.02e-15 QQLTAVQDDQ
GDSALHLAVINCQFEAIESLV SVMSGLPSTF
NFkB_Acropora               542  7.45e-15 ESFVNEYNFL
RQTPLHLAVITKQPRALDCLI KAGANPRLRD
NFkB_Acropora               575  8.49e-15 GANPRLRDRH
GNTAVHIACSYGDATCLKALL HYDVSKMVLN
NFkB_Amphimedon             806  1.25e-14 IPELVMRNND
GLTPLHLAAACGNPDCFKELV KAHADVNVQD
Relish_Biomphalaria         845  2.05e-14 AQVDLPDGKS
GKTALHHAVDNDDLPVASYLL LEARTDVNAR
IkB_Nev                     213  2.95e-14 GASVDLVDRN
GKTALHLACERGDIDSVREII RPLSDKAYNP
NFkB_Corallimorph           578  3.33e-14 RGDVKSRDRH
GNTAVHVVCAHGDAACLRVLL NYSETKAVLN
NFkB[Ciona                  829  3.75e-14 RHLTDVRDCN
GDSVLHVAVIHDQMQVLSSLL DVIVTLNNKQ
IkB_Nev                     144  7.53e-14 RGLLFAQDED
GDTALHLAIIHTNVQAVENIV AAAPSTKALD
NFkB_Acropora               611  8.43e-14 KMVLNWQNYQ
GLTPVHLAVLCGSKDVLKLLR SAGANMSAQD
NFkB_Capsaspora             858  9.44e-14 GASGNARDFG
KNTPLHLAARQGHIGIAALLV EAGATLSLNA
Relish_Dmel                 674  9.44e-14 GCNPNLKNNA
GNTPLHVAVKEEHLSCVESFL NGVPTVQLDL
NFkB2_Homo                  668  1.06e-13 RANVNARTFA
GNTPLHLAAGLGYPTLTRLLL KAGADIHAEN
NFkB[Ciona                 1009  2.53e-13 DADLEASTYE
GYTPLHVAASLDHCEIATLLL ACGADPEASS
NFkB_Amphimedon             763  3.12e-13 NANPLVSDRN
GDTPLHLACKYGFLQGIVPLL NRSTRINTEG
NFkB1_Homo                  616  3.12e-13 GADLSLLDRL
GNSVLHLAAKEGHDKVLSILL KHKKAALLLD
NFkB1_Homo                  544  3.85e-13 RHLTAVQDEN
GDSVLHLAIIHLHSQLVRDLL EVTSGLISDD
NFkB_Platygyra              620  4.74e-13 KTVLNWQNYQ
GLTPVHLAVLAGSKDVLKLLN SAGANMSAQD
NFkB_Capsaspora             672  5.25e-13 AEDLQSVNDM
GETVLHSAVIEKRAAIARLLL VAGADLGQSN
NFkB_Capsaspora             637  5.25e-13 RQLLAAPNEN
GDSPLHTAVAQGNLRSTMALL PLLAAEDLQS
Relish_Biomphalaria         879  5.25e-13 RTDVNARCFD
GNTALHIACARQLVGMVALLM TAGADMECEN
NFkB_Ed                     549  5.25e-13 STFINQYNYL
HQTPLHLAVLTRHPLAIDCLL RGKADPTLRD
Relish_Dmel                 711  5.82e-13 QLDLSLTNDD
GLTPLHMAIRQNKYDVAKKLI SYDRTSISVA
IkB_Nev                     180  6.44e-13 TKALDIFNYL
RQTPLHLATITKQSNIVRGLI ASGASVDLVD
```

```
NFkB_Acropora               645  6.44e-13 ANMSAQDGTS
GKTPLHLSVEQDNLSLSGFLI LEANCDVDAS
Relish_Biomphalaria         768  8.71e-13 GANPTIADRH
GNTCAHLAVLNKSESCLKILV KYLRPGQSNL
Relish_Biomphalaria         735  1.06e-12 KNHINSLNLL
RQTPLHLATVMCQDEMVEMLL QAGANPTIAD
NFkB_Platygyra              688  5.34e-12 NCDVDATTFN
GNTPLHIAAASGLKGQTALLV AAGADTALQN
IkB_Nev                     260  7.67e-12 SSILNTRNYD
GFTALHVAVFSNSIDIVSALT NVGADINVPD
NFkB1_Homo                  720  7.67e-12 DAHVDSTTYD
GTTPLHIAAGRGSTRLAALLK AAGADPLVEN
Relish_Dmel                 746  1.42e-11 TSISVANTMD
GNNALHMAVLEQSVELLVLIL DAQNENLTDI
--------------------------------------------------------------------


--------------------------------------------------------------------
      Motif 4 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB_Corallimorph                 3.3e-14  506_[4]_50_[4]_49_[4]_247
NFkB_Platygyra                    4.7e-13
512_[4]_50_[4]_15_[4]_13_[4]_13_
                                           [4]_210
NFkB1_Homo                        3.1e-13
543_[4]_18_[4]_12_[4]_49_[4]_13_
                                           [4]_229
NFkB_Acropora                     8.4e-14
503_[4]_17_[4]_12_[4]_15_[4]_13_
                                           [4]_239
NFkBb_Aiptasia                    9.3e-16
505_[4]_50_[4]_20_[4]_13_[4]_176
NFkB_Amphimedon                   1.2e-14
688_[4]_53_[4]_22_[4]_47_[4]_201
IkB_Nev                           6.4e-13
143_[4]_15_[4]_12_[4]_26_[4]_13_
                                           [4]_69
NFkB2_Homo                        1.1e-13
487_[4]_18_[4]_120_[4]_211
NFkB_Ed                           3.8e-15
510_[4]_17_[4]_12_[4]_54_[4]_183
Relish_Biomphalaria               2.1e-14
734_[4]_12_[4]_56_[4]_13_[4]_186
NFkB[Ciona                        3.7e-14  828_[4]_159_[4]_171
NFkB_Capsaspora                   5.3e-13
636_[4]_14_[4]_165_[4]_345
Relish_Dmel                       1.4e-11  673_[4]_16_[4]_14_[4]_205
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 4 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 4 width=21 seqs=50
NFkB_Corallimorph        (  507) GDTALHLAVINCQQEVIQCLL  1
NFkB_Platygyra           (  513) GDTALHLAVINSQQEVVQCLL  1
NFkB1_Homo               (  686) GRTALHLAVEHDNISLAGCLL  1
NFkB_Platygyra           (  654) GKTPLHHAVEQDNLAVAGFLI  1
NFkB_Corallimorph        (  648) GRTPLHHAVEQDNLAVAGFLI  1
NFkB_Acropora            (  504) GDTALHLAVINSQQEVIHCLV  1
NFkBb_Aiptasia           (  618) GYTPLHLAVIKGNREIIQILL  1
NFkB_Amphimedon          (  689) GDTALHLAIIHNHQDVVLQLL  1
IkB_Nev                  (  294) GKTALHHAVETNNLRLVSYLL  1
NFkB2_Homo               (  527) HQTPLHLAVITGQTSVVSFLL  1
NFkB2_Homo               (  488) GDTPLHLAIIHGQTSVIEQIV  1
NFkBb_Aiptasia           (  652) GRSPLHLAIEHDNLAIAGYLI  1
NFkBb_Aiptasia           (  506) GDTALHIAVINCQFTAIEGLV  1
NFkB_Amphimedon          (  874) GNTPLHCAAALGNVAIVSLLI  1
NFkB_Platygyra           (  584) GNTAVHIACMHGDAVCLKALL  1
NFkBb_Aiptasia           (  577) GNTPVHTACAQGDVHCLRVLL  1
NFkB_Ed                  (  582) GNTPVHIACVQGDVTCLQVLL  1
NFkB_Ed                  (  657) GRSPLHHAVETNNLAIAGYLI  1
NFkB1_Homo               (  583) YQTPLHLAVITKQEDVVEDLL  1
NFkB_Ed                  (  511) GDSALHLAVINCQFEAIESLV  1
NFkB_Acropora            (  542) RQTPLHLAVITKQPRALDCLI  1
NFkB_Acropora            (  575) GNTAVHIACSYGDATCLKALL  1
NFkB_Amphimedon          (  806) GLTPLHLAAACGNPDCFKELV  1
Relish_Biomphalaria      (  845) GKTALHHAVDNDDLPVASYLL  1
IkB_Nev                  (  213) GKTALHLACERGDIDSVREII  1
NFkB_Corallimorph        (  578) GNTAVHVVCAHGDAACLRVLL  1
NFkB[Ciona               (  829) GDSVLHVAVIHDQMQVLSSLL  1
IkB_Nev                  (  144) GDTALHLAIIHTNVQAVENIV  1
NFkB_Acropora            (  611) GLTPVHLAVLCGSKDVLKLLR  1
NFkB_Capsaspora          (  858) KNTPLHLAARQGHIGIAALLV  1
Relish_Dmel              (  674) GNTPLHVAVKEEHLSCVESFL  1
NFkB2_Homo               (  668) GNTPLHLAAGLGYPTLTRLLL  1
NFkB[Ciona               ( 1009) GYTPLHVAASLDHCEIATLLL  1
NFkB_Amphimedon          (  763) GDTPLHLACKYGFLQGIVPLL  1
NFkB1_Homo               (  616) GNSVLHLAAKEGHDKVLSILL  1
NFkB1_Homo               (  544) GDSVLHLAIIHLHSQLVRDLL  1
NFkB_Platygyra           (  620) GLTPVHLAVLAGSKDVLKLLN  1
NFkB_Capsaspora          (  672) GETVLHSAVIEKRAAIARLLL  1
NFkB_Capsaspora          (  637) GDSPLHTAVAQGNLRSTMALL  1
Relish_Biomphalaria      (  879) GNTALHIACARQLVGMVALLM  1
NFkB_Ed                  (  549) HQTPLHLAVLTRHPLAIDCLL  1
Relish_Dmel              (  711) GLTPLHMAIRQNKYDVAKKLI  1
IkB_Nev                  (  180) RQTPLHLATITKQSNIVRGLI  1
NFkB_Acropora            (  645) GKTPLHLSVEQDNLSLSGFLI  1
Relish_Biomphalaria      (  768) GNTCAHLAVLNKSESCLKILV  1
Relish_Biomphalaria      (  735) RQTPLHLATVMCQDEMVEMLL  1
NFkB_Platygyra           (  688) GNTPLHIAAASGLKGQTALLV  1
```

```
IkB_Nev                  (  260) GFTALHVAVFSNSIDIVSALT  1
NFkB1_Homo               (  720) GTTPLHIAAGRGSTRLAALLK  1
Relish_Dmel              (  746) GNNALHMAVLEQSVELLVLIL  1
//

----------------------------------------------------------------------

----------------------------------------------------------------------
      Motif 4 position-specific scoring matrix
----------------------------------------------------------------------
log-odds matrix: alength= 20 w= 21 n= 29610 bayes= 9.2075 E= 1.1e-
280
  -292   -425   -361   -420   -510    363     -4   -504   -162   -
571   -461   -339   -545   -504    -14   -387   -451   -486   -350
-79
  -253   -425    200    -87    -80   -374   -256   -379    107    -
18   -309    230   -432     97     85   -295   -115   -366   -323
69
  -364   -353   -487   -518   -475   -536   -467   -363   -417   -
502   -347   -130   -568   -467   -423     50    379   -360   -395
-481
   227     19   -663   -645   -632   -452   -635   -587   -624   -
637   -577   -602    293   -636   -603   -413   -434     32   -571
-643
  -178   -489   -768   -692   -352   -720   -652   -226   -656
328   -248   -712   -727   -652   -620   -688   -535    112   -437
-502
  -922   -808   -863   -959   -856   -795    524   -992   -912   -
931   -990   -914   -879   -952   -851   -963   -915   -993   -701
-802
  -318      9   -559   -477   -259   -492    168    156   -429
265     82   -470   -538   -462   -409   -216    -56     65   -264
-299
   376   -347   -659   -631   -585   -413   -628   -557   -622   -
596   -516   -587   -626   -641   -589   -187   -414   -153   -515
-600
   117    313   -799   -758   -520   -721   -784    151   -732   -
412   -418   -741   -800   -805   -752   -692    -55    303   -626
-610
    95   -351   -125    135    -68    -83   -305    270     36
21     -8   -315   -470   -306     -8   -110   -281    -47   -289
-297
  -123    100   -267     52   -396   -371    259   -375    -55    -
56    -20    134   -428    134     49   -101    115   -362   -319
69
  -262    200    145    -90   -409    234   -262   -389    107   -
190   -319     91   -439    -38    -72   -102   -116   -376   -332
-317
  -259   -429    127   -204    -80   -374    225   -385    -58   -
108   -315    209   -437    190    -71     29   -272   -372   -329
-21
```

```
    23      9    -39    -35     17   -396   -286     78     40
111    -12   -292      1     42    -81   -107      6     85   -298
-18
    94   -421    144    138   -396    -29    -28   -375    -55   -
188   -305    -97   -179     45     84     29     42   -149   -319
-305
    51    305   -559   -479   -272   -176   -407    198   -428
74     86   -459   -542   -153   -415   -121   -304    219   -260
-288
   158   -306   -569   -490    -56   -487   -419    183   -439
145   -207   -470   -553   -483   -427   -206      6    210   -271
-299
    23   -421    -33    121   -396     64    -28   -375    149   -
188    -20   -253   -428     45    157     49   -114    -67   -319
-305
    22    260    -42    -40    113    -83   -302     44    -82
126     -8   -113   -183    -47   -273    -61   -280      0   -289
167
  -565   -517   -775   -687    -61   -751   -625     85   -647
338   -208   -718   -719   -625   -600   -719   -562   -366   -392
-469
  -322   -314   -559   -476   -256   -495   -415    200   -136
263      6   -147   -537   -460   -121   -443   -137    137   -264
-301
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 21 nsites= 50 E= 1.1e-280
 0.000000  0.000000  0.000000  0.000000  0.000000  0.860000
0.040000  0.000000  0.020000  0.000000  0.000000  0.000000  0.000000
0.000000  0.060000  0.000000  0.000000  0.000000  0.000000  0.020000
 0.000000  0.000000  0.240000  0.020000  0.020000  0.000000
0.000000  0.000000  0.100000  0.080000  0.000000  0.280000  0.000000
0.120000  0.080000  0.000000  0.020000  0.000000  0.000000  0.040000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.020000  0.000000
0.000000  0.000000  0.140000  0.840000  0.000000  0.000000  0.000000
 0.340000  0.020000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.560000
0.000000  0.000000  0.000000  0.000000  0.080000  0.000000  0.000000
 0.020000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.840000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.140000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.020000  0.000000  0.000000  0.000000  0.000000
0.100000  0.140000  0.000000  0.540000  0.040000  0.000000  0.000000
0.000000  0.000000  0.020000  0.040000  0.100000  0.000000  0.000000
```

```
 0.960000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.020000  0.000000  0.020000  0.000000  0.000000
 0.160000  0.160000  0.000000  0.000000  0.000000  0.000000
0.000000  0.120000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.040000  0.520000  0.000000  0.000000
 0.140000  0.000000  0.020000  0.160000  0.020000  0.040000
0.000000  0.320000  0.060000  0.100000  0.020000  0.000000  0.000000
0.000000  0.040000  0.040000  0.000000  0.040000  0.000000  0.000000
 0.020000  0.040000  0.000000  0.080000  0.000000  0.000000
0.180000  0.000000  0.020000  0.060000  0.020000  0.140000  0.000000
0.160000  0.060000  0.040000  0.140000  0.000000  0.000000  0.040000
 0.000000  0.080000  0.160000  0.020000  0.000000  0.400000
0.000000  0.000000  0.100000  0.020000  0.000000  0.100000  0.000000
0.040000  0.020000  0.040000  0.020000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.140000  0.000000  0.020000  0.000000
0.140000  0.000000  0.020000  0.040000  0.000000  0.240000  0.000000
0.240000  0.020000  0.120000  0.000000  0.000000  0.000000  0.020000
 0.080000  0.020000  0.040000  0.040000  0.040000  0.000000
0.000000  0.080000  0.060000  0.200000  0.020000  0.000000  0.080000
0.080000  0.020000  0.040000  0.060000  0.120000  0.000000  0.020000
 0.140000  0.000000  0.160000  0.160000  0.000000  0.060000
0.020000  0.000000  0.020000  0.020000  0.000000  0.020000  0.020000
0.080000  0.080000  0.120000  0.080000  0.020000  0.000000  0.000000
 0.100000  0.160000  0.000000  0.000000  0.000000  0.020000
0.000000  0.180000  0.000000  0.140000  0.040000  0.000000  0.000000
0.020000  0.000000  0.040000  0.000000  0.300000  0.000000  0.000000
 0.220000  0.000000  0.000000  0.000000  0.020000  0.000000
0.000000  0.160000  0.000000  0.240000  0.000000  0.000000  0.000000
0.000000  0.000000  0.020000  0.060000  0.280000  0.000000  0.000000
 0.080000  0.000000  0.040000  0.140000  0.000000  0.120000
0.020000  0.000000  0.140000  0.020000  0.020000  0.000000  0.000000
0.080000  0.140000  0.140000  0.020000  0.040000  0.000000  0.000000
 0.080000  0.120000  0.040000  0.040000  0.080000  0.040000
0.000000  0.060000  0.020000  0.220000  0.020000  0.020000  0.020000
0.040000  0.000000  0.060000  0.000000  0.060000  0.000000  0.080000
 0.000000  0.000000  0.000000  0.000000  0.020000  0.000000
0.000000  0.080000  0.000000  0.900000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.200000  0.020000  0.520000  0.020000  0.020000  0.000000
0.000000  0.020000  0.000000  0.020000  0.180000  0.000000  0.000000
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 4 regular expression
--------------------------------------------------------------------
G[ND]T[PA]LHLAVIxG[NQ]LxV[VLA]xLL[LI]
--------------------------------------------------------------------




Time 302.02 secs.

********************************************************************


********************************************************************
MOTIF  5 MEME    width =  23  sites =  27  llr = 1155  E-value =
1.5e-236
********************************************************************
--------------------------------------------------------------------
      Motif 5 Description
--------------------------------------------------------------------
Simplified        A  ::1::::::::14::::::::::
pos.-specific     C  ::::::3:1:::1:::::1::::
probability       D  :::::::::11::::::::::13
matrix            E  ::::1:1:::1:::::::::::2
                  F  4::::::::::::::::::::::
                  G  :::::::4::8:1:::::::::1
                  H  :::::::::::::::::2:::::
                  I  :::3:4:::::::17:1::::::
                  K  ::::5::::1:::1:::::::3:
                  L  :::::21:::::::::::9::::
                  M  :::::::::::::::::::::::
                  N  ::::::16:1:::::::::::11
                  P  :a:::::::::6:::::::::::
                  Q  ::::3::::2:::::::1:::::
                  R  :::::::::::1:4:1:::::::
                  S  ::4::::::3:1:::::4:::43
                  T  ::4:::1::::::::3:1:191:
                  V  :::7:4::::::31249::7:::
                  W  :::::::::::::3:::::::::
                  Y  6:::::::9::::::::::::::

         bits    7.3
                 6.6
                 5.9
                 5.1
Relative         4.4         *
Entropy          3.7 **      *       *   *
(61.7 bits)      2.9 ** *   ** *  ** * ***
                 2.2 ****** ** * ********* *
                 1.5 ***********************
```

```
                 0.7 ***********************
                 0.0 -----------------------

Multilevel           YPTVKVCNYSGPARIVVSLVTSD
consensus            F SIQI G Q  VWVT H   KS
sequence                  L


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 5 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                   Site
-------------             ----- ---------            ---------------
NFkBb_Aiptasia               82  8.05e-25 GEFSDSKNKS
YPSVQVCNYQGPCRIVVSLVTED EPHMPHAHSL
NFkB_Acropora                82  1.12e-24 GEYSEKGKKS
YPSVQLCNYKGPARIVVSLVTSD ENPMPHAHSL
NFkBSer_Nev                  87  2.91e-24 GQFSTSKSKS
YPSVQVNNYQGPCRIVVTLVTKD EPYMLHAHSL
NFkBCys_Nev                  87  2.91e-24 GQFSTSKSKS
YPSVQVNNYQGPCRIVVTLVTKD EPYMLHAHSL
NFkB_Platygyra               82  1.13e-23 GQYSEKGKKS
YPSVQLCNYQGPARIVVSLVTVD EPPMPHAHSL
NFkB_Corallimorph            83  1.13e-23 GEYSEKSKKS
YPSVQLCNYQGPARIVVSLVTTE DPPMPHAHSL
NFkB_Ed                      87  2.33e-23 GQFSTSKNKS
YPSVQINNYKGPCRIVVTLVTSE EPHVLHAHSL
NFkB_Biomphalaria           153  1.58e-22 GENSTNDHRT
YPTIKIHNYNGPAIIVVSCVTKE NPPHCKPHPH
Dif_Dmel                    118  2.05e-22 MNSSSETGKT
FPTIEVCNYDGPVIIVVSCVTSD EPFRQHPHWL
NFAT_Ed                     252  4.99e-22 GPIHGSSDNT
FPTIKIANYSGSVWITVHLVTSS GMPHYHSIHG
NFAT_Nev                    546  9.24e-22 GPIHGSSDNT
FPTVKVLGYSGSVWITVHLVTSS GQPHYHSIHG
NFkB[Ciona                   63  1.18e-21 GGSSDKNKKT
FPAVKICNYQGYARIVVQLVTNE ENPRLHPHSL
NFkB2_Homo                   77  2.14e-21 GASSEKGRKT
YPTVKICNYEGPAKIEVDLVTHS DPPRAHAHSL
NFAT_Aiptasia               293  4.82e-21 GPIHGSSEST
YPTIKVSGYSGPVWITVYLTTSS GLPHYHSIHG
Relish_Biomphalaria          95  6.05e-21 GTKSERSRKS
YPSIKIENYSGAARVVVSLVTDE KVPRPHAHKL
Dorsal_Dmel                  86  4.46e-19 GVNSTPENKT
YPTIEIVGYKGRAVVVVSCVTKD TPYRPHPHNL
NFAT_Acropora               311  5.41e-19 GPIHGSQENT
FPTVKVTGYSDAIWITVHLTTSG GIPHYHSIHG
NFkB1_Homo                   82  6.57e-19 GASSEKNKKS
YPQVKICNYVGPAKVIVQLVTNG KNIHLHAHSL
```

```
NFATb_Platygyra             335  2.24e-18 GPIHGSQDNT
FPAVKVTGCDEAVWITVHLTTSS GVPHYHSIHG
NFATa_Platygyra             314  2.24e-18 GPIHGSQDNT
FPAVKVTGCDEAVWITVHLTTSS GVPHYHSIHG
NFkB_Amphimedon              87  2.46e-18 NSEKNRRQKT
YPTVHLKGYRGRARVMVSLVTDS DPAMPHAHSI
RelA_Homo                    58  1.48e-17 GERSTDTTKT
HPTIKINGYTGPGTVRISLVTKD PPHRPHPHEL
cRel                         47  3.22e-17 GEHSTDNNRT
YPSIQIMNYYGKGKVRITLVTKN DPYKPHPHDL
rel1[Ciona]                  44  1.23e-16 GKNTNGDRKT
WPSCQVLNYSGVAIMRVSLVSKD DPPRPHPHSL
NFAT_Corallimorph           350  3.79e-16 GPIHGSKDNT
FPTVMVTGASDTLWITVHLITSS GQPHYHSIHG
Relish_Dmel                 189  1.22e-15 GANSKRTPKT
FPEVTLCNYDGPAVIRCSLFQTN LDSPHSHQLV
NFAT5                       313  3.51e-12 GSVKDRTQQG
FPTVKLEGHNEPVVLQVFVGNDS GRVKPHGFYQ
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 5 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkBb_Aiptasia                    8.1e-25  81_[5]_744
NFkB_Acropora                     1.1e-24  81_[5]_800
NFkBSer_Nev                       2.9e-24  86_[5]_331
NFkBCys_Nev                       2.9e-24  86_[5]_331
NFkB_Platygyra                    1.1e-23  81_[5]_814
NFkB_Corallimorph                 1.1e-23  82_[5]_810
NFkB_Ed                           2.3e-23  86_[5]_751
NFkB_Biomphalaria                 1.6e-22  152_[5]_435
Dif_Dmel                            2e-22  117_[5]_527
NFAT_Ed                             5e-22  251_[5]_186
NFAT_Nev                          9.2e-22  545_[5]_353
NFkB[Ciona                        1.2e-21  62_[5]_1115
NFkB2_Homo                        2.1e-21  76_[5]_800
NFAT_Aiptasia                     4.8e-21  292_[5]_363
Relish_Biomphalaria               6.1e-21  94_[5]_968
Dorsal_Dmel                       4.5e-19  85_[5]_570
NFAT_Acropora                     5.4e-19  310_[5]_346
NFkB1_Homo                        6.6e-19  81_[5]_865
NFATb_Platygyra                   2.2e-18  334_[5]_193
NFATa_Platygyra                   2.2e-18  313_[5]_193
NFkB_Amphimedon                   2.5e-18  86_[5]_986
RelA_Homo                         1.5e-17  57_[5]_368
cRel                              3.2e-17  46_[5]_550
rel1[Ciona]                       1.2e-16  43_[5]_224
NFAT_Corallimorph                 3.8e-16  349_[5]_166
Relish_Dmel                       1.2e-15  188_[5]_760
```

```
NFAT5                            3.5e-12  312_[5]_1196
------------------------------------------------------------------------

------------------------------------------------------------------------
      Motif 5 in BLOCKS format
------------------------------------------------------------------------
BL   MOTIF 5 width=23 seqs=27
NFkBb_Aiptasia           (   82) YPSVQVCNYQGPCRIVVSLVTED  1
NFkB_Acropora            (   82) YPSVQLCNYKGPARIVVSLVTSD  1
NFkBSer_Nev              (   87) YPSVQVNNYQGPCRIVVTLVTKD  1
NFkBCys_Nev              (   87) YPSVQVNNYQGPCRIVVTLVTKD  1
NFkB_Platygyra           (   82) YPSVQLCNYQGPARIVVSLVTVD  1
NFkB_Corallimorph        (   83) YPSVQLCNYQGPARIVVSLVTTE  1
NFkB_Ed                  (   87) YPSVQINNYKGPCRIVVTLVTSE  1
NFkB_Biomphalaria        (  153) YPTIKIHNYNGPAIIVVSCVTKE  1
Dif_Dmel                 (  118) FPTIEVCNYDGPVIIVVSCVTSD  1
NFAT_Ed                  (  252) FPTIKIANYSGSVWITVHLVTSS  1
NFAT_Nev                 (  546) FPTVKVLGYSGSVWITVHLVTSS  1
NFkB[Ciona               (   63) FPAVKICNYQGYARIVVQLVTNE  1
NFkB2_Homo               (   77) YPTVKICNYEGPAKIEVDLVTHS  1
NFAT_Aiptasia            (  293) YPTIKVSGYSGPVWITVYLTTSS  1
Relish_Biomphalaria      (   95) YPSIKIENYSGAARVVVSLVTDE  1
Dorsal_Dmel              (   86) YPTIEIVGYKGRAVVVVSCVTKD  1
NFAT_Acropora            (  311) FPTVKVTGYSDAIWITVHLTTSG  1
NFkB1_Homo               (   82) YPQVKICNYVGPAKVIVQLVTNG  1
NFATb_Platygyra          (  335) FPAVKVTGCDEAVWITVHLTTSS  1
NFATa_Platygyra          (  314) FPAVKVTGCDEAVWITVHLTTSS  1
NFkB_Amphimedon          (   87) YPTVHLKGYRGRARVMVSLVTDS  1
RelA_Homo                (   58) HPTIKINGYTGPGTVRISLVTKD  1
cRel                     (   47) YPSIQIMNYYGKGKVRITLVTKN  1
rel1[Ciona]              (   44) WPSCQVLNYSGVAIMRVSLVSKD  1
NFAT_Corallimorph        (  350) FPTVMVTGASDTLWITVHLITSS  1
Relish_Dmel              (  189) FPEVTLCNYDGPAVIRCSLFQTN  1
NFAT5                    (  313) FPTVKLEGHNEPVVLQVFVGNDS  1
//

------------------------------------------------------------------------
------------

------------------------------------------------------------------------
------------
      Motif 5 position-specific scoring matrix
------------------------------------------------------------------------
------------
log-odds matrix: alength= 20 w= 23 n= 29532 bayes= 9.89428 E= 1.5e-
236
  -560   -483   -633   -619    342   -639     52   -473   -564   -
448   -442   -529   -676   -568   -518   -587   -565   -507    258
456
```

```
  -629   -666   -702   -732   -720   -664   -677   -764   -690   -
743   -760   -741    378   -743   -676   -715   -692   -755   -593
-695
    42   -293   -391    -91   -430   -413   -401   -343   -347   -
456   -320   -285   -496    -93   -362    180    300   -332   -353
-417
  -428    100   -723   -688   -446   -711   -746    273   -668   -
327   -339   -687   -744   -762   -698   -693   -439    337   -591
-557
  -337   -470   -368     35   -495   -438     45   -425    321   -
423     58   -317   -505    237   -106   -381    -62   -420   -350
-366
  -454   -403   -752   -713   -405   -730   -757    304   -687
136   -304   -705   -761   -756   -718   -714   -458    268   -536
-537
   -53    389   -221     42   -288   -313     42   -232      7    -
26     58    133   -372   -191   -164   -100    116    -62   -232
-228
  -529   -591   -431   -555   -696    239   -527   -777   -564   -
764   -751    361   -685   -624   -610   -528   -559   -731   -581
-605
   -89    195   -564   -547    -82   -542     52   -436   -507   -
424   -406   -491   -612   -536   -475   -488   -486   -456   -109
513
  -177   -349    124    -13   -324   -299   -180   -303    120   -
313   -233     49   -356    169      3    122    -41    -77   -247
52
  -255   -390    -27     10   -475    358   -379   -469   -338   -
533   -426   -282   -502   -448   -343   -343   -405   -450   -317
-402
    68   -375   -365   -331   -402   -394   -352   -371    -68   -
378   -363   -384    311   -354     26    -70    -92   -111   -370
13
   265    282   -519   -455   -283     -9   -416     11   -417    -
90   -205   -446   -533   -469   -408   -327   -285    191   -272
-307
  -347   -386   -500   -361   -386   -469   -311    123    135   -
336   -282   -373   -541   -287    298   -423    -61     75    520
-340
  -318   -317   -429   -420   -250   -476   -441    395   -359    -
37     10   -400   -527   -452   -395   -416   -293    143   -269
-276
  -226   -239   -419    -70   -216   -394   -309     18   -257   -
191     77   -349   -458    -70    155   -335    195    265   -198
-224
  -234     68   -499   -463   -358   -524   -452     92   -451   -
279   -273   -503   -526   -534   -426   -495   -288    372   -401
-455
  -238   -348    -41   -204     -8   -324    275   -358   -172   -
378   -302   -180   -415     21   -223    214    122   -357   -279
51
```

```
  -425    228   -626   -542   -231   -604   -499   -146   -502
327   -120   -573   -586   -499   -462   -563   -428    -61   -304
-370
  -135   -193   -396   -358    -77   -190   -337     42   -346   -
227   -207   -402   -422   -425   -315   -389     35    355   -290
-362
  -303   -286   -413   -446   -406   -473   -396   -294   -345   -
433   -278    -64   -501   -104   -353    -64    381   -291   -326
-411
  -203   -371     93    -20   -350   -304     45   -332    224   -
342   -263     54   -379   -193   -168    173     31    -79   -274
-257
  -405   -514    256    160   -569     10   -306   -625   -328   -
634   -593     74   -529   -388   -413    173   -365   -608   -505
-428
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 5 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 23 nsites= 27 E= 1.5e-236
 0.000000  0.000000  0.000000  0.000000  0.370370  0.000000
0.037037  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.037037  0.555556
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.111111  0.000000  0.000000  0.037037  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.037037  0.000000  0.370370  0.444444  0.000000  0.000000  0.000000
 0.000000  0.037037  0.000000  0.000000  0.000000  0.000000
0.000000  0.296296  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.074074  0.000000  0.000000
0.037037  0.000000  0.481481  0.000000  0.037037  0.000000  0.000000
0.333333  0.000000  0.000000  0.037037  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.370370  0.000000  0.222222  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.407407  0.000000  0.000000
 0.037037  0.333333  0.000000  0.074074  0.000000  0.000000
0.037037  0.000000  0.037037  0.074074  0.037037  0.148148  0.000000
0.000000  0.000000  0.037037  0.148148  0.037037  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.370370
0.000000  0.000000  0.000000  0.000000  0.000000  0.629630  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.037037  0.074074  0.000000  0.000000  0.000000  0.000000
0.037037  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.851852
 0.000000  0.000000  0.148148  0.037037  0.000000  0.000000
0.000000  0.000000  0.111111  0.000000  0.000000  0.074074  0.000000
0.222222  0.037037  0.259259  0.037037  0.037037  0.000000  0.037037
```

```
 0.000000  0.000000  0.074074  0.111111  0.000000  0.814815
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.148148  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.037037  0.000000  0.000000  0.000000  0.555556
0.000000  0.074074  0.074074  0.037037  0.037037  0.000000  0.037037
 0.444444  0.148148  0.000000  0.000000  0.000000  0.074074
0.000000  0.037037  0.000000  0.037037  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.259259  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.111111  0.111111  0.000000  0.000000  0.000000  0.000000
0.000000  0.370370  0.000000  0.037037  0.111111  0.259259  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.703704  0.000000  0.037037  0.037037  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.222222  0.000000  0.000000
 0.000000  0.000000  0.000000  0.037037  0.000000  0.000000
0.000000  0.037037  0.000000  0.000000  0.037037  0.000000  0.000000
0.037037  0.148148  0.000000  0.259259  0.444444  0.000000  0.000000
 0.000000  0.037037  0.000000  0.000000  0.000000  0.000000
0.000000  0.074074  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.888889  0.000000  0.000000
 0.000000  0.000000  0.037037  0.000000  0.037037  0.000000
0.222222  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.074074  0.000000  0.444444  0.148148  0.000000  0.000000  0.037037
 0.000000  0.111111  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.851852  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.037037  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.037037  0.037037
0.000000  0.037037  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.148148  0.740741  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.037037  0.000000
0.037037  0.000000  0.037037  0.888889  0.000000  0.000000  0.000000
 0.000000  0.000000  0.111111  0.037037  0.000000  0.000000
0.037037  0.000000  0.259259  0.000000  0.000000  0.074074  0.000000
0.000000  0.000000  0.370370  0.074074  0.037037  0.000000  0.000000
 0.000000  0.000000  0.333333  0.185185  0.000000  0.074074
0.000000  0.000000  0.000000  0.000000  0.000000  0.074074  0.000000
0.000000  0.000000  0.333333  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 5 regular expression
--------------------------------------------------------------------
[YF]P[TS][VI][KQ][VIL]C[NG]Y[SQ]GP[AV][RW][IV][VT]V[SH]LVT[SK][DS]
--------------------------------------------------------------------
```

```
Time 369.01 secs.

********************************************************************


********************************************************************
MOTIF  6 MEME    width =  50  sites =   8  llr = 1068  E-value =
7.9e-230
********************************************************************
--------------------------------------------------------------------
      Motif 6 Description
--------------------------------------------------------------------
Simplified        A
:::9::::::::::::::1::::::::::::3:::::::a::1::8:::3
pos.-specific     C
::::::::::::::::::::::::::::::::::::::::::::::::::
probability       D
4:::::9::::::::::::a::::1:::9:::::::::::::::::3:::
matrix            E
::::::1::::::::::a:::a::::::1::::::9::a:::::::6::5
                  F
:::::::::::::::::::::::::::::::::::::::::::a::::::
                  G
::::::::::::::::::9:::::::a::::::::::::::::::::::1
                  H
::::::::::::::::::::::::::::::::::::::::::::1:::::
                  I
:1::1:::::a::1:::::::::::::a:::::::::::::::::::a::
                  K
1:::::::::::::::::::4::59::::::::a811a::1:::::::::
                  L
:::::9::9::::9::::::::a::::::::::::::::::a9:::::::
                  M
:9:::1::::::::::::::::::::::::::::::::::1:::::::::
                  N
4::::::::1:::::a::::::::::::::::::::::::::::::::::
                  P
:::::::::::::::::::::::::::::a::::::::::::::::::a1
                  Q
::::1:::::::::::::::::::::::::::::::::::::::9:::::
                  R
::1::::11::aa:a:::::6::5:a::::9:::1:9:::8:::::::::
                  S
:::::::9:9:::::::::::::::::::::1::::::::::::::1:::
                  T
::9::::::::::::::::::::::::::::6::1::::::::::1::::
                  V
:::18:::::::::::::::::::::::::1::::::::::::::1::::
                  W
::::::::::::::::a:::::::::::::::a:::::::::::::::::
```

```
                  Y
1:::::::::::::::::::::::::::::::::::::::::::::::::

         bits    7.3                *               *
                 6.6                *               *
                 5.9                *               *
                 5.1  *              *               *          *
Relative         4.4  *        *** **** * *   * *    **   **    *
*
Entropy          3.7  ***  *   *** **************** ** ******* **
**
(192.6 bits)     2.9
*************************************************
                 2.2
**************************************************
                 1.5
**************************************************
                 0.7
**************************************************
                 0.0 -----------------------------------------------

Multilevel
DMTAVLDSLSIRRLRNWEGDRELKKRGIDPRTWKKERKEARLLFQAEIPE
consensus            N                   K  R       A              D
A
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 6 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value
Site
-------------             ----- ---------            ---------------
NFAT_Acropora               372  2.16e-64 AVQVMVGPDS
NMTAVLDSLSIRRLRNWEGDRELRKRGIDPRTWKKERKEARLLFQAEIPE QEGRPATKLL
NFATb_Platygyra             396  1.52e-63 AVQVMVAPDT
NMTAVLDSLSIRRLRNWEGDRELRKRGIDPRAWKKERKEARLLFQAEIPE KDGRPALKLS
NFATa_Platygyra             375  1.52e-63 AVQVMVAPDT
NMTAVLDSLSIRRLRNWEGDRELRKRGIDPRAWKKERKEARLLFQAEIPE KDGRPALKLS
NFAT_Corallimorph           411  7.88e-63 AVQLMVAPDN
DMTAVLDSLSIRRLRNWEGDRELKKRGIDPRTWKKERKEARLLFQTEIPE SNGQPAIKLT
NFAT_Nev                    607  2.43e-61 AVQVLVEPDC
DMTAILDSLSIRRLRNWEGDKELKKRGIDPRTWKKERKEARLLFQADIPA KDGLPEMKLS
NFAT_Aiptasia               354  8.56e-60 AVQLMVDPDS
KMTAVMDSLSIRRLRNWEGDKELKKRGIDPRTWKRERKEARLLFQAEIPG EDGQPDIKLT
NFAT_Ed                     313  8.56e-60 AVQVLVEPDC
DMTAVLDSLSIRRLRNWEGDRELKKRGIDPRSWKKERKEAMLLFQADIPA SDGCPETKLS
```

```
NFAT_Hydra                 1233  2.05e-36 KVYGHENRDG
YIRVQLERRNIRRIRNWEADKELRDRGIEPVTWKTKKKEAKLAFHVSIPP SKTHSGYELT
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 6 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFAT_Acropora                     2.2e-64  371_[6]_258
NFATb_Platygyra                   1.5e-63  395_[6]_105
NFATa_Platygyra                   1.5e-63  374_[6]_105
NFAT_Corallimorph                 7.9e-63  410_[6]_78
NFAT_Nev                          2.4e-61  606_[6]_265
NFAT_Aiptasia                     8.6e-60  353_[6]_275
NFAT_Ed                           8.6e-60  312_[6]_98
NFAT_Hydra                        2.1e-36  1232_[6]_693
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 6 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 6 width=50 seqs=8
NFAT_Acropora            (  372)
NMTAVLDSLSIRRLRNWEGDRELRKRGIDPRTWKKERKEARLLFQAEIPE  1
NFATb_Platygyra          (  396)
NMTAVLDSLSIRRLRNWEGDRELRKRGIDPRAWKKERKEARLLFQAEIPE  1
NFATa_Platygyra          (  375)
NMTAVLDSLSIRRLRNWEGDRELRKRGIDPRAWKKERKEARLLFQAEIPE  1
NFAT_Corallimorph        (  411)
DMTAVLDSLSIRRLRNWEGDRELKKRGIDPRTWKKERKEARLLFQTEIPE  1
NFAT_Nev                 (  607)
DMTAILDSLSIRRLRNWEGDKELKKRGIDPRTWKKERKEARLLFQADIPA  1
NFAT_Aiptasia            (  354)
KMTAVMDSLSIRRLRNWEGDKELKKRGIDPRTWKRERKEARLLFQAEIPG  1
NFAT_Ed                  (  313)
DMTAVLDSLSIRRLRNWEGDRELKKRGIDPRSWKKERKEAMLLFQADIPA  1
NFAT_Hydra               ( 1233)
YIRVQLERRNIRRIRNWEADKELRDRGIEPVTWKTKKKEAKLAFHVSIPP  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 6 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 50 n= 28479 bayes= 12.5343 E= 7.9e-
230
  -218   -337    261   -122   -359   -186   -144   -383    113   -
395   -334    260   -360   -204   -192   -170   -194   -373   -288
197
```

```
  -426   -343   -527   -526   -333   -524   -476   -102   -460   -
183    531   -505   -559   -526   -502   -508   -421   -284   -207
-281
  -215   -214   -336   -348   -331   -372   -306   -226   -212   -
352   -210   -199   -421   -303     66    -78    370   -222   -248
-322
   346    -74   -359   -312   -268   -169   -338   -200   -296   -
260   -192   -332   -447   -367   -291   -115   -185     15   -208
-292
   -91   -148   -350   -312   -232   -377   -292     95   -298   -
176   -157   -356   -378   -109   -269   -345   -152    354   -244
-315
  -315   -277   -490   -402   -110   -482   -360    -47   -361
324    163   -439   -451   -360   -320   -435   -310   -143   -176
-243
  -304   -352    399    -32   -378   -362   -261   -361   -338   -
416   -359    -91   -498   -370   -344   -352   -361   -370   -272
-308
  -155   -182   -302   -335   -321   -298   -301   -329   -213   -
366   -278   -182   -377   -335     33    297     54   -350   -248
-275
  -300   -270   -459   -372   -124   -454   -335    -59   -296
325     -2   -407   -432   -335      7   -408   -296   -146   -177
-234
  -155   -179   -232   -309   -317   -274   -278   -330   -242   -
369   -280     26   -368   -336   -252    295     62   -356   -249
-268
  -326   -307   -470   -464   -259   -483   -466    422   -407   -
105   -123   -444   -541   -493   -433   -455   -315     25   -292
-301
  -348   -280   -443   -440   -436   -413   -219   -376   -110   -
396   -370   -343   -422   -291    437   -414   -381   -468   -191
-357
  -348   -280   -443   -440   -436   -413   -219   -376   -110   -
396   -370   -343   -422   -291    437   -414   -381   -468   -191
-357
  -315   -277   -496   -409   -114   -487   -368     93   -369
323      1   -445   -458   -369   -329   -441   -311   -130   -181
-247
  -348   -280   -443   -440   -436   -413   -219   -376   -110   -
396   -370   -343   -422   -291    437   -414   -381   -468   -191
-357
  -366   -326   -228   -400   -358   -358   -128   -309   -299   -
419   -344    413   -450   -333   -331   -241   -274   -383   -229
-305
  -395   -325   -414   -413   -109   -422   -366   -367   -374   -
253   -283   -402   -504   -413   -334   -455   -402   -356    718
-108
  -479   -543   -214    404   -568   -520   -463   -492   -515   -
601   -537   -433   -674   -416   -521   -574   -528   -542   -451
-523
```

```
   -45   -307   -264   -323   -410    363   -331   -403   -288   -
468   -360   -242   -439   -408   -284   -276   -336   -377   -252
-343
  -329   -369    405   -108   -397   -379   -284   -384   -365   -
438   -384   -115   -514   -401   -366   -375   -384   -394   -289
-328
  -287   -338   -383   -243   -436   -365   -174   -335    260   -
330   -274   -248   -427   -151    374   -332   -274   -350   -222
-286
  -479   -543   -214    404   -568   -520   -463   -492   -515   -
601   -537   -433   -674   -416   -521   -574   -528   -542   -451
-523
  -360   -322   -519   -451   -161   -495   -401    -99   -409    
340    -50   -480   -489   -412   -368   -479   -359   -192   -219
-281
  -281   -364   -378   -226   -442   -361   -174   -331    326   -
325   -264   -239   -436   -139    322   -325   -263   -337   -239
-280
  -333   -349   -146   -345   -487   -433   -345   -358    419   -
448   -366   -318   -485   -377    -20   -433   -360   -440   -289
-393
  -348   -280   -443   -440   -436   -413   -219   -376   -110   -
396   -370   -343   -422   -291    437   -414   -381   -468   -191
-357
  -229   -352   -300   -361   -441    372   -363   -442   -325   -
501   -401   -280   -471   -444   -320   -324   -384   -422   -281
-373
  -326   -307   -470   -464   -259   -483   -466    422   -407   -
105   -123   -444   -541   -493   -433   -455   -315     25   -292
-301
  -304   -352    399    -32   -378   -362   -261   -361   -338   -
416   -359    -91   -498   -370   -344   -352   -361   -370   -272
-308
  -241   -373   -382   -363   -410   -389   -367   -395   -324   -
397   -390   -407    367   -383   -342   -341   -328   -383   -353
-411
  -324   -264   -428   -412   -416   -399   -203   -343    -87   -
372   -344   -324   -409   -269    432   -393   -358   -165   -177
-338
   136   -175   -366   -380   -349   -273   -345   -260   -306   -
373   -239   -235   -399   -346   -305     40    337   -230   -272
-352
  -395   -325   -414   -413   -109   -422   -366   -367   -374   -
253   -283   -402   -504   -413   -334   -455   -402   -356    718
-108
  -348   -353   -468   -415   -496   -460   -373   -364    423   -
460   -377   -362   -498   -417    -24   -469   -379   -453   -294
-408
  -329   -346   -446   -369   -484   -441   -328   -350    416   -
431   -351   -334   -483   -342     39   -436   -151   -426   -281
-382
```

```
  -375   -542   -161    397   -554   -466   -404   -463   -105   -
534   -467   -375   -555   -309   -394   -476   -437   -477   -440
-482
  -328   -265   -426   -406   -424   -399   -198   -356    -19   -
376   -346   -320   -406   -262    432   -393   -357   -444   -175
-340
  -348   -353   -468   -415   -496   -460   -373   -364    423   -
460   -377   -362   -498   -417    -24   -469   -379   -453   -294
-408
  -479   -543   -214    404   -568   -520   -463   -492   -515   -
601   -537   -433   -674   -416   -521   -574   -528   -542   -451
-523
   369   -160   -432   -403   -361   -239   -410   -326   -388   -
366   -297   -399   -472   -443   -373   -196   -253   -219   -288
-372
  -320   -270   -418   -372   -423   -394   -194   -351     14   -
368     -3   -308   -407   -243    426   -382   -343   -427   -179
-331
  -360   -322   -519   -451   -161   -495   -401    -99   -409
340    -50   -480   -489   -412   -368   -479   -359   -192   -219
-281
   -29   -260   -470   -387   -125   -433   -351    -54   -346
323     -5   -417   -437   -354   -310   -389   -290   -137   -182
-242
  -347   -248   -455   -446    472   -467   -382   -220   -431   -
171   -209   -449   -471   -505   -437   -394   -418   -281    -81
-16
  -242   -287   -346   -102   -367   -416     46   -313   -230   -
255   -143   -242   -365    380   -169   -322   -286   -335   -174
-321
   338    -70   -354   -306   -263   -165   -331   -205   -289   -
257   -186   -327   -443   -360   -285   -111    -11     11   -202
-286
  -211   -521    185    336   -499   -319   -269   -393   -153   -
410   -341   -201   -377   -150   -273    -10   -275   -353   -413
-375
  -326   -307   -470   -464   -259   -483   -466    422   -407   -
105   -123   -444   -541   -493   -433   -455   -315     25   -292
-301
  -241   -373   -382   -363   -410   -389   -367   -395   -324   -
397   -390   -407    367   -383   -342   -341   -328   -383   -353
-411
   151   -301    -68    286   -364     46   -210   -313   -106   -
330   -255   -176     38   -139   -184   -206   -192   -275   -289
-277
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 6 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 50 nsites= 8 E= 7.9e-230
 0.000000  0.000000  0.375000  0.000000  0.000000  0.000000
0.000000  0.000000  0.125000  0.000000  0.000000  0.375000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.125000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.125000  0.000000  0.000000  0.875000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.125000  0.000000  0.875000  0.000000  0.000000  0.000000
 0.875000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.125000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.125000  0.000000  0.000000  0.000000  0.000000  0.000000
0.125000  0.000000  0.000000  0.000000  0.750000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.875000  0.125000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.875000  0.125000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.125000  0.875000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.875000  0.000000  0.000000  0.000000
0.000000  0.125000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.125000  0.000000
0.000000  0.000000  0.875000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.125000  0.000000  0.875000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.125000  0.000000  0.000000  0.000000  0.000000  0.875000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.375000  0.000000  0.000000  0.000000  0.000000
0.000000  0.625000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.125000  0.000000  0.000000  0.000000
0.000000  0.000000  0.875000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.875000  0.125000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.875000  0.000000  0.000000  0.125000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.125000  0.625000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.750000  0.000000  0.000000  0.000000  0.000000
0.000000  0.125000  0.000000  0.125000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.875000  0.000000  0.000000
0.000000  0.000000  0.125000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.125000  0.000000  0.000000  0.000000  0.000000
0.000000  0.875000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.125000  0.000000  0.125000  0.000000  0.000000
0.000000  0.750000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.125000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.875000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.125000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.875000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.750000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.125000  0.125000  0.000000  0.000000
 0.000000  0.000000  0.250000  0.625000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.125000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.250000  0.000000  0.000000  0.500000  0.000000  0.125000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.125000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 6 regular expression
--------------------------------------------------------------------
[DN]MTAVLDSLSIRRLRNWEGD[RK]EL[KR]KRGIDPR[TA]WKKERKEARLLFQA[ED]IP[EA]
--------------------------------------------------------------------




Time 434.52 secs.

********************************************************************


********************************************************************
MOTIF  7 MEME    width =  21  sites =  25  llr = 948  E-value =
7.3e-173
********************************************************************
--------------------------------------------------------------------
      Motif 7 Description
--------------------------------------------------------------------
Simplified        A  11::::2::::::6:::::::
pos.-specific     C  ::::::::::7::::::::::
probability       D  :2:4:::::::::::::612:
matrix            E  :1::::1:::::1:::113::
                  F  :::::::::::a::4::::::
                  G  :2::::::::::::::::1:9
                  H  ::::::::::::::2::::::
                  I  2:2:::1::::::::2:::::
                  K  4::2::::1::::::::::::
                  L  ::::7::::a:::::6:::::
                  M  ::5:::::::1::::::::::
                  N  :1:424:::::::::::1:3:
                  P  ::::::::::::::::7:2::
                  Q  1:::::::::::6::::111:
                  R  ::2:::2:9:::2:::2::::
                  S  12:::41:::::::::::22:
                  T  :1:::2:::::::::::::::
                  V  ::1:::3a::2::4:1:::::
                  W  :::::::::::::::::::::
                  Y  ::::::::::::::3::::::

         bits    7.3
                 6.6
                 5.9
                 5.1
```

```
Relative         4.4            *
Entropy          3.7        *****        *
(54.7 bits)      2.9   **   ***** **     *
                 2.2   **** ***********  *
                 1.5 * *******************
                 0.7 *********************
                 0.0 ---------------------

Multilevel           KDMDLSVVRLCFQAFLPDENG
consensus               N NA      VY   SS
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                    Site
-------------             ----- ---------            ---------------
NFkB_Amphimedon             207  8.74e-25 EIHQQAQTLA
KSMNLSVVRLCFQAFLPDENG RYTIPIDPVF
NFkBb_Aiptasia              227  1.08e-24 KILKLVQEQS
KTMNLSAVRLCFQAYLPDENG NFTKPLKPCI
NFkB_Corallimorph           228  3.80e-24 KVRAMVEEQK
KNMNLSAVRLCFQAYLPDESG CFTKALPPCI
NFkB_Platygyra              224  3.78e-23 KVRQMVEEQK
QNMNLNAVRLCFQAYLPDESG CFTKALPPCI
NFkB_Acropora               223  3.13e-22 KVRSLVEKQK
NSMNLSVVRLCFQAYLPDDNG CFTKALPPCF
NFkBSer_Nev                 230  1.07e-21 KSREYAKQQA
AAMDLSAVRLCFQAYLPDQDG NFTRPLKPVY
NFkBCys_Nev                 230  1.07e-21 KSREYAEQQA
AAMDLSAVRLCFQAYLPDQDG NFTRPLKPVY
cRel                        141  5.50e-21 NVPEKQLNDI
EDCDLNVVRLCFQVFLPDEHG NLTTALPPVV
NFkB_Ed                     231  1.12e-20 KIKKIAEQQA
KEMNLSEVKLCFQAYLPDRNG NFTKALKPVY
NFkB_Biomphalaria           247  1.28e-19 PYQTGFDHAQ
SNIDLNVVRLCFQVFLPNEQG KVTRVVPPVC
NFkB[Ciona                  178  5.38e-19 RIAAKAQSEA
KSIDLSVVRLMFIAYLPDSNG AFTIMLKPVI
NFkB1_Homo                  206  1.07e-18 LIRQAALQQT
KEMDLSVVRLMFTAFLPDSTG SFTRRLEPVV
Relish_Biomphalaria         209  1.46e-17 TAKLQADEQS
KTMQLNVVKLCFQVFLRNPDG TFDKMLPPVV
rel1[Ciona]                 140  5.89e-17 TMLDGDERSA
VDVDLNIVRLCFEAFIPDARG KYTQKLEPVV
Relish_Dmel                 298  6.42e-17 ELHQETEREA
KDMNLNQVRLCFEAFKIEDNG AWVPLAPPVY
```

```
RelA_Homo                   150  6.42e-17 PFQVPIEEQR
GDYDLNAVRLCFQVTVRDPSG RPLRLPPVLS
RelB_Homo                   259  2.44e-15 PYNAGSLKNH
QEVDMNVVRICFQASYRDQQG QMRRMDPVLS
NFkB2_Homo                  183  3.07e-15 ELEQEAKELK
KVMDLSIVRLRFSAFLRASDG SFSLPLKPVI
NFAT1                       515  8.81e-15 DIELRKGETD
IGRKNTRVRLVFRVHIPESSG RIVSLQTASN
Dorsal_Dmel                 181  1.02e-14 KTGFSHRFQP
SSIDLNSVRLCFQVFMESEQK GRFTSPLPPV
NFAT4                       557  1.02e-14 DIELRKGETD
IGRKNTRVRLVFRVHIPQPSG KVLSLQIASI
NFAT2                        81  1.84e-14 DIELRKGETD
IGRKNTRVRLVFRVHVPQPSG RTLSLQVASN
NFAT3                       473  1.08e-13 DIELRKGETD
IGRKNTRVRLVFRVHVPQGGG KVVSVQAASV
NFkB_Hydra                  192  1.30e-12 DLQSEASSLM
KDLNVHSVVLAFHCFLEDSNG RYTINLPTVY
Dif_Dmel                    216  5.59e-11 NAKFDHKDQI
DKINRYELRLCYQAFITVGNS KVPLDPIVSS
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB_Amphimedon                   8.7e-25  206_[7]_868
NFkBb_Aiptasia                    1.1e-24  226_[7]_601
NFkB_Corallimorph                 3.8e-24  227_[7]_667
NFkB_Platygyra                    3.8e-23  223_[7]_674
NFkB_Acropora                     3.1e-22  222_[7]_661
NFkBSer_Nev                       1.1e-21  229_[7]_190
NFkBCys_Nev                       1.1e-21  229_[7]_190
cRel                              5.5e-21  140_[7]_458
NFkB_Ed                           1.1e-20  230_[7]_609
NFkB_Biomphalaria                 1.3e-19  246_[7]_343
NFkB[Ciona                        5.4e-19  177_[7]_1002
NFkB1_Homo                        1.1e-18  205_[7]_743
Relish_Biomphalaria               1.5e-17  208_[7]_856
rel1[Ciona]                       5.9e-17  139_[7]_130
Relish_Dmel                       6.4e-17  297_[7]_653
RelA_Homo                         6.4e-17  149_[7]_278
RelB_Homo                         2.4e-15  258_[7]_300
NFkB2_Homo                        3.1e-15  182_[7]_696
NFAT1                             8.8e-15  514_[7]_370
Dorsal_Dmel                         1e-14  180_[7]_477
NFAT4                               1e-14  556_[7]_498
NFAT2                             1.8e-14  80_[7]_252
NFAT3                             1.1e-13  472_[7]_339
NFkB_Hydra                        1.3e-12  191_[7]_265
```

```
Dif_Dmel                          5.6e-11  215_[7]_431
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
     Motif 7 in BLOCKS format
--------------------------------------------------------------------------------
BL   MOTIF 7 width=21 seqs=25
NFkB_Amphimedon         (  207) KSMNLSVVRLCFQAFLPDENG  1
NFkBb_Aiptasia          (  227) KTMNLSAVRLCFQAYLPDENG  1
NFkB_Corallimorph       (  228) KNMNLSAVRLCFQAYLPDESG  1
NFkB_Platygyra          (  224) QNMNLNAVRLCFQAYLPDESG  1
NFkB_Acropora           (  223) NSMNLSVVRLCFQAYLPDDNG  1
NFkBSer_Nev             (  230) AAMDLSAVRLCFQAYLPDQDG  1
NFkBCys_Nev             (  230) AAMDLSAVRLCFQAYLPDQDG  1
cRel                    (  141) EDCDLNVVRLCFQVFLPDEHG  1
NFkB_Ed                 (  231) KEMNLSEVKLCFQAYLPDRNG  1
NFkB_Biomphalaria       (  247) SNIDLNVVRLCFQVFLPNEQG  1
NFkB[Ciona              (  178) KSIDLSVVRLMFIAYLPDSNG  1
NFkB1_Homo              (  206) KEMDLSVVRLMFTAFLPDSTG  1
Relish_Biomphalaria     (  209) KTMQLNVVKLCFQVFLRNPDG  1
rel1[Ciona]             (  140) VDVDLNIVRLCFEAFIPDARG  1
Relish_Dmel             (  298) KDMNLNQVRLCFEAFKIEDNG  1
RelA_Homo               (  150) GDYDLNAVRLCFQVTVRDPSG  1
RelB_Homo               (  259) QEVDMNVVRICFQASYRDQQG  1
NFkB2_Homo              (  183) KVMDLSIVRLRFSAFLRASDG  1
NFAT1                   (  515) IGRKNTRVRLVFRVHIPESSG  1
Dorsal_Dmel             (  181) SSIDLNSVRLCFQVFMESEQK  1
NFAT4                   (  557) IGRKNTRVRLVFRVHIPQPSG  1
NFAT2                   (   81) IGRKNTRVRLVFRVHVPQPSG  1
NFAT3                   (  473) IGRKNTRVRLVFRVHVPQGGG  1
NFkB_Hydra              (  192) KDLNVHSVVLAFHCFLEDSNG  1
Dif_Dmel                (  216) DKINRYELRLCYQAFITVGNS  1
//

--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
     Motif 7 position-specific scoring matrix
--------------------------------------------------------------------------------
log-odds matrix: alength= 20 w= 21 n= 29610 bayes= 9.35975 E= 7.3e-
173
    24   -340    -26     -5   -315    -82   -172    151    276   -
304   -224    -16   -348     45   -133    -20   -183    -68   -239
-225
    23   -351    164    100   -327     92   -181   -307     22   -
317   -238    108   -358   -170   -146     60     39    -69   -251
-236
  -227    107   -486   -406   -193   -404   -335    181   -355    -
49    415   -387   -469   -398    164   -351   -231     58   -185
73
```

```
  -398   -500    294   -285   -557   -319   -294   -608    164   -
614   -573    276   -521    -53   -365   -315   -355   -595   -486
-415
  -343   -311   -508   -419   -170   -504   -384   -101   -375
315     65     62   -475   -385    -92   -452   -337    -79   -223
-284
  -380   -471   -184   -305   -497   -317     57   -579   -314   -
594   -546    275   -516   -384   -389    199    136   -570   -445
71
   158   -282   -252     46   -259   -329   -222     76   -136   -
239   -178   -232   -390    -40    166    -26   -204    210   -218
-224
  -359   -359   -634   -601   -391   -633   -600    -93   -584    -
87   -299   -621   -654   -660   -574   -614   -394    385   -481
-502
  -356   -289   -455   -444   -450   -427   -225   -383    -20   -
404   -375   -350   -432   -294    433   -422   -388   -236   -200
-368
  -441   -399   -631   -544   -215   -617   -496      5   -504
341   -106   -578   -586   -495   -461   -577   -437   -250   -290
-362
   -48    513   -572   -512   -327   -399   -455   -184   -444   -
290    172   -474   -531   -497    -21   -358   -307    134   -318
-350
  -386   -285   -495   -482    472   -514   -378   -258   -465   -
209   -246   -477   -512   -532   -468   -429   -454   -318    -94
71
  -263   -315   -358    -34   -393   -432     17   -152   -235   -
282   -171   -264   -390    366     36   -223   -168   -357   -203
-343
   307    116   -635   -619   -521   -373   -600   -311   -612   -
481   -443   -542   -560   -605   -566   -337   -354    245   -490
-554
  -352   -341   -451   -422    352   -488    237   -338   -396   -
337   -308   -411   -517   -451   -376   -134    -72   -363    -55
392
  -328   -301   -509   -421   -174   -493   -382    125   -100
300     68   -451   -477   -390   -344   -441   -324     37   -221
7
  -214   -370   -364     -6   -399   -390   -352    -64   -290   -
375   -363   -387    329   -354    126   -315    -86   -357   -369
-410
  -159   -397    376      7   -419   -381   -288   -398   -312   -
445   -384      0   -505    -19   -348   -204   -365   -170   -317
-342
   -52   -391     56    213   -366      2   -215   -338   -119   -
349   -270   -206     87     93      1     89   -225   -322   -289
-273
  -315   -450    153   -240   -466    -69     58   -476   -230   -
485   -416    255   -465     94    -11    124    -46   -463   -394
-351
```

```
  -238   -372   -308   -368   -459    368   -376   -453   -111   -
520   -410   -287   -492   -456   -329   -181   -399   -434   -299
-389
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 21 nsites= 25 E= 7.3e-173
 0.080000  0.000000  0.040000  0.040000  0.000000  0.040000
0.000000  0.160000  0.400000  0.000000  0.000000  0.040000  0.000000
0.080000  0.000000  0.080000  0.000000  0.040000  0.000000  0.000000
 0.080000  0.000000  0.200000  0.120000  0.000000  0.160000
0.000000  0.000000  0.040000  0.000000  0.000000  0.120000  0.000000
0.000000  0.000000  0.160000  0.080000  0.040000  0.000000  0.000000
 0.000000  0.040000  0.000000  0.000000  0.000000  0.000000
0.000000  0.160000  0.000000  0.040000  0.480000  0.000000  0.000000
0.000000  0.160000  0.000000  0.000000  0.080000  0.000000  0.040000
 0.000000  0.000000  0.440000  0.000000  0.000000  0.000000
0.000000  0.000000  0.160000  0.000000  0.000000  0.360000  0.000000
0.040000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.720000  0.040000  0.160000  0.000000
0.000000  0.040000  0.000000  0.000000  0.040000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.040000  0.000000  0.000000  0.000000  0.000000  0.360000  0.000000
0.000000  0.000000  0.400000  0.160000  0.000000  0.000000  0.040000
 0.240000  0.000000  0.000000  0.080000  0.000000  0.000000
0.000000  0.080000  0.000000  0.000000  0.000000  0.000000  0.000000
0.040000  0.160000  0.080000  0.000000  0.320000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.040000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.960000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.080000  0.000000  0.000000  0.000000  0.000000
0.000000  0.880000  0.000000  0.000000  0.040000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.040000  0.000000  0.960000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.040000  0.680000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.080000  0.000000  0.000000
0.000000  0.040000  0.000000  0.000000  0.160000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.960000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.040000
 0.000000  0.000000  0.000000  0.080000  0.000000  0.000000
0.040000  0.040000  0.000000  0.000000  0.000000  0.000000  0.000000
0.600000  0.160000  0.040000  0.040000  0.000000  0.000000  0.000000
 0.600000  0.040000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.360000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.440000  0.000000
0.160000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.040000  0.040000  0.000000  0.000000  0.320000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.160000  0.040000  0.600000  0.040000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.120000  0.000000  0.040000
 0.000000  0.000000  0.000000  0.080000  0.000000  0.000000
0.000000  0.040000  0.000000  0.000000  0.000000  0.000000  0.680000
0.000000  0.160000  0.000000  0.040000  0.000000  0.000000  0.000000
 0.040000  0.000000  0.600000  0.080000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.080000  0.000000
0.120000  0.000000  0.040000  0.000000  0.040000  0.000000  0.000000
 0.040000  0.000000  0.080000  0.280000  0.000000  0.080000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.160000
0.120000  0.040000  0.200000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.160000  0.000000  0.000000  0.040000
0.040000  0.000000  0.000000  0.000000  0.000000  0.320000  0.000000
0.120000  0.040000  0.240000  0.040000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.920000
0.000000  0.000000  0.040000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.040000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 regular expression
--------------------------------------------------------------------
KDM[DN]L[SN][VA]VRLCFQ[AV][FY]LPD[ES][NS]G
--------------------------------------------------------------------




Time 498.85 secs.

********************************************************************


********************************************************************
MOTIF  8 MEME    width =  31  sites =  17  llr = 1021  E-value =
3.6e-189
********************************************************************
--------------------------------------------------------------------
      Motif 8 Description
--------------------------------------------------------------------
Simplified        A  ::::1:1::::::::::11:14::::11:::
pos.-specific     C  :1:::::::::::::::::::::::::::::
probability       D  1::1::1:::::121a:1::1::::::::21
matrix            E  8::9::2:1:::121:161:11::::::1::
                  F  :::::1:a::1:::5:::::::::::::::8
                  G  ::::::::::::::::::1:5:::::111::
                  H  ::::::::::::::1::11::::::::::5:
```

```
                  I  :::::1:::::::1:::::7:::::::2:::
                  K  :1:::2:::::::11:5:::11a1284::::
                  L  :1:::1::1:3:12::1:11::::::1111:
                  M  :::::1::::1:12:::::::::::::2:::
                  N  ::::::::::::11::::11:::::::::1:
                  P  ::::6:4::::a::1:1:::::::::::7:1
                  Q  ::::::2:1:4:5:::1:3:11::2:::1::
                  R  :::::1::1:::1:1:1:2:12:9621::1:
                  S  ::a:3:::::1:::1:1::::1:::::::::
                  T  :6::::1:7::::1::1:::::::::3111:
                  V  12:::4::::1::1:::::2::::::13::1
                  W  :::::::::::::::::::::::::::::::
                  Y  :::::::::a1::::::1:::::::::1:::

         bits    7.3
                 6.6
                 5.9
                 5.1        * *
Relative         4.4        * *     *      *
Entropy          3.7   **   * * *   *      ** *    *
(86.7 bits)      2.9 * **   *** *   * * *  ****    *
                 2.2 ****** *** ** ** * *  ***** ***
                 1.5 *******************************
                 0.7 *******************************
                 0.0 -------------------------------

Multilevel           ETSEPVPFTYQPQxFDKEQIGAKRRKKVPHF
consensus             V  SKQ   L          R    TI
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value
Site
-------------             ----- ---------            ---------------
NFkB_Platygyra              361  7.60e-38 QLELRRKSDQ
ETSEPVEFTYQPQLFDKEQIGAKRRKKIPHF SDYFGGGGGG
NFkB_Ed                     368  2.22e-36 MLELRRKSDM
ETSESVQFTYQPQEFDKEQIGAKRRKKVPHF SDYFPPGGGG
NFkBSer_Nev                 368  6.40e-36 VELRRKKNGG
ETSEPVQFTYQPQLFDKEAIGAKRRKTVPHF TEFLSGGSSG
NFkBCys_Nev                 368  6.40e-36 VELRRKKNGG
ETSEPVQFTYQPQLFDKEAIGAKRRKTVPHF TDFLSGGSSG
NFkB_Acropora               359  4.54e-34 HLELRRKSDD
ETSDPVEFTYQPQMFDKEQIGSKRRKKIPHF SDYFKDGSGG
NFkBb_Aiptasia              363  4.37e-33 LLELRRKSDK
ETSEPFTFTYSPQMFDTEQIGAKRRKKVPHF SDYYPPGGPP
```

```
NFkB_Corallimorph           364  6.93e-33 HIELRRKSDR
EKSESVDFTYQPQMFDQEQIGAKRRKKVPHF QDYFGGGGQP
NFkB_Amphimedon             348  1.39e-30 WIALKRPSDH
ETSEPKPFLYLPQEFDEERIGQKRRKKITHF NNFFEGPGGG
NFkB1_Homo                  341  6.00e-26 FVQLRRKSDL
ETSEPKPFLYYPEIKDKEEVQRKRQKLMPNF SDSFGGGSGA
NFkB[Ciona                  314  5.42e-25 QVQLRRKSDN
EVSESRPFTYLPNKSDLELIDRKRRKVMPDF LDHTGNGSTG
NFkB_Biomphalaria           381  2.57e-23 LMQLQRPSDG
ETSEPIPFTYMPEDPDPDRIAEKRKRKAQRF LEYWNSTGVA
Relish_Biomphalaria         345  6.04e-23 LIMLQRKSDQ
EVSEPKAFTYFPQNRDKDNIASKKRKRIPLD GYEFGDGGLG
NFkB2_Homo                  316  3.77e-22 FLQLKRKRGG
DVSDSKQFTYYPLVEDKEEVQRKRRKALPTF SQPFGGGSHM
RelA_Homo                   279  1.89e-21 SMQLRRPSDR
ELSEPMEFQYLPDTDDRHRIEEKRKRTYETF KSIMKKSPFS
RelB_Homo                   388  2.43e-20 NVFLQRLTDG
VCSEPLPFTYLPRDHDSYGVDKKRKRGMPDV LGELNSSDPH
cRel                        270  5.15e-20 KMQLRRPSDQ
EVSESMDFRYLPDEKDTYGNKAKKQKTTLLF QKLCQDHVET
Dorsal_Dmel                 315  1.05e-17 FIQLRRPSDG
VTSEALPFEYVPMDSDPAHLRRKRQKTGGDP MHLLLQQQQK
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB_Platygyra                    7.6e-38  360_[8]_527
NFkB_Ed                           2.2e-36  367_[8]_462
NFkBSer_Nev                       6.4e-36  367_[8]_42
NFkBCys_Nev                       6.4e-36  367_[8]_42
NFkB_Acropora                     4.5e-34  358_[8]_515
NFkBb_Aiptasia                    4.4e-33  362_[8]_455
NFkB_Corallimorph                 6.9e-33  363_[8]_521
NFkB_Amphimedon                   1.4e-30  347_[8]_717
NFkB1_Homo                          6e-26  340_[8]_598
NFkB[Ciona                        5.4e-25  313_[8]_856
NFkB_Biomphalaria                 2.6e-23  380_[8]_199
Relish_Biomphalaria                 6e-23  344_[8]_710
NFkB2_Homo                        3.8e-22  315_[8]_553
RelA_Homo                         1.9e-21  278_[8]_139
RelB_Homo                         2.4e-20  387_[8]_161
cRel                              5.1e-20  269_[8]_319
Dorsal_Dmel                       1.1e-17  314_[8]_333
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 8 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 8 width=31 seqs=17
NFkB_Platygyra           (  361) ETSEPVEFTYQPQLFDKEQIGAKRRKKIPHF  1
NFkB_Ed                  (  368) ETSESVQFTYQPQEFDKEQIGAKRRKKVPHF  1
NFkBSer_Nev              (  368) ETSEPVQFTYQPQLFDKEAIGAKRRKTVPHF  1
NFkBCys_Nev              (  368) ETSEPVQFTYQPQLFDKEAIGAKRRKTVPHF  1
NFkB_Acropora            (  359) ETSDPVEFTYQPQMFDKEQIGSKRRKKIPHF  1
NFkBb_Aiptasia           (  363) ETSEPFTFTYSPQMFDTEQIGAKRRKKVPHF  1
NFkB_Corallimorph        (  364) EKSESVDFTYQPQMFDQEQIGAKRRKKVPHF  1
NFkB_Amphimedon          (  348) ETSEPKPFLYLPQEFDEERIGQKRRKKITHF  1
NFkB1_Homo               (  341) ETSEPKPFLYYPEIKDKEEVQRKRQKLMPNF  1
NFkB[Ciona               (  314) EVSESRPFTYLPNKSDLELIDRKRRKVMPDF  1
NFkB_Biomphalaria        (  381) ETSEPIPFTYMPEDPDPDRIAEKRKRKAQRF  1
Relish_Biomphalaria      (  345) EVSEPKAFTYFPQNRDKDNIASKKRKRIPLD  1
NFkB2_Homo               (  316) DVSDSKQFTYYPLVEDKEEVQRKRRKALPTF  1
RelA_Homo                (  279) ELSEPMEFQYLPDTDDRHRIEEKRKRTYETF  1
RelB_Homo                (  388) VCSEPLPFTYLPRDHDSYGVDKKRKRGMPDV  1
cRel                     (  270) EVSESMDFRYLPDEKDTYGNKAKKQKTTLLF  1
Dorsal_Dmel              (  315) VTSEALPFEYVPMDSDPAHLRRKRQKTGGDP  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 31 n= 29220 bayes= 10.8159 E= 3.6e-
189
  -355   -593    -37    388   -589   -472   -417   -480   -318   -
536   -468   -386   -531   -289   -426   -468   -430    -36   -482
-505
  -231    128   -411   -393   -255   -408   -338   -127    -12   -
61   -163   -276   -455   -363   -310   -162    327    151   -225
-271
  -441   -491   -634   -702   -636   -530   -618   -693   -652   -
693   -660   -590   -652   -699   -615    338   -414   -643   -513
-596
  -451   -556    -99    401   -576   -514   -456   -494   -458   -
591   -525   -425   -641   -387   -503   -551   -508   -531   -460
-524
   -17   -300   -384   -359   -409   -334   -372   -383   -323   -
393   -370   -387    319   -376   -341    118   -280   -346   -370
-420
  -175   -173   -429   -349     75   -351   -281     79    192
58    216   -332   -417   -342     21   -298   -180    229   -135
-164
   -22   -501    111    184   -474   -373   -296   -403   -178   -
415   -345   -273    204    177   -271   -323    -13   -372   -398
-376
```

```
  -455   -356   -550   -551    481   -548   -470   -334   -533   -
285   -322   -548   -565   -602   -530   -502   -521   -394   -185
-122
  -255   -284   -316    -26   -366   -397   -281   -269   -133     -
1   -244   -233   -442    -29     26   -150    347   -269   -278   -
325
  -687   -581   -685   -741   -277   -632   -453   -627   -680   -
591   -603   -648   -706   -688   -621   -713   -677   -659   -259
542
  -180   -179   -422   -344     76   -354   -279    -52   -294
164    134   -331   -419    222   -287    -75   -184     37   -134
208
  -453   -546   -568   -569   -591   -552   -549   -601   -529   -
594   -597   -599    376   -585   -534   -548   -532   -590   -497
-579
  -222   -306    -30     17   -359   -373    -53   -312   -173   -
146     13    -83   -364    352    -45   -287   -254   -322   -196
-296
  -138   -259    136    137   -234   -268   -155     28     54
74    250     18   -326   -147   -120   -192      7    -10   -181
-179
  -135   -305     14     34    328   -253     93   -260    126   -
270   -191   -133    -58   -124     52     20   -149   -247   -204
-185
  -426   -456    413   -209   -488   -464   -378   -481   -461   -
530   -480   -216   -593   -497   -458   -472   -478   -490   -374
-420
  -146   -315   -165     30   -293   -266   -144   -268    292    -
66   -198   -148     32     15     58    -50     80   -256   -211
-200
   -26   -581    116    337   -538   -388     92   -451   -210   -
464   -394   -274   -438   -212   -324   -356   -333   -411   -460
206
    64   -303   -149     96   -279     40     93   -257    -40    -
67   -187     23   -311    195    170   -175   -146   -244   -201
-188
  -294   -295   -401   -392   -226   -449   -412    395   -331    -
19    -59   -185   -500   -424   -366   -388   -267    124   -242
-249
    58   -342     90     42   -325    244   -174   -300     52   -
311   -232   -160   -347     80     42   -212   -188   -286   -242
-232
   223   -340   -189     97   -328   -293   -167   -296     75   -
303   -226   -176   -354     14    218     18   -189   -283   -236
-229
  -389   -391   -508   -460   -533   -496   -415   -405    427   -
500   -419   -404   -534   -464    -66   -511   -420   -494   -331
-448
  -346   -282   -445   -427   -442   -417   -216   -374      3   -
394   -364   -339   -424   -281    433   -412   -376   -463   -192
-358
```

```
  -361   -437   -464   -306   -522   -441   -248   -410    197   -
401   -342   -319   -512    142    376   -404   -342   -416   -311
-358
  -351   -362   -475   -406   -505   -466   -361   -368    418   -
457   -375   -361   -504   -386     68   -466   -378   -452   -300
-409
   -11   -298   -215   -137   -282    -42   -175   -223    280    -
56   -190   -187   -359   -161     61   -224    200    -16   -213
-214
   -10   -169   -428   -350   -144    -49   -280    229   -299     -
6    265   -330   -414   -343   -287   -295      6    205   -132
115
  -181   -337   -331    -60   -366    -91   -320   -336   -262   -
111   -331   -354    333    -64   -287   -282    -54   -324   -336
-378
  -279   -307     97   -224   -251   -322    433   -358   -208    -
27   -256     11   -401   -138      4   -260     29   -345   -173
-67
  -331   -231   -208   -430    465   -467   -401   -204   -419   -
154   -193   -441   -245   -501   -432   -377   -407   -163    -75
-13
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 8 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 31 nsites= 17 E= 3.6e-189
 0.000000  0.000000  0.058824  0.823529  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.117647  0.000000  0.000000
 0.000000  0.058824  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.058824  0.058824  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.588235  0.235294  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.117647  0.882353  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.058824  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.647059
0.000000  0.000000  0.294118  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.058824  0.000000
0.000000  0.058824  0.235294  0.117647  0.117647  0.000000  0.000000
0.000000  0.058824  0.000000  0.000000  0.352941  0.000000  0.000000
 0.058824  0.000000  0.117647  0.176471  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.352941
0.235294  0.000000  0.000000  0.058824  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.058824  0.000000  0.000000
0.000000  0.000000  0.000000  0.117647  0.000000  0.000000  0.000000
0.058824  0.058824  0.000000  0.705882  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.058824  0.000000
0.000000  0.000000  0.000000  0.294118  0.058824  0.000000  0.000000
0.352941  0.000000  0.058824  0.000000  0.058824  0.000000  0.117647
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.117647  0.117647  0.000000  0.000000
0.000000  0.000000  0.000000  0.058824  0.058824  0.058824  0.000000
0.529412  0.058824  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.176471  0.176471  0.000000  0.000000
0.000000  0.058824  0.058824  0.176471  0.176471  0.058824  0.000000
0.000000  0.000000  0.000000  0.058824  0.058824  0.000000  0.000000
 0.000000  0.000000  0.058824  0.058824  0.470588  0.000000
0.058824  0.000000  0.117647  0.000000  0.000000  0.000000  0.058824
0.000000  0.058824  0.117647  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.058824  0.000000  0.000000
0.000000  0.000000  0.470588  0.058824  0.000000  0.000000  0.117647
0.058824  0.058824  0.058824  0.117647  0.000000  0.000000  0.000000
 0.058824  0.000000  0.117647  0.647059  0.000000  0.000000
0.058824  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.117647
 0.117647  0.000000  0.000000  0.117647  0.000000  0.117647
0.058824  0.000000  0.000000  0.058824  0.000000  0.058824  0.000000
0.294118  0.176471  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.705882  0.000000  0.058824  0.000000  0.058824  0.000000
0.000000  0.000000  0.000000  0.000000  0.176471  0.000000  0.000000
 0.117647  0.000000  0.117647  0.058824  0.000000  0.470588
0.000000  0.000000  0.058824  0.000000  0.000000  0.000000  0.000000
0.117647  0.058824  0.000000  0.000000  0.000000  0.000000  0.000000
 0.411765  0.000000  0.000000  0.117647  0.000000  0.000000
0.000000  0.000000  0.058824  0.000000  0.000000  0.000000  0.000000
0.058824  0.235294  0.117647  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.117647  0.000000  0.000000  0.000000  0.000000
0.000000  0.882353  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.176471  0.000000  0.000000  0.000000  0.000000
0.176471  0.647059  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.823529  0.000000  0.000000  0.000000  0.000000
0.000000  0.176471  0.000000  0.000000  0.000000  0.000000  0.000000
 0.058824  0.000000  0.000000  0.000000  0.000000  0.058824
0.000000  0.000000  0.411765  0.058824  0.000000  0.000000  0.000000
0.000000  0.058824  0.000000  0.294118  0.058824  0.000000  0.000000
 0.058824  0.000000  0.000000  0.000000  0.000000  0.058824
0.000000  0.235294  0.000000  0.058824  0.176471  0.000000  0.000000
0.000000  0.000000  0.000000  0.058824  0.294118  0.000000  0.058824
 0.000000  0.000000  0.000000  0.058824  0.000000  0.058824
0.000000  0.000000  0.000000  0.058824  0.000000  0.000000  0.705882
0.058824  0.000000  0.000000  0.058824  0.000000  0.000000  0.000000
 0.000000  0.000000  0.176471  0.000000  0.000000  0.000000
0.470588  0.000000  0.000000  0.117647  0.000000  0.058824  0.000000
0.000000  0.058824  0.000000  0.117647  0.000000  0.000000  0.000000
 0.000000  0.000000  0.058824  0.000000  0.823529  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.058824
0.000000  0.000000  0.000000  0.000000  0.058824  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 regular expression
--------------------------------------------------------------------
E[TV]SE[PS][VK][PQ]FTY[QL]PQxFDKEQIG[AR]KRRK[KT][VI]PHF
--------------------------------------------------------------------



Time 561.27 secs.

********************************************************************


********************************************************************
MOTIF  9 MEME    width =  21  sites =  19  llr = 802  E-value =
3.7e-150
********************************************************************
--------------------------------------------------------------------
      Motif 9 Description
--------------------------------------------------------------------
Simplified        A  :1::::::11::::123::1:
pos.-specific     C  ::::1::3::::::::::1::
probability       D  ::::::::::::2::1:::3:
matrix            E  ::::::::::::2:221:23:
                  F  a:::::::::::::1::::::
                  G  ::::9:::::1:::21:::::
                  H  :::::::7:::::::::::::
                  I  :1:1:91::::::21:121::
                  K  :::::::::2992:13::112
                  L  :::9::2::::::1:1:7:1:
```

```
                  M  :::1::::::::111::13::
                  N  :19:::::::::3::::::::
                  P  :6::::::::::::1::::::
                  Q  :11:::7::::::::1::11:
                  R  ::::::1::111::::::118
                  S  :11:::::::::1::11:1::
                  T  :1::::::16::::112:21:
                  V  :::::1::9::::71:4::::
                  W  :::::::::::::::::::::
                  Y  ::::::::::::1::::::::

         bits    7.3
                 6.6
                 5.9
                 5.1 *
Relative         4.4 *    * *
Entropy          3.7 * * ** ** **        *
(60.9 bits)      2.9 * ********** *   *  *
                 2.2 ************ *  **  *
                 1.5 ************** ******
                 0.7 *********************
                 0.0 ---------------------

Multilevel           FPNLGIQHVTKKNVEKVLMDR
consensus                  LC K  K GEAI E
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name            Start   P-value                 Site
-------------            -----  ---------            ---------------
NFkBSer_Nev                144  3.71e-26 VGPDQHMTAS
FPNLGIQHVTKKNVVKVLMDR FIKWQTLQNA
NFkBCys_Nev                144  3.71e-26 VGPDQHMTAS
FPNLGIQHVTKKNVVKVLMDR FIKWQTLQNA
NFkB_Platygyra             138  7.80e-25 IGPEHGMTAS
FPNLGIQHVTKKSVGKVLMDR YIRMQTLHTA
NFkB_Ed                    144  1.45e-24 IGPDQGMTAS
FPNLGIQHVTKKMVTKVLMER YIKVQELHNA
NFkB_Acropora              138  3.85e-24 IGPEQGMTAS
FPNLGIQHVTKKNVGLVLMDR YLKMQMLHTA
NFkB_Corallimorph          139  5.55e-24 IGAEQGMTAS
FPNLGIQHVTKKSVGAVLMER YVRMQTLHTA
NFkBb_Aiptasia             139  4.99e-23 IGTEQGMTAS
FPNLGIQHVTKKKVAKTLTER YTKMQALQNA
NFkB[Ciona                 118  8.31e-22 QCGPKDMTAT
FPNLGIQHVTKKNVATILEER YIAAEMQLSS
```

```
NFkB1_Homo                  137  1.33e-19 TAGPKDMVVG
FANLGILHVTKKKVFETLEAR MTEACIRGYN
Dorsal_Dmel                 142  5.82e-19 EINSETMRAV
FSNLGIQCVKKKDIEAALKAR EEIRVDPFKT
RelB_Homo                   222  4.45e-18 LRPHVSPRHS
FNNLGIQCVRKKEIEAAIERK IQLGIDPYNA
cRel                        102  6.36e-18 EFGQERRPLF
FQNLGIRCVKKKEVKEAIITR IKAGINPFNV
NFkB_Amphimedon             143  9.03e-18 IGPETDMYAQ
FTSLGILHVTKKKVPEVLTRR LLQQTTPRGQ
rel1[Ciona]                 100  9.86e-18 VDPGNQMLGV
FPNLGIQCVRRREVGQAIQDR LNHGVNPFGT
RelA_Homo                   113  6.37e-17 ELCPDRCIHS
FQNLGIQCVKKRDLEQAISQR IQTNNNPFQV
Relish_Biomphalaria         150  8.15e-17 ELKSCLDVVS
FPNLCILHVTGKKLIDVLTER NIDTIKLNKK
NFkB2_Homo                  133  1.19e-15 SVGPKDMTAQ
FNNLGVLHVTKKNMMGTMIQK LQRQRLRSRP
NFkB_Biomphalaria           210  3.16e-15 RVKDTSDKIV
FPQIGIQCAKKKDVESSLRLR KEINVDPYQT
Relish_Dmel                 247  3.88e-14 VSKERGYVAQ
FINMGIIHTAKKYIFEELCKK KQDRLVFQMN
--------------------------------------------------------------------


--------------------------------------------------------------------
      Motif 9 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkBSer_Nev                       3.7e-26  143_[9]_276
NFkBCys_Nev                       3.7e-26  143_[9]_276
NFkB_Platygyra                    7.8e-25  137_[9]_760
NFkB_Ed                           1.4e-24  143_[9]_696
NFkB_Acropora                     3.8e-24  137_[9]_746
NFkB_Corallimorph                 5.6e-24  138_[9]_756
NFkBb_Aiptasia                      5e-23  138_[9]_689
NFkB[Ciona                        8.3e-22  117_[9]_1062
NFkB1_Homo                        1.3e-19  136_[9]_812
Dorsal_Dmel                       5.8e-19  141_[9]_516
RelB_Homo                         4.5e-18  221_[9]_337
cRel                              6.4e-18  101_[9]_497
NFkB_Amphimedon                     9e-18  142_[9]_932
rel1[Ciona]                       9.9e-18  99_[9]_170
RelA_Homo                         6.4e-17  112_[9]_315
Relish_Biomphalaria               8.1e-17  149_[9]_915
NFkB2_Homo                        1.2e-15  132_[9]_746
NFkB_Biomphalaria                 3.2e-15  209_[9]_380
Relish_Dmel                       3.9e-14  246_[9]_704
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 9 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 9 width=21 seqs=19
NFkBSer_Nev               (  144) FPNLGIQHVTKKNVVKVLMDR  1
NFkBCys_Nev               (  144) FPNLGIQHVTKKNVVKVLMDR  1
NFkB_Platygyra            (  138) FPNLGIQHVTKKSVGKVLMDR  1
NFkB_Ed                   (  144) FPNLGIQHVTKKMVTKVLMER  1
NFkB_Acropora             (  138) FPNLGIQHVTKKNVGLVLMDR  1
NFkB_Corallimorph         (  139) FPNLGIQHVTKKSVGAVLMER  1
NFkBb_Aiptasia            (  139) FPNLGIQHVTKKKVAKTLTER  1
NFkB[Ciona                (  118) FPNLGIQHVTKKNVATILEER  1
NFkB1_Homo                (  137) FANLGILHVTKKKVFETLEAR  1
Dorsal_Dmel               (  142) FSNLGIQCVKKKDIEAALKAR  1
RelB_Homo                 (  222) FNNLGIQCVRKKEIEAAIERK  1
cRel                      (  102) FQNLGIRCVKKKEVKEAIITR  1
NFkB_Amphimedon           (  143) FTSLGILHVTKKKVPEVLTRR  1
rel1[Ciona]               (  100) FPNLGIQCVRRREVGQAIQDR  1
RelA_Homo                 (  113) FQNLGIQCVKKRDLEQAISQR  1
Relish_Biomphalaria       (  150) FPNLCILHVTGKKLIDVLTER  1
NFkB2_Homo                (  133) FNNLGVLHVTKKNMMGTMIQK  1
NFkB_Biomphalaria         (  210) FPQIGIQCAKKKDVESSLRLR  1
Relish_Dmel               (  247) FINMGIIHTAKKYIFEELCKK  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 21 n= 29610 bayes= 10.7999 E= 3.7e-
150
  -486   -387   -576   -581    483   -570   -494   -367   -562   -
317   -355   -575   -592   -629   -556   -532   -550   -426   -215
-152
   -52   -344   -334   -302   -372   -363   -322    -39   -263   -
349   -334     32    317     16   -290   -115    -61   -330   -341
-379
  -358   -314   -215   -393   -347   -354   -109   -291   -285   -
405   -326    408   -442   -191   -319   -170   -258   -367   -217
-296
  -369   -331   -540   -451   -167   -535   -412     20   -412
331    100   -489   -502   -411   -371   -486   -363   -198   -232
-299
  -244     65   -324   -384   -469    370   -389   -464   -348   -
528   -422   -303   -499   -469   -344   -341   -402   -441   -310
-401
  -372   -339   -568   -551   -337   -590   -585    426   -501   -
182   -199   -534   -636   -593   -538   -547   -364     57   -407
-401
```

```
  -294   -333   -408   -176   -326   -458    -97    -50   -196
44   -165   -302   -429    361    -25   -376   -326   -318   -221
-336
  -572    415   -680   -759   -552   -600    468   -742   -706   -
717   -725   -670   -710   -726   -656   -659   -655   -718   -479
-461
   -50   -175   -378   -342   -275   -391   -323     13   -332   -
222   -202   -386   -403   -411   -299   -360    -79    365   -284
-364
   -47   -394   -433   -318   -487   -436   -275   -382    209   -
411   -329   -305   -510   -242    135   -297    327   -379   -327
-369
  -350   -356   -477   -422   -504   -289   -380   -365    421   -
465   -380   -367   -503   -426     -1   -475   -383   -457   -299
-416
  -351   -358   -477   -421   -505   -470   -378   -366    421   -
465   -380   -367   -504   -421     23   -475   -383   -457   -299
-416
  -161   -331    131    131   -309   -267   -159   -289    192   -
299     92    205   -337   -150   -126      9   -173   -276   -233
92
  -276   -293   -547   -507   -304   -556   -492    179   -490
25     98   -535   -565   -557   -470   -528   -318    340   -376
-424
    54   -227   -245    156    135    123   -202     39     26   -
181    108   -216    -70   -208   -175   -234     -4     70   -170
-182
    98   -314      3    162   -289    -53   -145   -267    217    -
78   -197   -145   -320     73   -106    -58     -4   -254   -212
-198
   152   -188   -398    -53   -199   -358   -300     59   -299   -
170   -125   -344   -419   -356   -293   -105    104    280   -188
-221
  -433   -388   -639   -552   -189   -618   -495    201   -512
310    120   -583   -587   -495   -467   -583   -430   -235   -271
-348
  -146    117   -171    127   -272   -270   -153     91     51   -
257    332   -155   -328      2     39    -60    117   -229   -204
-196
    52   -335    195    196   -309   -279   -163   -284     50    -
79   -215   -162   -334     74    111   -202     -8   -270   -232
-217
  -355   -301   -455   -414   -456   -427   -227   -385     66   -
402   -369   -344   -440   -279    429   -418   -379   -464   -210
-365
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 9 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 21 nsites= 19 E= 3.7e-150
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.052632  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.052632  0.000000  0.000000  0.000000  0.105263  0.578947
0.105263  0.000000  0.052632  0.052632  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.894737  0.000000
0.052632  0.000000  0.052632  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.052632  0.000000  0.894737  0.052632  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.052632  0.000000  0.000000  0.000000  0.947368
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.947368  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.052632  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.052632  0.000000  0.210526  0.000000  0.000000  0.000000
0.684211  0.052632  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.315789  0.000000  0.000000  0.000000  0.000000
0.684211  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.052632  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.052632  0.894737  0.000000  0.000000
 0.052632  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.210526  0.000000  0.000000  0.000000  0.000000
0.000000  0.105263  0.000000  0.631579  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.052632
0.000000  0.000000  0.894737  0.000000  0.000000  0.000000  0.000000
0.000000  0.052632  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.894737  0.000000  0.000000  0.000000  0.000000
0.000000  0.105263  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.157895  0.157895  0.000000  0.000000
0.000000  0.000000  0.210526  0.000000  0.052632  0.263158  0.000000
0.000000  0.000000  0.105263  0.000000  0.000000  0.000000  0.052632
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.157895  0.000000  0.105263  0.052632  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.684211  0.000000  0.000000
 0.105263  0.000000  0.000000  0.210526  0.105263  0.210526
0.000000  0.052632  0.052632  0.000000  0.052632  0.000000  0.052632
0.000000  0.000000  0.000000  0.052632  0.105263  0.000000  0.000000
```

```
 0.157895  0.000000  0.052632  0.210526  0.000000  0.052632
0.000000  0.000000  0.263158  0.052632  0.000000  0.000000  0.000000
0.105263  0.000000  0.052632  0.052632  0.000000  0.000000  0.000000
 0.263158  0.000000  0.000000  0.052632  0.000000  0.000000
0.000000  0.052632  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.052632  0.157895  0.421053  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.210526  0.000000  0.736842  0.052632  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.052632  0.000000  0.157895  0.000000  0.000000
0.000000  0.105263  0.052632  0.000000  0.315789  0.000000  0.000000
0.052632  0.052632  0.052632  0.157895  0.000000  0.000000  0.000000
 0.105263  0.000000  0.263158  0.263158  0.000000  0.000000
0.000000  0.000000  0.052632  0.052632  0.000000  0.000000  0.000000
0.105263  0.105263  0.000000  0.052632  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.157895  0.000000  0.000000  0.000000  0.000000
0.000000  0.842105  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 regular expression
--------------------------------------------------------------------
FPNLGI[QL][HC]V[TK]KK[NK]V[EG][KE][VA][LI]M[DE]R
--------------------------------------------------------------------




Time 623.67 secs.

********************************************************************


********************************************************************
MOTIF 10 MEME    width =  21  sites =  25  llr = 855  E-value =
5.5e-128
********************************************************************
--------------------------------------------------------------------
      Motif 10 Description
--------------------------------------------------------------------
Simplified        A  :1:::6:::::::2::::1:2
pos.-specific     C  :::::::::::::4::::31:
probability       D  ::::::::::::2::31::::
matrix            E  ::::::::::::1::11::1:
                  F  ::::::2::::::::::::::
                  G  ::::::::::8:::2:52:::
                  H  :2::a:8:::2:1::::::::
                  I  ::::::::11::2::::11::
                  K  ::1::::::::7::12:::::
                  L  12:2::::7::::::::::::
```

```
                  M  ::3::::::::::::::::::
                  N  2::::::::::3:32:::::
                  P  63:7:4::::::::::::::1
                  Q  ::::::::2:::1::::::::
                  R  ::4::::::::3::1::::::
                  S  ::1::::6:::::11::::::
                  T  :::::::::2:::2::1::52
                  V  :::::::::7:::::::4223
                  W  :::::::::::::::::::::
                  Y  :2:::::2::::::::::1::

         bits    7.3
                 6.6
                 5.9
                 5.1     *
Relative         4.4     * *
Entropy          3.7     * *    *
(49.3 bits)      2.9   * ***  ***
                 2.2 * ********** *    **
                 1.5 ************** ******
                 0.7 *********************
                 0.0 ---------------------

Multilevel           PPRPHAHSLVGKNCNDGVCTV
consensus              ML P     RDA K GVVA
sequence                            N    T


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                      Site
-------------             ----- ---------            ---------------
NFkB_Platygyra              106  1.80e-20 IVVSLVTVDE
PPMPHAHSLIGKNSNNGVVTV QIGPEHGMTA
NFkB_Corallimorph           107  1.80e-20 IVVSLVTTED
PPMPHAHSLIGKNSNNGVVTV QIGAEQGMTA
rel1[Ciona]                  68  2.06e-20 MRVSLVSKDD
PPRPHPHSLVGRDCNNGVCQI NVDPGNQMLG
NFkB_Acropora               106  2.94e-19 IVVSLVTSDE
NPMPHAHSLIGKNASNGVVTV QIGPEQGMTA
NFkB[Ciona                   87  3.31e-19 IVVQLVTNEE
NPRLHPHSLVGKQCQNGICTV QCGPKDMTAT
RelB_Homo                   190  1.07e-18 VTACLVWKDW
PHRVHPHSLVGKDCTDGICRV RLRPHVSPRH
RelA_Homo                    82  1.68e-18 VRISLVTKDP
PHRPHPHELVGKDCRDGFYEA ELCPDRCIHS
NFkBb_Aiptasia              106  2.11e-18 IVVSLVTEDE
PHMPHAHSLTGKHANNDGIVT VQIGTEQGMT
```

```
NFkB1_Homo                   106  2.63e-18 VIVQLVTNGK
NIHLHAHSLVGKHCEDGICTV TAGPKDMVVG
NFkB_Amphimedon              111  3.28e-18 VMVSLVTDSD
PAMPHAHSIVGKNAIDGRCVV EIGPETDMYA
cRel                          71  5.08e-18 VRITLVTKND
PYKPHPHDLVGKDCRDGYYEA EFGQERRPLF
NFkBSer_Nev                  111  1.19e-17 IVVTLVTKDE
PYMLHAHSLTGKNANEEGVVT VQVGPDQHMT
NFkBCys_Nev                  111  1.19e-17 IVVTLVTKDE
PYMLHAHSLTGKNANEEGVVT VQVGPDQHMT
Relish_Biomphalaria          119  1.32e-17 VVVSLVTDEK
VPRPHAHKLVGTNCKDGLCTV ELKSCLDVVS
Dorsal_Dmel                  110  1.33e-16 VVVSCVTKDT
PYRPHPHNLVGKEGCKKGVCT LEINSETMRA
NFkB_Biomphalaria            179  1.33e-16 VSCVTKENPP
HCKPHPHAIVGRDCKKGVCTL RVKDTSDKIV
NFkB2_Homo                   101  5.43e-16 IEVDLVTHSD
PPRAHAHSLVGKQCSELGICA VSVGPKDMTA
NFkB_Ed                      111  3.83e-15 IVVTLVTSEE
PHVLHAHSLTGKNANIDGAVA VQIGPDQGMT
NFAT3                        405  4.17e-15 QMFIGTADER
NLRPHAFYQVHRITGKMVATA SYEAVVSGTK
NFAT4                        489  6.38e-15 QMFIGTADDR
YLRPHAFYQVHRITGKTVATA SQEIIIASTK
NFAT2                         13  3.57e-14 QLFIGTADDR
LLRPHAFYQVHRITGKTVSTT SHEAILSNTK
NFAT1                        447  6.72e-14 QIFIGTADER
ILKPHAFYQVHRITGKTVTTT SYEKIVGNTK
Dif_Dmel                     142  3.87e-11 IVVSCVTSDE
PFRQHPHWLVSKEEADACKSG IYQKKLPPEE
Relish_Dmel                  212  6.89e-10 VIRCSLFQTN
LDSPHSHQLVVRKDDRDVCDP HDLHVSKERG
NFAT3                        187  3.97e-08 WLLLSAPGPT
PASPRPASPCGKRRYSSSGTP SSASPALSRR
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
     Motif 10 block diagrams
--------------------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB_Platygyra                    1.8e-20  105_[10]_792
NFkB_Corallimorph                 1.8e-20  106_[10]_788
rel1[Ciona]                       2.1e-20  67_[10]_202
NFkB_Acropora                     2.9e-19  105_[10]_778
NFkB[Ciona                        3.3e-19  86_[10]_1093
RelB_Homo                         1.1e-18  189_[10]_369
RelA_Homo                         1.7e-18  81_[10]_346
NFkBb_Aiptasia                    2.1e-18  105_[10]_722
NFkB1_Homo                        2.6e-18  105_[10]_843
NFkB_Amphimedon                   3.3e-18  110_[10]_964
```

```
cRel                              5.1e-18  70_[10]_528
NFkBSer_Nev                       1.2e-17  110_[10]_309
NFkBCys_Nev                       1.2e-17  110_[10]_309
Relish_Biomphalaria               1.3e-17  118_[10]_946
Dorsal_Dmel                       1.3e-16  109_[10]_548
NFkB_Biomphalaria                 1.3e-16  178_[10]_411
NFkB2_Homo                        5.4e-16  100_[10]_778
NFkB_Ed                           3.8e-15  110_[10]_729
NFAT3                             4.2e-15  186_[10]_197_[10]_407
NFAT4                             6.4e-15  488_[10]_566
NFAT2                             3.6e-14  12_[10]_320
NFAT1                             6.7e-14  446_[10]_438
Dif_Dmel                          3.9e-11  141_[10]_505
Relish_Dmel                       6.9e-10  211_[10]_739
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 10 width=21 seqs=25
NFkB_Platygyra           (  106) PPMPHAHSLIGKNSNNGVVTV  1
NFkB_Corallimorph        (  107) PPMPHAHSLIGKNSNNGVVTV  1
rel1[Ciona]              (   68) PPRPHPHSLVGRDCNNGVCQI  1
NFkB_Acropora            (  106) NPMPHAHSLIGKNASNGVVTV  1
NFkB[Ciona               (   87) NPRLHPHSLVGKQCQNGICTV  1
RelB_Homo                (  190) PHRVHPHSLVGKDCTDGICRV  1
RelA_Homo                (   82) PHRPHPHELVGKDCRDGFYEA  1
NFkBb_Aiptasia           (  106) PHMPHAHSLTGKHANNDGIVT  1
NFkB1_Homo               (  106) NIHLHAHSLVGKHCEDGICTV  1
NFkB_Amphimedon          (  111) PAMPHAHSIVGKNAIDGRCVV  1
cRel                     (   71) PYKPHPHDLVGKDCRDGYYEA  1
NFkBSer_Nev              (  111) PYMLHAHSLTGKNANEEGVVT  1
NFkBCys_Nev              (  111) PYMLHAHSLTGKNANEEGVVT  1
Relish_Biomphalaria      (  119) VPRPHAHKLVGTNCKDGLCTV  1
Dorsal_Dmel              (  110) PYRPHPHNLVGKEGCKKGVCT  1
NFkB_Biomphalaria        (  179) HCKPHPHAIVGRDCKKGVCTL  1
NFkB2_Homo               (  101) PPRAHAHSLVGKQCSELGICA  1
NFkB_Ed                  (  111) PHVLHAHSLTGKNANIDGAVA  1
NFAT3                    (  405) NLRPHAFYQVHRITGKMVATA  1
NFAT4                    (  489) YLRPHAFYQVHRITGKTVATA  1
NFAT2                    (   13) LLRPHAFYQVHRITGKTVSTT  1
NFAT1                    (  447) ILKPHAFYQVHRITGKTVTTT  1
Dif_Dmel                 (  142) PFRQHPHWLVSKEEADACKSG  1
Relish_Dmel              (  212) LDSPHSHQLVVRKDDRDVCDP  1
NFAT3                    (  187) PASPRPASPCGKRRYSSSGTP  1
//

--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
      Motif 10 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 21 n= 29610 bayes= 10.6991 E= 5.5e-
128
  -216   -328   -378   -342   -324   -391     13    -40   -301    -
42   -276    111    312   -360   -321   -320   -285    -81   -303
33
    19    101    -66   -356     47   -383    230     28   -313
84   -120   -353    164   -365   -308   -324   -222   -124   -144
273
  -386   -484   -473   -331   -538   -474     56   -437    152    -
434    344   -352   -548   -255    323    -32   -371    -71   -359
-390
   -76   -368   -367   -336   -396   -390   -354   -364   -297
64   -360   -389    329    -96   -322   -315   -303   -104   -368
-410
  -531   -471   -463   -505   -401   -549    512   -569   -497    -
511   -447   -320   -595   -319    -21   -498   -481   -553   -321
-216
   308   -306   -622   -618   -574   -355   -590   -566   -615    -
600   -514   -525    225   -592   -560    -98   -347   -437   -498
-579
   -92   -413   -460   -496    208   -512    485   -471   -503    -
430   -391   -314   -577   -320   -352   -451   -441   -474   -153
-51
   -47   -339    -27    -11   -325   -294   -183   -306     19    -
317   -237    -16   -358    -30   -146    227   -167   -295    232
244
  -371   -337   -540   -451   -183   -535   -414     56   -409
313    -62   -489   -152     70   -371   -484   -365   -207   -243
-306
  -249     84   -516   -479   -360   -535   -469    142   -466    -
278   -273   -515   -542   -548   -444   -506    108    343   -409
-454
  -235   -364   -319   -380   -467    354    162   -461   -345    -
526   -418   -296   -497   -464   -342   -169   -392   -145   -311
-399
  -406   -484   -512   -357   -570   -489   -304   -452    376    -
452   -390   -368   -562   -269    256   -455    -65   -464   -364
-409
  -196   -367    167     58   -346   -305    140    155     21    -
333   -254    238   -373     44      9   -234   -209   -311   -267
-252
   163    407    -27    -21   -366    -76   -223   -344   -141    -
359   -280   -194   -395   -219      1    -19    129   -325   -292
-279
   -42     85    -26     -5   -315     90   -172    -31     86    -
304   -224    215   -347    -24     82    -20    -33   -281   -238
60
```

```
  -225   -393    217    104   -378   -314   -216    -29    215   -
366   -289    204   -398   -208      4    -95   -235   -343   -298
-280
   -46   -344     94     54   -322    248   -182   -299     20   -
110     58   -179   -356   -170   -144    -91     84   -287   -245
-234
  -213    106   -471   -392     31    152   -321    146   -341    -
49   -112   -373   -456   -385    -24   -118   -218    251   -174
73
    72    391   -461   -382   -188    -90   -319    101    -37   -
164   -114   -368   -454   -378   -324   -117    -36    184   -175
162
  -239    170    -64     17   -357   -381   -277   -279   -195   -
361   -248   -226   -427    -67    -28    -68    307    123   -283
-312
   163   -218   -477   -399   -197    -89   -331     34   -349    -
53   -123   -380     -7   -393   -338   -340    185    222   -185
-213
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 21 nsites= 25 E= 5.5e-128
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.040000  0.040000  0.000000  0.080000  0.000000  0.160000  0.600000
0.000000  0.000000  0.000000  0.000000  0.040000  0.000000  0.040000
 0.080000  0.040000  0.040000  0.000000  0.040000  0.000000
0.160000  0.040000  0.000000  0.160000  0.000000  0.000000  0.280000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.160000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.040000  0.000000  0.120000  0.000000  0.280000  0.000000  0.000000
0.000000  0.440000  0.080000  0.000000  0.040000  0.000000  0.000000
 0.040000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.200000  0.000000  0.000000  0.680000
0.040000  0.000000  0.000000  0.000000  0.040000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.960000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.040000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.600000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.360000
0.000000  0.000000  0.040000  0.000000  0.000000  0.000000  0.000000
 0.040000  0.000000  0.000000  0.000000  0.160000  0.000000
0.800000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.040000  0.000000  0.040000  0.040000  0.000000  0.000000
0.000000  0.000000  0.040000  0.000000  0.000000  0.040000  0.000000
0.040000  0.000000  0.560000  0.000000  0.000000  0.040000  0.160000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.080000  0.000000  0.720000  0.000000  0.000000  0.040000
0.160000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.040000  0.000000  0.000000  0.000000  0.000000
0.000000  0.120000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.160000  0.680000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.760000
0.160000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.040000  0.000000  0.040000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.680000  0.000000  0.000000  0.000000  0.000000
0.000000  0.280000  0.000000  0.040000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.200000  0.080000  0.000000  0.000000
0.080000  0.160000  0.040000  0.000000  0.000000  0.320000  0.000000
0.080000  0.040000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.240000  0.360000  0.040000  0.040000  0.000000  0.040000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.040000  0.080000  0.160000  0.000000  0.000000  0.000000
 0.040000  0.040000  0.040000  0.040000  0.000000  0.160000
0.000000  0.040000  0.080000  0.000000  0.000000  0.280000  0.000000
0.040000  0.080000  0.080000  0.040000  0.000000  0.000000  0.040000
 0.000000  0.000000  0.280000  0.120000  0.000000  0.000000
0.000000  0.040000  0.240000  0.000000  0.000000  0.240000  0.000000
0.000000  0.040000  0.040000  0.000000  0.000000  0.000000  0.000000
 0.040000  0.000000  0.120000  0.080000  0.000000  0.480000
0.000000  0.000000  0.040000  0.040000  0.040000  0.000000  0.000000
0.000000  0.000000  0.040000  0.120000  0.000000  0.000000  0.000000
 0.000000  0.040000  0.000000  0.000000  0.040000  0.240000
0.000000  0.120000  0.000000  0.040000  0.000000  0.000000  0.000000
0.000000  0.040000  0.040000  0.000000  0.400000  0.000000  0.040000
 0.120000  0.320000  0.000000  0.000000  0.000000  0.040000
0.000000  0.080000  0.040000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.040000  0.040000  0.240000  0.000000  0.080000
 0.000000  0.080000  0.040000  0.080000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.040000  0.040000  0.040000  0.480000  0.200000  0.000000  0.000000
 0.240000  0.000000  0.000000  0.000000  0.000000  0.040000
0.000000  0.040000  0.000000  0.040000  0.000000  0.000000  0.080000
0.000000  0.000000  0.000000  0.240000  0.320000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 regular expression
--------------------------------------------------------------------
PP[RM][PL]H[AP]HSLVG[KR][ND][CA]N[DKN]G[VG][CV][TV][VAT]
--------------------------------------------------------------------




Time 684.06 secs.

********************************************************************
```

```
********************************************************************
MOTIF 11 MEME    width =  21  sites =  19  llr = 750  E-value =
1.7e-121
********************************************************************
--------------------------------------------------------------------
      Motif 11 Description
--------------------------------------------------------------------
Simplified        A  :::3:::::::3:::::6:16
pos.-specific     C  :::::::21::::::::::1:
probability       D  :1:::1::::3:::a:::::1
matrix            E  :::::1::::1::::::1:::
                  F  6:::::::1::::2:::::::
                  G  :::::::::::::::1:::11
                  H  ::::::::::1::1:::::::
                  I  ::2:1:::3:::5::::::::
                  K  ::31:3:::::1:::29:11:
                  L  1:1:8:::1::::1:::::::
                  M  :1:11:::::::::::::1::
                  N  :::1::::::3::::1:1:3:
                  P  :1:3:59::::5::::::7::
                  Q  1:1:::::::1::::::::::
                  R  1:32::::::1::1::1::::
                  S  :11::::::a:1:::6:3141
                  T  :81:::1::::1::::::1:2
                  V  1::11::83:1:5::::::::
                  W  :::::::::::::::::::::
                  Y  2:::::::2::::6:::::::

         bits    7.3
                 6.6
                 5.9
                 5.1
Relative         4.4               *
Entropy          3.7       ** *   ** *
(57.0 bits)      2.9 **  * ** *  *** * *
                 2.2 **  ****** ******** *
                 1.5 *********************
                 0.7 *********************
                 0.0 ---------------------

Multilevel           FTKPLPPVISDPIYDSKAPSA
consensus              RA K CV NAV  K S N
sequence                     Y


--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 11 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                    Site
-------------             ----- ---------            ---------------
NFkB_Platygyra              246  1.69e-22 QAYLPDESGC
FTKALPPCISNAVYDSKAPSA SNLKICRMDR
NFkB1_Homo                  228  3.04e-22 TAFLPDSTGS
FTRRLEPVVSDAIYDSKAPNA SNLKIVRMDR
NFkB[Ciona                  200  1.37e-21 IAYLPDSNGA
FTIMLKPVISDAIFDSKAPNA ATLKICRMDC
NFkBb_Aiptasia              249  2.29e-21 QAYLPDENGN
FTKPLKPCISNPVYDSKAPAS CQLKICRMDK
NFkBCys_Nev                 252  1.23e-20 QAYLPDQDGN
FTRPLKPVYSDAVLDSKAPSA SQLKICRMDK
NFkB_Acropora               245  1.74e-20 QAYLPDDNGC
FTKALPPCFSRSVYDSKAPSA ANLKICRMDR
NFkB_Corallimorph           250  3.40e-20 QAYLPDESGC
FTKALPPCISNSVYDSKSPAA STLKICRMDR
NFkB_Ed                     253  9.00e-20 QAYLPDRNGN
FTKALKPVYSDTVRDSKAPSA SQLKICRMDK
Relish_Biomphalaria         231  1.87e-19 QVFLRNPDGT
FDKMLPPVVSQPIYDSKSPGA SALKICRMDK
NFkBSer_Nev                 252  3.44e-19 QAYLPDQDGN
FTRPLKPVYSDAVLDSKEPSA SQLKICRMDK
Dorsal_Dmel                 204  3.81e-18 VFMESEQKGR
FTSPLPPVVSEPIFDKKAMSD LVICRLCSCS
NFkB_Amphimedon             229  5.02e-18 QAFLPDENGR
YTIPIDPVFSNKVYDSKAPSA GTLKICRLDR
NFkB2_Homo                  205  8.64e-18 SAFLRASDGS
FSLPLKPVISQPIHDSKSPGA SNLKISRMDK
rel1[Ciona]                 162  2.72e-17 EAFIPDARGK
YTQKLEPVVSDPIYDKKATCS SVLKICRVDK
cRel                        163  3.23e-17 QVFLPDEHGN
LTTALPPVVSNPIYDNRAPNT AELRICRVNK
RelB_Homo                   280  1.28e-14 FQASYRDQQG
QMRRMDPVLSEPVYDKKSTNT SELRICRINK
RelA_Homo                   171  1.28e-14 FQVTVRDPSG
RPLRLPPVLSHPIFDNRAPNT AELKICRVNR
NFkB_Hydra                  214  2.81e-14 HCFLEDSNGR
YTINLPTVYSVPIYDGKNKKG CEYKILRLSS
NFkB_Biomphalaria           269  3.99e-14 QVFLPNEQGK
VTRVVPPVCSHPIHDKKSSKD LVICRVDKSS
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB_Platygyra                    1.7e-22  245_[11]_652
```

```
NFkB1_Homo                           3e-22  227_[11]_721
NFkB[Ciona                         1.4e-21  199_[11]_980
NFkBb_Aiptasia                     2.3e-21  248_[11]_579
NFkBCys_Nev                        1.2e-20  251_[11]_168
NFkB_Acropora                      1.7e-20  244_[11]_639
NFkB_Corallimorph                  3.4e-20  249_[11]_645
NFkB_Ed                              9e-20  252_[11]_587
Relish_Biomphalaria                1.9e-19  230_[11]_834
NFkBSer_Nev                        3.4e-19  251_[11]_168
Dorsal_Dmel                        3.8e-18  203_[11]_454
NFkB_Amphimedon                      5e-18  228_[11]_846
NFkB2_Homo                         8.6e-18  204_[11]_674
rel1[Ciona]                        2.7e-17  161_[11]_108
cRel                               3.2e-17  162_[11]_436
RelB_Homo                          1.3e-14  279_[11]_279
RelA_Homo                          1.3e-14  170_[11]_257
NFkB_Hydra                         2.8e-14  213_[11]_243
NFkB_Biomphalaria                    4e-14  268_[11]_321
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 11 width=21 seqs=19
NFkB_Platygyra           (  246) FTKALPPCISNAVYDSKAPSA  1
NFkB1_Homo               (  228) FTRRLEPVVSDAIYDSKAPNA  1
NFkB[Ciona               (  200) FTIMLKPVISDAIFDSKAPNA  1
NFkBb_Aiptasia           (  249) FTKPLKPCISNPVYDSKAPAS  1
NFkBCys_Nev              (  252) FTRPLKPVYSDAVLDSKAPSA  1
NFkB_Acropora            (  245) FTKALPPCFSRSVYDSKAPSA  1
NFkB_Corallimorph        (  250) FTKALPPCISNSVYDSKSPAA  1
NFkB_Ed                  (  253) FTKALKPVYSDTVRDSKAPSA  1
Relish_Biomphalaria      (  231) FDKMLPPVVSQPIYDSKSPGA  1
NFkBSer_Nev              (  252) FTRPLKPVYSDAVLDSKEPSA  1
Dorsal_Dmel              (  204) FTSPLPPVVSEPIFDKKAMSD  1
NFkB_Amphimedon          (  229) YTIPIDPVFSNKVYDSKAPSA  1
NFkB2_Homo               (  205) FSLPLKPVISQPIHDSKSPGA  1
rel1[Ciona]              (  162) YTQKLEPVVSDPIYDKKATCS  1
cRel                     (  163) LTTALPPVVSNPIYDNRAPNT  1
RelB_Homo                (  280) QMRRMDPVLSEPVYDKKSTNT  1
RelA_Homo                (  171) RPLRLPPVLSHPIFDNRAPNT  1
NFkB_Hydra               (  214) YTINLPTVYSVPIYDGKNKKG  1
NFkB_Biomphalaria        (  269) VTRVVPPVCSHPIHDKKSSKD  1
//

--------------------------------------------------------------------
```

```
--------------------------------------------------------------------------------
        Motif 11 position-specific scoring matrix
--------------------------------------------------------------------------------
log-odds matrix: alength= 20 w= 21 n= 29610 bayes= 10.7999 E= 1.7e-
121
  -336   -241   -452   -435    455   -472   -370   -211   -420   -
108   -200   -443   -469   -197   -152   -384   -407   -146    -76
145
  -271   -253    -66   -415   -373   -445   -365   -260   -313   -
399     59   -238   -112   -364   -321    -32    368   -257   -293
-379
  -269   -391   -321   -221   -400   -378   -225    159    262
15   -279   -260   -443     -2    247    -82    -17   -332   -283
-297
   160   -316   -221   -147   -303   -306   -190   -254     47   -
281    181     -1    196   -177    160   -231   -196    -37   -235
-235
  -348   -313   -514   -425   -161   -511   -390     13   -386
325     90   -464   -479   -389   -346   -461   -342    -54   -220
-284
  -278   -521     96    124   -526   -388   -333   -452    245   -
461   -406   -272    255   -242   -299   -354   -339   -420   -451
-432
  -219   -370   -374   -346   -406   -391   -362   -379   -307   -
385   -373   -396    361   -367   -331   -321    -51   -365   -372
-417
  -353    346   -672   -655   -431   -551   -660   -107   -632   -
328   -337   -627   -661   -693   -633   -532   -409    359   -517
-512
  -226    140   -485   -408    150   -406   -333    245   -357
46   -108   -388   -469   -399   -345   -355   -230    197   -179
294
  -476   -524   -665   -736   -667   -557   -646   -730   -690   -
724   -701   -634   -679   -731   -648    338   -475   -676   -537
-626
  -187   -361    227     95   -342   -283    172   -321    -97   -
331   -253    210   -361     74     33   -220   -200    -40   -265
-246
   135   -335   -350   -321   -385   -359   -339   -356    -34   -
363   -348   -366    308   -342   -306    -32    -55   -339   -353
-395
  -399   -350   -691   -658   -398   -677   -731    351   -632   -
274   -288   -648   -715   -728   -677   -658   -403    288   -545
-507
  -198   -206   -304   -271    223   -350    147   -205   -251    -
28   -176   -287   -376   -326    -39   -267   -268   -227     24
453
  -455   -482    415   -240   -514   -489   -407   -510   -490   -
557   -510   -246   -616   -525   -485   -501   -506   -520   -399
-447
```

```
  -328   -422   -160   -274   -504    -34   -263   -539    198   -
550   -496    116   -481   -340   -306    259   -275   -522   -428
-375
  -351   -358   -477   -421   -505   -470   -378   -366    421   -
465   -380   -367   -504   -421     23   -475   -383   -457   -299
-416
   319   -178   -294    -49   -373   -242   -352   -342   -330   -
378   -304    -23   -487   -395   -352    108   -258   -231   -308
-369
  -190   -346   -342   -311   -375   -366   -329   -345    -40   -
351     46   -364    337   -332   -296   -117     20   -333   -345
-387
    63    143   -214   -262   -449     53   -281   -446    105   -
464   -390    226   -448   -316   -296    183   -268   -400   -376
-359
   312   -174     51   -377   -380    -51   -394   -348   -370   -
384   -309   -328   -491   -429   -376      2    102   -233   -314
-387
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 11 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 21 nsites= 19 E= 1.7e-121
 0.000000  0.000000  0.000000  0.000000  0.631579  0.000000
0.000000  0.000000  0.000000  0.052632  0.000000  0.000000  0.000000
0.052632  0.052632  0.000000  0.000000  0.052632  0.000000  0.157895
 0.000000  0.000000  0.052632  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.052632  0.000000  0.052632
0.000000  0.000000  0.052632  0.789474  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.157895  0.315789  0.105263  0.000000  0.000000  0.000000
0.052632  0.263158  0.052632  0.052632  0.000000  0.000000  0.000000
 0.263158  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.052632  0.000000  0.105263  0.052632  0.315789
0.000000  0.157895  0.000000  0.000000  0.052632  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.052632  0.000000  0.842105  0.052632  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.052632  0.000000  0.000000
 0.000000  0.000000  0.105263  0.105263  0.000000  0.000000
0.000000  0.000000  0.315789  0.000000  0.000000  0.000000  0.473684
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.947368
0.000000  0.000000  0.000000  0.052632  0.000000  0.000000  0.000000
 0.000000  0.210526  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.789474  0.000000  0.000000
 0.000000  0.052632  0.000000  0.000000  0.105263  0.000000
0.000000  0.263158  0.000000  0.105263  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.263158  0.000000  0.210526
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.315789  0.105263  0.000000  0.000000
0.105263  0.000000  0.000000  0.000000  0.000000  0.263158  0.000000
0.105263  0.052632  0.000000  0.000000  0.052632  0.000000  0.000000
 0.263158  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.052632  0.000000  0.000000  0.000000  0.526316
0.000000  0.000000  0.105263  0.052632  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.526316  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.473684  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.157895  0.000000
0.105263  0.000000  0.000000  0.105263  0.000000  0.000000  0.000000
0.000000  0.052632  0.000000  0.000000  0.000000  0.000000  0.578947
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.052632
0.000000  0.000000  0.210526  0.000000  0.000000  0.105263  0.000000
0.000000  0.000000  0.631579  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.894737  0.000000  0.000000  0.000000  0.000000
0.000000  0.105263  0.000000  0.000000  0.000000  0.000000  0.000000
 0.631579  0.000000  0.000000  0.052632  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.052632  0.000000
0.000000  0.000000  0.263158  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.052632  0.000000  0.052632  0.000000  0.736842
0.000000  0.000000  0.052632  0.105263  0.000000  0.000000  0.000000
 0.105263  0.052632  0.000000  0.000000  0.000000  0.105263
0.000000  0.000000  0.105263  0.000000  0.000000  0.263158  0.000000
0.000000  0.000000  0.368421  0.000000  0.000000  0.000000  0.000000
 0.578947  0.000000  0.105263  0.000000  0.000000  0.052632
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.105263  0.157895  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 regular expression
--------------------------------------------------------------------
FT[KR][PA]L[PK]P[VC][IVY]S[DN][PA][IV]YD[SK]K[AS]P[SN]A
--------------------------------------------------------------------




Time 743.15 secs.

********************************************************************
```

```
********************************************************************
MOTIF 12 MEME    width =  21  sites =  12  llr = 590  E-value =
4.5e-106
********************************************************************
--------------------------------------------------------------------
      Motif 12 Description
--------------------------------------------------------------------
Simplified        A  ::9:::::::::3::31::::
pos.-specific     C  :::::::::7::::::::::1
probability       D  :::::::::::::::1::4::
matrix            E  :11::8:a::::::::::3::
                  F  :::::::::::::::::::::
                  G  ::::::::a::a:::7::331
                  H  3::3::::::::::7:::::3
                  I  :::::::::::::7:::::::
                  K  ::::::::::1:::3::1:::
                  L  :::::1:::::::::::::::
                  M  :::::::::::::::::::::
                  N  :::1:::::::::::::::6:
                  P  1:::::::::::7:::11:::
                  Q  :::::::::::::::::311:
                  R  :9:7::::::9:::::1::::
                  S  ::::::7::3::1:::83:1:
                  T  :::::13::::::::::3::6
                  V  :::::::::::::3:::::::
                  W  :::::::::::::::::::::
                  Y  6:::a::::::::::::::::

         bits    7.3
                 6.6
                 5.9
                 5.1     *
Relative         4.4  *  *  * **   *
Entropy          3.7 *****  ***** **
(70.9 bits)      2.9 ****************    *
                 2.2 ***************** ***
                 1.5 *********************
                 0.7 *********************
                 0.0 ---------------------

Multilevel           YRARYESEGCRGPIHGSTDNT
consensus            H  H  T  S  AVKA QEGH
sequence                              SG


--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
     Motif 12 sites sorted by position p-value
---------------------------------------------------------------------
Sequence name             Start   P-value                     Site
-------------             ----- ---------            ---------------
NFATb_Platygyra             314  1.80e-27 IVIIEEPEEN
YRARYESEGCRGPIHGSQDNT FPAVKVTGCD
NFATa_Platygyra             293  1.80e-27 IVIIEEPEEN
YRARYESEGCRGPIHGSQDNT FPAVKVTGCD
NFAT_Acropora               290  4.85e-27 IVIIEEPEEN
YRARYESEGCRGPIHGSQENT FPTVKVTGYS
NFAT_Ed                     231  4.85e-27 LVLLEEPEEN
YRARYESEGCRGPIHGSSDNT FPTIKIANYS
NFAT_Corallimorph           329  6.84e-27 IMILEEPEEN
YRARYESEGCRGPIHGSKDNT FPTVMVTGAS
NFAT_Aiptasia               272  6.76e-25 LVILDEPEEN
YRARYESEGCRGPIHGSSEST YPTIKVSGYS
NFAT_Hydra                  745  2.01e-24 SVTAYGGHRT
YRARYESEGCKGPIHGSTENC FPSIKKMQQV
NFAT4                       443  3.92e-20 LKIEVQPKTH
HRAHYETEGSRGAVKASTGGH PVVKLLGYNE
NFAT1                       400  5.86e-19 LRIEVQPKPH
HRAHYETEGSRGAVKAPTGGH PVVQLHGYME
NFAT3                       359  2.05e-18 LRIEVQPRAH
HRAHYETEGSRGAVKAAPGGH PVVKLLGYSE
NFAT_Nev                    525  3.01e-18 CEPKLVLLEE
PEENYTSEGCRGPIHGSSDNT FPTVKVLGYS
NFAT5                       292  8.73e-16 LKIVVQPETQ
HRARYLTEGSRGSVKDRTQQG FPTVKLEGHN
---------------------------------------------------------------------


---------------------------------------------------------------------
     Motif 12 block diagrams
---------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFATb_Platygyra                   1.8e-27  313_[12]_216
NFATa_Platygyra                   1.8e-27  292_[12]_216
NFAT_Acropora                     4.8e-27  289_[12]_369
NFAT_Ed                           4.8e-27  230_[12]_209
NFAT_Corallimorph                 6.8e-27  328_[12]_189
NFAT_Aiptasia                     6.8e-25  271_[12]_386
NFAT_Hydra                          2e-24  744_[12]_1210
NFAT4                             3.9e-20  442_[12]_612
NFAT1                             5.9e-19  399_[12]_485
NFAT3                               2e-18  358_[12]_453
NFAT_Nev                            3e-18  524_[12]_376
NFAT5                             8.7e-16  291_[12]_1219
---------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 12 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 12 width=21 seqs=12
NFATb_Platygyra          (  314) YRARYESEGCRGPIHGSQDNT  1
NFATa_Platygyra          (  293) YRARYESEGCRGPIHGSQDNT  1
NFAT_Acropora            (  290) YRARYESEGCRGPIHGSQENT  1
NFAT_Ed                  (  231) YRARYESEGCRGPIHGSSDNT  1
NFAT_Corallimorph        (  329) YRARYESEGCRGPIHGSKDNT  1
NFAT_Aiptasia            (  272) YRARYESEGCRGPIHGSSEST  1
NFAT_Hydra               (  745) YRARYESEGCKGPIHGSTENC  1
NFAT4                    (  443) HRAHYETEGSRGAVKASTGGH  1
NFAT1                    (  400) HRAHYETEGSRGAVKAPTGGH  1
NFAT3                    (  359) HRAHYETEGSRGAVKAAPGGH  1
NFAT_Nev                 (  525) PEENYTSEGCRGPIHGSSDNT  1
NFAT5                    (  292) HRARYLTEGSRGSVKDRTQQG  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 21 n= 29610 bayes= 11.7159 E= 4.5e-
106
  -391   -351   -456   -450     14   -485    342   -346   -402   -
331   -315   -384     -5   -434   -375   -432   -419   -376     -9
458
  -339   -274   -431   -173   -434   -409   -210   -368    -96   -
388   -360   -332   -417   -278    434   -405   -371   -458   -186
-352
   354   -114   -349    -26   -313   -203   -364   -274   -316   -
312   -238   -348   -469   -380   -320   -151   -220   -160   -247
-331
  -323   -333   -307   -299   -426   -363    239   -381    -36   -
386   -340      9   -440   -227    398   -345   -319   -418   -232
-306
  -611   -513   -625   -671   -192   -578   -372   -543   -609   -
511   -519   -575   -650   -616   -553   -639   -605   -576   -179
540
  -402   -537   -184    398   -549   -487   -430   -460   -387   -
255   -481   -400   -591   -346   -452   -504   -198   -485   -447
-495
  -157   -176   -331   -374   -321   -313   -327   -325   -273   -
370   -276   -189   -379   -371   -267    284    182   -353   -251
-284
  -486   -547   -219    404   -572   -525   -468   -497   -527   -
607   -543   -439   -682   -423   -528   -581   -535   -548   -454
-528
```

```
  -278   -397   -348   -409   -485    376   -408   -490   -374   -
546   -449   -329   -515   -491   -367   -373   -432   -470   -325
-419
  -149    513   -527   -549   -492   -298   -507   -489   -537   -
529   -453   -447   -480   -528   -488    176   -293   -378   -413
-477
  -337   -269   -436   -425   -431   -407   -206   -363    -39   -
385   -356   -330   -413   -275    434   -403   -368   -456   -181
-349
  -278   -397   -348   -409   -485    376   -408   -490   -374   -
546   -449   -329   -515   -491   -367   -373   -432   -470   -325
-419
   122   -282   -334   -306   -363   -312   -322   -335   -270   -
343   -325   -346    326   -325   -290    -61   -247   -308   -328
-374
  -319   -290   -498   -482   -281   -527   -514    384   -430   -
120   -137   -464   -573   -523   -467   -479   -308    213   -340
-335
  -393   -455   -397   -336   -429   -433    450   -457    272   -
442   -389   -306   -529   -265   -106   -417   -376   -458   -312
-293
    65   -318    -49   -329   -428    349   -340   -423   -303   -
486   -379   -245   -453   -416   -303   -285   -341   -393   -274
-360
   -33   -177   -327   -356   -325   -301   -323   -331   -261   -
371   -280   -194   -104   -360    -24    290     58   -350   -256
-287
  -145   -266   -164   -106   -288   -263   -154   -245     80   -
280   -190   -131    -32    155    -96    106    237   -236   -207
-208
  -243   -547    271    227   -530    150   -291   -432   -182   -
444   -377   -207   -406     45   -302   -313   -301   -389   -447
-400
  -285   -377    -98   -219   -443    157   -194   -473   -225   -
505   -453    340   -426     30   -298    -15   -256   -471   -366
-319
  -153    188   -327   -374   -374      1    281   -302   -316   -
396   -285   -239   -434   -370   -329   -153    325   -274   -308
-355
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 21 nsites= 12 E= 4.5e-106
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.333333  0.000000  0.000000  0.000000  0.000000  0.000000  0.083333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.583333
 0.000000  0.000000  0.000000  0.083333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.916667  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.916667  0.000000  0.000000  0.083333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.000000  0.000000  0.000000  0.083333  0.000000
0.000000  0.666667  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.833333  0.000000  0.000000
0.000000  0.000000  0.000000  0.083333  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.083333  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.666667  0.333333  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.666667  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.333333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
0.000000  0.916667  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.666667
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.666667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.666667  0.000000  0.333333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.250000  0.000000  0.083333  0.000000  0.000000  0.666667
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.083333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.083333
0.000000  0.083333  0.750000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.083333
0.250000  0.000000  0.250000  0.333333  0.000000  0.000000  0.000000
 0.000000  0.000000  0.416667  0.250000  0.000000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.083333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.583333  0.000000
0.083333  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.083333  0.000000  0.000000  0.000000  0.083333
0.250000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.583333  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 regular expression
--------------------------------------------------------------------
[YH]RA[RH]YE[ST]EG[CS]RG[PA][IV][HK][GA]S[TQS][DEG][NG][TH]
--------------------------------------------------------------------




Time 801.93 secs.

********************************************************************


********************************************************************
MOTIF 13 MEME    width =  29  sites =  12  llr = 725  E-value =
2.7e-116
********************************************************************
--------------------------------------------------------------------
      Motif 13 Description
--------------------------------------------------------------------
Simplified        A  39::1:85:1:2:1::72:::::83::::
pos.-specific     C  11:::::::::::1:::::::::::::1:
probability       D  ::::8:::::a::::::::::::1::742
matrix            E  :::::::1:::::::::::::::::::31
                  F  :::1:3:::::::::::::::::1:::::
                  G  ::::1:1:18:::::::1::1::::::::
                  H  :::1:::::::::1::::1:6::::::::
                  I  :::::::::::3:::::1:::1:::::::
                  K  :::::::::1::1::::::::::::::1:
                  L  ::43::::::::::aa12:::93::::::
                  M  ::3::::::::2:2::::1::::::::::
                  N  3::::::::1::::::::::::::::3:6
                  P  :::::::::::::::::1:::::::1:::
                  Q  :::2::::::::::::::813::::8:11
                  R  2::3::::::::9::::::9:::::1:::
                  S  3:::1:2:2:::::::1:::1::::1::1
                  T  :::1:::18:::::::::::::71:::::
                  V  ::3::::3:::4::::24::::::8::::
                  W  :::::1:::::::::::::::::::::::
                  Y  :::::7:::::::6:::::::::::::::

         bits    7.3
```

```
                 6.6
                 5.9
                 5.1
Relative         4.4      *    * *      *
Entropy          3.7  *   *    * ****  **      *
(87.2 bits)      2.9  ** *** *** ****  *********
                 2.2 ***************** ***********
                 1.5 *****************************
                 0.7 *****************************
                 0.0 -----------------------------

Multilevel           AALRDYAATGDVRYLLAVQRHLTAVQDDN
consensus            N ML F V   I        Q L A NE
sequence             S V


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                Site
-------------             ----- ---------            ---------------
NFkB_Corallimorph           478  1.34e-34 LAWNLAERSA
CAMRDYSATGDVRYLLAVQRHLTAVQDDN GDTALHLAVI
NFkB_Platygyra              484  1.14e-32 LAWNLAEKSA
AAMRDYAATGDMRYLLAAQRHLTAVQDDS GDTALHLAVI
NFkB_Acropora               475  2.30e-31 LAWNVAAICA
AAVRDYAVSGDMRYLLVVQRHLTAVQDDN GDTALHLAVI
NFkB1_Homo                  515  3.56e-30 KAMQLAKRHA
NALFDYAVTGDVKMLLAVQRHLTAVQDEN GDSVLHLAII
NFkB_Ed                     482  9.31e-29 LAWALVEHAS
SAMRDYAATGDVRYLLAIQQQLTAVQDDQ GDSALHLAVI
NFkBb_Aiptasia              477  1.14e-28 LAWAIAKHTS
SAMQDYAATGDVRYLLSVQRQITAVQNDD GDTALHIAVI
Relish_Biomphalaria         666  1.16e-24 VTGHVAERTL
AALTDFAETGDIRHLLLVQRHLLAVSNKN GDPPFHLAVI
NFkB[Ciona                  800  2.08e-24 YAVKTMNRNS
SALHDFSVTGDIRMLLVLQRHLTDVRDCN GDSVLHVAVI
NFkB2_Homo                  459  7.70e-24 RLFGLAQRSA
RALLDYGVTADARALLAGQRHLLTAQDEN GDTPLHLAII
NFkB_Amphimedon             660  1.72e-23 MAFEVCDRMF
NALLAWATTKDIRYLLAAQRSLTAVQNQE GDTALHLAII
NFkB_Capsaspora             608  4.48e-22 KLHQLALSTV
RAVQGFAASGDARYLLALHRQLLAAPNEN GDSPLHTAVA
IkB_Nev                     115  1.62e-19 ISQSQSISPH
NCVLSYAAGNDVRCLLAPMRGLLFAQDED GDTALHLAII
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 13 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB_Corallimorph                 1.3e-34  477_[13]_409
NFkB_Platygyra                    1.1e-32  483_[13]_406
NFkB_Acropora                     2.3e-31  474_[13]_401
NFkB1_Homo                        3.6e-30  514_[13]_426
NFkB_Ed                           9.3e-29  481_[13]_350
NFkBb_Aiptasia                    1.1e-28  476_[13]_343
Relish_Biomphalaria               1.2e-24  665_[13]_391
NFkB[Ciona                        2.1e-24  799_[13]_372
NFkB2_Homo                        7.7e-24  458_[13]_412
NFkB_Amphimedon                   1.7e-23  659_[13]_407
NFkB_Capsaspora                   4.5e-22  607_[13]_587
IkB_Nev                           1.6e-19  114_[13]_240
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 13 width=29 seqs=12
NFkB_Corallimorph        (  478) CAMRDYSATGDVRYLLAVQRHLTAVQDDN  1
NFkB_Platygyra           (  484) AAMRDYAATGDMRYLLAAQRHLTAVQDDS  1
NFkB_Acropora            (  475) AAVRDYAVSGDMRYLLVVQRHLTAVQDDN  1
NFkB1_Homo               (  515) NALFDYAVTGDVKMLLAVQRHLTAVQDEN  1
NFkB_Ed                  (  482) SAMRDYAATGDVRYLLAIQQQLTAVQDDQ  1
NFkBb_Aiptasia           (  477) SAMQDYAATGDVRYLLSVQRQITAVQNDD  1
Relish_Biomphalaria      (  666) AALTDFAETGDIRHLLLVQRHLLAVSNKN  1
NFkB[Ciona               (  800) SALHDFSVTGDIRMLLVLQRHLTDVRDCN  1
NFkB2_Homo               (  459) RALLDYGVTADARALLAGQRHLLTAQDEN  1
NFkB_Amphimedon          (  660) NALLAWATTKDIRYLLAAQRSLTAVQNQE  1
NFkB_Capsaspora          (  608) RAVQGFAASGDARYLLALHRQLLAAPNEN  1
IkB_Nev                  (  115) NCVLSYAAGNDVRCLLAPMRGLLFAQDED  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 29 n= 29298 bayes= 10.9118 E= 2.7e-
116
   174    197   -221   -200   -354   -242   -235   -326   -157   -
351   -276    205   -376   -239    170    124   -194   -284   -282
-285
   355    156   -407   -364   -322   -203   -383   -284   -349   -
323   -249   -371   -463   -410   -339   -152   -218   -169   -257
-343
```

```
  -392   -347   -674   -598   -158   -607   -512    -73   -555
229    367   -596   -612   -526   -516   -587   -395    188   -249
-323
  -138   -242   -191   -113     90   -267    130   -152    -26
115   -133   -161   -328    119    251   -196     38   -163   -160
-158
  -118   -343    391   -105   -394   -134   -266   -381   -335   -
434   -376    -99   -490   -374   -350   -162   -340   -381   -291
-320
  -384   -340   -472   -450    284   -492   -148   -332   -409   -
317   -302   -396   -525   -435   -375   -429   -415   -363    355
475
   339   -109   -396   -356   -316    -22   -375   -280   -341   -
317   -242   -360   -458   -402   -331     32   -211   -163   -251
-338
   292   -136   -340      2   -270   -227   -329   -174   -283   -
253   -193   -327   -432   -342   -296   -176     13    185   -228
-281
  -192   -218   -365   -398   -363    -37   -352   -259   -308   -
389   -241   -228   -436   -355   -313     61    359   -246   -284
-367
   -78   -335   -267   -328   -422    358   -336   -415    -71   -
482   -372    -65   -454   -415   -290   -295   -359   -396   -262
-351
  -365   -401    408   -145   -430   -411   -318   -420   -401   -
472   -419   -152   -544   -436   -400   -411   -418   -429   -320
-362
   102   -235   -519   -462   -249   -475   -428    244   -425   -
173    256   -456   -523   -484   -421   -434   -262    272   -286
-305
  -337   -269   -436   -425   -431   -407   -206   -363    -39   -
385   -356   -330   -413   -275    434   -403   -368   -456   -181
-349
   -44     90   -265   -230    163   -308    108   -155   -210   -
170    147   -249   -336   -286   -201   -226   -221   -176     53
449
  -436   -393   -583   -529   -231   -550   -471   -172   -488
347   -124   -553   -556   -489   -444   -555   -435   -268   -287
-353
  -436   -393   -583   -529   -231   -550   -471   -172   -488
347   -124   -553   -556   -489   -444   -555   -435   -268   -287
-353
   335    -73   -357   -308   -263   -172   -333   -215   -290   -
117   -186   -335   -466   -366   -287    -52   -192     29   -202
-287
    59   -142   -368   -311   -161    -71   -265     96   -279
34    -87   -322    -81   -338   -259   -295   -147    301   -154
-193
  -248   -292   -354   -107   -375   -423     34   -318   -239   -
260    -25   -249   -370    379   -176   -328   -292   -340   -180
-330
```

```
  -338   -270   -436   -427   -431   -408   -207   -364    -95   -
386   -357   -331   -413   -152    434   -404   -370   -458   -181
-350
  -296   -273   -214   -262   -211    -91    461   -362   -270   -
310   -238    -89   -398    101   -144   -106   -256   -342   -133
-16
  -345   -306   -524   -436   -139   -515   -395     64   -396
330    -24   -473   -484   -395   -356   -470   -340   -162   -208
-275
  -311   -325   -527   -527   -253   -466   -464   -165   -444
185   -173   -419   -552   -486   -439   -304    339   -225   -296
-345
   340    -76    -86   -299    -17   -172   -328   -227   -284   -
266   -192   -321   -463   -359   -285   -117    -55   -116   -205
-288
   137   -205   -448   -415   -316   -365   -399    -28   -403   -
249   -236   -429   -450   -466   -374   -332   -226    349   -335
-393
  -246   -294   -347   -109   -376   -417    -28   -318   -221   -
262   -150   -246   -198    376    -73   -205   -289   -340   -182
-329
  -324   -399    364   -166   -442   -277   -239   -463   -280   -
499   -451    220   -467   -339   -341   -274   -310   -463   -353
-334
  -204    178    269    247   -421   -317   -236   -361     72   -
373   -299   -194   -374     44   -208   -270   -247   -333   -338
-315
  -286   -384    143     43   -422   -242   -180   -424   -208   -
465   -404    343   -416     22   -282    -25   -251   -436   -335
-308
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 13 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 29 nsites= 12 E= 2.7e-116
 0.250000  0.083333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.166667  0.250000  0.000000  0.000000  0.000000  0.000000
 0.916667  0.083333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.416667  0.333333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.083333  0.000000
0.083333  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
0.166667  0.333333  0.000000  0.083333  0.000000  0.000000  0.000000
 0.083333  0.000000  0.750000  0.000000  0.000000  0.083333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.083333  0.666667
 0.750000  0.000000  0.000000  0.000000  0.000000  0.083333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.083333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.083333  0.333333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.083333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.750000  0.000000  0.000000  0.000000
 0.083333  0.000000  0.000000  0.000000  0.000000  0.750000
0.000000  0.000000  0.083333  0.000000  0.000000  0.083333  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.416667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
0.000000  0.916667  0.000000  0.000000  0.000000  0.000000  0.000000
 0.083333  0.083333  0.000000  0.000000  0.000000  0.000000
0.083333  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.583333
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.666667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.083333  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.166667  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.083333
0.000000  0.083333  0.000000  0.166667  0.000000  0.000000  0.083333
0.000000  0.000000  0.000000  0.000000  0.416667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.083333  0.000000  0.000000  0.000000  0.083333  0.000000  0.000000
0.833333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.083333  0.916667  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.083333
0.583333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.083333  0.000000  0.916667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.333333  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
 0.750000  0.000000  0.083333  0.000000  0.083333  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.083333  0.000000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.750000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.083333
0.750000  0.083333  0.083333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.333333  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.083333  0.416667  0.333333  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
0.083333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.166667  0.083333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.583333  0.000000
0.083333  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 regular expression
--------------------------------------------------------------------
[ANS]A[LMV][RL]D[YF]A[AV]TGD[VI]RYLLAVQR[HQ]L[TL]A[VA]Q[DN][DE]N
--------------------------------------------------------------------




Time 859.15 secs.

********************************************************************


********************************************************************
MOTIF 14 MEME    width =  29  sites =   7  llr = 566  E-value =
2.3e-112
********************************************************************
--------------------------------------------------------------------
      Motif 14 Description
--------------------------------------------------------------------
Simplified        A  ::::::::::::::::::::::::::a::
pos.-specific     C  :::::::::::::::a:::::::::::::
probability       D  :::::::::::::::::::::::::::::
matrix            E  :::::::::::::::::a:::1:1:::::
                  F  ::::::::::::::::::3::::::::::
                  G  :::::::a:a::::::::::::99:::::
                  H  :a:a::a::::::::::::::::::::::
```

```
                  I  :::::a::::::::::::3:::::4::::
                  K  ::::::::::::a:::a::::::::::::
                  L  :::::::::::::::::::3a::::::::
                  M  :::::::::::::::::::::::::::::
                  N  :::::::::::::::::::::::::::::
                  P  a:::::::a:::::a::::::9:::a:::
                  Q  ::::::::::::::::::::::::::::a
                  R  ::::::::::::::::::::::1::::::
                  S  ::::a:::::a::::::::::::::::::
                  T  :::::::::::a::::::47:::::::::
                  V  :::::::::::::a::::::::::6::a:
                  W  :::::::::::::::::::::::::::::
                  Y  ::a::::::::::::::::::::::::::

         bits    7.3
                 6.6
                 5.9                *
                 5.1  ***  *        *
Relative         4.4  *** **    **  ***          *
Entropy          3.7 ******************  * *  ****
(116.6 bits)     2.9 *****************************
                 2.2 *****************************
                 1.5 *****************************
                 0.7 *****************************
                 0.0 -----------------------------

Multilevel           PHYHSIHGPGSTKVPCKETTLPGGVPAVQ
consensus                              FL    I
sequence                               I


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
NFATb_Platygyra             360  1.02e-36 TVHLTTSSGV
PHYHSIHGPGSTKVPCKETTLPGGVPAVQ VMVAPDTNMT
NFATa_Platygyra             339  1.02e-36 TVHLTTSSGV
PHYHSIHGPGSTKVPCKETTLPGGVPAVQ VMVAPDTNMT
NFAT_Corallimorph           375  1.02e-36 TVHLITSSGQ
PHYHSIHGPGSTKVPCKEITLPGGIPAVQ LMVAPDNDMT
NFAT_Aiptasia               318  1.02e-36 TVYLTTSSGL
PHYHSIHGPGSTKVPCKEITLPGGIPAVQ LMVDPDSKMT
NFAT_Acropora               336  5.50e-36 TVHLTTSGGI
PHYHSIHGPGSTKVPCKETTLEGGVPAVQ VMVGPDSNMT
NFAT_Ed                     277  8.65e-35 TVHLVTSSGM
PHYHSIHGPGSTKVPCKEFLLPRGVPAVQ VLVEPDCDMT
```

```
NFAT_Nev                    571  1.05e-34 TVHLVTSSGQ
PHYHSIHGPGSTKVPCKEFLLPGEIPAVQ VLVEPDCDMT
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFATb_Platygyra                     1e-36  359_[14]_162
NFATa_Platygyra                     1e-36  338_[14]_162
NFAT_Corallimorph                   1e-36  374_[14]_135
NFAT_Aiptasia                       1e-36  317_[14]_332
NFAT_Acropora                     5.5e-36  335_[14]_315
NFAT_Ed                           8.6e-35  276_[14]_155
NFAT_Nev                            1e-34  570_[14]_322
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 14 width=29 seqs=7
NFATb_Platygyra          (  360) PHYHSIHGPGSTKVPCKETTLPGGVPAVQ  1
NFATa_Platygyra          (  339) PHYHSIHGPGSTKVPCKETTLPGGVPAVQ  1
NFAT_Corallimorph        (  375) PHYHSIHGPGSTKVPCKEITLPGGIPAVQ  1
NFAT_Aiptasia            (  318) PHYHSIHGPGSTKVPCKEITLPGGIPAVQ  1
NFAT_Acropora            (  336) PHYHSIHGPGSTKVPCKETTLEGGVPAVQ  1
NFAT_Ed                  (  277) PHYHSIHGPGSTKVPCKEFLLPRGVPAVQ  1
NFAT_Nev                 (  571) PHYHSIHGPGSTKVPCKEFLLPGEIPAVQ  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 29 n= 29298 bayes= 12.6367 E= 2.3e-
112
  -216   -351   -359   -338   -387   -367   -345   -370   -299   -
373   -366   -383    365   -359   -318   -316   -304   -358   -334
-389
  -415   -357   -351   -396   -283   -425    510   -455   -409   -
400   -342   -216   -478   -218   -253   -389   -372   -442   -206
-106
  -459   -393   -509   -527    -55   -484   -235   -400   -472   -
378   -377   -450   -548   -492   -429   -499   -475   -433    -59
534
  -415   -357   -351   -396   -283   -425    510   -455   -409   -
400   -342   -216   -478   -218   -253   -389   -372   -442   -206
-106
```

```
  -197   -239   -380   -429   -386   -329   -383   -405   -352   -
439   -362   -272   -432   -436   -343    322    -40   -400   -305
-344
  -307   -291   -449   -441   -240   -467   -446    417   -383    -
82   -100   -421   -524   -470   -411   -432   -295     47   -272
-280
  -415   -357   -351   -396   -283   -425    510   -455   -409   -
400   -342   -216   -478   -218   -253   -389   -372   -442   -206
-106
  -217   -341   -289   -349   -430    371   -352   -431   -314   -
491   -389   -269   -461   -433   -309   -312   -372   -410   -271
-363
  -216   -351   -359   -338   -387   -367   -345   -370   -299   -
373   -366   -383    365   -359   -318   -316   -304   -358   -334
-389
  -217   -341   -289   -349   -430    371   -352   -431   -314   -
491   -389   -269   -461   -433   -309   -312   -372   -410   -271
-363
  -197   -239   -380   -429   -386   -329   -383   -405   -352   -
439   -362   -272   -432   -436   -343    322    -40   -400   -305
-344
  -261   -268   -402   -434   -384   -395   -381   -290   -344   -
410   -285   -278   -467   -397   -346   -153    393   -285   -299
-376
  -344   -350   -464   -410   -493   -457   -369   -360    423   -
456   -373   -358   -494   -411    -21   -465   -375   -449   -291
-404
  -152   -196   -410   -379   -272   -414   -359     17   -365   -
204   -197   -414   -435   -443   -337   -395   -211    374   -296
-350
  -216   -351   -359   -338   -387   -367   -345   -370   -299   -
373   -366   -383    365   -359   -318   -316   -304   -358   -334
-389
  -365    577   -526   -483   -445   -536   -478   -382   -507   -
466   -382   -504   -591   -553   -453   -502   -392   -459   -427
-478
  -344   -350   -464   -410   -493   -457   -369   -360    423   -
456   -373   -358   -494   -411    -21   -465   -375   -449   -291
-404
  -476   -543   -213    404   -567   -519   -461   -491   -511   -
599   -535   -432   -671   -413   -518   -571   -526   -540   -450
-521
  -176   -167   -414   -354    260   -360   -281    242   -299    -
66    -46   -315   -420   -343   -294   -257    251    -17   -120
-116
  -207   -214   -383   -377   -203   -371   -334    -99   -291
128   -117   -261   -438   -349   -297   -144    342   -137   -211
-257
  -342   -305   -503   -433   -145   -481   -384    -82   -391
337    -33   -463   -473   -394   -351   -461   -341   -174   -203
-264
```

```
  -134   -289   -271     10   -319   -307   -271   -290   -212   -
296   -284   -300    344   -272   -239   -234   -223   -278   -287
-328
  -188   -319   -257   -316   -407    363   -323   -401   -274   -
466   -358   -236   -440   -400    -21   -283   -345   -382   -248
-337
  -186   -318   -248    -64   -406    363   -320   -400   -276   -
465   -357   -229   -437   -395   -276   -279   -342   -380   -247
-335
  -239   -221   -490   -458   -252   -496   -476    320   -426   -
127   -137   -459   -528   -512   -441   -462   -254    297   -335
-335
  -216   -351   -359   -338   -387   -367   -345   -370   -299   -
373   -366   -383    365   -359   -318   -316   -304   -358   -334
-389
   365   -136   -408   -376   -336   -217   -387   -299   -362   -
340   -271   -376   -455   -420   -349   -172   -232   -192   -265
-349
  -152   -196   -410   -379   -272   -414   -359     17   -365   -
204   -197   -414   -435   -443   -337   -395   -211    374   -296
-350
  -277   -318   -372   -142   -393   -428    -62   -349   -262   -
293   -184   -279   -397    388   -205   -356   -321   -370   -207
-345
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 29 nsites= 7 E= 2.3e-112
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.285714  0.000000
0.000000  0.285714  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.428571  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.285714  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.714286  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.142857  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.857143
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.857143
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.142857  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.142857  0.000000  0.857143
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.428571  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.571429  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 regular expression
--------------------------------------------------------------------
PHYHSIHGPGSTKVPCKE[TFI][TL]LPGG[VI]PAVQ
--------------------------------------------------------------------




Time 915.75 secs.

********************************************************************


********************************************************************
MOTIF 15 MEME    width =  15  sites =  21  llr = 586  E-value =
6.0e-079
********************************************************************
--------------------------------------------------------------------
      Motif 15 Description
--------------------------------------------------------------------
Simplified        A  :::3:::::::::::
pos.-specific     C  :::::::::::::::
probability       D  1:::::::::::::9
matrix            E  42::1:::4::::::
                  F  ::::::1::::::::
                  G  :::::::::::::::
                  H  ::::::1::::::::
                  I  :::::::3:::::::
                  K  :1::2:1:1:1:51:
                  L  ::::::23:a:::::
                  M  :::::::1:::::::
                  N  ::::3:::::::::1
                  P  ::8:::::::::4::
```

```
                  Q  11::::1:3:1::::
                  R  :4:::::::7a:::
                  S  ::::::::::::8:
                  T  2:::1::::::::::
                  V  :::7:a:2:::::::
                  W  :::::::::::::::
                  Y  :::::::::::::::

         bits    7.3
                 6.6
                 5.9
                 5.1
Relative         4.4            *
Entropy          3.7      *   * *  *
(40.3 bits)      2.9   ** *   ******
                 2.2 **** * ********
                 1.5 ***************
                 0.7 ***************
                 0.0 ---------------

Multilevel           ERPVNVLIELRRKSD
consensus            T  AK  LQ   P
sequence                    V


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 15 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
NFkB_Corallimorph           348  1.10e-18 KTPPFWNIAT ERPVKVHIELRRKSD
REKSESVDFT
NFkB_Acropora               343  9.57e-18 KTPAYWNIAV ERPVKVHLELRRKSD
DETSDPVEFT
NFkB_Platygyra              345  2.89e-17 KTPPYWNVAT ERPVKVQLELRRKSD
QETSEPVEFT
NFkBb_Aiptasia              347  2.08e-16 KTPAYHNIAI ERPVEVLLELRRKSD
KETSEPFTFT
Dorsal_Dmel                 299  5.28e-15 KTPRYHTLDI TEPAKVFIQLRRPSD
GVTSEALPFE
cRel                        254  6.73e-15 FKTPPYCKAI TEPVTVKMQLRRPSD
QEVSESMDFR
NFkB[Ciona                  298  2.09e-14 RTPAYKDTEI KMPVNVQVQLRRKSD
NEVSESRPFT
NFkB_Ed                     352  3.94e-14 KTPPYWNVAI EKPAPVMLELRRKSD
METSESVQFT
NFkB1_Homo                  325  5.92e-14 KTPKYKDINI TKPASVFVQLRRKSD
LETSEPKPFL
```

```
NFkB_Biomphalaria          365  1.18e-13 RTPSYHNTEI TRPAEVLMQLQRPSD
GETSEPIPFT
NFkBSer_Nev                351  3.04e-13 KTPPYWNIAI ERPANVLVELRRKKN
GGETSEPVQF
NFkBCys_Nev                351  3.04e-13 KTPPYWNIAI ERPANVLVELRRKKN
GGETSEPVQF
NFkB_Amphimedon            332  4.38e-13 QTPTFYNQAI EHPVQVWIALKRPSD
HETSEPKPFL
RelA_Homo                  263  7.49e-13 RTPPYADPSL QAPVRVSMQLRRPSD
RELSEPMEFQ
Relish_Dmel                418  8.93e-13 QTPPYKDKDV DREVNVYIELIRPSD
DERSFPALPF
Relish_Biomphalaria        329  2.10e-12 KTPAYWNTNI DKAVNVLIMLQRKSD
QEVSEPKAFT
NFkB_Hydra                 310  8.37e-12 RTPPYKHKVL DQPVKVKIELRAASD
HMRCSKHFDY
rel1[Ciona]                254  9.79e-12 RTPPFCNENI QEKVDVQFKLRRPSD
METSKPLVFT
NFkB2_Homo                 300  1.33e-11 RTPPYHKMKI ERPVTVFLQLKRKRG
GDVSDSKQFT
Dif_Dmel                   330  6.39e-11 KTPRYRNTEI TQSVNVELKLVRPSD
GATSAPLPFE
RelB_Homo                  372  2.98e-10 KTPPYEDLEI VEPVTVNVFLQRLTD
GVCSEPLPFT
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 15 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB_Corallimorph                 1.1e-18  347_[15]_553
NFkB_Acropora                     9.6e-18  342_[15]_547
NFkB_Platygyra                    2.9e-17  344_[15]_559
NFkBb_Aiptasia                    2.1e-16  346_[15]_487
Dorsal_Dmel                       5.3e-15  298_[15]_365
cRel                              6.7e-15  253_[15]_351
NFkB[Ciona                        2.1e-14  297_[15]_888
NFkB_Ed                           3.9e-14  351_[15]_494
NFkB1_Homo                        5.9e-14  324_[15]_630
NFkB_Biomphalaria                 1.2e-13  364_[15]_231
NFkBSer_Nev                         3e-13  350_[15]_75
NFkBCys_Nev                         3e-13  350_[15]_75
NFkB_Amphimedon                   4.4e-13  331_[15]_749
RelA_Homo                         7.5e-13  262_[15]_171
Relish_Dmel                       8.9e-13  417_[15]_539
Relish_Biomphalaria               2.1e-12  328_[15]_742
NFkB_Hydra                        8.4e-12  309_[15]_153
rel1[Ciona]                       9.8e-12  253_[15]_22
NFkB2_Homo                        1.3e-11  299_[15]_585
Dif_Dmel                          6.4e-11  329_[15]_323
```

```
RelB_Homo                          3e-10  371_[15]_193
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 15 in BLOCKS format
---------------------------------------------------------------------
BL   MOTIF 15 width=15 seqs=21
NFkB_Corallimorph         (  348) ERPVKVHIELRRKSD  1
NFkB_Acropora             (  343) ERPVKVHLELRRKSD  1
NFkB_Platygyra            (  345) ERPVKVQLELRRKSD  1
NFkBb_Aiptasia            (  347) ERPVEVLLELRRKSD  1
Dorsal_Dmel               (  299) TEPAKVFIQLRRPSD  1
cRel                      (  254) TEPVTVKMQLRRPSD  1
NFkB[Ciona                (  298) KMPVNVQVQLRRKSD  1
NFkB_Ed                   (  352) EKPAPVMLELRRKSD  1
NFkB1_Homo                (  325) TKPASVFVQLRRKSD  1
NFkB_Biomphalaria         (  365) TRPAEVLMQLQRPSD  1
NFkBSer_Nev               (  351) ERPANVLVELRRKKN  1
NFkBCys_Nev               (  351) ERPANVLVELRRKKN  1
NFkB_Amphimedon           (  332) EHPVQVWIALKRPSD  1
RelA_Homo                 (  263) QAPVRVSMQLRRPSD  1
Relish_Dmel               (  418) DREVNVYIELIRPSD  1
Relish_Biomphalaria       (  329) DKAVNVLIMLQRKSD  1
NFkB_Hydra                (  310) DQPVKVKIELRAASD  1
rel1[Ciona]               (  254) QEKVDVQFKLRRPSD  1
NFkB2_Homo                (  300) ERPVTVFLQLKRKRG  1
Dif_Dmel                  (  330) TQSVNVELKLVRPSD  1
RelB_Homo                 (  372) VEPVTVNVFLQRLTD  1
//

---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 15 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 15 n= 29844 bayes= 10.7769 E= 6.0e-
079
  -284   -611    139    286   -563   -427   -357   -459      5   -
472   -400   -336   -454     65   -331   -385    180    -54   -478
-448
   -45   -405   -289    155   -411   -368     76   -360    166   -
362     87   -248   -431     67    310   -301   -263   -353   -291
-297
   -61   -354   -349    -78   -383   -375   -338   -354    -49   -
360   -348   -372    345   -341   -305   -126   -288   -342   -354
-396
   198   -318   -632   -614   -464   -421   -603   -171   -602   -
382   -375   -560   -580   -622   -572   -389   -360    344   -493
-529
```

```
  -154   -325     -7     75   -301   -273   -156   -280    207   -
290   -210    214    -79     -6     30    -68    106   -267   -224
-210
  -492   -484   -693   -713   -543   -636   -661   -252   -686   -
464   -474   -704   -707   -750   -658   -688   -532    396   -543
-594
  -152   -307   -175      9    169   -276    155   -253    102
111     79     -1   -333    107   -121    -70   -167   -247    251
104
  -430   -394   -705   -632     56   -637   -552    264   -587
178    257   -623   -659   -578   -558   -607   -433    186   -309
-376
   -37   -401   -160    270     24   -335   -223   -337    101   -
349     83   -223   -385    225   -168   -265   -234   -320   -295
-282
  -595   -539   -704   -695   -380   -652   -613   -329   -652
353   -284   -701   -688   -652   -603   -713   -595   -432   -425
-501
  -372   -383   -472   -352   -504   -449   -254    -39    100   -
415   -365   -342   -493     83    396   -423   -369    -87   -278
-375
  -199   -285   -455   -452   -448   -424   -226   -383   -118   -
405   -377   -351   -430   -299    436   -420   -388   -476   -199
-369
   -49   -391   -416   -324   -464   -407   -310   -399    320    -
96   -362   -353    242   -284   -134   -356   -330   -389   -356
-390
  -192   -201   -341   -372   -337   -346   -326   -342     -9   -
381   -290   -200   -398   -358    -73    296     83   -384   -264
-294
  -328   -373    399   -107   -400   -211   -279   -385   -360   -
440   -383    -14   -519   -397   -365   -366   -379   -394   -295
-328
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
        Motif 15 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 15 nsites= 21 E= 6.0e-079
 0.000000  0.000000  0.142857  0.428571  0.000000  0.000000
0.000000  0.000000  0.047619  0.000000  0.000000  0.000000  0.000000
0.095238  0.000000  0.000000  0.238095  0.047619  0.000000  0.000000
 0.047619  0.000000  0.000000  0.190476  0.000000  0.000000
0.047619  0.000000  0.142857  0.000000  0.047619  0.000000  0.000000
0.095238  0.428571  0.000000  0.000000  0.000000  0.000000  0.000000
 0.047619  0.000000  0.000000  0.047619  0.000000  0.000000
0.000000  0.000000  0.047619  0.000000  0.000000  0.000000  0.809524
0.000000  0.000000  0.047619  0.000000  0.000000  0.000000  0.000000
 0.285714  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.714286  0.000000  0.000000
```

```
 0.000000  0.000000  0.047619  0.095238  0.000000  0.000000
0.000000  0.000000  0.238095  0.000000  0.000000  0.285714  0.047619
0.047619  0.047619  0.047619  0.142857  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.047619  0.142857  0.000000
0.095238  0.000000  0.095238  0.238095  0.047619  0.047619  0.000000
0.142857  0.000000  0.047619  0.000000  0.000000  0.047619  0.047619
 0.000000  0.000000  0.000000  0.000000  0.047619  0.000000
0.000000  0.285714  0.000000  0.285714  0.142857  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.238095  0.000000  0.000000
 0.047619  0.000000  0.000000  0.428571  0.047619  0.000000
0.000000  0.000000  0.095238  0.000000  0.047619  0.000000  0.000000
0.333333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.047619  0.095238  0.000000  0.000000  0.000000  0.000000
0.142857  0.666667  0.000000  0.000000  0.047619  0.000000  0.000000
 0.047619  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.952381  0.000000  0.000000  0.000000  0.000000  0.000000
 0.047619  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.523810  0.047619  0.000000  0.000000  0.380952
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.095238  0.000000  0.000000  0.000000  0.000000
0.000000  0.047619  0.809524  0.047619  0.000000  0.000000  0.000000
 0.000000  0.000000  0.857143  0.000000  0.000000  0.047619
0.000000  0.000000  0.000000  0.000000  0.000000  0.095238  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 15 regular expression
--------------------------------------------------------------------
[ET]RP[VA][NK]VL[ILV][EQ]LRR[KP]SD
--------------------------------------------------------------------




Time 972.32 secs.

********************************************************************
```

```
********************************************************************
MOTIF 16 MEME    width =  29  sites =   7  llr = 469  E-value =
6.1e-060
********************************************************************
--------------------------------------------------------------------
      Motif 16 Description
--------------------------------------------------------------------
Simplified        A  ::::::13::::::::::1::::::::9:
pos.-specific     C  :::::::::::::::::::::::::::::
probability       D  ::::::::::6::::4::::::::a::::
matrix            E  :a::::3:::4::::6:::::::::::::
                  F  ::::::::::::1:::1::::1:::::::
                  G  :::::71:::::::::::::a::::::::
                  H  ::::::::::::::3::::::::::::::
                  I  ::::3::::::::1:73:::::1::9:::
                  K  ::1::::::::::::::::::::::::::
                  L  :::1::::a:::39:::1::::9:::::a
                  M  ::::::::::::6:3::4:::::::::::
                  N  :::::1::::::::3:::1::::::::::
                  P  :::::::::::::::::::a:::a:::::
                  Q  ::79::::::::::::::1::::::::::
                  R  ::1:::::::::::1:::1::::::::::
                  S  a::::14::::a::::::1:::::::91:
                  T  :::::::7:a:::::::13::::::11::
                  V  ::::7:::::::::::1::::::::::::
                  W  :::::::::::::::::::::::::::::
                  Y  :::::::::::::::::::::9:::::::

         bits    7.3
                 6.6
                 5.9
                 5.1                      *
Relative         4.4  *       *           *  *
Entropy          3.7 ** *    ** **   *  *** ***  *
(96.7 bits)      2.9 ****** *********** **********
                 2.2 ****************** **********
                 1.5 *****************************
                 0.7 *****************************
                 0.0 -----------------------------

Multilevel           SEQQVGSTLTDSMLHEIMTPGYLPDISAL
consensus                I EA  E L MD I
sequence                           N


--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 16 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
NFkB_Ed                       4  1.63e-34        MTQ
SEQQVGSTLTESMLHEIMAPGYLPDISAL QMPLDAGASG
NFkBSer_Nev                   4  3.79e-32        MAQ
SEQQVGSALTESMLNEIIRPGYLPDISAL HVPLGTNAEE
NFkBCys_Nev                   4  6.41e-32        MAQ
SEQQVGSALTESMLNEIIQPGYLPDISAL HVPLGTNAEE
NFkB_Platygyra                5  1.21e-31       MATN
SERQIGETLTDSLLMDIMTPGYLPDISAL QMPPATYSGP
NFkBb_Aiptasia                4  1.37e-31        MTH
SEQQVGGTLTDSMLHEIMTPGFLPDISSL NVQMEMGYEG
NFkB_Acropora                 5  1.89e-28       MATN
SEQQVNATLTDSLLMDVLNPGYLPDISAL QVPTGSYQGP
NFkB_Corallimorph             5  1.44e-21       MATD
SEKLISETLTDSFIRDFTSPGYIPDTTAL IANLTGSYTG
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB_Ed                           1.6e-34  3_[16]_828
NFkBSer_Nev                       3.8e-32  3_[16]_408
NFkBCys_Nev                       6.4e-32  3_[16]_408
NFkB_Platygyra                    1.2e-31  4_[16]_885
NFkBb_Aiptasia                    1.4e-31  3_[16]_816
NFkB_Acropora                     1.9e-28  4_[16]_871
NFkB_Corallimorph                 1.4e-21  4_[16]_882
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 16 width=29 seqs=7
NFkB_Ed                  (    4) SEQQVGSTLTESMLHEIMAPGYLPDISAL  1
NFkBSer_Nev              (    4) SEQQVGSALTESMLNEIIRPGYLPDISAL  1
NFkBCys_Nev              (    4) SEQQVGSALTESMLNEIIQPGYLPDISAL  1
NFkB_Platygyra           (    5) SERQIGETLTDSLLMDIMTPGYLPDISAL  1
NFkBb_Aiptasia           (    4) SEQQVGGTLTDSMLHEIMTPGFLPDISSL  1
NFkB_Acropora            (    5) SEQQVNATLTDSLLMDVLNPGYLPDISAL  1
NFkB_Corallimorph        (    5) SEKLISETLTDSFIRDFTSPGYIPDTTAL  1
//

--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
       Motif 16 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 29 n= 29298 bayes= 11.8747 E= 6.1e-
060
  -197   -239   -380   -429   -386   -329   -383   -405   -352   -
439   -362   -272   -432   -436   -343    322    -40   -400   -305
-344
  -476   -543   -213    404   -567   -519   -461   -491   -511   -
599   -535   -432   -671   -413   -518   -571   -526   -540   -450
-521
  -240   -311   -327   -131   -384   -364    -66   -306    110   -
271   -178   -220   -380    349    109   -300   -252   -317   -192
-280
  -242   -286   -346   -104   -351   -414    -23   -297   -225   -
136   -139   -244   -366    378   -168   -322   -285   -326   -174
-313
  -171   -189   -439   -402   -252   -454   -398    234   -386   -
158   -159   -431   -465   -468   -371   -425   -214    340   -318
-348
  -180   -310   -220   -293   -403    354   -299   -400   -266   -
462   -357    -12   -429   -379   -273    -95   -320   -378   -250
-328
    98   -208   -112    196   -304     68   -169   -280    -92   -
299   -222   -117   -311   -156   -148    179   -126   -241   -231
-225
   172   -161   -375   -377   -352   -238   -356   -267   -322   -
368   -255   -259   -387   -359   -317   -110    344   -227   -280
-353
  -342   -305   -503   -433   -145   -481   -384    -82   -391
337    -33   -463   -473   -394   -351   -461   -341   -174   -203
-264
  -261   -268   -402   -434   -384   -395   -381   -290   -344   -
410   -285   -278   -467   -397   -346   -153    393   -285   -299
-376
  -211   -460    330    251   -456   -321   -260   -373   -164   -
397   -332   -161   -381   -160   -276   -298   -280   -341   -360
-350
  -197   -239   -380   -429   -386   -329   -383   -405   -352   -
439   -362   -272   -432   -436   -343    322    -40   -400   -305
-344
  -360   -310   -623   -550    183   -558   -438    -40   -503
184    441   -546   -556   -463   -459   -543   -362   -158   -168
-230
  -306   -268   -490   -403   -106   -480   -361    103   -363
321      8   -438   -452   -362   -323   -434   -302   -119   -174
-240
  -154   -257   -151   -105   -225   -246    340   -223     11   -
235    270    178   -319    -89    133   -182   -152   -222   -144
-92
```

```
  -193   -541    261    318   -502   -320   -269   -379   -137   -
394   -326   -212   -360   -129   -265   -294   -268   -335   -413
-376
  -273   -265   -404   -391     16   -441   -403    391   -332    -
35    -51   -371   -491   -420   -363   -384   -252    125   -230
-237
  -185   -172   -441   -365    -92   -370   -299    248   -315
102    378   -351   -424   -349   -303   -322     91    -26   -123
-164
    63   -222    -91    -25   -216   -192    -78   -187     15   -
206   -124     92   -252     80    117     47    180   -177   -139
-130
  -216   -351   -359   -338   -387   -367   -345   -370   -299   -
373   -366   -383    365   -359   -318   -316   -304   -358   -334
-389
  -217   -341   -289   -349   -430    371   -352   -431   -314   -
491   -389   -269   -461   -433   -309   -312   -372   -410   -271
-363
  -300   -267   -392   -368    226   -417    -77   -257   -331   -
245   -227   -327   -449   -366   -302   -350   -339   -288     63
496
  -306   -268   -490   -403   -106   -480   -361    103   -363
321      8   -438   -452   -362   -323   -434   -302   -119   -174
-240
  -216   -351   -359   -338   -387   -367   -345   -370   -299   -
373   -366   -383    365   -359   -318   -316   -304   -358   -334
-389
  -322   -363    404   -101   -391   -372   -277   -377   -358   -
431   -377   -108   -508   -393   -359   -367   -376   -387   -283
-321
  -262   -257   -413   -397   -215   -434   -411    398   -338    -
50    -66   -378   -494   -427   -369   -381    -18     84   -243
-249
  -139   -154   -305   -348   -296   -296   -302   -303   -246   -
346   -253   -164   -356   -347   -242    294    126   -339   -227
-258
   345    -75   -358   -317   -281   -163   -339   -244   -302   -
282   -207   -324   -425   -366   -295      3   -178   -128   -216
-301
  -342   -305   -503   -433   -145   -481   -384    -82   -391
337    -33   -463   -473   -394   -351   -461   -341   -174   -203
-264
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 29 nsites= 7 E= 6.1e-060
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.142857  0.000000  0.000000  0.000000  0.000000
0.714286  0.142857  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.142857  0.000000  0.000000  0.000000
0.857143  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.285714  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.714286  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.714286
0.000000  0.000000  0.000000  0.000000  0.000000  0.142857  0.000000
0.000000  0.000000  0.142857  0.000000  0.000000  0.000000  0.000000
 0.142857  0.000000  0.000000  0.285714  0.000000  0.142857
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.428571  0.000000  0.000000  0.000000  0.000000
 0.285714  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.714286  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.571429  0.428571  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.142857  0.000000
0.000000  0.000000  0.000000  0.285714  0.571429  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.142857  0.000000  0.857143  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.285714  0.000000  0.000000  0.000000  0.285714  0.285714  0.000000
0.000000  0.142857  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.428571  0.571429  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.142857  0.000000
0.000000  0.714286  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.142857  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.285714  0.000000  0.142857  0.428571  0.000000  0.000000
0.000000  0.000000  0.000000  0.142857  0.000000  0.000000  0.000000
```

```
 0.142857  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.142857  0.000000
0.142857  0.142857  0.142857  0.285714  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.142857  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.857143
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.142857  0.000000  0.857143  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.857143  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.142857  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.857143  0.142857  0.000000  0.000000  0.000000
 0.857143  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.142857  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 regular expression
--------------------------------------------------------------------
SEQQ[VI]G[SE][TA]LT[DE]S[ML]L[HMN][ED]I[MI]TPGYLPDISAL
--------------------------------------------------------------------




Time 1028.51 secs.

********************************************************************
```

```
*********************************************************************
MOTIF 17 MEME    width =  21  sites =    7  llr = 376  E-value =
1.8e-056
*********************************************************************
---------------------------------------------------------------------
      Motif 17 Description
---------------------------------------------------------------------
Simplified        A  ::::6::::::::::::::::
pos.-specific     C  ::1::::::a::::::a::::
probability       D  7:::1::::::::::::::::
matrix            E  1:::3::::::::::::::::
                  F  ::::::::::::::a::::::
                  G  :a::::::::::::::::::a
                  H  :::::::::::::::::::::
                  I  :::::3:::::::4:::::::
                  K  ::::::a:::a:6::::::::
                  L  ::1::3:a1::::::::::::
                  M  :::::1:::::::::::::::
                  N  1::::::::::::::::::::
                  P  :::a:::::::::::::::::
                  Q  ::3::::::::::::a:::::
                  R  ::4:::::::::4::::::::
                  S  ::::::::6::a:::::aaa:
                  T  :::::3::3::::::::::::
                  V  :::::::::::::6:::::::
                  W  :::::::::::::::::::::
                  Y  :::::::::::::::::::::

         bits    7.3
                 6.6
                 5.9          *      *
                 5.1          *    * *
Relative         4.4       *  **   ***
Entropy          3.7  * *  ** **** *******
(77.5 bits)      2.9 ***** ** ************
                 2.2 *********************
                 1.5 *********************
                 0.7 *********************
                 0.0 ---------------------

Multilevel           DGRPAIKLSCKSKVFQCSSSG
consensus              Q EL  T   RI
sequence                    T


---------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 17 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name            Start   P-value                    Site
-------------            ----- ---------            ---------------
NFATb_Platygyra            447  1.02e-25 LLFQAEIPEK
DGRPALKLSCKSKVFQCSSSG PPGNPEIWWA
NFATa_Platygyra            426  1.02e-25 LLFQAEIPEK
DGRPALKLSCKSKVFQCSSSG PPGNPEIWWA
NFAT_Ed                    364  7.56e-25 LLFQADIPAS
DGCPETKLSCKSRIFQCSSSG AAGSPEIWWA
NFAT_Nev                   658  2.47e-24 LLFQADIPAK
DGLPEMKLSCKSRIFQCSSSG ATGNPEIWWT
NFAT_Aiptasia              405  3.22e-24 LLFQAEIPGE
DGQPDIKLTCKSRIFQCSSSG PTGSPEIWWT
NFAT_Corallimorph          462  2.79e-23 LLFQTEIPES
NGQPAIKLTCKSKVFQCSSSG PPGNPEIWWA
NFAT_Acropora              423  1.23e-22 LLFQAEIPEQ
EGRPATKLLCKSKVFQCSSSG PPGNPEIWWA
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 17 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFATb_Platygyra                     1e-25  446_[17]_83
NFATa_Platygyra                     1e-25  425_[17]_83
NFAT_Ed                           7.6e-25  363_[17]_76
NFAT_Nev                          2.5e-24  657_[17]_243
NFAT_Aiptasia                     3.2e-24  404_[17]_253
NFAT_Corallimorph                 2.8e-23  461_[17]_56
NFAT_Acropora                     1.2e-22  422_[17]_236
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 17 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 17 width=21 seqs=7
NFATb_Platygyra         (  447) DGRPALKLSCKSKVFQCSSSG  1
NFATa_Platygyra         (  426) DGRPALKLSCKSKVFQCSSSG  1
NFAT_Ed                 (  364) DGCPETKLSCKSRIFQCSSSG  1
NFAT_Nev                (  658) DGLPEMKLSCKSRIFQCSSSG  1
NFAT_Aiptasia           (  405) DGQPDIKLTCKSRIFQCSSSG  1
NFAT_Corallimorph       (  462) NGQPAIKLTCKSKVFQCSSSG  1
NFAT_Acropora           (  423) EGRPATKLLCKSKVFQCSSSG  1
//

--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 17 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 21 n= 29610 bayes= 11.8899 E= 1.8e-
056
  -301   -350    396    -29   -376   -353   -256   -359   -331   -
415   -357    -30   -493   -365   -339   -343   -354   -368   -271
-305
  -217   -341   -289   -349   -430    371   -352   -431   -314   -
491   -389   -269   -461   -433   -309   -312   -372   -410   -271
-363
  -179    206   -252   -158   -267   -293   -138   -192     33
6   -167   -188   -350    158    330   -237   -185   -209   -162   -
198
  -216   -351   -359   -338   -387   -367   -345   -370   -299   -
373   -366   -383    365   -359   -318   -316   -304   -358   -334
-389
   253   -387    133    242   -425   -281   -235   -338   -114   -
354   -283   -187   -343   -121   -221   -244   -229   -289   -346
-323
  -180   -168   -429   -354    -89   -362   -289    250   -304
172    228   -340   -415   -339   -292   -309    175    -22   -117
-157
  -344   -350   -464   -410   -493   -457   -369   -360    423   -
456   -373   -358   -494   -411    -21   -465   -375   -449   -291
-404
  -342   -305   -503   -433   -145   -481   -384    -82   -391
337    -33   -463   -473   -394   -351   -461   -341   -174   -203
-264
  -142   -155   -302   -334   -285   -300   -294   -271   -237   -
126   -233   -163   -356   -334   -235    278    166   -303   -219
-251
  -365    577   -526   -483   -445   -536   -478   -382   -507   -
466   -382   -504   -591   -553   -453   -502   -392   -459   -427
-478
  -344   -350   -464   -410   -493   -457   -369   -360    423   -
456   -373   -358   -494   -411    -21   -465   -375   -449   -291
-404
  -197   -239   -380   -429   -386   -329   -383   -405   -352   -
439   -362   -272   -432   -436   -343    322    -40   -400   -305
-344
  -281   -350   -380   -240   -441   -368   -192   -325    365   -
336   -272   -248   -436   -161    265   -336   -271   -345   -239
-290
  -239   -221   -490   -458   -252   -496   -476    320   -426   -
127   -137   -459   -528   -512   -441   -462   -254    297   -335
-335
  -339   -240   -448   -438    471   -460   -374   -211   -423   -
163   -200   -441   -464   -497   -429   -386   -410   -272    -72
-7
```

```
  -277   -318   -372   -142   -393   -428    -62   -349   -262   -
293   -184   -279   -397    388   -205   -356   -321   -370   -207
-345
  -365    577   -526   -483   -445   -536   -478   -382   -507   -
466   -382   -504   -591   -553   -453   -502   -392   -459   -427
-478
  -197   -239   -380   -429   -386   -329   -383   -405   -352   -
439   -362   -272   -432   -436   -343    322    -40   -400   -305
-344
  -197   -239   -380   -429   -386   -329   -383   -405   -352   -
439   -362   -272   -432   -436   -343    322    -40   -400   -305
-344
  -197   -239   -380   -429   -386   -329   -383   -405   -352   -
439   -362   -272   -432   -436   -343    322    -40   -400   -305
-344
  -217   -341   -289   -349   -430    371   -352   -431   -314   -
491   -389   -269   -461   -433   -309   -312   -372   -410   -271
-363
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 17 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 21 nsites= 7 E= 1.8e-056
 0.000000  0.000000  0.714286  0.142857  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.142857  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.142857  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.142857  0.000000  0.000000  0.000000
0.285714  0.428571  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.571429  0.000000  0.142857  0.285714  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.285714  0.000000  0.285714  0.142857  0.000000  0.000000
0.000000  0.000000  0.000000  0.285714  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.142857  0.000000  0.000000  0.000000
0.000000  0.000000  0.571429  0.285714  0.000000  0.000000  0.000000
```

```
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.571429  0.000000  0.000000  0.000000  0.000000
0.000000  0.428571  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.428571  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.571429  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 17 regular expression
--------------------------------------------------------------------
DG[RQ]P[AE][ILT]KL[ST]CKS[KR][VI]FQCSSSG
--------------------------------------------------------------------




Time 1084.25 secs.

********************************************************************
```

```
*********************************************************************
MOTIF 18 MEME    width =  29  sites =   6  llr = 427  E-value =
4.2e-056
*********************************************************************

---------------------------------------------------------------------
      Motif 18 Description
---------------------------------------------------------------------
Simplified        A  ::2::272:::7:::::::5:::3::::2
pos.-specific     C  ::::::::::a::::::::::::::::::
probability       D  :2:::::::a::::::::::a::::::::
matrix            E  :5::2:::::::::::::::::a::::7:
                  F  2::::::::::::::::::::::::::::
                  G  ::::::::::::a:::::::::::::a::
                  H  :::::::::::::::::::::::::::::
                  I  :::::22:7::::a:::::::7:::3:3:
                  K  :2:::::::::::::a:::::::::7:::
                  L  ::::::2:::::::a:a::::::7:::::
                  M  ::::8::::::::::::::::::::::::
                  N  ::87:::2::::::::::a::::::::::
                  P  8::::::::::::::::::::::::::::
                  Q  :::2:::::::::::::::::::::::::
                  R  :::::3:::::::::::a::::::a::::
                  S  :2:2:2:3:::::::::::5::::::::2
                  T  :::::2:2::::::::::::::::::::7
                  V  :::::::23::3:::::::::3:::::::
                  W  :::::::::::::::::::::::::::::
                  Y  :::::::::::::::::::::::::::::

         bits    7.3
                 6.6
                 5.9           *
                 5.1           *
Relative         4.4     *    **  * * ** * * *
Entropy          3.7 * * *   *** ******* *** ****
(102.7 bits)     2.9 * *** * *********************
                 2.2 ******* *********************
                 1.5 *****************************
                 0.7 *****************************
                 0.0 -----------------------------

Multilevel           PENNMRASIDCAGILKLRNADIELRKGET
consensus                    V  V       S V A I I
sequence


---------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 18 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name            Start   P-value                 Site
-------------            ----- ---------            ---------------
NFAT1                      485  5.96e-36 NTKVLEIPLE
PKNNMRATIDCAGILKLRNADIELRKGET DIGRKNTRVR
NFAT4                      527  1.14e-35 STKVLEIPLL
PENNMSASIDCAGILKLRNSDIELRKGET DIGRKNTRVR
NFAT3                      443  4.80e-35 GTKVLEMTLL
PENNMAANIDCAGILKLRNSDIELRKGET DIGRKNTRVR
NFAT2                       51  3.66e-33 NTKVLEIPLL
PENSMRAVIDCAGILKLRNSDIELRKGET DIGRKNTRVR
NFAT5                      374  5.19e-28 GTTVIEVGLD
PSNNMTLAVDCVGILKLRNADVEARIGIA GSKKKSTRAR
NFat?                       80  1.89e-23 VEGTKVIHIP
FDAQEIISVDCVGILKLRNADVEARIGIS RAKKRSQTVR
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 18 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFAT1                               6e-36  484_[18]_392
NFAT4                             1.1e-35  526_[18]_520
NFAT3                             4.8e-35  442_[18]_361
NFAT2                             3.7e-33  50_[18]_274
NFAT5                             5.2e-28  373_[18]_1129
NFat?                             1.9e-23  79_[18]_985
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 18 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 18 width=29 seqs=6
NFAT1                    (  485) PKNNMRATIDCAGILKLRNADIELRKGET  1
NFAT4                    (  527) PENNMSASIDCAGILKLRNSDIELRKGET  1
NFAT3                    (  443) PENNMAANIDCAGILKLRNSDIELRKGET  1
NFAT2                    (   51) PENSMRAVIDCAGILKLRNSDIELRKGET  1
NFAT5                    (  374) PSNNMTLAVDCVGILKLRNADVEARIGIA  1
NFat?                    (   80) FDAQEIISVDCVGILKLRNADVEARIGIS  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 18 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 29 n= 29298 bayes= 11.9121 E= 4.2e-
056
```

```
  -137   -285   -288   -260    100   -308   -267   -279   -221   -
284   -274   -308    342   -280   -244   -238   -226   -273   -246
-241
  -134   -373    141    287   -348   -246   -166   -292    138   -
303   -229   -126   -304    -91   -142     31   -174   -264   -268
-243
   -79   -278   -182   -326   -333   -297   -105   -282   -252   -
387   -311    402   -412   -293   -289   -197   -230   -339   -210
-277
  -291   -295   -148   -270   -329   -282    -95   -283   -211   -
380   -304    394   -400    -63   -256    -82   -220   -344   -208
-263
  -391   -339   -428   -171   -345   -489   -438   -215   -382   -
197    529   -454   -534   -455   -431   -468   -398   -299   -204
-273
    91   -154   -140    -70   -153   -202   -107    118    -21   -
136    -71   -109   -267   -105    210     51    129    -88   -106
-113
   311    -93   -367   -309   -164   -214   -306    119   -279
33    -84   -325   -431   -343   -278   -159   -175    -32   -160
-214
    69   -150   -205   -165   -228   -235   -189   -174   -118   -
231   -152     56   -314   -196   -151    203    163     25   -171
-189
  -267   -250   -420   -405   -218   -454   -428    385   -349    -
50    -67   -387   -503   -441   -383   -400   -252    179   -256
-259
  -315   -357    403    -94   -385   -366   -270   -371   -350   -
425   -370   -102   -502   -386   -353   -360   -370   -381   -277
-315
  -364    577   -525   -482   -444   -535   -477   -381   -506   -
465   -381   -503   -590   -552   -452   -501   -391   -457   -426
-477
   320    -88   -371   -323   -255   -183   -342   -108   -306   -
227   -177   -332   -419   -368   -301   -134   -176    159   -217
-284
  -206   -330   -278   -338   -420    370   -341   -420   -303   -
480   -378   -258   -451   -422   -298   -301   -361   -399   -261
-352
  -290   -277   -430   -420   -223   -452   -429    412   -362    -
63    -80   -401   -509   -450   -391   -413   -277     66   -254
-261
  -324   -288   -487   -415   -128   -468   -368    -65   -372
335    -16   -446   -458   -377   -333   -443   -323   -156   -187
-247
  -340   -347   -459   -404   -489   -453   -364   -357    423   -
452   -369   -354   -491   -404    -18   -460   -371   -445   -288
-400
  -324   -288   -487   -415   -128   -468   -368    -65   -372
335    -16   -446   -458   -377   -333   -443   -323   -156   -187
-247
```

```
  -337   -270   -432   -426   -426   -403   -208   -365    -98   -
385   -358   -332   -412   -279    436   -403   -369   -456   -181
-346
  -349   -311   -210   -380   -343   -342   -113   -293   -281   -
403   -328    411   -435   -316   -314   -224   -258   -367   -215
-289
   281   -114   -371   -356   -348   -171   -362   -323   -346   -
363   -283   -302   -365   -373   -329    206   -149   -214   -278
-348
  -315   -357    403    -94   -385   -366   -270   -371   -350   -
425   -370   -102   -502   -386   -353   -360   -370   -381   -277
-315
  -267   -250   -420   -405   -218   -454   -428    385   -349    -
50    -67   -387   -503   -441   -383   -400   -252    179   -256
-259
  -472   -541   -211    404   -566   -516   -459   -490   -504   -
597   -533   -429   -667   -410   -515   -567   -523   -538   -449
-519
   160   -205   -435   -364   -124   -334   -337    -41   -324
287    -26   -374   -419   -354   -307   -296   -233   -103   -171
-220
  -337   -270   -432   -426   -426   -403   -208   -365    -98   -
385   -358   -332   -412   -279    436   -403   -369   -456   -181
-346
  -253   -295   -352   -248   -321   -368   -231    178    380   -
257   -219   -265   -432   -214     -2   -336   -260   -191   -228
-264
  -206   -330   -278   -338   -420    370   -341   -420   -303   -
480   -378   -258   -451   -422   -298   -301   -361   -399   -261
-352
  -208   -352    -84    345   -326   -348   -286    205   -165   -
260   -231   -266   -396   -181   -252   -317   -261   -166   -308
-301
    53   -163   -322   -337   -311   -286   -303   -213   -255   -
334   -195   -188   -380   -304   -260     66    343   -198   -234
-311
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 18 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 29 nsites= 6 E= 4.2e-056
 0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.833333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.166667  0.500000  0.000000  0.000000
0.000000  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.833333  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.666667  0.000000
0.166667  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.833333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.166667  0.166667  0.000000  0.000000  0.000000
 0.666667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.333333  0.166667  0.166667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.666667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.666667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.666667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.666667  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
0.000000  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.666667  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 18 regular expression
--------------------------------------------------------------------
PENNMRAS[IV]DC[AV]GILKLRN[AS]D[IV]E[LA]R[KI]G[EI]T
--------------------------------------------------------------------




Time 1139.69 secs.

********************************************************************


********************************************************************
MOTIF 19 MEME    width =  31  sites =  12  llr = 609  E-value =
3.9e-050
********************************************************************
--------------------------------------------------------------------
      Motif 19 Description
--------------------------------------------------------------------
Simplified        A  152::::2::::1::21::::::::::11:
```

```
pos.-specific     C  ::1::1::::1::::::::::::::2:::::
probability       D  :::::::::::3:1:::1::::::::2:12:
matrix            E  :::::3::2:::::::1::::::3:1::111
                  F  :::11::::22:::::1:::::3:::11:::
                  G  3:1::::::::::::::1:::1:::::6121
                  H  13::::::::4::3::::11:1::::1::::
                  I  ::213:2:::::::8:::2:1:4:221::::
                  K  :::::2::::::2:::1::2::::::::316
                  L  ::3:321:::::1:121:::::1:22:::::
                  M  :11:::1::::::::1::1::::::::::::
                  N  3::::::::::5:2:::::1:4::::322:1
                  P  :::::::a6:::3::::8:1:::::::::::
                  Q  ::::::::1::131:::::2:1:1:::::::
                  R  :::::1::::2::2:11::1:1:::1::142
                  S  11::::::::2::::13::2:1:1:12:2::
                  T  :1:1:23::::122:51::2::::::12:::
                  V  1:184:4:::::::21::7:9:2:73:::::
                  W  :::::::::::::::::::::::::::::::
                  Y  2::::::::8:::::::::::2:5:::::::

         bits    7.3
                 6.6
                 5.9
                 5.1
Relative         4.4          *
Entropy          3.7        * *          *
(73.2 bits)      2.9    *   * ***  *  ** * ***
                 2.2  * ** ******* ** ** *****  * **
                 1.5 *******************************
                 0.7 *******************************
                 0.0 -------------------------------

Multilevel           GALVVEVPPYHNQHITSPVxVNIYVVNGKRK
consensus            NH  I T    DP         FE
sequence                 L


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                  Site
-------------             ----- ---------            ---------------
NFAT2                       182  1.76e-27 AKTDRDLCKP
NSLVVEIPPFRNQRITSPVHVSFYVCNGKRK RSQYQRFTYL
NFAT1                       616  3.09e-26 ATVDKDKSQP
NMLFVEIPEYRNKHIRTPVKVNFYVINGKRK RSQPQHFTYH
NFAT4                       658  4.42e-26 GKIIREKCQG
AHIVLEVPPYHNPAVTAAVQVHFYLCNGKRK KSQSQRFTYT
```

```
NFAT5                       502  2.06e-24 AEIDMELFHQ
NHLIVKVPPYHDQHITLPVSVGIYVVTNAGR SHDVQPFTYT
NFAT_Aiptasia               487  3.79e-23 AEVDKSKTHQ
GAAVILTPPYSNQDILFPVKVNIELVSGNAK NGKCSEPIEF
NFat?                       214  1.13e-22 GQLDKDTFNQ
SHMVVRVPAYHDPTITKPINVQVYVEHNGRK CDPHSFTYDP
NFAT_Acropora               504  3.60e-22 AEVDKSKSHQ
GAAVVLTPAYCDTQITSPITVNVEVVFGNGR DSKSSEPIEF
NFkB_Capsaspora             471  7.55e-21 PGANLFFHHQ
YAVVLTLPPYHTQTITAPVTVRISILDTDDE TESQYVEYTY
NFAT_Hydra                 1364  9.02e-21 ADIDRNKSSL
HACVFKVPPYFQTHLVSDVSVYIEVRIGSEK EPRISEPVQF
NFAT3                       574  9.02e-21 ATVNRLQSNE
VTLTLTVPEYSNKRVSRPVQVYFYVSNGRRK RSPTQSFRFL
NFAT_Nev                    740  1.51e-18 VDCDKNKSHQ
GAGVICTPPFFDLNIMSPMRVNLEVLSTSKN AKCSDPVEFT
NFkB_Sphaeroforma_arctic    405  4.90e-18 PLRIIQFHHQ
YAIVIEMPQYHNPNILEGHPINIQIIDFEDG TESAPARYTY
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFAT2                             1.8e-27  181_[19]_141
NFAT1                             3.1e-26  615_[19]_259
NFAT4                             4.4e-26  657_[19]_387
NFAT5                             2.1e-24  501_[19]_999
NFAT_Aiptasia                     3.8e-23  486_[19]_161
NFat?                             1.1e-22  213_[19]_849
NFAT_Acropora                     3.6e-22  503_[19]_145
NFkB_Capsaspora                   7.5e-21  470_[19]_722
NFAT_Hydra                          9e-21  1363_[19]_581
NFAT3                               9e-21  573_[19]_228
NFAT_Nev                          1.5e-18  739_[19]_151
NFkB_Sphaeroforma_arctic          4.9e-18  404_[19]_14
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 19 width=31 seqs=12
NFAT2                    (  182) NSLVVEIPPFRNQRITSPVHVSFYVCNGKRK  1
NFAT1                    (  616) NMLFVEIPEYRNKHIRTPVKVNFYVINGKRK  1
NFAT4                    (  658) AHIVLEVPPYHNPAVTAAVQVHFYLCNGKRK  1
NFAT5                    (  502) NHLIVKVPPYHDQHITLPVSVGIYVVTNAGR  1
NFAT_Aiptasia            (  487) GAAVILTPPYSNQDILFPVKVNIELVSGNAK  1
NFat?                    (  214) SHMVVRVPAYHDPTITKPINVQVYVEHNGRK  1
NFAT_Acropora            (  504) GAAVVLTPAYCDTQITSPITVNVEVVFGNGR  1
NFkB_Capsaspora          (  471) YAVVLTLPPYHTQTITAPVTVRISILDTDDE  1
NFAT_Hydra               ( 1364) HACVFKVPPYFQTHLVSDVSVYIEVRIGSEK  1
```

```
NFAT3                    (  574) VTLTLTVPEYSNKRVSRPVQVYFYVSNGRRK  1
NFAT_Nev                 (  740) GAGVICTPPFFDLNIMSPMRVNLEVLSTSKN  1
NFkB_Sphaeroforma_arctic (  405) YAIVIEMPQYHNPNILEGHPINIQIIDFEDG  1
//

--------------------------------------------------------------------
--------------------------------------------------------------------
     Motif 19 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 31 n= 29220 bayes= 10.9079 E= 3.9e-
050
   27   -255   -129    -88   -205    136    130   -194    -55   -
228   -159    187   -309   -133   -107    -17   -138     16   -171
239
  291   -135   -302   -246   -268   -213    247   -209   -212   -
258    122   -271   -404   -286   -239    -26     13   -155   -215
-259
  101    184   -396   -316   -109    -13   -246    181   -266
175    169   -298   -380   -309   -253   -263   -143     75    -99
-127
 -101   -159   -361   -324    -39   -390   -304     80   -313   -
192   -173   -369   -389   -392   -281   -358    -60    355   -259
-333
 -315   -285   -578   -521    114   -533   -476    255   -478
151   -111   -509   -571   -511   -471   -495   -319    259   -272
-313
 -129    168   -153    209   -263   -249   -124   -224    168
54   -168   -132   -308   -108     96   -174    115   -219   -183
-177
 -211   -204   -476   -409   -192   -417   -356    193   -366
16    165   -398   -471   -416   -356   -370    175    266   -208
-236
 -340   -457   -472   -460   -497   -469   -455   -492   -421   -
491   -488   -499    373   -479   -434   -438   -425   -481   -424
-493
   57   -324   -251     76   -353   -334   -293   -319   -224   -
326   -309   -317    317    -26   -261   -262   -249   -305   -319
-355
 -437   -371   -515   -499    238   -524   -177   -359   -449   -
337   -328   -420   -561   -458   -406   -470   -451   -394     -2
505
 -248    119   -246   -243    134   -337    429   -262   -202   -
265   -201   -125   -391   -125    106     -7   -234   -264   -111
-8
 -297   -402    247   -187   -453   -225   -198   -500   -216   -
512   -466    314   -423     37   -294   -218     40   -489   -385
-317
 -156   -304   -185   -104   -296   -274   -145   -252    173   -
29   -195   -159    142    209    -42   -203    116   -247   -206
-205
```

```
    25   -279     48    -58   -255   -223    277   -240    -23   -
249   -170    133   -291     45    154   -151    111   -228   -178
-156
  -293   -289   -409   -400   -227   -455   -421    395   -339      -
8    -63   -379   -505   -432   -375   -396   -269    127   -249   -
255
  -184   -181   -350   -321   -204   -357   -278   -102   -248
44    129   -227   -403   -303     29    -12    310     23   -171
-214
    94   -259   -121     62     71   -222   -106   -212     94   -
35   -150   -105   -280    -94     80    138     42   -203   -166
-154
   -17   -311    -28   -277   -344    -63   -297   -315   -241   -
321   -309   -323    338   -301   -266   -257   -247   -302   -314
-355
   -97   -154   -357   -319   -234   -382    -23    111   -305   -
182     21   -361   -383   -383   -275   -348   -158    350   -242
-312
  -102   -272   -119    -47   -248   -222    125   -226    160   -
236   -156     56    -25    117     85     52    112   -214   -170
-157
  -167   -205   -432   -396   -286   -457   -384    109   -384   -
206   -201   -435   -459   -466   -359   -428   -221    368   -330
-383
  -155   -303   -117    -97   -287    -10    128   -273    -59   -
290   -213    281   -323     33     70    -23   -157   -268   -210
224
  -329   -292   -605   -544    307   -552   -496    313   -503
36   -118   -531   -589   -530   -495   -518   -332    150   -282
-321
  -211   -384   -101    239   -189   -307   -196   -338   -128   -
349   -286   -181   -382     41   -198    -32   -247   -323   -215
407
  -258   -258   -534   -494   -286   -537   -491    193   -476
79   -192   -515   -553   -549   -466   -510   -291    334   -371
-398
  -133    274   -372     10   -111   -309   -237    182   -245
90    -36   -285   -374   -295     54    -40   -139    186    -98
-126
  -148   -281    112    -99     64   -237    115     34    -66   -
265   -190    271   -320   -142   -120     40     24   -236   -193
-187
  -204   -320   -196   -285     44    324   -282   -401   -271   -
455   -372    103   -440   -361   -299   -257     70   -381   -285
-313
    29   -275     48     66   -251     -8   -105   -231    201   -
241   -161    132   -282    -94     83     53   -117   -218   -174
-160
    24   -310    131     77   -291     81   -134   -265     97   -
274   -196   -119   -313   -116    278   -176   -151   -251   -209
-195
```

```
  -270   -368   -295      4   -426    -39   -217   -344    364   -
362   -292     18   -433   -197    161   -314   -270   -359   -268
-301
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 31 nsites= 12 E= 3.9e-050
 0.083333  0.000000  0.000000  0.000000  0.000000  0.250000
0.083333  0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.083333  0.000000  0.083333  0.000000  0.166667
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.000000  0.000000  0.083333  0.000000  0.000000
0.000000  0.000000  0.083333  0.083333  0.000000  0.000000  0.000000
 0.166667  0.083333  0.000000  0.000000  0.000000  0.083333
0.000000  0.166667  0.000000  0.333333  0.083333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.083333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.083333  0.000000
0.000000  0.083333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.083333  0.750000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.083333  0.000000
0.000000  0.250000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.416667  0.000000  0.000000
 0.000000  0.083333  0.000000  0.333333  0.000000  0.000000
0.000000  0.000000  0.166667  0.166667  0.000000  0.000000  0.000000
0.000000  0.083333  0.000000  0.166667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.083333  0.083333  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.416667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.583333
0.083333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.833333
 0.000000  0.083333  0.000000  0.000000  0.166667  0.000000
0.416667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.166667  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.333333  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.083333  0.000000  0.000000  0.083333  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.083333  0.000000  0.000000  0.250000
0.333333  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
 0.083333  0.000000  0.083333  0.000000  0.000000  0.000000
0.250000  0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.083333  0.166667  0.000000  0.166667  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.750000  0.000000  0.083333  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.166667  0.083333  0.000000  0.000000
0.000000  0.083333  0.083333  0.500000  0.083333  0.000000  0.000000
 0.166667  0.000000  0.000000  0.083333  0.083333  0.000000
0.000000  0.000000  0.083333  0.083333  0.000000  0.000000  0.000000
0.000000  0.083333  0.333333  0.083333  0.000000  0.000000  0.000000
 0.083333  0.000000  0.083333  0.000000  0.000000  0.083333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.750000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.083333  0.166667  0.000000  0.000000  0.083333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.083333  0.000000  0.166667  0.000000  0.000000  0.083333  0.083333
0.166667  0.083333  0.166667  0.166667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.083333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.916667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.083333
0.083333  0.000000  0.000000  0.000000  0.000000  0.416667  0.000000
0.083333  0.083333  0.083333  0.000000  0.000000  0.000000  0.166667
 0.000000  0.000000  0.000000  0.000000  0.333333  0.000000
0.000000  0.416667  0.000000  0.083333  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.083333  0.000000  0.083333  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
 0.000000  0.166667  0.000000  0.083333  0.000000  0.000000
0.000000  0.166667  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.083333  0.083333  0.000000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.166667  0.000000  0.083333  0.000000
0.083333  0.083333  0.000000  0.000000  0.000000  0.333333  0.000000
0.000000  0.000000  0.166667  0.083333  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.083333  0.583333
0.000000  0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
 0.083333  0.000000  0.083333  0.083333  0.000000  0.083333
0.000000  0.000000  0.250000  0.000000  0.000000  0.166667  0.000000
0.000000  0.083333  0.166667  0.000000  0.000000  0.000000  0.000000
 0.083333  0.000000  0.166667  0.083333  0.000000  0.166667
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
0.000000  0.416667  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.083333  0.000000  0.083333
0.000000  0.000000  0.583333  0.000000  0.000000  0.083333  0.000000
0.000000  0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
--------------------------------------------------------------------
--------------------------------------------------------------------
      Motif 19 regular expression
--------------------------------------------------------------------
[GN][AH]LV[VIL]E[VT]PPYH[ND][QP]HITSPVxVN[IF][YE]VVNGKRK
--------------------------------------------------------------------




Time 1195.40 secs.

********************************************************************


********************************************************************
MOTIF 20 MEME    width =  39  sites =   6  llr = 514  E-value =
1.5e-047
********************************************************************
--------------------------------------------------------------------
      Motif 20 Description
--------------------------------------------------------------------
Simplified        A  :::::aa:2::::22a:::a8:a:::3:::::2:2:::a
pos.-specific     C  ::::::::::::::2:::::::::2::::2:::::::::
probability       D  ::::::::::2::::::::::::7::::2::52:::7::
matrix            E  :::::::::::322:::::::::::::::2735::::2:
                  F  ::::2:::::::::::::::::::::2::2:::2:5:::
                  G  :::::::8:8::7::::::::a:::::::::2:::::::
                  H  :::a:::::::::2::::::::::::::::2::::::::
                  I  :::::::::::::::::::::::::::::::::2:::::
                  K  :::::::::::5:::::::::::::::2:::::::::::
                  L  ::a:5:::3:7:::::7a3:2:::::5::::::::2:7:
                  M  ::::::::::2::2:::::::::::2:::::::::::::
                  N  :::::::::2:::::::::::::2::::8::::::::::
                  P  :a::::::::::::::::::::::2::3::::::8::::
                  Q  :::::::::::::3:::::::::::::2::::2::::::
                  R  ::::::::5::::::::::::::::::::2:::::::::
                  S  :::::::2::::2::::::::::::::::3::::::3::
                  T  a:::::::::::::7:::::::::77:3::2::7:::::
                  V  ::::3::::::2::::3:7::::2:2:::::::::::::
                  W  :::::::::::::::::::::::::::::::::::::::
                  Y  :::::::::::::::::::::::::::::::::::3:2:

         bits    7.3
                 6.6
                 5.9
                 5.1    *
Relative         4.4 *  *
Entropy          3.7 **** **        * * * **      *      *  *
(123.6 bits)     2.9 **** *******  ************  * ** ******
```

```
                 2.2 ***************************************
                 1.5 ***************************************
                 0.7 ***************************************
                 0.0 ---------------------------------------

Multilevel           TPLHLAAGRGLKGQTALLVAAGADTTLPNSEDETPFDLA
consensus                V   L  E    V L       AT   E   YS
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
NFkB_Corallimorph           684  1.78e-43 DVNAVTLDGN
TPLHVAAGRGLKGQTALLVAAGADTTLQNCEEEIPFDLA NVAEVQEILD
NFkB_Acropora               681  8.93e-41 DVDASTFDGN
TPLHLAAGLGLKGHTALLVAAGADTTFPNSEDDTAFDLA NVAEVQEILD
NFkB_Ed                     693  1.24e-40 DVNVTTYDSH
TPLHVAAGRGLEGQTAVLVAAGAVTTATNEEDETPYDLA ATDQIRQLLD
NFkBb_Aiptasia              688  2.98e-39 DVDSLTYDDN
TPLHLAAGLGLVGETALLVAAGADTMATNSEDETPYSLA TTAEVKKILG
IkB_Nev                     330  5.86e-32 CVDAETFDEC
TPLHFAAGRGMESMAALLLAAGADPTLPNRTGATPLDEA ADNVRPMLQL
IkB_Hym                     252  1.39e-25 DVNSLNNCDV
TPLHLAASANDKEACAVLLALGANCVLKDFHEQFPFSYA TDDEIKEKLR
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB_Corallimorph                 1.8e-43  683_[20]_193
NFkB_Acropora                     8.9e-41  680_[20]_185
NFkB_Ed                           1.2e-40  692_[20]_129
NFkBb_Aiptasia                      3e-39  687_[20]_122
IkB_Nev                           5.9e-32  329_[20]_15
IkB_Hym                           1.4e-25  251_[20]_14
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 20 width=39 seqs=6
NFkB_Corallimorph        (  684)
TPLHVAAGRGLKGQTALLVAAGADTTLQNCEEEIPFDLA  1
```

```
NFkB_Acropora            (  681)
TPLHLAAGLGLKGHTALLVAAGADTTFPNSEDDTAFDLA  1
NFkB_Ed                  (  693)
TPLHVAAGRGLEGQTAVLVAAGAVTTATNEEDETPYDLA  1
NFkBb_Aiptasia           (  688)
TPLHLAAGLGLVGETALLVAAGADTMATNSEDETPYSLA  1
IkB_Nev                  (  330)
TPLHFAAGRGMESMAALLLAAGADPTLPNRTGATPLDEA  1
IkB_Hym                  (  252)
TPLHLAASANDKEACAVLLALGANCVLKDFHEQFPFSYA  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 39 n= 28908 bayes= 12.6815 E= 1.5e-
047
  -234   -242   -374   -403   -357   -372   -354   -259   -314   -
381   -255   -249   -443   -368   -317   -123    389   -255   -274
-349
  -192   -329   -336   -313   -365   -346   -322   -346   -275   -
350   -341   -359    362   -335   -295   -292   -280   -334   -314
-367
  -324   -288   -487   -415   -128   -468   -368    -65   -372
335    -16   -446   -458   -377   -333   -443   -323   -156   -187
-247
  -383   -328   -318   -361   -250   -400    506   -422   -375   -
368   -307   -181   -451   -182   -218   -355   -339   -408   -175
-72
  -252   -224   -494   -414    178   -441   -345      9   -370
259      8   -417   -459   -377   -341   -400   -254    190   -142
-184
   362   -114   -385   -350   -312   -196   -366   -273   -336   -
315   -246   -354   -439   -396   -326   -150   -211   -167   -244
-326
   362   -114   -385   -350   -312   -196   -366   -273   -336   -
315   -246   -354   -439   -396   -326   -150   -211   -167   -244
-326
  -166   -294   -251   -311   -400    361   -318   -394   -278   -
458   -351   -228   -428   -395   -275    -91   -321   -366   -245
-333
    68   -198   -262   -173   -197   -273   -159   -114      0
131   -109   -201   -342   -156    330   -222   -165   -140   -140
-173
  -181   -312   -237   -302   -400    361   -309   -396   -270   -
461   -353    -23   -431   -389   -271   -270   -332   -376   -243
-328
```

```
  -265   -241    -38   -332   -102   -426   -312    -33   -300
312    149   -376   -409   -315   -272   -374   -262   -115   -154
-211
  -134   -311    -74    222   -304   -255   -135   -237    287   -
256   -186   -143   -307    -83    -20   -195   -158     76   -205
-204
  -170   -302   -209    -31   -392    351   -287   -385   -245   -
443   -341   -190   -416   -349   -257    -84   -304   -362   -243
-317
   -11   -255   -167     49   -272   -273    120   -234    -65   -
219    102   -141   -297    319    -88   -192   -160   -235   -149
-194
    95    250   -358   -363   -310   -237   -326   -218   -292   -
323   -209   -228   -371   -329   -287    -77    337   -192   -244
-315
   362   -114   -385   -350   -312   -196   -366   -273   -336   -
315   -246   -354   -439   -396   -326   -150   -211   -167   -244
-326
  -271   -237   -505   -428   -114   -470   -385     17   -386
288    -12   -444   -476   -398   -359   -432   -274    188   -186
-239
  -324   -288   -487   -415   -128   -468   -368    -65   -372
335    -16   -446   -458   -377   -333   -443   -323   -156   -187
-247
  -204   -200   -476   -425   -160   -452   -397     57   -394
164    -73   -436   -481   -446   -382   -421   -231    321   -231
-269
   362   -114   -385   -350   -312   -196   -366   -273   -336   -
315   -246   -354   -439   -396   -326   -150   -211   -167   -244
-326
   340    -69   -346   -296   -235   -165   -319   -173   -276    -
33   -160   -319   -434   -349   -274   -111   -177    -96   -189
-265
  -206   -330   -278   -338   -420    370   -341   -420   -303   -
480   -378   -258   -451   -422   -298   -301   -361   -399   -261
-352
   362   -114   -385   -350   -312   -196   -366   -273   -336   -
315   -246   -354   -439   -396   -326   -150   -211   -167   -244
-326
  -295   -345    395    -77   -371   -345   -250   -353   -319   -
408   -351    -23   -486   -359   -330   -334   -344   -168   -267
-299
  -121    221   -324   -334   -293   -282   -298   -195   -252   -
307   -185   -194     22   -302   -259    -59    342   -183   -226
-295
  -170   -163   -334   -326   -207   -348   -282    -62   -243   -
176    180   -199   -392   -296   -249    -78    336     75   -180
-232
   158   -189   -429   -352    174   -365   -288     -6   -306
254      9   -353   -414   -331   -289   -318   -209    -72   -111
-130
```

```
   -96   -248   -126    -54   -247   -220   -108   -210    141   -
225   -156   -110    198     85    -27   -140    169   -201   -168
-167
  -320   -301    -28   -302   -336   -294    -97   -288   -246   -
395   -319    402   -413   -285   -290   -197   -233   -358   -211
-273
   -55    208   -100     99    129   -188    -74   -123      8   -
159    -89    -77   -247    -74    123    131    -39   -127   -105
-38
  -197   -389    -74    355   -375   -295    128   -326   -116   -
351   -280   -173   -370   -159   -186   -253     27   -313   -295
-281
  -212   -388    335    195   -403     16   -216   -358   -164   -
387   -323    -91   -379   -179   -254   -255   -256   -338   -310
-301
    77   -468    145    303   -425   -295   -223   -329    -93   -
342   -270   -198   -326    109   -201   -252   -221   -291   -341
-312
  -173   -162   -347   -330    141   -351   -272    133   -253   -
125    -79   -217   -395   -302   -256   -104    328    -64   -145
-164
    29   -267   -278   -247   -310   -290   -266   -280   -210   -
288   -275   -298    342   -270   -234   -219   -210   -265   -279
-321
  -279   -229   -385   -360    398   -409   -113   -192   -331
19   -171   -339   -429   -378   -312   -335   -329   -241     38
348
  -229   -320    364    -87   -379   -235   -199   -383   -220   -
420   -364    -48   -407   -274   -276     79   -249   -372   -290
-281
  -235   -227   -354     -1    -80   -387   -255    -41   -243
302      5   -322   -394   -284   -238   -333   -236   -113   -110
141
   362   -114   -385   -350   -312   -196   -366   -273   -336   -
315   -246   -354   -439   -396   -326   -150   -211   -167   -244
-326
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 39 nsites= 6 E= 1.5e-047
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.833333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.333333  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.833333
0.000000  0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.166667  0.000000  0.666667
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.166667  0.000000  0.000000
0.166667  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
0.333333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.166667  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.333333  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.833333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
 0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.166667
0.000000  0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.166667  0.000000  0.000000
 0.333333  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.000000  0.000000  0.000000  0.333333
0.166667  0.000000  0.000000  0.333333  0.000000  0.000000  0.000000
 0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.833333  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.166667  0.000000  0.166667  0.166667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.333333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
0.166667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.333333  0.000000  0.166667
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.166667  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.166667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.833333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.333333
 0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.333333  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.166667
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 regular expression
--------------------------------------------------------------------
TPLH[LV]AAG[RL]GL[KE]GQTA[LV]L[VL]AAGADTT[LA][PT]NSE[DE]ETP[FY][DS]L
A
--------------------------------------------------------------------




Time 1249.93 secs.

********************************************************************


********************************************************************
SUMMARY OF MOTIFS
********************************************************************

--------------------------------------------------------------------
      Combined block diagrams: non-overlapping sites with p-value <
0.0001
--------------------------------------------------------------------
SEQUENCE NAME            COMBINED P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NFkB[Ciona                       4.46e-217  24_[2(8.18e-
33)]_9_[5(1.18e-21)]_1_\
    [10(3.31e-19)]_10_[9(8.31e-22)]_39_[7(5.38e-19)]_1_[11(1.37e-
21)]_2_\
    [1(3.35e-33)]_14_[3(5.16e-32)]_1_[15(2.09e-14)]_1_[8(5.42e-
25)]_104_\
    [14(3.00e-05)]_322_[13(2.08e-24)]_[4(3.75e-14)]_19_[4(2.79e-
08)]_12_\
    [4(4.31e-09)]_52_[4(2.81e-13)]_13_[4(2.53e-13)]_17_[4(6.05e-
05)]_133
rel1[Ciona]                      9.53e-149  5_[2(3.44e-
32)]_9_[5(1.23e-16)]_1_\
    [10(2.06e-20)]_11_[9(9.86e-18)]_19_[7(5.89e-17)]_1_[11(2.72e-
17)]_2_\
    [1(3.88e-31)]_8_[3(1.65e-28)]_1_[15(9.79e-12)]_22
NFat?                             5.71e-34  44_[10(4.09e-
05)]_14_[18(1.89e-23)]_\
```

```
    1_[7(3.80e-05)]_25_[1(6.20e-11)]_27_[19(1.13e-22)]_34_[6(4.22e-
05)]_765
NFkB1_Homo                      1.52e-230  43_[2(4.12e-
34)]_9_[5(6.57e-19)]_1_\
    [10(2.63e-18)]_10_[9(1.33e-19)]_48_[7(1.07e-18)]_1_[11(3.04e-
22)]_2_\
    [1(3.34e-34)]_13_[3(8.08e-32)]_1_[15(5.92e-14)]_1_[8(6.00e-
26)]_143_\
    [13(3.56e-30)]_[4(3.85e-13)]_18_[4(3.83e-15)]_12_[4(3.12e-
13)]_15_\
    [4(1.59e-08)]_13_[4(2.92e-17)]_15_[20(5.88e-17)]_209
NFkB2_Homo                      8.98e-201  38_[2(2.80e-
34)]_9_[5(2.14e-21)]_1_\
    [10(5.43e-16)]_11_[9(1.19e-15)]_29_[7(3.07e-15)]_1_[11(8.64e-
18)]_2_\
    [1(1.15e-32)]_11_[3(3.18e-29)]_1_[15(1.33e-11)]_1_[8(3.77e-
22)]_112_\
    [13(7.70e-24)]_[4(7.99e-16)]_18_[4(5.07e-16)]_52_[4(1.96e-
10)]_13_\
    [4(1.96e-10)]_15_[20(1.02e-14)]_21_[4(8.51e-05)]_149
RelA_Homo                       3.16e-157  19_[2(1.81e-
33)]_9_[5(1.48e-17)]_1_\
    [10(1.68e-18)]_10_[9(6.37e-17)]_16_[7(6.42e-17)]_[11(1.28e-
14)]_2_\
    [1(7.55e-32)]_8_[3(6.40e-28)]_1_[15(7.49e-13)]_1_[8(1.89e-
21)]_139
RelB_Homo                       9.69e-141  125_[2(1.13e-
30)]_35_[10(1.07e-18)]_\
    11_[9(4.45e-18)]_16_[7(2.44e-15)]_[11(1.28e-14)]_2_[1(1.47e-
29)]_8_\
    [3(1.85e-28)]_1_[15(2.98e-10)]_1_[8(2.43e-20)]_161
cRel                            5.22e-157  8_[2(4.28e-
32)]_9_[5(3.22e-17)]_1_\
    [10(5.08e-18)]_10_[9(6.36e-18)]_18_[7(5.50e-21)]_1_[11(3.23e-
17)]_2_\
    [1(4.29e-32)]_8_[3(2.82e-29)]_[15(6.73e-15)]_1_[8(5.15e-20)]_319
NFAT1                            5.75e-75  399_[12(5.86e-19)]_26_\
    [10(6.72e-14)]_17_[18(5.96e-36)]_1_[7(8.81e-15)]_22_[1(1.43e-
07)]_27_\
    [19(3.09e-26)]_259
NFAT2                            2.59e-60  12_[10(3.57e-
14)]_17_[18(3.66e-33)]_\
    1_[7(1.84e-14)]_22_[1(1.42e-05)]_27_[19(1.76e-27)]_141
NFAT3                            2.32e-69  186_[10(3.97e-08)]_151_\
    [12(2.05e-18)]_25_[10(4.17e-15)]_17_[18(4.80e-35)]_1_[7(1.08e-
13)]_22_\
    [1(7.10e-08)]_27_[19(9.02e-21)]_228
NFAT4                            6.84e-80  442_[12(3.92e-20)]_25_\
    [10(6.38e-15)]_17_[18(1.14e-35)]_1_[7(1.02e-14)]_22_[1(5.93e-
09)]_27_\
    [19(4.42e-26)]_334_[9(7.43e-06)]_32
```

```
NFAT5                             7.25e-66  84_[11(2.92e-07)]_186_\
    [12(8.73e-16)]_[5(3.51e-12)]_6_[14(7.40e-06)]_3_[18(5.19e-
28)]_1_\
    [7(1.22e-06)]_20_[1(3.24e-14)]_26_[19(2.06e-24)]_134_[16(7.33e-
06)]_836
NFkBCys_Nev                      7.76e-245  3_[16(6.41e-
32)]_16_[2(6.43e-36)]_9_\
    [5(2.91e-24)]_1_[10(1.19e-17)]_12_[9(3.71e-26)]_65_[7(1.07e-
21)]_1_\
    [11(1.23e-20)]_2_[1(5.95e-40)]_15_[3(8.14e-37)]_1_[15(3.04e-
13)]_2_\
    [8(6.40e-36)]_42
NFkBSer_Nev                      3.34e-240  3_[16(3.79e-
32)]_16_[2(6.55e-32)]_9_\
    [5(2.91e-24)]_1_[10(1.19e-17)]_12_[9(3.71e-26)]_65_[7(1.07e-
21)]_1_\
    [11(3.44e-19)]_2_[1(5.95e-40)]_15_[3(8.14e-37)]_1_[15(3.04e-
13)]_2_\
    [8(6.40e-36)]_42
NFAT_Nev                         1.97e-160  225_[11(9.58e-05)]_278_\
    [12(3.01e-18)]_[5(9.24e-22)]_2_[14(1.05e-34)]_7_[6(2.43e-
61)]_1_\
    [17(2.47e-24)]_4_[1(1.82e-25)]_26_[19(1.51e-18)]_1_[8(8.92e-
07)]_119
NFkB_Ed                           0.00e+00  3_[16(1.63e-
34)]_16_[2(1.67e-34)]_9_\
    [5(2.33e-23)]_1_[10(3.83e-15)]_12_[9(1.45e-24)]_8_[20(8.43e-
05)]_19_\
    [7(1.12e-20)]_1_[11(9.00e-20)]_2_[1(4.22e-36)]_15_[3(4.03e-
33)]_1_\
    [15(3.94e-14)]_1_[8(2.22e-36)]_83_[13(9.31e-29)]_[4(5.02e-
15)]_17_\
    [4(5.25e-13)]_12_[4(2.91e-15)]_20_[4(4.50e-10)]_13_[4(3.83e-
15)]_15_\
    [20(1.24e-40)]_129
NFAT_Ed                          4.78e-152  230_[12(4.85e-
27)]_[5(4.99e-22)]_2_\
    [14(8.65e-35)]_7_[6(8.56e-60)]_1_[17(7.56e-25)]_4_[1(1.63e-
24)]_41
NFkBb_Aiptasia                    0.00e+00  3_[16(1.37e-
31)]_11_[2(3.43e-36)]_9_\
    [5(8.05e-25)]_1_[10(2.11e-18)]_12_[9(4.99e-23)]_67_[7(1.08e-
24)]_1_\
    [11(2.29e-21)]_2_[1(1.43e-36)]_14_[3(3.26e-32)]_1_[15(2.08e-
16)]_1_\
    [8(4.37e-33)]_83_[13(1.14e-28)]_[4(2.20e-15)]_17_[4(1.54e-
09)]_12_\
    [4(2.91e-15)]_20_[4(1.96e-16)]_13_[4(9.28e-16)]_15_[20(2.98e-
39)]_122
NFAT_Aiptasia                    6.63e-173  271_[12(6.76e-
25)]_[5(4.82e-21)]_2_\
```

```
    [14(1.02e-36)]_7_[6(8.56e-60)]_1_[17(3.22e-24)]_4_[1(3.09e-
23)]_26_\
    [19(3.79e-23)]_6_[2(4.01e-06)]_126
NFkB_Acropora                   0.00e+00  4_[16(1.89e-
28)]_10_[2(2.79e-37)]_9_\
    [5(1.12e-24)]_1_[10(2.94e-19)]_11_[9(3.85e-24)]_64_[7(3.13e-
22)]_1_\
    [11(1.74e-20)]_2_[1(1.73e-37)]_14_[3(8.08e-32)]_1_[15(9.57e-
18)]_1_\
    [8(4.54e-34)]_85_[13(2.30e-31)]_[4(1.01e-16)]_17_[4(7.45e-
15)]_12_\
    [4(8.49e-15)]_15_[4(8.43e-14)]_13_[4(6.44e-13)]_15_[20(8.93e-
41)]_185
NFAT_Acropora                  2.08e-173  77_[17(5.25e-05)]_191_\
    [12(4.85e-27)]_[5(5.41e-19)]_2_[14(5.50e-36)]_7_[6(2.16e-
64)]_1_\
    [17(1.23e-22)]_4_[1(1.66e-25)]_25_[19(3.60e-22)]_2_[8(6.08e-
05)]_112
NFkB_Corallimorph               0.00e+00  4_[16(1.44e-
21)]_11_[2(2.79e-37)]_9_\
    [5(1.13e-23)]_1_[10(1.80e-20)]_11_[9(5.55e-24)]_68_[7(3.80e-
24)]_1_\
    [11(3.40e-20)]_2_[1(2.81e-34)]_14_[3(2.42e-33)]_1_[15(1.10e-
18)]_1_\
    [8(6.93e-33)]_83_[13(1.34e-34)]_[4(1.06e-19)]_17_[4(2.53e-
13)]_12_\
    [4(3.33e-14)]_15_[4(1.23e-10)]_13_[4(1.01e-16)]_15_[20(1.78e-
43)]_193
NFAT_Corallimorph              3.75e-152  328_[12(6.84e-
27)]_[5(3.79e-16)]_2_\
    [14(1.02e-36)]_7_[6(7.88e-63)]_1_[17(2.79e-23)]_4_[1(4.36e-
26)]_21
NFkB_Hydra                      8.19e-77  15_[2(5.96e-
22)]_13_[5(3.73e-05)]_\
    111_[7(1.30e-12)]_1_[11(2.81e-14)]_2_[1(1.60e-21)]_12_[3(3.69e-
20)]_1_\
    [15(8.37e-12)]_2_[8(1.98e-10)]_120
NFAT_Hydra                      1.63e-64  156_[9(2.08e-05)]_174_\
    [18(1.03e-05)]_58_[15(4.34e-05)]_291_[12(2.01e-
24)]_216_[19(8.40e-06)]_186_\
    [19(2.00e-05)]_3_[6(2.05e-36)]_1_[17(7.17e-05)]_2_[1(4.87e-
13)]_26_\
    [19(9.02e-21)]_2_[8(1.17e-06)]_548
NFkB_Platygyra                  0.00e+00  4_[16(1.21e-
31)]_10_[2(6.43e-36)]_9_\
    [5(1.13e-23)]_1_[10(1.80e-20)]_11_[9(7.80e-25)]_65_[7(3.78e-
23)]_1_\
    [11(1.69e-22)]_2_[1(8.92e-40)]_15_[3(1.43e-33)]_1_[15(2.89e-
17)]_1_\
    [8(7.60e-38)]_92_[13(1.14e-32)]_[4(7.66e-18)]_17_[4(1.83e-
13)]_12_\
```

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    [4(2.91e-15)]_15_[4(4.74e-13)]_13_[4(7.13e-17)]_15_[20(2.72e-
33)]_190
NFATa_Platygyra                 1.87e-156  292_[12(1.80e-
27)]_[5(2.24e-18)]_2_\
    [14(1.02e-36)]_7_[6(1.52e-63)]_1_[17(1.02e-25)]_4_[1(1.03e-
25)]_48
NFATb_Platygyra                 1.93e-156  313_[12(1.80e-
27)]_[5(2.24e-18)]_2_\
    [14(1.02e-36)]_7_[6(1.52e-63)]_1_[17(1.02e-25)]_4_[1(1.03e-
25)]_48
NFkB_Biomphalaria               1.84e-161  114_[2(3.11e-
31)]_9_[5(1.58e-22)]_3_\
    [10(1.33e-16)]_10_[9(3.16e-15)]_16_[7(1.28e-19)]_1_[11(3.99e-
14)]_\
    [1(3.16e-28)]_14_[3(1.73e-29)]_1_[15(1.18e-13)]_1_[8(2.57e-
23)]_199
NFkB_Sphaeroforma_arctic         1.11e-25  203_[5(9.65e-
06)]_91_[1(8.97e-19)]_\
    56_[19(4.90e-18)]_14
Relish_Biomphalaria             1.22e-204  56_[2(5.14e-
31)]_9_[5(6.05e-21)]_1_\
    [10(1.32e-17)]_10_[9(8.15e-17)]_38_[7(1.46e-17)]_1_[11(1.87e-
19)]_2_\
    [1(6.56e-31)]_14_[3(2.39e-32)]_1_[15(2.10e-12)]_1_[8(6.04e-
23)]_290_\
    [13(1.16e-24)]_[4(1.68e-10)]_19_[4(1.06e-12)]_12_[4(8.71e-
13)]_22_\
    [4(1.08e-09)]_13_[4(2.05e-14)]_13_[4(5.25e-13)]_186
Relish_Dmel                      7.36e-97  150_[2(7.08e-
07)]_9_[5(1.22e-15)]_\
    [10(6.89e-10)]_14_[9(3.88e-14)]_30_[7(6.42e-17)]_1_[11(1.55e-
06)]_2_\
    [1(1.07e-20)]_14_[3(3.56e-26)]_1_[15(8.93e-13)]_166_[4(4.09e-
05)]_21_\
    [4(1.23e-10)]_12_[4(9.44e-14)]_16_[4(5.82e-13)]_14_[4(1.42e-
11)]_17_\
    [4(8.17e-07)]_167
Dorsal_Dmel                     4.70e-146  47_[2(2.16e-
26)]_9_[5(4.46e-19)]_1_\
    [10(1.33e-16)]_11_[9(5.82e-19)]_18_[7(1.02e-14)]_2_[11(3.81e-
18)]_\
    [1(5.79e-22)]_13_[3(4.82e-26)]_1_[15(5.28e-15)]_1_[8(1.05e-
17)]_333
Dif_Dmel                         6.91e-96  78_[2(2.54e-
24)]_10_[5(2.05e-22)]_1_\
    [10(3.87e-11)]_14_[9(3.52e-09)]_18_[7(5.59e-11)]_18_[1(6.02e-
23)]_14_\
    [3(7.52e-24)]_1_[15(6.39e-11)]_1_[8(2.34e-06)]_291
NFkB_Amphimedon                 4.03e-215  46_[2(1.37e-
31)]_11_[5(2.46e-18)]_1_\
```

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    [10(3.28e-18)]_11_[9(9.03e-18)]_43_[7(8.74e-25)]_1_[11(5.02e-
18)]_2_\
    [1(4.38e-30)]_19_[3(7.39e-25)]_1_[15(4.38e-13)]_1_[8(1.39e-
30)]_281_\
    [13(1.72e-23)]_[4(4.34e-16)]_20_[4(1.00e-11)]_12_[4(3.12e-
13)]_1_\
    [12(6.22e-05)]_[4(1.25e-14)]_13_[4(4.93e-09)]_13_[4(2.54e-
15)]_12_\
    [4(1.15e-05)]_31_[13(7.24e-05)]_108
NFkB_Capsaspora                  2.53e-59  277_[5(6.11e-
06)]_25_[9(9.27e-05)]_\
    18_[15(4.70e-05)]_17_[1(1.55e-20)]_43_[19(7.55e-21)]_[8(5.97e-
06)]_75_\
    [13(4.48e-22)]_[4(5.25e-13)]_14_[4(5.25e-13)]_87_[4(1.97e-
07)]_24_\
    [4(7.35e-08)]_12_[4(9.44e-14)]_345
IkB_Nev                          1.12e-42  114_[13(1.62e-
19)]_[4(7.53e-14)]_15_\
    [4(6.44e-13)]_12_[4(2.95e-14)]_26_[4(7.67e-12)]_13_[4(5.07e-
16)]_15_\
    [20(5.86e-32)]_15
IkB_Hym                          2.85e-19  63_[4(6.49e-
06)]_49_[4(5.62e-07)]_\
    57_[4(3.11e-06)]_19_[20(1.39e-25)]_14
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Stopped because nmotifs = 20 reached.
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CPU: meme-server

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A.11 IKK MEME Output

MEME

Multiple Em for Motif Elicitation

For further information on how to interpret these results or to get a copy of the MEME software please access http://meme-suite.org.

If you use MEME in your research, please cite the following paper:
Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994. [pdf]

DISCOVERED MOTIFS | MOTIF LOCATIONS | INPUTS & SETTINGS | PROGRAM INFORMATION

DISCOVERED MOTIFS

1.

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***E*-value:** 1.5e-269

Site Count: 18

Width: 41
Log Likelihood Ratio: 1347

Information Content: 113

Relative Entropy: 107.9

Bayes Threshold: 8.27414

Name	Start	*p*-value	Sites
9. TBK/E_Nematostella	105	3.35e-42	SLFTMLEHPS NAYGLSEQDCITVIRDVVAGMKHLHDNGIVHRDLKPGNIMR VYRDDGSCVY
3. TBK1_HUMAN	103	7.38e-42	SLYTVLEEPS NAYGLPESEFLIVLRDVVGGMNHLRENGIVHRDIKPGNIMR VIGEDGQSVY
5. TBK/E_Ciona	115	2.35e-39	SLYSMLDDPE NLYGLPESEFHRVLSHITAGMKHLHDKGIVHRDLKPGNIMR SLDDDGTAVY

Name	**Start**	***p*-value**	**Sites**		
4. IKKE_HUMAN	103	9.36e-39	SLLSV LESPE	NAFGLPEDEFLVVLRCVVAGMNH LRENGIVHRDIKPGNIMR	LVGEE GQSIY
13. TBK/E_Amphimedon	121	4.79e-37	SLYEV IDSPQ	NAYGLDEYQFKSVIFDVASGMRH LRDHGFVHRDIKPGNIMR	CINPD GSFVF
1. IKKA_HUMAN	112	1.99e-36	DLRKL LNKPE	NCCGLKESQILSLLSDIGSGIRY LHENKIIHRDLKPENIVL	QDVGG KIIHK
14. IKKAB_Hydra	434	2.56e-36	DLREV LSYTE	NCCGLIESMVLRVLEDVACGLNF LHEKNIIHRDLKPENILK	GHKGD QVVYK
12. TBK/E_Aiptasia	105	8.79e-36	SLYTL LEHPS	NSYGFSEKDCKDIIRDVVAGMEH LRKQGIVHRDLKPGNIMR	VFNDD GTCSY
6. IKKAB_Ciona	114	1.03e-34	DLRKF LTQPE	NCCGLPEFQVRNILQDIGSAIEH LHERQLVHRDLKPENIVM	KEKEK NVFQF
2. IKKB_HUMAN	113	1.30e-34	DLRKY LNQFE	NCCGLREGAILTLLSDIASALRY LHENRIIHRDLKPENIVL	QQGEQ RLIHK
8. TBK/E_Drosophila	106	6.11e-34	SLFNI LDDPE	NSYGLPEHEFLLVLEHLCAGMKH LRDNKLVHRDLKPGNIMK	FISED GQTIY
10. IKKAB_Nematostella	111	1.17e-33	DLRKV LNSPD	NCAGLKEASVLRVITDIANAVQF LHSKRIIHRDLKPENIVI	NFTNG NAVYK
11. IKKAB_Aiptasia	106	1.57e-32	DLRRI LNTPE	NIRGLKESTVIEVTADVAHAIEF LHSKRIIHRDLKPENIVI	QHTDG KDIYK
15. TBK/Epar_Hydra	105	1.30e-28	SLYEI IEEPE	NMFGVDDITLINIIQDVCAGMEY LKNSNVVHRDVKPGNILR	ADKGS GGYIY
16. IKKAB_Trichoplax	47	1.41e-28	GGDLA DHLAA	TRFGLDEVNIKKFINDISSAIAC IHSKRIIHRDIKPENILL	MSHNG EHTYK
17. IKK?_Mnemiopsis	350	5.85e-26	NGGDL KFHIH	SMGAFTEDRARFYTAEILCGIQH LHQCNIVYRDLKPENILL	DDAGH VRISD

	Name	Start	*p*-value	Sites		
19.	IKK?_Capsaspora	124	1.82e-25	AGGELFDYIV	ARQNLKEVEARRVFRQIISAVSYCHQSALIHRDLKPENLLL	DSDLNIKIID
20.	IKK?_Monosiga	134	3.57e-25	SGGEVFDYLV	SHGRMKEKEARIKFRQIVSALQYCHARGIVHRDLKAENLLL	DKDLQIKIAD

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***E*-value:** 1.3e-223

Site Count: 19

Width: 29
Log Likelihood Ratio: 1071

Information Content: 81.2

Relative Entropy: 81.3

Bayes Threshold: 9.69554

	Name	Start	*p*-value	Sites		
3.	TBK1_HUMAN	195	1.31e-31	YERAVLRKDH	QKKYGATVDLWSIGVTFYHAATGSLPFRP	FEGPRRNKEV
9.	TBK/E_Nematostella	197	8.74e-30	YERGVLRKAT	GKTFGAQVDLWSIGVTFYHIATGRLPFRP	FGGRQNKDTM
12.	TBK/E_Aiptasia	198	2.41e-29	YERGVLRKSS	GKTFGANVDLWSIGVTFYHIATGKLPFRP	QGGRQNKDTM
15.	TBK/Epar_Hydra	197	8.72e-29	YEKAVMKWSS	NKTFTSRVDMWSLGVTFYHLATGQLPFRP	AGGRQNKDIM
5.	TBK/E_Ciona	207	8.72e-29	YERAVLRKHA	GKMFSATVDLWSLGVTLYHVATGMLPFRP	YGGARRNKDV
8.	TBK/E_Drosophila	198	1.39e-28	YERAVLRKSI	QRSFTANVDLWSIGVTLYHVATGNLPFRP	FGGRKNRETM
4.	IKKE_HUMAN	195	3.41e-28	YERAVLRKPQ	QKAFGVTVDLWSIGVTLYHAATGSLPFIP	FGGPRRNKEI
11.	IKKAB_Aiptasia	190	9.34e-28	RYLAPELLAG	NGSYTKTVDYWSLGTVLFECITGIRPFPD	LSPVNWHREI
10.	IKKAB_Nematostella	195	2.81e-27	KYLAPELLAG	NGSYSKTVDYWSLGTVVFECITGRRPFPD	LSPVQWYMEI
2.	IKKB_HUMAN	196	4.79e-27	LQYLAPELLE	QQKYTVTVDYWSFGTLAFECITGFRPFLP	NWQPVQWHSK

	Name	Start	*p*-value	Sites		
7.	IKKAB_Drosophila	236	1.07e-25	RHYYAPEVVE	NGFYNSTVDLWSFGVIAYELVTGELPFIP	HQTLKNIILN
6.	IKKAB_Ciona	200	1.21e-25	YLAPEFYGAN	PLCYTATVDFWSFGLLVYECITGRRPFYP	SLELAQVLND
1.	IKKA_HUMAN	195	1.21e-25	LQYLAPELFE	NKPYTATVDYWSFGTMVFECIAGYRPFLH	HLQPFTWHEK
13.	TBK/E_Amphimedon	213	3.74e-24	YERALINYRS	KEEFLDKVDLWSLGATFFHLATGRLPFRP	YRKRQDRGTM
14.	IKKAB_Hydra	517	6.30e-24	NYMAPELYES	QSGYTKAADYWSFGTVIFECITGIRPFDL	IKENKLKVIC
16.	IKKAB_Trichoplax	134	3.51e-23	PYMAPEVQIR	IQEYTKSVDIWSFGVVIYECVTKSLPFSD	VSLQEMEKID
20.	IKK?_Monosiga	215	2.25e-20	PYAAPELFQG	REYTGPEVDVWSCGVILFTLISGALPFDG	STLKELRDRV
19.	IKK?_Capsaspora	205	2.89e-20	YYAAPEMIVG	QSYVGPEIDIWSMGVILYTLLCGHLPFDD	DNLTRLYEKV
17.	IKK?_Mnemiopsis	430	3.15e-20	VGYMAPEVIK	NERYSYSVDWWGLGCIIFEMIEGQAPFRS	RKERVKREEV

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***E*-value:** 3.1e-100

Site Count: 16

Width: 21
Log Likelihood Ratio: 638

Information Content: 59.5

Relative Entropy: 57.5

Bayes Threshold: 9.76539

	Name	Start	*p*-value	Sites		
3.	TBK1_HUMAN	166	3.99e-24	TDFGAARELE	DDEQFVSLYGTEEYLHPDMYE	RAVLRKDHQK
5.	TBK/E_Ciona	178	3.00e-23	TDFGAARELG	DDEQFMSLYGTEEYLHPDIYE	RAVLRKHAGK
4.	IKKE_HUMAN	166	4.51e-23	TDFGAARELD	DDEKFVSVYGTEEYLHPDMYE	RAVLRKPQQK
12.	TBK/E_Aiptasia	169	5.98e-22	DFGAARELEH	SAEQFMSVYGTEEYLHPDLYE	RGVLRKSSGK

	Name	Start	*p*-value	Sites		
15.	TBK/Epar_Hydra	168	9.88e-22	TDFGAARELG	EAEQFVSLYGTEEYLHPDIYE	KAVMKWSSNK
8.	TBK/E_Drosophila	169	3.01e-21	TDFGAARELE	DNQPFASLYGTEEYLHPDLYE	RAVLRKSIQR
9.	TBK/E_Nematostella	168	1.52e-20	TDFGAARELM	ESDQFVSIYGTEEYLHPDLYE	RGVLRKATGK
1.	IKKA_HUMAN	174	3.05e-19	IDLGYAKDVD	QGSLCTSFVGTLQYLAPELFE	NKPYTATVDY
13.	TBK/E_Amphimedon	184	9.91e-19	ADFGTARQLD	PNEHFTSLHGTEEYLYPAMYE	RALINYRSKE
2.	IKKB_HUMAN	175	9.91e-19	IDLGYAKELD	QGSLCTSFVGTLQYLAPELLE	QQKYTVTVDY
6.	IKKAB_Ciona	177	2.47e-17	IDLGYAKEIN	ENSFGTSFVGTMHYLAPEFYG	ANPLCYTATV
14.	IKKAB_Hydra	495	2.26e-16	IADFGFAKDL	DRSMCKTVLGTQNYMAPELYE	SQSGYTKAAD
10.	IKKAB_Nematostella	173	2.98e-16	IDLGYAKQLD	QGSMASTFVGTLKYLAPELLA	GNGSYSKTVD
11.	IKKAB_Aiptasia	168	5.13e-16	IDLGYAKQLD	QYSIATTFVGTLRYLAPELLA	GNGSYTKTVD
7.	IKKAB_Drosophila	215	1.64e-14	TDFGLARGTP	DQTMVQSVVGTRHYYAPEVVE	NGFYNSTVDL
20.	IKK?_Monosiga	193	5.26e-13	ADFGFANMYE	PDQKLNTFCGSPPYAAPELFQ	GREYTGPEVD

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***E*-value:** 3.8e-097

Site Count: 8

Width: 41
Log Likelihood Ratio: 692

Information Content: 127.6

Relative Entropy: 124.8

Bayes Threshold: 11.4615

	Name	Start	*p*-value	Sites		
12.	TBK/E_Aiptasia	228	1.11e-41	ATGKLPFRPQ	GGRQNKDTMYHITTAKASGMIAGVQRISDGVIEWSDKLPDH	TNLSRGFQDL

Name	Start	*p*-value	Sites		
9. TBK/E_Nematostella	227	2.37e-41	ATGRLPFRPF	GGRQNKDTMYHITTRKASGMIAGVQKSEGGEVEWTDKLPDH	TCLSQGFRNL
5. TBK/E_Ciona	238	1.17e-40	TGMLPFRPYG	GARRNKDVMYRITTEKPSGVISGVQHSERGSIEWSRELPKT	CRLSHGFKKI
3. TBK1_HUMAN	226	1.23e-39	TGSLPFRPFE	GPRRNKEVMYKIITGKPSGAISGVQKAENGPIDWSGDMPVS	CSLSRGLQVL
4. IKKE_HUMAN	226	1.55e-39	TGSLPFIPFG	GPRRNKEIMYRITTEKPAGAIAGAQRRENGPLEWSYTLPIT	CQLSLGLQSQ
8. TBK/E_Drosophila	228	1.95e-39	ATGNLPFRPF	GGRKNRETMHQITTKKASGVISGTQLSENGPIEWSTTLPPH	AHLSQGLKTL
15. TBK/Epar_Hydra	227	4.77e-29	ATGQLPFRPA	GGRQNKDIMFKMISEKSNDAISCYQDLDNGSLIYSNELPKK	TRISENLKMH
13. TBK/E_Amphimedon	243	3.37e-28	ATGRLPFRPY	RKRQDRGTMFKIINEKKTGIILGWQQEYNAPIYYSDRLPPD	IVISQGLRDI

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***E*-value:** 1.9e-093

Site Count: 19

Width: 21
Log Likelihood Ratio: 656

Information Content: 50.1

Relative Entropy: 49.8

Bayes Threshold: 9.71222

Name	Start	*p*-value	Sites		
12. TBK/E_Aiptasia	11	1.76e-19	MEIRSSPNFM	WHIKDVLGQGATGAVYKGRDK	KTGNEVAIKV
9. TBK/E_Nematostella	11	2.09e-19	METRSSSNYI	WNLKSVLGQGATGAVYTGRHK	KSGDVVAVKT
11. IKKAB_Aiptasia	9	8.91e-19	MQVSGHDD	WIEERCLGAGGFGTVTLWKHK	YNHEYLAIKK

Name	Start	*p*-value	Sites		
2. IKKB_HUMAN	15	3.93e-18	PSLTTQTCGA	WEMKERLGTGGFGNVIRWHNQ	ETGEQIAIKQ
5. TBK/E_Ciona	20	1.19e-17	SPIRSTLNYV	WSTTEILGQGATGFVFKGREK	KTGQEYAIKV
3. TBK1_HUMAN	9	1.76e-17	MQSTSNHL	WLLSDILGQGATANVFRGRHK	KTGDLFAIKV
1. IKKA_HUMAN	15	2.01e-17	PGLRPGAGGP	WEMRERLGTGGFGNVCLYQHR	ELDLKIAIKS
4. IKKE_HUMAN	9	2.60e-17	MQSTANYL	WHTDDLLGQGATASVYKARNK	KSGELVAVKV
6. IKKAB_Ciona	17	3.80e-17	PQRQPMQCGE	WTLIKILGSGGFGQVSLWKNK	QDVKLAVKQC
13. TBK/E_Amphimedon	28	7.05e-17	ETEYYSLSYI	WSSKDKLGQGATGQVFAGYSK	RSGDKVAIKM
8. TBK/E_Drosophila	12	7.05e-17	SFLRGSVSYV	WCTTSVLGKGATGSVFQGVNK	ITGESVAVKT
7. IKKAB_Drosophila	41	3.19e-16	ENNKMHSFGN	WERCRNLGEGGFGLVIHWRNR	TTGREIATKH
10. IKKAB_Nematostella	14	5.53e-16	NKLRQSSQDG	WVEERCVGTGSFGTVTLWENK	ITKEQIVLKK
15. TBK/Epar_Hydra	12	2.91e-15	NVVRQSLNYV	WSVQEVIGNGATGTVYKCLAK	KTGAPCAAKV
14. IKKAB_Hydra	336	3.55e-15	DMENGKVYGN	WKYEKQIGCGAFAKVSRWKNI	KTDKELVVKQ
17. IKK?_Mnemiopsis	259	8.91e-14	LEKKPIGKHT	FRHYRVLGKGGFGEVCATQSR	ASGKMYAEKK
18. IKK?_Pleurobrachia	22	2.47e-13	SRETEILLSH	LRLKRKIGYGGFGYVYEGTYR	GTKVAVKKMH
20. IKK?_Monosiga	44	6.62e-13	TERSAQTIGE	YIMYKTIGKGNFARVKLAKHK	LTNVEVAIKV
19. IKK?_Capsaspora	33	2.35e-12	EGSSTQFLGK	FKLLRTLGHGSYGKVKLAQHI	ETGQKVALKI

6.

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***E*-value:** 3.4e-095

Site Count: 14

Width: 29
Log Likelihood Ratio: 716

Information Content: 78.4

Relative Entropy: 73.8

Bayes Threshold: 10.5478

Name	Start	*p*-value		Sites	
4. IKKE_HUMAN	46	2.72e-27	AVKVFNTTSY	LRPREVQVREFEVLRKLNHQNIVKLFAVE	ETGGSRQKVL
3. TBK1_HUMAN	46	6.93e-27	AIKVFNNISF	LRPVDVQMREFEVLKKLNHKNIVKLFAIE	EETTTRHKVL
1. IKKA_HUMAN	52	2.57e-25	AIKSCRLELS	TKNRERWCHEIQIMKKLNHANVVKACDVP	EELNILIHDV
8. TBK/E_Drosophila	49	5.18e-25	AVKTFNPYSH	MRPADVQMREFEALKKVNHENIVKLLAIE	EDQEGRGKVI
9. TBK/E_Nematostella	48	1.03e-24	AVKTSNHLGM	MRPLEVRKREFDVLSKLDHENIVKIFASE	TELRSQNEII
11. IKKAB_Aiptasia	46	2.52e-24	AIKKCRLDLS	PANRQRWHQEVEILKKLDHANIVKAKDVP	AILDVSGGEI
10. IKKAB_Nematostella	51	3.92e-24	VLKKCRLDLS	PSNRNQWQKEVEIMKGLDHPNIVKAIDVP	AVLDVREGQL
12. TBK/E_Aiptasia	48	4.37e-24	AIKVTNHLGM	MRPLDVRKREFEVLNRLDHENIVRIFASE	NELRSQNEII
2. IKKB_HUMAN	52	4.47e-23	AIKQCRQELS	PRNRERWCLEIQIMRRLTHPNVVAARDVP	EGMQNLAPND
15. TBK/Epar_Hydra	49	4.00e-22	AAKVFNSQAD	RRPYEVRIREIELLKKLSHPNIIKLMGLE	QEIGSKATVL
5. TBK/E_Ciona	58	2.21e-21	IKVFNSLNYM	ARSLEARRREFEVLRKVDHKNVVRLFSVE	EELTTKHDVI
20. IKK?_Monosiga	82	3.20e-21	IKVIDKTRLK	ESHMLKVMREVRILKMLNHPNIVKLYEVI	DTPKYLYLVM
6. IKKAB_Ciona	53	3.82e-19	AVKQCKNQLS	RQNERRWRKEVEMMQRLNHPSIVNFVEVP	VEIQNAYVDH
19. IKK?_Capsaspora	72	2.64e-17	KILEKSNIKS	NKALKRIFREIGYLKVLHHPHIVALLEVI	ETTDRIILIM

7.

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***E*-value:** 5.2e-081

Site Count: 19

Width: 15
Log Likelihood Ratio: 540

Information Content: 42.8

Relative Entropy: 41

Bayes Threshold: 9.7246

Name	Start	*p*-value	Sites		
9. TBK/E_Nematostella	150	6.10e-18	PGNIMRVYRD	DGSCVYKLTDFGAAR	ELMESDQFVS
8. TBK/E_Drosophila	151	3.30e-17	PGNIMKFISE	DGQTIYKLTDFGAAR	ELEDNQPFAS
3. TBK1_HUMAN	148	3.30e-17	PGNIMRVIGE	DGQSVYKLTDFGAAR	ELEDDEQFVS
5. TBK/E_Ciona	160	1.29e-16	PGNIMRSLDD	DGTAVYKLTDFGAAR	ELGDDEQFMS
12. TBK/E_Aiptasia	150	5.82e-16	PGNIMRVFND	DGTCSYKLTDFGAAR	ELEHSAEQFM
4. IKKE_HUMAN	148	1.87e-15	PGNIMRLVGE	EGQSIYKLTDFGAAR	ELDDDEKFVS
11. IKKAB_Aiptasia	150	2.72e-15	KPENIVIQHT	DGKDIYKLIDLGYAK	QLDQYSIATT
7. IKKAB_Drosophila	197	4.97e-15	PDNIVIQRGV	DGKKIYKLTDFGLAR	GTPDQTMVQS
15. TBK/Epar_Hydra	150	1.52e-14	PGNILRADKG	SGGYIYKITDFGAAR	ELGEAEQFVS
13. TBK/E_Amphimedon	166	3.15e-14	PGNIMRCINP	DGSFVFKLADFGTAR	QLDPNEHFTS
10. IKKAB_Nematostella	155	7.02e-14	KPENIVINFT	NGNAVYKLIDLGYAK	QLDQGSMAST
14. IKKAB_Hydra	478	4.15e-13	KPENILKGHK	GDQVVYKIADFGFAK	DLDRSMCKTV
1. IKKA_HUMAN	156	5.41e-13	KPENIVLQDV	GGKIIHKIIDLGYAK	DVDQGSLCTS
16. IKKAB_Trichoplax	91	7.64e-12	KPENILLMSH	NGEHTYKLGDFGISK	FCTGAEPRTV
20. IKK?_Monosiga	175	1.91e-11	RDLKAENLLL	DKDLQIKIADFGFAN	MYEPDQKLNT

Name	Start	*p*-value	Sites		
18. IKK?_Pleurobrachia	159	1.91e-11	LDVKPANVIV	DDSDTCKLGDFGCAQ	RLGDSGNEFT
2. IKKB_HUMAN	157	2.77e-11	KPENIVLQQG	EQRLIHKIIDLGYAK	ELDQGSLCTS
6. IKKAB_Ciona	159	6.16e-11	PENIVMKEKE	KNVFQFKIIDLGYAK	EINENSFGTS
19. IKK?_Capsaspora	165	1.25e-10	RDLKPENLLL	DSDLNIKIIDFGFSN	VYRTDMVLNT

8.

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***E*-value:** 2.1e-079

Site Count: 13

Width: 21
Log Likelihood Ratio: 542

Information Content: 63.1

Relative Entropy: 60.1

Bayes Threshold: 11.2304

Name	Start	*p*-value	Sites		
1. IKKA_HUMAN	91	8.64e-22	EELNILIHDV	PLLAMEYCSGGDLRKLLNKPE	NCCGLKESQI
10. IKKAB_Nematostella	90	2.68e-21	AVLDVREGQL	PLLGMEYCEGGDLRKVLNSPD	NCAGLKEASV
11. IKKAB_Aiptasia	85	4.21e-21	AILDVSGGEI	PLLAMEYCEGGDLRRILNTPE	NIRGLKESTV
2. IKKB_HUMAN	92	4.71e-20	GMQNLAPNDL	PLLAMEYCQGGDLRKYLNQFE	NCCGLREGAI
9. TBK/E_Nematostella	84	5.33e-20	ASETELRSQN	EIIVMELCSGGSLFTMLEHPS	NAYGLSEQDC
12. TBK/E_Aiptasia	84	6.01e-20	ASENELRSQN	EIIAMELCSGGSLYTLLEHPS	NSYGFSEKDC
8. TBK/E_Drosophila	85	2.15e-19	AIEEDQEGRG	KVIVMELCTGGSLFNILDDPE	NSYGLPEHEF
13. TBK/E_Amphimedon	100	1.95e-18	LNEIEKKHQY	HIIAMELCNGGSLYEVIDSPQ	NAYGLDEYQF
5. TBK/E_Ciona	94	1.95e-18	SVEEELTTKH	DVIIMELCPNGSLYSMLDDPE	NLYGLPESEF

Name	Start	*p*-value	Sites		
4. IKKE_HUMAN	82	2.38e-18	AVEETGGSRQ	KVLVMEYCSSGSLLSVLESPE	NAFGLPEDEF
3. TBK1_HUMAN	82	3.89e-18	AIEEETTTRH	KVLIMEFCPCGSLYTVLEEPS	NAYGLPESEF
7. IKKAB_Drosophila	130	1.22e-17	YLNGMFSAKL	PVIVLEYCNGGDVRKRLQSPE	NANGLTEFEV
6. IKKAB_Ciona	93	2.32e-17	EIQNAYVDHY	VALGMEYCEAGDLRKFLTQPE	NCCGLPEFQV

9.

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***E*-value:** 5.2e-063

Site Count: 14

Width: 41
Log Likelihood Ratio: 803

Information Content: 86.5

Relative Entropy: 82.7

Bayes Threshold: 8.8942

Name	Start	*p*-value	Sites		
4. IKKE_HUMAN	297	8.41e-31	VEQAKCWGFD	QFFAETSDILQRVVVHVFSLSQAVLHHIYIHAHNTIAIFQE	AVHKQTSVAP
3. TBK1_HUMAN	297	2.75e-30	ADQEKCWGFD	QFFAETSDILHRMVIHVFSLQQMTAHKIYIHSYNTATIFHE	LVYKQTKIIS
5. TBK/E_Ciona	309	4.60e-30	CNPHKIWTFD	RYFAEVEDILSKKVINVFSVPNAMLHKVYISPEKTLVSFQE	AVAELTEVRS
12. TBK/E_Aiptasia	299	6.62e-28	SDPSKMMSFG	EFFRRVQDMVTRKVVSVYHVQTSSFHEIYIPPTAQFEAFQE	LISKETGLPP
9. TBK/E_Nematostella	298	9.33e-28	SDPAKMMSFD	QFFAYVQDMVSRKVLDVYCVSSSQFHKIYIRRTEMLNRFKQ	MVTEQTSVPC
13. TBK/E_Amphimedon	313	5.86e-26	DTFDSMWAFD	RFFKAIDGIKKQNVVHIFCVSRCTCHMIYVDDAGEADIIPK	FKELIARQTS

Name	Start	*p*-value	Sites		
2. IKKB_HUMAN	298	1.82e-25	RGTDPTYGPN	GCFKALDDILNLKLVHILNMVTGTIHTYPVTEDESLQSLKA	RIQQDTGIPE
10. IKKAB_Nematostella	297	4.52e-25	GGRQREDGVQ	DCFHVIQELANAKVVHVYCVANSVIFSYEVVAEETVGSLKQ	KLQNDTEIPI
8. TBK/E_Drosophila	299	1.75e-23	ENREKTWSFD	RFFHEVTLILRKRVIHVFFTNRTSSVEVFLEPDEQIDNFRE	RIFLQTEVPL
11. IKKAB_Aiptasia	292	3.73e-22	GGQVHEDGSR	QCYKLLHKILDSKVVHIFCAFTSTLLTFEVTQTDRREDINA	RIYEETGIAL
1. IKKA_HUMAN	299	4.07e-22	GPVDLTLKQP	RCFVLMDHILNLKIVHILNMTSAKIISFLLPPDESLHSLQS	RIERETGINT
6. IKKAB_Ciona	301	1.75e-21	QLRGGGVGNN	EWFKTVERILREKCIHVYNTQNNSVFTIPVLDERMSIAKMQ	EAIMRATNIP
14. IKKAB_Hydra	610	2.45e-21	CHDADKRGTT	ECFSMIKDILSINEIHLFDIMTCQETSYACKPGDTVQNLKL	FIKQEFGIEA
7. IKKAB_Drosophila	340	2.90e-21	RGQLAANNVP	VVFADLDKILNMNVLTIFAVNNCERLEYAVSAEMTMKDLIA	LIVLDTGMDE

10.

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***E*-value:** 1.2e-035

Site Count: 9

Width: 8
Log Likelihood Ratio: 216

Information Content: 34.1

Relative Entropy: 34.7

Bayes Threshold: 11.4713

Name	Start	*p*-value	Sites		
17. IKK?_Mnemiopsis	146	2.54e-11	QTDRYHVRTE	QTDRYHVR	TEQVRTEQTS
17. IKK?_Mnemiopsis	136	2.54e-11	QTDRYHVRTE	QTDRYHVR	TEQTDRYHVR

Name	Start	*p*-value	Sites
17. IKK?_Mnemiopsis	126	2.54e-11	QTDRYHVRTE QTDRYHVR TEQTDRYHVR
17. IKK?_Mnemiopsis	116	2.54e-11	QTDRYHVRSE QTDRYHVR TEQTDRYHVR
17. IKK?_Mnemiopsis	106	2.54e-11	QTDRYHVRSE QTDRYHVR SEQTDRYHVR
17. IKK?_Mnemiopsis	96	2.54e-11	QTDRYHVRSE QTDRYHVR SEQTDRYHVR
17. IKK?_Mnemiopsis	86	2.54e-11	QTDRYHVRTE QTDRYHVR SEQTDRYHVR
17. IKK?_Mnemiopsis	76	2.54e-11	QTDRFHVRTE QTDRYHVR TEQTDRYHVR
17. IKK?_Mnemiopsis	66	5.58e-11	AWVVTHVRTE QTDRFHVR TEQTDRYHVR

11.

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***E*-value:** 2.1e-021

Site Count: 7

Width: 21
Log Likelihood Ratio: 304

Information Content: 65.8

Relative Entropy: 62.7

Bayes Threshold: 11.5649

Name	Start	*p*-value	Sites
3. TBK1_HUMAN	276	1.39e-22	SCSLSRGLQV LLTPVLANILEADQEKCWGFD QFFAETSDIL
9. TBK/E_Nematostella	277	5.27e-22	HTCLSQGFRN LLTPLLAGVLESDPAKMMSFD QFFAYVQDMV
4. IKKE_HUMAN	276	4.98e-20	TCQLSLGLQS QLVPILANILEVEQAKCWGFD QFFAETSDIL
12. TBK/E_Aiptasia	278	6.72e-20	HTNLSRGFQD LLVPILAGVLESDPSKMMSFG EFFRRVQDMV
8. TBK/E_Drosophila	278	5.64e-19	HAHLSQGLKT LVTPLLAGLLEENREKTWSFD RFFHEVTLIL
5. TBK/E_Ciona	288	5.98e-18	TCRLSHGFKK IFTVVLSGILECNPHKIWTFD RYFAEVEDIL

Name	Start	*p*-value	Sites		
15. TBK/Epar_Hydra	277	1.94e-13	KTRISENLKM	HLTPILKCLLQIQQQFMLSYD	DFFKEIKELV

12.

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***E*-value:** 2.0e-020

Site Count: 6

Width: 30
Log Likelihood Ratio: 360

Information Content: 90.6

Relative Entropy: 86.6

Bayes Threshold: 9.00132

Name	Start	*p*-value	Sites		
1. IKKA_HUMAN	254	8.95e-32	ACEEMSGEVR	FSSHLPQPNSLCSLVVEPMENWLQLMLNWD	PQQRGGPVDL
2. IKKB_HUMAN	255	2.25e-27	VSEDLNGTVK	FSSSLPYPNNLNSVLAERLEKWLQLMLMWH	PRQRGTDPTY
10. IKKAB_Nematostella	253	7.98e-26	AYFDAAGELK	FSELLPTPNSLTSFYQERYVFLLRLLLLWD	AKERGGRQRE
11. IKKAB_Aiptasia	248	1.97e-24	AFYNASDEMT	FSEVFPELNTLSRCFQEKYVNLLRLLLLWD	PVKRGGQVHE
6. IKKAB_Ciona	260	1.11e-22	TVETQGSTHV	YSSTIPQPHSLNPIFAKKIESWLQQMLQLD	PQLRGGGVGN
16. IKKAB_Trichoplax	194	9.79e-20	TFLDSNGKVQ	FSTELPIENNLYAPTIQKITNFLQLLLDGN	PKRRGGYNEV

13.

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***E*-value:** 3.5e-020

Site Count: 6

Width: 39
Log Likelihood Ratio: 444

Information Content: 112.1

Relative Entropy: 106.8

Bayes Threshold: 11.5913

Name	Start	*p*-value		Sites	
3. TBK1_HUMAN	558	1.64e-38	NVEKLQVLLN	CMTEIYYQFKKDKAERRLAYNEEQIHKFDKQKLYYHATK	AMTHFTDECV
12. TBK/E_Aiptasia	580	1.54e-32	LFPLVSSLTS	KIEDIYSRYRKDKHLRRLPYAEEQNHNFDRKRLGQLTDK	VTDATNQMFD
9. TBK/E_Nematostella	579	6.50e-32	LLCTVSTLRA	RIEEFYNRFRKEKHLRRLSLADEQNHVFDRRKLSAECKR	VMELTKHSAE
4. IKKE_HUMAN	549	8.33e-30	SIQQIQCCLD	KMNFIYKQFKKSRMRPGLGYNEEQIHKLDKVNFSHLAKR	LLQVFQEECV
5. TBK/E_Ciona	584	2.95e-26	LEERMKVASE	KSREISRLFKTHKKIRRLSHSDDQLHKFEKQRLAEVCEA	SVTLFTDKSV
8. TBK/E_Drosophila	559	1.22e-24	ASAQAKYLVE	RLRDSWQHLLRDRATRTLTYNDEQFHALEKIKVDHNGKR	IKALLLDNVN

14.

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***E*-value:** 8.0e-013

Site Count: 8

Width: 15
Log Likelihood Ratio: 240

Information Content: 46

Relative Entropy: 43.4

Bayes Threshold: 8.39663

Name	Start	*p*-value		Sites	
5. TBK/E_Ciona	41	2.92e-15	TGFVFKGREK	KTGQEYAIKVFNSLN	YMARSLEARR
3. TBK1_HUMAN	30	3.22e-15	TANVFRGRHK	KTGDLFAIKVFNNIS	FLRPVDVQMR
4. IKKE_HUMAN	30	1.39e-14	TASVYKARNK	KSGELVAVKVFNTTS	YLRPREVQVR
12. TBK/E_Aiptasia	32	3.86e-14	TGAVYKGRDK	KTGNEVAIKVTNHLG	MMRPLDVRKR

	Name	Start	*p*-value		Sites	
15.	TBK/Epar_Hydra	33	1.66e-13	TGTVYKCLAK	KTGAPCAAKVFNSQA	DRRPYEVRIR
9.	TBK/E_Nematostella	32	7.08e-13	TGAVYTGRHK	KSGDVVAVKTSNHLG	MMRPLEVRKR
8.	TBK/E_Drosophila	33	1.46e-12	TGSVFQGVNK	ITGESVAVKTFNPYS	HMRPADVQMR
13.	TBK/E_Amphimedon	49	4.18e-12	TGQVFAGYSK	RSGDKVAIKMFTSPS	EYKAMQSEMQ

15.

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***E*-value:** 4.3e-009

Site Count: 6

Width: 40
Log Likelihood Ratio: 431

Information Content: 111.2

Relative Entropy: 103.6

Bayes Threshold: 10.8004

	Name	Start	*p*-value		Sites	
2.	IKKB_HUMAN	460	1.17e-36	GQRAAMMNLL	RNNSCLSKMKNSMASMSQQLKAKLDFFKTSIQIDLEKYSE	QTEFGITSDK
1.	IKKA_HUMAN	457	2.41e-35	GQRAAMLSLL	RYNANLTKMKNTLISASQQLKAKLEFFHKSIQLDLERYSE	QMTYGISSEK
10.	IKKAB_Nematostella	454	8.27e-32	AHRAAMKHAL	KLNAHLTKLRSSLQNDLLRLRERVAFFKESLSTDLQHYSD	EALHLKSDGV
11.	IKKAB_Aiptasia	447	1.21e-27	AHLTLLKYTL	KLHSRLSQLRTNLTSDCIRLEERITFCRESLHTDIEHFSD	VAVDLHANDM
6.	IKKAB_Ciona	456	1.56e-24	ALATLSESIE	RHTNYYEQQLKSFSDAFNMFRGKVDFFKFSIEKDLSNCIE	TDICDNNELL
14.	IKKAB_Hydra	760	2.66e-24	GKNALIKILK	CRMETIDELKNELTELIIQNETGIHFFNKSLETDIQLYGT	DVPQDEWLKA

16.

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***E*-value:** 1.1e-013

Site Count: 5

Width: 50
Log Likelihood Ratio: 483

Information Content: 145.6

Relative Entropy: 139.3

Bayes Threshold: 11.6349

	Name	Start	*p*-value	Sites		
10.	IKKAB_Nematostella	400	3.63e-44	PQSPYRPIFS	LSPSVQAIVTEPKTLLLFEELKKAQGEALHFCQDQKENFQHLLQAHRAAM	KHALKLNAHL
1.	IKKA_HUMAN	403	4.57e-44	VYEGPFASRS	LSDCVNYIVQDSKIQLPIIQLRKVWAEAVHYVSGLKEDYSRLFQGQRAAM	LSLLRYNANL
2.	IKKB_HUMAN	406	5.10e-42	TYETQISPRP	QPESVSCILQEPKRNLAFFQLRKVWGQVWHSIQTLKEDCNRLQQGQRAAM	MNLLRNNSCL
11.	IKKAB_Aiptasia	393	2.17e-33	IPASPRPLFT	LPSTLQSVVTESKTLLPYLEQKRIHAEALSFCYKQMKNYKYLIQAHLTLL	KYTLKLHSRL
14.	IKKAB_Hydra	706	2.01e-29	IDATYKINKD	MPDRVKELLGHYEEIQKYHELLLKWSHCIYYCTKQSNNYDRLLEGKNALI	KILKCRMETI

17.

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***E*-value:** 3.8e-009

Site Count: 4

Width: 49
Log Likelihood Ratio: 402

Information Content: 153.2

Relative Entropy: 144.8

Bayes Threshold: 11.7075

Name	Start	*p*-value	Sites		
1. IKKA_HUMAN	605	2.47e-42	QSQDRVLKEL	FGHLSKLLGCKQKIIDLLPKVEVALSNIKEADNTVMFMQGKRQKEIWHL	LKIACTQSSA
11. IKKAB_Aiptasia	599	7.24e-40	TKREKLNKEM	FTHLRRILQCSTELQNVVPKVIEKTRQISHHKDHILQIQKQRQEDVWCL	ISNKQDSVDS
2. IKKB_HUMAN	609	9.07e-40	QSFEKKVRVI	YTQLSKTVVCKQKALELLPKVEEVVSLMNEDEKTVVRLQEKRQKELWNL	LKIACSKVRG
10. IKKAB_Nematostella	604	1.60e-38	VTREKLLRDV	NTHISCIFQVTQNLQTLVPQLEEKREEINYRHLEIAKLQRKRQEDVWSL	RSQAMEDEIT

18.

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***E*-value:** 7.7e-008

Site Count: 4

Width: 27
Log Likelihood Ratio: 243

Information Content: 87.7

Relative Entropy: 87.7

Bayes Threshold: 11.7542

Name	Start	*p*-value	Sites		
10. IKKAB_Nematostella	224	1.02e-28	CITGRRPFPD	LSPVQWYMEIREKSARDIHAYFDAAGE	LKFSELLPTP
11. IKKAB_Aiptasia	219	1.65e-26	CITGIRPFPD	LSPVNWHREIGQKSPRHIHAFYNASDE	MTFSEVFPEL
1. IKKA_HUMAN	225	4.56e-23	IAGYRPFLHH	LQPFTWHEKIKKKDPKCIFACEEMSGE	VRFSSHLPQP
2. IKKB_HUMAN	226	1.05e-22	ITGFRPFLPN	WQPVQWHSKVRQKSEVDIVVSEDLNGT	VKFSSSLPYP

19.

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***E*-value:** 7.9e-007

Site Count: 7

Width: 15
Log Likelihood Ratio: 214

Information Content: 47.4

Relative Entropy: 44.1

Bayes Threshold: 10.8151

Name	Start	*p*-value	Sites		
19 IKK?_Capsasp . ora	604	7.67e-18	GAAPQAAAEP	AVAAAAAAAAAVTPA	PVAAAPVVAS
19 IKK?_Capsasp . ora	542	8.19e-17	KPVQQQPSAT	TAAAAAAAATATTAA	PVAAAAPAAA
19 IKK?_Capsasp . ora	559	1.23e-16	AATATTAAPV	AAAAPAAAAPAMTPA	ERMQMLMANA
19 IKK?_Capsasp . ora	731	1.83e-13	TATASSAGPM	TTTAAAAAGGAVPPA	SSVAKSSAKA
19 IKK?_Capsasp . ora	355	9.26e-13	EKRDRDLKKF	AAAAAANNAAALSAS	QSVAHMRSGS
19 IKK?_Capsasp . ora	394	1.27e-12	PMNVVPASAE	EVAAAKAAATAQQSA	QQSRLAQLRE
19 IKK?_Capsasp . ora	714	2.46e-11	ELPVPDLPAS	STPATAATATASSAG	PMTTTAAAAA

20.

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***E*-value:** 4.4e-006

Site Count: 4

Width: 46
Log Likelihood Ratio: 377

Information Content: 141.4

Relative Entropy: 136

Bayes Threshold: 8.98905

Name	Start	*p*-value	Sites		
4 IKKE_HU . MAN	338	1.45 e-39	AHNTIAIFQE	AVHKQTSVAPRHQEYLFEGHLCVLEPSVSAQHIAHTTASSPLTLFS	TAIPKGLAFR
3 TBK1_HU . MAN	338	1.08 e-38	SYNTATIFHE	LVYKQTKIISSNQELIYEGRRLVLEPGRLAQHFPKTTEENPIFVVS	REPLNTIGLI
9 TBK/E_Ne . matostella	339	1.15 e-36	RTEMLNRFKQ	MVTEQTSVPCDQQELFYEFQYFQPPDMCPAADFPNTSRDRPVIMIG	GEQLAPDKLV

Name	Start	*p*-value	Sites		
5. TBK/E_Ciona	350	1.92e-35	PEKTLVSFQE	AVAELTEVRSSKQLLLFDGEQFEMEQFVAVKSYPHTTPEHPLILFS	SDINDFQAIT

21.

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⇢

***E*-value:** 1.2e-004

Site Count: 7

Width: 29
Log Likelihood Ratio: 345

Information Content: 73.2

Relative Entropy: 71.1

Bayes Threshold: 11.5483

Name	Start	*p*-value	Sites		
9. TBK/E_Nematostella	399	2.83e-25	APDKLVNLAI	PKITELPPEWTLEGDAAVSKIMANCAYSC	EHSVAVYSDS
8. TBK/E_Drosophila	402	1.63e-23	NVQLPQQLDL	PKFPVFPPNVSVENDASLAKSACSVGHEC	KRRVDIFTSM
3. TBK1_HUMAN	397	4.15e-22	LNTIGLIYEK	ISLPKVHPRYDLDGDASMAKAITGVVCYA	CRIASTLLLY
12. TBK/E_Aiptasia	401	8.12e-22	LPEDLTPRKI	PIVTKLQKDYTLESDAAAAKIRANCAHAC	KVSTLFYTQV
5. TBK/E_Ciona	410	7.18e-20	DFQAITIPHT	CKPPKVKPSLSLDNDSSLAKVCSSTLFDI	RKSVSYLLLV
13. TBK/E_Amphimedon	416	4.09e-19	KPDKLATPVV	TQPPNMPPETTMVDDLRYAKDCTKAIWVM	YRAAETMDRY
4. IKKE_HUMAN	397	6.13e-19	PKGLAFRDPA	LDVPKFVPKVDLQADYNTAKGVLGAGYQA	LRLARALLDG

22.

↥

⇢

***E*-value:** 4.8e-002

Site Count: 5

Width: 15
Log Likelihood Ratio: 162

Information Content: 46.6

Relative Entropy: 46.9

Bayes Threshold: 12.4006

	Name	Start	*p*-value	Sites		
10.	IKKAB_Nematostella	697	3.97e-16	FAQAITSVKE	EQNTITQSLDWSFLE	DDDHTNS
2.	IKKB_HUMAN	729	1.08e-15	LENAIQDTVR	EQDQSFTALDWSWLQ	TEEEEHSCLE
1.	IKKA_HUMAN	730	3.13e-15	LSTIIHEANE	EQGNSMMNLDWSWLT	E
11.	IKKAB_Aiptasia	700	9.07e-14	SEVVQSVKVE	YGNVAPESLDWSFLE	EDTEV
17.	IKK?_Mnemiopsis	514	4.19e-13	GVKGDKWTTA	KQHKFFDKIDWIFLE	AGSATPEFVP

MOTIF LOCATIONS

Only Motif Sites
Motif Sites+Scanned Sites
All Sequences

	Name	*p*-value	Motif Location
1.	IKKA_HUMAN	0.00e+0	
2.	IKKB_HUMAN	4.12e-277	
3.	TBK1_HUMAN	0.00e+0	
4.	IKKE_HUMAN	3.68e-278	
5.	TBK/E_Ciona	2.18e-267	
6.	IKKAB_Ciona	3.80e-150	
7.	IKKAB_Drosophila	5.57e-74	
8.	TBK/E_Drosophila	2.15e-230	
9.	TBK/E_Nematostella	0.00e+0	
10.	IKKAB_Nematostella	2.23e-279	
11.	IKKAB_Aiptasia	2.49e-258	
12.	TBK/E_Aiptasia	2.04e-250	
13.	TBK/E_Amphimedon	2.69e-159	
14.	IKKAB_Hydra	5.99e-131	
15.	TBK/Epar_Hydra	8.12e-135	
16.	IKKAB_Trichoplax	3.71e-63	

	Name	*p*-value	Motif Location
17.	IKK?_Mnemiopsis	2.88e-51	
18.	IKK?_Pleurobrachia	5.05e-24	
19.	IKK?_Capsaspora	1.03e-72	
20.	IKK?_Monosiga	3.35e-66	

INPUTS & SETTINGS

Sequences

Source	Alphabet	Sequence Count
sequences.fa	Protein	20

Background

	Name	Freq.	Bg.
A	Alanine	0.061	0.061
C	Cysteine	0.019	0.019
D	Aspartic acid	0.053	0.053
E	Glutamic acid	0.077	0.077
F	Phenylalanine	0.037	0.037
G	Glycine	0.050	0.050
H	Histidine	0.028	0.028
I	Isoleucine	0.058	0.058
K	Lysine	0.069	0.069
L	Leucine	0.100	0.100
M	Methionine	0.026	0.026

	Name	Freq.	Bg.
N	Asparagine	0.045	0.045
P	Proline	0.040	0.040
Q	Glutamine	0.048	0.048
R	Arginine	0.057	0.057
S	Serine	0.071	0.071
T	Threonine	0.056	0.056
V	Valine	0.064	0.064
W	Tryptophan	0.011	0.011
Y	Tyrosine	0.031	0.031

	Name	Freq.	Bg.
A	Alanine	0.061	0.061
C	Cysteine	0.019	0.019
D	Aspartic acid	0.053	0.053
E	Glutamic acid	0.077	0.077
F	Phenylalanine	0.037	0.037
G	Glycine	0.050	0.050
H	Histidine	0.028	0.028
I	Isoleucine	0.058	0.058
K	Lysine	0.069	0.069

	Name	Freq.	Bg.
L	Leucine	0.100	0.100
M	Methionine	0.026	0.026
N	Asparagine	0.045	0.045
P	Proline	0.040	0.040
Q	Glutamine	0.048	0.048
R	Arginine	0.057	0.057
S	Serine	0.071	0.071
T	Threonine	0.056	0.056
V	Valine	0.064	0.064
W	Tryptophan	0.011	0.011
Y	Tyrosine	0.031	0.031

Other Settings

Motif Site Distribution	ANR: Any number of sites per sequence
Site Strand Handling	This alphabet only has one strand
Maximum Number of Motifs	22
Motif E-value Threshold	no limit
Minimum Motif Width	6
Maximum Motif Width	50
Minimum Sites per Motif	2

Maximum Sites per Motif	50
Bias on Number of Sites	0.8
Sequence Prior	Mega-weight Dirichlets Mix Plus
Sequence Prior Strength	71705
EM Starting Point Source	From substrings in input sequences
EM Starting Point Map Type	Point Accepted Mutation
EM Starting Point Fuzz	120
EM Maximum Iterations	50
EM Improvement Threshold	0.00001
Trim Gap Open Cost	11
Trim Gap Extend Cost	1
End Gap Treatment	Same cost as other gaps

Hide Advanced Settings

MEME version

4.11.2 (Release date: Mon Oct 24 12:27:06 2016 -0700)

Reference

Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994.

Command line

A.12 TAK1 MEME Output

```
********************************************************************
MEME - Motif discovery tool
********************************************************************
MEME version 4.11.3 (Release date: Sat Mar 11 20:16:08 2017 -0800)

For further information on how to interpret these results or to get
a copy of the MEME software please access http://meme-suite.org .

This file may be used as input to the MAST algorithm for searching
sequence databases for matches to groups of motifs.  MAST is
available
for interactive use and downloading at http://meme-suite.org .
********************************************************************


********************************************************************
REFERENCE
********************************************************************
If you use this program in your research, please cite:

Timothy L. Bailey and Charles Elkan,
"Fitting a mixture model by expectation maximization to discover
motifs in biopolymers", Proceedings of the Second International
Conference on Intelligent Systems for Molecular Biology, pp. 28-36,
AAAI Press, Menlo Park, California, 1994.
********************************************************************


********************************************************************
TRAINING SET
********************************************************************
DATAFILE= TAK1_Training_Set_v5.txt
ALPHABET= ACDEFGHIKLMNPQRSTVWY
Sequence name            Weight Length  Sequence name  Weight Length
-------------            ------ ------  -------------  ------ ------
TAK1_HUMAN               1.0000    606  TAK1_DROSOPHILA
1.0000    393
TAK1_CIONA               1.0000    608  TAK1_TRICHOPLAX
1.0000    261
TAK1_NEMATOSTELLA        1.0000    280  TAK1_AMPHIMEDON
1.0000    477
********************************************************************

********************************************************************
COMMAND LINE SUMMARY
********************************************************************
This information can also be useful in the event you wish to report
a problem with the MEME software.
```

```
command: meme TAK1_Training_Set_v5.txt -protein -oc . -nostatus -
time 18000 -maxsize 60000 -mod anr -nmotifs 20 -minw 6 -maxw 50

model:  mod=           anr    nmotifs=        20    evt=
inf
object function=  E-value of product of p-values
width:  minw=            6    maxw=           50
width:  wg=             11    ws=              1    endgaps=
yes
nsites: minsites=        2    maxsites=       30    wnsites=
0.8
theta:  spmap=         pam    spfuzz=        120
global: substring=     yes    branching=      no    wbranch=
no
em:     prior=       megap    b=           13125    maxiter=
50
        distance=    1e-05
data:   n=            2625    N=               6    shuffle=
-1

sample: seed=            0    ctfrac=         -1    maxwords=
-1
Dirichlet mixture priors file: prior30.plib
Letter frequencies in dataset:
A 0.059 C 0.021 D 0.051 E 0.074 F 0.030 G 0.054 H 0.031 I 0.054 K
0.061
L 0.075 M 0.033 N 0.038 P 0.064 Q 0.046 R 0.057 S 0.085 T 0.054 V
0.066
W 0.014 Y 0.032
Background letter frequencies (from dataset with add-one prior
applied):
A 0.059 C 0.021 D 0.051 E 0.074 F 0.030 G 0.054 H 0.031 I 0.054 K
0.061
L 0.075 M 0.033 N 0.038 P 0.064 Q 0.047 R 0.057 S 0.085 T 0.054 V
0.065
W 0.014 Y 0.032
********************************************************************


********************************************************************
MOTIF  1 MEME    width =  41  sites =   6  llr = 611  E-value =
1.6e-104
********************************************************************
--------------------------------------------------------------------
      Motif 1 Description
--------------------------------------------------------------------
Simplified        A  ::2::::75::a::2:::::::2:::::::3:::::::2::
pos.-specific     C  ::::::::::::::::::2:::::a::::::::::::::::
probability       D  ::2:::::::::::::::2::::::a:::::::::::::::
matrix            E  :::::::::::::a::5:::::7::::::::::::a:::::
                  F  :::::::::::::::7:::::::::::7:7:::::::::::
```

```
                  G  :::::a:::::::::::8::::::::::::7::::::::::
                  H  :::::::::::::::::2:::::::::::::::::::::::
                  I  ::::2::::::::::3::::::::::2::::a7:::23:::
                  K  2:::7:::::::::::3::3:::a:::::::::::::::::
                  L  :::::::2::::::::::2:::::::::::::::8::23:::
                  M  7::2::::::a::::::::::::::::::::::22::33:::
                  N  ::57::::::::::::::23:::::::::::::::::::::
                  P  ::::::::2:::a::::::2:::::::::::::::::::::
                  Q  ::::2:::::::::::2::2::::::::::::::::::::3
                  R  ::::::::3:::::::::2:::::::::::::::::::::a7
                  S  :::2::7:::::::::::2::5::::::a:::::::::2::
                  T  :a::::3::::::::::::::52:::::::::2:::::7::
                  V  ::2::::2::::::8::::::::::::8:::::::::3::::
                  W  :::::::::7:::::::::::::::::::3::::a::::::
                  Y  2::::::::3::::::::::a::::::3:::::::::::::

         bits    6.2                                   *
                 5.5                         *         *
                 4.9          **         *   *         *
                 4.3  *   *   ***        *  *** * * *  *    *
Relative         3.7 **   *   ***** * *  *  *** *** *  **   *
Entropy          3.1 ** ****  ******* *  ** *************  ***
(146.9 bits)     2.5 ****************** **********************
                 1.8 *****************************************
                 1.2 *****************************************
                 0.6 *****************************************
                 0.0 -----------------------------------------

Multilevel           MTNNKGSAAWMAPEVFEGXKYSEKCDVFSFGIILWEMITRR
consensus                  T RY     IK  N T     Y WA     VL  Q
sequence                                                    M


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
TAK1_CIONA                  173  2.83e-51  FGTACDQHTH
MTNNKGSAAWMAPEVFEGCQYSEKCDVFSWGIILWEVLTRR KPFDDLGGPA
TAK1_HUMAN                  186  2.83e-51  FGTACDIQTH
MTNNKGSAAWMAPEVFEGSNYSEKCDVFSWGIILWEVITRR KPFDEIGGPA
TAK1_NEMATOSTELLA           164  3.39e-50  FGTACDLKTY
MTNNKGSAAWMAPEVFEGNNYTEKCDVYSFGIILWEMISRR KPFDDMAGSP
TAK1_TRICHOPLAX             146  2.71e-46  FGTVCTAHTQ
MTVNKGSAPWMAPEVFQGRKYSEKCDVFSFAIIMWEIMTRR EPYDHMGTER
TAK1_AMPHIMEDON             155  9.64e-35  TCRNLETNLL
YTASIGTVRYMAPEVIKGDPYTTKCDIFSFAITLWEMLARQ VPTIESVSAN
```

```
TAK1_DROSOPHILA             163  1.59e-34 FGLATDMSNN
KTDMQGTLRYMAPEAIKHLKYTAKCDVYSFGIMLWELMTRQ LPYSHLENPN
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_CIONA                        2.8e-51  172_[1]_395
TAK1_HUMAN                        2.8e-51  185_[1]_380
TAK1_NEMATOSTELLA                 3.4e-50  163_[1]_76
TAK1_TRICHOPLAX                   2.7e-46  145_[1]_75
TAK1_AMPHIMEDON                   9.6e-35  154_[1]_282
TAK1_DROSOPHILA                   1.6e-34  162_[1]_190
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 1 width=41 seqs=6
TAK1_CIONA               (  173)
MTNNKGSAAWMAPEVFEGCQYSEKCDVFSWGIILWEVLTRR  1
TAK1_HUMAN               (  186)
MTNNKGSAAWMAPEVFEGSNYSEKCDVFSWGIILWEVITRR  1
TAK1_NEMATOSTELLA        (  164)
MTNNKGSAAWMAPEVFEGNNYTEKCDVYSFGIILWEMISRR  1
TAK1_TRICHOPLAX          (  146)
MTVNKGSAPWMAPEVFQGRKYSEKCDVFSFAIIMWEIMTRR  1
TAK1_AMPHIMEDON          (  155)
YTASIGTVRYMAPEVIKGDPYTTKCDIFSFAITLWEMLARQ  1
TAK1_DROSOPHILA          (  163)
KTDMQGTLRYMAPEAIKHLKYTAKCDVYSFGIMLWELMTRQ  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 41 n= 2385 bayes= 8.28917 E= 1.6e-
104
  -292   -326   -398   -379   -200   -390   -326   -211    -59   -
164    459   -315   -463   -305   -272   -370   -304   -250   -261
24
  -212   -268   -366   -437   -339   -336   -377   -287   -348   -
364   -308   -207   -425   -334   -354   -108    399   -261   -391
-398
    49   -282     85   -134   -252   -180   -120   -250   -129   -
260   -260    380   -306   -130   -187   -138   -142     14   -302
-244
```

```
  -276   -312   -177   -356   -301   -278   -117   -291   -270   -
348    -68    441   -393   -247   -311   -103   -214   -333   -313
-313
  -225   -346   -306   -243   -369   -316   -229      8    355   -
306   -309   -196   -393     52    -13   -297   -242   -322   -346
-325
  -184   -357   -270   -372   -403    407   -364   -447   -337   -
462   -432   -216   -433   -389   -335   -286   -351   -405   -377
-400
  -113   -178   -292   -374   -276   -254   -320   -319   -275   -
323   -298   -119   -336   -306   -275    298    181   -325   -340
-305
   347    -95   -339   -327   -189   -139   -330   -122   -304     -
6   -181   -274   -416   -308   -306   -105   -159     46   -289   -
287
   271   -192   -202   -173   -261   -161   -203   -261    -80   -
244   -246   -138    111   -134    200   -131   -134   -200   -317
-269
  -381   -345   -427   -466     14   -402   -240   -359   -415   -
236   -326   -336   -490   -368   -374   -428   -388   -350    570
236
  -406   -372   -514   -557   -335   -480   -496   -248   -490   -
180    480   -460   -538   -493   -536   -488   -416   -317   -323
-328
   384   -141   -377   -383   -295   -160   -389   -300   -369   -
297   -299   -312   -421   -363   -363   -135   -200   -173   -360
-374
  -170   -356   -328   -347   -347   -310   -345   -373   -309   -
332   -395   -318    380   -301   -332   -276   -270   -340   -431
-415
  -450   -568   -203    370   -548   -480   -482   -517   -538   -
579   -586   -388   -650   -377   -552   -552   -512   -544   -565
-568
    28   -168   -342   -346   -219   -315   -317     20   -334   -
163   -215   -311   -356   -345   -308   -304   -139    350   -364
-367
  -280   -259   -466   -480    448   -429   -357    167   -451    -
54   -146   -393   -460   -423   -446   -387   -323   -127   -189
-61
  -130   -414    -28    250   -359   -242   -196   -324    198   -
286   -286   -131   -305    148   -105   -214   -184   -278   -383
-307
  -164   -342   -240   -344   -380    398     36   -426   -308   -
444   -410   -184   -418   -362   -311   -262   -328   -386   -360
-372
   -35    186    112    -44   -170   -136    -79   -184     -8
38   -157    160   -220    -21     96     59    -52   -158   -236
-150
   -84   -288    -83    -72   -238   -161   -106   -252    200   -
214   -210    249     68    141    -35   -121   -102   -220   -278
-201
```

```
  -389   -383   -462   -513      1   -418   -216   -384   -461   -
321   -387   -370   -498   -422   -428   -440   -424   -395   -143
482
  -116   -186   -294   -371   -282   -258   -320   -281   -278   -
321   -275   -125   -348   -289   -282    255    273   -265   -344
-323
    71   -377    -50    312   -370   -251   -258   -342   -157   -
327   -326   -165   -336   -113   -245   -230     67   -295   -426
-351
  -318   -374   -451   -438   -472   -416   -387   -384    389   -
434   -423   -312   -473   -371    -55   -445   -361   -451   -404
-448
  -342    550   -517   -516   -426   -498   -500   -408   -540   -
448   -435   -462   -572   -519   -489   -485   -380   -463   -542
-525
  -294   -384    411   -128   -368   -329   -293   -399   -384   -
408   -424    -60   -485   -353   -390   -345   -360   -387   -394
-363
   -98   -187   -376   -381   -219   -371   -356    123   -368   -
142   -206   -345   -393   -382   -346   -362   -164    348   -392
-378
  -328   -291   -434   -461    444   -416   -178   -269   -421   -
186   -274   -327   -456   -378   -395   -372   -373   -296    -73
293
  -150   -239   -342   -430   -340   -270   -378   -401   -352   -
392   -384   -198   -389   -372   -350    332      4   -379   -396
-364
  -362   -310   -466   -501    445   -434   -206   -272   -450   -
185   -276   -345   -479   -394   -417   -402   -393   -307    386
80
   145   -253   -276   -366   -379    377   -360   -413   -338   -
424   -397   -210   -389   -364   -334   -203   -250   -329   -378
-394
  -268   -303   -422   -454   -205   -416   -452    384   -396    -
45   -134   -359   -491   -417   -428   -397   -267     60   -371
-310
  -216   -259   -384   -400   -159   -370   -384    356   -342    -
10     70   -307   -444   -354   -368   -334    -14     84   -312
-259
  -277   -289   -470   -423    -77   -431   -370    -59   -382
338    129   -384   -421   -315   -345   -406   -285   -133   -277
-276
  -365   -344   -399   -439    -84   -379   -382   -387   -400   -
228   -328   -353   -480   -373   -364   -432   -384   -354    601
-148
  -450   -568   -203    370   -548   -480   -482   -517   -538   -
579   -586   -388   -650   -377   -552   -552   -512   -544   -565
-568
  -183   -212   -452   -430    -95   -369   -364    197   -383
127    276   -341   -435   -353   -377   -346   -199    212   -275
-246
```

```
  -271   -284   -539   -508    -61   -455   -422    243   -462
225    289   -430   -489   -387   -435   -445   -284    -78   -274
-275
    75   -190   -315   -371   -293   -250   -326   -241   -289   -
316   -248   -146   -362   -270   -298     81    354   -204   -350
-359
  -315   -296   -424   -460   -408   -366   -231   -392   -132   -
368   -412   -290   -394   -246    399   -388   -359   -462   -297
-394
  -250   -317   -334   -275   -381   -314   -191   -351     -9   -
310   -331   -203   -381    162    361   -308   -266   -361   -305
-326
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 1 position-specific probability matrix
---------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 41 nsites= 6 E= 1.6e-104
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.000000  0.666667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.166667
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.666667  0.000000
0.000000  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.666667  0.000000  0.000000  0.000000  0.000000
0.166667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.666667  0.333333  0.000000  0.000000  0.000000
 0.666667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.166667
0.000000  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.666667  0.333333
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.833333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.666667  0.000000
0.000000  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.333333  0.000000  0.000000  0.000000  0.000000
0.166667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.833333
0.166667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.166667  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.166667  0.000000
0.000000  0.166667  0.166667  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.333333  0.000000  0.000000  0.333333  0.166667
0.166667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.500000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.666667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.833333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.666667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.333333
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.666667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.333333  0.000000
 0.333333  0.000000  0.000000  0.000000  0.000000  0.666667
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.666667  0.000000  0.000000  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.833333  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.166667  0.333333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.333333  0.333333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.666667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.333333  0.666667  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 1 regular expression
--------------------------------------------------------------------------------
MTNNKG[ST]A[AR][WY]MAPEV[FI][EK]GX[KN]Y[ST]EKCDV[FY]S[FW][GA]IILWE[M
V][ILM]TR[RQ]
--------------------------------------------------------------------------------
```

```
Time  1.90 secs.

*********************************************************************


*********************************************************************
MOTIF  2 MEME    width =  29  sites =   6  llr = 427  E-value = 
4.1e-066
*********************************************************************
---------------------------------------------------------------------
      Motif 2 Description
---------------------------------------------------------------------
Simplified        A  :::::::::::::2:2::::::::::7::
pos.-specific     C  ::::::::::::::3::::::a::::27:
probability       D  :::a:::::::::::::2::::a:::::7
matrix            E  ::::::::::::::::2::::::::::::
                  F  ::::::::::::3::::::::::a:::::
                  G  :::::::::::::227::::::::a::::
                  H  :a:::::::::::::2:::::::::::::
                  I  5:::3:::::::::::::::7::::::::
                  K  :::::a:::::::::::::a:::::::::
                  L  2:::7::2:7a8::::::8:2::::2:::
                  M  2::::::::3:2:::::::::::::::::
                  N  ::::::::a::::53:::::::::::::2
                  P  ::::::85:::::::::::::::::::::
                  Q  :::::::2::::::2::::::::::::::
                  R  ::a::::::::::2:::2:::::::::2:
                  S  ::::::22::::::::2::::::::::::
                  T  ::::::::::::3:::7::::::::8:22
                  V  2:::::::::::2::::72:2:::::2::
                  W  :::::::::::::::::::::::::::::
                  Y  ::::::::::::2::::::::::::::::

         bits    6.2
                 5.5                      *
                 4.9  *      *            * *
                 4.3  *** *  *          * ****
Relative         3.7  *** *  * *        * ***** *
Entropy          3.1  ****** ****  ** ************
(102.6 bits)     2.5 ******* *********************
                 1.8 *****************************
                 1.2 *****************************
                 0.6 *****************************
                 0.0 -----------------------------

Multilevel           IHRDLKPPNLLLFNCGTVLKICDFGTACD
consensus                I    M  T N
sequence


---------------------------------------------------------------------
```

```
---------------------------------------------------------------------
     Motif 2 sites sorted by position p-value
---------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
TAK1_CIONA                  140  1.76e-37 YLHNMKPKAL
IHRDLKPPNLLLTNNGTVLKICDFGTACD QHTHMTNNKG
TAK1_NEMATOSTELLA           131  6.03e-35 YLHSMKPKAI
IHRDLKPPNLLLTRCGTVVKICDFGTACD LKTYMTNNKG
TAK1_HUMAN                  153  6.82e-35 YLHSMQPKAL
IHRDLKPPNLLLVAGGTVLKICDFGTACD IQTHMTNNKG
TAK1_TRICHOPLAX             113  1.45e-28 YLHSMTPKPL
MHRDLKPLNMLMFNCATVLKVCDFGTVCT AHTQMTVNKG
TAK1_DROSOPHILA             130  2.15e-26 AYLHSLDRPI
VHRDIKPQNMLLYNQHEDLKICDFGLATD MSNNKTDMQG
TAK1_AMPHIMEDON             120  1.79e-24 GLKHIHSKRI
LHRDIKSSNLLLFGNGSRLKLCDFGTCRN LETNLLYTAS
---------------------------------------------------------------------

---------------------------------------------------------------------
     Motif 2 block diagrams
---------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_CIONA                        1.8e-37  139_[2]_440
TAK1_NEMATOSTELLA                   6e-35  130_[2]_121
TAK1_HUMAN                        6.8e-35  152_[2]_425
TAK1_TRICHOPLAX                   1.4e-28  112_[2]_120
TAK1_DROSOPHILA                   2.1e-26  129_[2]_235
TAK1_AMPHIMEDON                   1.8e-24  119_[2]_329
---------------------------------------------------------------------

---------------------------------------------------------------------
     Motif 2 in BLOCKS format
---------------------------------------------------------------------
BL   MOTIF 2 width=29 seqs=6
TAK1_CIONA               (  140) IHRDLKPPNLLLTNNGTVLKICDFGTACD  1
TAK1_NEMATOSTELLA        (  131) IHRDLKPPNLLLTRCGTVVKICDFGTACD  1
TAK1_HUMAN               (  153) IHRDLKPPNLLLVAGGTVLKICDFGTACD  1
TAK1_TRICHOPLAX          (  113) MHRDLKPLNMLMFNCATVLKVCDFGTVCT  1
TAK1_DROSOPHILA          (  130) VHRDIKPQNMLLYNQHEDLKICDFGLATD  1
TAK1_AMPHIMEDON          (  120) LHRDIKSSNLLLFGNGSRLKLCDFGTCRN  1
//

---------------------------------------------------------------------
```

```
---------------------------------------------------------------------
      Motif 2 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 29 n= 2457 bayes= 9.12259 E= 4.1e-
066
  -241   -285   -387   -413   -169   -391   -408    354   -353
43     44   -318   -460   -370   -385   -355   -233    119   -327
-273
  -361   -355   -310   -395   -233   -363    483   -449   -408   -
350   -360   -139   -434   -149   -255   -340   -329   -414   -291
-120
  -315   -296   -424   -460   -408   -366   -231   -392   -132   -
368   -412   -290   -394   -246    399   -388   -359   -462   -297
-394
  -294   -384    411   -128   -368   -329   -293   -399   -384   -
408   -424    -60   -485   -353   -390   -345   -360   -387   -394
-363
  -278   -286   -514   -476    -79   -457   -413    210   -434
309    -48   -421   -466   -365   -403   -443   -289    -80   -290
-287
  -318   -374   -451   -438   -472   -416   -387   -384    389   -
434   -423   -312   -473   -371    -55   -445   -361   -451   -404
-448
   -97   -296   -267   -281   -294   -255   -288   -310   -244   -
272   -330   -251    360   -237   -271    -18   -201   -274   -395
-369
   -90   -288   -228   -225   -263   -241   -247   -271   -187    -
17   -285   -204    330     48   -223    -18   -176   -242   -360
-319
  -327   -337   -202   -413   -325   -305   -136   -321   -315   -
386   -381    452   -418   -283   -351   -209   -248   -373   -331
-337
  -294   -302   -516   -471    -64   -461   -402    -51   -427
316    255   -424   -458   -350   -389   -446   -304   -134   -276
-279
  -302   -315   -480   -449   -111   -431   -391    -92   -406
353    -70   -404   -440   -344   -370   -428   -313   -162   -304
-295
  -277   -289   -470   -423    -77   -431   -370    -59   -382
338    129   -384   -421   -315   -345   -406   -285   -133   -277
-276
  -117   -162   -314   -301    309   -265   -120    -59   -259    -
72   -103   -213   -336   -244   -255   -215    183     93    -95
256
    90   -275    -73   -134   -265    100   -126   -285    -85   -
269   -267    350   -292   -109     87   -124   -130   -259   -313
-240
  -103    332    -48   -139   -269    126   -139   -292   -109   -
277   -281    283   -295    140   -168   -118   -130   -260   -336
-244
```

```
    -7   -320   -233   -330   -374    390     27   -410   -296   -
427   -395   -176   -405   -344   -302   -243   -302   -364   -357
-370
  -150   -213   -226     -4   -278   -280   -275   -224   -223   -
297   -230   -103   -355   -216   -252     69    353   -198   -335
-328
   -59   -175    -40   -234   -207   -289   -258      6   -211   -
162   -204   -221   -332   -243    -44   -270   -127    336   -332
-315
  -262   -277   -466   -422    -88   -423   -372    -44   -381
335    -43   -379   -422   -320   -348   -399   -272     49   -285
-278
  -318   -374   -451   -438   -472   -416   -387   -384    389   -
434   -423   -312   -473   -371    -55   -445   -361   -451   -404
-448
  -250   -293   -388   -418   -187   -401   -425    362   -359
34    -99   -323   -470   -382   -395   -364   -240    121   -345
-285
  -342    550   -517   -516   -426   -498   -500   -408   -540   -
448   -435   -462   -572   -519   -489   -485   -380   -463   -542
-525
  -294   -384    411   -128   -368   -329   -293   -399   -384   -
408   -424    -60   -485   -353   -390   -345   -360   -387   -394
-363
  -309   -260   -433   -465    487   -418   -389   -230   -450   -
137   -245   -392   -439   -457   -459   -363   -392   -270   -181
-48
  -184   -357   -270   -372   -403    407   -364   -447   -337   -
462   -432   -216   -433   -389   -335   -286   -351   -405   -377
-400
  -167   -215   -329   -377   -222   -320   -325   -154   -284
34   -193   -160   -389   -276   -296    -61    370   -152   -325
-313
   356    123   -335   -328   -229   -118   -340   -212   -310   -
222   -223   -274   -416   -315   -310    -84   -159     14   -303
-318
  -284    544   -476   -473   -398   -431   -455   -376   -415   -
409   -402   -405   -533   -445   -197   -410   -168   -406   -506
-479
  -261   -369    395   -116   -355   -263   -249   -390   -313   -
395   -409     66   -441   -295   -347   -274    -67   -375   -388
-338
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------------------
      Motif 2 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 29 nsites= 6 E= 4.1e-066
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.166667  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.833333
0.000000  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.500000
0.166667  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.333333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.833333  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.333333  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.333333  0.166667  0.000000  0.166667
 0.166667  0.000000  0.000000  0.000000  0.000000  0.166667
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.333333  0.000000  0.000000  0.000000  0.166667
0.000000  0.000000  0.000000  0.000000  0.000000  0.333333  0.000000
0.166667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.166667  0.000000  0.000000  0.000000  0.000000  0.666667
0.166667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.166667  0.666667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.000000  0.666667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.833333  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.666667  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.833333  0.000000  0.000000  0.000000
 0.666667  0.166667  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
 0.000000  0.666667  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.166667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 2 regular expression
--------------------------------------------------------------------
IHRD[LI]KPPN[LM]LL[FT]N[CN]GTVLKICDFGTACD
--------------------------------------------------------------------




Time  3.45 secs.

********************************************************************


********************************************************************
MOTIF  3 MEME    width =  47  sites =   5  llr = 533  E-value =
9.3e-058
********************************************************************
--------------------------------------------------------------------
      Motif 3 Description
--------------------------------------------------------------------
Simplified        A  :4:2:::6::::2::::::::::::::::::::22::2:::::::::
pos.-specific     C  ::::::::::::::::::::2::::::::::8:::::::::::::::
probability       D  :::::::::::::::2:::::::::::::::::4:8:4:::::22::
matrix            E  ::::::::::2::::::::::::::84::2::::::::4::::26::
                  F  ::8::::::::::::::::::::2::::::::::::::::::4::::
                  G  :::::::::::a:::::::6:::::::::::::::::::::::::::
                  H  :::::::::6::::::::::2::::::::::::::::::::::::::
                  I  ::::a:::::2::::::8::4:::4:::2::::::::::::::::8:
                  K  ::::::::::::4::::6:::6::::::::2:::42::2::::2:::
                  L  :::::4::::::::::a2::2:::2::a2:::::::::::2::::2:
                  M  :::::6::2:::::::::::::::::::6:::::::::::::4::::
                  N  2:::::::::2::::::::4:::::22::::::::::2:::::2:::
                  P  62::::::::::::a8:::::a26::::::::::::a:::8::::::
                  Q  :::::::4::2:::::::2:::2:::::::::::4:::2::::::::
                  R  2::6::::::::2a::::::::::::::::6::::::::a::::2::
                  S  :4:::::::2::::::::::::::::4:::22:4:::2:::822:::
                  T  :::2::::::2:2::::::::::::::::8:::::::::::2:::::
                  V  ::::::::82::::::::2::::24:::::::::::::2:::::::a
                  W  ::::::8:::::::::::::::::::::::::a::::::::::::::
                  Y  ::2:::2::::::::::::::::::::::::::::::::::::::::

         bits    6.2                                 *
                 5.5                                 *
                 4.9       *                         *
                 4.3   * * *    * *                 **      *
Relative         3.7   * *** *  * ** ** * *     * * **  **  *     **
Entropy          3.1 * * ****** * ***** * * * * *** **  **  ****  **
(153.7 bits)     2.5 ********** *************************** **** ***
                 1.8 ***********************************************
                 1.2 ***********************************************
```

```
                 0.6 ***********************************************
                 0.0 -----------------------------------------------

Multilevel           PAFRIMWAVHEGKRPPLIKGIPKPIEELMTRCWDKDPDERPSFDEIV
consensus            NSYA LYQMSI A  D LQNC PFVNS IEKS SQK AK LTMEDL
sequence             RP T     VN R     V H QVL N L S  AA  NQ   SKR
                               Q T       L                SV    N
                               T                                S
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
TAK1_HUMAN                  235  3.80e-52 RRKPFDEIGG
PAFRIMWAVHNGTRPPLIKNLPKPIESLMTRCWSKDPSQRPSMEEIV KIMTHLMRYF
TAK1_NEMATOSTELLA           214  3.33e-49 RKPFDDMAGS
PPFRIMWAVHIGRRPPLIKNIPKPIEELITSCWDKDPDKRPSFSRIV IFLNHLMQFF
TAK1_CIONA                  222  2.03e-47 RRKPFDDLGG
PAFRIMWAVHTGARPDLIQGCPQPVESLMTRCWSAKPNERPSMDEIV VAMSDLMQFF
TAK1_TRICHOPLAX             197  6.09e-44 EPYDHMGTER
RSFTILWQVSEGKRPPLIKGIPKVLENLMTRSWAQDPDERPSFKEIV QKLEYLYQVN
TAK1_AMPHIMEDON             205  1.48e-31 QVPTIESVSA
NSYAILYQMVQGKRPPLLVGHPPFVNELLEKCWDQDPAVRLTSNDLV DKFNKICEHF
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_HUMAN                        3.8e-52  234_[3]_325
TAK1_NEMATOSTELLA                 3.3e-49  213_[3]_20
TAK1_CIONA                          2e-47  221_[3]_340
TAK1_TRICHOPLAX                   6.1e-44  196_[3]_18
TAK1_AMPHIMEDON                   1.5e-31  204_[3]_226
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 3 width=47 seqs=5
TAK1_HUMAN               (  235)
PAFRIMWAVHNGTRPPLIKNLPKPIESLMTRCWSKDPSQRPSMEEIV  1
TAK1_NEMATOSTELLA        (  214)
PPFRIMWAVHIGRRPPLIKNIPKPIEELITSCWDKDPDKRPSFSRIV  1
TAK1_CIONA               (  222)
PAFRIMWAVHTGARPDLIQGCPQPVESLMTRCWSAKPNERPSMDEIV  1
TAK1_TRICHOPLAX          (  197)
RSFTILWQVSEGKRPPLIKGIPKVLENLMTRSWAQDPDERPSFKEIV  1
```

```
TAK1_AMPHIMEDON           (  205)
NSYAILYQMVQGKRPPLLVGHPPFVNELLEKCWDQDPAVRLTSNDLV  1
//
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 3 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 47 n= 2349 bayes= 9.12486 E= 9.3e-
058
   -94   -293   -190   -212   -274   -222   -223   -289   -142   -
252   -296    102    332   -171     50   -180   -173   -257   -360
-312
   263   -136   -273   -280   -285   -125   -299   -301   -260   -
291   -289   -191    133   -248   -280    186    -94   -200   -354
-330
  -301   -251   -422   -450    476   -411   -291   -225   -429   -
132   -237   -359   -432   -420   -429   -351   -375   -262   -128
126
    51   -240   -249   -226   -295   -232   -182   -278    -57   -
263   -276   -162   -320   -141    351   -204     51   -265   -282
-287
  -254   -291   -406   -436   -191   -403   -436    379   -378    -
29   -117   -343   -478   -399   -411   -381   -252     75   -355
-294
  -303   -305   -541   -521    -70   -469   -432    -53   -465
214    403   -448   -497   -396   -447   -469   -318   -139   -268
-271
  -358   -336   -394   -432    -58   -376   -348   -373   -392   -
218   -318   -342   -475   -362   -356   -423   -375   -344    596
-10
   305   -163   -185   -139   -263   -143   -231   -266   -142   -
254   -256   -153   -309    248   -181   -120   -138   -187   -327
-286
   -91   -177   -368   -366   -169   -346   -334     41   -346    -
94    117   -323   -380   -352   -327   -334   -154    341   -338
-319
  -151   -226   -187   -226   -135   -236    425   -226   -205   -
197   -204    -39   -319    -52   -141    -17   -161      7   -207
-39
   -27   -233    -50     97   -167   -133    -72     82      4   -
152   -147    162   -211    156    -53    -75    118   -146   -229
-150
  -172   -346   -259   -361   -392    406   -354   -436   -326   -
452   -421   -205   -423   -378   -325   -275   -339   -394   -368
-390
    92   -283   -150   -107   -250   -199   -125   -243    270   -
213   -211    -77   -278    -49    133   -151     98   -220   -274
-214
  -309   -292   -418   -452   -403   -361   -226   -387   -125   -
362   -406   -284   -389   -240    398   -382   -353   -455   -293
```

```
-388
  -146   -335   -305   -323   -325   -289   -323   -349   -285   -
309   -371   -294    377   -278   -309   -253   -246   -316   -411
-393
  -103   -304     53   -246   -291   -251   -276   -308   -233   -
269   -328   -219    356   -225   -264   -205   -200   -275   -390
-360
  -284   -298   -464   -431    -95   -417   -375    -76   -387
350    -54   -387   -425   -327   -353   -410   -295   -144   -288
-278
  -249   -288   -396   -423   -159   -403   -421    364   -364
62    -87   -329   -469   -379   -396   -369   -241     86   -330
-278
  -148   -308   -203   -141   -290   -241   -154   -258    314   -
234   -239   -120   -322    128     12   -207   -164     56   -297
-250
  -153   -319   -126   -261   -365    365   -250   -421   -250   -
423   -409    220   -376   -275   -286   -197   -247   -375   -372
-338
   -89    198   -324   -299    -50   -248    141    275   -246
117    -38   -212   -328   -231   -248   -215   -103     50   -183
-124
  -146   -335   -305   -323   -325   -289   -323   -349   -285   -
309   -371   -294    377   -278   -309   -253   -246   -316   -411
-393
  -149   -319   -186   -133   -308   -240   -161   -287    319   -
256   -257   -115     55    115      0   -206   -169   -271   -309
-261
   -91   -250   -269   -273    132   -251   -262   -166   -233   -
167   -218   -239    332   -225   -258   -203   -174     42   -301
-224
  -211   -250   -403   -421   -170   -394   -413    328   -369
70   -106   -332   -458   -383   -395   -364   -219    198   -341
-287
  -357   -539   -154    363   -512   -398   -404   -486   -378   -
516   -521    -77   -539   -291   -445   -428   -412   -486   -540
-505
  -103   -303     -3    196   -274   -123   -125   -306    -80   -
275   -274    207   -270    -79   -150    167   -104   -269   -335
-233
  -284   -298   -464   -431    -95   -417   -375    -76   -387
350    -54   -387   -425   -327   -353   -410   -295   -144   -288
-278
  -288   -292   -520   -512   -101   -448   -429    115   -458
116    423   -426   -492   -405   -453   -442   -301   -124   -275
-276
  -137   -225   -159     58   -276   -253   -254   -224   -184   -
284   -234    -96   -339   -178   -227    -47    357   -198   -335
-312
  -227   -295   -304   -265   -361   -296   -177   -334     83   -
297   -317   -185   -357   -130    363    -46   -245   -347   -287
```

```
-315
  -279    547   -500   -506   -416   -429   -488   -400   -523   -
437   -425   -435   -542   -499   -477   -240   -349   -434   -528
-509
  -361   -341   -396   -436    -80   -376   -378   -383   -397   -
224   -325   -349   -477   -369   -360   -429   -381   -351    600
-144
   140   -227    255    -84   -278   -125   -166   -307   -130   -
286   -284     -3   -280   -127   -191    176    -93   -251   -341
-258
   114   -287   -124    -67   -253   -190   -108   -247    226   -
207   -205    -67   -271    251      5   -148   -117   -218   -273
-212
  -257   -371    400    -93   -353   -288   -259   -380    -83   -
384   -397    -37   -443   -280   -323   -296   -310   -364   -383
-340
  -146   -335   -305   -323   -325   -289   -323   -349   -285   -
309   -371   -294    377   -278   -309   -253   -246   -316   -411
-393
    90   -306    307    -92   -288   -137   -143   -330   -129   -
306   -309    186   -304   -132   -192     52   -144   -298   -344
-250
   -65   -304    -28    201   -239   -176   -121   -238    132   -
206   -201    -59   -245    159    -68   -130   -102     76   -287
-209
  -309   -292   -418   -452   -403   -361   -226   -387   -125   -
362   -406   -284   -389   -240    398   -382   -353   -455   -293
-388
   -99   -296   -265   -276   -267   -258   -282   -277   -236
0   -300   -252    357   -231   -264   -207   -199   -255   -378   -
347
  -109   -174   -285   -367   -270   -250   -315   -319   -269   -
318   -296   -114   -330   -302   -269    305    148   -330   -335
-298
  -104   -163   -309   -290    360   -250   -206    -48   -244    -
32    267   -213   -334   -234   -255     40   -131    -63   -143
2
   -62   -276    162    111   -220   -123    -94   -248    123   -
213   -207    189   -236    -36    -92     72    -81   -212   -277
-187
  -168   -472    118    315   -406   -271   -258   -371   -150   -
348   -347   -157   -343   -102     53   -256   -233   -325   -450
-367
  -249   -288   -396   -423   -159   -403   -421    364   -364
62    -87   -329   -469   -379   -396   -369   -241     86   -330
-278
   -95   -191   -369   -376   -222   -348   -347     19   -361   -
155   -217   -338   -385   -374   -338   -346   -167    360   -380
-364
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 3 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 47 nsites= 5 E= 9.3e-058
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.200000  0.600000
0.000000  0.200000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.400000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.200000
0.000000  0.000000  0.400000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.800000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.200000
 0.200000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.600000  0.000000  0.200000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.400000  0.600000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.800000  0.200000
 0.600000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.400000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.800000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.600000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.200000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
0.000000  0.200000  0.000000  0.000000  0.000000  0.200000  0.000000
0.200000  0.000000  0.000000  0.200000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.200000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.400000  0.000000  0.000000  0.000000  0.000000
0.000000  0.200000  0.000000  0.200000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.800000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.800000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.600000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.600000
0.000000  0.000000  0.000000  0.000000  0.000000  0.400000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
0.200000  0.400000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.600000  0.000000  0.000000  0.000000  0.200000
0.200000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.600000
0.000000  0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.400000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.400000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.800000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.400000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
0.000000  0.000000  0.400000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.200000  0.000000  0.200000  0.600000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.800000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
0.000000  0.600000  0.200000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.800000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.200000  0.000000  0.400000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.400000  0.000000  0.000000  0.000000  0.000000
 0.200000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.400000  0.000000  0.000000  0.000000  0.000000
0.400000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.800000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.200000  0.000000  0.400000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.400000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.200000  0.000000  0.000000  0.800000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.800000  0.200000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.400000  0.000000
0.000000  0.000000  0.000000  0.000000  0.400000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.200000  0.200000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.200000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.200000  0.600000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.200000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.800000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 3 regular expression
--------------------------------------------------------------------
[PNR][ASP][FY][RAT]I[ML][WY][AQ][VM][HSV][EINQT]G[KART]RP[PD]L[IL][K
QV][GN][ICHL]P[KPQ][PFV][IVL][EN][ESN]L[MIL][TE][RKS][CS]W[DSA][KQA]
[DK]P[DANS][EKQV]R[PL][ST][FMS][DEKNS][EDR][IL]V
--------------------------------------------------------------------



Time  5.01 secs.

********************************************************************

********************************************************************
MOTIF  4 MEME    width =  29  sites =   5  llr = 345  E-value =
1.2e-040
********************************************************************
--------------------------------------------------------------------
     Motif 4 Description
--------------------------------------------------------------------
Simplified        A  ::::44:8:::4:::8:4:4::::::::6
pos.-specific     C  :::::::::::4::8::::::::::::::
probability       D  :::::::::::::::::::2:::::2:::
matrix            E  :2:::2:::::::::::::2:::::::::
                  F  :::::::::::::::::::::::::::::
                  G  :::::2:::2:::::::6:::::::::::
                  H  :2::::8:::::::::::::::a::::::
                  I  :2::::::4:::::::::::::::::::2
                  K  ::::::::::::::::4::::::::4:8:
                  L  2:::::::::::a:::::2::a::2::::
                  M  ::::::::4::2::::::::::::8::::
                  N  :::::::::::::::::::::::2:::::
                  P  6:::::::::::::::::::::::::822
                  Q  :2::::2::::::a::2::2:::::2:::
                  R  :::::::::2::::::::::::::::2::
                  S  ::::22:::6::::222::::::8:::::
                  T  :::a::::::::::::2::::::::2:::
                  V  ::::2::22:::::::::8::::::::::
                  W  2:::::::::a::::::::::::::::::
                  Y  :2a:2:::::::::::::::a::::::::

         bits    6.2           *
                 5.5           *
                 4.9   *       *         * *
                 4.3   **  *   *  **     * *
Relative         3.7   **  *   * ***     *** *
Entropy          3.1 * **  *** ****** ** ***** **
(99.7 bits)      2.5 * *** ********** ************
                 1.8 *****************************
                 1.2 *****************************
```

```
                 0.6 *****************************
                 0.0 -----------------------------

Multilevel           PEYTAAHAISWALQCAKGVAYLHSMKPKA
consensus            LH  SEQVMG C  SSQALD   NLDRPI
sequence             WI  VG  VR M   S   E     Q  P
                      Q  YS         T   Q     T
                      Y
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
TAK1_HUMAN                  123  1.62e-34 YNVLHGAEPL
PYYTAAHAMSWCLQCSQGVAYLHSMQPKA LIHRDLKPPN
TAK1_CIONA                  110  8.86e-33 YNLLHGPGNQ
PHYTSGHAMSWCLQCATGVQYLHNMKPKA LIHRDLKPPN
TAK1_NEMATOSTELLA           101  5.05e-32 LHWKKSTSRA
PIYTASHVISWALQCASGVEYLHSMKPKA IIHRDLKPPN
TAK1_TRICHOPLAX              83  3.65e-27 LQKVLHNQKD
LQYTYAHAIGWMLQSAKAVDYLHSMTPKP LMHRDLKPLN
TAK1_DROSOPHILA             101  1.79e-22 LHNYLYGDDK
WEYTVEQAVRWALQCAKALAYLHSLDRPI VHRDIKPQNM
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_HUMAN                        1.6e-34  122_[4]_455
TAK1_CIONA                        8.9e-33  109_[4]_470
TAK1_NEMATOSTELLA                   5e-32  100_[4]_151
TAK1_TRICHOPLAX                   3.7e-27  82_[4]_150
TAK1_DROSOPHILA                   1.8e-22  100_[4]_264
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 4 width=29 seqs=5
TAK1_HUMAN               (  123) PYYTAAHAMSWCLQCSQGVAYLHSMQPKA  1
TAK1_CIONA               (  110) PHYTSGHAMSWCLQCATGVQYLHNMKPKA  1
TAK1_NEMATOSTELLA        (  101) PIYTASHVISWALQCASGVEYLHSMKPKA  1
TAK1_TRICHOPLAX          (   83) LQYTYAHAIGWMLQSAKAVDYLHSMTPKP  1
TAK1_DROSOPHILA          (  101) WEYTVEQAVRWALQCAKALAYLHSLDRPI  1
//

--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 4 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 29 n= 2457 bayes= 9.88264 E= 1.2e-
040
  -100   -268   -268   -273   -167   -257   -259   -200   -228
31   -222   -240    333   -224   -253   -208   -185   -200    232
-209
   -60   -216   -101     52      4   -170    239     52    -44   -
146   -150    -40   -240    163    -83   -114    -88   -154   -164
214
  -334   -340   -416   -458     45   -382   -170   -335   -410   -
277   -339   -327   -459   -379   -382   -389   -376   -346   -108
476
  -184   -242   -337   -405   -312   -313   -350   -257   -317   -
334   -279   -178   -401   -305   -325    -80    394   -232   -366
-370
   309    -92   -261   -243   -110   -128   -226   -121   -211   -
136   -147   -192   -337   -215   -231     25   -112     61   -231
118
   298   -127   -149     40   -226     94   -201   -238   -138   -
222   -217   -108   -303   -143   -184     46   -116   -137   -292
-253
  -269   -267   -210   -283   -149   -300    454   -353   -294   -
252   -252    -27   -354     55   -143   -236   -226   -315   -206
-19
   359    -85   -331   -323   -225   -117   -338   -185   -306   -
213   -219   -269   -405   -310   -307    -85   -155     38   -304
-315
  -191   -217   -429   -427   -132   -378   -392    300   -377    -
19    268   -336   -448   -371   -391   -354   -201    161   -310
-265
   -64   -194   -154   -198   -264     97   -204   -294   -121   -
278   -270    -61   -295   -162     81    261     28   -262   -322
-263
  -361   -341   -396   -436    -80   -376   -378   -383   -397   -
224   -325   -349   -477   -369   -360   -429   -381   -351    600
-144
   282    346   -337   -325   -166   -140   -299   -119   -290   -
141    168   -241   -338   -275   -289   -115   -123    -81   -272
-247
  -284   -298   -464   -431    -95   -417   -375    -76   -387
350    -54   -387   -425   -327   -353   -410   -295   -144   -288
-278
  -230   -323   -337   -151   -353   -371    -62   -352   -265   -
252   -214   -212   -358    417   -217   -316   -286   -352   -302
-370
  -279    547   -500   -506   -416   -429   -488   -400   -523   -
437   -425   -435   -542   -499   -477   -240   -349   -434   -528
-509
```

```
   360    -88   -327   -328   -248   -110   -341   -255   -314   -
248   -244   -259   -385   -310   -312     37   -149   -120   -317
-332
   -51   -252    -81    -51   -202   -150    -89   -212    207   -
181   -174    -23   -232    147    -21     71    132   -182   -248
-173
   188   -214   -274   -354   -357    362   -351   -386   -331   -
393   -372   -205   -366   -343   -327   -171   -213   -291   -371
-382
  -102   -184   -380   -380   -169   -361   -348     44   -360
57   -157   -336   -391   -365   -341   -350   -163    340   -347
-327
   202   -359    162    175   -295   -194   -165   -285    -67   -
252   -248    -81   -261    158   -151   -160   -138   -236   -350
-261
  -334   -340   -416   -458     45   -382   -170   -335   -410   -
277   -339   -327   -459   -379   -382   -389   -376   -346   -108
476
  -284   -298   -464   -431    -95   -417   -375    -76   -387
350    -54   -387   -425   -327   -353   -410   -295   -144   -288
-278
  -331   -327   -279   -362   -202   -339    478   -417   -373   -
319   -328   -106   -408   -117   -223   -308   -298   -383   -262
-88
  -113   -193   -170   -285   -279   -202   -257   -334   -233   -
328   -312    105   -325   -257   -256    299     83   -335   -345
-289
  -385   -358   -517   -550   -249   -480   -484   -193   -484    -
43    473   -457   -532   -473   -520   -485   -394   -268   -310
-315
   -48   -265    130    -12   -204   -140    -88   -221    205   -
186   -180    -10   -226    150    -41    -93    118   -187   -254
-174
  -100   -301   -260   -269   -287   -256   -276   -303   -214   -
264   -321   -243    357   -222     33   -206   -199   -270   -385
-356
  -289   -364   -392   -366   -445   -383   -342   -369    382   -
403   -395   -273   -129   -303    -45   -395   -327   -418   -390
-416
   317   -109   -281   -262   -171   -139   -273     85   -237   -
150   -168   -215     89   -237   -255   -107   -127    -69   -270
-246
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 29 nsites= 5 E= 1.2e-040
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.200000  0.000000  0.000000  0.600000
0.000000  0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
```

```
 0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
0.200000  0.200000  0.000000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.000000  0.000000  0.000000  0.000000  0.200000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.400000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.200000  0.000000  0.200000
 0.400000  0.000000  0.000000  0.200000  0.000000  0.200000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.800000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.800000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.400000  0.000000  0.000000  0.400000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.200000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.200000  0.600000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.400000  0.400000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.800000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
 0.800000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.400000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.200000  0.200000  0.000000  0.000000  0.000000
 0.400000  0.000000  0.000000  0.000000  0.000000  0.600000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.800000  0.000000  0.000000
 0.400000  0.000000  0.200000  0.200000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
0.000000  0.000000  0.800000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.200000  0.800000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.400000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.000000  0.200000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.800000
0.000000  0.200000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.800000  0.000000  0.000000  0.000000  0.200000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.600000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.200000  0.000000  0.000000  0.000000  0.000000  0.200000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 regular expression
--------------------------------------------------------------------
[PLW][EHIQY]YT[ASVY][AEGS][HQ][AV][IMV][SGR]W[ACM]LQ[CS][AS][KQST][G
A][VL][ADEQ]YLH[SN][ML][KDQT][PR][KP][AIP]
--------------------------------------------------------------------




Time  6.44 secs.

********************************************************************
```

```
*******************************************************************
MOTIF  5 MEME    width =  41  sites =   4  llr = 384  E-value =
1.6e-030
*******************************************************************
-------------------------------------------------------------------
      Motif 5 Description
-------------------------------------------------------------------
Simplified        A  ::3:::a:::::::3:::8:::::::::::::::::::::8
pos.-specific     C  ::::::::::::::::::::::::::::::3::::::::::
probability       D  ::::3::::::::3::::::::::3:::::3::::::::::
matrix            E  :3:::::::::a:8:8:33:::a::::::::::::::::::
                  F  :::3:::::::::::::::8::::::::::::::::::3::
                  G  :::::::::::::::::::::::::::::::::::::::a:
                  H  :::::::::::::::::::::::::::::::a:::::::::
                  I  :::353:3:3a:3::::3:35:::::::::::::a8::::3
                  K  ::33::::a:::::::35:::3::::::::::::::5::::
                  L  :::::::::::::::::::::::5::a::3:::::::a:::
                  M  :::::::::3::::::::::3::::::::::::::::::::
                  N  ::3::::::::::::3::::::::::::::3::a:::::::
                  P  ::::::::::::::::::::::::::::::::8::::::::
                  Q  :::33::::3::::3:3:::3:::3a::3:::::::3::::
                  R  38::::::::::::::5:::::::5:::8:::3:::3::::
                  S  ::3:::::::::8:5::::::::::::a::3::::::::::
                  T  :::::::::3:::::::::::3:::::::::::::::::::
                  V  :::::8:8:::::::::::::5:5:::::8:::::3:::::
                  W  8::::::::::::::::::::::::::::::::::::::::
                  Y  ::::::::::::::::::::::::::::::::::::::8::

         bits    6.2
                 5.5
                 4.9 *                              * *
                 4.3 *     * * *        *     *     * **   **
Relative         3.7 *     * * **       *  *  ****  * **  ***
Entropy          3.1 **  ***** **** *  *** ** ***** ***** ****
(138.4 bits)     2.5 ** **************************************
                 1.8 *****************************************
                 1.2 *****************************************
                 0.6 *****************************************
                 0.0 -----------------------------------------

Multilevel           WRAFIVAVKIIESESERKAFIVELRQLSRVCHPNIIKLYGA
consensus            REKIDI I M  IDANKEEIMK VD   QLD R  VQ F I
sequence               NKQ    Q    Q QI  QT  Q     N     R
                       SQ     T                    S

-------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 5 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
TAK1_HUMAN                   55  5.26e-46 GAFGVVCKAK
WRAKDVAIKQIESESERKAFIVELRQLSRVNHPNIVKLYGA CLNPVCLVME
TAK1_CIONA                   42  1.12e-44 GSFGVVYLAI
WRNIQVAVKMIESESERIAFMTELRQLSRVCHPNIIRLYGA CRNPVSLVME
TAK1_NEMATOSTELLA            28  2.62e-39 AFGVVYKARW
REKFIVAVKTIESEAEKKAFIVEVQQLSRVSHRNIIKLYGA VTKHEPVCLV
TAK1_TRICHOPLAX              14  2.62e-31 GSFGVVHKAR
WRSQIIAVKIIEIDQNQEEIQKEVDQLSQLDHPNIIQLFGI SILQSAPSLL
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 5 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_HUMAN                        5.3e-46  54_[5]_511
TAK1_CIONA                        1.1e-44  41_[5]_526
TAK1_NEMATOSTELLA                 2.6e-39  27_[5]_212
TAK1_TRICHOPLAX                   2.6e-31  13_[5]_207
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 5 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 5 width=41 seqs=4
TAK1_HUMAN               (   55)
WRAKDVAIKQIESESERKAFIVELRQLSRVNHPNIVKLYGA  1
TAK1_CIONA               (   42)
WRNIQVAVKMIESESERIAFMTELRQLSRVCHPNIIRLYGA  1
TAK1_NEMATOSTELLA        (   28)
REKFIVAVKTIESEAEKKAFIVEVQQLSRVSHRNIIKLYGA  1
TAK1_TRICHOPLAX          (   14)
WRSQIIAVKIIEIDQNQEEIQKEVDQLSQLDHPNIIQLFGI  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 5 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 41 n= 2385 bayes= 9.21735 E= 1.6e-
030
  -346   -334   -385   -417    -73   -368   -360   -370   -346   -
217   -315   -333   -468   -346   -155   -413   -365   -339    596
-134
```

```
  -224   -290   -244    -17   -357   -293   -184   -337    -44   -
305   -329   -187   -348   -144    375   -286   -255   -354   -285
-323
   142   -219    -43    -42   -182   -111    -78   -202    134   -
174   -168    195   -210    -20    -54    100    -31   -166   -240
-157
   -38   -168   -119    -84    203   -160    -88    140    127    -
57    -86    -56   -230    157    -60   -110    -59    -47   -168
-25
   -80   -239    125    -20   -161   -184   -142    268    -69    -
82   -126    -64   -260    130   -125   -146   -102    -14   -257
-181
   -94   -176   -367   -371   -192   -357   -348    177   -353   -
104   -171   -327   -386   -366   -337   -345   -154    332   -366
-340
   374   -101   -330   -329   -251   -122   -345   -251   -318   -
251   -253   -268   -385   -316   -317    -96   -161   -129   -320
-330
   -94   -176   -367   -371   -192   -357   -348    177   -353   -
104   -171   -327   -386   -366   -337   -345   -154    332   -366
-340
  -309   -368   -435   -417   -462   -406   -372   -376    388   -
423   -412   -300   -464   -350    -48   -431   -350   -439   -396
-436
   -46   -127   -198   -162    -56   -192   -145    180   -119     -
6    180   -113   -265    153   -148   -125    150     18   -170   -
120
  -241   -279   -393   -420   -177   -391   -421    374   -362    -
16   -104   -328   -465   -384   -395   -366   -238     87   -341
-279
  -438   -565   -197    369   -544   -472   -475   -512   -514   -
570   -577   -380   -635   -365   -539   -540   -501   -535   -561
-561
   -72   -159   -261   -296   -195   -214   -273     72   -228   -
190   -208   -122   -310   -249   -241    286     80   -147   -292
-240
  -332   -556    -27    361   -521   -407   -409   -477   -357   -
501   -505   -303   -514   -259   -445   -434   -406   -467   -546
-514
   167   -162   -125   -108   -214   -129   -156   -229    -85   -
213   -207    -61   -240    144   -131    212      4   -180   -279
-215
  -306   -507   -124    357   -474   -348   -352   -456   -308   -
470   -474    -14   -481   -245   -381   -364   -353   -445   -510
-455
  -188   -301   -269   -196   -338   -262   -142   -300    163   -
255   -267   -142   -337    136    323   -241   -196   -293   -280
-272
   -86   -273    -93     99   -225   -190   -128     90    280   -
190   -194    -72   -262    -44    -18   -148   -112   -183   -269
-204
```

```
   338   -116   -132     70   -237   -121   -252   -234   -175   -
226   -225   -165   -325   -162   -225    -91   -140   -123   -306
-286
  -271   -234   -420   -441    473   -403   -366      1   -422    -
81   -180   -369   -423   -421   -431   -343   -337   -185   -167
-33
  -139   -198   -308   -285    -91   -289   -265    319   -228
20    140   -226   -361     73   -252   -252   -147     66   -235
-187
   -46   -158   -210   -182   -145   -227   -190      9     62   -
107   -135   -146   -286   -147   -135   -171    107    286   -253
-210
  -438   -565   -197    369   -544   -472   -475   -512   -514   -
570   -577   -380   -635   -365   -539   -540   -501   -535   -561
-561
  -166   -199   -431   -406    -79   -365   -357     68   -364
248    -57   -338   -414   -335   -355   -347   -191    248   -273
-244
  -106   -278    112    -54   -260   -185   -110   -264      4   -
228   -230    -55   -268    137    299   -152   -130   -242   -269
-223
  -219   -314   -321   -139   -342   -360    -53   -340   -249   -
242   -205   -200   -348    415   -204   -304   -274   -340   -293
-357
  -265   -281   -447   -412    -80   -401   -358    -59   -368
346    -39   -368   -410   -310   -336   -391   -277   -126   -272
-260
  -103   -192   -283   -363   -289   -227   -324   -343   -289   -
338   -328   -140   -342   -313   -293    320     59   -327   -351
-312
  -268   -285   -360   -340   -380   -329   -197   -356    -62   -
326   -358   -233   -370    -10    386   -333   -298   -398   -282
-350
   -97   -174   -372   -369   -142   -346   -334     67   -345
86   -129   -320   -382   -346   -329   -333   -153    330   -320
-295
  -101    226    216   -110   -250   -115   -108   -286   -108   -
272   -273    259   -276   -114   -169    106    -65   -262   -311
-216
  -301   -301   -250   -330   -174   -315    472   -387   -337   -
291   -299    -77   -383    -88   -194   -279   -268   -353   -236
-59
   -90   -290   -244   -250   -275   -243   -259   -290   -187   -
252   -307   -224    352   -204     49   -195   -186   -258   -370
-338
  -308   -324   -183   -387   -311   -287   -122   -307   -295   -
371   -367    450   -403   -266   -333   -194   -232   -358   -319
-321
  -241   -279   -393   -420   -177   -391   -421    374   -362    -
16   -104   -328   -465   -384   -395   -366   -238     87   -341
-279
```

```
  -231   -269   -388   -416   -182   -395   -423    362   -358    -
12   -100   -322   -464   -382   -394   -361   -226    144   -346
-283
  -175   -322   -255   -177   -337   -256   -146   -290    305   -
250   -255   -130   -341    151    174   -231   -181   -277   -298
-264
  -265   -281   -447   -412    -80   -401   -358    -59   -368
346    -39   -368   -410   -310   -336   -391   -277   -126   -272
-260
  -183   -217   -297   -310    284   -301    -28   -208   -280   -
159   -206   -218   -350   -264   -263   -249   -247   -214    -10
417
  -161   -335   -248   -349   -382    404   -343   -424   -314   -
441   -410   -194   -413   -367   -314   -263   -327   -382   -358
-379
   346    -90   -318   -304   -181   -130   -315     86   -282   -
147   -174   -253   -379   -287   -289    -98   -142    -39   -284
-273
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 5 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 41 nsites= 4 E= 1.6e-030
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.000000  0.750000  0.000000
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.750000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.250000  0.250000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.750000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.750000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.250000  0.000000  0.000000
0.250000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.750000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.250000  0.750000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.750000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
0.250000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.250000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.750000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.750000  0.000000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.250000  0.000000  0.000000
0.250000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.750000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.750000  0.000000  0.000000
 0.000000  0.250000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.750000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.750000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.250000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.750000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.750000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
      Motif 5 regular expression
---------------------------------------------------------------------
[WR][RE][AKNS][FIKQ][IDQ][VI]A[VI]K[IMQT]IE[SI][ED][SAQ][EN][RKQ][KE
I][AE][FI][IMQ][VKT]E[LV][RDQ]QLS[RQ][VL][CDNS]H[PR]NI[IV][KQR]L[YF]
G[AI]
---------------------------------------------------------------------




Time  7.80 secs.

*********************************************************************


*********************************************************************
MOTIF  6 MEME    width =  20  sites =   5  llr = 240  E-value =
5.7e-024
*********************************************************************
---------------------------------------------------------------------
      Motif 6 Description
---------------------------------------------------------------------
Simplified        A  2:::::::6:::::::::::
pos.-specific     C  ::4:::::::4:::::::::
probability       D  :2:::::::2::::::::::
matrix            E  ::::::a::82:::::::::
                  F  :::::::4::::::::::::
                  G  ::::::::::4a:::::::6
                  H  ::::::::::::::2:::8:
                  I  ::::::::::::::::::::
                  K  2::::::::::::::2::::
                  L  :::a4:::2::::a::4a::
                  M  :::::a::::::::::::::
                  N  :::::::::::::::8:::2
                  P  62::::::::::::::::::
                  Q  ::::::::::::::2:::::
                  R  ::::::::::::::::::::
                  S  ::4:::::2:::a:::::::
                  T  ::::::::::::::::::::
                  V  :6::6:::::::::::4:::
                  W  :::::::::::::::::::2
                  Y  ::2::::6::::::6:2:2:

         bits    6.2
                 5.5
                 4.9      *
                 4.3      * *   *      *
Relative         3.7    * ***   ***** **
Entropy          3.1   ****** ******* ***
(69.3 bits)      2.5 ********************
```

```
                 1.8 ********************
                 1.2 ********************
                 0.6 ********************
                 0.0 --------------------

Multilevel           PVCLVMEYAECGSLYNLLHG
consensus            ADS L  FLDG   HKV YN
sequence             KPY     S E   Q Y  W

---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 6 sites sorted by position p-value
---------------------------------------------------------------------
Sequence name             Start   P-value                     Site
-------------             ----- ---------            ----------------
TAK1_HUMAN                   99  9.04e-26 IVKLYGACLN
PVCLVMEYAEGGSLYNVLHG AEPLPYYTAA
TAK1_CIONA                   86  1.27e-24 IIRLYGACRN
PVSLVMEFAECGSLYNLLHG PGNQPHYTSG
TAK1_NEMATOSTELLA            74  2.65e-24 KLYGAVTKHE
PVCLVMEYAEGGSLYNLLHW KKSTSRAPIY
TAK1_DROSOPHILA              78  1.06e-17 RVIGRASNGK
KDYLLMEYLEEGSLHNYLYG DDKWEYTVEQ
TAK1_TRICHOPLAX              60  2.20e-15 QLFGISILQS
APSLLMEFSDCGSLQKVLHN QKDLQYTYAH
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 6 block diagrams
---------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_HUMAN                          9e-26  98_[6]_488
TAK1_CIONA                        1.3e-24  85_[6]_503
TAK1_NEMATOSTELLA                 2.7e-24  73_[6]_187
TAK1_DROSOPHILA                   1.1e-17  77_[6]_296
TAK1_TRICHOPLAX                   2.2e-15  59_[6]_182
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 6 in BLOCKS format
---------------------------------------------------------------------
BL   MOTIF 6 width=20 seqs=5
TAK1_HUMAN               (   99) PVCLVMEYAEGGSLYNVLHG  1
TAK1_CIONA               (   86) PVSLVMEFAECGSLYNLLHG  1
TAK1_NEMATOSTELLA        (   74) PVCLVMEYAEGGSLYNLLHW  1
TAK1_DROSOPHILA          (   78) KDYLLMEYLEEGSLHNYLYG  1
TAK1_TRICHOPLAX          (   60) APSLLMEFSDCGSLQKVLHN  1
//
---------------------------------------------------------------------
```

```
----------------------------------------------------------------------
     Motif 6 position-specific scoring matrix
----------------------------------------------------------------------
log-odds matrix: alength= 20 w= 20 n= 2511 bayes= 9.91404 E= 5.7e-
024
    55   -289   -238   -240   -276   -243   -259   -289     20   -
252   -305   -220    343   -202   -229   -191   -184   -256   -374
-341
   -54   -173      0   -190   -197   -265   -251      3   -227   -
155   -195   -199     -1   -229   -244   -245   -122    325   -323
-296
   -39    357   -253   -281    -58   -173   -201   -169   -233   -
179   -197   -152   -316   -230   -250    197    -54   -150   -189
216
  -284   -298   -464   -431    -95   -417   -375    -76   -387
350    -54   -387   -425   -327   -353   -410   -295   -144   -288
-278
  -174   -212   -454   -439   -113   -393   -394     48   -402
208    -95   -370   -444   -381   -395   -380   -206    294   -313
-282
  -402   -370   -512   -553   -330   -477   -492   -244   -486   -
176    480   -457   -536   -490   -532   -485   -413   -313   -320
-325
  -445   -567   -200    370   -546   -477   -479   -515   -528   -
576   -583   -385   -644   -372   -547   -547   -508   -541   -564
-565
  -225   -249   -335   -350    338   -335    -59   -239   -318   -
185   -236   -246   -385   -293   -296   -287   -283   -248    -25
403
   348    -83   -305   -295   -213   -113   -310   -206   -273    -
22   -208   -243   -382   -278   -282     17   -143    -96   -290
-293
  -369   -566    -71    365   -536   -435   -438   -494   -407   -
530   -535   -336   -556   -295   -483   -475   -442   -495   -557
-538
   -55    338   -149     68   -280    300   -231   -285   -188   -
287   -288    -87   -317   -201   -228   -145   -160   -238   -336
-288
  -172   -346   -259   -361   -392    406   -354   -436   -326   -
452   -421   -205   -423   -378   -325   -275   -339   -394   -368
-390
  -126   -214   -313   -398   -314   -248   -351   -372   -321   -
365   -355   -168   -365   -343   -321    327     34   -353   -373
-337
  -284   -298   -464   -431    -95   -417   -375    -76   -387
350    -54   -387   -425   -327   -353   -410   -295   -144   -288
-278
  -144   -202   -233   -243    171   -263    205   -199   -199   -
158   -192   -159   -318     76   -198   -208   -206   -198    -43
390
```

```
  -279   -322   -153   -314   -311   -257   -117   -306    -46   -
357   -353    440   -387   -224   -251   -181   -215   -348   -319
-310
  -131   -171   -384   -352    -29   -300   -257     32   -302
226    -44   -267   -367   -274   -293   -271   -150    212   -186
191
  -284   -298   -464   -431    -95   -417   -375    -76   -387
350    -54   -387   -425   -327   -353   -410   -295   -144   -288
-278
  -284   -273   -229   -309    -81   -315    453   -349   -335   -
250   -257    -43   -366    -50   -163   -251   -240   -317   -165
131
  -150   -327   -209   -312   -346    388   -306   -397   -277   -
412   -384     38   -399   -324   -289   -240   -297   -360    141
-334
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 6 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 20 nsites= 5 E= 5.7e-024
 0.200000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.600000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.200000
0.000000  0.000000  0.000000  0.000000  0.600000  0.000000  0.000000
 0.000000  0.400000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.400000  0.000000  0.000000  0.000000  0.200000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.400000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.600000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.400000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.600000
 0.600000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.200000  0.800000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.400000  0.000000  0.200000  0.000000  0.400000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.000000  0.000000  0.000000  0.000000  0.600000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.800000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.400000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.400000  0.000000  0.200000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.800000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.200000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.600000
0.000000  0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 6 regular expression
--------------------------------------------------------------------
[PAK][VDP][CSY]L[VL]ME[YF][ALS][ED][CGE]GSL[YHQ][NK][LVY]L[HY][GNW]
--------------------------------------------------------------------




Time  9.00 secs.

********************************************************************


********************************************************************
MOTIF  7 MEME    width =  11  sites =   6  llr = 154  E-value =
6.5e-011
********************************************************************
```

```
--------------------------------------------------------------------
      Motif 7 Description
--------------------------------------------------------------------
Simplified        A  :2:5::2:::a
pos.-specific     C  ::::::::3::
probability       D  :::::::::::
matrix            E  2::::::::::
                  F  ::::7::::::
                  G  8:a:2a:::::
                  H  :2::::::2::
                  I  :::::::::::
                  K  :2:::::::7:
                  L  :::::::::2:
                  M  :::::::::::
                  N  :::::::::::
                  P  :::::::::::
                  Q  :2:::::::::
                  R  :3::::2:22:
                  S  :::5:::::::
                  T  :::::::::::
                  V  ::::::7a:::
                  W  :::::::::::
                  Y  ::::2:::3::

         bits    6.2
                 5.5
                 4.9
                 4.3   *  *    *
Relative         3.7 * * ** *  *
Entropy          3.1 * **** ** *
(37.0 bits)      2.5 * *********
                 1.8 ***********
                 1.2 ***********
                 0.6 ***********
                 0.0 -----------

Multilevel           GRGAFGVVCKA
consensus               S    Y
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value              Site
-------------             ----- ---------            -----------
TAK1_NEMATOSTELLA            15  1.23e-14 SDELEVIENV GHGAFGVVYKA
RWREKFIVAV
```

```
TAK1_HUMAN                    43  1.76e-14 YKEIEVEEVV GRGAFGVVCKA
KWRAKDVAIK
TAK1_TRICHOPLAX                2  1.53e-13          V GRGSFGVVHKA
RWRSQIIAVK
TAK1_CIONA                    30  5.01e-12 YNEMELKEVV GKGSFGVVYLA
IWRNIQVAVK
TAK1_DROSOPHILA               18  7.44e-10 AEVKLSEKFL GAGSGGAVRKA
TFQNQEIAVK
TAK1_AMPHIMEDON               35  7.51e-09 LEFKPDQKFV EQGAYGRVCRA
THEGKDVAVK
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_NEMATOSTELLA                 1.2e-14  14_[7]_255
TAK1_HUMAN                        1.8e-14  42_[7]_553
TAK1_TRICHOPLAX                   1.5e-13  1_[7]_249
TAK1_CIONA                          5e-12  29_[7]_568
TAK1_DROSOPHILA                   7.4e-10  17_[7]_365
TAK1_AMPHIMEDON                   7.5e-09  34_[7]_432
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 7 width=11 seqs=6
TAK1_NEMATOSTELLA        (   15) GHGAFGVVYKA  1
TAK1_HUMAN               (   43) GRGAFGVVCKA  1
TAK1_TRICHOPLAX          (    2) GRGSFGVVHKA  1
TAK1_CIONA               (   30) GKGSFGVVYLA  1
TAK1_DROSOPHILA          (   18) GAGSGGAVRKA  1
TAK1_AMPHIMEDON          (   35) EQGAYGRVCRA  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 11 n= 2565 bayes= 9.18476 E= 6.5e-
011
  -159   -340   -232    -88   -384    398   -336   -422   -302   -
442   -405   -180   -414   -352   -307   -258   -324   -381   -360
-378
    94   -297   -157   -110   -262   -205    170   -260    146   -
219   -218    -80   -285    141    233   -159   -127   -234   -276
-217
```

```
  -184   -357   -270   -372   -403    407   -364   -447   -337   -
462   -432   -216   -433   -389   -335   -286   -351   -405   -377
-400
   303   -140   -363   -390   -331   -135   -385   -351   -379   -
345   -336   -260   -348   -340   -366    221   -138   -220   -394
-396
  -291   -251   -413   -440    469    -53   -278   -225   -419   -
136   -238   -353   -429   -414   -420   -345   -366   -260   -134
130
  -184   -357   -270   -372   -403    407   -364   -447   -337   -
462   -432   -216   -433   -389   -335   -286   -351   -405   -377
-400
    15   -163   -319   -316   -204   -305   -290     18   -281   -
156   -202   -283   -341   -305    -79   -290   -128    343   -338
-336
  -111   -206   -385   -393   -238   -362   -364      5   -379   -
170   -233   -354   -401   -391   -355   -362   -183    364   -396
-381
  -141    276   -238   -235    139   -261    192   -184   -154   -
157   -186   -160   -322   -178     61   -209   -191   -182    -68
346
  -280   -365   -400   -342   -436   -371   -293   -358    372   -
106   -367   -255   -440   -229     46   -373   -304   -392   -376
-388
   384   -141   -377   -383   -295   -160   -389   -300   -369   -
297   -299   -312   -421   -363   -363   -135   -200   -173   -360
-374
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 11 nsites= 6 E= 6.5e-011
 0.000000  0.000000  0.000000  0.166667  0.000000  0.833333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.166667  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
0.166667  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.666667  0.166667
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.166667
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.000000  0.666667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.333333  0.000000  0.000000  0.000000  0.000000
0.166667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.000000  0.000000  0.000000  0.333333
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.666667  0.166667  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 regular expression
--------------------------------------------------------------------
GRG[AS]FGVV[CY]KA
--------------------------------------------------------------------




Time 10.21 secs.

********************************************************************


********************************************************************
MOTIF  8 MEME    width =  50  sites =   2  llr = 265  E-value =
6.6e-007
********************************************************************

--------------------------------------------------------------------
      Motif 8 Description
--------------------------------------------------------------------
Simplified        A
::a:::::::::::5:::::::::a::::::::a::::::::::a:::::
pos.-specific     C
::::::::::::::::5:::::::::::::a:::::::::::::::::::
probability       D
:::::::5:::::::::::::::::::::::::::5::::::::::::::
matrix            E
:::::::5:::::::::::::a:::::5::::::55::::::a:::::::
                  F
::::::::::::::::::::::::::5:::::::::::::::::::::::
                  G
::::::::::::::::::::::::::::::::::::::::::::::::::
```

```
                  H
::::::::55::::::::::::::::5::a::::::::::::::::::::
                  I
::::5::::::::::::::::::::5:::::::::::::::::a::::::
                  K
::::::::::::::::::::a::::::::::5::::::5::::::::5::
                  L
::::5:a:5:a::a::::::::::::::::::5::::5:::::::aa5::
                  M
:5:::::::::::::::::::::a:::::::55::::5::::::::::::
                  N
::::::::::::::::::5:::::::::::::::::::::::::::::::
                  P
a:::::::::::a:5a:5::::::::::::::::::::::::::::::::
                  Q
:::::::::5:a:::::::::::::::5a:::::5:::::a:::::::a:
                  R
:5::::::::::::::::::::::::::::::::::::5::::::::::a
                  S
::::::::::::::::5:5a::a:::::::::::::::::::::::::::
                  T
:::::a:::::::::::5:::::::::::::::::::::::a::::::::
                  V
:::::::::::::::::::::::::5:::::::::::::a::::::::::
                  W
::::::::::::::::::::::::::::::::::::::::::::::::::
                  Y
:::a::::::::::::::::::::::::::::::::a:::::::::::::

         bits    6.2
                 5.5                               *
                 4.9    *                   *     **     *
                 4.3   ** *     *        *  ** * ***  *  *   ** **
**
Relative         3.7 **** **  ***** **  ****** * **** *  *  ********
**
Entropy          3.1
**************************************************
(191.2 bits)     2.5
**************************************************
                 1.8
**************************************************
                 1.2
**************************************************
                 0.6
**************************************************
                 0.0
--------------------------------------------------

Multilevel
PMAYITLDHHLQPLAPCPNSKESMAIFEQHCKLAEDYLKVQTEIALLKQR
```

```
consensus             R  L  ELQ    P STS      VHQ   MM QE MR
L
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
TAK1_HUMAN                  497  1.59e-59 TDTNGSDNSI
PMAYLTLDHQLQPLAPCPNSKESMAVFEQHCKMAQEYMKVQTEIALLLQR KQELVAELDQ
TAK1_CIONA                  501  7.64e-56 SGSDSQCDSL
PRAYITLELHLQPLPPSTSSKESMAIHQQHCMLAEDYLRVQTEIALLKQR GEQLRLGLAD
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_HUMAN                        1.6e-59  496_[8]_60
TAK1_CIONA                        7.6e-56  500_[8]_58
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 8 width=50 seqs=2
TAK1_HUMAN               (  497)
PMAYLTLDHQLQPLAPCPNSKESMAVFEQHCKMAQEYMKVQTEIALLLQR  1
TAK1_CIONA               (  501)
PRAYITLELHLQPLPPSTSSKESMAIHQQHCMLAEDYLRVQTEIALLKQR  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 50 n= 2331 bayes= 10.1855 E= 6.6e-
007
   -77   -267   -229   -240   -251   -219   -252   -272   -208   -
236   -295   -214    362   -204   -234   -182   -174   -240   -345
-315
  -107   -192   -199   -177   -139   -199   -113   -105     14    -
69    255   -121   -264    -57    286   -185   -128   -127   -160
-162
```

```
   357    -70   -252   -245   -197    -79   -279   -187   -236   -
194   -203   -202   -290   -239   -248    -62   -115    -79   -273
-264
  -150   -194   -244   -265    183   -241    -13   -166   -224   -
125   -175   -172   -309   -220   -219   -218   -203   -174      7
429
  -176   -211   -364   -364    -51   -342   -327    298   -310
206    -24   -284   -384   -290   -314   -313   -186     75   -230
-207
   -88   -162   -222   -259   -209   -214   -242   -153   -195   -
214   -187    -89   -289   -197   -215     24    361   -130   -278
-259
  -205   -234   -381   -350    -35   -346   -304     -3   -303
333     -8   -307   -357   -259   -284   -331   -222    -73   -215
-206
  -214   -408    292    270   -373   -273   -263   -373   -229   -
370   -376    -94   -384   -172   -303   -285   -275   -344   -403
-353
  -108   -175   -160   -181      1   -211    318    -45   -127
187    -70    -45   -249      0    -97   -180   -127    -77    -90
22
  -168   -263   -182   -122   -195   -257    307   -285   -142   -
207   -190    -55   -291    334   -104   -210   -186   -265   -218
-107
  -205   -234   -381   -350    -35   -346   -304     -3   -303
333     -8   -307   -357   -259   -284   -331   -222    -73   -215
-206
  -183   -291   -254   -106   -302   -307    -35   -302   -184   -
215   -186   -161   -311    406   -162   -262   -230   -299   -270
-309
   -77   -267   -229   -240   -251   -219   -252   -272   -208   -
236   -295   -214    362   -204   -234   -182   -174   -240   -345
-315
  -205   -234   -381   -350    -35   -346   -304     -3   -303
333     -8   -307   -357   -259   -284   -331   -222    -73   -215
-206
   169   -166   -178   -178   -191   -126   -207   -203   -155   -
191   -227   -150    303   -146   -179   -110   -111   -133   -277
-237
   -77   -267   -229   -240   -251   -219   -252   -272   -208   -
236   -295   -214    362   -204   -234   -182   -174   -240   -345
-315
     1    467   -269   -321   -205   -177   -276   -234   -268   -
255   -260   -156   -306   -262   -260    129    -15   -197   -297
-260
   -37   -177   -160   -169   -182   -161   -180   -173   -131   -
176   -202    -96    280   -129   -158    -32    184   -129   -253
-220
   -98   -218    -41   -170   -226   -118    -89   -249   -137   -
266   -264    358   -266   -136   -179    142      4   -248   -267
-218
```

```
    -42   -152   -201   -258   -225   -161   -244   -266   -205   -
266   -262    -77   -266   -225   -220    298    100   -248   -295
-245
   -278   -353   -377   -350   -425   -366   -330   -354    384   -
387   -382   -262   -429   -291    -34   -384   -313   -401   -376
-397
   -399   -547   -176    368   -519   -443   -445   -491   -445   -
535   -543   -350   -582   -328   -488   -495   -460   -504   -543
-529
    -42   -152   -201   -258   -225   -161   -244   -266   -205   -
266   -262    -77   -266   -225   -220    298    100   -248   -295
-245
   -349   -342   -472   -494   -273   -438   -447   -200   -431   -
138    476   -416   -498   -432   -469   -442   -362   -263   -301
-298
    357    -70   -252   -245   -197    -79   -279   -187   -236   -
194   -203   -202   -290   -239   -248    -62   -115    -79   -273
-264
   -132   -195   -351   -364   -140   -341   -349    311   -321    -
10    -92   -288   -394   -334   -335   -316   -163    233   -304
-255
   -158   -192   -201   -246    334   -245    322   -162   -217   -
108   -167    -74   -300    -97   -170   -208   -185   -165    -11
199
   -131   -329    -43    247   -301   -235    -98   -293   -107   -
243   -230   -115   -280    287   -151   -208   -181   -264   -302
-280
   -183   -291   -254   -106   -302   -307    -35   -302   -184   -
215   -186   -161   -311    406   -162   -262   -230   -299   -270
-309
   -224   -253   -181   -245   -115   -248    453   -309   -230   -
229   -241    -23   -318    -33   -132   -217   -202   -280   -186
-8
   -325    550   -507   -508   -412   -480   -489   -393   -526   -
432   -424   -450   -559   -507   -478   -468   -369   -441   -529
-507
   -103   -223   -176   -144   -157   -199   -153   -109    275    -
98    272   -106   -264    -72     -7   -179   -122   -139   -195
-174
   -197   -225   -390   -370    -32   -353   -308     20   -318
245    345   -308   -379   -259   -309   -330   -217    -69   -191
-200
    357    -70   -252   -245   -197    -79   -279   -187   -236   -
194   -203   -202   -290   -239   -248    -62   -115    -79   -273
-264
   -131   -329    -43    247   -301   -235    -98   -293   -107   -
243   -230   -115   -280    287   -151   -208   -181   -264   -302
-280
   -214   -408    292    270   -373   -273   -263   -373   -229   -
370   -376    -94   -384   -172   -303   -285   -275   -344   -403
-353
```

```
  -150   -194   -244   -265    183   -241    -13   -166   -224   -
125   -175   -172   -309   -220   -219   -218   -203   -174      7
429
  -197   -225   -390   -370    -32   -353   -308     20   -318
245    345   -308   -379   -259   -309   -330   -217    -69   -191
-200
  -220   -307   -304   -260   -361   -294   -205   -316    316   -
304   -313   -188   -359   -149    248   -291   -241   -333   -301
-316
   -52   -151   -313   -313   -156   -290   -293     89   -293    -
88   -153   -275   -332   -305   -283   -283   -120    339   -308
-281
  -183   -291   -254   -106   -302   -307    -35   -302   -184   -
215   -186   -161   -311    406   -162   -262   -230   -299   -270
-309
   -88   -162   -222   -259   -209   -214   -242   -153   -195   -
214   -187    -89   -289   -197   -215     24    361   -130   -278
-259
  -399   -547   -176    368   -519   -443   -445   -491   -445   -
535   -543   -350   -582   -328   -488   -495   -460   -504   -543
-529
  -200   -244   -356   -375   -140   -352   -374    362   -319
10    -78   -290   -418   -338   -349   -326   -200    109   -303
-242
   357    -70   -252   -245   -197    -79   -279   -187   -236   -
194   -203   -202   -290   -239   -248    -62   -115    -79   -273
-264
  -205   -234   -381   -350    -35   -346   -304     -3   -303
333     -8   -307   -357   -259   -284   -331   -222    -73   -215
-206
  -205   -234   -381   -350    -35   -346   -304     -3   -303
333     -8   -307   -357   -259   -284   -331   -222    -73   -215
-206
  -100   -212   -178   -146    -96   -205   -150    -51    266
165   -102   -108   -243    -77     -1   -181   -125   -100   -150
-157
  -183   -291   -254   -106   -302   -307    -35   -302   -184   -
215   -186   -161   -311    406   -162   -262   -230   -299   -270
-309
  -273   -276   -370   -382   -369   -326   -202   -355    -82   -
330   -370   -248   -363   -205    393   -343   -311   -406   -275
-351
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 50 nsites= 2 E= 6.6e-007
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.500000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 8 regular expression
--------------------------------------------------------------------
P[MR]AY[IL]TL[DE][HL][HQ]LQPL[AP]P[CS][PT][NS]SKESMA[IV][FH][EQ]QHC[
KM][LM]A[EQ][DE]Y[LM][KR]VQTEIALL[KL]QR
--------------------------------------------------------------------




Time 11.38 secs.

********************************************************************


********************************************************************
MOTIF  9 MEME    width =  15  sites =   3  llr = 118  E-value =
6.2e-006
********************************************************************
--------------------------------------------------------------------
      Motif 9 Description
--------------------------------------------------------------------
Simplified        A  :::::::7:::::::
pos.-specific     C  ::::::::::3::::
probability       D  ::::::::7::::::
matrix            E  :::::::::3:::::
                  F  :::7a::::::::7:
                  G  ::::::a3:::::::
                  H  :::::::::::::::
                  I  :::::::::::::::
                  K  :::::::::::::::
                  L  a::::::::::a:::
                  M  :a:::::::::::::
                  N  ::::::::3:::3::
                  P  :::::a::::7:::a
                  Q  ::7:::::::::3::
                  R  ::3::::::::::::
                  S  :::::::::3:::::
                  T  :::::::::3:::::
                  V  ::::::::::::3::
                  W  :::::::::::::::
                  Y  :::3:::::::::3:

         bits    6.2
                 5.5
                 4.9  *  *
                 4.3  * ** *      *
Relative         3.7 ******* * ** **
Entropy          3.1 ********* *****
(56.6 bits)      2.5 ***************
                 1.8 ***************
```

```
                 1.2 ***************
                 0.6 ***************
                 0.0 ---------------

Multilevel           LMQFFPGADEPLNFP
consensus              RY   GNSC QY
sequence                      T  V


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                Site
-------------             ----- ---------            ---------------
TAK1_NEMATOSTELLA           266  6.32e-19 FSRIVIFLNH LMQFFPGADTCLVFP
TAK1_CIONA                  274  9.09e-18 MDEIVVAMSD LMQFFPGGNSPLNFP
LHDSDSIPSS
TAK1_HUMAN                  287  2.08e-16 MEEIVKIMTH LMRYFPGADEPLQYP
CQYSDEGQSN
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_NEMATOSTELLA                 6.3e-19  265_[9]
TAK1_CIONA                        9.1e-18  273_[9]_320
TAK1_HUMAN                        2.1e-16  286_[9]_305
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 9 width=15 seqs=3
TAK1_NEMATOSTELLA        (  266) LMQFFPGADTCLVFP  1
TAK1_CIONA               (  274) LMQFFPGGNSPLNFP  1
TAK1_HUMAN               (  287) LMRYFPGADEPLQYP  1
//

--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
     Motif 9 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 15 n= 2541 bayes= 10.1724 E= 6.2e-
006
  -243   -262   -425   -389    -63   -382   -338    -39   -343
342    -24   -346   -391   -291   -316   -369   -255   -105   -254
-239
  -383   -360   -500   -533   -308   -465   -478   -227   -468   -
162    479   -444   -525   -472   -510   -471   -396   -293   -313
-315
  -163   -291   -232   -109   -300   -275    -44   -288    -39   -
213   -190   -131   -306    376    103   -229   -194   -276   -268
-279
  -252   -231   -371   -392    453   -364   -163   -205   -365   -
124   -215   -297   -396   -350   -356   -309   -318   -234    -72
231
  -285   -240   -412   -441    483   -398   -356   -204   -424   -
114   -220   -367   -420   -430   -434   -342   -365   -244   -158
-20
  -100   -292   -259   -273   -280   -247   -279   -301   -237   -
263   -324   -246    369   -232   -263   -207   -200   -269   -373
-348
  -149   -323   -236   -336   -370    403   -332   -411   -302   -
427   -398   -181   -401   -354   -303   -251   -313   -369   -348
-367
   332    -86   -266   -279   -236    176   -298   -242   -266   -
238   -235   -199   -324   -265   -274    -71   -127   -119   -301
-302
  -248   -358    397   -100   -341   -255   -237   -375   -299   -
380   -394     83   -428   -280   -332   -267   -288   -360   -374
-326
   -40   -195    -66     94   -198   -150   -131   -202    -62   -
200   -186    -20   -226    -63   -114    179    207   -174   -262
-190
   -57    233   -247   -261   -243   -205   -260   -250   -220   -
230   -279   -217    339   -214   -243   -167   -160   -215   -344
-305
  -243   -262   -425   -389    -63   -382   -338    -39   -343
342    -24   -346   -391   -291   -316   -369   -255   -105   -254
-239
   -44   -205    -68    -57   -150   -147    -30    -95    -27   -
127   -138    241   -223    216    -70   -102    -59    109   -213
-148
  -252   -231   -371   -392    453   -364   -163   -205   -365   -
124   -215   -297   -396   -350   -356   -309   -318   -234    -72
231
  -100   -292   -259   -273   -280   -247   -279   -301   -237   -
263   -324   -246    369   -232   -263   -207   -200   -269   -373
-348
---------------------------------------------------------------------
```

```
--------------------------------------------------------------------------------
      Motif 9 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 15 nsites= 3 E= 6.2e-006
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.666667  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.666667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.333333
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.666667  0.000000  0.000000  0.000000  0.000000  0.333333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.333333  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.333333  0.333333  0.000000  0.000000  0.000000
 0.000000  0.333333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.666667
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.333333  0.000000
0.333333  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.666667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.333333
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------------------
```

```
----------------------------------------------------------------------
      Motif 9 regular expression
----------------------------------------------------------------------
LM[QR][FY]FPG[AG][DN][EST][PC]L[NQV][FY]P
----------------------------------------------------------------------




Time 12.58 secs.

**********************************************************************


**********************************************************************
MOTIF 10 MEME    width =   8  sites =   3  llr = 64  E-value =
1.9e+000
**********************************************************************
----------------------------------------------------------------------
      Motif 10 Description
----------------------------------------------------------------------
Simplified        A  ::::::3:
pos.-specific     C  ::::::::
probability       D  :::a7:::
matrix            E  ::::3:::
                  F  ::a:::::
                  G  ::::::7a
                  H  ::::::::
                  I  :::::3::
                  K  a:::::::
                  L  :::::3::
                  M  :::::3::
                  N  ::::::::
                  P  :a::::::
                  Q  ::::::::
                  R  ::::::::
                  S  ::::::::
                  T  ::::::::
                  V  ::::::::
                  W  ::::::::
                  Y  ::::::::

         bits    6.2
                 5.5
                 4.9   *
                 4.3 * **   *
Relative         3.7 ****   *
Entropy          3.1 ***** **
(30.7 bits)      2.5 ********
                 1.8 ********
                 1.2 ********
```

```
                 0.6 ********
                 0.0 --------

Multilevel           KPFDDIGG
consensus                ELA
sequence                  M

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name            Start   P-value              Site
-------------            ----- ---------            --------
TAK1_CIONA                 214  1.44e-10 IILWEVLTRR KPFDDLGG
PAFRIMWAVH
TAK1_NEMATOSTELLA          205  3.14e-10 IILWEMISRR KPFDDMAG
SPPFRIMWAV
TAK1_HUMAN                 227  4.57e-10 IILWEVITRR KPFDEIGG
PAFRIMWAVH
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_CIONA                        1.4e-10  213_[10]_387
TAK1_NEMATOSTELLA                 3.1e-10  204_[10]_68
TAK1_HUMAN                        4.6e-10  226_[10]_372
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 10 width=8 seqs=3
TAK1_CIONA              (  214) KPFDDLGG  1
TAK1_NEMATOSTELLA       (  205) KPFDDMAG  1
TAK1_HUMAN              (  227) KPFDEIGG  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 8 n= 2583 bayes= 10.1961 E= 1.9e+000
  -299   -363   -418   -396   -451   -395   -359   -369    387   -
412   -403   -288   -455   -330    -43   -417   -339   -428   -390
-424
  -100   -292   -259   -273   -280   -247   -279   -301   -237   -
```

```
263   -324   -246    369   -232   -263   -207   -200   -269   -373
-348
  -285   -240   -412   -441    483   -398   -356   -204   -424   -
114   -220   -367   -420   -430   -434   -342   -365   -244   -158
-20
  -272   -369    408   -107   -351   -307   -274   -381   -354   -
390   -405    -42   -463   -325   -367   -322   -336   -368   -379
-345
  -226   -377    390     54   -352   -283   -256   -367   -267   -
368   -378    -42   -410   -221   -324   -288   -292   -344   -383
-338
  -189   -220   -405   -389    -45   -355   -333    255   -339
215    227   -311   -401   -301   -332   -328   -199     22   -232
-211
    86   -243   -227   -309   -337    382   -314   -363   -282   -
375   -353   -168   -359   -315   -286   -187   -235   -295   -338
-348
  -149   -323   -236   -336   -370    403   -332   -411   -302   -
427   -398   -181   -401   -354   -303   -251   -313   -369   -348
-367
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 8 nsites= 3 E= 1.9e+000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.666667  0.333333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.333333  0.333333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.333333  0.000000  0.000000  0.000000  0.000000  0.666667
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 10 regular expression
--------------------------------------------------------------------
KPFD[DE][ILM][GA]G
--------------------------------------------------------------------




Time 13.91 secs.

********************************************************************


********************************************************************
MOTIF 11 MEME    width =  19  sites =   2  llr = 102  E-value =
3.6e+000
********************************************************************
--------------------------------------------------------------------
      Motif 11 Description
--------------------------------------------------------------------
Simplified        A  ::::::::5::::::::::
pos.-specific     C  :::::::::::::::::::
probability       D  :::::::::::::::5:::
matrix            E  :::::::::::::::::::
                  F  :::::::::::::5:::::
                  G  :::::::::::::::::::
                  H  :::::::::a5:::::::a
                  I  ::::::::::5::::::::
                  K  :::::::::::::::5:::
                  L  ::::::5::::::::::::
                  M  :::::::::::::::::::
                  N  aa::::::5::::::::::
                  P  :::a:::5::::::5:a::
                  Q  :::::::::::a:::::::
                  R  ::5::::::::::5:::5:
                  S  :::::a::::::a::::::
                  T  :::::::5:::::::::5:
                  V  ::::a::::::::::::::
                  W  :::::::::::::::::::
                  Y  ::5:::5:::::::5::::

         bits    6.2
                 5.5
                 4.9 **       *        *
                 4.3 **       * *      *
Relative         3.7 ******  ******* * *
Entropy          3.1 *******************
(73.2 bits)      2.5 *******************
                 1.8 *******************
                 1.2 *******************
```

```
                 0.6 *******************
                 0.0 -------------------

Multilevel           NNRPVSLPAHHQSFPDPRH
consensus              Y   YTN I  RYK T
sequence

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                   Site
-------------             ----- ---------            ---------------
TAK1_CIONA                  469  2.61e-24 GPTSPQTTPT
NNRPVSYTNHIQSFYDPRH QLSSGSDSQC
TAK1_AMPHIMEDON             440  6.02e-22 RQYLHIEQAN
NNYPVSLPAHHQSRPKPTH SSYSDTYSRS
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_CIONA                        2.6e-24  468_[11]_121
TAK1_AMPHIMEDON                     6e-22  439_[11]_19
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 11 width=19 seqs=2
TAK1_CIONA               (  469) NNRPVSYTNHIQSFYDPRH  1
TAK1_AMPHIMEDON          (  440) NNYPVSLPAHHQSRPKPTH  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 19 n= 2517 bayes= 10.2963 E=
3.6e+000
  -263   -304   -133   -315   -286   -240   -104   -287   -247   -
341   -340    444   -369   -230   -288   -171   -200   -327   -301
-290
  -263   -304   -133   -315   -286   -240   -104   -287   -247   -
341   -340    444   -369   -230   -288   -171   -200   -327   -301
-290
  -117   -199   -179   -180     70   -193     10   -174    -10   -
```

```
149   -183   -105   -269    -96    285   -178   -150   -178    -29
258
   -77   -267   -229   -240   -251   -219   -252   -272   -208   -
236   -295   -214    362   -204   -234   -182   -174   -240   -345
-315
   -52   -151   -313   -313   -156   -290   -293     89   -293    -
88   -153   -275   -332   -305   -283   -283   -120    339   -308
-281
   -42   -152   -201   -258   -225   -161   -244   -266   -205   -
266   -262    -77   -266   -225   -220    298    100   -248   -295
-245
  -117   -164   -251   -257    181   -250    -53      0   -209
210    -37   -178   -297   -189   -204   -214   -155    -61     34
296
   -37   -177   -160   -169   -182   -161   -180   -173   -131   -
176   -202    -96    280   -129   -158    -32    184   -129   -253
-220
   204   -141    -13   -107   -171    -43    -91   -175    -85   -
188   -195    307   -204    -85   -126    -56    -61   -120   -222
-173
  -224   -253   -181   -245   -115   -248    453   -309   -230   -
229   -241    -23   -318    -33   -132   -217   -202   -280   -186
-8
   -82   -146   -152   -179    -19   -195    272    231   -122    -
10    -74    -23   -252    -44   -106   -170    -96     53   -135
7
  -183   -291   -254   -106   -302   -307    -35   -302   -184   -
215   -186   -161   -311    406   -162   -262   -230   -299   -270
-309
   -42   -152   -201   -258   -225   -161   -244   -266   -205   -
266   -262    -77   -266   -225   -220    298    100   -248   -295
-245
  -128   -186   -215   -222    329   -217    -87   -136    -62    -
89   -167   -143   -273   -137    260   -201   -164   -145    -13
63
   -69   -178   -157   -175    126   -170    -20   -140   -134   -
117   -156   -105    233   -132   -144   -143   -126   -136    -20
292
  -102   -281    284     -3   -244   -134   -131   -254    213   -
241   -243      6   -247    -71    -64   -142   -129   -230   -265
-212
   -77   -267   -229   -240   -251   -219   -252   -272   -208   -
236   -295   -214    362   -204   -234   -182   -174   -240   -345
-315
   -81   -183   -155   -146   -199   -171   -111   -176     23   -
179   -191    -67   -231    -68    282    -44    184   -146   -207
-192
  -224   -253   -181   -245   -115   -248    453   -309   -230   -
229   -241    -23   -318    -33   -132   -217   -202   -280   -186
-8
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 11 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 19 nsites= 2 E= 3.6e+000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
```

```
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 regular expression
--------------------------------------------------------------------
NN[RY]PVS[LY][PT][AN]H[HI]QS[FR][PY][DK]P[RT]H
--------------------------------------------------------------------




Time 15.30 secs.

********************************************************************


********************************************************************
MOTIF 12 MEME    width =  11  sites =   2  llr = 61  E-value =
2.3e+001
********************************************************************
--------------------------------------------------------------------
      Motif 12 Description
--------------------------------------------------------------------
Simplified        A  :::::::::::
pos.-specific     C  :::::::::::
probability       D  :::::5:::::
matrix            E  :::::::::::
                  F  :::::::5:::
                  G  :::5:::::::
                  H  ::::::a::5:
                  I  :::::::::::
                  K  :::::::::::
                  L  :5:::::::::
                  M  ::::::::5:5
                  N  :::::5:::5:
                  P  :::::::::::
                  Q  :::5:::::::
                  R  :5:::::::::
                  S  :::::::::::
```

```
                  T  :::::::::::
                  V  ::::a::55::
                  W  ::::::::::5
                  Y  a:a::::::::

         bits    6.2
                 5.5
                 4.9 * *   *
                 4.3 * *   *   *
Relative         3.7 * * *******
Entropy          3.1 ***********
(43.9 bits)      2.5 ***********
                 1.8 ***********
                 1.2 ***********
                 0.6 ***********
                 0.0 -----------

Multilevel           YLYGVDHFMHM
consensus             R Q N VVNW
sequence

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value              Site
-------------             ----- ---------            -----------
TAK1_AMPHIMEDON              93  5.44e-15 RVLHGSHPHR YRYGVDHVMHW
SRQTAVGLKH
TAK1_TRICHOPLAX             248  3.53e-13 SFKEIVQKLE YLYQVNHFVNM MVL
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_AMPHIMEDON                   5.4e-15  92_[12]_374
TAK1_TRICHOPLAX                   3.5e-13  247_[12]_3
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 12 width=11 seqs=2
TAK1_AMPHIMEDON          (   93) YRYGVDHVMHW  1
TAK1_TRICHOPLAX          (  248) YLYQVNHFVNM  1
//

--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 12 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 11 n= 2565 bayes= 10.3236 E=
2.3e+001
  -150   -194   -244   -265    183   -241    -13   -166   -224   -
125   -175   -172   -309   -220   -219   -218   -203   -174      7
429
  -126   -200   -226   -205    -99   -229   -134    -68    -15
171   -107   -146   -265    -91    289   -211   -154   -110   -133
-166
  -150   -194   -244   -265    183   -241    -13   -166   -224   -
125   -175   -172   -309   -220   -219   -218   -203   -174      7
429
   -58   -233    -93    -91   -230    297    -89   -247    -85   -
223   -220    -43   -236    230   -104   -139   -137   -216   -226
-215
   -52   -151   -313   -313   -156   -290   -293     89   -293    -
88   -153   -275   -332   -305   -283   -283   -120    339   -308
-281
  -204   -321    355    -90   -302   -180   -156   -332   -215   -
341   -350    246   -356   -203   -263   -190   -210   -324   -330
-281
  -224   -253   -181   -245   -115   -248    453   -309   -230   -
229   -241    -23   -318    -33   -132   -217   -202   -280   -186
-8
   -94   -153   -309   -318    375   -279   -222     62   -282     -
3    -88   -241   -327   -272   -284   -249   -150    189    -86
10
   -78   -153   -312   -306    -64   -274   -264    133   -261
28    317   -239   -333   -241   -270   -252   -123    216   -200
-178
  -194   -265    -68   -205   -184   -187    305   -276   -168   -
264   -266    363   -311    -67   -154   -150   -160   -276   -230
-98
  -230   -261   -343   -366    -29   -318   -270   -148   -304    -
81    293   -275   -408   -262   -289   -330   -255   -187    527
-91
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 12 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 11 nsites= 2 E= 2.3e+001
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 regular expression
--------------------------------------------------------------------
Y[LR]Y[GQ]V[DN]H[FV][MV][HN][MW]
--------------------------------------------------------------------




Time 16.54 secs.

********************************************************************


********************************************************************
MOTIF 13 MEME    width =   9  sites =   4  llr = 85  E-value =
3.0e+001
********************************************************************
--------------------------------------------------------------------
      Motif 13 Description
--------------------------------------------------------------------
Simplified        A  :::::::a
```

```
pos.-specific     C  :::::::::
probability       D  8:3::::::
matrix            E  ::5:a::::
                  F  :::::::::
                  G  :53::::::
                  H  :::::::::
                  I  :::::::::
                  K  :::::::::
                  L  :::::::::
                  M  :::::::::
                  N  3::::::::
                  P  :::::::::
                  Q  :::::::::
                  R  :::a::5a:
                  S  ::::::3::
                  T  :3:::8:::
                  V  :3:::33::
                  W  :::::::::
                  Y  :::::::::

         bits    6.2
                 5.5
                 4.9
                 4.3    *   **
Relative         3.7 *  **  **
Entropy          3.1 *  *** **
(30.6 bits)      2.5 *********
                 1.8 *********
                 1.2 *********
                 0.6 *********
                 0.0 ---------

Multilevel           DGERETRRA
consensus            NTD  VS
sequence              VG   V


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value              Site
-------------             ----- ---------            ---------
TAK1_DROSOPHILA             364  1.53e-10 TERETSRAAH NGERETRRA
GQDVGRETVR
TAK1_DROSOPHILA             342  1.76e-10 VVREMAKAAA DGDREVRRA
EKDTERETSR
TAK1_DROSOPHILA             353  2.86e-10 GDREVRRAEK DTERETSRA
AHNGERETRR
```

```
TAK1_DROSOPHILA             375  1.37e-09 GERETRRAGQ DVGRETVRA
VKKIGKKLRF
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_DROSOPHILA                   1.5e-10
341_[13]_2_[13]_2_[13]_2_[13]_10
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 13 width=9 seqs=4
TAK1_DROSOPHILA          (  364) NGERETRRA  1
TAK1_DROSOPHILA          (  342) DGDREVRRA  1
TAK1_DROSOPHILA          (  353) DTERETSRA  1
TAK1_DROSOPHILA          (  375) DVGRETVRA  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 9 n= 2577 bayes= 9.32924 E= 3.0e+001
  -266   -367    403   -108   -351   -287   -260   -382   -337   -
390   -405     43   -455   -313   -358   -299   -319   -369   -381
-340
   -22   -166   -226   -249   -189    316   -249   -129   -213   -
173   -187   -150   -305   -221   -234   -134    129    104   -274
-240
  -151   -421    171    289   -374     98   -218   -360   -144   -
337   -338    -73   -321    -96   -240   -210   -204   -314   -424
-331
  -302   -287   -411   -440   -397   -355   -221   -381   -118   -
356   -399   -277   -385   -233    398   -375   -346   -447   -288
-381
  -438   -565   -197    369   -544   -472   -475   -512   -514   -
570   -577   -380   -635   -365   -539   -540   -501   -535   -561
-561
  -118   -175   -299   -334   -210   -275   -296    -86   -255   -
186   -177   -137   -352   -247   -269    -37    353     96   -305
-290
   -59   -198   -168   -137   -178   -180   -132   -144    -14   -
153   -166    -93   -259    -79    289     53    -81     85   -234
-187
```

```
  -302   -287   -411   -440   -397   -355   -221   -381   -118   -
356   -399   -277   -385   -233    398   -375   -346   -447   -288
-381
   374   -101   -330   -329   -251   -122   -345   -251   -318   -
251   -253   -268   -385   -316   -317    -96   -161   -129   -320
-330
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 9 nsites= 4 E= 3.0e+001
 0.000000  0.000000  0.750000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.250000  0.500000  0.000000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.750000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.250000  0.000000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 regular expression
--------------------------------------------------------------------
[DN][GTV][EDG]RE[TV][RSV]RA
--------------------------------------------------------------------



Time 17.70 secs.
********************************************************************
```

```
********************************************************************
MOTIF 14 MEME    width =  36  sites =   2  llr = 181  E-value =
3.6e+001
********************************************************************
--------------------------------------------------------------------
      Motif 14 Description
--------------------------------------------------------------------
Simplified        A  ::::::::::5::::::::::::::::5::::::::
pos.-specific     C  ::::::::::::::::::::::5:::::::::::::
probability       D  ::::::::::5:::::::::5::::5::::::::::
matrix            E  ::::a::::::a:::::::::::::::5:::5::::
                  F  ::::::::::::::::::::::::::::::::::::
                  G  ::::::::::::::::::::::::::::::::::::
                  H  :::::5::::::::::::::::::::::::::::5:
                  I  :::::::::::::::::::::::::::::5::::::
                  K  ::::::55:::::5:::5:::5:aa::::::::::a
                  L  :a::::::a5:::::a::::::::::a:::::::::
                  M  ::::::::::::::::::::::5:::::::::::::
                  N  ::5:::::::::a:::::::::::::::::::5:::
                  P  ::::::::::::::::::::::::::::::::::::
                  Q  :::5::55::::::::5:::55:::5::::::5a5:
                  R  a:::::::::::::::::::::::::::5:a:::::
                  S  ::::::::::::::a:5::::::::::::::5::::
                  T  :::::::::::::5:::5::::::::::::::::::
                  V  ::55:::::5::::::::::::::::::55::::::
                  W  ::::::::::::::::::5:::::::::::::::::
                  Y  :::::5::::::::::::5a::::::::::::::::

         bits    6.2
                 5.5
                 4.9             *      *
                 4.3 *           *     **  ***     *  * *
Relative         3.7 **  **  *  ** **  **  *** *   * ****
Entropy          3.1 ******************************* ****
(130.4 bits)     2.5 ************************************
                 1.8 ************************************
                 1.2 ************************************
                 0.6 ************************************
                 0.0 ------------------------------------

Multilevel           RLNQEHKKLLAENKSLQKWYDKCKKDLARIRENQHK
consensus              VV YQQ VD  T  STY QQM  Q EVV SQ Q
sequence


--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
     Motif 14 sites sorted by position p-value
---------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
TAK1_CIONA                  570  2.42e-39 DDEREKSEDD
RLNVEYQQLVAENTSLQKWYDKMKKDLARVRENQHK TRN
TAK1_HUMAN                  566  6.22e-38 QDEKDQQNTS
RLVQEHKKLLDENKSLSTYYQQCKKQLEVIRSQQQK RQGTS
---------------------------------------------------------------------

---------------------------------------------------------------------
     Motif 14 block diagrams
---------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_CIONA                        2.4e-39  569_[14]_3
TAK1_HUMAN                        6.2e-38  565_[14]_5
---------------------------------------------------------------------

---------------------------------------------------------------------
     Motif 14 in BLOCKS format
---------------------------------------------------------------------
BL   MOTIF 14 width=36 seqs=2
TAK1_CIONA               (  570)
RLNVEYQQLVAENTSLQKWYDKMKKDLARVRENQHK  1
TAK1_HUMAN               (  566)
RLVQEHKKLLDENKSLSTYYQQCKKQLEVIRSQQQK  1
//

---------------------------------------------------------------------

---------------------------------------------------------------------
     Motif 14 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 36 n= 2415 bayes= 10.2366 E=
3.6e+001
  -273   -276   -370   -382   -369   -326   -202   -355    -82   -
330   -370   -248   -363   -205    393   -343   -311   -406   -275
-351
  -205   -234   -381   -350    -35   -346   -304     -3   -303
333     -8   -307   -357   -259   -284   -331   -222    -73   -215
-206
   -50   -164    -63   -169   -122   -152   -103     33   -131   -
103   -144    313   -256   -132   -164   -136    -66    190   -193
-164
   -35   -163   -145    -92   -117   -188    -69     23    -86    -
65   -110    -96   -222    267   -105   -160    -82    195   -176
-160
```

```
  -399   -547   -176    368   -519   -443   -445   -491   -445   -
535   -543   -350   -582   -328   -488   -495   -460   -504   -543
-529
  -157   -199   -187   -233    132   -241    363   -204   -208   -
155   -183    -56   -302    -76   -147   -194   -184   -199    -33
307
   -97   -262   -120    -59   -240   -181    -70   -228    249   -
189   -188    -57   -241    257     42   -152   -116   -210   -233
-201
   -97   -262   -120    -59   -240   -181    -70   -228    249   -
189   -188    -57   -241    257     42   -152   -116   -210   -233
-201
  -205   -234   -381   -350    -35   -346   -304     -3   -303
333     -8   -307   -357   -259   -284   -331   -222    -73   -215
-206
   -94   -160   -329   -319    -37   -296   -277    157   -277
218    -31   -256   -333   -254   -274   -273   -138    222   -194
-186
   155   -204    325    -18   -221    -94   -164   -234   -131   -
239   -246    -12   -231   -119   -182   -131   -137   -165   -270
-217
  -399   -547   -176    368   -519   -443   -445   -491   -445   -
535   -543   -350   -582   -328   -488   -495   -460   -504   -543
-529
  -263   -304   -133   -315   -286   -240   -104   -287   -247   -
341   -340    444   -369   -230   -288   -171   -200   -327   -301
-290
   -78   -211   -129   -111   -207   -169   -135   -178    276   -
188   -189    -50   -228    -67     -2    -51    180   -156   -234
-195
   -42   -152   -201   -258   -225   -161   -244   -266   -205   -
266   -262    -77   -266   -225   -220    298    100   -248   -295
-245
  -205   -234   -381   -350    -35   -346   -304     -3   -303
333     -8   -307   -357   -259   -284   -331   -222    -73   -215
-206
   -31   -194    -78    -52   -183   -127    -30   -200    -44   -
171   -167     -5   -188    287    -69    125     -1   -176   -212
-171
   -78   -211   -129   -111   -207   -169   -135   -178    276   -
188   -189    -50   -228    -67     -2    -51    180   -156   -234
-195
  -262   -270   -333   -365     89   -324   -138   -265   -321   -
173   -244   -260   -407   -294   -291   -327   -296   -262    556
221
  -150   -194   -244   -265    183   -241    -13   -166   -224   -
125   -175   -172   -309   -220   -219   -218   -203   -174      7
429
  -103   -288    297     40   -249   -154    -75   -264    -85   -
235   -233      5   -247    222   -132   -151   -138   -234   -264
-221
```

```
   -97   -262   -120    -59   -240   -181    -70   -228    249   -
189   -188    -57   -241    257     42   -152   -116   -210   -233
-201
  -137    484   -371   -381   -143   -315   -317   -115   -327   -
110    257   -293   -402   -291   -317   -288   -204   -134   -256
-244
  -278   -353   -377   -350   -425   -366   -330   -354    384   -
387   -382   -262   -429   -291    -34   -384   -313   -401   -376
-397
  -278   -353   -377   -350   -425   -366   -330   -354    384   -
387   -382   -262   -429   -291    -34   -384   -313   -401   -376
-397
  -103   -288    297     40   -249   -154    -75   -264    -85   -
235   -233      5   -247    222   -132   -151   -138   -234   -264
-221
  -205   -234   -381   -350    -35   -346   -304     -3   -303
333     -8   -307   -357   -259   -284   -331   -222    -73   -215
-206
   179   -204     -1    261   -219   -125   -168   -217    -87   -
213   -220    -90   -214    -47   -151   -130   -124   -145   -277
-215
   -43   -158   -194   -179   -129   -190   -140     22    -19    -
85   -139   -129   -246   -105    238   -182    -95    217   -179
-169
  -132   -195   -351   -364   -140   -341   -349    311   -321    -
10    -92   -288   -394   -334   -335   -316   -163    233   -304
-255
  -273   -276   -370   -382   -369   -326   -202   -355    -82   -
330   -370   -248   -363   -205    393   -343   -311   -406   -275
-351
   -43   -236     15    252   -209   -122   -129   -230    -65   -
217   -220    -24   -209    -36   -124    108    -45   -197   -263
-192
  -115   -254    -41    -78   -226   -150      7   -240    -68   -
214   -207    311   -252    270    -94   -124   -112   -231   -234
-201
  -183   -291   -254   -106   -302   -307    -35   -302   -184   -
215   -186   -161   -311    406   -162   -262   -230   -299   -270
-309
  -168   -263   -182   -122   -195   -257    307   -285   -142   -
207   -190    -55   -291    334   -104   -210   -186   -265   -218
-107
  -278   -353   -377   -350   -425   -366   -330   -354    384   -
387   -382   -262   -429   -291    -34   -384   -313   -401   -376
-397
---------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 14 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 36 nsites= 2 E= 3.6e+001
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.500000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 regular expression
--------------------------------------------------------------------
RL[NV][QV]E[HY][KQ][KQ]L[LV][AD]EN[KT]SL[QS][KT][WY]Y[DQ][KQ][CM]KK[
DQ]L[AE][RV][IV]R[ES][NQ]Q[HQ]K
--------------------------------------------------------------------




Time 18.91 secs.

********************************************************************


********************************************************************
MOTIF 15 MEME    width =  11  sites =   4  llr = 98  E-value =
1.2e+002
********************************************************************
--------------------------------------------------------------------
      Motif 15 Description
--------------------------------------------------------------------
Simplified        A  :::::::::::
pos.-specific     C  :::::::::::
probability       D  ::a:5::::::
matrix            E  a3:3:a:a:3a
                  F  :::::::::::
                  G  :::::::::::
                  H  :::::::::::
                  I  :8::::3::3:
                  K  ::::3::::3:
                  L  ::::::3:3::
                  M  ::::::3::::
                  N  ::::3::::::
                  P  :::::::::::
                  Q  :::::::::::
                  R  :::::::::::
```

```
                  S  :::3::3::::
                  T  :::::::::3:
                  V  ::::::::8::
                  W  :::::::::::
                  Y  :::5:::::::

         bits    6.2
                 5.5
                 4.9
                 4.3   *
Relative         3.7 * *  * *  *
Entropy          3.1 ****** ** *
(35.5 bits)      2.5 ****** ** *
                 1.8 ***********
                 1.2 ***********
                 0.6 ***********
                 0.0 -----------

Multilevel           EIDYDEIEVEE
consensus             E EK L LI
sequence                SN M  K
                           S  T

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 15 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value              Site
-------------             ----- ---------            -----------
TAK1_HUMAN                   30  3.32e-12 EAPSQVLNFE EIDYKEIEVEE
VVGRGAFGVV
TAK1_NEMATOSTELLA             2  6.27e-12          E EIDSDELEVIE
NVGHGAFGVV
TAK1_CIONA                   17  1.51e-11 VIERHPGFIE EIDYNEMELKE
VVGKGSFGVV
TAK1_AMPHIMEDON             282  4.86e-10 DSDDEDDDED EEDEDESEVTE
VPPPSPPLAL
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 15 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_HUMAN                        3.3e-12  29_[15]_566
TAK1_NEMATOSTELLA                 6.3e-12  1_[15]_268
TAK1_CIONA                        1.5e-11  16_[15]_581
TAK1_AMPHIMEDON                   4.9e-10  281_[15]_185
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 15 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 15 width=11 seqs=4
TAK1_HUMAN               (   30) EIDYKEIEVEE  1
TAK1_NEMATOSTELLA        (    2) EIDSDELEVIE  1
TAK1_CIONA               (   17) EIDYNEMELKE  1
TAK1_AMPHIMEDON          (  282) EEDEDESEVTE  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 15 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 11 n= 2565 bayes= 9.32249 E=
1.2e+002
  -438   -565   -197    369   -544   -472   -475   -512   -514   -
570   -577   -380   -635   -365   -539   -540   -501   -535   -561
-561
  -194   -264   -262    -29   -168   -333   -336    354   -258    -
16    -97   -252   -404   -269   -304   -300   -200     85   -312
-249
  -280   -374    409   -115   -357   -316   -281   -387   -368   -
396   -412    -48   -472   -337   -377   -331   -346   -375   -384
-352
   -67   -191    -93     63    126   -168    -17   -169    -84   -
143   -161    -53   -248    -94   -126     39   -108   -157    -94
348
  -169   -329    351    -75   -304   -166   -162   -343     61   -
324   -331    167   -332   -155   -205   -165   -182   -317   -350
-269
  -438   -565   -197    369   -544   -472   -475   -512   -514   -
570   -577   -380   -635   -365   -539   -540   -501   -535   -561
-561
   -90   -143   -318   -291    -43   -252   -236    231   -242
175    180   -211   -323   -223   -244     20   -102     39   -185
-141
  -438   -565   -197    369   -544   -472   -475   -512   -514   -
570   -577   -380   -635   -365   -539   -540   -501   -535   -561
-561
   -97   -174   -372   -369   -142   -346   -334     67   -345
86   -129   -320   -382   -346   -329   -333   -153    330   -320
-295
   -25   -213    -55    110   -147   -136    -80    114    141   -
125   -129    -18   -208     -7    -38    -76    137    -99   -217
-140
  -438   -565   -197    369   -544   -472   -475   -512   -514   -
570   -577   -380   -635   -365   -539   -540   -501   -535   -561
-561
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------------------
	Motif 15 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 11 nsites= 4 E= 1.2e+002 
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000 
0.000000  0.750000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.500000 
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.250000  0.000000  0.000000  0.250000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.250000  0.000000  0.250000  0.250000  0.000000  0.000000 
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.750000  0.000000  0.000000 
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000 
0.000000  0.250000  0.250000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
	Motif 15 regular expression
--------------------------------------------------------------------------------
E[IE]D[YES][DKN]E[ILMS]E[VL][EIKT]E
--------------------------------------------------------------------------------




Time 20.06 secs.

********************************************************************************
```

```
********************************************************************
MOTIF 16 MEME    width =   6  sites =   2  llr = 34  E-value =
3.1e+002
********************************************************************
--------------------------------------------------------------------
      Motif 16 Description
--------------------------------------------------------------------
Simplified        A  :::::5
pos.-specific     C  55::::
probability       D  :::a::
matrix            E  ::::::
                  F  :5::::
                  G  ::::::
                  H  ::::::
                  I  ::::a:
                  K  ::::::
                  L  ::::::
                  M  ::a:::
                  N  :::::5
                  P  ::::::
                  Q  ::::::
                  R  ::::::
                  S  5:::::
                  T  ::::::
                  V  ::::::
                  W  ::::::
                  Y  ::::::

         bits    6.2
                 5.5
                 4.9   *
                 4.3  ****
Relative         3.7 ******
Entropy          3.1 ******
(24.7 bits)      2.5 ******
                 1.8 ******
                 1.2 ******
                 0.6 ******
                 0.0 ------

Multilevel           CCMDIA
consensus            SF   N
sequence


--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 16 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value             Site
-------------             ----- ---------            ------
TAK1_DROSOPHILA             247  1.57e-09 CPEGIKQLME CCMDIN
PEKRPSMKEI
TAK1_HUMAN                  318  1.59e-07 GQSNSATSTG SFMDIA
STNTSNKSDT
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_DROSOPHILA                   1.6e-09  246_[16]_141
TAK1_HUMAN                        1.6e-07  317_[16]_283
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 16 width=6 seqs=2
TAK1_DROSOPHILA          (  247) CCMDIN  1
TAK1_HUMAN               (  318) SFMDIA  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 6 n= 2595 bayes= 10.3404 E= 3.1e+002
     1    467   -269   -321   -205   -177   -276   -234   -268   -
255   -260   -156   -306   -262   -260    129    -15   -197   -297
-260
  -165    440   -360   -386    356   -326   -261   -155   -354   -
121   -198   -293   -390   -342   -338   -288   -243   -166   -111
-11
  -349   -342   -472   -494   -273   -438   -447   -200   -431   -
138    476   -416   -498   -432   -469   -442   -362   -263   -301
-298
  -257   -360    405    -93   -340   -286   -261   -369   -328   -
377   -392    -34   -439   -300   -348   -304   -316   -355   -370
-333
  -200   -244   -356   -375   -140   -352   -374    362   -319
10    -78   -290   -418   -338   -349   -326   -200    109   -303
-242
```

```
   204   -141    -13   -107   -171    -43    -91   -175    -85   -
188   -195    307   -204    -85   -126    -56    -61   -120   -222
-173
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 16 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 6 nsites= 2 E= 3.1e+002
 0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.500000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 16 regular expression
--------------------------------------------------------------------------------
[CS][CF]MDI[AN]
--------------------------------------------------------------------------------




Time 21.12 secs.

********************************************************************************


********************************************************************************
MOTIF 17 MEME    width =   8  sites =   2  llr = 43  E-value =
9.5e+002
********************************************************************************
--------------------------------------------------------------------------------
      Motif 17 Description
--------------------------------------------------------------------------------
Simplified        A  ::::::::
```

```
pos.-specific     C  ::::::::
probability       D  ::::::a:
matrix            E  ::::::::
                  F  ::::::::
                  G  ::::::::
                  H  ::::::::
                  I  ::::5:::
                  K  ::::::::
                  L  :::::::a
                  M  ::::::::
                  N  ::::::::
                  P  ::::::::
                  Q  :::::a::
                  R  aaa:::::
                  S  :::a5:::
                  T  ::::::::
                  V  ::::::::
                  W  ::::::::
                  Y  ::::::::

         bits    6.2
                 5.5
                 4.9
                 4.3 ***  **
Relative         3.7 **** ***
Entropy          3.1 ********
(31.3 bits)      2.5 ********
                 1.8 ********
                 1.2 ********
                 0.6 ********
                 0.0 --------

Multilevel           RRRSIQDL
consensus                S
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 17 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name            Start   P-value              Site
-------------            ----- ---------            --------
TAK1_HUMAN                 436  1.48e-10 EIVISGNGQP RRRSIQDL
TVTGTEPGQV
TAK1_CIONA                 391  3.82e-10 ALSKVTKCES RRRSSQDL
IAEFEQTTIT
--------------------------------------------------------------------

--------------------------------------------------------------------
```

```
      Motif 17 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_HUMAN                        1.5e-10  435_[17]_163
TAK1_CIONA                        3.8e-10  390_[17]_210
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 17 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 17 width=8 seqs=2
TAK1_HUMAN               (  436) RRRSIQDL  1
TAK1_CIONA               (  391) RRRSSQDL  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 17 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 8 n= 2583 bayes= 10.3337 E= 9.5e+002
  -273   -276   -370   -382   -369   -326   -202   -355    -82    -
330   -370   -248   -363   -205    393   -343   -311   -406   -275
-351
  -273   -276   -370   -382   -369   -326   -202   -355    -82    -
330   -370   -248   -363   -205    393   -343   -311   -406   -275
-351
  -273   -276   -370   -382   -369   -326   -202   -355    -82    -
330   -370   -248   -363   -205    393   -343   -311   -406   -275
-351
   -42   -152   -201   -258   -225   -161   -244   -266   -205    -
266   -262    -77   -266   -225   -220    298    100   -248   -295
-245
   -12   -128   -188   -208    -64   -169   -194    254   -158     -
21    -79    -81   -237   -163   -180    121     25     62   -193
-136
  -183   -291   -254   -106   -302   -307    -35   -302   -184    -
215   -186   -161   -311    406   -162   -262   -230   -299   -270
-309
  -257   -360    405    -93   -340   -286   -261   -369   -328    -
377   -392    -34   -439   -300   -348   -304   -316   -355   -370
-333
  -205   -234   -381   -350    -35   -346   -304     -3   -303
333     -8   -307   -357   -259   -284   -331   -222    -73   -215
-206
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 17 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 8 nsites= 2 E= 9.5e+002
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 17 regular expression
--------------------------------------------------------------------
RRRS[IS]QDL
--------------------------------------------------------------------




Time 22.20 secs.

********************************************************************


********************************************************************
MOTIF 18 MEME    width =   6  sites =   2  llr = 33  E-value =
9.6e+002
********************************************************************
--------------------------------------------------------------------
      Motif 18 Description
--------------------------------------------------------------------
```

```
Simplified        A  :::::5
pos.-specific     C  ::::::
probability       D  :::a::
matrix            E  ::::::
                  F  ::::a:
                  G  ::::::
                  H  ::::::
                  I  ::::::
                  K  5:::::
                  L  ::::::
                  M  5:::::
                  N  ::::::
                  P  ::::::
                  Q  :5::::
                  R  :5::::
                  S  ::::::
                  T  ::::::
                  V  ::a:::
                  W  :::::5
                  Y  ::::::

         bits    6.2
                 5.5
                 4.9     *
                 4.3    ***
Relative         3.7 * ****
Entropy          3.1 ******
(24.2 bits)      2.5 ******
                 1.8 ******
                 1.2 ******
                 0.6 ******
                 0.0 ------

Multilevel           KQVDFA
consensus            MR   W
sequence


--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 18 sites sorted by position p-value
--------------------------------------------------------------------------------
Sequence name             Start   P-value              Site
-------------             ----- ---------            ------
TAK1_DROSOPHILA             302  7.48e-09 YHVDSSGSRI MRVDFW
RHQLPSIRMT
TAK1_DROSOPHILA               3  1.33e-07         MV KQVDFA
EVKLSEKFLG
--------------------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 18 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_DROSOPHILA                   7.5e-09  2_[18]_293_[18]_86
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 18 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 18 width=6 seqs=2
TAK1_DROSOPHILA          (  302) MRVDFW  1
TAK1_DROSOPHILA          (    3) KQVDFA  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 18 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 6 n= 2595 bayes= 10.3404 E= 9.6e+002
  -103   -223   -176   -144   -157   -199   -153   -109    275    -
98    272   -106   -264    -72     -7   -179   -122   -139   -195
-174
  -142   -258   -191   -126   -269   -223    -55   -262     19    -
213   -217   -107   -273    256    292   -200   -165   -252   -230
-235
   -52   -151   -313   -313   -156   -290   -293     89   -293    -
88   -153   -275   -332   -305   -283   -283   -120    339   -308
-281
  -257   -360    405    -93   -340   -286   -261   -369   -328    -
377   -392    -34   -439   -300   -348   -304   -316   -355   -370
-333
  -266   -231   -394   -422    479   -379   -322   -186   -401    -
100   -205   -345   -404   -404   -410   -327   -340   -225   -135
2
   159   -168   -244   -268    -35   -154   -225   -179   -215    -
145   -192   -197   -305   -205   -209   -175   -169   -132    530
-71
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 18 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 6 nsites= 2 E= 9.6e+002
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 18 regular expression
--------------------------------------------------------------------
[KM][QR]VDF[AW]
--------------------------------------------------------------------


Time 23.24 secs.

********************************************************************


********************************************************************
MOTIF 19 MEME    width =  10  sites =   2  llr = 53  E-value =
1.1e+003
********************************************************************
--------------------------------------------------------------------
      Motif 19 Description
--------------------------------------------------------------------
Simplified        A  :55:::::::
pos.-specific     C  ::::::::::
probability       D  :5::::::::
matrix            E  ::::5:::::
                  F  ::::::::::
                  G  :::::::a::
                  H  :::5::::::
                  I  ::::::::::
                  K  ::::::::::
                  L  ::::::::::
                  M  a::5::::::
                  N  ::5:::::::
                  P  ::::::::::
                  Q  ::::::::::
                  R  ::::::::::
```

```
                  S  ::::5:::5:
                  T  :::::aa::a
                  V  ::::::::::
                  W  ::::::::::
                  Y  ::::::::5:

         bits    6.2
                 5.5
                 4.9 *
                 4.3 *    *** *
Relative         3.7 * ** *** *
Entropy          3.1 **** *****
(38.2 bits)      2.5 **********
                 1.8 **********
                 1.2 **********
                 0.6 **********
                 0.0 ----------

Multilevel           MAAHETTGST
consensus             DNMS   Y
sequence

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value               Site
-------------             ----- ---------            ----------
TAK1_AMPHIMEDON             408  4.17e-14 VVVVDHEVHE MDNHETTGYT
SLDENRLRFD
TAK1_AMPHIMEDON             316  5.42e-11 QSDMSYVKSK MAAMSTTGST
SDPPGDANND
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_AMPHIMEDON                   4.2e-14  315_[19]_82_[19]_60
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 19 width=10 seqs=2
TAK1_AMPHIMEDON          (  408) MDNHETTGYT  1
TAK1_AMPHIMEDON          (  316) MAAMSTTGST  1
//
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 19 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 10 n= 2571 bayes= 10.327 E= 1.1e+003
  -349   -342   -472   -494   -273   -438   -447   -200   -431   -
138    476   -416   -498   -432   -469   -442   -362   -263   -301
-298
   155   -204    325    -18   -221    -94   -164   -234   -131   -
239   -246    -12   -231   -119   -182   -131   -137   -165   -270
-217
   204   -141    -13   -107   -171    -43    -91   -175    -85   -
188   -195    307   -204    -85   -126    -56    -61   -120   -222
-173
  -107   -179   -153   -171    -43   -200    321    -93   -119    -
55    290    -32   -264     32    -99   -172   -120   -107   -127
8
   -43   -236     15    252   -209   -122   -129   -230    -65   -
217   -220    -24   -209    -36   -124    108    -45   -197   -263
-192
   -88   -162   -222   -259   -209   -214   -242   -153   -195   -
214   -187    -89   -289   -197   -215     24    361   -130   -278
-259
   -88   -162   -222   -259   -209   -214   -242   -153   -195   -
214   -187    -89   -289   -197   -215     24    361   -130   -278
-259
  -131   -306   -219   -315   -350    400   -314   -389   -283   -
404   -379   -165   -381   -332   -286   -234   -291   -347   -334
-349
   -29   -145   -124   -161    136   -134      2   -126   -119   -
119   -142    -40   -228   -124   -138    152     -2   -127    -26
298
   -88   -162   -222   -259   -209   -214   -242   -153   -195   -
214   -187    -89   -289   -197   -215     24    361   -130   -278
-259
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 10 nsites= 2 E= 1.1e+003
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 regular expression
--------------------------------------------------------------------
M[AD][AN][HM][ES]TTG[SY]T
--------------------------------------------------------------------




Time 24.30 secs.

********************************************************************


********************************************************************
MOTIF 20 MEME    width =   9  sites =   2  llr = 48  E-value =
5.3e+002
********************************************************************
--------------------------------------------------------------------
      Motif 20 Description
--------------------------------------------------------------------
Simplified        A  :::::::::
pos.-specific     C  :::::::::
probability       D  :::::::::
matrix            E  :5:::::5:
                  F  ::::::::a
                  G  :::::::::
                  H  :::::::::
```

```
                  I  ::::a::::
                  K  :::::::::
                  L  :5:::::::
                  M  ::::::a::
                  N  :::::::::
                  P  ::a::::::
                  Q  a::::::::
                  R  :::::5:::
                  S  :::5:::::
                  T  :::::::5:
                  V  :::::5:::
                  W  :::::::::
                  Y  :::5:::::

         bits    6.2
                 5.5
                 4.9       * *
                 4.3 *   * * *
Relative         3.7 * * * * *
Entropy          3.1 * *******
(34.6 bits)      2.5 *********
                 1.8 *********
                 1.2 *********
                 0.6 *********
                 0.0 ---------

Multilevel           QEPSIRMEF
consensus             L Y V T
sequence

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                  Site
-------------             ----- ---------            ---------
TAK1_AMPHIMEDON              68  3.42e-12 KSVEEKRGYK QEPYIVMEF
APYSLERVLH
TAK1_DROSOPHILA             310  9.10e-11 RIMRVDFWRH QLPSIRMTF
PIVKREAERL
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
TAK1_AMPHIMEDON                   3.4e-12  67_[20]_401
TAK1_DROSOPHILA                   9.1e-11  309_[20]_75
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 20 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 20 width=9 seqs=2
TAK1_AMPHIMEDON          (   68) QEPYIVMEF  1
TAK1_DROSOPHILA          (  310) QLPSIRMTF  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 9 n= 2577 bayes= 10.3304 E= 5.3e+002
  -183   -291   -254   -106   -302   -307    -35   -302   -184   -
215   -186   -161   -311    406   -162   -262   -230   -299   -270
-309
   -94   -221    -39    243    -89   -205   -161    -61   -103
161   -111   -116   -242    -40   -149   -186   -138    -99   -161
-162
   -77   -267   -229   -240   -251   -219   -252   -272   -208   -
236   -295   -214    362   -204   -234   -182   -174   -240   -345
-315
   -29   -145   -124   -161    136   -134      2   -126   -119   -
119   -142    -40   -228   -124   -138    152     -2   -127    -26
298
  -200   -244   -356   -375   -140   -352   -374    362   -319
10    -78   -290   -418   -338   -349   -326   -200    109   -303
-242
   -43   -158   -194   -179   -129   -190   -140     22    -19    -
85   -139   -129   -246   -105    238   -182    -95    217   -179
-169
  -349   -342   -472   -494   -273   -438   -447   -200   -431   -
138    476   -416   -498   -432   -469   -442   -362   -263   -301
-298
   -66   -225     -4    257   -210   -157   -139   -193    -66   -
199   -204    -48   -221    -38   -125    -74    161   -154   -257
-201
  -266   -231   -394   -422    479   -379   -322   -186   -401   -
100   -205   -345   -404   -404   -410   -327   -340   -225   -135
2
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 9 nsites= 2 E= 5.3e+002
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 regular expression
--------------------------------------------------------------------
Q[EL]P[SY]I[RV]M[ET]F
--------------------------------------------------------------------




Time 25.27 secs.

********************************************************************


********************************************************************
SUMMARY OF MOTIFS
********************************************************************

--------------------------------------------------------------------
      Combined block diagrams: non-overlapping sites with p-value <
0.0001
--------------------------------------------------------------------
SEQUENCE NAME            COMBINED P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
```

```
TAK1_HUMAN                       0.00e+00  29_[15(3.32e-
12)]_2_[7(1.76e-14)]_1_\
    [5(5.26e-46)]_3_[6(9.04e-26)]_4_[4(1.62e-34)]_1_[2(6.82e-
35)]_4_\
    [1(2.83e-51)]_[10(4.57e-10)]_[3(3.80e-52)]_5_[9(2.08e-16)]_16_\
    [16(1.59e-07)]_112_[17(1.48e-10)]_53_[8(1.59e-59)]_19_[14(6.22e-
38)]_5
TAK1_DROSOPHILA                 2.00e-109  2_[18(1.33e-
07)]_9_[7(7.44e-10)]_3_\
    [5(1.15e-08)]_5_[6(1.06e-17)]_3_[4(1.79e-22)]_[2(2.15e-26)]_4_\
    [1(1.59e-34)]_43_[16(1.57e-09)]_49_[18(7.48e-09)]_2_[20(9.10e-
11)]_23_\
    [13(1.76e-10)]_2_[13(2.86e-10)]_2_[13(1.53e-10)]_2_[13(1.37e-
09)]_10
TAK1_CIONA                       0.00e+00  16_[15(1.51e-
11)]_2_[7(5.01e-12)]_1_\
    [5(1.12e-44)]_3_[6(1.27e-24)]_4_[4(8.86e-33)]_1_[2(1.76e-
37)]_4_\
    [1(2.83e-51)]_[10(1.44e-10)]_[3(2.03e-47)]_5_[9(9.09e-18)]_102_\
    [17(3.82e-10)]_70_[11(2.61e-24)]_13_[8(7.64e-56)]_19_[14(2.42e-
39)]_3
TAK1_TRICHOPLAX                 1.52e-170  1_[7(1.53e-
13)]_1_[5(2.62e-31)]_5_\
    [6(2.20e-15)]_3_[4(3.65e-27)]_1_[2(1.45e-28)]_4_[1(2.71e-
46)]_10_\
    [3(6.09e-44)]_4_[12(3.53e-13)]_3
TAK1_NEMATOSTELLA               3.08e-225  1_[15(6.27e-
12)]_2_[7(1.23e-14)]_2_\
    [5(2.62e-39)]_5_[6(2.65e-24)]_7_[4(5.05e-32)]_1_[2(6.03e-
35)]_4_\
    [1(3.39e-50)]_[10(3.14e-10)]_1_[3(3.33e-49)]_5_[9(6.32e-19)]
TAK1_AMPHIMEDON                 1.55e-120  34_[7(7.51e-
09)]_22_[20(3.42e-12)]_\
    16_[12(5.44e-15)]_16_[2(1.79e-24)]_6_[1(9.64e-35)]_9_[3(1.48e-
31)]_30_\
    [15(4.86e-10)]_23_[19(5.42e-11)]_82_[19(4.17e-14)]_22_[11(6.02e-
22)]_19
--------------------------------------------------------------------

********************************************************************


********************************************************************
Stopped because requested number of motifs (20) found.
********************************************************************

CPU: meme-server

********************************************************************
```

A.13 NIK MEME Output

```
********************************************************************
MEME - Motif discovery tool
********************************************************************
MEME version 4.11.3 (Release date: Sat Mar 11 20:16:08 2017 -0800)

For further information on how to interpret these results or to get
a copy of the MEME software please access http://meme-suite.org .

This file may be used as input to the MAST algorithm for searching
sequence databases for matches to groups of motifs.  MAST is
available
for interactive use and downloading at http://meme-suite.org .
********************************************************************


********************************************************************
REFERENCE
********************************************************************
If you use this program in your research, please cite:

Timothy L. Bailey and Charles Elkan,
"Fitting a mixture model by expectation maximization to discover
motifs in biopolymers", Proceedings of the Second International
Conference on Intelligent Systems for Molecular Biology, pp. 28-36,
AAAI Press, Menlo Park, California, 1994.
********************************************************************


********************************************************************
TRAINING SET
********************************************************************
DATAFILE= NIK_Training_Set_v6.txt
ALPHABET= ACDEFGHIKLMNPQRSTVWY
Sequence name            Weight Length  Sequence name
Weight Length
-------------            ------ ------  -------------
NIK_HOMO                 1.0000    947  NIK_AIPTASIA
1.0000    633
NIK_DROSOPHILA           1.0000    505  NIK_BRANCHIOSTOMA
1.0000   1633
********************************************************************

********************************************************************
COMMAND LINE SUMMARY
********************************************************************
This information can also be useful in the event you wish to report
a problem with the MEME software.
```

```
command: meme NIK_Training_Set_v6.txt -protein -oc . -nostatus -time
18000 -maxsize 60000 -mod anr -nmotifs 20 -minw 6 -maxw 50

model:  mod=           anr    nmotifs=        20    evt=
inf
object function=  E-value of product of p-values
width:  minw=            6    maxw=           50
width:  wg=             11    ws=              1    endgaps=
yes
nsites: minsites=        2    maxsites=       20    wnsites=
0.8
theta:  spmap=         pam    spfuzz=        120
global: substring=     yes    branching=      no    wbranch=
no
em:     prior=       megap    b=           18590    maxiter=
50
        distance=    1e-05
data:   n=            3718    N=               4    shuffle=
-1

sample: seed=            0    ctfrac=         -1    maxwords=
-1
Dirichlet mixture priors file: prior30.plib
Letter frequencies in dataset:
A 0.069 C 0.024 D 0.048 E 0.078 F 0.027 G 0.070 H 0.033 I 0.036 K
0.049
L 0.092 M 0.022 N 0.034 P 0.083 Q 0.055 R 0.053 S 0.085 T 0.055 V
0.058
W 0.009 Y 0.018
Background letter frequencies (from dataset with add-one prior
applied):
A 0.069 C 0.024 D 0.048 E 0.078 F 0.027 G 0.070 H 0.033 I 0.036 K
0.049
L 0.092 M 0.022 N 0.034 P 0.083 Q 0.055 R 0.053 S 0.085 T 0.055 V
0.058
W 0.010 Y 0.018
********************************************************************


********************************************************************
MOTIF  1 MEME    width =  49  sites =   4  llr = 413  E-value =
4.1e-017
********************************************************************
--------------------------------------------------------------------
      Motif 1 Description
--------------------------------------------------------------------
Simplified        A
:::3:3::3:::::::::::::::55::::::::3:33::::::a::::
pos.-specific     C
:::3::::::::::::::::3::::::::::::::::::3::::::3::
```

```
probability       D
:::::::::::::::::::::a:::3:::::35:::::::a::::::::
matrix            E
:::::::8::33:33::::::::::3:::::::::::::::::::::::
                  F
33::::3::::3::::::::::::::::5::::::::::::8:::::::
                  G
:::3::::8:::::::3:::3:::3:::::::35:::::5::a::::::
                  H
:::::::::::::8:3:::a:::::::::::::::5:::::::3:3:::
                  I
:3:::::::::::::::83:::5::::3::::::::3::3:::::3:5:
                  K
::::::::::3:::3::::::::a:::::::::::::8::::::::3::
                  L
::8::35::5::a::3::3:::::::::35::::::5:a::::::::5:
                  M
::::::3::::::::::::::::::::33::::::::::::::3:::::
                  N
::::::::::::::::::::::::::a:::3:::3::::::::::::::
                  P
::::::::::::::::::::::::::::::::::::::::::::::::5
                  Q
:::38::::::::::3::::::::::::::::::::::::::::::3:5
                  R
3::::::::::::::35:::3::::::::::::::::::::::::::::
                  S
:::::::3::3:::5:3:::3:::::::::55:333:::::::5:::::
                  T
::3:::::::::::::::::::::3::::3::3:3:::::::::::3::
                  V
:::::5:::53::::::35:::5::::5:33::::::::::::::5:::
                  W
:::::::::::::::::::::::::::::::::::::::::::::::::
                  Y
55:::::::::5:::::::::::::::::::::::::::::3:::::::

         bits    6.7
                 6.0
                 5.3
                 4.7                    * *    *             **
Relative         4.0 **           *   * * * *  *             *** *
Entropy          3.3 **      *  ***   * * ***  ***        ** *** *
*
(148.8 bits)     2.7 *** ****** ***  **** ******** * *
*************
                 2.0 ******************************* *
***************
                 1.3
*************************************************
```

```
                 0.7
*************************************************
                 0.0 -----------------------------------------------
--

Multilevel
YYLAQVLEGLEYLHSHRIVHCDIKAANVFLSSDGAHLKLGDFGSAVCIP
consensus            FFTC AFSAVKE EELGVI G V GD ILTNDGSNSAA C Y H
HKLQ
sequence             RI G LM   SF  KQS L R   TE MMVV T S I  I   M IQ
                        Q      V    R    S             T           T

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
NIK_BRANCHIOSTOMA           709  3.95e-47 YRTLHQYMAL
FYLCQVFEGLVYLEEQRIVHSDVKAANMMVSSDGAHLKLIDFGMAHTIP DGADWVEPQR
NIK_HOMO                    494  8.27e-46 QGCLPEDRAL
YYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVCLQ PDGLGKSLLT
NIK_DROSOPHILA              331  2.78e-39 TGNLPEALTR
RFTAQLLSGVSELHKHGIVHRDIKTANIFLVDGSNSLKLGDFGSAVKIQ AHTTVPGELQ
NIK_AIPTASIA                264  2.66e-36 SGHLDERCCI
YILQXVMEAVKFLHSLSVIHCDIKGENVFTNXTXTXIKLGDYGSAIQLP LGLECIRLQK
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_BRANCHIOSTOMA                   4e-47  708_[1]_876
NIK_HOMO                          8.3e-46  493_[1]_405
NIK_DROSOPHILA                    2.8e-39  330_[1]_126
NIK_AIPTASIA                      2.7e-36  263_[1]_321
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 1 width=49 seqs=4
NIK_BRANCHIOSTOMA        (  709)
FYLCQVFEGLVYLEEQRIVHSDVKAANMMVSSDGAHLKLIDFGMAHTIP  1
NIK_HOMO                 (  494)
YYLGQALEGLEYLHSRRILHGDVKADNVLLSSDGSHAALCDFGHAVCLQ  1
NIK_DROSOPHILA           (  331)
RFTAQLLSGVSELHKHGIVHRDIKTANIFLVDGSNSLKLGDFGSAVKIQ  1
```

```
NIK_AIPTASIA             (  264)
YILQXVMEAVKFLHSLSVIHCDIKGENVFTNXTXTXIKLGDYGSAIQLP  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 49 n= 3526 bayes= 9.78218 E= 4.1e-
017
  -156   -206   -244   -267    287   -303    -10   -121   -199   -
168   -119   -173   -351   -258     68   -208   -210   -162     33
474
  -160   -205   -259   -282    298   -310    -26    143   -219   -
141    -99   -185   -359   -271   -228   -217   -207   -137     25
466
  -211   -252   -378   -358    -54   -377   -321     25   -271
293     28   -282   -410   -293   -278   -306     60    -64   -196
-143
   222    219   -176   -181   -182    127   -198   -138   -109   -
222   -136   -104   -307    119   -164    -82   -101   -106   -218
-137
  -219   -308   -297   -128   -307   -375    -41   -259   -210   -
246   -124   -166   -351    385   -178   -279   -253   -295   -220
-260
    81   -163   -320   -322   -107   -313   -287    118   -255
41    -56   -244   -375   -309   -266   -252   -119    320   -213
-149
  -260   -275   -456   -430    233   -441   -357     37   -349
265    257   -350   -454   -337   -337   -383   -254    -80   -179
-119
  -263   -484    -93    344   -425   -359   -335   -362   -222   -
449   -363   -194   -465   -224   -321    -85   -305   -374   -430
-335
    11   -305   -229   -339   -349    355   -342   -341   -270   -
445   -326   -164   -427   -370   -291   -220   -279   -323   -298
-283
  -187   -220   -422   -413    -63   -403   -367    125   -332
218      1   -321   -452   -360   -344   -347   -194    266   -220
-158
   -35   -247    -30    111   -146   -165    -83   -103    172   -
175    -85      8   -238    -24    -25     75    -44    108   -172
-55
  -137   -193   -222    -19    281   -288      1   -109   -185   -
160   -107   -161   -335   -246   -201   -191   -194   -150     28
474
  -286   -302   -438   -418    -64   -439   -368     -2   -336
316     19   -352   -448   -335   -325   -391   -280   -108   -220
-174
  -228   -296   -120     20   -146   -285    427   -272   -155   -
```

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279   -192     -4   -363    -61   -121   -205   -198   -274   -168
44
   -69   -277    -22    122   -196   -177   -107   -169    173   -
224   -131      8   -263    -44    -39    175    -46   -175   -211
-96
  -132   -279   -147   -112   -176   -250    257   -172     19     -
1   -121    -44   -311    228    145   -161   -132   -192   -179
-39
   -99   -251   -130   -161   -249    102   -156   -215     -8   -
278   -195    -50   -316   -128    314     51   -129   -226   -226
-157
  -252   -289   -379   -422   -167   -433   -433    418   -327    -
42    -42   -305   -502   -407   -383   -361   -229    161   -294
-198
  -168   -222   -380   -400   -129   -401   -377    323   -323
67    -47   -304   -453   -383   -348   -341   -181    276   -265
-190
  -322   -322   -241   -336   -158   -352    462   -330   -306   -
321   -241    -61   -421   -114   -183   -279   -271   -335   -183
26
    14    219   -134   -154   -185    157   -166   -149    -55   -
231   -143    -54   -291   -137    155    114    -51   -147   -214
-113
  -301   -395    418   -122   -341   -354   -291   -330   -336   -
426   -354    -32   -511   -362   -366   -331   -348   -357   -331
-266
  -204   -247   -390   -422   -165   -428   -422    380   -339    -
66    -61   -318   -486   -414   -381   -365   -205    254   -306
-214
  -329   -388   -426   -424   -446   -443   -382   -319    419   -
453   -354   -283   -503   -375    -36   -431   -353   -421   -344
-350
   295   -116   -262   -284   -226    103   -303   -187   -226   -
272   -181   -179   -356   -276   -261    -72    122   -114   -259
-218
   210   -331    199    177   -279   -210   -183   -226    -48   -
285   -195    -50   -298    -67   -157   -150   -143   -203   -300
-181
  -329   -345   -174   -393   -296   -324   -133   -251   -263   -
401   -309    467   -441   -291   -322   -194   -235   -340   -266
-235
  -151   -209   -369   -385   -122   -382   -355    314   -308    -
61    208   -289   -437   -367   -330   -322   -166    282   -250
-176
  -266   -259   -441   -451    431   -439   -362      2   -380
118    236   -355   -466   -390   -387   -363   -282   -110   -134
5
  -133   -180   -343   -326    -44   -320   -278    109   -240
228     21   -229   -381   -274   -257   -243    113    165   -163
-94
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   -57   -191   -116   -162   -167   -190   -171   -108    -85   -
212   -128    200   -301   -156   -148    225     52     91   -212
-113
   -62   -188    108   -110   -163   -192   -138   -160    -40   -
216   -132    -12   -250   -105   -101    247     72   -178   -188
-84
  -149   -312    336    -88   -274     94   -165   -265   -115   -
338   -255     51   -344   -171   -197   -134    103   -271   -291
-172
   -54   -249   -126   -150   -204    311   -175   -192    -82   -
254   -173    -67   -283   -150   -138     21   -118   -196   -205
-122
    98   -195   -136   -177   -208   -203   -192   -174    -98   -
266   -160    167   -313   -165   -160    196    197   -179   -237
-147
  -155   -235   -131   -162    -95   -240    410   -198   -114   -
215   -137     13   -286    -30    -90    -19   -131   -202   -130
88
    76   -200   -364   -347    -42   -340   -299    243   -263
234     27   -255   -397   -291   -277   -273   -160     27   -171
-106
   -79   -360   -326   -305   -389   -375   -310   -285    407   -
393   -300   -218   -450   -272    -25   -334   -284   -351   -318
-291
  -286   -302   -438   -418    -64   -439   -368     -2   -336
316     19   -352   -448   -335   -325   -391   -280   -108   -220
-174
   -61    198   -250   -305   -141    291   -278    172   -223   -
163   -100   -163   -366   -287   -249   -176   -147    -57   -203
-133
  -301   -395    418   -122   -341   -354   -291   -330   -336   -
426   -354    -32   -511   -362   -366   -331   -348   -357   -331
-266
  -309   -266   -399   -441    485   -435   -254   -162   -379   -
160   -173   -322   -460   -422   -394   -339   -360   -236    -55
251
  -182   -356   -239   -356   -366    367   -353   -368   -283   -
471   -352   -177   -451   -392   -303   -263   -330   -365   -305
-293
   -62   -194   -116   -125   -101   -199    189    -78    -35   -
163    204    -23   -282    -97    -94    204     24   -108   -161
-9
   354   -122   -321   -336   -236   -160   -355   -194   -286   -
281   -195   -251   -423   -342   -305    -96   -164   -111   -267
-244
   -88   -177   -310   -320   -123   -334     50    239   -250   -
104    -68   -243   -379   -311   -262   -274   -124    324   -223
-146
   -58    203    -80    -64   -153   -185    -89   -107    181   -
178    -88     -9   -258    150     -7    -70    150   -121   -173
-68
```

```
  -247   -270   -426   -437    -64   -438   -399    360   -347
198     14   -334   -483   -376   -369   -377   -235     52   -225
-167
  -121   -307   -178   -156   -256   -267   -196   -230   -115   -
276   -215   -146    260    226   -170   -191   -181   -239   -286
-214
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 49 nsites= 4 E= 4.1e-017
 0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.750000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
 0.250000  0.250000  0.000000  0.000000  0.000000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.017142  0.006106  0.011992  0.019415  0.006708  0.017543
0.008313  0.009049  0.012326  0.023027  0.005571  0.008514  0.020820
0.763864  0.013129  0.021288  0.013864  0.014466  0.002428  0.004434
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.000000  0.500000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.750000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.000000  0.000000  0.750000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.250000  0.250000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
0.750000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
0.250000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.250000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.750000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.250000  0.000000  0.000000  0.000000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.250000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.250000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.250000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.250000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.500000  0.000000  0.250000  0.000000  0.000000
 0.017142  0.006106  0.261992  0.019415  0.006708  0.017543
0.008313  0.009049  0.012326  0.023027  0.005571  0.008514  0.020820
0.013864  0.013129  0.521288  0.013864  0.014466  0.002428  0.004434
 0.000000  0.000000  0.500000  0.000000  0.000000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
 0.017142  0.006106  0.011992  0.019415  0.006708  0.517543
0.008313  0.009049  0.012326  0.023027  0.005571  0.008514  0.020820
0.013864  0.013129  0.271288  0.013864  0.014466  0.002428  0.004434
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.250000  0.250000  0.000000  0.000000  0.000000
 0.017142  0.006106  0.011992  0.019415  0.006708  0.017543
0.508313  0.009049  0.012326  0.023027  0.005571  0.008514  0.020820
0.013864  0.013129  0.271288  0.013864  0.014466  0.002428  0.004434
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.750000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.250000  0.000000  0.000000  0.000000  0.500000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.750000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 1 regular expression
--------------------------------------------------------------------
[YFR][YFI][LT][ACGQ]Q[VAL][LFM][ES][GA][LV][EKSV][YEF]L[HE][SEK][HLQ
R][RGS][IV][VIL]H[CGRS]D[IV]K[AGT][ADE]N[VIM][FLM][LTV][SNV][SD][DGT
][GS][ANST][HS][LAI][KA]L[GCI]D[FY]G[SHM]A[VHI][CKQT][IL][PQ]
--------------------------------------------------------------------




Time  2.88 secs.

********************************************************************


********************************************************************
MOTIF  2 MEME    width =  28  sites =   3  llr = 220  E-value =
2.6e-014
********************************************************************
--------------------------------------------------------------------
      Motif 2 Description
--------------------------------------------------------------------
Simplified        A  ::333::::::::::::3::::::3:::
pos.-specific     C  3:3:::::::7a::::::::7:::::::
probability       D  :3:::a:::::::::::::::::::::3
matrix            E  :::::::::::::::3::::::::::::
                  F  ::::::::::::::::::::::::::73
                  G  :3:::::::33::3:::::a::::::::
                  H  7::::::::::::::7:::::7::::::
                  I  ::::::3:::::::::::::::::3:::
                  K  :::7::::::::::::::::3:::::::
                  L  ::::::::::::::7::7::::::::::
                  M  ::::::::::::33::a:::::::::::
                  N  :3::::::::::::::::7:::::::::
                  P  ::::::::::::::::::::::a:::::
                  Q  :::::::::::::::::::::::::7::
                  R  ::3::::::::::::::::::3:::33:
                  S  ::::::::a3::::::::3:::::::::
                  T  ::::::::::::::::::::::::3:::
                  V  ::::7:7::3::733:::::::::::::
                  W  :::::::a:::::::::::::::a::::
                  Y  :::::::::::::::::::::::::::3
```

```
         bits    6.7        *               *
                 6.0        *               *
                 5.3        *   *    *      *
                 4.7      * *   *    *      *
Relative         4.0 *    * *  **    *  *** *  *
Entropy          3.3 *  ****** ***  ** ****** ***
(105.8 bits)     2.7 ********* ******************
                 2.0 ****************************
                 1.3 ****************************
                 0.7 ****************************
                 0.0 ----------------------------

Multilevel           HDAKVDVWSGCCVGLHMLNGCHPWAQFD
consensus            CGCAA I  SG MMVE AS KR  IRRF
sequence              NR      V   V           T  Y

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 2 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
NIK_HOMO                    573  3.37e-35 MAPEVVLGRS
CDAKVDVWSSCCMMLHMLNGCHPWTQFF RGPLCLKIAS
NIK_BRANCHIOSTOMA           788  1.91e-34 MPTEVAECKP
HNCKVDVWSGCCVGLHMLNGCHPWIRRY SHAATLLLII
NIK_DROSOPHILA              411  1.34e-23 EVFTKTNSDG
HGRAADIWSVGCVVVEMASGKRPWAQFD SNFQIMFKVG
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 2 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_HOMO                          3.4e-35  572_[2]_347
NIK_BRANCHIOSTOMA                 1.9e-34  787_[2]_818
NIK_DROSOPHILA                    1.3e-23  410_[2]_67
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 2 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 2 width=28 seqs=3
NIK_HOMO                 (  573) CDAKVDVWSSCCMMLHMLNGCHPWTQFF  1
NIK_BRANCHIOSTOMA        (  788) HNCKVDVWSGCCVGLHMLNGCHPWIRRY  1
NIK_DROSOPHILA           (  411) HGRAADIWSVGCVVVEMASGKRPWAQFD  1
//
--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
     Motif 2 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 28 n= 3610 bayes= 10.6794 E= 2.6e-
014
  -194    187   -187   -266    -92   -279    422   -202   -204   -
240   -163    -17   -358    -70   -130   -201   -184   -216   -136
79
  -165   -323    278   -112   -280    177   -136   -292   -115   -
365   -284    262   -339   -174   -199   -119   -154   -305   -286
-165
   207    305   -215   -216   -165   -170   -201   -111    -67   -
205   -129   -136   -308   -174    203   -105   -113    -78   -197
-115
     3   -321   -234   -211   -315   -300   -242   -235    390   -
326   -237   -152   -375   -193    -13   -248   -213   -272   -279
-219
    94   -160   -302   -312   -160   -284   -297     96   -258   -
153   -113   -248   -362   -319   -266   -230   -117    344   -260
-208
  -293   -389    416   -114   -336   -345   -284   -324   -323   -
420   -347    -26   -501   -350   -356   -322   -338   -350   -327
-259
  -126   -199   -354   -375   -154   -387   -358    299   -310    -
91    -77   -296   -426   -379   -325   -333   -157    320   -288
-216
  -374   -355   -381   -436    -58   -407   -380   -317   -358   -
247   -259   -326   -509   -388   -342   -421   -376   -325    652
-49
  -100   -193   -241   -327   -249   -241   -303   -255   -223   -
339   -242    -97   -353   -304   -252    312     78   -278   -277
-199
    62   -148   -170   -200   -145    200   -210    -43   -130   -
184   -110    -88   -285   -190   -178    108    -51    164   -195
-110
  -194    514   -411   -459   -353    -21   -439   -301   -412   -
416   -326   -329   -499   -453   -409   -307   -286   -334   -412
-352
  -355    529   -504   -519   -405   -528   -505   -344   -503   -
471   -372   -440   -605   -540   -474   -478   -378   -436   -484
-432
   -97   -173   -332   -336    -87   -338   -302    161   -264    -
52    241   -257   -389   -319   -279   -281   -127    325   -213
-146
   -12   -136   -226   -226    -40    124   -202    127   -146    -
39    281   -137   -311   -198   -182   -159    -75    208   -121
-42
  -197   -228   -397   -378    -37   -389   -333    116   -296
270     36   -298   -418   -311   -300   -327   -197    157   -189
-134
```

```
  -165   -288    -61     82   -141   -237    397   -227    -78   -
254   -168      9   -318    -31    -95   -165   -155   -232   -169
37
  -404   -380   -491   -540   -292   -503   -489   -171   -436   -
192    537   -427   -563   -498   -499   -471   -399   -276   -261
-229
   105   -197   -308   -290    -39   -283   -275     49   -214
265     27   -223   -346   -249   -237   -221   -156    -26   -167
-102
  -229   -310    -98   -268   -272   -240   -116   -235   -184   -
365   -274    444   -385   -230   -254     -1   -152   -301   -257
-197
  -169   -344   -227   -343   -354    365   -342   -354   -271   -
457   -340   -165   -440   -379   -292   -251   -316   -351   -296
-281
  -285    519   -399   -406   -348   -432   -396   -287    -58   -
398   -312   -318   -517   -378   -286   -378   -308   -347   -406
-327
  -226   -280   -178   -223   -134   -291    415   -247    -61   -
258   -174    -11   -358    -48    127   -207   -189   -257   -151
54
  -121   -313   -250   -280   -265   -284   -289   -245   -206   -
293   -266   -230    330   -257   -252   -207   -203   -251   -320
-262
  -374   -355   -381   -436    -58   -407   -380   -317   -358   -
247   -259   -326   -509   -388   -342   -421   -376   -325    652
-49
   168   -129   -226   -225    -71   -208   -215    246   -145    -
75    -20   -127   -302   -200   -187    -81    175     92   -151
-67
  -184   -312   -223   -115   -285   -312    -55   -231     -7   -
243   -132   -115   -344    351    114   -229   -196   -259   -216
-193
  -228   -245   -309   -322    467   -353   -216   -115   -185   -
133   -131   -231   -398   -289     66   -274   -256   -178    -61
142
  -152   -204    105   -237    345   -290    -19   -110   -187   -
154   -113   -143   -344   -244   -211   -200   -200   -155     34
427
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 2 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 28 nsites= 3 E= 2.6e-014
 0.000000  0.333333  0.000000  0.000000  0.000000  0.000000
0.666667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.333333  0.000000  0.000000  0.333333
0.000000  0.000000  0.000000  0.000000  0.000000  0.333333  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.333333  0.333333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
 0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.666667  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.333333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.333333  0.000000  0.333333  0.000000  0.000000
 0.000000  0.666667  0.000000  0.000000  0.000000  0.333333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.333333
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
0.666667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.666667  0.000000
0.000000  0.000000  0.333333  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.666667  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.333333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.666667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.333333  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.666667  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.666667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.333333  0.000000  0.333333  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.333333
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 2 regular expression
--------------------------------------------------------------------
[HC][DGN][ACR][KA][VA]D[VI]WS[GSV][CG]C[VM][GMV][LV][HE]M[LA][NS]G[C
K][HR]PW[AIT][QR][FR][DFY]
--------------------------------------------------------------------




Time  5.57 secs.

********************************************************************


********************************************************************
MOTIF  3 MEME    width =  20  sites =   4  llr = 183  E-value =
2.8e-007
********************************************************************
--------------------------------------------------------------------
      Motif 3 Description
--------------------------------------------------------------------
```

```
Simplified        A  ::33:::8::::::::::::
pos.-specific     C  :3::::::::::::::::::
probability       D  :::3::::::33::::::::
matrix            E  ::::::::3:5:35:::::a
                  F  :::::5:::::::3:::a::
                  G  ::::::a::::5::::::::
                  H  ::::3:::::3:::::::::
                  I  :5:::::3::::::::a:::
                  K  ::::::::::::::::::::
                  L  :33:5:::::::::33::::
                  M  ::::::::::::::::::a:
                  N  3::::::::::::::3::::
                  P  :::3::::::::3:::::::
                  Q  :::::::::3::3:::::::
                  R  5::3:::::5:33:::::::
                  S  ::::::::::::::::::::
                  T  ::::::::::::::33::::
                  V  ::5:::::83::::5:::::
                  W  :::::::::::::3::::::
                  Y  3:::35:::::::::3::::

         bits    6.7
                 6.0
                 5.3                  **
                 4.7      *          ***
Relative         4.0      **         ****
Entropy          3.3 **   ****    *  ****
(65.9 bits)      2.7 *** ******** *******
                 2.0 ********************
                 1.3 ********************
                 0.7 ********************
                 0.0 --------------------

Multilevel           RIVALFGAVREGEEVLIFME
consensus            NCADHY IEQDDPFLN
sequence             YLLPY    VHRQWTT
                        R        R  Y

--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 3 sites sorted by position p-value
--------------------------------------------------------------------------------
Sequence name             Start   P-value                      Site
-------------             ----- ---------             ---------------
NIK_HOMO                    451  1.56e-24 LMACAGLTSP
RIVPLYGAVREGPWVNIFME LLEGGSLGQL
NIK_BRANCHIOSTOMA           666  3.76e-21 LEICCCLDNP
YIAAHFGAVREGRETYIFME FLEGYTLEKI
NIK_AIPTASIA                219  1.15e-18 IWSKLSGQNI
RCLDLFGAVQDDQFVTIFME YMEEGSLANL
```

```
NIK_DROSOPHILA              288  1.14e-15 LKILEGIKHK
NLVRYYGIEVHREELLIFME LCSEGTLESL
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_HOMO                          1.6e-24  450_[3]_477
NIK_BRANCHIOSTOMA                 3.8e-21  665_[3]_948
NIK_AIPTASIA                      1.2e-18  218_[3]_395
NIK_DROSOPHILA                    1.1e-15  287_[3]_198
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 3 width=20 seqs=4
NIK_HOMO                 (  451) RIVPLYGAVREGPWVNIFME  1
NIK_BRANCHIOSTOMA        (  666) YIAAHFGAVREGRETYIFME  1
NIK_AIPTASIA             (  219) RCLDLFGAVQDDQFVTIFME  1
NIK_DROSOPHILA           (  288) NLVRYYGIEVHREELLIFME  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 20 n= 3642 bayes= 10.5665 E= 2.8e-
007
  -158   -283   -142   -162   -114   -241    -84   -195     20   -
253   -179    162   -333   -112    325   -177   -156   -226   -158
250
  -186    178   -375   -387    -84   -372   -348    378   -296
92     -4   -273   -443   -345   -327   -305   -177     95   -211
-132
    81   -163   -320   -322   -107   -313   -287    118   -255
41    -56   -244   -375   -309   -266   -252   -119    320   -213
-149
    97   -261    141    -37   -172   -170   -105   -150     16   -
206   -119     -5    138    -54    129    -88    -73   -151   -198
-82
  -192   -234   -281   -295    123   -328    227    -58   -207
191    -63   -169   -384   -224   -218   -248   -200   -121     -4
369
  -240   -255   -322   -353    393   -367    -72   -163   -283   -
190   -162   -226   -415   -315   -282   -280   -279   -215     33
455
```

```
  -182   -356   -239   -356   -366    367   -353   -368   -283   -
471   -352   -177   -451   -392   -303   -263   -330   -365   -305
-293
   325   -111   -309   -311   -165   -168   -325    143   -251   -
177   -116   -236   -418   -312   -278    -99   -145    -21   -231
-187
   -77   -190   -220    -22   -179   -329   -283     82   -212   -
172   -131   -228   -368   -271   -245   -275   -129    354   -277
-223
  -146   -277   -184   -148   -226   -260   -132   -156     61   -
226   -151    -92   -329    114    320   -188   -147     79   -200
-136
  -163   -427    186    279   -331   -256    147   -285    -97   -
346   -258    -61   -352   -111   -205   -204   -195   -281   -347
-216
  -146   -332     80   -186   -304    323   -224   -296   -130   -
374   -271    -47   -374   -219     48   -182   -214   -299   -277
-209
   -69   -284    -45    107   -192   -193    -85   -162     40   -
210   -115    -18     63    188    139   -105    -83   -169   -198
-94
  -174   -265   -181    215    265   -296   -132   -116   -140   -
174   -127   -142   -370   -188   -194   -222   -183   -157    424
196
   -91   -164   -322   -323    -92   -320   -282    133   -248
62    -39   -235   -377   -301   -263   -251     96    310   -199
-131
   -66   -169   -125   -131     46   -207    -54     10    -51
65    -23    195   -285   -114   -109    -92    132    -33    -75
314
  -261   -300   -384   -427   -162   -429   -431    431   -330    -
46    -46   -311   -503   -409   -384   -366   -241    105   -289
-194
  -315   -267   -411   -457    500   -443   -381   -157   -403   -
152   -172   -360   -466   -467   -433   -350   -379   -236   -114
54
  -417   -387   -499   -554   -306   -511   -498   -181   -449   -
201    537   -436   -571   -509   -514   -481   -410   -288   -265
-236
  -459   -585   -188    363   -528   -510   -485   -455   -483   -
600   -519   -363   -674   -391   -528   -540   -504   -518   -509
-475
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 20 nsites= 4 E= 2.8e-007
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.250000
```

```
 0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.250000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.750000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.750000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.250000  0.500000  0.000000  0.000000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.250000  0.500000  0.000000  0.000000
0.250000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.250000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
0.250000  0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.500000  0.250000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.250000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.250000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 3 regular expression
--------------------------------------------------------------------
[RNY][ICL][VAL][ADPR][LHY][FY]G[AI][VE][RQV][EDH][GDR][EPQR][EFW][VL
T][LNTY]IFME
--------------------------------------------------------------------




Time  8.29 secs.

********************************************************************


********************************************************************
MOTIF  4 MEME    width =  14  sites =   4  llr = 129  E-value =
9.4e-002
********************************************************************
--------------------------------------------------------------------
      Motif 4 Description
--------------------------------------------------------------------
Simplified        A  ::::::3::5:::5
pos.-specific     C  ::::::::::::::
probability       D  ::::::::::::::
matrix            E  ::3::5:::::a::
                  F  3::::::3:::::3
                  G  3::a::::::::::
                  H  :::::::5::::::
                  I  :5::::::::::::
                  K  ::::::::::::::
                  L  ::::::::::::::
                  M  ::::::::a:::::
                  N  ::3:::::::::::
                  P  :33:::3::38:::
                  Q  :::::5::::::::
                  R  ::::::::::::::
                  S  ::::::::::3:::
                  T  3:::a:5:::3:::
                  V  ::3:::::::::a3
                  W  ::::::::::::::
                  Y  33:::::3::::::
```

```
         bits    6.7
                 6.0
                 5.3        *
                 4.7        *
Relative         4.0   **  **  **
Entropy          3.3  * **  **  **
(46.4 bits)      2.7 ** ****** ****
                 2.0 **************
                 1.3 **************
                 0.7 **************
                 0.0 --------------

Multilevel           FIEGTETHMAPEVA
consensus            GPN  QAF PT  F
sequence             TYP   PY S   V
                     Y V

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            --------------
NIK_HOMO                    555  1.31e-16 GLGKSLLTGD YIPGTETHMAPEVV
LGRSCDAKVD
NIK_DROSOPHILA              390  2.59e-14 AHTTVPGELQ GYVGTQAYMAPEVF
TKTNSDGHGR
NIK_AIPTASIA                323  3.68e-14 LGLECIRLQK TINGTEPFMSPEVA
TLEQPPPLPR
NIK_BRANCHIOSTOMA           770  1.25e-13 ADWVEPQRNA FPEGTQTHMPTEVA
ECKPHNCKVD
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_HOMO                          1.3e-16  554_[4]_379
NIK_DROSOPHILA                    2.6e-14  389_[4]_102
NIK_AIPTASIA                      3.7e-14  322_[4]_297
NIK_BRANCHIOSTOMA                 1.2e-13  769_[4]_850
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 4 width=14 seqs=4
NIK_HOMO                 (  555) YIPGTETHMAPEVV  1
NIK_DROSOPHILA           (  390) GYVGTQAYMAPEVF  1
```

```
NIK_AIPTASIA             (  323) TINGTEPFMSPEVA  1
NIK_BRANCHIOSTOMA        (  770) FPEGTQTHMPTEVA  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 4 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 14 n= 3666 bayes= 9.83842 E= 9.4e-
002
  -104   -177   -202   -216    285     19    -26    -50   -148   -
126    -68   -130   -321   -208   -180   -158     62    -90      5
421
  -127   -189   -272   -274     14   -290   -192    349   -187    -
43    -10   -179     35   -244   -225   -216   -128     61   -105
273
   -51   -250    -24    104   -151   -173    -99    -97     15   -
182    -98    194     96    -45    -63    -89    -64    113   -186
-69
  -182   -356   -239   -356   -366    367   -353   -368   -283   -
471   -352   -177   -451   -392   -303   -263   -330   -365   -305
-293
  -178   -237   -298   -375   -268   -326   -333   -169   -253   -
333   -192   -134   -414   -301   -285    -52    385   -184   -289
-256
  -146   -406     -5    220   -335   -282   -148   -262    -70   -
297   -195   -111   -329    286   -161   -217   -194   -259   -307
-234
   131   -177   -205   -217   -210   -189   -242   -148   -148   -
251   -158   -114    138   -201   -200    -44    269   -140   -252
-180
  -251   -265   -279   -333    274   -356    353   -193   -278   -
220   -173   -128   -408   -191   -222   -266   -259   -233     19
391
  -417   -387   -499   -554   -306   -511   -498   -181   -449   -
201    537   -436   -571   -509   -514   -481   -410   -288   -265
-236
   269   -139   -232   -245   -230   -150   -275   -198   -188   -
274   -190   -161    126   -239   -233     92   -108   -137   -266
-207
  -100   -295   -236   -263   -256   -272   -278   -226   -189   -
280   -247   -209    314   -241   -238   -185     56   -231   -320
-257
  -459   -585   -188    363   -528   -510   -485   -455   -483   -
600   -519   -363   -674   -391   -528   -540   -504   -518   -509
-475
  -102   -198   -345   -366   -190   -372   -342     91   -312   -
169   -143   -305   -410   -382   -311   -330   -155    374   -310
-260
   281   -112   -294   -291    177   -185   -264     14   -221   -
```

```
115    -56   -206   -378   -274   -246   -115   -116    145   -168
-55
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 4 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 14 nsites= 4 E= 9.4e-002
 0.000000  0.000000  0.000000  0.000000  0.250000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.250000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.250000  0.250000
0.000000  0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.250000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.750000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
      Motif 4 regular expression
---------------------------------------------------------------------
[FGTY][IPY][ENPV]GT[EQ][TAP][HFY]M[APS][PT]EV[AFV]
---------------------------------------------------------------------



Time 10.85 secs.

*********************************************************************


*********************************************************************
MOTIF  5 MEME    width =   7  sites =   4  llr = 76  E-value = 1.8e-
001
*********************************************************************
---------------------------------------------------------------------
      Motif 5 Description
---------------------------------------------------------------------
Simplified        A  :3:::::
pos.-specific     C  :3:::3:
probability       D  3::::::
matrix            E  :::::3:
                  F  5::::::
                  G  ::3::::
                  H  :::::::
                  I  ::::::5
                  K  :3:8:::
                  L  :::::::
                  M  :::::::
                  N  :3:::::
                  P  :::::::
                  Q  :::::::
                  R  :::::5:
                  S  :::3:::
                  T  3::::::
                  V  ::::::5
                  W  ::8:a::
                  Y  :::::::

         bits    6.7     *
                 6.0     *
                 5.3   * *
                 4.7   * *
Relative         4.0   * *
Entropy          3.3 * *** *
(27.4 bits)      2.7 *******
                 2.0 *******
                 1.3 *******
                 0.7 *******
```

```
                 0.0 -------

Multilevel           FAWKWRI
consensus            DCGS CV
sequence             TK   E
                      N

---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 5 sites sorted by position p-value
---------------------------------------------------------------------
Sequence name             Start   P-value             Site
-------------             ----- ---------            -------
NIK_AIPTASIA                613  1.19e-09 LQRASEEDWY TKWKWRV
DLHGNIQRND
NIK_BRANCHIOSTOMA          1607  1.98e-09 LSVEVVAVAG DNWKWCI
NEQCILEYQG
NIK_HOMO                    932  5.56e-09 LQCTLAPDGS FAWSWRV
KHGQLENRP
NIK_HOMO                     51  1.62e-07 KLEAVEKSPV FCGKWEI
LNDVITKGTA
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 5 block diagrams
---------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_AIPTASIA                      1.2e-09  612_[5]_14
NIK_BRANCHIOSTOMA                   2e-09  1606_[5]_20
NIK_HOMO                          5.6e-09  50_[5]_874_[5]_9
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 5 in BLOCKS format
---------------------------------------------------------------------
BL   MOTIF 5 width=7 seqs=4
NIK_AIPTASIA             (  613) TKWKWRV  1
NIK_BRANCHIOSTOMA        ( 1607) DNWKWCI  1
NIK_HOMO                 (  932) FAWSWRV  1
NIK_HOMO                 (   51) FCGKWEI  1
//

---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 5 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 7 n= 3694 bayes= 9.84941 E= 1.8e-001
  -127   -223    108   -157    406   -232   -154    -86   -108   -
```

```
148   -105    -55   -321   -171   -175   -141    101   -125   -112
124
   151    204    -65    -73   -147   -153   -103   -108    173   -
183    -95    203   -258    -61    -44    -71    -58   -108   -178
-64
  -356   -352   -376   -432    -62   -150   -379   -317   -353   -
251   -261   -319   -506   -386   -341   -407   -368   -323    648
-53
  -239   -354   -267   -267   -365   -339   -268   -277    400   -
370   -279   -166   -427   -227    -18    -72   -248   -332   -304
-258
  -379   -358   -384   -439    -61   -410   -384   -322   -362   -
251   -263   -329   -512   -391   -346   -425   -380   -329    652
-54
  -150    144   -170     17   -242   -257   -148   -194     20   -
258   -181    -94   -327   -112    346   -189   -161   -223   -206
-148
  -204   -247   -390   -422   -165   -428   -422    380   -339    -
66    -61   -318   -486   -414   -381   -365   -205    254   -306
-214
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 5 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 7 nsites= 4 E= 1.8e-001
 0.000000  0.000000  0.250000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.250000  0.000000  0.000000  0.000000
 0.250000  0.250000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.250000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.750000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.750000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.250000  0.000000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 5 regular expression
--------------------------------------------------------------------
[FDT][ACKN][WG][KS]W[RCE][IV]
--------------------------------------------------------------------




Time 13.48 secs.

********************************************************************


********************************************************************
MOTIF  6 MEME    width =  19  sites =   2  llr = 105  E-value =
2.7e-001
********************************************************************
--------------------------------------------------------------------
      Motif 6 Description
--------------------------------------------------------------------
Simplified        A  :::::::::::::::::::
pos.-specific     C  :::::::::::::::::::
probability       D  5::::::::::::::::::
matrix            E  ::::::::5::::::::::
                  F  :5::::::::::::a::::
                  G  ::::::5:::a:a::a:::
                  H  5:5:5::::::::::::::
                  I  ::::::55:5:::::::::
                  K  ::::::::5:::::::5::
                  L  :::::::::5:::::::::
                  M  :::::::5:::::::::::
                  N  :::::::::::::::::::
                  P  :::::::::::::::::::
                  Q  :5:::::::::5:::::::
                  R  ::5::5:::::::a:::::
                  S  :::::5:::::5:::::::
                  T  ::::::::::::::::5::
                  V  :::::::::::::::::a:
                  W  :::a5::::::::::::::
                  Y  ::::::::::::::::::a

         bits    6.7    *
                 6.0    *              *
                 5.3    *          *   *
                 4.7    **         *   *
Relative         4.0  * **  *  * **** **
Entropy          3.3 ***** ***** *******
(75.9 bits)      2.7 *******************
                 2.0 *******************
                 1.3 *******************
```

```
                 0.7 *******************
                 0.0 -------------------

Multilevel           DFHWHRGIEIGQGRFGKVY
consensus            HQR WSIMKL S    T
sequence

---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 6 sites sorted by position p-value
---------------------------------------------------------------------
Sequence name             Start   P-value                   Site
-------------             ----- ---------            ---------------
NIK_DROSOPHILA              227  2.83e-24 DKVHIRARSV
HFRWHRGIKIGQGRFGKVY TAVNNNTGEL
NIK_BRANCHIOSTOMA           610  2.08e-22 LPPCDAQFRL
DQHWWSIMELGSGRFGTVY LSCLASEEQE
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 6 block diagrams
---------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_DROSOPHILA                    2.8e-24  226_[6]_260
NIK_BRANCHIOSTOMA                 2.1e-22  609_[6]_1005
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 6 in BLOCKS format
---------------------------------------------------------------------
BL   MOTIF 6 width=19 seqs=2
NIK_DROSOPHILA           (  227) HFRWHRGIKIGQGRFGKVY  1
NIK_BRANCHIOSTOMA        (  610) DQHWWSIMELGSGRFGTVY  1
//

---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 6 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 19 n= 3646 bayes= 9.98268 E= 2.7e-
001
  -177   -301    338    -66   -184   -200    248   -237   -121   -
298   -217     60   -333   -108   -153   -172   -176   -247   -198
-32
  -126   -206   -163   -147    354   -251    -21    -59    -97    -
89    -70    -86   -285    226   -122   -179   -141   -111     42
154
  -196   -268   -186   -211   -183   -266    267   -222     14   -
```

```
265   -195    -56   -332    -60    326   -215   -190   -249   -157
-23
  -366   -350   -375   -429    -52   -400   -370   -307   -350   -
242   -253   -319   -503   -381   -335   -414   -368   -318    651
-42
  -242   -277   -221   -288     28   -301    265   -199   -197   -
206   -171    -81   -392   -123   -147   -264   -235   -223    572
143
   -76   -213   -127   -147   -188   -172   -115   -161     38   -
233   -157    -33   -257    -96    295    128    -13   -181   -162
-100
   -58   -184   -178   -235    -94    243   -237    277   -153    -
88    -57   -109   -315   -231   -191   -177   -133     46   -148
-92
  -187   -224   -346   -366    -60   -365   -329    338   -270
17    369   -256   -426   -311   -306   -300   -178     82   -178
-115
  -103   -312     -3    212   -233   -202   -139   -184    263   -
247   -161    -42   -274    -43    -18   -148   -122   -194   -217
-127
  -197   -232   -355   -371    -36   -380   -337    355   -279
176     34   -268   -422   -316   -303   -313   -189     92   -177
-121
  -152   -326   -210   -322   -335    362   -324   -332   -252   -
434   -321   -148   -419   -357   -275   -234   -294   -330   -281
-263
   -52   -215    -69    -59   -167   -164    -40   -143    -13   -
201   -110     12   -226    262    -58    125     -4   -159   -160
-85
  -152   -326   -210   -322   -335    362   -324   -332   -252   -
434   -321   -148   -419   -357   -275   -234   -294   -330   -281
-263
  -294   -296   -361   -389   -353   -364   -212   -298    -50   -
359   -312   -231   -401   -230    405   -343   -314   -388   -222
-265
  -287   -251   -385   -428    495   -416   -332   -129   -370   -
130   -147   -329   -442   -430   -399   -327   -343   -207    -83
88
  -152   -326   -210   -322   -335    362   -324   -332   -252   -
434   -321   -148   -419   -357   -275   -234   -294   -330   -281
-263
   -99   -232   -120   -118   -191   -206   -145   -121    308   -
218   -132    -34   -267    -92      9    -51    178   -138   -181
-110
   -73   -171   -304   -320   -141   -328   -303    146   -261   -
118    -95   -258   -370   -330   -272   -284   -123    357   -255
-195
  -171   -214   -235   -272    199   -279    -23   -109   -193   -
155   -117   -156   -348   -246   -207   -218   -206   -156     59
515
---------------------------------------------------------------------
```

```
--------------------------------------------------------------------------------
      Motif 6 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 19 nsites= 2 E= 2.7e-001
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 6 regular expression
--------------------------------------------------------------------
[DH][FQ][HR]W[HW][RS][GI][IM][EK][IL]G[QS]GRFG[KT]VY
--------------------------------------------------------------------




Time 16.28 secs.

********************************************************************


********************************************************************
MOTIF  7 MEME    width =   9  sites =   3  llr = 72  E-value =
6.9e+000
********************************************************************
--------------------------------------------------------------------
      Motif 7 Description
--------------------------------------------------------------------
Simplified        A  ::a::::::
pos.-specific     C  :::::::::
probability       D  :::::::::
matrix            E  :::7::a::
                  F  :3:::::::
                  G  :::3:3:::
                  H  ::::a::::
                  I  :::::::::
                  K  :::::::::
                  L  ::::::::a
                  M  37:::::::
                  N  7::::::::
                  P  :::::::::
                  Q  :::::::a:
                  R  :::::::::
                  S  :::::3:::
                  T  :::::::::
                  V  :::::::::
                  W  :::::3:::
```

```
                  Y  :::::::::

         bits    6.7
                 6.0
                 5.3
                 4.7  *  *
Relative         4.0 *** * **
Entropy          3.3 *** *****
(34.6 bits)      2.7 *********
                 2.0 *********
                 1.3 *********
                 0.7 *********
                 0.0 ---------

Multilevel           NMAEHGEQL
consensus            MF G S
sequence                  W

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                Site
-------------             ----- ---------            ---------
NIK_AIPTASIA                398  4.28e-12 QMPNESIEHD NMAEHGEQL
SVHVNGELQP
NIK_AIPTASIA                447  1.08e-11 HVPLNVHDVN NMAEHSEQL
LPEHEELHQL
NIK_BRANCHIOSTOMA           564  7.73e-10 VSVIPPRHVS MFAGHWEQL
AEELLTTNRR
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_AIPTASIA                      4.3e-12  397_[7]_40_[7]_178
NIK_BRANCHIOSTOMA                 7.7e-10  563_[7]_1061
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 7 width=9 seqs=3
NIK_AIPTASIA             (  398) NMAEHGEQL  1
NIK_AIPTASIA             (  447) NMAEHSEQL  1
NIK_BRANCHIOSTOMA        (  564) MFAGHWEQL  1
//
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------------------
      Motif 7 position-specific scoring matrix
--------------------------------------------------------------------------------
log-odds matrix: alength= 20 w= 9 n= 3686 bayes= 10.7095 E= 6.9e+000
  -219   -293   -133   -264   -208   -271   -110   -154   -158   -
262    108    442   -381   -212   -219   -161   -163   -216   -221
-154
  -267   -284   -428   -440    222   -421   -326    -18   -348    -
31    489   -330   -476   -373   -373   -367   -266   -119   -145
-20
   347   -106   -292   -303   -214   -142   -330   -168   -255   -
257   -173   -225   -394   -313   -279    -79   -144    -90   -248
-219
  -238   -448    -82    334   -390     17   -304   -339   -198   -
423   -337   -157   -435   -212   -290   -289   -282   -350   -394
-299
  -290   -299   -212   -302   -131   -327    455   -298   -263   -
293   -213    -35   -396    -88   -155   -250   -242   -305   -159
52
   -33   -219   -158   -213   -119    232   -199   -165   -134   -
240   -168    -72   -324   -202   -179     78    -90   -174    448
-45
  -446   -581   -182    362   -522   -502   -476   -449   -460   -
590   -509   -354   -658   -379   -512   -526   -491   -509   -504
-466
  -227   -326   -289   -133   -313   -381    -56   -270   -194   -
261   -138   -170   -375    387   -178   -289   -262   -308   -232
-256
  -263   -283   -416   -395    -47   -420   -348     18   -312
312     34   -329   -429   -317   -305   -369   -258    -87   -202
-153
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 7 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 9 nsites= 3 E= 6.9e+000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.666667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.333333  0.000000
0.000000  0.000000  0.000000  0.000000  0.666667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.666667  0.000000  0.333333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.333333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.333333  0.000000  0.000000  0.333333  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 7 regular expression
--------------------------------------------------------------------
[NM][MF]A[EG]H[GSW]EQL
--------------------------------------------------------------------



Time 18.80 secs.

********************************************************************


********************************************************************
MOTIF  8 MEME    width =   6  sites =   2  llr = 37  E-value =
8.3e+000
********************************************************************
--------------------------------------------------------------------
      Motif 8 Description
--------------------------------------------------------------------
Simplified        A  ::::::
pos.-specific     C  :aaa5:
probability       D  :::::a
matrix            E  ::::::
                  F  ::::::
                  G  ::::::
                  H  ::::::
                  I  5:::::
                  K  ::::::
                  L  ::::5:
                  M  ::::::
                  N  ::::::
                  P  ::::::
                  Q  ::::::
                  R  ::::::
                  S  5:::::
```

```
                  T  ::::::
                  V  ::::::
                  W  ::::::
                  Y  ::::::

         bits    6.7
                 6.0
                 5.3  ***
                 4.7  *** *
Relative         4.0  *** *
Entropy          3.3 ******
(27.0 bits)      2.7 ******
                 2.0 ******
                 1.3 ******
                 0.7 ******
                 0.0 ------

Multilevel           ICCCCD
consensus            S   L
sequence

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value             Site
-------------             ----- ---------            ------
NIK_AIPTASIA                 10  2.07e-09  MPDSQKVYP SCCCCD
GSTDERLQTR
NIK_BRANCHIOSTOMA           658  8.62e-09 VTQVRRDELE ICCCLD
NPYIAAHFGA
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_AIPTASIA                      2.1e-09  9_[8]_618
NIK_BRANCHIOSTOMA                 8.6e-09  657_[8]_970
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 8 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 8 width=6 seqs=2
NIK_AIPTASIA             (   10) SCCCCD  1
NIK_BRANCHIOSTOMA        (  658) ICCCLD  1
//
--------------------------------------------------------------------
```

```
----------------------------------------------------------------------
      Motif 8 position-specific scoring matrix
----------------------------------------------------------------------
log-odds matrix: alength= 20 w= 6 n= 3698 bayes= 10.8517 E= 8.3e+000
   -33   -148   -180   -215    -48   -206   -204    311   -126    -
51    -21    -65   -275   -188   -169    121     23     79   -140
-50
  -346    529   -498   -514   -397   -517   -499   -336   -494   -
462   -366   -433   -597   -533   -467   -468   -371   -423   -476
-421
  -346    529   -498   -514   -397   -517   -499   -336   -494   -
462   -366   -433   -597   -533   -467   -468   -371   -423   -476
-421
  -346    529   -498   -514   -397   -517   -499   -336   -494   -
462   -366   -433   -597   -533   -467   -468   -371   -423   -476
-421
  -145    457   -348   -368    -48   -346   -306      8   -278
106    -50   -263   -405   -302   -273   -280   -197    -63   -143
-124
  -277   -381    414   -100   -325   -323   -271   -312   -296   -
407   -334    -18   -477   -325   -337   -304   -318   -337   -317
-247
----------------------------------------------------------------------

----------------------------------------------------------------------
      Motif 8 position-specific probability matrix
----------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 6 nsites= 2 E= 8.3e+000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
----------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 8 regular expression
--------------------------------------------------------------------
[IS]CCC[CL]D
--------------------------------------------------------------------




Time 21.30 secs.

********************************************************************


********************************************************************
MOTIF  9 MEME    width =  33  sites =   2  llr = 169  E-value =
1.1e+001
********************************************************************
--------------------------------------------------------------------
      Motif 9 Description
--------------------------------------------------------------------
Simplified        A  ::::a5::::5::::::55::5:::::::::::
pos.-specific     C  5::5:::::5:::::::5:::::a:5::a::::
probability       D  ::::::::::::::::::::::::::::::5::
matrix            E  :5:::::::::::::::::::::::::::::::
                  F  :5:::::5:::::::::::::::::::5:::::
                  G  ::::::::::::::::5:::::::::5::::::
                  H  :::::::::::5:55:::::5:5:::::::::5
                  I  ::a::::::::::::::::::::::5:::::::
                  K  ::::::::::::::::::::::::::::::::5
                  L  :::::5::::5::::::::::::::::::::::
                  M  :::::::::::::::::::::::::::::5:::
                  N  ::::::::::::::::::55::::5::::::::
                  P  ::::::::::::::::::::::::5::::::::
                  Q  5::5:::::::::5:::::::::::::::::::
                  R  ::::::::::::5::a:::::5:::::::5:::
                  S  ::::::::5:::5:5:5:::::5:::55:::::
                  T  :::::::5:::::::::::5:::::::::::::
                  V  ::::::a::::5::::::::::::::::::5a:
                  W  ::::::::::::::::::::5::::::::::::
                  Y  ::::::::55:::::::::::::::::::::::

         bits    6.7
                 6.0
                 5.3                        *    *
                 4.7   *      *          *  *    *
Relative         4.0 * *** ****     *    *  * *  ** *
Entropy          3.3 ***** **** * *** ********* ******
(121.7 bits)     2.7 *********************************
                 2.0 *********************************
                 1.3 *********************************
```

```
               0.7 *********************************
               0.0 ---------------------------------

Multilevel           CEICAAVFSCAHRHHRGAANHAHCNCGFCMDVH
consensus            QF Q L TYYLVSQS SCNTWRS PISS RV K
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                  Site
-------------             ----- ---------            ---------------
NIK_BRANCHIOSTOMA           206  4.54e-37 VTACSKPAGQ
CEICAAVFYCAVSHSRSCNTHRHCPIGFCRDVK IKLHEVNPGP
NIK_BRANCHIOSTOMA           158  1.61e-32 VVFPEQDQVQ
QFIQALVTSYLHRQHRGAANWASCNCSSCMVVH GAVKHVTACS
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_BRANCHIOSTOMA                 4.5e-37  157_[9]_15_[9]_1395
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 9 width=33 seqs=2
NIK_BRANCHIOSTOMA        (  206) CEICAAVFYCAVSHSRSCNTHRHCPIGFCRDVK
1
NIK_BRANCHIOSTOMA        (  158) QFIQALVTSYLHRQHRGAANWASCNCSSCMVVH
1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 33 n= 3590 bayes= 10.809 E= 1.1e+001
  -139    447   -235   -209   -204   -288   -123   -170   -152   -
243   -166   -148   -346    203   -144   -223   -179   -191   -195
-161
  -150   -237    -61    224    350   -259   -156    -99   -132   -
148   -130   -122   -319   -152   -193   -207   -180   -143    -11
127
```

```
  -221   -265   -347   -382   -124   -389   -384    419   -287    -
20    -20   -273   -456   -364   -338   -326   -202    126   -250
-157
  -139    447   -235   -209   -204   -288   -123   -170   -152    -
243   -166   -148   -346    203   -144   -223   -179   -191   -195
-161
   336    -91   -243   -251   -182   -117   -289   -130   -205    -
224   -145   -185   -329   -265   -237    -62   -117    -61   -220
-178
   215   -116   -206   -213    -13   -176   -210     71   -137
164      7   -147   -259   -175   -171   -118    -97     31    -94
-48
   -73   -171   -304   -320   -141   -328   -303    146   -261    -
118    -95   -258   -370   -330   -272   -284   -123    357   -255
-195
   -91   -150   -205   -241    375   -246   -151      8   -154    -
71    -46   -102   -297   -206   -192    -55    184    -32      8
139
   -50   -165   -115   -168    152   -172     -8    -69    -88    -
149    -85    -23   -267   -149   -127    152     -4   -110     27
384
  -138    443   -261   -308    124   -293    -93    -92   -224    -
179   -122   -186   -380   -276   -227   -224   -190   -136      5
329
   215   -116   -206   -213    -13   -176   -210     71   -137
164      7   -147   -259   -175   -171   -118    -97     31    -94
-48
   -58   -162   -138   -177    -31   -222    266     85    -96    -
97    -55    -31   -278    -74   -108   -166    -86    245    -93
73
   -76   -213   -127   -147   -188   -172   -115   -161     38    -
233   -157    -33   -257    -96    295    128    -13   -181   -162
-100
  -189   -284   -173   -129   -180   -295    297   -228   -111    -
237   -132    -38   -329    309    -93   -210   -189   -248   -166
-21
   -71   -203    -57   -126    -85   -152    319   -149    -50    -
211   -130     84   -246    -30    -67    131    -12   -160   -126
66
  -294   -296   -361   -389   -353   -364   -212   -298    -50    -
359   -312   -231   -401   -230    405   -343   -314   -388   -222
-265
   -13   -204   -128   -220   -233    295   -225   -224   -155    -
316   -221    -46   -301   -227   -197    114    -72   -210   -225
-170
   195    449   -316   -348   -207   -196   -337   -158   -275    -
270   -192   -245   -378   -323   -286   -140   -164   -109   -261
-208
   183   -162     -4   -114   -156    -81   -102   -119    -53    -
217   -137    324   -242   -111   -115    -56    -64   -102   -170
-87
```

```
  -120   -216    -48   -169   -192   -182   -105   -132    -87   -
256   -157    349   -300   -146   -148      8    215   -156   -195
-126
  -242   -277   -221   -288     28   -301    265   -199   -197   -
206   -171    -81   -392   -123   -147   -264   -235   -223    572
143
   161   -174   -150   -151   -179   -148   -140   -133     44   -
212   -143    -86   -247   -102    300   -119   -115   -107   -158
-105
   -71   -203    -57   -126    -85   -152    319   -149    -50   -
211   -130     84   -246    -30    -67    131    -12   -160   -126
66
  -346    529   -498   -514   -397   -517   -499   -336   -494   -
462   -366   -433   -597   -533   -467   -468   -371   -423   -476
-421
  -108   -255    -40   -148   -189   -161   -102   -172    -81   -
253   -189    334    190   -132   -133   -108   -109   -192   -197
-124
  -157    459   -359   -387   -119   -361   -348    226   -297   -
116    -92   -268   -437   -354   -309   -296   -188     32   -234
-161
   -13   -204   -128   -220   -233    295   -225   -224   -155   -
316   -221    -46   -301   -227   -197    114    -72   -210   -225
-170
   -76   -176   -198   -251    407   -230   -155    -63   -173   -
119    -97    -98   -299   -227   -210    106    -39   -112     -7
156
  -346    529   -498   -514   -397   -517   -499   -336   -494   -
462   -366   -433   -597   -533   -467   -468   -371   -423   -476
-421
  -128   -213   -190   -184   -124   -237   -123    -48     45   -
99    312   -104   -303    -83    297   -185   -131   -109   -107
-77
   -99   -232    322    -68   -156   -221   -195     45   -141   -
188   -141    -28   -314   -188   -200   -201   -140    187   -186
-125
   -73   -171   -304   -320   -141   -328   -303    146   -261   -
118    -95   -258   -370   -330   -272   -284   -123    357   -255
-195
  -126   -270   -106   -112   -162   -203    237   -169    307   -
227   -146     -2   -284    -31     62   -150   -121   -189   -159
-16
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 9 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 33 nsites= 2 E= 1.1e+001
 0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.500000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 9 regular expression
--------------------------------------------------------------------
[CQ][EF]I[CQ]A[AL]V[FT][SY][CY][AL][HV][RS][HQ][HS]R[GS][AC][AN][NT]
[HW][AR][HS]C[NP][CI][GS][FS]C[MR][DV]V[HK]
--------------------------------------------------------------------




Time 23.84 secs.

********************************************************************


********************************************************************
MOTIF 10 MEME    width =   6  sites =   2  llr = 37  E-value =
2.4e+001
********************************************************************
--------------------------------------------------------------------
     Motif 10 Description
--------------------------------------------------------------------
Simplified        A  ::::::
pos.-specific     C  ::::::
probability       D  :a::5:
matrix            E  ::::::
                  F  ::a:::
                  G  ::::::
                  H  a::::5
                  I  :::a5:
                  K  ::::::
                  L  ::::::
                  M  ::::::
                  N  :::::5
                  P  ::::::
                  Q  ::::::
                  R  ::::::
                  S  ::::::
                  T  ::::::
                  V  ::::::
                  W  ::::::
                  Y  ::::::

         bits    6.7
                 6.0
                 5.3   *
                 4.7 ****
Relative         4.0 **** *
Entropy          3.3 ******
(26.8 bits)      2.7 ******
                 2.0 ******
                 1.3 ******
```

```
                 0.7 ******
                 0.0 ------

Multilevel           HDFIDH
consensus                IN
sequence

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value              Site
-------------             ----- ---------            ------
NIK_AIPTASIA                118  4.45e-09 PPSNKKIPQE HDFIIN
NCAKGSDKEV
NIK_DROSOPHILA              464  6.93e-09 QAPESLSQEG HDFIDH
CLQHDPKRRL
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_AIPTASIA                      4.5e-09  117_[10]_510
NIK_DROSOPHILA                    6.9e-09  463_[10]_36
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 10 width=6 seqs=2
NIK_AIPTASIA             (  118) HDFIIN  1
NIK_DROSOPHILA           (  464) HDFIDH  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 6 n= 3698 bayes= 10.8517 E= 2.4e+001
  -245   -273   -172   -252   -100   -286    443   -252   -198   -
259   -183     -6   -356    -58   -121   -217   -205   -262   -133
78
  -277   -381    414   -100   -325   -323   -271   -312   -296   -
407   -334    -18   -477   -325   -337   -304   -318   -337   -317
-247
  -287   -251   -385   -428    495   -416   -332   -129   -370   -
130   -147   -329   -442   -430   -399   -327   -343   -207    -83
```

```
88
  -221   -265   -347   -382   -124   -389   -384    419   -287    -
20    -20   -273   -456   -364   -338   -326   -202    126   -250
-157
  -155   -247    321    -84   -136   -242   -212    255   -153   -
128   -102    -24   -338   -205   -211   -215   -162     18   -189
-114
  -215   -285    -59   -211   -168   -225    295   -219   -136   -
294   -208    380   -349    -92   -143   -151   -162   -258   -177
-13
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 6 nsites= 2 E= 2.4e+001
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 10 regular expression
--------------------------------------------------------------------
HDFI[DI][HN]
--------------------------------------------------------------------




Time 26.38 secs.

********************************************************************
```

```
********************************************************************
MOTIF 11 MEME    width =  15  sites =   2  llr = 81  E-value =
6.6e+001
********************************************************************
--------------------------------------------------------------------
     Motif 11 Description
--------------------------------------------------------------------
Simplified        A  ::a::::::::::::
pos.-specific     C  :::a:::::::::::
probability       D  :::::a::::::5::
matrix            E  :::::::::::::::
                  F  :::::::::::::::
                  G  ::::::::::::5::
                  H  ::::::::::::::a
                  I  :::::::::::::::
                  K  a:::::::a::::::
                  L  :a::::::::a::::
                  M  :::::::::::::::
                  N  :::::::::::::::
                  P  :::::::5:a:a:a:
                  Q  :::::::5:::::::
                  R  :::::::::::::::
                  S  ::::::a::::::::
                  T  :::::::::::::::
                  V  ::::a::::::::::
                  W  :::::::::::::::
                  Y  :::::::::::::::

         bits    6.7
                 6.0
                 5.3    *
                 4.7    * *        *
Relative         4.0 * ****  *     *
Entropy          3.3 ******* *******
(58.5 bits)      2.7 ***************
                 2.0 ***************
                 1.3 ***************
                 0.7 ***************
                 0.0 ---------------

Multilevel           KLACVDSPKPLPDPH
consensus                   Q    G
sequence

--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 11 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
NIK_HOMO                    286  4.19e-19 KPHPLESFLG KLACVDSQKPLPDPH
LSKLACVDSP
NIK_HOMO                    303  2.58e-18 QKPLPDPHLS KLACVDSPKPLPGPH
LEPSCLSRGA
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_HOMO                          4.2e-19  285_[11]_2_[11]_630
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 11 width=15 seqs=2
NIK_HOMO                 (  286) KLACVDSQKPLPDPH  1
NIK_HOMO                 (  303) KLACVDSPKPLPGPH  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 15 n= 3662 bayes= 10.8376 E=
6.6e+001
  -299   -374   -368   -357   -409   -404   -341   -297    415   -
417   -324   -246   -467   -317    -23   -384   -316   -383   -323
-311
  -226   -255   -372   -357    -20   -383   -314     54   -272
303     50   -291   -395   -285   -273   -332   -224    -56   -162
-120
   336    -91   -243   -251   -182   -117   -289   -130   -205   -
224   -145   -185   -329   -265   -237    -62   -117    -61   -220
-178
  -346    529   -498   -514   -397   -517   -499   -336   -494   -
462   -366   -433   -597   -533   -467   -468   -371   -423   -476
-421
   -73   -171   -304   -320   -141   -328   -303    146   -261   -
118    -95   -258   -370   -330   -272   -284   -123    357   -255
-195
  -277   -381    414   -100   -325   -323   -271   -312   -296   -
407   -334    -18   -477   -325   -337   -304   -318   -337   -317
```

```
-247
   -63  -173  -192  -265  -210  -198  -255  -209  -173   -
296  -204   -60  -304  -251  -209   298    97  -230  -243
-159
   -95  -264  -129   -95  -200  -225   -85  -174   -65   -
215  -144   -81   209   249   -95  -153  -134  -185  -193
-142
  -299  -374  -368  -357  -409  -404  -341  -297   415   -
417  -324  -246  -467  -317   -23  -384  -316  -383  -323
-311
   -98  -288  -220  -247  -236  -256  -262  -215  -177   -
266  -237  -198   324  -229  -223  -182  -176  -222  -292
-229
  -226  -255  -372  -357   -20  -383  -314    54  -272
303    50  -291  -395  -285  -273  -332  -224   -56  -162
-120
   -98  -288  -220  -247  -236  -256  -262  -215  -177   -
266  -237  -198   324  -229  -223  -182  -176  -222  -292
-229
  -143  -313   277  -112  -280   268  -208  -276  -160   -
365  -273     0  -352  -223  -220  -178  -209  -281  -249
-191
   -98  -288  -220  -247  -236  -256  -262  -215  -177   -
266  -237  -198   324  -229  -223  -182  -176  -222  -292
-229
  -245  -273  -172  -252  -100  -286   443  -252  -198   -
259  -183    -6  -356   -58  -121  -217  -205  -262  -133
78
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif 11 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 15 nsites= 2 E= 6.6e+001
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
```

```
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 11 regular expression
--------------------------------------------------------------------
KLACVDS[PQ]KPLP[DG]PH
--------------------------------------------------------------------




Time 28.82 secs.

********************************************************************


********************************************************************
MOTIF 12 MEME    width =   8  sites =   2  llr = 45  E-value =
8.5e+001
********************************************************************
```

```
--------------------------------------------------------------------
      Motif 12 Description
--------------------------------------------------------------------
Simplified        A  ::::::::
pos.-specific     C  ::::::::
probability       D  ::::::::
matrix            E  :::::5::
                  F  ::::::::
                  G  ::::::::
                  H  ::::5:::
                  I  ::::::::
                  K  ::::::::
                  L  ::55::::
                  M  :::::::a
                  N  ::::::::
                  P  ::::::::
                  Q  :5:5:5::
                  R  :5::5:::
                  S  ::::::::
                  T  ::5:::::
                  V  ::::::::
                  W  ::::::::
                  Y  a:::::a:

         bits    6.7
                 6.0 *     *
                 5.3 *     **
                 4.7 *     **
Relative         4.0 *     **
Entropy          3.3 **  * **
(32.5 bits)      2.7 ********
                 2.0 ********
                 1.3 ********
                 0.7 ********
                 0.0 --------

Multilevel           YQLLHEYM
consensus             RTQRQ
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value               Site
-------------             ----- ---------            --------
NIK_BRANCHIOSTOMA           293  5.87e-11 GPASLPVFPG YQLQREYM
SLPYGPGTQP
```

```
NIK_BRANCHIOSTOMA           699  1.55e-10 GYTLEKIIDQ YRTLHQYM
ALFYLCQVFE
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_BRANCHIOSTOMA                5.9e-11  292_[12]_398_[12]_927
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 12 width=8 seqs=2
NIK_BRANCHIOSTOMA        (  293) YQLQREYM  1
NIK_BRANCHIOSTOMA        (  699) YRTLHQYM  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 8 n= 3690 bayes= 10.8486 E= 8.5e+001
  -171   -214   -235   -272    199   -279    -23   -109   -193   -
155   -117   -156   -348   -246   -207   -218   -206   -156     59
515
  -163   -278   -182   -133   -253   -261    -65   -205     50   -
243   -159    -90   -311    230    303   -201   -167   -235   -177
-149
   -75   -146   -205   -217    -12   -245   -189    102   -122
188     28   -106   -277   -165   -158    -70    192     28    -80
-45
  -132   -231   -180   -121    -75   -275    -64     -5    -76
148    -17   -105   -287    281    -98   -198   -145    -90    -91
-82
  -196   -268   -186   -211   -183   -266    267   -222     14   -
265   -195    -56   -332    -60    326   -215   -190   -249   -157
-23
  -152   -350    -34    240   -286   -272   -108   -236    -75   -
273   -172    -99   -318    261   -140   -208   -184   -246   -250
-194
  -171   -214   -235   -272    199   -279    -23   -109   -193   -
155   -117   -156   -348   -246   -207   -218   -206   -156     59
515
  -369   -363   -463   -501   -258   -476   -457   -143   -400   -
168    534   -399   -537   -457   -458   -443   -365   -245   -248
-212
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 12 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 8 nsites= 2 E= 8.5e+001
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000 
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.500000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000 
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000 
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000 
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000 
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 12 regular expression
--------------------------------------------------------------------
Y[QR][LT][LQ][HR][EQ]YM
--------------------------------------------------------------------




Time 31.42 secs.

********************************************************************


********************************************************************
MOTIF 13 MEME    width =   9  sites =   2  llr = 51  E-value = 
3.0e+002
********************************************************************
--------------------------------------------------------------------
      Motif 13 Description
--------------------------------------------------------------------
```

```
Simplified        A  a:::a::::
pos.-specific     C  :::::::::
probability       D  :::::::::
matrix            E  :::::::::
                  F  :::::::::
                  G  :::a:::::
                  H  :::::::::
                  I  :::::::::
                  K  :::::::a:
                  L  ::a::::::
                  M  :a::::::5
                  N  :::::::::
                  P  ::::::a::
                  Q  :::::::::
                  R  :::::a:::
                  S  :::::::::
                  T  ::::::::5
                  V  :::::::::
                  W  :::::::::
                  Y  :::::::::

         bits    6.7
                 6.0
                 5.3  *
                 4.7  *
Relative         4.0 ** *** **
Entropy          3.3 *********
(36.5 bits)      2.7 *********
                 2.0 *********
                 1.3 *********
                 0.7 *********
                 0.0 ---------

Multilevel           AMLGARPKM
consensus                    T
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 13 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value              Site
-------------             ----- ---------            ---------
NIK_BRANCHIOSTOMA           351  3.26e-12 GNTFGQAGQS AMLGARPKM
TQQQPPPSEQ
NIK_BRANCHIOSTOMA           318  1.14e-11 TQPPPSLPPS AMLGARPKT
LDIKPAGPPL
--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
      Motif 13 block diagrams
---------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_BRANCHIOSTOMA                 3.3e-12  317_[13]_24_[13]_1274
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 13 in BLOCKS format
---------------------------------------------------------------------
BL   MOTIF 13 width=9 seqs=2
NIK_BRANCHIOSTOMA        (  351) AMLGARPKM  1
NIK_BRANCHIOSTOMA        (  318) AMLGARPKT  1
//

---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 13 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 9 n= 3686 bayes= 10.8471 E= 3.0e+002
   336    -91   -243   -251   -182   -117   -289   -130   -205   -
224   -145   -185   -329   -265   -237    -62   -117    -61   -220
-178
  -369   -363   -463   -501   -258   -476   -457   -143   -400   -
168    534   -399   -537   -457   -458   -443   -365   -245   -248
-212
  -226   -255   -372   -357    -20   -383   -314     54   -272
303     50   -291   -395   -285   -273   -332   -224    -56   -162
-120
  -152   -326   -210   -322   -335    362   -324   -332   -252   -
434   -321   -148   -419   -357   -275   -234   -294   -330   -281
-263
   336    -91   -243   -251   -182   -117   -289   -130   -205   -
224   -145   -185   -329   -265   -237    -62   -117    -61   -220
-178
  -294   -296   -361   -389   -353   -364   -212   -298    -50   -
359   -312   -231   -401   -230    405   -343   -314   -388   -222
-265
   -98   -288   -220   -247   -236   -256   -262   -215   -177   -
266   -237   -198    324   -229   -223   -182   -176   -222   -292
-229
  -299   -374   -368   -357   -409   -404   -341   -297    415   -
417   -324   -246   -467   -317    -23   -384   -316   -383   -323
-311
   -76   -149   -201   -217    -71   -240   -193     45   -119    -
56    370    -91   -299   -159   -166    -38    224    -11   -121
-66
---------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 13 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 9 nsites= 2 E= 3.0e+002
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 13 regular expression
--------------------------------------------------------------------
AMLGARPK[MT]
--------------------------------------------------------------------




Time 33.89 secs.

********************************************************************


********************************************************************
MOTIF 14 MEME    width =   6  sites =   2  llr = 40  E-value = 9.1e-
002
********************************************************************
```

```
--------------------------------------------------------------------------------
	Motif 14 Description
--------------------------------------------------------------------------------
Simplified        A  ::::::
pos.-specific     C  ::::::
probability       D  ::::::
matrix            E  ::::::
                  F  :::5::
                  G  ::::::
                  H  ::a:::
                  I  ::::::
                  K  ::::::
                  L  ::::::
                  M  5a:::a
                  N  :::5::
                  P  ::::::
                  Q  ::::::
                  R  ::::::
                  S  ::::::
                  T  ::::::
                  V  ::::a:
                  W  5:::::
                  Y  ::::::

         bits    6.7
                 6.0
                 5.3 **   *
                 4.7 ***  *
Relative         4.0 ******
Entropy          3.3 ******
(29.1 bits)      2.7 ******
                 2.0 ******
                 1.3 ******
                 0.7 ******
                 0.0 ------

Multilevel           MMHFVM
consensus            W  N
sequence


--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
	Motif 14 sites sorted by position p-value
--------------------------------------------------------------------------------
Sequence name            Start   P-value             Site
-------------            ----- ---------            ------
NIK_DROSOPHILA               2  2.50e-10          M WMHFVM
ERAERGRGMR
```

```
NIK_BRANCHIOSTOMA          1300  2.39e-09 LQPGLQSLPA MMHNVM
FTNTPNPPPT
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_DROSOPHILA                    2.5e-10  1_[14]_498
NIK_BRANCHIOSTOMA                 2.4e-09  1299_[14]_328
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 14 width=6 seqs=2
NIK_DROSOPHILA           (    2) WMHFVM  1
NIK_BRANCHIOSTOMA        ( 1300) MMHNVM  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 6 n= 3698 bayes= 10.8517 E= 9.1e-002
  -250   -281   -334   -373    -13   -356   -280    -91   -273   -
111    351   -259   -446   -287   -278   -331   -258   -169    579
-5
  -369   -363   -463   -501   -258   -476   -457   -143   -400   -
168    534   -399   -537   -457   -458   -443   -365   -245   -248
-212
  -245   -273   -172   -252   -100   -286    443   -252   -198   -
259   -183     -6   -356    -58   -121   -217   -205   -262   -133
78
  -161   -221    -72   -223    350   -221    -60    -86   -145   -
152   -126    332   -329   -191   -191   -154   -141   -143     11
140
   -73   -171   -304   -320   -141   -328   -303    146   -261   -
118    -95   -258   -370   -330   -272   -284   -123    357   -255
-195
  -369   -363   -463   -501   -258   -476   -457   -143   -400   -
168    534   -399   -537   -457   -458   -443   -365   -245   -248
-212
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 6 nsites= 2 E= 9.1e-002
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 14 regular expression
--------------------------------------------------------------------
[MW]MH[FN]VM
--------------------------------------------------------------------




Time 36.41 secs.

********************************************************************


********************************************************************
MOTIF 15 MEME    width =   6  sites =   2  llr = 35  E-value =
5.0e+002
********************************************************************
--------------------------------------------------------------------
      Motif 15 Description
--------------------------------------------------------------------
Simplified        A  :::5::
pos.-specific     C  5:a:::
probability       D  ::::::
matrix            E  ::::::
                  F  5:::::
                  G  ::::::
                  H  ::::::
                  I  ::::::
                  K  :::::a
                  L  ::::::
```

```
                  M  ::::::
                  N  ::::::
                  P  ::::::
                  Q  :a::::
                  R  :::5::
                  S  ::::::
                  T  ::::::
                  V  ::::a:
                  W  ::::::
                  Y  ::::::

         bits    6.7
                 6.0
                 5.3   *
                 4.7   *
Relative         4.0 *** **
Entropy          3.3 ******
(25.3 bits)      2.7 ******
                 2.0 ******
                 1.3 ******
                 0.7 ******
                 0.0 ------

Multilevel           CQCAVK
consensus            F  R
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 15 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value             Site
-------------             ----- ---------            ------
NIK_BRANCHIOSTOMA          1540  4.95e-09 VTFLNRGNTL CQCRVK
PAKTIGELCE
NIK_HOMO                    424  2.40e-08 VHRMEDKQTG FQCAVK
KVRLEVFRAE
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 15 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_BRANCHIOSTOMA                   5e-09  1539_[15]_88
NIK_HOMO                          2.4e-08  423_[15]_518
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 15 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 15 width=6 seqs=2
NIK_BRANCHIOSTOMA        ( 1540) CQCRVK  1
NIK_HOMO                 (  424) FQCAVK  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 15 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 6 n= 3698 bayes= 10.8517 E= 5.0e+002
  -186    419   -352   -393    372   -363   -272    -98   -323   -
151   -140   -276   -428   -367   -327   -288   -245   -148    -58
75
  -203   -312   -245   -113   -286   -345    -45   -246   -153   -
245   -128   -144   -349    380   -151   -262   -233   -281   -217
-223
  -346    529   -498   -514   -397   -517   -499   -336   -494   -
462   -366   -433   -597   -533   -467   -468   -371   -423   -476
-421
   161   -174   -150   -151   -179   -148   -140   -133     44   -
212   -143    -86   -247   -102    300   -119   -115   -107   -158
-105
   -73   -171   -304   -320   -141   -328   -303    146   -261   -
118    -95   -258   -370   -330   -272   -284   -123    357   -255
-195
  -299   -374   -368   -357   -409   -404   -341   -297    415   -
417   -324   -246   -467   -317    -23   -384   -316   -383   -323
-311
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 15 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 6 nsites= 2 E= 5.0e+002
 0.000000  0.500000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 15 regular expression
--------------------------------------------------------------------
[CF]QC[AR]VK
--------------------------------------------------------------------




Time 38.93 secs.

********************************************************************


********************************************************************
MOTIF 16 MEME    width =   6  sites =   2  llr = 34  E-value =
5.7e+002
********************************************************************
--------------------------------------------------------------------
      Motif 16 Description
--------------------------------------------------------------------
Simplified        A  ::::::
pos.-specific     C  ::::::
probability       D  ::::::
matrix            E  ::::::
                  F  ::::::
                  G  ::::::
                  H  5::::a
                  I  ::::::
                  K  :::a::
                  L  ::::5:
                  M  ::::::
                  N  ::::::
                  P  :5::5:
                  Q  5:::::
                  R  ::::::
                  S  ::::::
                  T  ::::::
                  V  :5::::
                  W  ::a:::
                  Y  ::::::

         bits    6.7   *
```

```
                 6.0   *
                 5.3   *
                 4.7   *  *
Relative         4.0   ** *
Entropy          3.3 * ** *
(24.8 bits)      2.7 ******
                 2.0 ******
                 1.3 ******
                 0.7 ******
                 0.0 ------

Multilevel           HPWKLH
consensus            QV  P
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value            Site
-------------             ----- ---------            ------
NIK_HOMO                    273  1.30e-08 LPHPFPFHPL QPWKPH
PLESFLGKLA
NIK_HOMO                    238  2.42e-08 KLISPLQCLN HVWKLH
HPQDGGPLPL
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_HOMO                          1.3e-08  237_[16]_29_[16]_669
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 16 width=6 seqs=2
NIK_HOMO                 (  273) QPWKPH  1
NIK_HOMO                 (  238) HVWKLH  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 6 n= 3698 bayes= 10.8517 E= 5.7e+002
```

```
  -189   -284   -173   -129   -180   -295    297   -228   -111   -
237   -132    -38   -329    309    -93   -210   -189   -248   -166
-21
   -50   -181   -198   -214   -105   -231   -218     72   -145   -
122    -92   -152    205   -196   -183   -169   -102    238   -174
-114
  -366   -350   -375   -429    -52   -400   -370   -307   -350   -
242   -253   -319   -503   -381   -335   -414   -368   -318    651
-42
  -299   -374   -368   -357   -409   -404   -341   -297    415   -
417   -324   -246   -467   -317    -23   -384   -316   -383   -323
-311
   -95   -213   -202   -215    -36   -249   -205      9   -134
159    -29   -152    223   -166   -163   -176   -136    -61   -107
-83
  -245   -273   -172   -252   -100   -286    443   -252   -198   -
259   -183     -6   -356    -58   -121   -217   -205   -262   -133
78
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 6 nsites= 2 E= 5.7e+002
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 16 regular expression
--------------------------------------------------------------------
[HQ][PV]WK[LP]H
--------------------------------------------------------------------
```

```
Time 41.42 secs.

********************************************************************


********************************************************************
MOTIF 17 MEME    width =   9  sites =   2  llr = 50  E-value =
3.5e+002
********************************************************************
--------------------------------------------------------------------
      Motif 17 Description
--------------------------------------------------------------------
Simplified        A  :::::::::
pos.-specific     C  :::::::::
probability       D  :::5:::::
matrix            E  :::::::a:
                  F  :a:::::::
                  G  ::::a:a::
                  H  :::::::::
                  I  :::::::::
                  K  ::5:::::5
                  L  :::::::::
                  M  5::::5::5
                  N  :::::::::
                  P  :::::::::
                  Q  ::5::::::
                  R  :::::::::
                  S  :::::::::
                  T  :::::::::
                  V  :::5:::::
                  W  :::::::::
                  Y  5::::5:::

         bits    6.7
                 6.0
                 5.3  *
                 4.7 **   *
Relative         4.0 **  *****
Entropy          3.3 *********
(36.3 bits)      2.7 *********
                 2.0 *********
                 1.3 *********
                 0.7 *********
                 0.0 ---------

Multilevel           MFKDGMGEK
consensus            Y QV Y  M
sequence


--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 17 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value              Site
-------------             ----- ---------            ---------
NIK_DROSOPHILA              444  6.34e-12 WAQFDSNFQI MFKVGMGEK
PQAPESLSQE
NIK_BRANCHIOSTOMA           491  6.90e-12 TQNNRAAVHA YFQDGYGEM
TFNDNELPCL
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 17 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_DROSOPHILA                    6.3e-12  443_[17]_53
NIK_BRANCHIOSTOMA                 6.9e-12  490_[17]_1134
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 17 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 17 width=9 seqs=2
NIK_DROSOPHILA           (  444) MFKVGMGEK  1
NIK_BRANCHIOSTOMA        (  491) YFQDGYGEM  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 17 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 9 n= 3686 bayes= 10.8471 E= 3.5e+002
  -150   -201   -248   -273    141   -292    -77      7   -184    -
52    422   -170   -360   -223   -213   -223   -168    -79     30
347
  -287   -251   -385   -428    495   -416   -332   -129   -370   -
130   -147   -329   -442   -430   -399   -327   -343   -207    -83
88
  -117   -283   -111    -65   -225   -218    -81   -172    281   -
219   -130    -41   -279    231     53   -152   -119   -192   -180
-115
   -99   -232    322    -68   -156   -221   -195     45   -141   -
188   -141    -28   -314   -188   -200   -201   -140    187   -186
-125
  -152   -326   -210   -322   -335    362   -324   -332   -252   -
434   -321   -148   -419   -357   -275   -234   -294   -330   -281
-263
  -150   -201   -248   -273    141   -292    -77      7   -184    -
52    422   -170   -360   -223   -213   -223   -168    -79     30
```

```
347
  -152   -326   -210   -322   -335    362   -324   -332   -252   -
434   -321   -148   -419   -357   -275   -234   -294   -330   -281
-263
  -420   -567   -167    361   -504   -481   -455   -434   -414   -
565   -485   -334   -620   -353   -477   -496   -463   -486   -490
-443
  -124   -243   -167   -151   -141   -237   -163    -52    306   -
128    329    -90   -303    -97      4   -179   -125   -121   -143
-88
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 17 position-specific probability matrix
---------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 9 nsites= 2 E= 3.5e+002
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 17 regular expression
---------------------------------------------------------------------
[MY]F[KQ][DV]G[MY]GE[KM]
---------------------------------------------------------------------
```

```
Time 43.94 secs.

********************************************************************


********************************************************************
MOTIF 18 MEME     width =   6  sites =   2  llr = 35  E-value =
6.6e+002
********************************************************************
--------------------------------------------------------------------
      Motif 18 Description
--------------------------------------------------------------------
Simplified        A  ::::::
pos.-specific     C  ::::::
probability       D  ::::::
matrix            E  ::::::
                  F  ::a:5:
                  G  ::::::
                  H  a::::5
                  I  ::::::
                  K  ::::::
                  L  ::::::
                  M  ::::::
                  N  ::::::
                  P  :a:a::
                  Q  ::::::
                  R  ::::::
                  S  :::::5
                  T  ::::::
                  V  ::::::
                  W  ::::::
                  Y  ::::5:

         bits    6.7
                 6.0
                 5.3   *
                 4.7 * * *
Relative         4.0 * * *
Entropy          3.3 ******
(25.1 bits)      2.7 ******
                 2.0 ******
                 1.3 ******
                 0.7 ******
                 0.0 ------

Multilevel           HPFPFH
consensus                YS
sequence


--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif 18 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name            Start   P-value             Site
-------------            ----- ---------            ------
NIK_HOMO                   265  5.53e-09 THPFPYSRLP HPFPFH
PLQPWKPHPL
NIK_HOMO                   256  3.27e-08 QDGGPLPLPT HPFPYS
RLPHPFPFHP
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 18 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME           POSITION P-VALUE  MOTIF DIAGRAM
-------------           ----------------  -------------
NIK_HOMO                         5.5e-09  255_[18]_3_[18]_677
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 18 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 18 width=6 seqs=2
NIK_HOMO                ( 265) HPFPFH  1
NIK_HOMO                ( 256) HPFPYS  1
//
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif 18 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 6 n= 3698 bayes= 10.8517 E= 6.6e+002
  -245   -273   -172   -252   -100   -286    443   -252   -198   -
259   -183     -6   -356    -58   -121   -217   -205   -262   -133
78
   -98   -288   -220   -247   -236   -256   -262   -215   -177   -
266   -237   -198    324   -229   -223   -182   -176   -222   -292
-229
  -287   -251   -385   -428    495   -416   -332   -129   -370   -
130   -147   -329   -442   -430   -399   -327   -343   -207    -83
88
   -98   -288   -220   -247   -236   -256   -262   -215   -177   -
266   -237   -198    324   -229   -223   -182   -176   -222   -292
-229
  -202   -217   -287   -321    419   -337    -66   -112   -254   -
138   -120   -208   -381   -298   -263   -247   -248   -171     60
402
   -71   -203    -57   -126    -85   -152    319   -149    -50   -
211   -130     84   -246    -30    -67    131    -12   -160   -126
66
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 18 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 6 nsites= 2 E= 6.6e+002
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 18 regular expression
--------------------------------------------------------------------
HPFP[FY][HS]
--------------------------------------------------------------------




Time 46.48 secs.

********************************************************************


********************************************************************
MOTIF 19 MEME    width =   6  sites =   2  llr = 34  E-value =
9.5e+002
********************************************************************
--------------------------------------------------------------------
      Motif 19 Description
--------------------------------------------------------------------
Simplified        A  ::5:::
pos.-specific     C  a:::::
probability       D  :555::
matrix            E  ::::::
                  F  ::::a:
                  G  ::::::
```

```
                  H  :5::::
                  I  ::::::
                  K  ::::::
                  L  ::::::
                  M  ::::::
                  N  ::::::
                  P  ::::::
                  Q  :::5::
                  R  :::::a
                  S  ::::::
                  T  ::::::
                  V  ::::::
                  W  ::::::
                  Y  ::::::

         bits    6.7
                 6.0
                 5.3 *   *
                 4.7 *   *
Relative         4.0 *   **
Entropy          3.3 ******
(24.9 bits)      2.7 ******
                 2.0 ******
                 1.3 ******
                 0.7 ******
                 0.0 ------

Multilevel           CDADFR
consensus             HDQ
sequence

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value             Site
-------------             ----- ---------            ------
NIK_BRANCHIOSTOMA           449  6.43e-09 HFNVGALEGF CHDDFR
LENPIGRRDV
NIK_BRANCHIOSTOMA           603  4.09e-08 LDLHAEKLPP CDAQFR
LDQHWWSIME
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_BRANCHIOSTOMA                 6.4e-09  448_[19]_148_[19]_1025
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif 19 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 19 width=6 seqs=2
NIK_BRANCHIOSTOMA        (  449) CHDDFR  1
NIK_BRANCHIOSTOMA        (  603) CDAQFR  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 6 n= 3698 bayes= 10.8517 E= 9.5e+002
  -346    529   -498   -514   -397   -517   -499   -336   -494   -
462   -366   -433   -597   -533   -467   -468   -371   -423   -476
-421
  -177   -301    338    -66   -184   -200    248   -237   -121   -
298   -217     60   -333   -108   -153   -172   -176   -247   -198
-32
   134   -225    334    -25   -206   -132   -174   -177   -100   -
269   -188      5   -269   -144   -171   -131   -140   -148   -217
-131
  -124   -308    306     33   -234   -192    -85   -207    -54   -
265   -175     21   -285    197   -121   -151   -140   -217   -211
-135
  -287   -251   -385   -428    495   -416   -332   -129   -370   -
130   -147   -329   -442   -430   -399   -327   -343   -207    -83
88
  -294   -296   -361   -389   -353   -364   -212   -298    -50   -
359   -312   -231   -401   -230    405   -343   -314   -388   -222
-265
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 19 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 6 nsites= 2 E= 9.5e+002
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 19 regular expression
---------------------------------------------------------------------
C[DH][AD][DQ]FR
---------------------------------------------------------------------




Time 48.91 secs.

*********************************************************************


*********************************************************************
MOTIF 20 MEME    width =   7  sites =   2  llr = 39  E-value =
1.5e+003
*********************************************************************
---------------------------------------------------------------------
      Motif 20 Description
---------------------------------------------------------------------
Simplified        A  :5:::::
pos.-specific     C  :::55::
probability       D  :5:::::
matrix            E  :::::::
                  F  :::::::
                  G  :::::::
                  H  ::::::5
                  I  ::::5::
                  K  ::::::5
                  L  :::::::
                  M  a::::::
                  N  :::::::
                  P  :::::::
                  Q  :::::::
                  R  ::a::::
                  S  :::::5:
                  T  :::::::
                  V  :::5:::
                  W  :::::5:
                  Y  :::::::

         bits    6.7
```

```
                 6.0
                 5.3 *
                 4.7 *
Relative         4.0 * ****
Entropy          3.3 *******
(28.4 bits)      2.7 *******
                 2.0 *******
                 1.3 *******
                 0.7 *******
                 0.0 -------

Multilevel           MARCCSH
consensus             D VIWK
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value             Site
-------------             ----- ---------            -------
NIK_HOMO                    129  3.36e-10 NNVAHATEGK MARVCWK
GKRRSKARKK
NIK_DROSOPHILA               52  1.52e-08 DDEFEALKQQ MDRCISH
VIGITSEPEK
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_HOMO                          3.4e-10  128_[20]_812
NIK_DROSOPHILA                    1.5e-08  51_[20]_447
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF 20 width=7 seqs=2
NIK_HOMO                 (  129) MARVCWK  1
NIK_DROSOPHILA           (   52) MDRCISH  1
//

--------------------------------------------------------------------
```

```
---------------------------------------------------------------------
      Motif 20 position-specific scoring matrix
---------------------------------------------------------------------
log-odds matrix: alength= 20 w= 7 n= 3694 bayes= 9.08278 E= 1.5e+003
  -369   -363   -463   -501   -258   -476   -457   -143   -400   -
168    534   -399   -537   -457   -458   -443   -365   -245   -248
-212
   134   -225    334    -25   -206   -132   -174   -177   -100   -
269   -188      5   -269   -144   -171   -131   -140   -148   -217
-131
  -294   -296   -361   -389   -353   -364   -212   -298    -50   -
359   -312   -231   -401   -230    405   -343   -314   -388   -222
-265
   -60    420   -323   -350   -121   -306   -310     81   -275   -
139   -102   -250   -388   -326   -284   -250   -142    229   -214
-157
  -157    459   -359   -387   -119   -361   -348    226   -297   -
116    -92   -268   -437   -354   -309   -296   -188     32   -234
-161
  -119   -236   -214   -273    -12   -227   -202   -160   -177   -
198   -158   -107   -348   -225   -190     67    -70   -187    590
27
  -126   -270   -106   -112   -162   -203    237   -169    307   -
227   -146     -2   -284    -31     62   -150   -121   -189   -159
-16
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif 20 position-specific probability matrix
---------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 7 nsites= 2 E= 1.5e+003
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.500000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif 20 regular expression
--------------------------------------------------------------------
M[AD]R[CV][CI][SW][HK]
--------------------------------------------------------------------




Time 51.29 secs.

********************************************************************


********************************************************************
SUMMARY OF MOTIFS
********************************************************************

--------------------------------------------------------------------
      Combined block diagrams: non-overlapping sites with p-value <
0.0001
--------------------------------------------------------------------
SEQUENCE NAME            COMBINED P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
NIK_HOMO                       3.61e-123  50_[5(1.62e-
07)]_71_[20(3.36e-10)]_\
    102_[16(2.42e-08)]_12_[18(3.27e-08)]_3_[18(5.53e-
09)]_2_[16(1.30e-08)]_7_\
    [11(4.19e-19)]_2_[11(2.58e-18)]_79_[6(1.77e-05)]_8_[15(2.40e-
08)]_21_\
    [3(1.56e-24)]_23_[1(8.27e-46)]_12_[4(1.31e-16)]_4_[2(3.37e-
35)]_294_\
    [3(7.38e-05)]_17_[5(5.56e-09)]_9
NIK_AIPTASIA                    1.11e-65  9_[8(2.07e-
09)]_102_[10(4.45e-09)]_\
    9_[8(5.31e-05)]_80_[3(1.15e-18)]_25_[1(2.66e-36)]_10_[4(3.68e-
14)]_61_\
    [7(4.28e-12)]_40_[7(1.08e-11)]_157_[5(1.19e-09)]_14
NIK_DROSOPHILA                 7.13e-101  1_[14(2.50e-
10)]_44_[20(1.52e-08)]_\
    168_[6(2.83e-24)]_42_[3(1.14e-15)]_23_[1(2.78e-39)]_10_[4(2.59e-
14)]_7_\
    [2(1.34e-23)]_5_[17(6.34e-12)]_11_[10(6.93e-09)]_36
NIK_BRANCHIOSTOMA              1.67e-174  46_[4(2.56e-
05)]_97_[9(1.61e-32)]_\
    15_[9(4.54e-37)]_54_[12(5.87e-11)]_17_[13(1.14e-
11)]_24_[13(3.26e-12)]_89_\
```

```
    [19(6.43e-09)]_36_[17(6.90e-12)]_64_[7(7.73e-10)]_30_[19(4.09e-
08)]_1_\
    [6(2.08e-22)]_29_[8(8.62e-09)]_2_[3(3.76e-21)]_13_[12(1.55e-
10)]_2_\
    [1(3.95e-47)]_12_[4(1.25e-13)]_4_[2(1.91e-34)]_484_[14(2.39e-
09)]_234_\
    [15(4.95e-09)]_61_[5(1.98e-09)]_20
--------------------------------------------------------------------

********************************************************************


********************************************************************
Stopped because requested number of motifs (20) found.
********************************************************************

CPU: meme-server

********************************************************************
```

A.14 SOD MEME Output

```
********************************************************************
MEME - Motif discovery tool
********************************************************************
************
MEME version 4.11.4 (Release date: Fri Apr 07 15:22:08 2017 -0700)

For further information on how to interpret these results or to get
a copy of the MEME software please access http://meme-suite.org .

This file may be used as input to the MAST algorithm for searching
sequence databases for matches to groups of motifs.  MAST is
available
for interactive use and downloading at http://meme-suite.org .
********************************************************************


********************************************************************
REFERENCE
********************************************************************
If you use this program in your research, please cite:

Timothy L. Bailey and Charles Elkan,
"Fitting a mixture model by expectation maximization to discover
motifs in biopolymers", Proceedings of the Second International
Conference on Intelligent Systems for Molecular Biology, pp. 28-36,
AAAI Press, Menlo Park, California, 1994.
********************************************************************


********************************************************************
TRAINING SET
********************************************************************
DATAFILE= sequences.fa
ALPHABET= ACDEFGHIKLMNPQRSTVWY
Sequence name            Weight Length  Sequence name  Weight Length
-------------            ------ ------  -------------  ------ ------
CCS_Homo                 1.0000    274  CuZnSOD1_Homo
1.0000    154
MnSOD_Homo               1.0000    222  CuZnSOD2_Homo
1.0000    240
CCS_Ciona                1.0000    263  CuZnSOD_Ciona
1.0000    154
MnSOD_Ciona              1.0000    217  CuZnSOD1_Biomphalaria
1.0000    128
CuZnSOD2_Biomphalaria    1.0000    155  CuZnSOD3_Biomphalaria
1.0000    192
MnSOD_Biomphalaria       1.0000    223  CCS_Crassostrea
1.0000    248
```

```
CuZnSOD_Crassostrea      1.0000    156  MnSOD_Crassostrea
1.0000    225
CCS_Drosophila           1.0000    263  CuZnSOD_Drosophila
1.0000    152
MnSOD_Drosophila         1.0000    129  CuZnSOD2_Drosophila
1.0000    145
CuZnSOD_Caenorhabditis   1.0000    180  MnSOD_Caenorhabditis
1.0000    221
CCS_Hydra                1.0000    243  CuZn_Hydra
1.0000    152
MnSOD_Hydra              1.0000    219  CCS_Acropora
1.0000    221
CuZnSOD_Acropora         1.0000    177  MnSOD_Acropora
1.0000    126
CCS_Amphimedon           1.0000    245  CuZnSOD_Amphimedon
1.0000    166
MnSOD_Amphimedon         1.0000    221  CCS_Trichoplax
1.0000    251
CuZnSOD_Trichoplax       1.0000    154  MnSOD_Trichoplax
1.0000    224
CCS_Capsaspora           1.0000    306  CuZnSOD_Capsaspora
1.0000    151
FeMnSOD_Capsaspora       1.0000    229  CCS_Nematostella
1.0000    265
CuZnSOD3_Nematostella    1.0000    133  CuZnSOD2_Nematostella
1.0000    156
CuZnSOD1_Nematostella    1.0000    154  MnSOD1_Nematostella
1.0000    221
MnSOD2_Nematostella      1.0000    255
********************************************************************

********************************************************************
COMMAND LINE SUMMARY
********************************************************************
This information can also be useful in the event you wish to report
a problem with the MEME software.

command: meme sequences.fa -protein -oc . -nostatus -time 18000 -
maxsize 60000 -mod anr -nmotifs 20 -minw 6 -maxw 50

model:  mod=           anr    nmotifs=        20    evt=
inf
object function=  E-value of product of p-values
width:  minw=            6    maxw=           50
width:  wg=             11    ws=              1    endgaps=
yes
nsites: minsites=        2    maxsites=       50    wnsites=
0.8
theta:  spmap=         pam    spfuzz=        120
global: substring=     yes    branching=      no    wbranch=
no
```

```
em:     prior=       megap    b=           41050    maxiter=
50
        distance=    1e-05
data:   n=            8210    N=              41    shuffle=
-1

sample: seed=            0    ctfrac=         -1    maxwords=
-1
Dirichlet mixture priors file: prior30.plib
Letter frequencies in dataset:
A 0.081 C 0.022 D 0.056 E 0.055 F 0.029 G 0.114 H 0.043 I 0.057 K
0.056
L 0.080 M 0.017 N 0.053 P 0.038 Q 0.035 R 0.037 S 0.067 T 0.052 V
0.077
W 0.012 Y 0.019
Background letter frequencies (from dataset with add-one prior
applied):
A 0.081 C 0.022 D 0.056 E 0.055 F 0.029 G 0.113 H 0.043 I 0.057 K
0.056
L 0.079 M 0.017 N 0.053 P 0.038 Q 0.035 R 0.037 S 0.067 T 0.052 V
0.077
W 0.012 Y 0.020
********************************************************************


********************************************************************
MOTIF LTPGKHGFHIHZFGDLTNGCTSAGPHFNP MEME-1    width =  29  sites =
27  llr = 1644  E-value = 3.4e-435
********************************************************************
--------------------------------------------------------------------
      Motif LTPGKHGFHIHZFGDLTNGCTSAGPHFNP MEME-1 Description
--------------------------------------------------------------------
Simplified        A  :21:::1:::::::::::::::5:1::::
pos.-specific     C  :::::::::::::::::::a::2::::::
probability       D  ::::::::::::::a::1::::::2::::
matrix            E  :11:1::::::6::::::::1::::::::
                  F  :::::::7::::6:::::::::::::6::
                  G  :::9::8::::::a::::a::::a1::::
                  H  :::::9::8:a::::::::::::::8:::
                  I  :::::::1:7::::::::::1::::1:::
                  K  ::1:3:::1::::::::::::::::::::
                  L  8:::3::2::::1::3:::::::::::::
                  M  ::::::::::::::::::::1::::::::
                  N  ::::1:::1::::::3:6::1:::1::a:
                  P  :16:::::::::::::::::::::4:::9
                  Q  :::::::::::3:::::2:::::::::::
                  R  :::::::::::::::::::::::::::::
                  S  :1:::::::::::::141:::91::::::
                  T  :3::::::::::::::5:::3:2::::::
                  V  :::::::::3:::::1::::1::::1:::
                  W  :::::::::::::::::::::::::::::
```

```
                  Y  ::::::::::::2::1::::::::::4::

         bits    6.4
                 5.7
                 5.1                    *
                 4.5      *    *   *    *        *
Relative         3.8      *  * *   *    *     ****
Entropy          3.2      * ******** * ** * * ****
(87.9 bits)      2.5 * ** * ******** **** *** ****
                 1.9 * ************* **** ********
                 1.3 *****************************
                 0.6 *****************************
                 0.0 -----------------------------

Multilevel           LTPGKHGFHIHEFGDLTNGCTSAGPHFNP
consensus             A  L  L V QY  NS     T   Y
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LTPGKHGFHIHZFGDLTNGCTSAGPHFNP MEME-1 sites sorted by
position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
CuZnSOD_Capsaspora           36  1.22e-34 ATKVEGTIEG
LAPGKHGFHIHEFGDNTNGCISAGPHFNP AGKTHGAPED
CuZnSOD_Acropora             62  2.31e-32 ECRIYGELTG
LTPGKHGFHVHQFGDGTNGCTSAGPHFNP EGKLHGGPVD
CuZnSOD1_Nematostella        39  2.74e-32 PCTLRGRITG
LTEGKHGFHIHEFGDNTNGCTSAGAHYNP HGKMHGAPED
CuZnSOD1_Biomphalaria         6  2.74e-32      GEISG
LSPGLHGFHIHQYGDSTNGCISAGPHFNP FGKVHGGPQE
CuZnSOD_Caenorhabditis       60  3.82e-32 QAVIEGEIKG
LTPGLHGFHVHQYGDSTNGCISAGPHFNP FGKTHGGPKS
CuZnSOD2_Biomphalaria        40  3.82e-32 CTVVSGKVSG
LAPGNHGFHIHQFGDYSNGCISAGAHFNP ANKNHGGPCD
CCS_Nematostella            124  4.50e-32 NCIIDGTIDG
LTPGNHGFHIHEFGDFSNGCTSTGAHFNP TNNQHGARED
CuZnSOD_Crassostrea          41  4.50e-32 PVTLSGEIKG
LTPGQHGFHVHQFGDNTNGCTSAGAHFNP FNKEHGAPED
CuZnSOD_Trichoplax           38  6.21e-32 PIRISGEVKG
LAPGKHGFHVHEFGDNTQGCTSAGGHYNP HKKVHGAPGD
CuZnSOD_Drosophila           36  4.55e-31 PVKVTGEVLG
LAKGLHGFHVHEFGDNTNGCMSSGPHFNP RNKEHGAPTD
CuZnSOD2_Drosophila          29  5.26e-31 PVKVTGEVTG
LSKGLHGFHVHEFGDNTNGCMSSGPHFNP YSKEHGAPGD
CuZnSOD1_Homo                39  1.89e-30 PVKVWGSIKG
LTEGLHGFHVHEFGDNTAGCTSAGPHFNP LSRKHGGPKD
```

```
CuZn_Hydra                   37  2.49e-30 THVSGKITGL
QPPGKHGFHIHQFGDYSGGCMSTGPHFNP FNKEHGGPED
CuZnSOD_Ciona                39  7.28e-30 PCKISGSLTG
LAAGKHGFHIHEFGDHTNGCTSTGGHFNP QKCDHGAPEA
CuZnSOD_Amphimedon           50  3.40e-29 ITKVTGKVTS
LAPGDHGFHIHQFGDYTSGCVSAGSHFNP AGKNHGGPKD
CuZnSOD2_Nematostella        39  1.66e-28 PCKITGTIEG
LKAGNHGFHIHVYGDNTNGCVSAGPHFNP FKKEHGGPSD
CCS_Homo                    122  3.80e-28 RCLIEGTIDG
LEPGLHGLHVHQYGDLTNNCNSCGNHFNP DGASHGGPQD
CCS_Acropora                119  1.20e-27 VCIIDGAVDG
LTPGLHGLNIHELGDLSQGCFSTGDHYNP GNSRHGAPED
CCS_Ciona                   114  1.68e-27 LCLIEGTVDG
LSPGKHGLNIHEFGDLSDGCSSCGEHYNP YNYKHGGKND
CCS_Drosophila              115  4.06e-27 GVVVDGVVDG
LEPGLHGFHIHESGDVSNGCASVGNHYNP RNSPHGSPNA
CCS_Capsaspora              123  1.35e-24 ECVIEGTLDG
LSKGEHGLHIHEYGDLSQGWKSAGGIYNP KQMPHGPPSK
CCS_Hydra                   116  8.30e-23 CIIDGSISKL
SPFCKHAVHIHELGDLSNGCESTGDVYNP MPSTNEKVVG
CCS_Trichoplax              116  9.89e-23 KCMIEGTVDN
LRPGNYDIKIHEYGDLSDGCNNCGDIFNP YEYPHGNNNT
CuZnSOD3_Biomphalaria        77  9.89e-23 GFKTYSPDTP
ETQLLHGFHIHEFGDVASGCLAAGGHYNP KNSNHGDITD
CuZnSOD2_Homo               106  3.93e-22 FFALEGFPTE
PNSSSRAIHVHQFGDLSQGCESTGPHYNP LAVPHPQHPG
CCS_Crassostrea             121  1.20e-19 KCIIDGTIDG
LPEGKHKLFIHELGDISQGCDSCGDILGR LSPQTEKPLG
CCS_Amphimedon              117  5.40e-19 CVIEGTIDGL
TPNKEHLLKIHDHGDLSNGCESCGDVYNV MMSKNGKSVS
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LTPGKHGFHIHZFGDLTNGCTSAGPHFNP MEME-1 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CuZnSOD_Capsaspora                1.2e-34  35_[1]_87
CuZnSOD_Acropora                  2.3e-32  61_[1]_87
CuZnSOD1_Nematostella             2.7e-32  38_[1]_87
CuZnSOD1_Biomphalaria             2.7e-32  5_[1]_94
CuZnSOD_Caenorhabditis            3.8e-32  59_[1]_92
CuZnSOD2_Biomphalaria             3.8e-32  39_[1]_87
CCS_Nematostella                  4.5e-32  123_[1]_113
CuZnSOD_Crassostrea               4.5e-32  40_[1]_87
CuZnSOD_Trichoplax                6.2e-32  37_[1]_88
CuZnSOD_Drosophila                4.5e-31  35_[1]_88
CuZnSOD2_Drosophila               5.3e-31  28_[1]_88
CuZnSOD1_Homo                     1.9e-30  38_[1]_87
CuZn_Hydra                        2.5e-30  36_[1]_87
CuZnSOD_Ciona                     7.3e-30  38_[1]_87
```

```
CuZnSOD_Amphimedon                3.4e-29  49_[1]_88
CuZnSOD2_Nematostella             1.7e-28  38_[1]_89
CCS_Homo                          3.8e-28  121_[1]_124
CCS_Acropora                      1.2e-27  118_[1]_74
CCS_Ciona                         1.7e-27  113_[1]_121
CCS_Drosophila                    4.1e-27  114_[1]_120
CCS_Capsaspora                    1.4e-24  122_[1]_155
CCS_Hydra                         8.3e-23  115_[1]_99
CCS_Trichoplax                    9.9e-23  115_[1]_107
CuZnSOD3_Biomphalaria             9.9e-23  76_[1]_87
CuZnSOD2_Homo                     3.9e-22  105_[1]_106
CCS_Crassostrea                   1.2e-19  120_[1]_99
CCS_Amphimedon                    5.4e-19  116_[1]_100
--------------------------------------------------------------------


--------------------------------------------------------------------
      Motif LTPGKHGFHIHZFGDLTNGCTSAGPHFNP MEME-1 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF LTPGKHGFHIHZFGDLTNGCTSAGPHFNP width=29 seqs=27
CuZnSOD_Capsaspora       (   36) LAPGKHGFHIHEFGDNTNGCISAGPHFNP  1
CuZnSOD_Acropora         (   62) LTPGKHGFHVHQFGDGTNGCTSAGPHFNP  1
CuZnSOD1_Nematostella    (   39) LTEGKHGFHIHEFGDNTNGCTSAGAHYNP  1
CuZnSOD1_Biomphalaria    (    6) LSPGLHGFHIHQYGDSTNGCISAGPHFNP  1
CuZnSOD_Caenorhabditis   (   60) LTPGLHGFHVHQYGDSTNGCISAGPHFNP  1
CuZnSOD2_Biomphalaria    (   40) LAPGNHGFHIHQFGDYSNGCISAGAHFNP  1
CCS_Nematostella         (  124) LTPGNHGFHIHEFGDFSNGCTSTGAHFNP  1
CuZnSOD_Crassostrea      (   41) LTPGQHGFHVHQFGDNTNGCTSAGAHFNP  1
CuZnSOD_Trichoplax       (   38) LAPGKHGFHVHEFGDNTQGCTSAGGHYNP  1
CuZnSOD_Drosophila       (   36) LAKGLHGFHVHEFGDNTNGCMSSGPHFNP  1
CuZnSOD2_Drosophila      (   29) LSKGLHGFHVHEFGDNTNGCMSSGPHFNP  1
CuZnSOD1_Homo            (   39) LTEGLHGFHVHEFGDNTAGCTSAGPHFNP  1
CuZn_Hydra               (   37) QPPGKHGFHIHQFGDYSGGCMSTGPHFNP  1
CuZnSOD_Ciona            (   39) LAAGKHGFHIHEFGDHTNGCTSTGGHFNP  1
CuZnSOD_Amphimedon       (   50) LAPGDHGFHIHQFGDYTSGCVSAGSHFNP  1
CuZnSOD2_Nematostella    (   39) LKAGNHGFHIHVYGDNTNGCVSAGPHFNP  1
CCS_Homo                 (  122) LEPGLHGLHVHQYGDLTNNCNSCGNHFNP  1
CCS_Acropora             (  119) LTPGLHGLNIHELGDLSQGCFSTGDHYNP  1
CCS_Ciona                (  114) LSPGKHGLNIHEFGDLSDGCSSCGEHYNP  1
CCS_Drosophila           (  115) LEPGLHGFHIHESGDVSNGCASVGNHYNP  1
CCS_Capsaspora           (  123) LSKGEHGLHIHEYGDLSQGWKSAGGIYNP  1
CCS_Hydra                (  116) SPFCKHAVHIHELGDLSNGCESTGDVYNP  1
CCS_Trichoplax           (  116) LRPGNYDIKIHEYGDLSDGCNNCGDIFNP  1
CuZnSOD3_Biomphalaria    (   77) ETQLLHGFHIHEFGDVASGCLAAGGHYNP  1
CuZnSOD2_Homo            (  106) PNSSSRAIHVHQFGDLSQGCESTGPHYNP  1
CCS_Crassostrea          (  121) LPEGKHKLFIHELGDISQGCDSCGDILGR  1
CCS_Amphimedon           (  117) TPNKEHLLKIHDHGDLSNGCESCGDVYNV  1
//

--------------------------------------------------------------------
```

```
----------------------------------------------------------------------
     Motif LTPGKHGFHIHZFGDLTNGCTSAGPHFNP MEME-1 position-specific
scoring matrix
----------------------------------------------------------------------
log-odds matrix: alength= 20 w= 29 n= 7062 bayes= 8.59627 E= 3.4e-
435
  -367   -348   -500   -139   -152   -572   -452   -140   -394
333     -4   -457    -91    -72   -314   -164   -117   -220   -322
-264
   124   -384   -204     57   -308   -373   -255   -342     -6   -
310   -197    -32    167   -101     25    100    226   -324   -349
-216
   -33   -407   -336     58    -12   -450   -389   -400     54   -
363   -303    -87    399    -20   -261    -90   -271   -382   -448
-353
  -265    -28   -320   -363   -442    292   -450   -492   -139   -
206   -372   -299   -403   -388   -310   -138   -386   -467   -399
-370
  -259   -439    -35     62   -369   -398   -298   -403    239
182   -259    134   -316     30   -163    -57   -230   -383   -406
-269
  -394   -344   -304   -326   -200   -487    426   -434   -393   -
332   -228   -149   -352    -67    -32   -278   -294   -411   -246
89
   -80   -410   -129   -362   -442    290   -450   -491   -139   -
206   -372   -298   -402   -388   -310   -290   -386   -467   -398
-370
  -539   -484   -768   -698    445   -796   -692     47   -700
152   -136   -720   -618   -574   -617   -646   -511    -87   -419
-325
  -388   -341   -293   -318    -27   -477    415   -432    -55   -
329   -225      3   -347    -62   -154   -271   -288   -408   -250
-11
  -464   -427   -720   -675   -415   -779   -820    350   -675   -
296   -279   -680   -655   -677   -674   -636   -425    211   -664
-512
  -835   -742   -765   -838   -706   -772    454   -916   -830   -
813   -817   -779   -691   -727   -711   -798   -788   -910   -689
-620
  -355   -781    -16    340   -651   -554   -499   -558   -299   -
528   -426   -409   -408    308   -388   -404   -399   -115   -678
-517
  -585   -497   -646   -620    433   -710    -24   -480   -596
39   -379   -543   -577   -504   -507    -95   -551   -519   -204
351
  -498   -602   -543   -591   -632    312   -652   -712   -586   -
704   -599   -532   -582   -601   -529   -518   -597   -688   -587
-568
  -604   -622    412   -368   -606   -661   -598   -674   -633   -
664   -597   -390   -613   -576   -576   -578   -609   -676   -598
-541
```

```
  -245   -255   -476   -380     44   -169    -36     -9   -362
177    -81    222   -369   -315   -309      6   -209     20   -279
232
   -78   -337   -548   -549   -492   -452   -587   -483   -516   -
533   -377   -417   -439   -449   -454    262    330   -423   -532
-492
  -110   -534     54   -300   -537   -147   -368   -649   -349   -
619   -545    339   -434    227   -384     20   -342   -634   -587
-397
  -280   -422   -332   -376   -455    301   -463   -506   -373   -
528   -387   -110   -415   -402   -324   -303   -399   -481   -412
-383
  -401    544   -545   -484   -434   -621   -559   -429   -541   -
469   -352   -523   -510   -493   -442   -467   -386   -501   -145
-464
   -78   -312    -57     93     28   -404   -297    121    -29    -
79    246     36   -300   -156   -174    -59    209     -3   -311
-200
   -86   -310   -431   -474   -441   -429   -517   -504   -441   -
499   -376    -63   -395   -419   -389    367    -83   -465   -488
-405
   256    299   -637   -606   -538   -427   -660   -572   -632   -
570   -454   -540   -455   -523   -534     24    205   -101   -584
-546
  -498   -602   -543   -591   -632    312   -652   -712   -586   -
704   -599   -532   -582   -601   -529   -518   -597   -688   -587
-568
    77   -521    167    -40   -514     30   -370   -603   -331   -
568   -491     64    320   -303   -360    -63   -332   -582   -569
-389
  -461   -432   -609   -599   -332   -701    415    105   -612   -
298   -273   -483   -588   -411   -479   -536   -425     18   -479
-279
  -657   -550   -696   -677    430   -747   -388   -526   -635   -
105   -418   -561   -625   -520   -530   -589   -588   -565   -209
424
  -452   -428   -301   -455   -411   -220   -269   -417   -391   -
482   -374    409   -426   -330   -379   -260   -325   -484   -398
-356
  -246   -412   -382   -336   -387   -470   -433   -414   -328   -
376   -333   -406    452   -295    -39   -276   -296   -140   -475
-397
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif LTPGKHGFHIHZFGDLTNGCTSAGPHFNP MEME-1 position-specific
probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 29 nsites= 27 E= 3.4e-435
 0.000000  0.000000  0.000000  0.037037  0.000000  0.000000
0.000000  0.000000  0.000000  0.814815  0.000000  0.000000  0.037037
```

```
0.037037  0.000000  0.037037  0.037037  0.000000  0.000000  0.000000
 0.222222  0.000000  0.000000  0.074074  0.000000  0.000000
0.000000  0.000000  0.037037  0.000000  0.000000  0.037037  0.148148
0.000000  0.037037  0.148148  0.296296  0.000000  0.000000  0.000000
 0.074074  0.000000  0.000000  0.111111  0.037037  0.000000
0.000000  0.000000  0.111111  0.000000  0.000000  0.037037  0.555556
0.037037  0.000000  0.037037  0.000000  0.000000  0.000000  0.000000
 0.000000  0.037037  0.000000  0.000000  0.000000  0.851852
0.000000  0.000000  0.037037  0.037037  0.000000  0.000000  0.000000
0.000000  0.000000  0.037037  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.037037  0.074074  0.000000  0.000000
0.000000  0.000000  0.333333  0.333333  0.000000  0.148148  0.000000
0.037037  0.000000  0.037037  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.925926  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.037037  0.000000  0.000000  0.000000  0.000000  0.037037
 0.074074  0.000000  0.037037  0.000000  0.000000  0.814815
0.000000  0.000000  0.037037  0.037037  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.666667  0.000000
0.000000  0.074074  0.000000  0.222222  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.037037  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.037037  0.000000
0.814815  0.000000  0.074074  0.000000  0.000000  0.074074  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.666667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.333333  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.037037  0.592593  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.333333  0.000000  0.000000  0.000000  0.037037  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.592593  0.000000
0.037037  0.000000  0.000000  0.111111  0.000000  0.000000  0.000000
0.000000  0.000000  0.037037  0.000000  0.000000  0.000000  0.222222
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.037037  0.037037
0.037037  0.037037  0.000000  0.296296  0.000000  0.296296  0.000000
0.000000  0.000000  0.074074  0.000000  0.074074  0.000000  0.111111
 0.037037  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.444444  0.518519  0.000000  0.000000  0.000000
 0.037037  0.000000  0.074074  0.000000  0.000000  0.037037
0.000000  0.000000  0.000000  0.000000  0.000000  0.592593  0.000000
```

```
0.185185  0.000000  0.074074  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.962963
0.000000  0.000000  0.000000  0.000000  0.000000  0.037037  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.962963  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.037037  0.000000
 0.037037  0.000000  0.037037  0.111111  0.037037  0.000000
0.000000  0.148148  0.037037  0.037037  0.111111  0.074074  0.000000
0.000000  0.000000  0.037037  0.259259  0.074074  0.000000  0.000000
 0.037037  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.037037  0.000000
0.000000  0.000000  0.925926  0.000000  0.000000  0.000000  0.000000
 0.481481  0.185185  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.074074  0.222222  0.037037  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.148148  0.000000  0.185185  0.037037  0.000000  0.148148
0.000000  0.000000  0.000000  0.000000  0.000000  0.074074  0.370370
0.000000  0.000000  0.037037  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.814815  0.111111  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.074074  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.592593  0.000000
0.000000  0.000000  0.000000  0.037037  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.370370
 0.000000  0.000000  0.000000  0.000000  0.000000  0.037037
0.000000  0.000000  0.000000  0.000000  0.000000  0.962963  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.925926
0.000000  0.037037  0.000000  0.000000  0.037037  0.000000  0.000000
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif LTPGKHGFHIHZFGDLTNGCTSAGPHFNP MEME-1 regular expression
--------------------------------------------------------------------------------
L[TA]PG[KL]HG[FL]H[IV]H[EQ][FY]GD[LN][TS]NGCTS[AT]GPH[FY]NP
--------------------------------------------------------------------------------




Time  8.80 secs.

********************************************************************************
```

```
********************************************************************
MOTIF CPNQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI MEME-2   width =  41
sites =  10  llr = 1142  E-value = 1.3e-294
********************************************************************
--------------------------------------------------------------------
      Motif CPNQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI MEME-2
Description
--------------------------------------------------------------------
Simplified        A  :4::::::8:::::::::::::::a:::::::1:1::::a:
pos.-specific     C  9::::::::::::::::::::::::::::::::::::::::
probability       D  ::::a::::::::::::::a:::::::::::::::9:::::
matrix            E  :::::::2::::::::::::::a::::::::::::::::::
                  F  :1::::::::::::::4::::::::::::::::::::::::
                  G  ::::::::1::a:::::a:::::::::::::::::::::::
                  H  :::::::1::::1::::::::::a:::::::::::::::::
                  I  :::::::::::::3::::a::::::::::::::::::1::a
                  K  ::::::::::::::::::::::::::::::9:::::::5::
                  L  1:::::a1:1::8::a6::::::::::a::::::1::2:::
                  M  :::::::::::::::::::::::::::::::::::::::::
                  N  ::a::::::::::::::::::::::::::::a:::1::5::
                  P  :4:::a::1:::::a:::::::::::::::::::8::::::
                  Q  :::a:::6::::::::::::::::::::a::::::::::::
                  R  ::::::::::::::::::::::::::::::1::a:::::::
                  S  :1:::::::::::::::::::::::::::::::::::::::
                  T  :::::::::9a::1:::::::::::::::::::::::::::
                  V  :::::::::::::5::::::a:::::::::::9::::7:::
                  W  :::::::::::::::::::::a:::::::::::::::::::
                  Y  ::::::::::::11:::::::::::aa::a::::::a::::

         bits    6.4                      *
                 5.7                      *   **  *      *
                 5.1 *  *                 *   ** **      *
                 4.5 * ****    *   *   ** *** ** ** * *  *   *
Relative         3.8 * *****  **   **  ************** ****  **
Entropy          3.2 * ****** **** *********************** ***
(164.7 bits)     2.5 *****************************************
                 1.9 *****************************************
                 1.3 *****************************************
                 0.6 *****************************************
                 0.0 -----------------------------------------

Multilevel           CANQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI
consensus             P     E     I  F                    LN
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif CPNQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI MEME-2 sites
sorted by position p-value
```

```
--------------------------------------------------------------------
Sequence name             Start   P-value                  Site
-------------             ----- ---------            ---------------
MnSOD_Amphimedon            167  2.39e-52 QVTGRLQIAT
CPNQDPLQATTGLVPLLGIDVWEHAYYLQYRNVRPDYVKAI WDVINWDDVS
MnSOD1_Nematostella         163  9.43e-52 KVNKRLAIAT
CFNQDPLQPTTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI YDVINWTNVA
MnSOD_Caenorhabditis        163  1.41e-51 PKGKILKVAT
CANQDPLEATTGLVPLFGIDVWEHAYYLQYKNVRPDYVNAI WKIANWKNVS
MnSOD_Ciona                 161  2.35e-51 KEKGQLQVVA
CPNQDPLHATTGLVPLFGIDVWEHAYYLQYKNVRPDYIKAI FNVVNWENVG
MnSOD_Homo                  164  4.00e-51 KERGHLQIAA
CPNQDPLQGTTGLIPLLGIDVWEHAYYLQYKNVRPDYLKAI WNVINWENVT
MnSOD_Trichoplax            166  1.03e-50 KESNSLKIAT
CANQDPLQATTGYVPLLGIDVWEHAYYLQYKNVRPNYVNAI FDVINWNDVA
MnSOD_Crassostrea           168  1.82e-50 KAAHSLRVVT
CANQDPLLATTGLYPLFGIDVWEHAYYLQYKNVRPDYVNAI WHIIDWKSVT
MnSOD_Biomphalaria          163  4.71e-49 PATGKVQVAT
CSNQDPLEATTGLIPLFGIDVWEHAYYLQYKNVRADYVNAI FNIANWQDVS
MnSOD_Hydra                 162  3.14e-48 SVTKRLAITA
LPNQDPLQATTGLIPLLGIDVWEHAYYLQYKNVRLDYVNAI FNIIDWKNVS
FeMnSOD_Capsaspora          170  2.35e-47 KTKGRVVITA
CANQDPLQALTGHTPLLGIDVWEHAYYLQYKNARPDYLKAI WKVVNWNNVN
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif CPNQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI MEME-2 block
diagrams
--------------------------------------------------------------------
------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
MnSOD_Amphimedon                  2.4e-52  166_[2]_14
MnSOD1_Nematostella               9.4e-52  162_[2]_18
MnSOD_Caenorhabditis              1.4e-51  162_[2]_18
MnSOD_Ciona                       2.3e-51  160_[2]_16
MnSOD_Homo                          4e-51  163_[2]_18
MnSOD_Trichoplax                    1e-50  165_[2]_18
MnSOD_Crassostrea                 1.8e-50  167_[2]_17
MnSOD_Biomphalaria                4.7e-49  162_[2]_20
MnSOD_Hydra                       3.1e-48  161_[2]_17
FeMnSOD_Capsaspora                2.3e-47  169_[2]_19
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif CPNQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI MEME-2 in
BLOCKS format
--------------------------------------------------------------------
BL   MOTIF CPNQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI width=41
seqs=10
```

```
MnSOD_Amphimedon         (  167)
CPNQDPLQATTGLVPLLGIDVWEHAYYLQYRNVRPDYVKAI  1
MnSOD1_Nematostella      (  163)
CFNQDPLQPTTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI  1
MnSOD_Caenorhabditis     (  163)
CANQDPLEATTGLVPLFGIDVWEHAYYLQYKNVRPDYVNAI  1
MnSOD_Ciona              (  161)
CPNQDPLHATTGLVPLFGIDVWEHAYYLQYKNVRPDYIKAI  1
MnSOD_Homo               (  164)
CPNQDPLQGTTGLIPLLGIDVWEHAYYLQYKNVRPDYLKAI  1
MnSOD_Trichoplax         (  166)
CANQDPLQATTGYVPLLGIDVWEHAYYLQYKNVRPNYVNAI  1
MnSOD_Crassostrea        (  168)
CANQDPLLATTGLYPLFGIDVWEHAYYLQYKNVRPDYVNAI  1
MnSOD_Biomphalaria       (  163)
CSNQDPLEATTGLIPLFGIDVWEHAYYLQYKNVRADYVNAI  1
MnSOD_Hydra              (  162)
LPNQDPLQATTGLIPLLGIDVWEHAYYLQYKNVRLDYVNAI  1
FeMnSOD_Capsaspora       (  170)
CANQDPLQALTGHTPLLGIDVWEHAYYLQYKNARPDYLKAI  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif CPNQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI MEME-2
position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 41 n= 6570 bayes= 10.302 E= 1.3e-294
  -387   543  -534  -473  -420  -609  -548  -411  -529  -
343  -336  -511  -499  -481  -430  -454  -373  -482  -523
-453
   184  -258  -354  -307   118  -338  -399  -349  -306  -
330  -260  -340   364  -263  -277    32  -204  -305  -402
-322
  -409  -376  -255  -411  -355  -447  -217  -363  -341  -
428  -321   408  -374  -280  -327  -212  -276  -431  -343
-301
  -347  -394  -425  -182  -415  -534  -180  -432  -335  -
331  -192  -334  -347   467  -231  -355  -351  -447  -347
-366
  -368  -417   400  -115  -391  -464  -369  -435  -403  -
444  -358  -139  -434  -345  -358  -342  -382  -439  -399
-320
  -314  -449  -434  -402  -433  -500  -482  -479  -395  -
436  -398  -461   465  -359  -365  -341  -359  -462  -486
-430
  -420  -390  -557  -479  -174  -593  -505  -170  -470
353   -45  -524  -429  -378  -382  -467  -379  -259  -349
-293
  -264  -323  -341     1  -350  -485   -29  -348  -248  -
```

```
157   -104   -250   -272    445   -147   -272   -267   -364   -274
-301
   320   -146   -403   -350   -304    -63   -448   -326   -370   -
320   -211   -361     63   -330   -313    -96   -187   -203   -355
-321
  -261   -268   -390   -395   -287   -474   -424   -232   -327    -
20   -162   -248   -359   -286   -288    -61    393   -240   -360
-307
  -365   -382   -487   -511   -442   -528   -527   -417   -455   -
485   -335   -375   -442   -411   -406   -195    419   -405   -465
-428
  -275   -407   -330   -374   -441    304   -454   -500   -371   -
514   -383   -311   -399   -395   -320   -299   -389   -475   -399
-372
  -358   -327   -491   -400    -48   -549     27   -136   -382
325     -4   -420   -371   -297   -300   -382   -310   -213   -184
176
  -184   -213   -420   -354   -178   -467   -399    219   -353   -
122    -70   -379   -338   -324   -295   -304     36    268   -307
150
  -314   -449   -434   -402   -433   -500   -482   -479   -395   -
436   -398   -461    465   -359   -365   -341   -359   -462   -486
-430
  -420   -390   -557   -479   -174   -593   -505   -170   -470
353    -45   -524   -429   -378   -382   -467   -379   -259   -349
-293
  -447   -399   -674   -593    356   -681   -495   -126   -577
286    -12   -592   -509   -433   -475   -556   -408   -242   -272
-145
  -275   -407   -330   -374   -441    304   -454   -500   -371   -
514   -383   -311   -399   -395   -320   -299   -389   -475   -399
-372
  -392   -378   -526   -509   -284   -588   -581    396   -486   -
150   -136   -504   -487   -473   -461   -459   -346    -58   -434
-328
  -368   -417    400   -115   -391   -464   -369   -435   -403   -
444   -358   -139   -434   -345   -358   -342   -382   -439   -399
-320
  -241   -289   -479   -437   -309   -536   -494    -73   -454   -
250   -213   -484   -402   -437   -382   -408   -258    354   -450
-381
  -426   -367   -429   -412    -97   -500   -445   -412   -405   -
254   -251   -418   -418   -350   -320   -415   -393   -395    623
-94
  -505   -578   -224    414   -549   -593   -535   -529   -544   -
595   -499   -443   -585   -348   -502   -529   -514   -575   -549
-502
  -535   -480   -458   -492   -363   -568    448   -592   -532   -
492   -411   -336   -465   -260   -338   -445   -457   -574   -397
-192
   351   -243   -486   -448   -390   -355   -525   -416   -464   -
```

```
411   -311   -452   -412   -419   -399   -196   -281   -304   -430
-397
  -587   -508   -596   -617   -125   -618   -397   -532   -588   -
458   -432   -541   -524   -503   -491   -546   -547   -560   -234
562
  -587   -508   -596   -617   -125   -618   -397   -532   -588   -
458   -432   -541   -524   -503   -491   -546   -547   -560   -234
562
  -420   -390   -557   -479   -174   -593   -505   -170   -470
353    -45   -524   -429   -378   -382   -467   -379   -259   -349
-293
  -347   -394   -425   -182   -415   -534   -180   -432   -335   -
331   -192   -334   -347    467   -231   -355   -351   -447   -347
-366
  -587   -508   -596   -617   -125   -618   -397   -532   -588   -
458   -432   -541   -524   -503   -491   -546   -547   -560   -234
562
  -363   -381   -473   -398   -473   -529   -435   -391    400   -
444   -327   -363   -400   -334     36   -414   -354   -475   -385
-381
  -409   -376   -255   -411   -355   -447   -217   -363   -341   -
428   -321    408   -374   -280   -327   -212   -276   -431   -343
-301
   -37   -193   -374   -321   -236   -444   -383     -4   -343   -
192   -142   -380   -298   -327   -266   -293   -149    333   -367
-322
  -383   -324   -461   -443   -427   -494   -301   -423   -145   -
400   -341   -363   -339   -232    462   -378   -375   -510   -299
-346
   -29   -332   -306   -259   -309   -391   -357   -335   -252    -
65   -254   -329    436   -218   -232   -198   -218   -317   -397
-320
  -332   -387    393    -77   -360   -433   -332   -399   -367   -
412   -322    -47   -409   -309   -325   -304   -346   -404   -371
-287
  -587   -508   -596   -617   -125   -618   -397   -532   -588   -
458   -432   -541   -524   -503   -491   -546   -547   -560   -234
562
  -241   -262   -497   -440   -233   -567   -509    106   -454
100   -122   -482   -416   -431   -393   -419   -239    310   -423
-341
  -328   -432   -189   -219   -429   -361   -280   -456    297   -
407   -320    300   -353   -150    -61   -230   -263   -446   -411
-286
   351   -243   -486   -448   -390   -355   -525   -416   -464   -
411   -311   -452   -412   -419   -399   -196   -281   -304   -430
-397
  -392   -378   -526   -509   -284   -588   -581    396   -486   -
150   -136   -504   -487   -473   -461   -459   -346    -58   -434
-328
---------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif CPNQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI MEME-2
position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 41 nsites= 10 E= 1.3e-294
 0.000000  0.900000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.400000  0.000000  0.000000  0.000000  0.100000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.400000
0.000000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
0.100000  0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
0.600000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.800000  0.000000  0.000000  0.000000  0.000000  0.100000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.100000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.900000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.100000  0.000000  0.000000  0.800000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.100000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.300000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.100000  0.500000  0.000000  0.100000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.400000  0.000000
0.000000  0.000000  0.000000  0.600000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.900000  0.000000  0.000000  0.000000  0.000000
0.000000  0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.900000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.100000  0.000000  0.000000  0.800000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.900000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.100000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.100000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.700000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif CPNQDPLQATTGLVPLLGIDVWEHAYYLQYKNVRPDYVKAI MEME-2 regular
expression
--------------------------------------------------------------------
C[AP]NQDPL[QE]ATTGL[VI]PL[LF]GIDVWEHAYYLQYKNVRPDY[VL][KN]AI
--------------------------------------------------------------------




Time 16.06 secs.

********************************************************************


********************************************************************
MOTIF RAKHTLPDLPYDYNALEPVISAEIMELHHSKHHATYVNNLNAAEEKLAEA MEME-3
      width =  50  sites =  13  llr = 1524  E-value = 1.6e-370
********************************************************************
--------------------------------------------------------------------
      Motif RAKHTLPDLPYDYNALEPVISAEIMELHHSKHHATYVNNLNAAEEKLAEA MEME-
3 Description
--------------------------------------------------------------------
```

```
Simplified        A
12:::::::::1:28:::1::51::::::1:::54::::::48::::418
pos.-specific     C
::::::::::::::::::::2:::::::::::::::::::::::::1::1
probability       D
::::1::5:::7:21:::::1:2:::::::::::::::::::::::::::
matrix            E
:11:1::3:::1::1:9::::25::5:::::::::::::::::981:19:
                  F
::::::::::::1:::::::::::::::::::::::::::::::::::::
                  G
:2:::::::1:1:1:::::::1::::::::1:::::::::::::1:::::
                  H
:1:9::::::::::::::2::1:::::a8::aa::::::::::::::2::
                  I
::::::::::::::::::1a:::9::2::::::::::::::21:::::::
                  K
1:9::::1:1:1:1::1::::::::2:::18::::::21:::::18:2::
                  L
:1:::a::9::::::a::::::::1:7::1:::::::::a:::1::51::
                  M
11::::::1:::::::::::::::9:::::::::::::::::::::1:::
                  N
:1:::::::::::4::::::2::::::::::::::::89:a:1:::::::
                  P
::::::a1:8:::::::a::::::::::::::::::::::::::::::::
                  Q
:1::::::::::::::::::::2::2:::2:::5:::::::1:::2:1::
                  R
81:::::::::::::::::::1:::2:::1:::::::::::::::::1::
                  S
:1::2::::::::2::::::61:::::::4:::::::::::::::::::1
                  T
::::6:::::::::::::2::1:1::1::1::::6:11:::11:::::::
                  V
::::1:::::::::::::2:::::::1:::1:::::9::::2::::::::
                  W
::::::::::::::::::::::::::::::::::::::::::::::1:::
                  Y
:::1::::::a:9:::::2:::::::::2::::::a::::::::::2:::

         bits    6.4
                 5.7           *                        *
                 5.1           * *           *          *
                 4.5    *  *   * *    * *    *  *   **  *    *
Relative         3.8 * ** **  ** *  *** *   **  **  **  *  ***  *
*
Entropy          3.2 * ** ** *** * **** *   **  ** ***********  ***
**
(169.2 bits)     2.5 * *********** **** ** ******* *********** *****
**
```

```
                 1.9 * ******************* *************************
**
                 1.3 *
************************************************
                 0.6
**************************************************
                 0.0 -----------------------------------------------
---

Multilevel
RAKHTLPDLPYDYNALEPHISAEIMELHHSKHHATYVNNLNAAEEKLAEA
consensus                   E          T   D  K   Q   QA      I    Y
sequence                               V                      V


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif RAKHTLPDLPYDYNALEPVISAEIMELHHSKHHATYVNNLNAAEEKLAEA MEME-
3 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                Site
-------------             ----- ---------            ---------------
MnSOD_Crassostrea            26  2.36e-61 SISALGAMGM
RMKHTLPDLPYDYNALEPYISADIMKLHHSKHHQTYVNNLNVAEEKLAEA MEKKDVNKII
FeMnSOD_Capsaspora           28  3.62e-57 TAAVAAAVPM
RAKHTLPDMPYDYSALEPVISAEIMKIHHSKHHQAYVNNLNIAEEKYAEA TAKNDLSAQI
MnSOD1_Nematostella          22  7.46e-56 RKAVLPVALV
RAKHTLPDLPYDYDALEPTINTEIMRLHHSKHHATYVNNLNIAEEKCLEA QAKGDVATAI
MnSOD_Ciona                  20  1.62e-55 TSKVVPVWAS
RGKHTLPDLPYDYSALEPHISAEIMETHYAKHHATYVNNLNIAEEKLHEA EAKNDISSII
MnSOD_Drosophila             10  3.93e-55  ISQTASLAV
RGKHTLPKLPYDYAALEPIICREIMELHHQKHHQTYVNNLNAAEEQLEEA KSKSDTTKLI
MnSOD_Trichoplax             25  2.25e-53 CHSALLITQA
RRKHDLPPLPYAYNALEPTISAEIMELHHSKHHQTYVTNLNAAEEKLAEA TSKNDISGVI
MnSOD_Homo                   23  3.54e-53 LAPALGYLGS
RQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNVNEEKYQEA LAKGDVTAQI
MnSOD_Caenorhabditis         23  1.35e-52 VQPITGVAAV
RSKHSLPDLPYDYADLEPVISHEIMQLHHQKHHATYVNNLNQIEEKLHEA VSKGNVKEAI
MnSOD_Biomphalaria           22  3.29e-51 LKRCFGVSLL
RLKHTLPDLKYDFNALEPYISADIMKLHYQKHHQAYVNNLNVAEEKLKAA VDKGDVNTII
MnSOD_Hydra                  21  4.80e-49 VFRKISRIAF
ANKHTLPELGYEYNALEPTISSQIMEIHHRKHHQAYVNNLNTAEEQLAEA QHKGDTSKII
MnSOD_Amphimedon             26  6.56e-47 SLSSLSSISR
RHKHVLPELPYGYKALEPVISGDIMELHHTKHHATYVNNLNATEGKMKEC LEAGDVSGAV
MnSOD_Acropora               26  7.81e-46 LTSVCAGVSS
KAKHELPELPYKYDALKPAICEEIMELHHKVHHATYVKNLNAAEEKYAEA QAEDNLGAMI
MnSOD2_Nematostella          34  7.23e-34 GNPYHEIVKY
MEEYTLPELPYDYNELEPHIDEATLRVHHLGHHAAYTKKLNAALKEWRES GKEKDLASKS
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif RAKHTLPDLPYDYNALEPVISAEIMELHHSKHHATYVNNLNAAEEKLAEA MEME-
3 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
MnSOD_Crassostrea                 2.4e-61  25_[3]_150
FeMnSOD_Capsaspora                3.6e-57  27_[3]_152
MnSOD1_Nematostella               7.5e-56  21_[3]_150
MnSOD_Ciona                       1.6e-55  19_[3]_148
MnSOD_Drosophila                  3.9e-55  9_[3]_70
MnSOD_Trichoplax                  2.3e-53  24_[3]_150
MnSOD_Homo                        3.5e-53  22_[3]_150
MnSOD_Caenorhabditis              1.3e-52  22_[3]_149
MnSOD_Biomphalaria                3.3e-51  21_[3]_152
MnSOD_Hydra                       4.8e-49  20_[3]_149
MnSOD_Amphimedon                  6.6e-47  25_[3]_146
MnSOD_Acropora                    7.8e-46  25_[3]_51
MnSOD2_Nematostella               7.2e-34  33_[3]_172
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif RAKHTLPDLPYDYNALEPVISAEIMELHHSKHHATYVNNLNAAEEKLAEA MEME-
3 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF RAKHTLPDLPYDYNALEPVISAEIMELHHSKHHATYVNNLNAAEEKLAEA
width=50 seqs=13
MnSOD_Crassostrea        (   26)
RMKHTLPDLPYDYNALEPYISADIMKLHHSKHHQTYVNNLNVAEEKLAEA  1
FeMnSOD_Capsaspora       (   28)
RAKHTLPDMPYDYSALEPVISAEIMKIHHSKHHQAYVNNLNIAEEKYAEA  1
MnSOD1_Nematostella      (   22)
RAKHTLPDLPYDYDALEPTINTEIMRLHHSKHHATYVNNLNIAEEKCLEA  1
MnSOD_Ciona              (   20)
RGKHTLPDLPYDYSALEPHISAEIMETHYAKHHATYVNNLNIAEEKLHEA  1
MnSOD_Drosophila         (   10)
RGKHTLPKLPYDYAALEPIICREIMELHHQKHHQTYVNNLNAAEEQLEEA  1
MnSOD_Trichoplax         (   25)
RRKHDLPPLPYAYNALEPTISAEIMELHHSKHHQTYVTNLNAAEEKLAEA  1
MnSOD_Homo               (   23)
RQKHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAYVNNLNVNEEKYQEA  1
MnSOD_Caenorhabditis     (   23)
RSKHSLPDLPYDYADLEPVISHEIMQLHHQKHHATYVNNLNQIEEKLHEA  1
MnSOD_Biomphalaria       (   22)
RLKHTLPDLKYDFNALEPYISADIMKLHYQKHHQAYVNNLNVAEEKLKAA  1
MnSOD_Hydra              (   21)
ANKHTLPELGYEYNALEPTISSQIMEIHHRKHHQAYVNNLNTAEEQLAEA  1
MnSOD_Amphimedon         (   26)
RHKHVLPELPYGYKALEPVISGDIMELHHTKHHATYVNNLNATEGKMKEC  1
MnSOD_Acropora           (   26)
KAKHELPELPYKYDALKPAICEEIMELHHKVHHATYVKNLNAAEEKYAEA  1
```

```
MnSOD2_Nematostella      (   34)
MEEYTLPELPYDYNELEPHIDEATLRVHHLGHHAAYTKKLNAALKEWRES  1
//

--------------------------------------------------------------

--------------------------------------------------------------
      Motif RAKHTLPDLPYDYNALEPVISAEIMELHHSKHHATYVNNLNAAEEKLAEA MEME-
3 position-specific scoring matrix
--------------------------------------------------------------
log-odds matrix: alength= 20 w= 50 n= 6201 bayes= 10.0609 E= 1.6e-
370
  -206   -306   -442   -404   -411   -478   -276   -399    -53   -
375    -24   -336   -321   -199    453   -352   -348   -482   -280
-325
   112   -307   -128     70   -228     -6     48   -263    -36    -
33    167     41   -189    113    100     27   -100   -245   -269
-136
  -367   -388   -461   -192   -478   -530   -434   -397    400   -
447   -332   -363   -404   -326      2   -414   -357   -479   -391
-384
  -378   -326   -291   -313   -137   -468    422   -409   -378   -
309   -211   -137   -336    -56   -148   -264   -280   -391   -200
156
  -258   -263    -34    -26   -321   -468   -387   -269   -281   -
355   -175   -208   -337   -241   -254     96    363    -59   -359
-315
  -477   -444   -605   -539   -227   -633   -558   -226   -529
357   -101   -579   -479   -436   -440   -525   -436   -317   -400
-347
  -387   -510   -499   -473   -496   -557   -545   -550   -465   -
504   -469   -528    468   -429   -432   -413   -430   -533   -536
-489
  -270   -618    303    258   -526   -447   -390   -465     32   -
436   -335   -269     71   -113   -290   -299   -303   -417   -554
-401
  -370   -343   -529   -424   -119   -586   -462   -113   -416
340    174   -479   -389   -320   -330   -420   -325   -205   -303
-252
  -187   -353   -321   -275   -329   -139   -373   -356    -31   -
318   -274   -342    440   -235   -247   -216   -237   -338   -416
-338
  -652   -562   -646   -678   -190   -661   -461   -598   -647   -
520   -498   -599   -569   -560   -546   -607   -605   -625   -293
564
  -177   -399    384    -11   -370   -243   -335   -407   -144   -
415   -324   -109   -399   -278   -317   -299   -338   -407   -382
-294
  -515   -436   -567   -541    175   -629   -277   -424   -511   -
353   -317   -453   -505   -413   -416   -464   -470   -456   -112
545
```

```
    73   -413    141   -163   -383    -59   -257   -456     43   -
422   -324    267   -305   -170   -213    110   -214   -438   -430
-262
   319   -165    -21     25   -299   -280   -392   -312   -278   -
303   -198   -281   -358   -223   -275   -110   -207   -197   -351
-301
  -477   -444   -605   -539   -227   -633   -558   -226   -529
357   -101   -579   -479   -436   -440   -525   -436   -317   -400
-347
  -464   -584   -205    412   -550   -578   -518   -523   -240   -
574   -476   -426   -537   -305   -457   -493   -481   -553   -551
-493
  -387   -510   -499   -473   -496   -557   -545   -550   -465   -
504   -469   -528    468   -429   -432   -413   -430   -533   -536
-489
    -3   -177   -386   -291    -93   -387    196     71   -274    -
86     -4   -298   -288   -229   -225   -212    182    143   -200
259
  -465   -441   -603   -597   -359   -642   -649    405   -578   -
242   -227   -591   -546   -558   -542   -545   -424   -148   -507
-408
  -266    232     42   -239   -393   -319   -305   -479   -268   -
463   -360    136   -326   -248   -280    307    -77   -477   -444
-295
   234   -223   -163    105   -237    -99     24   -266    -77   -
240   -130   -149   -225    -64     73     19     29   -212   -281
-166
   -17   -677    190    325   -554   -462   -406   -468   -210   -
438   -336   -313   -319    193   -297   -312   -308   -415   -582
-422
  -335   -335   -489   -460   -253   -564   -557    380   -435   -
105    -89   -456   -463   -430   -422   -399     -5     -1   -412
-295
  -461   -384   -537   -520   -332   -599   -550   -257   -486   -
148    574   -516   -470   -460   -485   -464   -415   -346   -306
-263
  -304   -462   -247    285   -449   -455   -293   -408    203   -
359   -262   -275   -351    197    206   -290   -271   -394   -397
-300
  -335   -312   -514   -413   -140   -562   -457     97   -405
314     -1   -459   -384   -322   -326   -394    -16    -16   -315
-251
  -622   -559   -548   -590   -457   -628    451   -685   -621   -
585   -517   -447   -533   -373   -440   -543   -552   -670   -482
-299
  -403   -347   -320   -341   -107   -492    416   -419   -400   -
322   -232   -167   -361    -87   -178   -291   -306   -408   -185
246
    -4   -312   -145    -55   -240   -308   -188   -270     71    -
33   -127   -127   -203    228    103    208     52   -254   -278
-148
```

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  -360   -383   -469   -393   -474   -309   -433   -394    398   -
444   -329   -362   -402   -326      2   -406   -353   -253   -390
-381
  -622   -559   -548   -590   -457   -628    451   -685   -621   -
585   -517   -447   -533   -373   -440   -543   -552   -670   -482
-299
  -622   -559   -548   -590   -457   -628    451   -685   -621   -
585   -517   -447   -533   -373   -440   -543   -552   -670   -482
-299
   267   -305   -464   -395   -473   -384   -539   -521   -413   -
507   -405   -428   -395    358   -376   -234   -288   -417   -509
-442
   218   -261   -522   -507   -453   -352   -559   -464   -516   -
487   -362   -420   -368   -422   -433   -179    346   -368   -495
-453
  -652   -562   -646   -678   -190   -661   -461   -598   -647   -
520   -498   -599   -569   -560   -546   -607   -605   -625   -293
564
  -153   -218   -402   -350   -256   -479   -412    -18   -371   -
206   -159   -408   -328   -356   -296   -329    -17    338   -393
-342
  -359   -359   -190   -312   -342   -387   -193   -348      6   -
404   -297    390   -343   -224   -237   -175    -61   -409   -332
-273
  -376   -346   -215   -369   -324   -416   -178   -326   -143   -
394   -283    401   -345   -239   -283   -172   -238   -396   -312
-269
  -477   -444   -605   -539   -227   -633   -558   -226   -529    
357   -101   -579   -479   -436   -440   -525   -436   -317   -400
-347
  -443   -410   -291   -447   -389   -479   -253   -399   -377   -
462   -357    411   -405   -316   -361   -248   -312   -467   -376
-335
   195   -193   -411   -319   -129   -398   -348    184   -304   -
112    -33   -328   -315     78   -255   -227     50    149   -236
-144
   319   -115   -364   -301   -251   -249   -407    -71   -315   -
259   -155    -82   -373   -297   -269    -74    -36   -148   -306
-271
  -496   -580   -220    413   -546   -591   -533   -525   -525   -
364   -490   -441   -576   -339   -494   -522   -507   -567   -549
-499
  -407   -587   -176    406   -546   -253   -483   -512   -139   -
539   -440   -381   -469   -248   -396   -431   -428   -519   -551
-471
  -335   -444   -318     35   -467   -474   -310   -412    365   -
376   -280   -289   -377    174      1   -320   -294   -417   -395
-316
  -319    129   -517   -423    -82   -534   -384   -127   -408    
279    194   -433   -392   -327   -332   -367   -279   -191    215
309
```

```
   179   -329   -157     65   -257   -320    139   -285    139    -
30   -139   -139   -215    113    112   -124   -125   -268   -288
-159
  -323   -577   -215    413   -549   -584   -528   -526   -505   -
586   -488   -435   -561   -327   -487   -507   -496   -563   -551
-499
   325     89   -389   -326   -275   -258   -430   -293   -342   -
287   -180   -361   -373   -318   -291      4   -189   -171   -328
-296
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif RAKHTLPDLPYDYNALEPVISAEIMELHHSKHHATYVNNLNAAEEKLAEA MEME-
3 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 50 nsites= 13 E= 1.6e-370
 0.076923  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.076923  0.000000  0.076923  0.000000  0.000000
0.000000  0.769231  0.000000  0.000000  0.000000  0.000000  0.000000
 0.230769  0.000000  0.000000  0.076923  0.000000  0.153846
0.076923  0.000000  0.000000  0.076923  0.076923  0.076923  0.000000
0.076923  0.076923  0.076923  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.076923  0.000000  0.000000
0.000000  0.000000  0.923077  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.923077  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.076923
 0.000000  0.000000  0.076923  0.076923  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.153846  0.615385  0.076923  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.538462  0.307692  0.000000  0.000000
0.000000  0.000000  0.076923  0.000000  0.000000  0.000000  0.076923
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.923077  0.076923  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.076923
0.000000  0.000000  0.076923  0.000000  0.000000  0.000000  0.846154
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.076923  0.000000  0.692308  0.076923  0.000000  0.076923
0.000000  0.000000  0.076923  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.076923  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.923077
 0.153846  0.000000  0.153846  0.000000  0.000000  0.076923
0.000000  0.000000  0.076923  0.000000  0.000000  0.384615  0.000000
0.000000  0.000000  0.153846  0.000000  0.000000  0.000000  0.000000
 0.846154  0.000000  0.076923  0.076923  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.923077  0.000000  0.000000
0.000000  0.000000  0.076923  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.076923  0.000000  0.000000  0.000000  0.000000  0.000000
0.230769  0.076923  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.230769  0.230769  0.000000  0.153846
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.153846  0.076923  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.153846  0.000000
0.000000  0.000000  0.615385  0.000000  0.000000  0.000000  0.000000
 0.461538  0.000000  0.000000  0.153846  0.000000  0.076923
0.076923  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.076923  0.076923  0.076923  0.000000  0.000000  0.000000
 0.076923  0.000000  0.230769  0.538462  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.153846  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.923077  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.076923  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.076923  0.923077  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.461538  0.000000  0.000000
0.000000  0.000000  0.230769  0.000000  0.000000  0.000000  0.000000
0.153846  0.153846  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.153846  0.000000  0.692308  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.076923  0.076923  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.846154  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.153846
 0.076923  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.076923  0.076923  0.000000  0.000000  0.000000
0.230769  0.076923  0.384615  0.076923  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.076923
0.000000  0.000000  0.846154  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.076923  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.538462  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.461538  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.384615  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.615385  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.076923  0.923077  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.153846  0.000000  0.000000  0.769231  0.000000
0.000000  0.000000  0.000000  0.076923  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.076923  0.000000  0.000000  0.923077  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.384615  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.230769  0.000000  0.000000  0.000000  0.000000  0.000000
0.076923  0.000000  0.000000  0.076923  0.230769  0.000000  0.000000
 0.769231  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.076923  0.000000  0.000000  0.000000  0.076923  0.000000
0.000000  0.000000  0.000000  0.076923  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.923077  0.000000  0.000000
0.000000  0.000000  0.000000  0.076923  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.846154  0.000000  0.076923
0.000000  0.000000  0.076923  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.076923  0.000000  0.000000
0.000000  0.000000  0.769231  0.000000  0.000000  0.000000  0.000000
```

```
0.153846  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.076923  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.538462  0.076923  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.076923  0.230769
 0.384615  0.000000  0.000000  0.076923  0.000000  0.000000
0.153846  0.000000  0.153846  0.076923  0.000000  0.000000  0.000000
0.076923  0.076923  0.000000  0.000000  0.000000  0.000000  0.000000
 0.076923  0.000000  0.000000  0.923077  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.846154  0.076923  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.076923  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif RAKHTLPDLPYDYNALEPVISAEIMELHHSKHHATYVNNLNAAEEKLAEA MEME-
3 regular expression
--------------------------------------------------------------------
RAKHTLP[DE]LPYDYNALEP[HTV]ISA[ED]IM[EK]LHH[SQ]KHH[AQ][TA]YVNNLN[AIV]
AEEK[LY]AEA
--------------------------------------------------------------------




Time 22.72 secs.

********************************************************************


********************************************************************
MOTIF DKLVSLVGVWSIIGRSVVVHADEDDLGKGGHELSKTTGNAG MEME-4   width =  41
sites =  26  llr = 1749  E-value = 3.7e-381
********************************************************************
--------------------------------------------------------------------
      Motif DKLVSLVGVWSIIGRSVVVHADEDDLGKGGHELSKTTGNAG MEME-4
Description
--------------------------------------------------------------------
Simplified        A  :::1::1:1::::::3::::5:2:::::::::11::::16:
pos.-specific     C  :1:::::::::::::::::::::::::::::::::::::::
probability       D  71:31:::22::::::::::13:9a::::::12::::::::
matrix            E  ::2:::::1:1:::::::::3:3::::::::51:12:::::
                  F  :1:::::::::::::::::::::::::::::::::::::::
                  G  :::::::7:::::a:::::::3::::9:871::::::8::a
                  H  :::::::::1:::::::::9::::::::::5:::::::1::
                  I  ::13::1:1::58:::212:::1::::::::::::2:::::
                  K  :21:1::2:::::::::::::2:::::4::::1:41::1::
                  L  :13::61:::::::::3:1::::::9:1::::3:2::1:::
                  M  :11:::::::::::::2::::::::::::::::::::::::
                  N  :::::::::3:::::::::::1::::::::3:::::2:7::
```

```
                  P  ::::1:::3:::::::::::::1::::::::2:::::::::
                  Q  ::1::1::::::::::::::::1:::::::::1::::::::
                  R  2:::::::::::::a::::::1:::::3:::::1:::::::
                  S  :1::3:1:::6::::5:::::::::::::2:::8:12::2:
                  T  ::::312::::::::2::::::::::::::::::146::1:
                  V  ::13::3:3::42:::497:::11:::::::::::::::::
                  W  :::::::::3:::::::::::::::::::::::::::::::
                  Y  ::::::1::1:::::::::::::::::::::::::::::::

         bits    6.4
                 5.7
                 5.1
                 4.5               *
Relative         3.8               *    *   **
Entropy          3.2             ***  * *   ***       *      *
(97.0 bits)      2.5 *      * ******* ****  **** * *  *  *** *
                 1.9 *  * * * ************* ********* * ******
                 1.3 * ***************************************
                 0.6 *****************************************
                 0.0 -----------------------------------------

Multilevel           DXLISLVGVWSIIGRSVVVHADEDDLGKGGHELSKTTGNAG
consensus            R  VT  KPNDV   AL   EG     R  NP
sequence                D                 K


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif DKLVSLVGVWSIIGRSVVVHADEDDLGKGGHELSKTTGNAG MEME-4 sites
sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                  Site
-------------             ----- ---------            ---------------
CuZnSOD_Crassostrea         104  1.68e-38 DDGVAKISIT
DKMIDLAGPQSIIGRTMVIHADVDDLGKGGHELSKTTGNAG GRLACGVIGI
CuZnSOD_Drosophila           99  5.33e-38 GDSPTAVSIT
DSKITLFGADSIIGRTVVVHADADDLGKGGHELSKTTGNAG ARIGCGVIGI
CuZnSOD_Trichoplax          101  1.39e-37 EQGVASINMT
DRMVTLTGPYSCIGRTIVVHEGVDDLGKGGHELSLTTGNAG ARVACGVIGI
CuZnSOD2_Drosophila          92  8.74e-37 GDGPTTVNIS
DCKITLVGADSIIGRRVVVHADADDLGKGGHELSKSTGNAG ARIGCGVIGI
CuZnSOD1_Nematostella       102  5.00e-36 ANGIADVSIT
DCLVSLTGQCSIIGRSLVVHEGMDDLGAGGHELSLTTGNAG GRVACGVIGI
CuZnSOD2_Biomphalaria       103  5.00e-36 DDGVADVSIK
DQQISLIGENSIIGRSLVVHDKEDDLGKGGNEESLKTGNAG PRLACGVIGI
CuZnSOD2_Nematostella       102  8.78e-36 DDGKACIDMT
DALVTLVGEHSVVGRSVVVHADEDDLGRGGHEDSKTTGHAG GRLACGVIGI
CCS_Nematostella            184  8.78e-36 IANQNGRATF
RFEDKTVKVWDIIGRAIVVHADEDDLGRGGHELSKSTGNSG ARVGCGIIAR
```

```
CuZnSOD_Amphimedon          112  2.31e-35 TGGDTEIELY
DDQIPLTGPNSIIGRSVVVHADPDDLGKDGHPDSLTTGHAG ARLACGVIGS
CuZnSOD_Capsaspora           99  1.14e-34 ADGIAKFTIT
DNLIQVSGVNSIVGRSVVIHADIDDLGKGGHELSKTTGNAG GRLACGVIGV
CuZnSOD_Acropora            125  1.14e-34 EQGVAKVDMT
DKLVSLVGKDSVVGRTIVVHEKADDLGKGGNEESTKTGNAG GRLACGVIGI
CuZn_Hydra                  100  1.69e-34 DYGNADVNIE
DSQIPLDGPNSIIGRALVVHQNEDDLGLGGHKDSKTTGNAG ARLSCGVIGL
CuZnSOD_Ciona               102  8.76e-34 SSGVAEVNIS
DKYVTLTGINSVIGRAVVVHADVDDLGLTSHPQSKTTGNAG GRLACGVIGI
CuZnSOD1_Homo               102  1.84e-33 KDGVADVSIE
DSVISLSGDHCIIGRTLVVHEKADDLGKGGNEESTKTGNAG SRLACGVIGI
CCS_Homo                    182  2.64e-31 RADADGRAIF
RMEDEQLKVWDVIGRSLIIDEGEDDLGRGGHPLSKITGNSG ERLACGIIAR
CuZnSOD3_Biomphalaria       140  9.65e-30 LDGTLEKVIE
DKIATLYGTYSVLSRAVVVHEKPDDLGRGGNPASLLNGNAG ARLACCSIVI
CCS_Ciona                   174  2.65e-29 EARSNGRATF
RFLDDKVKVWEIIGRSMVVHEGEDDEGKGGRETSKINGASG PGIACAIVAR
CCS_Acropora                179  3.96e-29 LADKNGRAHF
RMEDRNVKVWDVIGRSLVVHSREDDLGRGSNVLSQINGNSG PG
CuZnSOD2_Homo               162  1.42e-28 RDGSLWRYRA
GLAASLAGPHSIVGRAVVVHAGEDDLGRGGNQASVENGNAG RRLACCVVGV
CuZnSOD3_Nematostella        79  1.76e-25 YHGNVRTSFF
DHMVSLYGPDSVIGRSIVLHAERDDLGRGIGEYRTGSLATG NAGARLACCV
CCS_Drosophila              177  3.79e-25 RADETGRATF
RFVDPALDIWEIIGRAIVITANADDLGCGSNPQSRIDGNSG ERIACGIIAR
CuZnSOD_Caenorhabditis      123  1.45e-24 ADGVAKIKLT
DTLVTLYGPNTVVGRSMVVHAGQDDLGEGVGDKAEESKKTG NAGARAACGV
CuZnSOD1_Biomphalaria        69  1.86e-24 ENGVASFSMK
DDLVKIHGINSVIGRSMVVHAGIDDLGKGEGDKKEESLKTG NAGARVACGV
CCS_Capsaspora              186  2.19e-22 ASDAQGRATF
TLSASQLNVWDIIGHALVVHERPDDFGLGNAPRSSENGNVG AGVGAGIIAR
CCS_Hydra                   170  2.05e-18 SADLKGNSIF
KYIDHYIKVWDVIGRSVCLHEKDVDLKTSKHSDAGESIACG IIARSAGMLE
CCS_Trichoplax              176  5.14e-16 TANKNGRAMF
RIEDDTVKVWDVIGRSVIIHDKQVESSGKSLASRITCGIIA RSAGLFENSK
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif DKLVSLVGVWSIIGRSVVVHADEDDLGKGGHELSKTTGNAG MEME-4 block
diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------           -----------------  -------------
CuZnSOD_Crassostrea               1.7e-38  103_[4]_12
CuZnSOD_Drosophila                5.3e-38  98_[4]_13
CuZnSOD_Trichoplax                1.4e-37  100_[4]_13
CuZnSOD2_Drosophila               8.7e-37  91_[4]_13
CuZnSOD1_Nematostella               5e-36  101_[4]_12
CuZnSOD2_Biomphalaria               5e-36  102_[4]_12
CuZnSOD2_Nematostella             8.8e-36  101_[4]_14
```

```
CCS_Nematostella                 8.8e-36  183_[4]_41
CuZnSOD_Amphimedon               2.3e-35  111_[4]_14
CuZnSOD_Capsaspora               1.1e-34  98_[4]_12
CuZnSOD_Acropora                 1.1e-34  124_[4]_12
CuZn_Hydra                       1.7e-34  99_[4]_12
CuZnSOD_Ciona                    8.8e-34  101_[4]_12
CuZnSOD1_Homo                    1.8e-33  101_[4]_12
CCS_Homo                         2.6e-31  181_[4]_52
CuZnSOD3_Biomphalaria            9.6e-30  139_[4]_12
CCS_Ciona                        2.7e-29  173_[4]_49
CCS_Acropora                       4e-29  178_[4]_2
CuZnSOD2_Homo                    1.4e-28  161_[4]_38
CuZnSOD3_Nematostella            1.8e-25  78_[4]_14
CCS_Drosophila                   3.8e-25  176_[4]_46
CuZnSOD_Caenorhabditis           1.4e-24  122_[4]_17
CuZnSOD1_Biomphalaria            1.9e-24  68_[4]_19
CCS_Capsaspora                   2.2e-22  185_[4]_80
CCS_Hydra                        2.1e-18  169_[4]_33
CCS_Trichoplax                   5.1e-16  175_[4]_35
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif DKLVSLVGVWSIIGRSVVVHADEDDLGKGGHELSKTTGNAG MEME-4 in
BLOCKS format
--------------------------------------------------------------------
BL   MOTIF DKLVSLVGVWSIIGRSVVVHADEDDLGKGGHELSKTTGNAG width=41
seqs=26
CuZnSOD_Crassostrea      (  104)
DKMIDLAGPQSIIGRTMVIHADVDDLGKGGHELSKTTGNAG  1
CuZnSOD_Drosophila       (   99)
DSKITLFGADSIIGRTVVVHADADDLGKGGHELSKTTGNAG  1
CuZnSOD_Trichoplax       (  101)
DRMVTLTGPYSCIGRTIVVHEGVDDLGKGGHELSLTTGNAG  1
CuZnSOD2_Drosophila      (   92)
DCKITLVGADSIIGRRVVVHADADDLGKGGHELSKSTGNAG  1
CuZnSOD1_Nematostella    (  102)
DCLVSLTGQCSIIGRSLVVHEGMDDLGAGGHELSLTTGNAG  1
CuZnSOD2_Biomphalaria    (  103)
DQQISLIGENSIIGRSLVVHDKEDDLGKGGNEESLKTGNAG  1
CuZnSOD2_Nematostella    (  102)
DALVTLVGEHSVVGRSVVVHADEDDLGRGGHEDSKTTGHAG  1
CCS_Nematostella         (  184)
RFEDKTVKVWDIIGRAIVVHADEDDLGRGGHELSKSTGNSG  1
CuZnSOD_Amphimedon       (  112)
DDQIPLTGPNSIIGRSVVVHADPDDLGKDGHPDSLTTGHAG  1
CuZnSOD_Capsaspora       (   99)
DNLIQVSGVNSIVGRSVVIHADIDDLGKGGHELSKTTGNAG  1
CuZnSOD_Acropora         (  125)
DKLVSLVGKDSVVGRTIVVHEKADDLGKGGNEESTKTGNAG  1
CuZn_Hydra               (  100)
DSQIPLDGPNSIIGRALVVHQNEDDLGLGGHKDSKTTGNAG  1
```

```
CuZnSOD_Ciona            (  102)
DKYVTLTGINSVIGRAVVVHADVDDLGLTSHPQSKTTGNAG  1
CuZnSOD1_Homo            (  102)
DSVISLSGDHCIIGRTLVVHEKADDLGKGGNEESTKTGNAG  1
CCS_Homo                 (  182)
RMEDEQLKVWDVIGRSLIIDEGEDDLGRGGHPLSKITGNSG  1
CuZnSOD3_Biomphalaria    (  140)
DKIATLYGTYSVLSRAVVVHEKPDDLGRGGNPASLLNGNAG  1
CCS_Ciona                (  174)
RFLDDKVKVWEIIGRSMVVHEGEDDEGKGGRETSKINGASG  1
CCS_Acropora             (  179)
RMEDRNVKVWDVIGRSLVVHSREDDLGRGSNVLSQINGNSG  1
CuZnSOD2_Homo            (  162)
GLAASLAGPHSIVGRAVVVHAGEDDLGRGGNQASVENGNAG  1
CuZnSOD3_Nematostella    (   79)
DHMVSLYGPDSVIGRSIVLHAERDDLGRGIGEYRTGSLATG  1
CCS_Drosophila           (  177)
RFVDPALDIWEIIGRAIVITANADDLGCGSNPQSRIDGNSG  1
CuZnSOD_Caenorhabditis   (  123)
DTLVTLYGPNTVVGRSMVVHAGQDDLGEGVGDKAEESKKTG  1
CuZnSOD1_Biomphalaria    (   69)
DDLVKIHGINSVIGRSMVVHAGIDDLGKGEGDKKEESLKTG  1
CCS_Capsaspora           (  186)
TLSASQLNVWDIIGHALVVHERPDDFGLGNAPRSSENGNVG  1
CCS_Hydra                (  170)
KYIDHYIKVWDVIGRSVCLHEKDVDLKTSKHSDAGESIACG  1
CCS_Trichoplax           (  176)
RIEDDTVKVWDVIGRSVIIHDKQVESSGKSLASRITCGIIA  1
//

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--------------------------------------------------------------------
      Motif DKLVSLVGVWSIIGRSVVVHADEDDLGKGGHELSKTTGNAG MEME-4
position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 41 n= 6570 bayes= 7.73004 E= 3.7e-
381
  -415   -530    342   -279   -533   -149   -368   -578    -25   -
534   -447   -188   -437   -264    253   -293    -40   -565   -537
-388
   -69    144     37   -111    166   -366    -21    -68    135    -
21    188    -28   -259     43     30     69    -19   -308   -335
82
   -76   -275   -336    129   -196   -429   -335     51     37
159    256   -295   -327    151   -223    -64   -194     14   -290
89
    45   -409    214   -638   -403   -722   -757    244   -656   -
309   -281   -654   -623   -636   -636   -574   -406    202   -624
-488
```

```
  -199   -380     86      1   -301   -366    -21   -337     60   -
303   -190   -184    132     43     31    175    210   -318   -342
-208
  -136   -308   -478   -378   -156   -522   -422    -35   -109
303    -22   -109   -370     46   -302   -348      2    -85   -304
41
    -4   -249    -74   -379     48   -463    -31     62   -361
61    -76   -381   -365   -313   -306     10    143    170   -274
236
  -321   -456    -64   -326   -481    266   -404   -548    151   -
555   -431    -48   -416   -348   -329   -278   -362   -525   -460
-381
    -5   -365    -40     63   -286   -385   -271     77    -11   -
283   -179   -211    256     36   -141   -189    -23    169   -342
-216
  -413     68    143   -300   -294   -416    134   -561   -329   -
519   -444    228   -431     14   -349   -284   -342   -556    452
194
  -346     64    192     46   -500   -399   -388   -584   -348   -
562   -464   -177   -414   -318   -369    310    -22   -556   -550
-391
  -461     72   -738   -688   -420   -786   -842    321   -694   -
309   -290   -695   -662   -697   -694   -648   -425    244   -686
-526
  -371   -370   -486   -458   -268   -592   -562    366   -432    -
43    -89   -456   -477   -431   -422   -416   -310    119   -416
-300
  -274   -415   -334   -377   -454    301   -464   -505   -374   -
526   -385   -313   -413   -401   -325   -126   -392   -477   -412
-383
  -386   -326   -468   -449   -433   -503   -145   -425   -146   -
402   -343   -365   -344   -234    461   -381   -379   -514   -301
-351
   163   -321   -536   -540   -488   -427   -585   -542   -508   -
537   -414   -417   -420   -464     -9    290    183   -460   -532
-468
  -492   -454   -770   -696   -289   -787   -735    179   -694
176    309   -707   -640   -605   -637   -650   -455    228   -506
-443
  -247     37   -496   -443   -329   -585   -511     60   -463   -
264   -225   -501   -423   -452   -392   -437   -262    342   -487
-424
  -419   -406   -689   -636   -391   -751   -742    180   -649
0   -270   -663   -609   -638   -613   -611   -399    320   -628   -
508
  -400   -362    -99   -330   -238   -478    427   -457   -397   -
355   -251   -157   -365    -87   -181   -284    -92   -432   -278
-40
   245   -731     60    272   -629   -536   -483   -551   -293   -
521   -419   -380   -402     28   -378    -82   -387   -499   -659
-498
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  -394   -523    236    -31   -508    113   -358   -581    194   -
542   -452     69   -414   -271    100   -267   -325   -563   -544
-374
   106   -379    -36    229   -299   -379   -263     22   -122   -
297    100   -201    134    111     26   -183   -182     36   -347
-217
  -396   -448    397   -146   -422   -498   -402   -452   -437   -
472   -386   -170   -471   -378   -392   -373   -412   -102   -434
-352
  -357   -411    397    -57   -383   -462   -359   -422   -394   -
435   -345   -125   -435   -335   -350   -333   -373   -427   -394
-311
  -369   -347   -513   -138     -5   -576   -454   -137   -400
339     -1   -464   -380   -312   -316   -163   -322   -218   -320
-260
  -263   -407   -317   -360   -440    298   -448   -490   -136   -
513   -371   -297   -401   -386   -309   -135   -383   -465   -397
-368
   -88     58   -291    -23   -375   -160   -300   -386    276
37   -247   -256   -336   -138    271   -248    -31   -374   -391
-272
  -264   -408   -126   -359   -440    292   -447   -490   -136   -
513   -371   -294   -400   -385   -308   -135   -131   -466   -397
-367
  -263   -407   -311   -128   -436    276   -440   -153   -131   -
503   -364   -111   -397   -371   -302     24   -375   -189   -396
-363
  -126   -410   -241   -293   -315    -35    360   -482   -282   -
129   -307    199   -381   -148     -2   -267   -304   -462   -354
-128
   -95   -620     57    315   -524   -507   -426   -497    -40   -
466   -359   -348    241     30   -305    -77   -336   -109   -559
-414
    -3   -378    122    106   -298   -365   -246   -333     60
178   -187   -184   -258    112     31    -42    -19   -315   -339
80
   -31   -303   -404   -389   -397   -445   -429   -446    -60   -
433   -315   -278   -368   -295     69    347    -27   -451   -428
-341
  -200   -374   -204     61   -295   -157   -250    -67    251
99   -184   -189   -263     43     31    -43    101    -99   -338
-207
  -221   -351   -236    161   -289   -163   -284    115     95    -
98   -179   -216   -291   -131   -148     24    271   -285   -344
-225
  -329     37    -87   -411   -393   -512   -449   -341   -363   -
433   -248    140   -407   -322   -333    105    355   -332   -431
-386
  -264   -407   -318   -361   -437    292   -448   -155   -135   -
110   -366   -298   -401   -386   -307   -289   -383   -460   -396
-367
```

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   -75   -377   -235   -360   -356   -433    -16   -158    -61   -
416   -308    386   -369   -249   -263   -201   -263   -420   -345
-294
   303     20   -402   -337   -284   -280   -443   -121   -352   -
293   -188   -382   -413   -334   -304     82     30    -97   -338
-306
  -135   -410   -332   -374   -451    301   -461   -501   -371   -
523   -382   -311   -410   -399   -322   -295   -388   -473   -409
-381
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif DKLVSLVGVWSIIGRSVVVHADEDDLGKGGHELSKTTGNAG MEME-4
position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 41 nsites= 26 E= 3.7e-381
 0.000000  0.000000  0.653846  0.000000  0.000000  0.038462
0.000000  0.000000  0.038462  0.000000  0.000000  0.000000  0.000000
0.000000  0.230769  0.000000  0.038462  0.000000  0.000000  0.000000
 0.038462  0.076923  0.076923  0.000000  0.115385  0.000000
0.038462  0.038462  0.153846  0.076923  0.076923  0.038462  0.000000
0.038462  0.038462  0.115385  0.038462  0.000000  0.000000  0.038462
 0.038462  0.000000  0.000000  0.153846  0.000000  0.000000
0.000000  0.076923  0.076923  0.269231  0.115385  0.000000  0.000000
0.115385  0.000000  0.038462  0.000000  0.076923  0.000000  0.038462
 0.115385  0.000000  0.269231  0.000000  0.000000  0.000000
0.000000  0.307692  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.307692  0.000000  0.000000
 0.000000  0.000000  0.115385  0.038462  0.000000  0.000000
0.038462  0.000000  0.076923  0.000000  0.000000  0.000000  0.115385
0.038462  0.038462  0.269231  0.269231  0.000000  0.000000  0.000000
 0.038462  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.038462  0.038462  0.615385  0.000000  0.038462  0.000000
0.076923  0.000000  0.000000  0.076923  0.038462  0.000000  0.038462
 0.076923  0.000000  0.038462  0.000000  0.038462  0.000000
0.038462  0.076923  0.000000  0.115385  0.000000  0.000000  0.000000
0.000000  0.000000  0.076923  0.153846  0.269231  0.000000  0.115385
 0.000000  0.000000  0.038462  0.000000  0.000000  0.692308
0.000000  0.000000  0.230769  0.000000  0.000000  0.038462  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.076923  0.000000  0.038462  0.076923  0.000000  0.000000
0.000000  0.115385  0.038462  0.000000  0.000000  0.000000  0.269231
0.038462  0.000000  0.000000  0.038462  0.307692  0.000000  0.000000
 0.000000  0.038462  0.153846  0.000000  0.000000  0.000000
0.115385  0.000000  0.000000  0.000000  0.000000  0.269231  0.000000
0.038462  0.000000  0.000000  0.000000  0.000000  0.307692  0.076923
 0.000000  0.038462  0.230769  0.076923  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.615385  0.038462  0.000000  0.000000  0.000000
```

```
 0.000000  0.038462  0.000000  0.000000  0.000000  0.000000
0.000000  0.538462  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.423077  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.769231  0.000000  0.038462  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.192308  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.961538
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.038462  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.038462  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.961538  0.000000  0.000000  0.000000  0.000000  0.000000
 0.269231  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.038462  0.500000  0.192308  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.192308  0.000000  0.269231  0.153846  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.384615  0.000000  0.000000
 0.000000  0.038462  0.000000  0.000000  0.000000  0.000000
0.000000  0.076923  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.884615  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.192308  0.000000  0.076923  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.730769  0.000000  0.000000
 0.000000  0.000000  0.038462  0.000000  0.000000  0.000000
0.923077  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.038462  0.000000  0.000000  0.000000
 0.500000  0.000000  0.076923  0.346154  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.038462  0.000000  0.038462  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.307692  0.038462  0.000000  0.269231
0.000000  0.000000  0.230769  0.000000  0.000000  0.076923  0.000000
0.000000  0.076923  0.000000  0.000000  0.000000  0.000000  0.000000
 0.192308  0.000000  0.038462  0.307692  0.000000  0.000000
0.000000  0.076923  0.000000  0.000000  0.038462  0.000000  0.115385
0.076923  0.038462  0.000000  0.000000  0.115385  0.000000  0.000000
 0.000000  0.000000  0.923077  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.076923  0.000000  0.000000
 0.000000  0.000000  0.961538  0.038462  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.038462  0.038462  0.000000
0.000000  0.000000  0.000000  0.884615  0.000000  0.000000  0.000000
0.000000  0.000000  0.038462  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.923077
0.000000  0.000000  0.038462  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.038462  0.000000  0.000000  0.000000  0.000000
 0.038462  0.038462  0.000000  0.038462  0.000000  0.038462
0.000000  0.000000  0.423077  0.115385  0.000000  0.000000  0.000000
0.000000  0.269231  0.000000  0.038462  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.038462  0.000000  0.000000  0.846154
0.000000  0.000000  0.038462  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.038462  0.038462  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.038462  0.000000  0.653846
0.000000  0.038462  0.038462  0.000000  0.000000  0.038462  0.000000
0.000000  0.000000  0.153846  0.000000  0.038462  0.000000  0.000000
 0.038462  0.000000  0.000000  0.000000  0.000000  0.115385
0.500000  0.000000  0.000000  0.038462  0.000000  0.269231  0.000000
0.000000  0.038462  0.000000  0.000000  0.000000  0.000000  0.000000
 0.038462  0.000000  0.076923  0.500000  0.000000  0.000000
0.000000  0.000000  0.038462  0.000000  0.000000  0.000000  0.230769
0.038462  0.000000  0.038462  0.000000  0.038462  0.000000  0.000000
 0.076923  0.000000  0.153846  0.115385  0.000000  0.000000
0.000000  0.000000  0.076923  0.346154  0.000000  0.000000  0.000000
0.076923  0.038462  0.038462  0.038462  0.000000  0.000000  0.038462
 0.076923  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.038462  0.000000  0.000000  0.000000  0.000000
0.000000  0.076923  0.807692  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.076923  0.000000  0.038462
0.000000  0.038462  0.384615  0.192308  0.000000  0.000000  0.000000
0.038462  0.038462  0.038462  0.115385  0.038462  0.000000  0.000000
 0.000000  0.000000  0.000000  0.192308  0.000000  0.038462
0.000000  0.153846  0.115385  0.038462  0.000000  0.000000  0.000000
0.000000  0.000000  0.076923  0.384615  0.000000  0.000000  0.000000
 0.000000  0.038462  0.038462  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.192308  0.000000
0.000000  0.000000  0.153846  0.576923  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.846154
0.000000  0.038462  0.038462  0.076923  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.115385  0.000000  0.000000  0.000000  0.000000  0.000000
0.076923  0.038462  0.076923  0.000000  0.000000  0.692308  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.576923  0.038462  0.000000  0.000000  0.000000  0.000000
0.000000  0.038462  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.192308  0.115385  0.038462  0.000000  0.000000
 0.038462  0.000000  0.000000  0.000000  0.000000  0.961538
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif DKLVSLVGVWSIIGRSVVVHADEDDLGKGGHELSKTTGNAG MEME-4 regular
expression
--------------------------------------------------------------------
[DR]XL[IVD][ST]LV[GK][VP][WN][SD][IV]IGR[SA][VL]VVH[AE][DGK]EDDLG[KR
]GG[HN][EP]LSKTTGNAG
--------------------------------------------------------------------
```

```
Time 28.67 secs.

******************************************************************


******************************************************************
MOTIF KEHGGPEDEERHVGDLGNIEADEBGVAKV MEME-5    width =  29  sites =
23  llr = 1167  E-value = 1.6e-240
******************************************************************
------------------------------------------------------------------
      Motif KEHGGPEDEERHVGDLGNIEADEBGVAKV MEME-5 Description
------------------------------------------------------------------
Simplified        A  ::::4::11:::1:::::::812:::8::
pos.-specific     C  :::::::::::::::::::::::::::::
probability       D  :::::::7:1::::a::::::324:::2:
matrix            E  :2::::3:54:::::::::3::2::::1:
                  F  ::::::::::::::::::::::::::::3
                  G  :::95:1::::::a::a::::21:9::::
                  H  ::a::::::::a:::::::::::::::::
                  I  :::::::::1::::::::61:::::1:12
                  K  61::::1:::::::::::::::1::::2:
                  L  ::::::::::::2::9:::::::::::::
                  M  :::::::::::::::::::::::::::::
                  N  :1::1:1::2:::::::a:::2:3:1:::
                  P  :::::8:::::::::::::::::::1:::
                  Q  ::::::1::::::::::::::::1:::::
                  R  ::::::::1:a::::::::1:::::3:::
                  S  1:::::::1:::::::::::1:1::::1:
                  T  :1::::1:1::::::::::3:::::112:
                  V  :1:::::::1::6:::::41:::::3::3
                  W  :::::::::::::::::::::::::::::
                  Y  1::::::::::::::::::::::::::::

         bits    6.4
                 5.7
                 5.1
                 4.5   *       **  *
Relative         3.8   *       **  *  *
Entropy          3.2   *  *    ** *****  *
(73.2 bits)      2.5 * ** * *  ** ****** *   * * *
                 1.9 * **** ************ *  **** *
                 1.3 * ***************************
                 0.6 *****************************
                 0.0 -----------------------------

Multilevel           KEHGGPEDEERHVGDLGNIEADXDGVAXF
consensus                A             VT G N R  V
sequence


------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif KEHGGPEDEERHVGDLGNIEADEBGVAKV MEME-5 sites sorted by
position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                Site
-------------             ----- ---------            ---------------
CuZnSOD_Capsaspora           67  2.80e-29 SAGPHFNPAG
KTHGAPEDEERHVGDLGNVEAGADGIAKF TITDNLIQVS
CuZnSOD_Crassostrea          72  2.39e-28 SAGAHFNPFN
KEHGAPEDTERHVGDLGNVTAGDDGVAKI SITDKMIDLA
CuZnSOD1_Homo                70  5.97e-28 SAGPHFNPLS
RKHGGPKDEERHVGDLGNVTADKDGVADV SIEDSVISLS
CuZnSOD2_Biomphalaria        71  5.70e-27 SAGAHFNPAN
KNHGGPCDTERHVGDLGNIVAGDDGVADV SIKDQQISLI
CuZnSOD1_Nematostella        70  3.45e-26 SAGAHYNPHG
KMHGAPEDKDRHLGDLGNIEADANGIADV SITDCLVSLT
CuZnSOD_Trichoplax           69  5.64e-26 SAGGHYNPHK
KVHGAPGDEIRHVGDLGNIEANEQGVASI NMTDRMVTLT
CCS_Acropora                150  6.37e-26 STGDHYNPGN
SRHGAPEDNERHVGDLGNILADKNGRAHF RMEDRNVKVW
CCS_Nematostella            155  1.16e-25 STGAHFNPTN
NQHGAREDEERHVGDLGNIIANQNGRATF RFEDKTVKVW
CuZnSOD2_Nematostella        70  1.64e-25 SAGPHFNPFK
KEHGGPSDENRHVGDLGNVVAGDDGKACI DMTDALVTLV
CuZn_Hydra                   68  1.85e-25 STGPHFNPFN
KEHGGPEDENRHAGDLGNIVSDDYGNADV NIEDSQIPLD
CuZnSOD1_Biomphalaria        37  6.42e-25 SAGPHFNPFG
KVHGGPQEEIRHVGDLGNVTAAENGVASF SMKDDLVKIH
CuZnSOD_Caenorhabditis       91  8.94e-25 SAGPHFNPFG
KTHGGPKSEIRHVGDLGNVEAGADGVAKI KLTDTLVTLY
CuZnSOD_Acropora             93  1.11e-24 SAGPHFNPEG
KLHGGPVDEERHHGDLGNIIANEQGVAKV DMTDKLVSLV
CuZnSOD2_Drosophila          60  4.42e-24 SSGPHFNPYS
KEHGAPGDENRHLGDLGNIEASGDGPTTV NISDCKITLV
CCS_Homo                    153  1.23e-23 SCGNHFNPDG
ASHGGPQDSDRHRGDLGNVRADADGRAIF RMEDEQLKVW
CCS_Ciona                   145  1.50e-23 SCGEHYNPYN
YKHGGKNDAQRHVGDLGNIEARSNGRATF RFLDDKVKVW
CuZnSOD_Drosophila           67  7.13e-22 SSGPHFNPRN
KEHGAPTDENRHLGDLGNIQAAGDSPTAV SITDSKITLF
CuZnSOD_Ciona                70  7.79e-22 STGGHFNPQK
CDHGAPEAEVRHFGDLGNVTADSSGVAEV NISDKYVTLT
CuZnSOD3_Nematostella        47  1.06e-18 SAKGHFNPYG
KTHAGPRKRDRHVGDLGNVWSDYHGNVRT SFFDHMVSLY
CuZnSOD_Amphimedon           81  2.58e-18 SAGSHFNPAG
KNHGGPKDGERHAGDLGNITSTGGDTEIE LYDDQIPLTG
CCS_Drosophila              148  2.18e-17 GNHYNPRNSP
HGSPNADAAERHAGDLGNIRADETGRATF RFVDPALDIW
CuZnSOD3_Biomphalaria       108  1.20e-16 AAGGHYNPKN
SNHGDITDRVRHVGDFGNIKQELDGTLEK VIEDKIATLY
```

```
CCS_Trichoplax              147  2.04e-16 NCGDIFNPYE
YPHGNNNTSARKLGDIGSMTANKNGRAMF RIEDDTVKVW
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif KEHGGPEDEERHVGDLGNIEADEBGVAKV MEME-5 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CuZnSOD_Capsaspora                2.8e-29  66_[5]_56
CuZnSOD_Crassostrea               2.4e-28  71_[5]_56
CuZnSOD1_Homo                       6e-28  69_[5]_56
CuZnSOD2_Biomphalaria             5.7e-27  70_[5]_56
CuZnSOD1_Nematostella             3.5e-26  69_[5]_56
CuZnSOD_Trichoplax                5.6e-26  68_[5]_57
CCS_Acropora                      6.4e-26  149_[5]_43
CCS_Nematostella                  1.2e-25  154_[5]_82
CuZnSOD2_Nematostella             1.6e-25  69_[5]_58
CuZn_Hydra                        1.8e-25  67_[5]_56
CuZnSOD1_Biomphalaria             6.4e-25  36_[5]_63
CuZnSOD_Caenorhabditis            8.9e-25  90_[5]_61
CuZnSOD_Acropora                  1.1e-24  92_[5]_56
CuZnSOD2_Drosophila               4.4e-24  59_[5]_57
CCS_Homo                          1.2e-23  152_[5]_93
CCS_Ciona                         1.5e-23  144_[5]_90
CuZnSOD_Drosophila                7.1e-22  66_[5]_57
CuZnSOD_Ciona                     7.8e-22  69_[5]_56
CuZnSOD3_Nematostella             1.1e-18  46_[5]_58
CuZnSOD_Amphimedon                2.6e-18  80_[5]_57
CCS_Drosophila                    2.2e-17  147_[5]_87
CuZnSOD3_Biomphalaria             1.2e-16  107_[5]_56
CCS_Trichoplax                      2e-16  146_[5]_76
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif KEHGGPEDEERHVGDLGNIEADEBGVAKV MEME-5 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF KEHGGPEDEERHVGDLGNIEADEBGVAKV width=29 seqs=23
CuZnSOD_Capsaspora       (   67) KTHGAPEDEERHVGDLGNVEAGADGIAKF  1
CuZnSOD_Crassostrea      (   72) KEHGAPEDTERHVGDLGNVTAGDDGVAKI  1
CuZnSOD1_Homo            (   70) RKHGGPKDEERHVGDLGNVTADKDGVADV  1
CuZnSOD2_Biomphalaria    (   71) KNHGGPCDTERHVGDLGNIVAGDDGVADV  1
CuZnSOD1_Nematostella    (   70) KMHGAPEDKDRHLGDLGNIEADANGIADV  1
CuZnSOD_Trichoplax       (   69) KVHGAPGDEIRHVGDLGNIEANEQGVASI  1
CCS_Acropora             (  150) SRHGAPEDNERHVGDLGNILADKNGRAHF  1
CCS_Nematostella         (  155) NQHGAREDEERHVGDLGNIIANQNGRATF  1
CuZnSOD2_Nematostella    (   70) KEHGGPSDENRHVGDLGNVVAGDDGKACI  1
CuZn_Hydra               (   68) KEHGGPEDENRHAGDLGNIVSDDYGNADV  1
CuZnSOD1_Biomphalaria    (   37) KVHGGPQEEIRHVGDLGNVTAAENGVASF  1
CuZnSOD_Caenorhabditis   (   91) KTHGGPKSEIRHVGDLGNVEAGADGVAKI  1
CuZnSOD_Acropora         (   93) KLHGGPVDEERHHGDLGNIIANEQGVAKV  1
```

```
CuZnSOD2_Drosophila      (   60) KEHGAPGDENRHLGDLGNIEASGDGPTTV  1
CCS_Homo                 (  153) ASHGGPQDSDRHRGDLGNVRADADGRAIF  1
CCS_Ciona                (  145) YKHGGKNDAQRHVGDLGNIEARSNGRATF  1
CuZnSOD_Drosophila       (   67) KEHGAPTDENRHLGDLGNIQAAGDSPTAV  1
CuZnSOD_Ciona            (   70) CDHGAPEAEVRHFGDLGNVTADSSGVAEV  1
CuZnSOD3_Nematostella    (   47) KTHAGPRKRDRHVGDLGNVWSDYHGNVRT  1
CuZnSOD_Amphimedon       (   81) KNHGGPKDGERHAGDLGNITSTGGDTEIE  1
CCS_Drosophila           (  148) HGSPNADAAERHAGDLGNIRADETGRATF  1
CuZnSOD3_Biomphalaria    (  108) SNHGDITDRVRHVGDFGNIKQELDGTLEK  1
CCS_Trichoplax           (  147) YPHGNNNTSARKLGDIGSMTANKNGRAMF  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif KEHGGPEDEERHVGDLGNIEADEBGVAKV MEME-5 position-specific
scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 29 n= 7062 bayes= 8.66129 E= 1.6e-
240
   -83     54   -254   -164   -351   -409    -21   -367    331   -
338   -229    -34   -306   -126     52     18   -218   -359   -367
174
  -182   -364    -24    179   -284   -143   -232   -320     74    -
89    111    107      5     57     44    -28    114     -6   -325
-192
  -480   -470   -441   -473   -361   -575    441   -584   -528   -
486   -389   -305   -478   -232   -320    -74   -430   -554   -401
-176
  -130   -397   -315   -357   -436    297   -445   -485   -354   -
508   -366   -294    -81   -382   -305   -280   -374   -458   -393
-365
   214   -442    -13   -316   -524    199   -388   -622   -367   -
599   -508     81   -420   -337   -390   -253   -325   -557   -566
-405
   -92   -395   -364   -317   -370   -453   -414    -92    -78   -
358   -315    -84    436   -276    -25   -258   -278   -379   -457
-380
  -182     61    -24    221   -285    -61   -232   -320    116   -
286   -174     59   -245    126     44    -28     66    -89   -325
-192
  -146   -411    386    -44   -382   -451   -353   -421   -188   -
432   -342   -122   -424   -315   -340   -187   -175   -424   -394
-308
    10   -374   -183    294   -296   -143   -240   -330     11   -
296   -184    -13   -253    -86    115     37     66   -312   -336
-202
   -78   -558    119    282   -469   -474   -388     98   -222   -
426   -320    150   -348     46   -267   -301   -301      0   -509
-368
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  -504   -442   -571   -562   -537   -598   -423   -546   -272   -
518   -464   -484   -452   -356    469   -498   -495   -629   -416
-461
  -581   -542   -499   -522   -420   -633    444   -641    -46   -
544   -453   -373   -530   -297   -351   -485   -499   -622   -456
-242
    27   -220   -418   -345     17   -458    -63    -61   -345
64    -93   -375   -327   -312    -31   -294   -173    291   -297
-217
  -446   -559   -495   -542   -590    311   -609   -664   -537   -
663   -550   -481   -542   -555   -482   -468   -551   -640   -546
-525
  -540   -569    410   -297   -550   -611   -536   -608   -572   -
606   -531   -320   -569   -514   -518   -514   -548   -612   -547
-482
  -424   -395   -584   -479     37   -640   -516    -27   -471
343    -33   -533   -443   -374   -384   -475   -378   -255   -353
-301
  -446   -559   -495   -542   -590    311   -609   -664   -537   -
663   -550   -481   -542   -555   -482   -468   -551   -640   -546
-525
  -389   -359   -235   -395   -339   -435   -193   -339   -321   -
410   -298    404   -361   -258   -309   -120   -253   -410   -326
-285
  -430   -400   -647   -606   -360   -721   -729    329   -596   -
231    123   -609   -598   -593   -589   -566   -387    227   -573
-441
  -199   -316   -232    201   -237   -379   -266     47     -1   -
69   -134   -211   -274     46    112   -185    206     58    151
-189
   328   -204   -463   -407   -359   -327   -507   -379   -424   -
373   -265   -426   -420    -15   -369     73   -253   -256   -410
-377
     5   -467    249    -12   -425     79   -314   -487   -232   -
453   -350    167   -354   -212     24    -37    -18   -468   -470
-310
    90   -367    136    153   -287     -9   -234   -322    116   -
89   -176   -172   -246     57   -103     37   -158   -303   -328
93
  -374   -500    284   -255   -482   -127     -1   -572   -291   -
537   -447    224   -392    122   -318    -39    -20   -554   -532
104
  -256   -400   -118   -352   -433    297   -440   -483   -349   -
506   -363   -288   -393   -378   -301   -127   -376   -458   -390
-361
  -246   -315   -328   -229   -241   -434   -318     57      0   -
226   -137     54     98   -174    260   -250     67    196   -317
-215
   322   -131   -387   -127   -270   -267   -429   -284   -336   -
149   -173   -368   -404   -320   -289    -91    -16    -90   -324
-292
```

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   -56     61    135     76   -284   -351     -8     31    149   -
285    111   -170   -245    -78     44     38    150   -300   -325
-192
  -244   -251   -481    -47    334   -469   -400    157    -49   -
158    -78   -387   -371   -319   -311   -298    -11    204   -281
-189
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif KEHGGPEDEERHVGDLGNIEADEBGVAKV MEME-5 position-specific
probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 29 nsites= 23 E= 1.6e-240
 0.043478  0.043478  0.000000  0.000000  0.000000  0.000000
0.043478  0.000000  0.608696  0.000000  0.000000  0.043478  0.000000
0.000000  0.043478  0.086957  0.000000  0.000000  0.000000  0.086957
 0.000000  0.000000  0.043478  0.217391  0.000000  0.043478
0.000000  0.000000  0.086957  0.043478  0.043478  0.130435  0.043478
0.043478  0.043478  0.043478  0.130435  0.086957  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.956522  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.043478  0.000000  0.000000  0.000000  0.000000
 0.043478  0.000000  0.000000  0.000000  0.000000  0.913043
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.043478
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.391304  0.000000  0.043478  0.000000  0.000000  0.478261
0.000000  0.000000  0.000000  0.000000  0.000000  0.086957  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.043478  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.043478  0.043478  0.000000  0.000000  0.043478  0.782609
0.000000  0.043478  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.043478  0.043478  0.304348  0.000000  0.086957
0.000000  0.000000  0.130435  0.000000  0.000000  0.086957  0.000000
0.086957  0.043478  0.043478  0.086957  0.043478  0.000000  0.000000
 0.086957  0.000000  0.739130  0.043478  0.000000  0.000000
0.000000  0.000000  0.043478  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.043478  0.043478  0.000000  0.000000  0.000000
 0.086957  0.000000  0.000000  0.521739  0.000000  0.043478
0.000000  0.000000  0.043478  0.000000  0.000000  0.043478  0.000000
0.000000  0.086957  0.086957  0.086957  0.000000  0.000000  0.000000
 0.043478  0.000000  0.130435  0.391304  0.000000  0.000000
0.000000  0.130435  0.000000  0.000000  0.000000  0.173913  0.000000
0.043478  0.000000  0.000000  0.000000  0.086957  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.956522  0.000000  0.043478  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.130435  0.000000  0.000000  0.000000  0.043478  0.000000
0.043478  0.000000  0.000000  0.173913  0.000000  0.000000  0.000000
```

```
0.000000  0.043478  0.000000  0.000000  0.565217  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.043478  0.000000
0.000000  0.043478  0.000000  0.913043  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.956522  0.000000
0.000000  0.000000  0.043478  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.565217  0.000000  0.000000  0.043478  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.391304  0.000000  0.000000
 0.000000  0.000000  0.000000  0.260870  0.000000  0.000000
0.000000  0.086957  0.043478  0.043478  0.000000  0.000000  0.000000
0.043478  0.086957  0.000000  0.260870  0.130435  0.043478  0.000000
 0.826087  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.043478  0.000000  0.130435  0.000000  0.000000  0.000000  0.000000
 0.086957  0.000000  0.347826  0.043478  0.000000  0.217391
0.000000  0.000000  0.000000  0.000000  0.000000  0.173913  0.000000
0.000000  0.043478  0.043478  0.043478  0.000000  0.000000  0.000000
 0.173913  0.000000  0.173913  0.173913  0.000000  0.130435
0.000000  0.000000  0.130435  0.043478  0.000000  0.000000  0.000000
0.043478  0.000000  0.086957  0.000000  0.000000  0.000000  0.043478
 0.000000  0.000000  0.434783  0.000000  0.000000  0.043478
0.043478  0.000000  0.000000  0.000000  0.000000  0.260870  0.000000
0.086957  0.000000  0.043478  0.043478  0.000000  0.000000  0.043478
 0.000000  0.000000  0.043478  0.000000  0.000000  0.913043
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.043478  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.086957  0.043478  0.000000  0.000000  0.086957  0.086957
0.000000  0.260870  0.000000  0.086957  0.347826  0.000000  0.000000
 0.782609  0.000000  0.000000  0.043478  0.000000  0.000000
0.000000  0.000000  0.000000  0.043478  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.086957  0.043478  0.000000  0.000000
 0.043478  0.043478  0.173913  0.086957  0.000000  0.000000
0.043478  0.086957  0.173913  0.000000  0.043478  0.000000  0.000000
0.000000  0.043478  0.086957  0.173913  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.043478  0.347826  0.000000
0.000000  0.173913  0.043478  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.043478  0.347826  0.000000  0.000000
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif KEHGGPEDEERHVGDLGNIEADEBGVAKV MEME-5 regular expression
--------------------------------------------------------------------
KEHG[GA]PEDEERHVGDLGN[IV][ET]A[DG]X[DN]G[VR]AX[FV]
--------------------------------------------------------------------




Time 33.27 secs.

********************************************************************


********************************************************************
MOTIF KGDVSKIIALQPALKFNGGGHINHSIFWTNLSPNGGGEPTG MEME-6   width =  41
sites =  12  llr = 1079  E-value = 2.6e-224
********************************************************************
--------------------------------------------------------------------
      Motif KGDVSKIIALQPALKFNGGGHINHSIFWTNLSPNGGGEPTG MEME-6
Description
--------------------------------------------------------------------
Simplified        A  1:::133:5:21a::::::::::::::::::2:1:::::1:
pos.-specific     C  :::::::::::::::::::::::::::::::::::::::1:
probability       D  :18::::::::::::::::::::::::::::::2:::1:12
matrix            E  1::::1::::1:::::::::::::::::2:::::::14::1
                  F  :::::::::::::::a::::::::::a::::::::::::::
                  G  :5::12::::12:::::aaa::::::::::::::8871::7
                  H  ::::::::::::::::::::a::a:::::::::::::::::
                  I  :::2::39:::::2:::::::8:::a:::::::::::::::
                  K  81::13::::::::7:::::::::::::1:::111::1:1:
                  L  :::2::1::a:::7:::::::3::::::::a::::::1:::
                  M  ::::::1::::::::::::::::::::::::::::::::::
                  N  :32:2:::::::::::a:::::a:::::18::16:::::::
                  P  :::::::::::7::::::::::::::::::::8::::281:
                  Q  ::::::2:2:7:::::::::::::::::1::::1:11::2:
                  R  ::::::::::::::3::::::::::::::::::::::::::
                  S  :1::41::3::1::::::::::::8:::1::8::112:3:1
                  T  :::222::1:::::::::::::::2:::52:::::::1:3:
                  V  :::5::11:::::1:::::::::::::::::::::::::1:
                  W  :::::::::::::::::::::::::::a:::::::::::::
                  Y  :::::::::::::1:::::::::::::::::::::::::::

         bits    6.4                            *
                 5.7                            *
                 5.1                *          **
                 4.5                **   * ** ***
Relative         3.8   *    * *  *  **   * ** *** ** *     *
Entropy          3.2 * *    * **** ************** ****     *
(129.7 bits)     2.5 * *    * ******************* *******  *
                 1.9 ***** ***********************************
```

```
                 1.3 *****************************************
                 0.6 *****************************************
                 0.0 -----------------------------------------

Multilevel           KGDVSAIIALQPALKFNGGGHINHSIFWTNLSPNGGGEPTG
consensus             N   KA S     R      L                S
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif KGDVSKIIALQPALKFNGGGHINHSIFWTNLSPNGGGEPTG MEME-6 sites
sorted by position p-value
--------------------------------------------------------------------
Sequence name            Start   P-value                  Site
-------------            ----- ---------            ---------------
MnSOD_Homo                  75  4.30e-47 NEEKYQEALA
KGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGEPKG ELLEAIKRDF
MnSOD_Hydra                 73  1.98e-44 AEEQLAEAQH
KGDTSKIISLAPALKFNGGGHINHSIFWTNLSPNGGGKPTG ELLEAILKDF
MnSOD1_Nematostella         74  1.35e-43 AEEKCLEAQA
KGDVATAIALQPAVKFNGGGHLNHSIFWTNLSPNGGGEPTG ELMEAIKRDF
MnSOD_Biomphalaria          74  2.96e-43 AEEKLKAAVD
KGDVNTIISLQPALKFNGGGHINHTIFWSNLSPKGGGEPTG DLLQLIKEEF
MnSOD_Ciona                 72  2.32e-40 AEEKLHEAEA
KNDISSIISLGPALKFNGGGHINHSIFWETLSPNGGSEPCG ELKTAIDRDF
MnSOD_Trichoplax            77  1.61e-38 AEEKLAEATS
KNDISGVITLQGALRFNGGGHINHSIFWKNLSNDGGGLPTG ELGDAINACF
MnSOD_Acropora              78  3.27e-38 AEEKYAEAQA
EDNLGAMIALQPALKFNGGGHLNHSIFWTNLSPNGGGDPVG TVKDIFVY
MnSOD_Crassostrea           78  4.00e-38 AEEKLAEAME
KKDVNKIIQLQAAIRFNGGGHLNHSIFWETLSPQGGGEPQD GALKDLILEE
MnSOD_Amphimedon            78  3.86e-37 TEGKMKECLE
AGDVSGAVALEGAYRFNGGGHINHSIFWNNLSPNGGGTPQG KLMEAIERDF
MnSOD_Caenorhabditis        75  4.15e-36 IEEKLHEAVS
KGNVKEAIALQPALKFNGGGHINHSIFWTNLAKDGGEPSAE LLTAIKSDFG
MnSOD_Drosophila            62  7.71e-35 AEEQLEEAKS
KSDTTKLIQLAPALRFNGGGHINHTIFWQNLSPNKSQPSDD LKKAIESQWK
FeMnSOD_Capsaspora          80  2.44e-34 AEEKYAEATA
KNDLSAQIALQSAIKFNGGGHINHSIFWTNLAPASQSGSPS AELNKAINAE
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif KGDVSKIIALQPALKFNGGGHINHSIFWTNLSPNGGGEPTG MEME-6 block
diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
MnSOD_Homo                       4.3e-47  74_[6]_107
MnSOD_Hydra                        2e-44  72_[6]_106
```

```
MnSOD1_Nematostella              1.3e-43  73_[6]_107
MnSOD_Biomphalaria                 3e-43  73_[6]_109
MnSOD_Ciona                      2.3e-40  71_[6]_105
MnSOD_Trichoplax                 1.6e-38  76_[6]_107
MnSOD_Acropora                   3.3e-38  77_[6]_8
MnSOD_Crassostrea                  4e-38  77_[6]_107
MnSOD_Amphimedon                 3.9e-37  77_[6]_103
MnSOD_Caenorhabditis             4.1e-36  74_[6]_106
MnSOD_Drosophila                 7.7e-35  61_[6]_27
FeMnSOD_Capsaspora               2.4e-34  79_[6]_109
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif KGDVSKIIALQPALKFNGGGHINHSIFWTNLSPNGGGEPTG MEME-6 in
BLOCKS format
--------------------------------------------------------------------
BL   MOTIF KGDVSKIIALQPALKFNGGGHINHSIFWTNLSPNGGGEPTG width=41
seqs=12
MnSOD_Homo               (   75)
KGDVTAQIALQPALKFNGGGHINHSIFWTNLSPNGGGEPKG  1
MnSOD_Hydra              (   73)
KGDTSKIISLAPALKFNGGGHINHSIFWTNLSPNGGGKPTG  1
MnSOD1_Nematostella      (   74)
KGDVATAIALQPAVKFNGGGHLNHSIFWTNLSPNGGGEPTG  1
MnSOD_Biomphalaria       (   74)
KGDVNTIISLQPALKFNGGGHINHTIFWSNLSPKGGGEPTG  1
MnSOD_Ciona              (   72)
KNDISSIISLGPALKFNGGGHINHSIFWETLSPNGGSEPCG  1
MnSOD_Trichoplax         (   77)
KNDISGVITLQGALRFNGGGHINHSIFWKNLSNDGGGLPTG  1
MnSOD_Acropora           (   78)
EDNLGAMIALQPALKFNGGGHLNHSIFWTNLSPNGGGDPVG  1
MnSOD_Crassostrea        (   78)
KKDVNKIIQLQAAIRFNGGGHLNHSIFWETLSPQGGGEPQD  1
MnSOD_Amphimedon         (   78)
AGDVSGAVALEGAYRFNGGGHINHSIFWNNLSPNGGGTPQG  1
MnSOD_Caenorhabditis     (   75)
KGNVKEAIALQPALKFNGGGHINHSIFWTNLAKDGGEPSAE  1
MnSOD_Drosophila         (   62)
KSDTTKLIQLAPALRFNGGGHINHTIFWQNLSPNKSQPSDD  1
FeMnSOD_Capsaspora       (   80)
KNDLSAQIALQSAIKFNGGGHINHSIFWTNLAPASQSGSPS  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif KGDVSKIIALQPALKFNGGGHINHSIFWTNLSPNGGGEPTG MEME-6
position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 41 n= 6570 bayes= 8.75234 E= 2.6e-
```

```
224
  -207   -386   -423   -157   -471   -518   -419   -394    396   -
438   -323   -350   -395   -296      3   -396   -345   -468   -388
-374
  -304   -424     67   -203   -427    203   -278   -527     37   -
502   -413    205   -332   -224   -270     30   -247   -507   -461
-295
  -337   -393    391    -84   -366   -429   -334   -407   -365   -
419   -330      2   -410   -309   -328   -301   -345   -411   -378
-291
  -262   -269   -518   -450   -238   -557   -504    159   -452
89   -129   -472   -428   -423   -399   -400    135    269   -401
-305
   -61   -229   -229   -221   -284   -152   -310   -341    -35   -
330   -210     56   -262   -192   -181    302    149   -357   -331
-225
   124   -304   -127     76   -236      6   -183   -270    181   -
237   -126   -113   -195    -30    -51     34    132   -250   -277
-144
   129   -179   -405   -310    -95   -395   -325    231   -292
40    212   -312   -296    178   -238   -223   -135     48   -205
-114
  -330   -323   -460   -431   -233   -561   -535    374   -406    -
74    -59   -429   -446   -404   -396   -388   -272     77   -389
-271
   263   -209   -370   -315   -359   -304   -428   -386   -325   -
376   -266   -328   -332    188   -297    167     55   -281   -407
-343
  -458   -426   -589   -519   -210   -620   -541   -207   -509
356    -82   -560   -462   -417   -421   -506   -417   -298   -383
-329
   -40   -335   -262      9   -361   -199   -123   -362   -229   -
271   -130   -239   -279    436   -159   -254   -258   -367   -300
-304
   -19   -315   -338   -295   -341    -21   -390   -370   -290   -
334   -283   -349    419   -252   -266    -12   -229   -337   -423
-350
   355   -293   -532   -501   -441   -399   -568   -472   -517   -
465   -367   -497   -445   -466   -447   -245   -325   -361   -475
-443
  -334   -313   -510   -408   -119   -555   -444     99   -399
313     15   -453   -376   -311   -317   -388   -291    -22   -294
121
  -354   -424   -446   -290   -470   -491   -318   -406    361   -
380   -283   -309   -392   -148    265   -344   -307   -427   -383
-321
  -410   -321   -497   -475    498   -568   -486   -297   -491   -
204   -210   -493   -413   -470   -449   -385   -439   -352   -216
-32
  -431   -398   -278   -434   -377   -468   -240   -386   -364   -
450   -344    410   -394   -303   -349   -235   -299   -454   -364
```

```
-323
  -301   -430   -354   -399   -464    306   -478   -525   -395   -
537   -408   -336   -421   -419   -344   -324   -414   -499   -421
-395
  -301   -430   -354   -399   -464    306   -478   -525   -395   -
537   -408   -336   -421   -419   -344   -324   -414   -499   -421
-395
  -301   -430   -354   -399   -464    306   -478   -525   -395   -
537   -408   -336   -421   -419   -344   -324   -414   -499   -421
-395
  -595   -534   -520   -559   -427   -610    450   -656   -593   -
556   -483   -411   -512   -336   -408   -512   -522   -639   -455
-265
  -374   -357   -528   -490   -178   -612   -562    358   -467
139    -42   -492   -482   -430   -440   -449   -321    -37   -366
-284
  -431   -398   -278   -434   -377   -468   -240   -386   -364   -
450   -344    410   -394   -303   -349   -235   -299   -454   -364
-323
  -595   -534   -520   -559   -427   -610    450   -656   -593   -
556   -483   -411   -512   -336   -408   -512   -522   -639   -455
-265
  -180   -204   -331   -357   -292   -385   -390   -356   -286   -
354   -229   -188   -279   -294   -236    345    150   -387   -340
-251
  -441   -420   -578   -568   -334   -625   -627    402   -548   -
211   -197   -562   -527   -530   -515   -516   -398   -118   -483
-382
  -410   -321   -497   -475    498   -568   -486   -297   -491   -
204   -210   -493   -413   -470   -449   -385   -439   -352   -216
-32
  -437   -377   -439   -422   -109   -510   -455   -423   -416   -
265   -262   -429   -428   -361   -330   -426   -404   -406    624
-105
  -163   -310   -142    132   -263   -321   -214   -282     58   -
268   -147     46   -225    106    -82     37    293   -265   -302
-177
  -354   -352   -209   -352   -339   -401   -197   -347   -305   -
411   -302    396   -349   -250   -298   -179     20   -408   -331
-279
  -458   -426   -589   -519   -210   -620   -541   -207   -509
356    -82   -560   -462   -417   -421   -506   -417   -298   -383
-329
   101   -238   -463   -467   -413   -339   -513   -467   -453   -
462   -341   -349   -338   -393   -380    350   -103   -375   -457
-396
  -183   -348   -306   -266   -323   -401   -363   -351    -24   -
312   -268    -29    438   -226   -236   -209   -230   -333   -410
-330
   -32   -390    122   -146   -359   -317   -229   -400     29   -
397   -295    338   -301     86   -199   -159   -210   -409   -384
```

```
-255
  -223   -367   -276   -319   -401    292   -407   -450    -92   -
473   -331   -254   -360   -344   -268    -92   -341   -425   -358
-328
  -221   -363   -276   -320   -402    291   -408   -452   -317   -
474   -332   -255   -360    -36   -270    -87   -338   -425   -360
-330
  -227   -370   -233    -45   -402    276   -378   -452   -288   -
465   -331   -215   -351     -3   -259     13   -315   -425   -369
-321
  -148   -343     51    258   -263    -78   -205   -291     68    -
25   -147   -137    163    -35    -76   -125     53   -270   -304
-169
  -196   -349   -347   -307   -354   -410   -401   -385   -302   -
348   -301   -362    430   -266   -279    125   -253   -359   -434
-360
     5    124     36    -40   -217   -294   -176   -243     72   -
218   -107   -113     67    187    -45    -91    219    -24   -262
-132
  -239   -381     48    -34   -409    274   -367   -465   -295   -
479   -346   -188   -353   -297   -271    -53   -314   -440   -378
-322
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif KGDVSKIIALQPALKFNGGGHINHSIFWTNLSPNGGGEPTG MEME-6
position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 41 nsites= 12 E= 2.6e-224
 0.083333  0.000000  0.000000  0.083333  0.000000  0.000000
0.000000  0.000000  0.833333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.083333  0.000000  0.000000  0.500000
0.000000  0.000000  0.083333  0.000000  0.000000  0.250000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.833333  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.166667  0.500000  0.000000  0.000000
 0.083333  0.000000  0.000000  0.000000  0.000000  0.083333
0.000000  0.000000  0.083333  0.000000  0.000000  0.166667  0.000000
0.000000  0.000000  0.416667  0.166667  0.000000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.083333  0.000000  0.166667
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.166667  0.000000  0.000000  0.000000
 0.250000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.083333  0.083333  0.000000  0.000000
0.166667  0.000000  0.000000  0.000000  0.083333  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.916667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.083333  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.166667  0.000000  0.250000  0.083333  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.083333  0.000000  0.083333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.666667  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.083333  0.000000  0.000000  0.000000  0.000000  0.166667
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.666667
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.166667  0.000000  0.666667  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.083333  0.000000  0.083333
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.666667  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.750000  0.000000  0.250000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.833333  0.166667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  0.166667  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.083333  0.000000
0.083333  0.000000  0.083333  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.833333  0.000000
0.000000  0.000000  0.000000  0.166667  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.166667  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.833333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.083333  0.833333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.083333  0.000000  0.166667  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.583333  0.000000
0.083333  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.833333
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.833333
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.083333  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.083333  0.000000  0.666667
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.083333  0.000000  0.166667  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.083333  0.416667  0.000000  0.083333
0.000000  0.000000  0.083333  0.083333  0.000000  0.000000  0.166667
0.000000  0.000000  0.000000  0.083333  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.750000
0.000000  0.000000  0.250000  0.000000  0.000000  0.000000  0.000000
 0.083333  0.083333  0.083333  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.083333
0.166667  0.000000  0.000000  0.333333  0.083333  0.000000  0.000000
 0.000000  0.000000  0.166667  0.083333  0.000000  0.666667
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.083333  0.000000  0.000000  0.000000  0.000000
```

```
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif KGDVSKIIALQPALKFNGGGHINHSIFWTNLSPNGGGEPTG MEME-6 regular
expression
--------------------------------------------------------------------
K[GN]DVS[AK][IA]I[AS]LQPAL[KR]FNGGGH[IL]NHSIFWTNLSPNGGGE[PS]TG
--------------------------------------------------------------------




Time 37.58 secs.

********************************************************************


********************************************************************
MOTIF LLEAIKRDFGSFDNFKEKLTAATVAVQGSGWGWLGYDKETG MEME-7   width =  41
sites =  11  llr = 913  E-value = 4.8e-154
********************************************************************
--------------------------------------------------------------------
      Motif LLEAIKRDFGSFDNFKEKLTAATVAVQGSGWGWLGYDKETG MEME-7
Description
--------------------------------------------------------------------
Simplified        A  :::7::2::::::3::11:155116:::::::::::::21:
pos.-specific     C  :::::::1::::::::::::::::::::::::::1:2::::
probability       D  ::3::2:5::::5::::::1::::::::::::::::5::::
matrix            E  ::4::123::::41::3:::3:::::::::::::::::3::
                  F  ::::::::9::9::5:::3:::::::1::::::::3:::::
                  G  :2:::::::8::::::::::::::3::a:a:7::9::::15
                  H  ::::::::1:::::::::::::::::::::::::::::::1
                  I  1:::a::::::::::::::::::2:3:::::::::::::::
                  K  :21::42::::::1:834:::1:::::::::::::::5123
                  L  94:3:2:::::1::3::17::::::::::::::a:1:::::
                  M  :2:::::::::::12::::::::::1:::::::::::::::
                  N  :1:::2::::1::5:::::2:::1::::::::::::3::11
                  P  :::::::::::::::::::::1:::::::::::::::2:::
                  Q  ::1::::::::::::112:::2::::9::::::::1:1:::
                  R  ::::::4::::::::::2:::1:::::::::::::::::1:
                  S  ::::::11:17:1:::2::3114:1:::a::2:::::1:2:
                  T  ::2:::::::2:::::1::41:5::::::::1::::::23:
                  V  :::::::::1:::::1::::::16:6:::::::::::13::
                  W  :::::::::::::::::1::::::::::::9:a::::::::
                  Y  ::::::::::::::::::::::::::::::1::::5:::::

         bits    6.4                                 *
                 5.7                               * *
                 5.1                               * *
                 4.5     *   *  *              *   * *
Relative         3.8     *   *  *              * * * ** *
```

```
Entropy          3.2 *   *   * **  **  *       ***** *****
(119.8 bits)     2.5 *  **  *********  * * ****************
                 1.9 *************************************** *
                 1.3 *****************************************
                 0.6 *****************************************
                 0.0 -----------------------------------------

Multilevel           LLEAIKRDFGSFDNFKEKLTAATVAVQGSGWGWLGYDKETG
consensus              DL   E    EAL K FSE S GI         FN V K
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LLEAIKRDFGSFDNFKEKLTAATVAVQGSGWGWLGYDKETG MEME-7 sites
sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                  Site
-------------             ----- ---------            ---------------
MnSOD1_Nematostella         116  5.18e-44  PNGGGEPTGE
LMEAIKRDFGSFENFKERFNAATIAVQGSGWGWLGYDKVNK RLAIATCFNQ
MnSOD_Homo                  117  1.10e-42  PNGGGEPKGE
LLEAIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKERG HLQIAACPNQ
MnSOD_Amphimedon            120  8.60e-42  PNGGGTPQGK
LMEAIERDFGSFDEFKSQLTARTVAIQGSGWGWLGFNQVTG RLQIATCPNQ
MnSOD_Trichoplax            119  9.86e-39  NDGGGLPTGE
LGDAINACFGSFDNFKSKLSAATIAIQGSGWGWLGYCKESN SLKIATCANQ
MnSOD_Ciona                 114  3.64e-38  PNGGSEPCGE
LKTAIDRDFGSFENLKAKLTAASVGVQGSGWSWLGLDKEKG QLQVVACPNQ
MnSOD_Hydra                 115  4.70e-38  PNGGGKPTGE
LLEAILKDFGSFEAMKTRLSSPAVAVQGSGWGWLGYDSVTK RLAITALPNQ
FeMnSOD_Capsaspora          123  1.32e-35  ASQSGSPSAE
LNKAINAEFGSFDAFVEKFNTQTAAVQGSGWGWLGYDKTKG RVVITACANQ
MnSOD_Caenorhabditis        116  2.59e-35  AKDGGEPSAE
LLTAIKSDFGSLDNLQKQLSASTVAVQGSGWGWLGYCPKGK ILKVATCANQ
MnSOD_Biomphalaria          116  3.94e-34  PKGGGEPTGD
LLQLIKEEFSTFENMKKLLAEKSVAIQGSGWGWLGFNPATG KVQVATCSNQ
MnSOD_Crassostrea           121  2.59e-33  QGGGEPQDGA
LKDLILEEFVTFDALKKALTEASVGVQGSGWSWLGYDKAAH SLRVVTCANQ
MnSOD2_Nematostella         144  2.95e-23  KSEPRTPTGK
IGDLIDKSHGNFSMFKQWFDEQVNSMFGSGYTWLCQDVTSG FLTILNMGNQ
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LLEAIKRDFGSFDNFKEKLTAATVAVQGSGWGWLGYDKETG MEME-7 block
diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
MnSOD1_Nematostella               5.2e-44  115_[7]_65
```

```
MnSOD_Homo                        1.1e-42  116_[7]_65
MnSOD_Amphimedon                  8.6e-42  119_[7]_61
MnSOD_Trichoplax                  9.9e-39  118_[7]_65
MnSOD_Ciona                       3.6e-38  113_[7]_63
MnSOD_Hydra                       4.7e-38  114_[7]_64
FeMnSOD_Capsaspora                1.3e-35  122_[7]_66
MnSOD_Caenorhabditis              2.6e-35  115_[7]_65
MnSOD_Biomphalaria                3.9e-34  115_[7]_67
MnSOD_Crassostrea                 2.6e-33  120_[7]_64
MnSOD2_Nematostella               2.9e-23  143_[7]_71
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LLEAIKRDFGSFDNFKEKLTAATVAVQGSGWGWLGYDKETG MEME-7 in
BLOCKS format
--------------------------------------------------------------------
BL   MOTIF LLEAIKRDFGSFDNFKEKLTAATVAVQGSGWGWLGYDKETG width=41
seqs=11
MnSOD1_Nematostella      (  116)
LMEAIKRDFGSFENFKERFNAATIAVQGSGWGWLGYDKVNK  1
MnSOD_Homo               (  117)
LLEAIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKERG  1
MnSOD_Amphimedon         (  120)
LMEAIERDFGSFDEFKSQLTARTVAIQGSGWGWLGFNQVTG  1
MnSOD_Trichoplax         (  119)
LGDAINACFGSFDNFKSKLSAATIAIQGSGWGWLGYCKESN  1
MnSOD_Ciona              (  114)
LKTAIDRDFGSFENLKAKLTAASVGVQGSGWSWLGLDKEKG  1
MnSOD_Hydra              (  115)
LLEAILKDFGSFEAMKTRLSSPAVAVQGSGWGWLGYDSVTK  1
FeMnSOD_Capsaspora       (  123)
LNKAINAEFGSFDAFVEKFNTQTAAVQGSGWGWLGYDKTKG  1
MnSOD_Caenorhabditis     (  116)
LLTAIKSDFGSLDNLQKQLSASTVAVQGSGWGWLGYCPKGK  1
MnSOD_Biomphalaria       (  116)
LLQLIKEEFSTFENMKKLLAEKSVAIQGSGWGWLGFNPATG  1
MnSOD_Crassostrea        (  121)
LKDLILEEFVTFDALKKALTEASVGVQGSGWSWLGYDKAAH  1
MnSOD2_Nematostella      (  144)
IGDLIDKSHGNFSMFKQWFDEQVNSMFGSGYTWLCQDVTSG  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LLEAIKRDFGSFDNFKEKLTAATVAVQGSGWGWLGYDKETG MEME-7
position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 41 n= 6570 bayes= 9.57545 E= 4.8e-
154
```

```
  -360   -332   -523   -419   -112   -579   -457     36   -411
338     24   -472   -384   -316   -325   -414   -315   -184   -297
-245
  -166   -250   -216   -130   -171     19   -232   -147    145
183    291     48   -246    -87    -59   -160   -133   -161   -248
-141
  -224   -523    204    275   -431   -405   -328   -405     59   -
372   -267   -239   -278    128   -208   -240    144   -364   -465
-319
   306   -233   -492   -437   -261   -354   -509   -238   -446
152   -167   -439   -396   -393   -384   -193   -255   -231   -385
-328
  -416   -399   -552   -538   -309   -607   -604    400   -517   -
180   -166   -533   -507   -502   -488   -488   -372    -87   -459
-355
  -173   -356    141    101   -288   -308   -212   -320    231
75   -177    147   -228    -57    -83   -132   -145   -299   -325
-187
    84   -343   -170    151   -280   -334   -203   -299    163   -
261   -154   -152   -232    -39    290     34   -143   -283   -298
-176
  -301     52    363    123   -375   -385   -315   -415   -285   -
415   -323   -100   -364   -230   -288    -68   -296   -408   -395
-289
  -382   -292   -471   -444    488   -551    -30   -267   -455   -
175   -178   -447   -390   -423   -409   -353   -405   -321   -151
44
  -210   -349   -282   -324   -399    290   -411   -446   -321   -
469   -328   -260   -356   -346   -272    -74   -327   -128   -360
-330
  -181   -199   -313   -344   -282   -384   -377   -347   -274   -
345   -220    -62   -272   -283   -225    339    152   -385   -331
-241
  -350   -261   -448   -417    488   -534   -458   -227   -437    -
79   -139   -444   -363   -422   -403   -326   -383   -286   -164
18
  -265   -535    312    263   -481   -400   -351   -455   -211   -
430   -332   -187   -314   -117   -282     11   -283   -413   -509
-360
   131   -317   -119     89   -244   -300   -188   -271     83   -
241    189    254   -204    -33    -46   -111   -116   -255   -284
-152
  -451   -401   -700   -614    406   -704   -565   -126   -606
187    325   -630   -523   -454   -506   -571   -417   -246   -305
-224
  -352   -390   -445   -334   -462   -508   -380   -389    392   -
413   -304   -336   -391    -33     13   -377   -329   -163   -381
-351
    13   -309   -111    196   -230   -293   -175   -263    188   -
229   -117   -112   -186    128    -39    108     63   -244   -270
-137
```

```
     2   -371   -251   -137   -328   -379   -227   -325    252     -
7   -183   -197   -280    211    221   -196   -186   -315    245   -
211
  -436   -394   -641   -548    293   -666   -504   -129   -536
313    -11   -572   -483   -410   -440   -527   -395   -240   -291
-183
   -22   -288     33   -208   -329   -335   -293   -340   -215   -
370   -230    130   -295   -192   -215    205    277   -333   -373
-261
   269   -207   -232    191   -328   -296   -365   -347   -241   -
335   -226   -267   -308   -198   -241     39     52   -253   -376
-297
   199   -297   -141    -49   -238   -298   -181   -267     89   -
233   -122   -123     78    197    122     38   -108   -245   -272
-144
   -16   -232   -380   -382   -325   -395   -419   -294   -325   -
361   -200   -239   -323   -284   -281    221    321    -33   -369
-319
   -58   -184   -358   -304   -220   -450   -363     74   -325   -
180   -126   -130   -286   -310   -248   -298   -137    322   -346
-301
   295   -185   -448   -411   -363     91   -493   -392   -433   -
385   -273   -386   -345   -369   -364     47   -205   -265   -411
-375
  -257   -273   -512   -456   -260   -581   -532    211   -469   -
175    199   -495   -434   -452   -414   -433   -251    299   -452
-358
  -292   -344   -380   -124      0   -505   -119   -364   -282   -
265   -128   -278   -299    454   -176   -300   -295   -385   -272
-215
  -288   -419   -342   -387   -453    305   -466   -512   -383   -
525   -395   -324   -410   -407   -332   -311   -401   -487   -410
-384
  -328   -386   -506   -546   -481   -492   -564   -569   -509   -
548   -453   -419   -442   -486   -446    382   -176   -540   -501
-438
  -288   -419   -342   -387   -453    305   -466   -512   -383   -
525   -395   -324   -410   -407   -332   -311   -401   -487   -410
-384
  -409   -350   -414   -394    -73   -489   -422   -392   -387   -
234   -231   -400   -406   -332   -302   -398   -375   -375    619
9
  -182   -312   -298   -343   -409    277   -425   -459   -345   -
473   -338   -269   -351   -352   -296     54    -10   -401   -384
-349
  -431   -372   -434   -417   -103   -505   -450   -417   -410   -
259   -256   -423   -423   -355   -325   -420   -398   -400    623
-100
  -439   -408   -573   -499   -192   -607   -523   -189   -489
354    -63   -542   -445   -397   -402   -486   -398   -278   -366
-311
```

```
  -225     62   -293   -336   -409    295   -422   -460   -333   -
481   -342   -272   -367   -358   -283   -252   -343   -430   -369
-340
  -226   -239   -315   -266    290   -421    -92   -235   -276    -
31   -130   -291   -284     50   -217   -221   -251   -254    -52
471
  -314    254    325   -169   -416   -305   -279   -508   -263   -
491   -414    208   -341   -234   -289   -182   -252   -493   -457
-292
  -178   -337   -188    -89   -280   -340   -209   -293    292   -
260   -155   -160    181    127     -3     31   -148    -11   -299
-180
    85   -299   -121    206   -225   -320   -212   -223     73   -
217   -114   -150   -213    -44    -75   -129    142    132   -281
-157
    10   -295   -122    -40   -226    -74   -174   -259    142   -
228   -115     56   -187    -21    112    118    193   -241   -266
-134
  -270   -399   -144   -205   -401    224     60   -454    180   -
429   -326     66   -327   -185   -144   -189   -247   -438   -400
-280
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LLEAIKRDFGSFDNFKEKLTAATVAVQGSGWGWLGYDKETG MEME-7
position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 41 nsites= 11 E= 4.8e-154
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.090909  0.000000  0.909091  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.181818
0.000000  0.000000  0.181818  0.363636  0.181818  0.090909  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.272727  0.363636  0.000000  0.000000
0.000000  0.000000  0.090909  0.000000  0.000000  0.000000  0.000000
0.090909  0.000000  0.000000  0.181818  0.000000  0.000000  0.000000
 0.727273  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.272727  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.181818  0.090909  0.000000  0.000000
0.000000  0.000000  0.363636  0.181818  0.000000  0.181818  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.181818  0.000000  0.000000  0.181818  0.000000  0.000000
0.000000  0.000000  0.181818  0.000000  0.000000  0.000000  0.000000
0.000000  0.363636  0.090909  0.000000  0.000000  0.000000  0.000000
 0.000000  0.090909  0.545455  0.272727  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.090909  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.909091  0.000000
0.090909  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.818182
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.090909  0.000000  0.090909  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.090909  0.000000
0.000000  0.000000  0.727273  0.181818  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.909091  0.000000
0.000000  0.000000  0.000000  0.090909  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.545455  0.363636  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.090909  0.000000  0.000000  0.000000  0.000000
 0.272727  0.000000  0.000000  0.090909  0.000000  0.000000
0.000000  0.000000  0.090909  0.000000  0.090909  0.454545  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.545455  0.000000
0.000000  0.000000  0.000000  0.272727  0.181818  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.818182  0.000000  0.000000  0.000000  0.000000
0.090909  0.000000  0.000000  0.000000  0.090909  0.000000  0.000000
 0.090909  0.000000  0.000000  0.272727  0.000000  0.000000
0.000000  0.000000  0.272727  0.000000  0.000000  0.000000  0.000000
0.090909  0.000000  0.181818  0.090909  0.000000  0.000000  0.000000
 0.090909  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.363636  0.090909  0.000000  0.000000  0.000000
0.181818  0.181818  0.000000  0.000000  0.000000  0.090909  0.000000
 0.000000  0.000000  0.000000  0.000000  0.272727  0.000000
0.000000  0.000000  0.000000  0.727273  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.090909  0.000000  0.090909  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.181818  0.000000
0.000000  0.000000  0.272727  0.363636  0.000000  0.000000  0.000000
 0.545455  0.000000  0.000000  0.272727  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.090909  0.090909  0.000000  0.000000  0.000000
 0.454545  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.090909  0.000000  0.000000  0.000000  0.090909
0.181818  0.090909  0.090909  0.000000  0.000000  0.000000  0.000000
 0.090909  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.363636  0.454545  0.090909  0.000000  0.000000
 0.090909  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.181818  0.000000  0.000000  0.000000  0.090909  0.000000
0.000000  0.000000  0.000000  0.000000  0.636364  0.000000  0.000000
 0.636364  0.000000  0.000000  0.000000  0.000000  0.272727
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.090909  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.272727  0.000000  0.000000  0.090909  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.636364  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.090909  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.909091  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.909091  0.090909
 0.000000  0.000000  0.000000  0.000000  0.000000  0.727273
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.181818  0.090909  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.090909  0.000000  0.000000  0.000000  0.909091
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.272727  0.000000
0.000000  0.000000  0.000000  0.090909  0.000000  0.000000  0.000000
0.090909  0.000000  0.000000  0.000000  0.000000  0.000000  0.545455
 0.000000  0.181818  0.545455  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.272727  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.545455  0.000000  0.000000  0.000000  0.181818
0.090909  0.000000  0.090909  0.000000  0.090909  0.000000  0.000000
 0.181818  0.000000  0.000000  0.272727  0.000000  0.000000
0.000000  0.000000  0.090909  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.181818  0.272727  0.000000  0.000000
 0.090909  0.000000  0.000000  0.000000  0.000000  0.090909
0.000000  0.000000  0.181818  0.000000  0.000000  0.090909  0.000000
0.000000  0.090909  0.181818  0.272727  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.545455
0.090909  0.000000  0.272727  0.000000  0.000000  0.090909  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif LLEAIKRDFGSFDNFKEKLTAATVAVQGSGWGWLGYDKETG MEME-7 regular
expression
--------------------------------------------------------------------
LL[ED][AL]IKR[DE]FGSF[DE][NA][FL]K[EK]K[LF][TS][AE]A[TS]V[AG][VI]QGS
GWGWLG[YF][DN]K[EV]T[GK]
--------------------------------------------------------------------




Time 42.09 secs.

********************************************************************


********************************************************************
MOTIF ARLACGVIGIA MEME-8     width =  11  sites =  23  llr = 511  E-
value = 1.5e-082
********************************************************************
--------------------------------------------------------------------
      Motif ARLACGVIGIA MEME-8 Description
--------------------------------------------------------------------
Simplified        A  4::7::::3:3
pos.-specific     C  ::::a1:::::
probability       D  :::::::::::
matrix            E  1::::::::::
                  F  :::::::::::
                  G  3::1:9::6::
                  H  :::::::::::
                  I  ::1:::2a:5:
                  K  :::::::::::
                  L  ::7::::::1:
                  M  :::::::::::
                  N  :::::::::::
                  P  :::::::::::
                  Q  :::::::::::
                  R  1a:::::::2:
                  S  :::1::::::3
                  T  ::::::::::3
                  V  ::2:::7:11:
                  W  :::::::::::
                  Y  :::::::::::

         bits    6.4
                 5.7     *
                 5.1     *
                 4.5  *  *
Relative         3.8  *  *  *
Entropy          3.2  *  ** *
(32.0 bits)      2.5  *******
```

```
                 1.9  **********
                 1.3 ***********
                 0.6 ***********
                 0.0 -----------

Multilevel           ARLACGVIGIA
consensus            G     I ART
sequence                       S


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif ARLACGVIGIA MEME-8 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value               Site
-------------             ----- ---------            -----------
CuZnSOD2_Nematostella       143  8.67e-13 EDSKTTGHAG GRLACGVIGIT QAS
CuZnSOD_Acropora            166  8.67e-13 EESTKTGNAG GRLACGVIGIT K
CuZnSOD_Crassostrea         145  8.67e-13 ELSKTTGNAG GRLACGVIGIT K
CuZnSOD_Ciona               143  8.67e-13 PQSKTTGNAG GRLACGVIGIT K
CuZnSOD_Trichoplax          142  2.09e-12 ELSLTTGNAG ARVACGVIGIT KC
CuZnSOD2_Biomphalaria       144  2.37e-12 EESLKTGNAG PRLACGVIGIT V
CuZnSOD1_Homo               143  6.06e-12 EESTKTGNAG SRLACGVIGIA Q
CuZnSOD1_Nematostella       143  1.20e-11 ELSLTTGNAG GRVACGVIGIA L
CuZnSOD_Amphimedon          153  1.20e-11 PDSLTTGHAG ARLACGVIGST KLQ
CuZnSOD_Capsaspora          140  1.94e-11 ELSKTTGNAG GRLACGVIGVA K
CCS_Homo                    223  3.36e-11 PLSKITGNSG ERLACGIIARS
AGLFQNPKQI
CuZnSOD1_Biomphalaria       113  4.07e-11 EESLKTGNAG ARVACGVIALA
APVEN
CuZn_Hydra                  141  5.98e-11 KDSKTTGNAG ARLSCGVIGLA K
CuZnSOD2_Drosophila         133  7.22e-11 ELSKSTGNAG ARIGCGVIGIA KI
CuZnSOD_Drosophila          140  7.22e-11 ELSKTTGNAG ARIGCGVIGIA KI
CCS_Drosophila              218  1.26e-10 PQSRIDGNSG ERIACGIIARS
AGILQNFKRI
CCS_Amphimedon              207  1.51e-10 HSSIPSVYGT RRLMCGIIARS
AGLFQNTKKV
CuZnSOD_Caenorhabditis      167  1.80e-10 EESKKTGNAG ARAACGVIALA APQ
CuZnSOD3_Biomphalaria       181  2.99e-10 PASLLNGNAG ARLACCSIVIS P
CCS_Nematostella            225  5.87e-10 ELSKSTGNSG ARVGCGIIARS
AGLFQNTKKY
CuZnSOD3_Nematostella       123  8.10e-10 TGSLATGNAG ARLACCVIVHV
CuZnSOD2_Homo               203  9.49e-10 QASVENGNAG RRLACCVVGVC
GPGLWERQAR
CCS_Crassostrea             202  8.64e-09 VVHRGSPNIQ QKLSCGIIARS
AGLFQNSEKK
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
	Motif ARLACGVIGIA MEME-8 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CuZnSOD2_Nematostella             8.7e-13  142_[8]_3
CuZnSOD_Acropora                  8.7e-13  165_[8]_1
CuZnSOD_Crassostrea               8.7e-13  144_[8]_1
CuZnSOD_Ciona                     8.7e-13  142_[8]_1
CuZnSOD_Trichoplax                2.1e-12  141_[8]_2
CuZnSOD2_Biomphalaria             2.4e-12  143_[8]_1
CuZnSOD1_Homo                     6.1e-12  142_[8]_1
CuZnSOD1_Nematostella             1.2e-11  142_[8]_1
CuZnSOD_Amphimedon                1.2e-11  152_[8]_3
CuZnSOD_Capsaspora                1.9e-11  139_[8]_1
CCS_Homo                          3.4e-11  222_[8]_41
CuZnSOD1_Biomphalaria             4.1e-11  112_[8]_5
CuZn_Hydra                          6e-11  140_[8]_1
CuZnSOD2_Drosophila               7.2e-11  132_[8]_2
CuZnSOD_Drosophila                7.2e-11  139_[8]_2
CCS_Drosophila                    1.3e-10  217_[8]_35
CCS_Amphimedon                    1.5e-10  206_[8]_28
CuZnSOD_Caenorhabditis            1.8e-10  166_[8]_3
CuZnSOD3_Biomphalaria               3e-10  180_[8]_1
CCS_Nematostella                  5.9e-10  224_[8]_30
CuZnSOD3_Nematostella             8.1e-10  122_[8]
CuZnSOD2_Homo                     9.5e-10  202_[8]_27
CCS_Crassostrea                   8.6e-09  201_[8]_36
--------------------------------------------------------------------

--------------------------------------------------------------------
	Motif ARLACGVIGIA MEME-8 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF ARLACGVIGIA width=11 seqs=23
CuZnSOD2_Nematostella    (  143) GRLACGVIGIT  1 
CuZnSOD_Acropora         (  166) GRLACGVIGIT  1 
CuZnSOD_Crassostrea      (  145) GRLACGVIGIT  1 
CuZnSOD_Ciona            (  143) GRLACGVIGIT  1 
CuZnSOD_Trichoplax       (  142) ARVACGVIGIT  1 
CuZnSOD2_Biomphalaria    (  144) PRLACGVIGIT  1 
CuZnSOD1_Homo            (  143) SRLACGVIGIA  1 
CuZnSOD1_Nematostella    (  143) GRVACGVIGIA  1 
CuZnSOD_Amphimedon       (  153) ARLACGVIGST  1 
CuZnSOD_Capsaspora       (  140) GRLACGVIGVA  1 
CCS_Homo                 (  223) ERLACGIIARS  1 
CuZnSOD1_Biomphalaria    (  113) ARVACGVIALA  1 
CuZn_Hydra               (  141) ARLSCGVIGLA  1 
CuZnSOD2_Drosophila      (  133) ARIGCGVIGIA  1 
CuZnSOD_Drosophila       (  140) ARIGCGVIGIA  1 
CCS_Drosophila           (  218) ERIACGIIARS  1 
CCS_Amphimedon           (  207) RRLMCGIIARS  1 
```

```
CuZnSOD_Caenorhabditis   (  167) ARAACGVIALA  1
CuZnSOD3_Biomphalaria    (  181) ARLACCSIVIS  1
CCS_Nematostella         (  225) ARVGCGIIARS  1
CuZnSOD3_Nematostella    (  123) ARLACCVIVHV  1
CuZnSOD2_Homo            (  203) RRLACCVVGVC  1
CCS_Crassostrea          (  202) QKLSCGIIARS  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif ARLACGVIGIA MEME-8 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 11 n= 7800 bayes= 7.44201 E= 1.5e-
082
   218   -360   -198     76   -315     88   -264   -348   -122   -
316   -205   -192      4     49    113    -33   -184   -320   -356
-226
  -376   -317   -459   -437   -425   -494   -291   -415    -83   -
392   -332   -355   -334   -222    460   -371   -369   -504   -292
-343
   -99   -395   -656   -570   -270   -693   -625    122   -565
299   -142   -599   -536   -493   -500   -537   -386    115   -465
-387
   317   -163   -423   -360   -309    -42   -465   -327   -376   -
321     66   -397   -412   -353   -325     17   -225   -205   -362
-330
  -409    545   -552   -493   -444   -626   -566   -438   -549   -
478   -362   -531   -516   -501   -450   -475   -395   -510   -542
-475
  -348    222   -445   -488   -540    293   -563   -600   -485   -
609   -483   -424   -488   -499   -431   -378   -458   -557   -504
-478
  -274   -315   -528   -474   -339   -606   -546    177   -493   -
265   -230   -526   -453   -482   -427    -96   -284    322   -510
-432
  -433   -403   -650   -611   -364   -721   -734    397   -601   -
235   -219   -613   -601   -598   -594   -568   -390     -2   -578
-445
   189   -329   -593   -584   -534    237   -638   -555   -607   -
570   -453   -507   -435   -507   -512   -261   -319     12   -570
-532
  -236   -245   -464   -371   -164   -458    -23    292   -334
72    -63   -372   -360   -302    221    -66   -199     41   -270
-177
   208     95   -610   -586   -517   -413   -633   -538   -600   -
549   -426   -501   -432   -494   -507    192    252    -80   -562
-522
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif ARLACGVIGIA MEME-8 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 11 nsites= 23 E= 1.5e-082
 0.434783  0.000000  0.000000  0.086957  0.000000  0.260870
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.043478
0.043478  0.086957  0.043478  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.043478  0.000000  0.000000  0.000000  0.000000
0.000000  0.956522  0.000000  0.000000  0.000000  0.000000  0.000000
 0.043478  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.130435  0.000000  0.652174  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.173913  0.000000  0.000000
 0.739130  0.000000  0.000000  0.000000  0.000000  0.130435
0.000000  0.000000  0.000000  0.000000  0.043478  0.000000  0.000000
0.000000  0.000000  0.086957  0.000000  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.130435  0.000000  0.000000  0.000000  0.869565
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.217391  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.043478  0.000000  0.739130  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.956522  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.043478  0.000000  0.000000
 0.304348  0.000000  0.000000  0.000000  0.000000  0.608696
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.086957  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.043478  0.478261  0.000000  0.130435  0.000000  0.000000  0.000000
0.000000  0.217391  0.043478  0.000000  0.086957  0.000000  0.000000
 0.347826  0.043478  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.260870  0.304348  0.043478  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif ARLACGVIGIA MEME-8 regular expression
--------------------------------------------------------------------
[AG]RLACG[VI]I[GA][IR][ATS]
--------------------------------------------------------------------




Time 46.34 secs.

********************************************************************
```

```
********************************************************************
MOTIF LQGVZGIKSVEVDLDEZQVIVETSLPSSZVQELLESTGRLAVLRGQG MEME-9   width
=  47  sites =  10  llr = 823  E-value = 2.5e-086
********************************************************************
--------------------------------------------------------------------
      Motif LQGVZGIKSVEVDLDEZQVIVETSLPSSZVQELLESTGRLAVLRGQG MEME-9
Description
--------------------------------------------------------------------
Simplified        A  1:1:11:::::::12::::::::11::1:::11:::::::61:::::
pos.-specific     C  :::::::::::::::::1:::::::::::::::::::::::::::::
probability       D  :2::1::21:1:7:311::::2:::::::::2:::::::::::::::
matrix            E  :1::3:::::2:::143::::4::::::2::3::9::1:::::::::
                  F  :::::::::2::::::::::::::::1:::::::::::::::2::2:
                  G  ::5:18:2::::::1:1::::::::1:2:::::::1:9::::::a:a
                  H  ::::::::1:1:1::::::::1::::::::2::::::::::::::2:
                  I  ::::::5::::2:::::::61:::::::1::::3::::::13:::::
                  K  :::1:::3:::::::3:::::1:1::::1::11::2::32:::1:::
                  L  62:2:1::1::::8:::::1::::9::::21:57::::23::6::1:
                  M  ::::::::::1::::::1::::::::1:::::2:::::1:::11:1:
                  N  :12::::11:::1:12:::::::1::::1::1:::1:::::::::::
                  P  ::111:::::::::1::::::::::7:::::::::::::::::::::
                  Q  :21:3::1::1:::::53:::1:::::24:71:::::::1:::1:3:
                  R  11:::::::::::::::3::::::::::::::::::::42:::6:::
                  S  :1:::::16:2:1::::1::::43:165:::11::41::1:::1:::
                  T  1::1::::::1:::1::::::163:11:1::::::29::12::::::
                  V  1::5::5::6:8:1:::1a39::1:::::8::::1:::::16:::::
                  W  ::::::::::::::::::::::::::1::::::::::::::::::::
                  Y  :::::::::21:::::::::::::::::::::::::::::::1::1:

         bits    6.4
                 5.7
                 5.1
                 4.5
Relative         3.8                   *               * *
Entropy          3.2       *  * *      * * * **   **  ** *      ** *
(118.7 bits)     2.5      **  * *** ****** * ***  **  ** *** *******
                 1.9 * ***** ****** **************** ***************
                 1.3 ***********************************************
                 0.6 ***********************************************
                 0.0 -----------------------------------------------

Multilevel           LDGVEGIKSVEVDLDEQQVIVETSLPSSQVQELLESTGRLAVLRGQG
consensus             LNLQ VD FSI  AKER V DST    GELHDMI K  KKTIF  F
sequence              Q     G Y     N           Q       T  LR     H


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LQGVZGIKSVEVDLDEZQVIVETSLPSSZVQELLESTGRLAVLRGQG MEME-9
sites sorted by position p-value
```

```
---------------------------------------------------------------------
Sequence name             Start   P-value                  Site
-------------             ----- ---------            ---------------
CCS_Hydra                    27  2.30e-40 SSCVDKVSSS
LDQLQGIKSFEVDLDKQSVIVTTNLPSSIVQESLESTGMLAVYRGQG ENSVNLGAAV
CCS_Nematostella             32  5.65e-39 EKCVNKVKQV
LDGVQGVSSYSVDLGEQCVIVDTVLPSGQVQEMLEKTELKTILRGHG AGRAGKTAQH
CCS_Crassostrea              31  5.65e-39 EGCVKSVKNS
LQGVEGVKSVHVDLNKDQVVVESSLTSSQVQSLIEKTGKSAVLQGYG GFNETPLESG
CCS_Amphimedon               24  4.44e-36 CKSCEEAVKA
ALNVPGINSVYVDVPNEVVIVETSLPSSNVHKLLESTGKLIVFRGFG GQEQAPTSHQ
CCS_Acropora                 29  5.92e-36 QKCVDAVNNA
LEGKEGIKSFTVNLDNEQVIVETTLSTGKVQELLENSGRLAILRGLG ASGTQVSHLG
CCS_Homo                     33  7.15e-36 QSCVDAVRKS
LQGVAGVQDVEVHLEDQMVLVHTTLPSQEVQALLEGTGRQAVLKGMG SGQLQNLGAA
CCS_Capsaspora               32  1.32e-32 VNEAMQQLKQ
TSPPGAVGSVQVDLAEQRVVVESSLPSSTLLQAIESTGRKTVLRGQG DSFGRNLGSA
CCS_Drosophila               24  5.95e-32 KDVKSCADKL
RRALQGIGHVDIDATEGRVIVQTTAPWSEVQDKIESTGRRAVLSGFG GQSAVALINT
CCS_Ciona                    25  1.11e-30 CNGCVDSVKK
VLNTDLVDLVSVDLDKQRVVVKSKLGFQQVQDMLETTGKRAAFMGHG ASMQRQHLGA
CCS_Trichoplax               26  9.20e-30 NTCVDKVKDA
LNGVEGIDNYMISLAEEQVIIDSALPMAQLHNLLVTTGLTVIMRGQG AATEGASHLG
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif LQGVZGIKSVEVDLDEZQVIVETSLPSSZVQELLESTGRLAVLRGQG MEME-9
block diagrams
---------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CCS_Hydra                         2.3e-40  26_[9]_170
CCS_Nematostella                  5.7e-39  31_[9]_187
CCS_Crassostrea                   5.7e-39  30_[9]_171
CCS_Amphimedon                    4.4e-36  23_[9]_175
CCS_Acropora                      5.9e-36  28_[9]_146
CCS_Homo                          7.2e-36  32_[9]_195
CCS_Capsaspora                    1.3e-32  31_[9]_228
CCS_Drosophila                      6e-32  23_[9]_193
CCS_Ciona                         1.1e-30  24_[9]_192
CCS_Trichoplax                    9.2e-30  25_[9]_179
---------------------------------------------------------------------

---------------------------------------------------------------------
      Motif LQGVZGIKSVEVDLDEZQVIVETSLPSSZVQELLESTGRLAVLRGQG MEME-9
in BLOCKS format
---------------------------------------------------------------------
BL   MOTIF LQGVZGIKSVEVDLDEZQVIVETSLPSSZVQELLESTGRLAVLRGQG width=47
seqs=10
CCS_Hydra                (   27)
LDQLQGIKSFEVDLDKQSVIVTTNLPSSIVQESLESTGMLAVYRGQG  1
```

```
CCS_Nematostella         (   32)
LDGVQGVSSYSVDLGEQCVIVDTVLPSGQVQEMLEKTELKTILRGHG  1
CCS_Crassostrea          (   31)
LQGVEGVKSVHVDLNKDQVVVESSLTSSQVQSLIEKTGKSAVLQGYG  1
CCS_Amphimedon           (   24)
ALNVPGINSVYVDVPNEVVIVETSLPSSNVHKLLESTGKLIVFRGFG  1
CCS_Acropora             (   29)
LEGKEGIKSFTVNLDNEQVIVETTLSTGKVQELLENSGRLAILRGLG  1
CCS_Homo                 (   33)
LQGVAGVQDVEVHLEDQMVLVHTTLPSQEVQALLEGTGRQAVLKGMG  1
CCS_Capsaspora           (   32)
TSPPGAVGSVQVDLAEQRVVVESSLPSSTLLQAIESTGRKTVLRGQG  1
CCS_Drosophila           (   24)
RRALQGIGHVDIDATEGRVIVQTTAPWSEVQDKIESTGRRAVLSGFG  1
CCS_Ciona                (   25)
VLNTDLVDLVSVDLDKQRVVVKSKLGFQQVQDMLETTGKRAAFMGHG  1
CCS_Trichoplax           (   26)
LNGVEGIDNYMISLAEEQVIIDSALPMAQLHNLLVTTGLTVIMRGQG  1
//

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--------------------------------------------------------------------
      Motif LQGVZGIKSVEVDLDEZQVIVETSLPSSZVQELLESTGRLAVLRGQG MEME-9
position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 47 n= 6324 bayes= 7.83372 E= 2.5e-
086
   -49   -227   -409   -309    -93   -438   -349    -66   -289
297     35   -341   -302   -233     37   -265      8     -3   -232
-155
  -111   -294    131     95   -215   -277   -160   -250    -20
71   -104     66   -173    205    122     49    -85   -231   -256
-122
   -27   -343   -172   -195   -358    240   -302   -407   -208   -
398   -280    109     47     65   -203   -177   -234   -380   -359
-268
  -122   -170   -337   -259   -136   -395   -312    -12    -21
51    -42   -299     25   -227   -199   -227     25    282   -245
-163
    15   -417     85    244   -334    -57   -257   -342   -103   -
309   -200   -178     97    267   -135   -174   -177   -311   -373
-233
   -79   -348   -277   -319   -392    289   -406   -438   -316   -
137   -322   -256   -352   -342   -267   -235   -325   -409   -354
-324
  -331   -302   -565   -521   -276   -631   -643    310   -516   -
154   -135   -527   -508   -512   -506   -480   -292    253   -496
-360
  -186   -348    158    -83   -292     45   -201   -341    206   -
307   -200     97   -233    133   -108     56   -143   -323   -334
```

```
-185
  -205   -287     49   -156   -305   -300     55   -363   -164    -
35   -234     70   -261   -150   -170    299    -12   -366   -353
-218
  -432   -375   -550   -513    279   -587   -271   -264   -479   -
255   -218   -426   -469   -380   -386   -427   -384    275    -94
345
  -105   -287     54    154   -204   -274     71   -242    -15   -
208    189    -93   -168    135    -24    115     72   -224   -247
172
  -204   -242   -456   -403   -261   -540   -476    157   -422   -
185   -151   -455   -382   -411   -357   -393   -212    326   -437
-358
  -327   -390    384    -86   -365   -397    -77   -411   -336   -
420   -331    -11   -391   -287   -313   -113   -320   -414   -380
-284
   -78   -296   -484   -381   -111   -528   -424    -82   -372
327     31   -430   -350   -286   -291   -360   -274    -25   -284
-224
    93   -322    199     95   -253    -53   -184   -292    -59   -
259   -149     81     93    -41    -71   -101     73   -273   -295
-155
  -232   -468     95    277   -410   -345   -288   -416    207   -
383   -281    163   -277    -91   -194   -197   -223   -380   -447
-290
  -235   -540     94    256   -465    -54   -323   -426   -172   -
391   -285   -216   -284    346   -236   -246   -255   -382   -490
-344
  -132    155   -185    -91   -154   -316   -201   -134    -58   -
144    207   -156   -213    260    248     39   -103     21   -227
-116
  -241   -289   -479   -437   -309   -536   -494    -73   -454   -
250   -213   -484   -402   -437   -382   -408   -258    354   -450
-381
  -313   -314   -427   -398   -207   -532   -499    350   -372
13    -28   -396   -417   -369   -361   -355   -252    134   -353
-239
  -170   -222   -419   -366   -248   -508   -433     85   -386   -
183   -145   -423   -346   -374   -315   -359   -185    335   -406
-343
  -161   -378    152    265   -297   -331     77   -315     79   -
281   -171   -153   -220    137   -100   -147     68   -289   -336
-198
  -204   -236   -358   -373   -323   -412   -407   -285   -312   -
365   -189   -219   -325   -271   -270    216    351   -270   -362
-318
   -32   -232   -225   -166   -254   -358   -274   -259      9   -
277   -145     12   -247   -131   -137    233    255    -55   -300
-202
   -67   -309   -492   -392   -116   -522   -435   -103   -384
336     24   -441   -357   -295   -300   -359   -289   -182   -291
```

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-233
  -161   -320   -307   -265   -317   -111   -362   -345   -260   -
308   -261   -322    426   -225   -239    -11     12   -321   -402
-325
  -175   -193   -320   -330     -5   -382   -363   -276   -266   -
285     68   -180   -268   -269   -217    330    132   -307     98
-199
    55   -233   -291   -274   -382     65   -385   -424   -288   -
409   -295   -247   -300    226   -273    273   -170   -335   -425
-333
  -126   -302   -118    152   -229   -295   -160     16     83   -
222   -109     56   -186    309    -33    -99     63   -242   -262
-137
  -252   -273   -508   -451   -217   -572   -515    -21   -464
107   -108   -493   -423   -434   -401   -427   -251    323   -410
-331
  -267   -323   -356    -95   -344   -489     15   -348   -250   -
157   -104   -252   -274    448   -147   -276   -270   -366   -272
-294
    19   -323    141    215   -244   -295   -185   -275     85   -
241   -130     66   -191    136    -57     46   -109   -254   -284
-149
   -30   -221   -341   -245    -99   -405   -312    -73      3
275    268   -288   -281   -188   -183    -19   -164   -114   -226
-142
  -392   -355   -609   -512   -118   -641   -531    211   -503
308      0   -551   -459   -393   -417   -494   -351   -165   -321
-274
  -479   -575   -212    413   -543   -583   -525   -512   -499   -
576   -481   -433   -559   -325   -482   -507   -494   -333   -547
-494
  -185   -261   -154   -161   -289    -91   -259   -340    104   -
324   -208     48   -252   -143   -147    273    166   -342   -334
-211
  -231   -241   -357   -368   -314   -448   -398   -261   -300   -
353   -168   -209   -331   -256   -261     64    392   -249   -352
-317
  -221   -364   -272    -72   -397    295   -404   -447   -313   -
470   -328   -252   -357   -341   -266   -244   -339   -423   -355
-325
  -297   -398   -374   -214   -383   -436   -253   -342    238
101    219   -253   -345    -77    325   -272   -243   -345   -341
-254
  -170   -330   -184    -84   -269   -332   -195   -282    176
140   -141   -151   -230    139    220     42     72   -270   -286
-167
   290   -140   -395   -324   -213   -291   -409     34   -331   -
194   -113   -356   -365   -305   -284   -117    108     19   -301
-239
   -16   -229   -435   -381   -248   -515   -448    191   -398   -
180   -141   -432   -361   -384   -331   -365   -195    303   -409
```

```
-334
  -366   -336   -540   -441    219   -582   -424   -109   -430
300    216   -474   -401   -330   -344   -420   -322   -202   -248
176
  -305   -333   -361   -255   -389   -439   -254   -372     59   -
336    129   -272   -313     62    420    -47   -272   -401   -297
-276
  -275   -407   -330   -374   -441    304   -454   -500   -371   -
514   -383   -311   -399   -395   -320   -299   -389   -475   -399
-372
  -241   -255   -336   -270    253   -430    206   -180   -270
14    206   -266   -312    254   -212   -243   -217   -201   -102
298
  -275   -407   -330   -374   -441    304   -454   -500   -371   -
514   -383   -311   -399   -395   -320   -299   -389   -475   -399
-372
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LQGVZGIKSVEVDLDEZQVIVETSLPSSZVQELLESTGRLAVLRGQG MEME-9
position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 47 nsites= 10 E= 2.5e-086
 0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.600000  0.000000  0.000000  0.000000
0.000000  0.100000  0.000000  0.100000  0.100000  0.000000  0.000000
 0.000000  0.000000  0.200000  0.100000  0.000000  0.000000
0.000000  0.000000  0.000000  0.200000  0.000000  0.100000  0.000000
0.200000  0.100000  0.100000  0.000000  0.000000  0.000000  0.000000
 0.100000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.200000  0.100000
0.100000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.100000  0.200000  0.000000  0.000000  0.100000
0.000000  0.000000  0.000000  0.100000  0.500000  0.000000  0.000000
 0.100000  0.000000  0.100000  0.300000  0.000000  0.100000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.100000
0.300000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.100000  0.000000  0.000000  0.000000  0.000000  0.800000
0.000000  0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.200000  0.000000  0.000000  0.200000
0.000000  0.000000  0.300000  0.000000  0.000000  0.100000  0.000000
0.100000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
0.100000  0.000000  0.000000  0.100000  0.000000  0.100000  0.000000
0.000000  0.000000  0.600000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
```

```
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.600000  0.000000  0.200000
 0.000000  0.000000  0.100000  0.200000  0.000000  0.000000
0.100000  0.000000  0.000000  0.000000  0.100000  0.000000  0.000000
0.100000  0.000000  0.200000  0.100000  0.000000  0.000000  0.100000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.200000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.800000  0.000000  0.000000
 0.000000  0.000000  0.700000  0.000000  0.000000  0.000000
0.100000  0.000000  0.000000  0.000000  0.000000  0.100000  0.000000
0.000000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
 0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.800000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.100000  0.000000  0.000000
 0.200000  0.000000  0.300000  0.100000  0.000000  0.100000
0.000000  0.000000  0.000000  0.000000  0.000000  0.100000  0.100000
0.000000  0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.100000  0.400000  0.000000  0.000000
0.000000  0.000000  0.300000  0.000000  0.000000  0.200000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.100000  0.300000  0.000000  0.100000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.100000  0.000000  0.000000
0.300000  0.300000  0.100000  0.000000  0.100000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.600000  0.000000  0.100000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.300000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.900000  0.000000  0.000000
 0.000000  0.000000  0.200000  0.400000  0.000000  0.000000
0.100000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
0.100000  0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.400000  0.600000  0.000000  0.000000  0.000000
 0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.100000  0.000000  0.000000  0.100000  0.000000
0.000000  0.000000  0.300000  0.300000  0.100000  0.000000  0.000000
 0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.900000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.100000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.700000
0.000000  0.000000  0.100000  0.100000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.100000  0.000000
```

```
0.000000  0.000000  0.000000  0.000000  0.100000  0.000000  0.000000
0.000000  0.000000  0.600000  0.100000  0.000000  0.100000  0.000000
 0.100000  0.000000  0.000000  0.000000  0.000000  0.200000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
0.000000  0.100000  0.100000  0.000000  0.000000  0.100000  0.000000
0.400000  0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.800000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.200000  0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
0.700000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.100000  0.000000  0.200000  0.300000  0.000000  0.000000
0.000000  0.000000  0.100000  0.000000  0.000000  0.100000  0.000000
0.100000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
 0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.100000  0.500000  0.200000  0.000000  0.000000
0.000000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.300000  0.000000  0.700000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.900000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.100000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.100000
0.000000  0.000000  0.200000  0.000000  0.000000  0.100000  0.000000
0.000000  0.000000  0.400000  0.200000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.100000  0.900000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.100000  0.000000  0.900000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.300000  0.200000  0.100000  0.000000  0.000000
0.000000  0.400000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.300000  0.000000  0.000000  0.000000
0.100000  0.200000  0.100000  0.100000  0.000000  0.000000  0.000000
 0.600000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.200000  0.100000  0.000000  0.000000
 0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.300000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.600000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
0.000000  0.000000  0.000000  0.600000  0.100000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.100000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.100000  0.000000  0.100000  0.000000  0.000000
0.100000  0.600000  0.100000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
0.200000  0.000000  0.000000  0.100000  0.100000  0.000000  0.000000
0.300000  0.000000  0.000000  0.000000  0.000000  0.000000  0.100000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif LQGVZGIKSVEVDLDEZQVIVETSLPSSZVQELLESTGRLAVLRGQG MEME-9
regular expression
--------------------------------------------------------------------
L[DLQ][GN][VL][EQ]G[IV][KDG]S[VFY][ES][VI]DL[DA][EKN][QE][QR]V[IV]V[
ED][TS][ST]LPS[SGQ][QE][VL][QH][ED][LM][LI]E[SKT]TG[RKL][LKR][AT][VI
][LF]RG[QFH]G
--------------------------------------------------------------------




Time 50.44 secs.

********************************************************************


********************************************************************
MOTIF VKGTVRFVQESPGKP MEME-10     width =  15  sites =  26  llr =
556  E-value = 2.8e-061
********************************************************************
--------------------------------------------------------------------
     Motif VKGTVRFVQESPGKP MEME-10 Description
--------------------------------------------------------------------
Simplified        A  1:::::::::21:1:
pos.-specific     C  ::::::::::::::4
probability       D  ::::::::1:1121:
matrix            E  :::::::2:21212:
                  F  :::::18::::::::
                  G  ::a:::::::2131:
                  H  :::::::::::::::
                  I  1::14::::1:::::
                  K  :4:::1:::2:::21
                  L  :::2::11:2:::::
                  M  :::::::::::::::
                  N  :::::1::::::2::
                  P  :::::::::::2::3
                  Q  :2::::::9::1:::
```

```
                 R  :::::4:::::::::
                 S  :1:::::1::3211:
                 T  :2:4:::2::1:::1
                 V  8::35::3:2:::::
                 W  :::::::::::::::
                 Y  :::::::::::::::

         bits    6.4
                 5.7
                 5.1
                 4.5       *
Relative         3.8       * *
Entropy          3.2   *   * *
(30.9 bits)      2.5 * * * * *     *
                 1.9 ******* *     *
                 1.3 ************* *
                 0.6 ***************
                 0.0 ---------------

Multilevel           VKGTVRFVQESPGXC
consensus               VI  T    N P
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif VKGTVRFVQESPGKP MEME-10 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
CuZnSOD2_Nematostella        15  6.04e-14 AVCCMSGTEG VKGTIKFVQEAEGKP
CKITGTIEGL
CCS_Trichoplax               93  9.96e-14 AAVSILSGTS VKGLVRFTQLSADKC
MIEGTVDNLR
CCS_Capsaspora              100  2.56e-13 SILERDGTQD VIGVVRFVQISENEC
VIEGTLDGLS
CCS_Homo                     99  6.16e-13 AVAILGGPGT VQGVVRFLQLTPERC
LIEGTIDGLE
CuZnSOD1_Nematostella        15  4.43e-12 GVCCLVGDNE VKGVIHFTQQAPDGP
CTLRGRITGL
CuZnSOD_Crassostrea          17  5.00e-12 AVCVLKGDSN VTGTVQFSQEAPGSP
VTLSGEIKGL
CuZnSOD_Drosophila           12  1.28e-11 VKAVCVINGD AKGTVFFEQETSEAP
VKVTGEVLGL
CuZnSOD1_Homo                15  1.43e-11 AVCVLKGDGP VQGIINFEQKESNGP
VKVWGSIKGL
CuZnSOD2_Drosophila           5  2.00e-11       INGD AKGTVFFEQEGSGAP
VKVTGEVTGL
CuZnSOD_Ciona                15  2.00e-11 AVCVMKGSES VSGTIKFSQVGDGEP
CKISGSLTGL
```

```
CuZnSOD_Trichoplax           14  4.72e-11 KAVCCLQGPV VSGTIFFQQESGTGP
IRISGEVKGL
CCS_Nematostella            101  5.80e-11 AAVAMIDCEK VQGLTRFVQVSGDNC
IIDGTIDGLT
CuZnSOD2_Biomphalaria        16  1.06e-10 CVLSPGSATG ITGTITFTQEKAGDC
TVVSGKVSGL
CuZnSOD_Acropora             40  1.73e-10 CVLLESKSKE VKGVINFEQKQGECR
IYGELTGLTP
CCS_Acropora                 96  2.53e-10 AAVAEMSSGS VLGVARFVQVSEDVC
IIDGAVDGLT
CCS_Ciona                    91  4.83e-10 AAVAEISGRF VKGVVRLLQLDQNLC
LIEGTVDGLS
CuZnSOD_Caenorhabditis       36  5.28e-10 RAVAVLRGET VTGTIWITQKSENDQ
AVIEGEIKGL
CCS_Hydra                    92  5.78e-10 AVAILKNDHQ TYGLVRFVQKDLNSC
IIDGSISKLS
CuZn_Hydra                   13  7.55e-10 KSAICVLEGI VKGTIKFEDIGDGKT
HVSGKITGLQ
CCS_Crassostrea              98  1.07e-09 VVQLNAGDSN IQGVIRLVQSNPSKC
IIDGTIDGLP
CuZnSOD3_Biomphalaria        44  1.17e-09 LQPDPASTQK VSGIVIFNQTGPSEP
LKMTIHLSGF
CuZnSOD_Amphimedon           27  1.39e-09 AVCILASSDD VKGTIEFIQNEQGIT
KVTGKVTSLA
CCS_Amphimedon               93  1.39e-09 AVVVMKGSGP VNGLLRMVQVSSNEC
VIEGTIDGLT
CuZnSOD2_Homo                78  1.65e-09 SATLDAAQPR VTGVVLFRQLAPRAK
LDAFFALEGF
CCS_Drosophila               90  6.30e-08 TTGCVVDRTP VQGAVRFTTITDKHA
GVVVDGVVDG
CuZnSOD_Capsaspora           14  7.26e-08 LVAVLKGDGA VKGTVVFTDDGAATK
VEGTIEGLAP
--------------------------------------------------------------------


--------------------------------------------------------------------
      Motif VKGTVRFVQESPGKP MEME-10 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CuZnSOD2_Nematostella               6e-14  14_[10]_127
CCS_Trichoplax                      1e-13  92_[10]_144
CCS_Capsaspora                    2.6e-13  99_[10]_192
CCS_Homo                          6.2e-13  98_[10]_161
CuZnSOD1_Nematostella             4.4e-12  14_[10]_125
CuZnSOD_Crassostrea                 5e-12  16_[10]_125
CuZnSOD_Drosophila                1.3e-11  11_[10]_126
CuZnSOD1_Homo                     1.4e-11  14_[10]_125
CuZnSOD2_Drosophila                 2e-11  4_[10]_126
CuZnSOD_Ciona                       2e-11  14_[10]_125
CuZnSOD_Trichoplax                4.7e-11  13_[10]_126
CCS_Nematostella                  5.8e-11  100_[10]_150
```

```
CuZnSOD2_Biomphalaria            1.1e-10  15_[10]_125
CuZnSOD_Acropora                 1.7e-10  39_[10]_123
CCS_Acropora                     2.5e-10  95_[10]_111
CCS_Ciona                        4.8e-10  90_[10]_158
CuZnSOD_Caenorhabditis           5.3e-10  35_[10]_130
CCS_Hydra                        5.8e-10  91_[10]_137
CuZn_Hydra                       7.6e-10  12_[10]_125
CCS_Crassostrea                  1.1e-09  97_[10]_136
CuZnSOD3_Biomphalaria            1.2e-09  43_[10]_134
CuZnSOD_Amphimedon               1.4e-09  26_[10]_125
CCS_Amphimedon                   1.4e-09  92_[10]_138
CuZnSOD2_Homo                    1.6e-09  77_[10]_148
CCS_Drosophila                   6.3e-08  89_[10]_159
CuZnSOD_Capsaspora               7.3e-08  13_[10]_123
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif VKGTVRFVQESPGKP MEME-10 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF VKGTVRFVQESPGKP width=15 seqs=26
CuZnSOD2_Nematostella    (   15) VKGTIKFVQEAEGKP  1
CCS_Trichoplax           (   93) VKGLVRFTQLSADKC  1
CCS_Capsaspora           (  100) VIGVVRFVQISENEC  1
CCS_Homo                 (   99) VQGVVRFLQLTPERC  1
CuZnSOD1_Nematostella    (   15) VKGVIHFTQQAPDGP  1
CuZnSOD_Crassostrea      (   17) VTGTVQFSQEAPGSP  1
CuZnSOD_Drosophila       (   12) AKGTVFFEQETSEAP  1
CuZnSOD1_Homo            (   15) VQGIINFEQKESNGP  1
CuZnSOD2_Drosophila      (    5) AKGTVFFEQEGSGAP  1
CuZnSOD_Ciona            (   15) VSGTIKFSQVGDGEP  1
CuZnSOD_Trichoplax       (   14) VSGTIFFQQESGTGP  1
CCS_Nematostella         (  101) VQGLTRFVQVSGDNC  1
CuZnSOD2_Biomphalaria    (   16) ITGTITFTQEKAGDC  1
CuZnSOD_Acropora         (   40) VKGVINFEQKQGECR  1
CCS_Acropora             (   96) VLGVARFVQVSEDVC  1
CCS_Ciona                (   91) VKGVVRLLQLDQNLC  1
CuZnSOD_Caenorhabditis   (   36) VTGTIWITQKSENDQ  1
CCS_Hydra                (   92) TYGLVRFVQKDLNSC  1
CuZn_Hydra               (   13) VKGTIKFEDIGDGKT  1
CCS_Crassostrea          (   98) IQGVIRLVQSNPSKC  1
CuZnSOD3_Biomphalaria    (   44) VSGIVIFNQTGPSEP  1
CuZnSOD_Amphimedon       (   27) VKGTIEFIQNEQGIT  1
CCS_Amphimedon           (   93) VNGLLRMVQVSSNEC  1
CuZnSOD2_Homo            (   78) VTGVVLFRQLAPRAK  1
CCS_Drosophila           (   90) VQGAVRFTTITDKHA  1
CuZnSOD_Capsaspora       (   14) VKGTVVFTDDGAATK  1
//

--------------------------------------------------------------------
```

```
----------------------------------------------------------------
     Motif VKGTVRFVQESPGKP MEME-10 position-specific scoring matrix
----------------------------------------------------------------
log-odds matrix: alength= 20 w= 15 n= 7636 bayes= 7.94791 E= 2.8e-
061
   -56   -211   -383   -330   -253   -479   -390     37   -352   -
213   -161   -395   -311   -339   -274   -328    -85    331   -380
-342
  -207   -379   -212   -122   -301   -376   -256    -67    252   -
100   -190    -30   -270    223   -113     69    138   -313   -343
81
  -485   -591   -531   -579   -622    312   -642   -700   -574   -
694   -587   -519   -572   -590   -517   -506   -586   -677   -577
-558
  -100   -369   -644   -564   -321   -646   -604     71   -552
94   -212   -563   -540   -513   -508   -479    291    199   -475
-370
  -108   -400   -671   -614   -375   -715   -705    289   -609    -
78   -245   -620   -597   -593   -585   -560    -46    253   -571
-446
  -198   -372   -202     -1    166   -368    -21    -67    102   -
100   -182     45   -261     43    306   -170    -19    -99    133
-205
  -380   -291   -481   -449    486   -566   -498   -133   -469    -
60      8   -478   -394   -452   -435   -358   -413   -311   -198
-19
  -208   -327   -240    163   -249   -389   -277    -47   -146     -
9   -145    -36   -284     32     21     20    193    154   -318   -
200
  -314   -376    -59   -141   -405   -500   -151   -408   -300   -
308   -165   -270   -325    454   -205   -309   -124   -422   -332
-351
  -197   -372    -38    188   -293   -367   -249     74    135
69   -183    -28   -261     43   -118    -43    -19     72   -337
-205
    78   -391     40     62   -314     48   -257   -351     -5   -
317   -205    -24   -272     40   -130    177    102   -332   -355
-220
    42   -415     91    149   -336    -20   -279   -366   -136   -
105   -221   -210    233    112   -150    104   -202   -345   -377
-242
   -80   -416    131    106   -345    100   -277   -386    -15   -
352   -242    193   -298   -136     21     25    -25   -367   -387
-247
    43     48     37    139   -298    -23    -21    -70    135   -
102   -187    -27   -258    -91     31     24    -19   -102   -338
-205
   -97    382   -376   -278   -424   -479   -362   -427     59   -
390   -305   -331    323     17     34   -297     41   -414   -442
-344
----------------------------------------------------------------
```

```
--------------------------------------------------------------------------------
      Motif VKGTVRFVQESPGKP MEME-10 position-specific probability
matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 15 nsites= 26 E= 2.8e-061
 0.076923  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.076923  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.038462  0.807692  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.038462  0.384615  0.038462  0.000000  0.038462  0.000000
0.192308  0.000000  0.115385  0.153846  0.000000  0.000000  0.038462
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.038462  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.076923  0.000000  0.153846  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.423077  0.307692  0.000000  0.000000
 0.038462  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.423077  0.000000  0.038462  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.038462  0.461538  0.000000  0.000000
 0.000000  0.000000  0.000000  0.038462  0.115385  0.000000
0.038462  0.038462  0.115385  0.038462  0.000000  0.076923  0.000000
0.038462  0.384615  0.000000  0.038462  0.038462  0.038462  0.000000
 0.000000  0.000000  0.000000  0.000000  0.846154  0.000000
0.000000  0.038462  0.000000  0.076923  0.038462  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.192308  0.000000  0.000000
0.000000  0.038462  0.000000  0.076923  0.000000  0.038462  0.000000
0.038462  0.038462  0.076923  0.230769  0.269231  0.000000  0.000000
 0.000000  0.000000  0.076923  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.884615  0.000000  0.000000  0.038462  0.000000  0.000000  0.000000
 0.000000  0.000000  0.038462  0.230769  0.000000  0.000000
0.000000  0.115385  0.153846  0.153846  0.000000  0.038462  0.000000
0.038462  0.000000  0.038462  0.038462  0.153846  0.000000  0.000000
 0.153846  0.000000  0.076923  0.076923  0.000000  0.192308
0.000000  0.000000  0.038462  0.000000  0.000000  0.038462  0.000000
0.038462  0.000000  0.269231  0.115385  0.000000  0.000000  0.000000
 0.115385  0.000000  0.115385  0.153846  0.000000  0.115385
0.000000  0.000000  0.000000  0.038462  0.000000  0.000000  0.230769
0.076923  0.000000  0.153846  0.000000  0.000000  0.000000  0.000000
 0.038462  0.000000  0.153846  0.115385  0.000000  0.269231
0.000000  0.000000  0.038462  0.000000  0.000000  0.230769  0.000000
0.000000  0.038462  0.076923  0.038462  0.000000  0.000000  0.000000
 0.115385  0.038462  0.076923  0.153846  0.000000  0.115385
0.038462  0.038462  0.153846  0.038462  0.000000  0.038462  0.000000
0.000000  0.038462  0.076923  0.038462  0.038462  0.000000  0.000000
 0.038462  0.384615  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.076923  0.000000  0.000000  0.000000  0.346154
0.038462  0.038462  0.000000  0.076923  0.000000  0.000000  0.000000
--------------------------------------------------------------------------------
```

```
----------------------------------------------------------------------
     Motif VKGTVRFVQESPGKP MEME-10 regular expression
----------------------------------------------------------------------
VKG[TV][VI]RF[VT]QESP[GN]X[CP]
----------------------------------------------------------------------



Time 53.62 secs.

**********************************************************************


**********************************************************************
MOTIF TKMEFAVQMTCESCV MEME-11     width =  15  sites =  10  llr =
354  E-value = 3.3e-057
**********************************************************************
----------------------------------------------------------------------
     Motif TKMEFAVQMTCESCV MEME-11 Description
----------------------------------------------------------------------
Simplified        A  1::::9::::::1::
pos.-specific     C  1:::::::::8::9:
probability       D  1::::::::111:::
matrix            E  :1:a:::3:::2::2
                  F  ::::a::::::::::
                  G  :::::::::::12::
                  H  :::::::1:::::::
                  I  1:1::::::::::::
                  K  :4::::::::1121:
                  L  ::1::::::::::::
                  M  ::7:::::a::::::
                  N  :::::::2:::2:::
                  P  :::::::::::::::
                  Q  :::::::3:::2:::
                  R  :2:::::1:::::::
                  S  :::::1:::::13:1
                  T  511::::::9::1::
                  V  :2::::a:::::1:7
                  W  :::::::::::::::
                  Y  1::::::::::::::

         bits    6.4
                 5.7         *
                 5.1     *   *    *
                 4.5    **   * *  *
Relative         3.8   *** * ***  *
Entropy          3.2   ***** ***  *
(51.1 bits)      2.5 * *********  **
                 1.9 ***********  **
                 1.3 ***************
                 0.6 ***************
```

```
                 0.0 ---------------

Multilevel           TKMEFAVEMTCESCV
consensus             R     Q   NG E
sequence              V     N   QK

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif TKMEFAVQMTCESCV MEME-11 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
CCS_Nematostella             11  7.84e-20 MASMSEVPTE TRMEFAVEMTCEKCV
NKVKQVLDGV
CCS_Amphimedon                4  6.99e-19        MAD TKMEFAVQMTCKSCE
EAVKAALNVP
CCS_Trichoplax                5  1.39e-18       MATP TRMEFAVHMTCNTCV
DKVKDALNGV
CCS_Acropora                  8  2.88e-18    MASNTSV IKMEFAVRMTCQKCV
DAVNNALEGK
CCS_Ciona                     5  2.88e-18       MDVQ TEMEFAVEMTCNGCV
DSVKKVLNTD
CCS_Crassostrea              10  7.52e-17  MAASSGQEN AVMEFAVNMTCEGCV
KSVKNSLQGV
CCS_Homo                     12  2.82e-16 ASDSGNQGTL CTLEFAVQMTCQSCV
DAVRKSLQGV
CCS_Capsaspora                5  3.09e-14       MSSS YVTEFAVEMTCGACE
KAVNEAMQQL
CCS_Hydra                     6  5.72e-14      MENLF DKMEFSVNMTDSSCV
DKVSSSLDQL
CCS_Drosophila                4  5.36e-10        MDS TKIEFAVQMDKDVKS
CADKLRRALQ
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif TKMEFAVQMTCESCV MEME-11 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CCS_Nematostella                  7.8e-20  10_[11]_240
CCS_Amphimedon                      7e-19  3_[11]_227
CCS_Trichoplax                    1.4e-18  4_[11]_232
CCS_Acropora                      2.9e-18  7_[11]_199
CCS_Ciona                         2.9e-18  4_[11]_244
CCS_Crassostrea                   7.5e-17  9_[11]_224
CCS_Homo                          2.8e-16  11_[11]_248
CCS_Capsaspora                    3.1e-14  4_[11]_287
CCS_Hydra                         5.7e-14  5_[11]_223
CCS_Drosophila                    5.4e-10  3_[11]_245
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif TKMEFAVQMTCESCV MEME-11 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF TKMEFAVQMTCESCV width=15 seqs=10
CCS_Nematostella         (   11) TRMEFAVEMTCEKCV  1
CCS_Amphimedon           (    4) TKMEFAVQMTCKSCE  1
CCS_Trichoplax           (    5) TRMEFAVHMTCNTCV  1
CCS_Acropora             (    8) IKMEFAVRMTCQKCV  1
CCS_Ciona                (    5) TEMEFAVEMTCNGCV  1
CCS_Crassostrea          (   10) AVMEFAVNMTCEGCV  1
CCS_Homo                 (   12) CTLEFAVQMTCQSCV  1
CCS_Capsaspora           (    5) YVTEFAVEMTCGACE  1
CCS_Hydra                (    6) DKMEFSVNMTDSSCV  1
CCS_Drosophila           (    4) TKIEFAVQMDKDVKS  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif TKMEFAVQMTCESCV MEME-11 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 15 n= 7636 bayes= 11.0499 E= 3.3e-
057
    -6    141     10   -240   -154   -385   -303     48   -216   -
152    -50   -210   -276   -183   -190    -71    317   -126   -241
162
  -208   -358   -227     78   -311   -365   -216   -311    260   -
273   -170   -182   -265    -48    229   -181     71     94   -309
-198
  -402   -353   -538   -501   -240   -581   -523    -49   -472    -
49    558   -500   -455   -429   -449   -438    -85   -253   -299
-249
  -505   -578   -224    414   -549   -593   -535   -529   -544   -
595   -499   -443   -585   -348   -502   -529   -514   -575   -549
-502
  -388   -300   -478   -454    495   -551   -467   -274   -471   -
182   -187   -473   -393   -450   -430   -363   -418   -330   -195
-11
   329   -132   -393   -336   -286   -256   -435   -306   -353   -
299   -192   -357   -352   -320   -298     32   -183   -183   -337
-304
  -241   -289   -479   -437   -309   -536   -494    -73   -454   -
250   -213   -484   -402   -437   -382   -408   -258    354   -450
-381
  -159   -335   -119    209   -269   -309     79   -296    -33   -
259   -148    147   -216    274    128   -125   -131   -278   -297
-168
  -462   -387   -536   -522   -345   -595   -551   -267   -488   -
200    576   -517   -470   -463   -485   -464   -418   -353   -310
-266
  -271   -282     22   -332   -346   -445   -400   -300   -314   -
```

```
387   -209   -210   -353   -273   -285    -61    395   -290   -382
-333
  -384    542   -313   -455   -423   -592   -533   -416   -312   -
456   -339   -471   -493   -462   -413   -439   -369   -486   -522
-449
  -139   -318     69    163   -245    -54   -180   -283     85   -
249   -139    152   -196    210    -61     51   -109   -264   -287
-148
    33   -252   -156    -71   -221     29   -203   -236    149   -
222   -115   -135   -202    -51    -70    181     83      2   -272
-149
  -388    544   -532   -472   -424   -608   -547   -417   -335   -
458   -341   -510   -499   -479   -427   -453   -374   -488   -524
-455
  -134   -220   -240    108   -247   -392   -357    -62   -262   -
215   -151   -299   -290   -222   -238    -20   -162    307   -356
-280
---------------------------------------------------------------------

---------------------------------------------------------------------
     Motif TKMEFAVQMTCESCV MEME-11 position-specific probability
matrix
---------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 15 nsites= 10 E= 3.3e-057
 0.100000  0.100000  0.100000  0.000000  0.000000  0.000000
0.000000  0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.100000
 0.000000  0.000000  0.000000  0.100000  0.000000  0.000000
0.000000  0.000000  0.400000  0.000000  0.000000  0.000000  0.000000
0.000000  0.200000  0.000000  0.100000  0.200000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.100000  0.000000  0.100000  0.700000  0.000000  0.000000
0.000000  0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.900000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.300000  0.000000  0.000000
0.100000  0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
0.300000  0.100000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.900000  0.000000  0.000000  0.000000
 0.000000  0.800000  0.100000  0.000000  0.000000  0.000000
0.000000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.100000  0.200000  0.000000  0.100000
0.000000  0.000000  0.100000  0.000000  0.000000  0.200000  0.000000
0.200000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
 0.100000  0.000000  0.000000  0.000000  0.000000  0.200000
0.000000  0.000000  0.200000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.300000  0.100000  0.100000  0.000000  0.000000
 0.000000  0.900000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.100000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.200000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.100000  0.000000  0.700000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif TKMEFAVQMTCESCV MEME-11 regular expression
--------------------------------------------------------------------
T[KRV]MEFAV[EQN]MTC[ENQ][SGK]C[VE]
--------------------------------------------------------------------




Time 55.96 secs.

********************************************************************


********************************************************************
MOTIF LFQNSKKICACDGVTJWEERN MEME-12     width =  21  sites =   9
llr = 428  E-value = 8.8e-064
********************************************************************
--------------------------------------------------------------------
      Motif LFQNSKKICACDGVTJWEERN MEME-12 Description
--------------------------------------------------------------------
Simplified        A  ::::1::::6:::::::::11
pos.-specific     C  ::::::::a:a::::::::::
probability       D  :::::::::::9:::::33::
matrix            E  ::2:1::::::::::::47:1
                  F  16::1::1:::::::::::::
                  G  ::1:::::::::a:::::::1
                  H  :::::::::::::::::::::
                  I  1::::::3:::::::3:::::
                  K  :::::a6::::::3:::::2:
                  L  73:::::::::::1:6:::::
```

```
                  M  1::::::::::::::::::::
                  N  ::191::::::::::::1::4
                  P  ::::1:::::::::::::::2
                  Q  :16:::2::::::::::::::
                  R  ::::::2::::::1:::::6:
                  S  :::12::::2:1::1::1:1:
                  T  ::::2::1:2::::9::::::
                  V  :::::::3:::::4:1:::::
                  W  ::::::::::::::::a::::
                  Y  :::::::1:::::::::::::

         bits    6.4                 *
                 5.7         * *     *
                 5.1         * *     *
                 4.5      *  * *     *
Relative         3.8    * *  * **  * *
Entropy          3.2  * * ** * *** * * *
(68.6 bits)      2.5 **** ** ***** ******
                 1.9 **** ****************
                 1.3 *********************
                 0.6 *********************
                 0.0 ---------------------

Multilevel           LFQNSKKICACDGVTLWEERN
consensus             LE T QV S   K I DDKP
sequence                    R  T


-----------------------------------------------------------------

-----------------------------------------------------------------
      Motif LFQNSKKICACDGVTJWEERN MEME-12 sites sorted by position
p-value
-----------------------------------------------------------------
Sequence name            Start   P-value                 Site
-------------            ----- ---------          ---------------
CCS_Nematostella           238  9.97e-24 GCGIIARSAG
LFQNTKKYCACDGRTLWEDKP LKASSQL
CCS_Drosophila             231  2.77e-23 ACGIIARSAG
ILQNFKRICACDGVTLWDERN KPLAGKGRAT
CCS_Homo                   236  9.30e-23 ACGIIARSAG
LFQNPKQICSCDGLTIWEERG RPIAGKGRKE
CCS_Trichoplax             221  1.05e-22 TCGIIARSAG
LFENSKKFCACDGKTLWEDKP LTNKSPQASL
CCS_Amphimedon             220  3.67e-22 MCGIIARSAG
LFQNTKKVCTCDGVTIWDEAA SQRQK
CCS_Ciona                  228  4.10e-22 ACAIVARSAG
LFQNNKQTCACDGVSVWDERN VPLAGAERSK
CCS_Hydra                  218  3.31e-20 ACGIIARSAG
MLENSKKVCTCSGKTLWEERE ETRVH
```

```
CCS_Capsaspora              240  2.76e-19 GAGIIARSAG
LLGNAKRVCACDGKTLWSDSN PGALLPNKRV
CCS_Crassostrea             216  3.02e-19 CGIIARSAGL
FQNSEKKICSCDGVTIWNERN VPLAGSGRKS
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LFQNSKKICACDGVTJWEERN MEME-12 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CCS_Nematostella                    1e-23  237_[12]_7
CCS_Drosophila                    2.8e-23  230_[12]_12
CCS_Homo                          9.3e-23  235_[12]_18
CCS_Trichoplax                      1e-22  220_[12]_10
CCS_Amphimedon                    3.7e-22  219_[12]_5
CCS_Ciona                         4.1e-22  227_[12]_15
CCS_Hydra                         3.3e-20  217_[12]_5
CCS_Capsaspora                    2.8e-19  239_[12]_46
CCS_Crassostrea                     3e-19  215_[12]_12
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LFQNSKKICACDGVTJWEERN MEME-12 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF LFQNSKKICACDGVTJWEERN width=21 seqs=9
CCS_Nematostella         (  238) LFQNTKKYCACDGRTLWEDKP  1
CCS_Drosophila           (  231) ILQNFKRICACDGVTLWDERN  1
CCS_Homo                 (  236) LFQNPKQICSCDGLTIWEERG  1
CCS_Trichoplax           (  221) LFENSKKFCACDGKTLWEDKP  1
CCS_Amphimedon           (  220) LFQNTKKVCTCDGVTIWDEAA  1
CCS_Ciona                (  228) LFQNNKQTCACDGVSVWDERN  1
CCS_Hydra                (  218) MLENSKKVCTCSGKTLWEERE  1
CCS_Capsaspora           (  240) LLGNAKRVCACDGKTLWSDSN  1
CCS_Crassostrea          (  216) FQNSEKKICSCDGVTIWNERN  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LFQNSKKICACDGVTJWEERN MEME-12 position-specific scoring
matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 21 n= 7390 bayes= 11.0852 E= 8.8e-
064
  -344   -318   -509   -404    112   -562   -440     48   -396
316    204   -456   -368   -300   -310   -396   -299   -179   -278
-227
  -371   -320   -528   -470    426   -576   -410   -142   -452
175    -37   -472   -426    102   -392   -402   -353   -234   -192
-20
```

```
  -230   -362   -123    147   -349    -87   -161   -368   -159   -
299   -171     46   -261    397   -147   -186   -209   -359   -331
-257
  -359   -334   -204   -360   -315   -404   -169   -316   -292   -
386   -275    400   -334   -232   -282    -92   -227   -385   -303
-260
    18   -260   -119     81    106   -281   -170   -236    -33   -
212    -99     60     81    -19    -39    169    165   -224   -251
-120
  -374   -389   -479   -410   -478   -534   -447   -402    402   -
455   -340   -373   -407   -350     -5   -424   -365   -486   -393
-389
  -306   -409   -385   -214   -427   -437   -248   -372    315   -
320   -226   -250   -347    236    253   -278   -248   -369   -344
-261
  -179   -189   -391   -315    118   -408   -339    272   -296    -
49      8   -315   -304   -257   -248   -235     45    175   -216
163
  -390    544   -534   -475   -426   -609   -549   -419   -531   -
460   -343   -513   -499   -483   -432   -456   -376   -491   -525
-457
   277   -173   -426   -387   -349   -275   -469   -375   -405   -
371   -258   -360   -319   -341   -341    150    178   -256   -397
-356
  -390    544   -534   -475   -426   -609   -549   -419   -531   -
460   -343   -513   -499   -483   -432   -456   -376   -491   -525
-457
  -328   -386    393    -78   -361   -425   -331   -401   -361   -
413   -324    -98   -405   -304   -323   -150   -340   -404   -373
-287
  -263   -396   -318   -362   -430    303   -443   -488   -359   -
503   -371   -299   -388   -384   -308   -287   -378   -463   -388
-361
  -239   -314   -334   -194   -267   -404   -244   -212    240
26   -136   -236   -309    -76    174   -235   -194    213   -294
-201
  -224   -234   -349   -360   -307   -441   -390   -253   -293   -
346   -161   -202   -324   -249   -254     71    390   -242   -345
-310
  -337   -306   -577   -496   -153   -608   -542    240   -489
269    -34   -517   -458   -414   -429   -456   -298     74   -354
-284
  -422   -362   -425   -407    -92   -496   -440   -407   -400   -
249   -246   -413   -414   -345   -315   -410   -388   -390    622
-89
  -249   -451    238    283   -418   -311   -273   -448   -180   -
416   -321    103   -284   -114   -230     56   -222   -412   -462
-288
  -246   -618    218    354   -519   -426   -375   -444   -191   -
417   -316   -266   -298    -86   -275   -282   -283   -395   -544
-390
```

```
   -23   -343   -321   -207   -374   -411   -241   -357    159   -
316   -225   -238   -304    -90    396      3   -237   -366   -304
-251
    27   -340    -81     98   -308    -28   -214   -356   -120   -
326   -223    270    218    -98   -137   -118   -154   -335   -353
-204
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LFQNSKKICACDGVTJWEERN MEME-12 position-specific
probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 21 nsites= 9 E= 8.8e-064
 0.000000  0.000000  0.000000  0.000000  0.111111  0.000000
0.000000  0.111111  0.000000  0.666667  0.111111  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.555556  0.000000
0.000000  0.000000  0.000000  0.333333  0.000000  0.000000  0.000000
0.111111  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.222222  0.000000  0.111111
0.000000  0.000000  0.000000  0.000000  0.000000  0.111111  0.000000
0.555556  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.888889  0.000000
0.000000  0.000000  0.111111  0.000000  0.000000  0.000000  0.000000
 0.111111  0.000000  0.000000  0.111111  0.111111  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.111111  0.111111
0.000000  0.000000  0.222222  0.222222  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.555556  0.000000  0.000000  0.000000  0.000000
0.222222  0.222222  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.111111  0.000000
0.000000  0.333333  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.111111  0.333333  0.000000  0.111111
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.555556  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.222222  0.222222  0.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.888889  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.111111  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.333333  0.111111  0.000000  0.000000  0.000000
0.000000  0.111111  0.000000  0.000000  0.444444  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.111111  0.888889  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.333333  0.000000  0.555556  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.111111  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.333333  0.444444  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.111111  0.000000
0.000000  0.000000  0.111111  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.333333  0.666667  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.111111  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.222222  0.000000  0.000000  0.000000  0.000000
0.000000  0.555556  0.111111  0.000000  0.000000  0.000000  0.000000
 0.111111  0.000000  0.000000  0.111111  0.000000  0.111111
0.000000  0.000000  0.000000  0.000000  0.000000  0.444444  0.222222
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif LFQNSKKICACDGVTJWEERN MEME-12 regular expression
--------------------------------------------------------------------
L[FL][QE]N[ST]K[KQR][IV]C[AST]CDG[VK]T[LI]W[ED][ED][RK][NP]
--------------------------------------------------------------------



Time 58.20 secs.

********************************************************************


********************************************************************
MOTIF WBIINWENVSERFAA MEME-13     width =  15  sites =  10  llr =
309  E-value = 3.7e-031
********************************************************************
--------------------------------------------------------------------
      Motif WBIINWENVSERFAA MEME-13 Description
--------------------------------------------------------------------
Simplified        A  :::2:::::21::35
pos.-specific     C  :::::::::::::::
probability       D  :2::3::2::1:::1
matrix            E  ::::::3:::6::1:
```

```
                  F  4:::::::::::6::
                  G  :::::::::1:::::
                  H  :2:::::::::::::
                  I  ::45:::::::::::
                  K  :2::::3:::1::12
                  L  ::1::::::::13::
                  M  :::::::::::::1:
                  N  :4::7:26:211::1
                  P  :::::::::::::::
                  Q  ::::::1::::::1:
                  R  :::::::1:::8:1:
                  S  :::::::1:3:::::
                  T  ::::::1::2:::1:
                  V  ::53::::a::::1:
                  W  5::::a::::::::1
                  Y  1:::::::::::1::

         bits    6.4      *
                 5.7      *
                 5.1      *
                 4.5 *    *
Relative         3.8 *    *  *  *
Entropy          3.2 *   **  *  **
(44.5 bits)      2.5 ****** ** ***
                 1.9 ************* *
                 1.3 ***************
                 0.6 ***************
                 0.0 ---------------

Multilevel           WNVINWENVSERFAA
consensus            FDIVD KD A  L K
sequence              H A  N  N
                      K       T

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WBIINWENVSERFAA MEME-13 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                 Site
-------------             ----- ---------            ---------------
MnSOD_Homo                  205  1.61e-17 NVRPDYLKAI WNVINWENVTERYMA
CKK
FeMnSOD_Capsaspora          211  7.13e-17 NARPDYLKAI WKVVNWNNVNERFAA
ASRK
MnSOD_Caenorhabditis        204  7.13e-17 NVRPDYVNAI WKIANWKNVSERFAK
AQQ
MnSOD_Crassostrea           209  1.39e-15 NVRPDYVNAI WHIIDWKSVTERFKA
AL
MnSOD_Hydra                 203  3.96e-15 NVRLDYVNAI FNIIDWKNVSARFVA
AK
```

```
MnSOD1_Nematostella         204  2.67e-14 NVRPDYVKAI YDVINWTNVAERLQA
ASS
MnSOD_Ciona                 202  4.85e-14 NVRPDYIKAI FNVVNWENVGKRFTD
A
MnSOD_Biomphalaria          204  3.17e-13 NVRADYVNAI FNIANWQDVSDRLAK
ARLRS
MnSOD_Trichoplax            207  4.88e-12 NVRPNYVNAI FDVINWNDVANNFRN
AKA
MnSOD2_Nematostella         231  3.22e-11 NKRPGYVHSW WHLVDWERVNELLEW
WQNQNIHDEL
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif WBIINWENVSERFAA MEME-13 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
MnSOD_Homo                        1.6e-17  204_[13]_3
FeMnSOD_Capsaspora                7.1e-17  210_[13]_4
MnSOD_Caenorhabditis              7.1e-17  203_[13]_3
MnSOD_Crassostrea                 1.4e-15  208_[13]_2
MnSOD_Hydra                         4e-15  202_[13]_2
MnSOD1_Nematostella               2.7e-14  203_[13]_3
MnSOD_Ciona                       4.9e-14  201_[13]_1
MnSOD_Biomphalaria                3.2e-13  203_[13]_5
MnSOD_Trichoplax                  4.9e-12  206_[13]_3
MnSOD2_Nematostella               3.2e-11  230_[13]_10
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif WBIINWENVSERFAA MEME-13 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF WBIINWENVSERFAA width=15 seqs=10
MnSOD_Homo               (  205) WNVINWENVTERYMA  1
FeMnSOD_Capsaspora       (  211) WKVVNWNNVNERFAA  1
MnSOD_Caenorhabditis     (  204) WKIANWKNVSERFAK  1
MnSOD_Crassostrea        (  209) WHIIDWKSVTERFKA  1
MnSOD_Hydra              (  203) FNIIDWKNVSARFVA  1
MnSOD1_Nematostella      (  204) YDVINWTNVAERLQA  1
MnSOD_Ciona              (  202) FNVVNWENVGKRFTD  1
MnSOD_Biomphalaria       (  204) FNIANWQDVSDRLAK  1
MnSOD_Trichoplax         (  207) FDVINWNDVANNFRN  1
MnSOD2_Nematostella      (  231) WHLVDWERVNELLEW  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif WBIINWENVSERFAA MEME-13 position-specific scoring matrix
--------------------------------------------------------------------
```

```
log-odds matrix: alength= 20 w= 15 n= 7636 bayes= 11.0499 E= 3.7e-
031
  -527   -419   -563   -544    369   -615   -258   -406   -502   -
328   -298   -430   -494   -389   -398   -458   -457   -440    518
280
  -282   -405    173   -155   -391   -276    192   -478    159   -
443   -355    273   -299   -169   -201   -145   -208   -461   -435
-258
  -316   -298   -528   -484   -244   -600   -582    291   -474
34   -102   -491   -475   -462   -453   -442   -278    246   -437
-322
    90   -288   -538   -487   -255   -582   -579    311   -477   -
143   -118   -489   -473   -463   -456   -424   -272    191   -443
-320
  -330   -415    213   -203   -411   -301   -251   -493   -254   -
494   -413    358   -331   -222   -283   -168   -240   -506   -442
-289
  -426   -367   -429   -412    -97   -500   -445   -412   -405   -
254   -251   -418   -418   -350   -320   -415   -393   -395    623
-94
  -152   -337   -108    215   -265   -308   -196   -292    205   -
257   -147    148   -210    137    -41   -121     71   -272   -298
-166
  -315   -379    127   -210   -366   -307   -212   -408   -231   -
435   -338    354   -315   -200     71     21   -219   -443   -381
-264
  -241   -289   -479   -437   -309   -536   -494    -73   -454   -
250   -213   -484   -402   -437   -382   -408   -258    354   -450
-381
   105   -243   -216   -233   -339    -48   -326   -383   -238   -
374   -257    152   -284   -213   -230    228    180   -338   -385
-276
     9   -501     91    331   -419   -383   -312   -401     65   -
370   -265     61   -273    -75   -204   -223   -231   -362   -454
-306
  -353   -300   -432   -402   -402   -472   -271   -393   -108   -
208   -308   -156   -315   -197    455   -347   -344   -476   -274
-318
  -398   -310   -493   -462    456   -566   -347   -251   -465
109   -154   -444   -408   -406   -403   -373   -404   -316   -129
203
   136   -282   -111     91   -205   -276   -158   -235     91   -
205    190    -97   -171    134    122    -79     71     -9   -248
-116
   218   -280     59    -57   -243   -277   -188   -276    149   -
246   -137     71   -208    -44    -59    -96   -114   -246    233
-153
--------------------------------------------------------------------------------
```

```
--------------------------------------------------------------------------------
      Motif WBIINWENVSERFAA MEME-13 position-specific probability
matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 15 nsites= 10 E= 3.7e-031
 0.000000  0.000000  0.000000  0.000000  0.400000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.100000
 0.000000  0.000000  0.200000  0.000000  0.000000  0.000000
0.200000  0.000000  0.200000  0.000000  0.000000  0.400000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.400000  0.000000  0.100000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.200000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.300000  0.000000  0.000000
 0.000000  0.000000  0.300000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.700000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  0.300000  0.000000  0.000000
0.000000  0.000000  0.300000  0.000000  0.000000  0.200000  0.000000
0.100000  0.000000  0.000000  0.100000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.200000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.600000  0.000000
0.000000  0.100000  0.100000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.200000  0.000000  0.000000  0.000000  0.000000  0.100000
0.000000  0.000000  0.000000  0.000000  0.000000  0.200000  0.000000
0.000000  0.000000  0.300000  0.200000  0.000000  0.000000  0.000000
 0.100000  0.000000  0.100000  0.600000  0.000000  0.000000
0.000000  0.000000  0.100000  0.000000  0.000000  0.100000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.100000  0.000000  0.100000  0.000000
0.000000  0.800000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.600000  0.000000
0.000000  0.000000  0.000000  0.300000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.100000
 0.300000  0.000000  0.000000  0.100000  0.000000  0.000000
0.000000  0.000000  0.100000  0.000000  0.100000  0.000000  0.000000
0.100000  0.100000  0.000000  0.100000  0.100000  0.000000  0.000000
 0.500000  0.000000  0.100000  0.000000  0.000000  0.000000
0.000000  0.000000  0.200000  0.000000  0.000000  0.100000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.100000  0.000000
--------------------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif WBIINWENVSERFAA MEME-13 regular expression
--------------------------------------------------------------------
[WF][NDHK][VI][IVA][ND]W[EKN][ND]V[SANT]ER[FL]A[AK]
--------------------------------------------------------------------




Time 60.45 secs.

********************************************************************


********************************************************************
MOTIF MAJKAVCVLKG MEME-14    width =  11  sites =  11  llr = 224  E-
value = 1.7e-009
********************************************************************
--------------------------------------------------------------------
     Motif MAJKAVCVLKG MEME-14 Description
--------------------------------------------------------------------
Simplified        A  141:9:1::1:
pos.-specific     C  ::::::93:::
probability       D  :::::::::::
matrix            E  :::1:::::11
                  F  :::::::::::
                  G  :1::1::1::7
                  H  :::::::::::
                  I  ::2::1:1:::
                  K  ::14:::::3:
                  L  :13:::::71:
                  M  7:::::::2::
                  N  ::1::::::::
                  P  11:::::::::
                  Q  ::11:::::1:
                  R  :::4:::::11
                  S  1111:::::21
                  T  ::1:::::1::
                  V  :3:::9:5:1:
                  W  :::::::::::
                  Y  :::::::::::

         bits    6.4
                 5.7
                 5.1       *
                 4.5       *
Relative         3.8 *     *
Entropy          3.2 *   *** *
(29.4 bits)      2.5 *  ******
                 1.9 *  ****** *
                 1.3 ***********
```

```
                 0.6 ***********
                 0.0 -----------

Multilevel           MALKAVCVLKG
consensus             V R   C
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif MAJKAVCVLKG MEME-14 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value               Site
-------------             ----- ---------            -----------
CuZnSOD_Trichoplax            1  4.81e-13          . MALKAVCCLQG
PVVSGTIFFQ
CuZnSOD1_Homo                 1  5.77e-13          . MATKAVCVLKG
DGPVQGIINF
CuZnSOD_Ciona                 1  3.29e-11          . MVLEAVCVMKG
SESVSGTIKF
CuZnSOD2_Nematostella         1  6.61e-11          . MPIQAVCCMSG
TEGVKGTIKF
CuZnSOD_Crassostrea           3  1.29e-10         MS SALKAVCVLKG
DSNVTGTVQF
CuZn_Hydra                    1  2.26e-10          . MAKSAICVLEG
IVKGTIKFED
CuZnSOD1_Nematostella         1  3.55e-10          . MVIRGVCCLVG
DNEVKGVIHF
CuZnSOD_Caenorhabditis       23  1.18e-08 IFPQVEAAQK MSNRAVAVLRG
ETVTGTIWIT
MnSOD_Homo                    1  4.99e-08          . MLSRAVCGTSR
QLAPALGYLG
CuZnSOD_Amphimedon           13  6.59e-08 VDKAKFETSP PVARAVCILAS
SDDVKGTIEF
CuZnSOD_Acropora             24  8.67e-08 CPRFLEQRIM AGQKAVCVLLE
SKSKEVKGVI
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif MAJKAVCVLKG MEME-14 block diagrams
--------------------------------------------------------------------
------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CuZnSOD_Trichoplax                4.8e-13  [14]_143
CuZnSOD1_Homo                     5.8e-13  [14]_143
CuZnSOD_Ciona                     3.3e-11  [14]_143
CuZnSOD2_Nematostella             6.6e-11  [14]_145
CuZnSOD_Crassostrea               1.3e-10  2_[14]_143
CuZn_Hydra                        2.3e-10  [14]_141
```

```
CuZnSOD1_Nematostella             3.6e-10  [14]_143
CuZnSOD_Caenorhabditis            1.2e-08  22_[14]_147
MnSOD_Homo                          5e-08  [14]_211
CuZnSOD_Amphimedon                6.6e-08  12_[14]_143
CuZnSOD_Acropora                  8.7e-08  23_[14]_143
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif MAJKAVCVLKG MEME-14 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF MAJKAVCVLKG width=11 seqs=11
CuZnSOD_Trichoplax       (    1) MALKAVCCLQG  1
CuZnSOD1_Homo            (    1) MATKAVCVLKG  1
CuZnSOD_Ciona            (    1) MVLEAVCVMKG  1
CuZnSOD2_Nematostella    (    1) MPIQAVCCMSG  1
CuZnSOD_Crassostrea      (    3) SALKAVCVLKG  1
CuZn_Hydra               (    1) MAKSAICVLEG  1
CuZnSOD1_Nematostella    (    1) MVIRGVCCLVG  1
CuZnSOD_Caenorhabditis   (   23) MSNRAVAVLRG  1
MnSOD_Homo               (    1) MLSRAVCGTSR  1
CuZnSOD_Amphimedon       (   13) PVARAVCILAS  1
CuZnSOD_Acropora         (   24) AGQKAVCVLLE  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif MAJKAVCVLKG MEME-14 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 11 n= 7800 bayes= 11.0026 E= 1.7e-
009
   -33   -279   -483   -442   -347   -392   -506   -300   -439   -
259    547   -425     30   -388   -401    -26   -269   -317   -353
-300
   256   -137   -354   -278   -195    -91   -362   -174   -281    -
30    -99   -312     35   -251   -242     19   -156    110   -273
-205
    14   -250   -146    -57   -170   -298   -185    116     73
124    -66     51   -193    120    -56     37     66   -168   -236
-115
  -264   -401   -294     64   -378   -410   -245   -360    257   -
312   -213   -225   -315    133    308     26   -219   -350   -342
-242
   332   -154   -414   -360   -309    -75   -456   -331   -377   -
324   -216   -376   -364   -341   -320   -106   -200   -208   -360
-327
  -179   -230   -428   -375   -256   -517   -443     79   -395   -
190   -152   -432   -355   -384   -325   -368   -194    337   -416
-351
  -303    543   -533   -473   -424   -599   -548   -417   -529   -
458   -340   -510   -496   -480   -430   -443   -370   -485   -525
```

```
-456
  -210    309   -474   -406   -221    -80   -453     95   -408   -
169   -116   -426   -378   -375   -349   -328   -208    280   -362
-270
  -343   -319   -504   -399   -107   -557   -439    -98   -390
323    252   -452   -367   -299   -306   -390    -18   -183   -287
-232
    14   -296   -118     84   -217   -285   -165   -250    188    -
18   -105   -104   -178    127    116    108    -89    -18   -257
-125
  -221   -364   -266    -82   -396    286   -398   -446   -303   -
467   -326   -245   -355   -332    -29    -86   -334   -421   -355
-323
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif MAJKAVCVLKG MEME-14 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 11 nsites= 11 E= 1.7e-009
 0.090909  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.727273  0.000000  0.090909
0.000000  0.000000  0.090909  0.000000  0.000000  0.000000  0.000000
 0.363636  0.000000  0.000000  0.000000  0.000000  0.090909
0.000000  0.000000  0.000000  0.090909  0.000000  0.000000  0.090909
0.000000  0.000000  0.090909  0.000000  0.272727  0.000000  0.000000
 0.090909  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.181818  0.090909  0.272727  0.000000  0.090909  0.000000
0.090909  0.000000  0.090909  0.090909  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.090909  0.000000  0.000000
0.000000  0.000000  0.363636  0.000000  0.000000  0.000000  0.000000
0.090909  0.363636  0.090909  0.000000  0.000000  0.000000  0.000000
 0.909091  0.000000  0.000000  0.000000  0.000000  0.090909
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.090909  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.909091  0.000000  0.000000
 0.090909  0.909091  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.272727  0.000000  0.000000  0.000000  0.090909
0.000000  0.090909  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.545455  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.727273  0.181818  0.000000  0.000000
0.000000  0.000000  0.000000  0.090909  0.000000  0.000000  0.000000
 0.090909  0.000000  0.000000  0.090909  0.000000  0.000000
0.000000  0.000000  0.272727  0.090909  0.000000  0.000000  0.000000
0.090909  0.090909  0.181818  0.000000  0.090909  0.000000  0.000000
 0.000000  0.000000  0.000000  0.090909  0.000000  0.727273
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.090909  0.090909  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif MAJKAVCVLKG MEME-14 regular expression
--------------------------------------------------------------------
M[AV]L[KR]AVC[VC]LKG
--------------------------------------------------------------------




Time 62.56 secs.

********************************************************************


********************************************************************
MOTIF QHLGAAVAIL MEME-15     width =  10  sites =   8  llr = 170  E-
value = 5.1e-004
********************************************************************
--------------------------------------------------------------------
      Motif QHLGAAVAIL MEME-15 Description
--------------------------------------------------------------------
Simplified        A  ::::9a:6::
pos.-specific     C  ::::::::::
probability       D  ::::::::::
matrix            E  ::::::::3:
                  F  ::::::::::
                  G  :::a::::::
                  H  :6::::::::
                  I  ::::::::53
                  K  ::::::::::
                  L  ::9::::::5
                  M  ::::::::13
                  N  :4::::::::
                  P  ::::::::::
                  Q  4:1:::::::
                  R  1:::::::::
                  S  4:::1::3::
                  T  ::::::::::
                  V  1:::::a11:
                  W  ::::::::::
                  Y  ::::::::::

         bits    6.4
                 5.7
                 5.1
                 4.5
Relative         3.8      **
Entropy          3.2  ******
```

```
(30.6 bits)      2.5 **********
                 1.9 **********
                 1.3 **********
                 0.6 **********
                 0.0 ----------

Multilevel           QHLGAAVAIL
consensus            SN     SEI
sequence                      M


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif QHLGAAVAIL MEME-15 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value               Site
-------------             ----- ---------            ----------
CCS_Homo                     84  2.38e-11 VLKGMGSGQL QNLGAAVAIL
GGPGTVQGVV
CCS_Nematostella             87  3.89e-11 HGAGRAGKTA QHLGAAVAMI
DCEKVQGLTR
CCS_Acropora                 82  5.11e-11 RGLGASGTQV SHLGAAVAEM
SSGSVLGVAR
CCS_Trichoplax               79  7.94e-11 RGQGAATEGA SHLGAAVSIL
SGTSVKGLVR
CCS_Ciona                    77  1.04e-10 FMGHGASMQR QHLGAAVAEI
SGRFVKGVVR
CCS_Hydra                    77  2.67e-10 AVYRGQGENS VNLGAAVAIL
KNDHQTYGLV
CCS_Capsaspora               83  4.26e-09 VLRGQGDSFG RNLGSAVSIL
ERDGTQDVIG
CCS_Amphimedon               78  7.57e-09 GFGGQEQAPT SHQGAAVVVM
KGSGPVNGLL
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif QHLGAAVAIL MEME-15 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CCS_Homo                          2.4e-11  83_[15]_181
CCS_Nematostella                  3.9e-11  86_[15]_169
CCS_Acropora                      5.1e-11  81_[15]_130
CCS_Trichoplax                    7.9e-11  78_[15]_163
CCS_Ciona                           1e-10  76_[15]_177
CCS_Hydra                         2.7e-10  76_[15]_157
CCS_Capsaspora                    4.3e-09  82_[15]_214
CCS_Amphimedon                    7.6e-09  77_[15]_158
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif QHLGAAVAIL MEME-15 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF QHLGAAVAIL width=10 seqs=8
CCS_Homo                 (   84) QNLGAAVAIL  1
CCS_Nematostella         (   87) QHLGAAVAMI  1
CCS_Acropora             (   82) SHLGAAVAEM  1
CCS_Trichoplax           (   79) SHLGAAVSIL  1
CCS_Ciona                (   77) QHLGAAVAEI  1
CCS_Hydra                (   77) VNLGAAVAIL  1
CCS_Capsaspora           (   83) RNLGSAVSIL  1
CCS_Amphimedon           (   78) SHQGAAVVVM  1
//
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif QHLGAAVAIL MEME-15 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 10 n= 7841 bayes= 9.93535 E= 5.1e-
004
  -138   -283   -159    -62   -231   -304   -181   -238      5   -
216   -112   -131   -208    289    160    192   -108     22   -263
-145
  -328   -336   -168   -237   -211   -356    384   -429   -271   -
341   -244    207   -312    -77   -155   -202   -243   -408   -260
-30
  -323   -303   -466   -362    -97   -528   -409    -89   -344
334     44   -419   -340     35   -268   -362   -279   -172   -271
-209
  -251   -385   -306   -351   -420    302   -432   -477   -347   -
492   -359   -287   -377   -372   -297   -275   -366   -451   -377
-350
   325   -116   -374   -316   -268   -240   -417   -287   -333   -
281   -174   -340   -339   -302   -280     44   -167   -165   -320
-286
   346   -193   -439   -393   -339   -309   -479   -361   -410   -
357   -256   -406   -378   -371   -350   -147   -236   -248   -384
-349
  -195   -248   -436   -390   -269   -500   -449    -35   -407   -
212   -174   -441   -360   -392   -335   -366   -213    348   -411
-344
   306   -108   -366   -304   -253   -236   -406   -266   -319   -
264   -158   -336   -342   -292   -268     94   -163    -13   -307
-272
  -241   -245   -397     87   -154   -465   -410    326   -324    -
44    187   -352   -357   -301   -297   -291   -194     94   -284
-181
  -369   -335   -597   -497    -82   -614   -503    188   -487
271    349   -529   -439   -370   -399   -466   -328   -167   -285
-241
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif QHLGAAVAIL MEME-15 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 10 nsites= 8 E= 5.1e-004
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.375000  0.125000  0.375000  0.000000  0.125000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.625000  0.000000  0.000000  0.000000  0.000000  0.375000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.875000  0.000000  0.000000  0.000000
0.125000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.875000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.125000  0.000000  0.000000  0.000000  0.000000
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.625000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.250000  0.000000  0.125000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.125000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.125000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.250000  0.000000  0.500000  0.250000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif QHLGAAVAIL MEME-15 regular expression
--------------------------------------------------------------------
[QS][HN]LGAAV[AS][IE][LIM]
--------------------------------------------------------------------




Time 64.55 secs.

********************************************************************
```

```
**********************************************************************
MOTIF IIEGTIDG MEME-16 width =    8  sites =    8  llr = 143  E-value
= 2.0e-002
**********************************************************************
----------------------------------------------------------------------
      Motif IIEGTIDG MEME-16 Description
----------------------------------------------------------------------
Simplified        A  ::::1:::
pos.-specific     C  ::::::::
probability       D  ::4:::a:
matrix            E  ::6:::::
                  F  ::::::::
                  G  :::a:::9
                  H  ::::::::
                  I  4a:::5::
                  K  ::::::::
                  L  3::::1::
                  M  1:::::::
                  N  :::::::1
                  P  ::::::::
                  Q  ::::::::
                  R  ::::::::
                  S  ::::::::
                  T  ::::9:::
                  V  3::::4::
                  W  ::::::::
                  Y  ::::::::

         bits    6.4
                 5.7
                 5.1
                 4.5  *    *
Relative         3.8  *  * *
Entropy          3.2  **** *
(25.8 bits)      2.5  *******
                 1.9 ********
                 1.3 ********
                 0.6 ********
                 0.0 --------

Multilevel           IIEGTIDG
consensus            L D  V
sequence             V


----------------------------------------------------------------------

----------------------------------------------------------------------
      Motif IIEGTIDG MEME-16 sites sorted by position p-value
----------------------------------------------------------------------
```

```
Sequence name            Start   P-value              Site
-------------            ----- ---------            --------
CCS_Nematostella           116  7.44e-10 RFVQVSGDNC IIDGTIDG
LTPGNHGFHI
CCS_Crassostrea            113  7.44e-10 RLVQSNPSKC IIDGTIDG
LPEGKHKLFI
CCS_Amphimedon             108  1.85e-09 RMVQVSSNEC VIEGTIDG
LTPNKEHLLK
CCS_Homo                   114  2.37e-09 RFLQLTPERC LIEGTIDG
LEPGLHGLHV
CCS_Ciona                  106  7.44e-09 RLLQLDQNLC LIEGTVDG
LSPGKHGLNI
CCS_Capsaspora             115  1.44e-08 RFVQISENEC VIEGTLDG
LSKGEHGLHI
CCS_Acropora               111  3.72e-08 RFVQVSEDVC IIDGAVDG
LTPGLHGLNI
CCS_Trichoplax             108  4.25e-08 RFTQLSADKC MIEGTVDN
LRPGNYDIKI
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif IIEGTIDG MEME-16 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME           POSITION P-VALUE  MOTIF DIAGRAM
-------------           ----------------  -------------
CCS_Nematostella                 7.4e-10  115_[16]_142
CCS_Crassostrea                  7.4e-10  112_[16]_128
CCS_Amphimedon                   1.9e-09  107_[16]_130
CCS_Homo                         2.4e-09  113_[16]_153
CCS_Ciona                        7.4e-09  105_[16]_150
CCS_Capsaspora                   1.4e-08  114_[16]_184
CCS_Acropora                     3.7e-08  110_[16]_103
CCS_Trichoplax                   4.2e-08  107_[16]_136
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif IIEGTIDG MEME-16 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF IIEGTIDG width=8 seqs=8
CCS_Nematostella        (  116) IIDGTIDG  1
CCS_Crassostrea         (  113) IIDGTIDG  1
CCS_Amphimedon          (  108) VIEGTIDG  1
CCS_Homo                (  114) LIEGTIDG  1
CCS_Ciona               (  106) LIEGTVDG  1
CCS_Capsaspora          (  115) VIEGTLDG  1
CCS_Acropora            (  111) IIDGAVDG  1
CCS_Trichoplax          (  108) MIEGTVDN  1
//

--------------------------------------------------------------------
```

```
--------------------------------------------------------------------------------
      Motif IIEGTIDG MEME-16 position-specific scoring matrix
--------------------------------------------------------------------------------
log-odds matrix: alength= 20 w= 8 n= 7923 bayes= 10.6879 E= 2.0e-002
  -292   -291   -432   -392   -160   -514   -467    323   -367
94    176   -391   -398   -348   -344   -341   -237    127   -313
-215
  -348   -340   -477   -454   -238   -553   -536    387   -429    -
96    -81   -451   -447   -420   -410   -406   -298     -5   -388
-278
  -231   -602    234    343   -503   -409   -357   -430   -174   -
401   -300   -245   -281    -70   -258   -264   -267   -379   -530
-373
  -251   -385   -306   -351   -420    302   -432   -477   -347   -
492   -359   -287   -377   -372   -297   -275   -366   -451   -377
-350
    27   -217   -371   -372   -323   -366   -413   -279   -322   -
357   -190   -236   -313   -272   -278    -40    387   -253   -365
-325
  -302   -297   -436   -404   -200   -534   -502    337   -380
32    -32   -403   -418   -375   -367   -360   -246    163   -355
-242
  -352   -402    398    -98   -376   -449   -353   -419   -387   -
429   -342   -122   -420   -328   -343   -326   -366   -423   -385
-304
  -212   -355   -259   -305   -388    293   -392   -439   -303   -
461   -320    -46   -347   -331   -257   -233   -327   -414   -347
-315
--------------------------------------------------------------------------------

--------------------------------------------------------------------------------
      Motif IIEGTIDG MEME-16 position-specific probability matrix
--------------------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 8 nsites= 8 E= 2.0e-002
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.375000  0.000000  0.250000  0.125000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.250000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.375000  0.625000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.125000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.875000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.125000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.000000  0.000000  0.375000  0.000000  0.000000
 0.000000  0.000000  1.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.875000
0.000000  0.000000  0.000000  0.000000  0.000000  0.125000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif IIEGTIDG MEME-16 regular expression
--------------------------------------------------------------------
------------
[ILV]I[ED]GT[IV]DG
--------------------------------------------------------------------




Time 66.72 secs.

********************************************************************


********************************************************************
MOTIF RIDFRLKNERLKVWEMIGRSIILHRGIP MEME-17    width =  28  sites =
2  llr = 144  E-value = 3.2e+001
********************************************************************
--------------------------------------------------------------------
      Motif RIDFRLKNERLKVWEMIGRSIILHRGIP MEME-17 Description
--------------------------------------------------------------------
Simplified        A  :5::::::::::::::::::::::::::
pos.-specific     C  ::::::::::::::::::::::::::::
probability       D  ::5:::::::::::5:::::::::::::
matrix            E  ::::::::a:::::5:::::::::::::
                  F  :::a::::::::::::::::::::::::
                  G  :::::::::::::::::a:::::::5::
                  H  :::::::::::::::::::::::a::::
                  I  :5::::::::::::::a:::55::::5:
                  K  ::::::5::::a::::::::::::::::
                  L  :::::5::::5:::::::::::5:::::
                  M  :::::::::::::::5::::5:::::::
                  N  :::::::5::::::::::::::::::::
                  P  :::::::::::::::::::::::::::a
                  Q  ::::5:::::::::::::::::::::::
                  R  a:::5::::a::::::::a:::::5:::
                  S  ::5::::5:::::::::::a::::555:
                  T  :::::55:::::::::::::::::::::
                  V  ::::::::::5:a::5:::::55:::::
                  W  :::::::::::::5::::::::::::::
                  Y  :::::::::::::5::::::::::::::
```

```
         bits    6.4
                 5.7
                 5.1    *         *
                 4.5 *  *    ** * *  * *    *   *
Relative         3.8 *  **   ** *** ** ***  *   *
Entropy          3.2 ********** *********** ** **
(103.9 bits)     2.5 ****************************
                 1.9 ****************************
                 1.3 ****************************
                 0.6 ****************************
                 0.0 ----------------------------

Multilevel           RADFQLKNERLKVWDMIGRSIILHRGIP
consensus             IS RTTS  V  YEV    MVV SSS
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif RIDFRLKNERLKVWEMIGRSIILHRGIP MEME-17 sites sorted by
position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                Site
-------------             ----- ---------            ---------------
CCS_Crassostrea             171  6.30e-33 LGEVEVSTNG
RADFRLTNERLKVWEMIGRSIVVHRGSP NIQQKLSCGI
CCS_Amphimedon              174  2.11e-29 IAALQSDGSG
RISFQTKSERVKVYDVIGRSMILHSSIP SVYGTRRLMC
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif RIDFRLKNERLKVWEMIGRSIILHRGIP MEME-17 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CCS_Crassostrea                   6.3e-33  170_[17]_50
CCS_Amphimedon                    2.1e-29  173_[17]_44
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif RIDFRLKNERLKVWEMIGRSIILHRGIP MEME-17 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF RIDFRLKNERLKVWEMIGRSIILHRGIP width=28 seqs=2
CCS_Crassostrea          (  171) RADFRLTNERLKVWEMIGRSIVVHRGSP  1
CCS_Amphimedon           (  174) RISFQTKSERVKVYDVIGRSMILHSSIP  1
//

--------------------------------------------------------------------
```

```
--------------------------------------------------------------------------------
      Motif RIDFRLKNERLKVWEMIGRSIILHRGIP MEME-17 position-specific
scoring matrix
--------------------------------------------------------------------------------
log-odds matrix: alength= 20 w= 28 n= 7103 bayes= 11.7938 E=
3.2e+001
  -318   -282   -385   -338   -365   -433   -248   -363    -70   -
338   -275   -296   -287   -166    454   -310   -304   -429   -254
-279
   168   -107   -254   -195    -73   -268   -285    241   -187    -
24     18   -229   -186   -163   -158   -110    -85     90   -190
-91
  -131   -250    308      0   -228   -212   -181   -277   -115   -
274   -175     -2   -171    -82   -118    139    -45   -266   -259
-142
  -311   -237   -408   -377    483   -485   -368   -194   -389   -
108   -110   -394   -328   -365   -349   -293   -332   -248   -115
74
  -187   -264   -205    -82   -265   -330   -102   -269     31   -
222   -122   -155   -197    295    352   -167   -157   -275   -210
-163
   -99   -132   -229   -166    -24   -315   -226     37   -142
209     65   -171   -163   -101   -109    -37    203    -13   -112
-59
  -123   -217   -143    -67   -203   -275   -181   -186    288   -
197    -95    -99   -152    -28     59    -17    188   -179   -214
-124
  -142   -225    -55   -126   -222   -225   -136   -257   -125   -
274   -169    310   -190    -97   -119    176     12   -271   -247
-146
  -443   -553   -191    412   -515   -550   -491   -498   -433   -
544   -449   -399   -506   -289   -428   -462   -453   -527   -522
-457
  -318   -282   -385   -338   -365   -433   -248   -363    -70   -
338   -275   -296   -287   -166    454   -310   -304   -429   -254
-279
  -139   -166   -344   -275    -33   -403   -323    150   -265
209     64   -305   -257   -215   -214   -239   -130    199   -174
-114
  -323   -359   -391   -306   -421   -473   -377   -361    396   -
395   -287   -311   -352   -252     27   -350   -306   -424   -355
-326
   -97   -157   -327   -269   -152   -397   -340     82   -281    -
97    -58   -323   -256   -266   -222   -250   -112    316   -288
-209
  -307   -277   -348   -321     93   -430   -185   -272   -309   -
182   -149   -309   -331   -255   -231   -293   -289   -285    576
293
  -258   -414    278    314   -369   -380   -310   -380   -217   -
379   -282   -143   -307   -133   -243   -251   -268   -368   -383
-281
```

```
  -122   -159   -326   -262    -60   -381   -311    126   -249
19    412   -288   -257   -202   -210   -219   -115    193   -180
-107
  -245   -250   -371   -331   -135   -458   -420    355   -307
1     17   -338   -342   -299   -288   -292   -192     85   -282   -
171
  -175   -312   -234   -271   -346    293   -360   -396   -271   -
413   -284   -214   -304   -293   -226   -200   -284   -370   -314
-277
  -318   -282   -385   -338   -365   -433   -248   -363    -70   -
338   -275   -296   -287   -166    454   -310   -304   -429   -254
-279
   -86   -159   -215   -214   -221   -268   -291   -273   -193   -
275   -167   -125   -190   -186   -160    332    107   -271   -275
-173
  -210   -209   -369   -315    -71   -434   -366    274   -289
38    406   -321   -311   -246   -257   -266   -168     41   -210
-129
  -177   -201   -365   -320   -136   -448   -395    304   -309    -
19      2   -336   -317   -294   -274   -282   -156    210   -283
-184
  -139   -166   -344   -275    -33   -403   -323    150   -265
209     64   -305   -257   -215   -214   -239   -130    199   -174
-114
  -269   -259   -196   -201   -111   -355    407   -316   -218   -
238   -146    -71   -242      7    -71   -183   -194   -303   -165
64
   -99   -199   -150    -96   -199   -241   -151   -226     18   -
212   -120    -98   -142    -31    344    162     -2   -222   -195
-115
   -37   -190   -151   -169   -244    225   -262   -289   -174   -
295   -184   -111   -186   -163   -148    148    -62   -251   -257
-184
   -56   -134   -203   -164    -60   -276   -240    247   -146    -
29     16   -130   -161   -124   -119    155     33     39   -173
-64
  -122   -273   -244   -196   -247   -325   -298   -279   -196   -
244   -200   -263    438   -165   -173   -148   -166   -263   -324
-243
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif RIDFRLKNERLKVWEMIGRSIILHRGIP MEME-17 position-specific
probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 28 nsites= 2 E= 3.2e+001
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.500000  0.500000
 0.000000  0.000000  0.500000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
0.000000  1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
1.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif RIDFRLKNERLKVWEMIGRSIILHRGIP MEME-17 regular expression
--------------------------------------------------------------------
R[AI][DS]F[QR][LT][KT][NS]ER[LV]KV[WY][DE][MV]IGRS[IM][IV][LV]H[RS][
GS][IS]P
--------------------------------------------------------------------




Time 69.12 secs.

*******************************************************************


*******************************************************************
MOTIF WERDFY MEME-18   width =   6  sites =   2  llr = 36  E-value =
3.2e+002
*******************************************************************
```

```
--------------------------------------------------------------------
      Motif WERDFY MEME-18 Description
--------------------------------------------------------------------
Simplified        A  :::5::
pos.-specific     C  ::::::
probability       D  :::5::
matrix            E  :5::::
                  F  ::::5:
                  G  ::::::
                  H  ::5:::
                  I  :5::::
                  K  ::::::
                  L  ::::::
                  M  ::::5:
                  N  ::::::
                  P  ::::::
                  Q  ::::::
                  R  ::5:::
                  S  ::::::
                  T  ::::::
                  V  ::::::
                  W  a:::::
                  Y  :::::a

         bits    6.4 *
                 5.7 *    *
                 5.1 *    *
                 4.5 *   **
Relative         3.8 * * **
Entropy          3.2 ******
(26.2 bits)      2.5 ******
                 1.9 ******
                 1.3 ******
                 0.6 ******
                 0.0 ------

Multilevel           WEHAFY
consensus             IRDM
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WERDFY MEME-18 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name            Start   P-value              Site
-------------            ----- ---------            ------
CuZnSOD2_Homo               34  2.59e-09 SAEPNSDSAE WIRDMY
AKVTEIWQEV
```

```
MnSOD2_Nematostella         211  1.84e-08 RLNPVLVIDL WEHAFY
LKHQNKRPGY
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WERDFY MEME-18 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CuZnSOD2_Homo                    2.6e-09  33_[18]_201
MnSOD2_Nematostella              1.8e-08  210_[18]_39
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WERDFY MEME-18 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF WERDFY width=6 seqs=2
CuZnSOD2_Homo            (   34) WIRDMY  1
MnSOD2_Nematostella      (  211) WEHAFY  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WERDFY MEME-18 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 6 n= 8005 bayes= 11.9663 E= 3.2e+002
  -390   -336   -398   -378    -64   -470   -407   -372   -369   -
220   -216   -384   -388   -317   -286   -380   -357   -358    619
-56
  -166   -232    -79    308   -147   -341   -263    184   -139    -
94    -57   -197   -215    -74   -140   -188   -148    -23   -232
-130
  -220   -253   -209   -160   -194   -335    231   -286     -6   -
244   -158   -121   -218      4    375   -181   -179   -290   -189
-37
   111   -210    311     26   -217   -201   -210   -241   -119   -
247   -152    -61   -155    -80   -122    -97   -129   -188   -249
-145
  -215   -196   -356   -306    395   -422   -275    -42   -296
28    374   -317   -284   -236   -251   -245   -201   -115    -50
88
  -194   -200   -258   -221    187   -348    -60   -173   -212   -
134    -80   -221   -233   -181   -158   -184   -195   -197     27
500
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WERDFY MEME-18 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 6 nsites= 2 E= 3.2e+002
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.500000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.500000  0.000000
0.000000  0.000000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WERDFY MEME-18 regular expression
--------------------------------------------------------------------
W[EI][HR][AD][FM]Y
--------------------------------------------------------------------




Time 71.59 secs.

********************************************************************


********************************************************************
MOTIF MVKAVCV MEME-19  width =   7  sites =   2  llr = 42  E-value =
3.3e+002
********************************************************************
--------------------------------------------------------------------
      Motif MVKAVCV MEME-19 Description
--------------------------------------------------------------------
Simplified        A  :::a:::
pos.-specific     C  :::::a:
probability       D  :::::::
matrix            E  :::::::
                  F  :::::::
                  G  :::::::
                  H  :::::::
                  I  :::::::
                  K  ::a::::
                  L  :::::::
```

```
                  M  a::::::
                  N  :::::::
                  P  :::::::
                  Q  :::::::
                  R  :::::::
                  S  :::::::
                  T  :::::::
                  V  :a::a:a
                  W  :::::::
                  Y  :::::::

         bits    6.4
                 5.7 *    *
                 5.1 *    *
                 4.5 * *  *
Relative         3.8 *******
Entropy          3.2 *******
(30.2 bits)      2.5 *******
                 1.9 *******
                 1.3 *******
                 0.6 *******
                 0.0 -------

Multilevel           MVKAVCV
consensus
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif MVKAVCV MEME-19 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value              Site
-------------             ----- ---------            -------
CuZnSOD_Drosophila            1  7.89e-10          . MVKAVCV
INGDAKGTVF
CuZnSOD2_Biomphalaria         1  7.89e-10          . MVKAVCV
LSPGSATGIT
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif MVKAVCV MEME-19 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CuZnSOD_Drosophila                7.9e-10  [19]_145
CuZnSOD2_Biomphalaria             7.9e-10  [19]_148
--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
      Motif MVKAVCV MEME-19 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF MVKAVCV width=7 seqs=2
CuZnSOD_Drosophila       (    1) MVKAVCV  1
CuZnSOD2_Biomphalaria    (    1) MVKAVCV  1
//

--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif MVKAVCV MEME-19 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 7 n= 7964 bayes= 11.9589 E= 3.3e+002
  -393   -348   -486   -450   -269   -545   -493   -207   -419   -
147    571   -464   -422   -393   -408   -409   -354   -286   -280
-226
   -97   -157   -327   -269   -152   -397   -340     82   -281    -
97    -58   -323   -256   -266   -222   -250   -112    316   -288
-209
  -323   -359   -391   -306   -421   -473   -377   -361    396   -
395   -287   -311   -352   -252     27   -350   -306   -424   -355
-326
   312    -77   -266   -200   -193   -186   -325   -195   -224   -
203   -108   -250   -214   -200   -188    -28   -107   -102   -253
-192
   -97   -157   -327   -269   -152   -397   -340     82   -281    -
97    -58   -323   -256   -266   -222   -250   -112    316   -288
-209
  -370    543   -521   -463   -408   -587   -536   -400   -514   -
441   -329   -498   -483   -468   -418   -434   -361   -464   -508
-435
   -97   -157   -327   -269   -152   -397   -340     82   -281    -
97    -58   -323   -256   -266   -222   -250   -112    316   -288
-209
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif MVKAVCV MEME-19 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 7 nsites= 2 E= 3.3e+002
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 1.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
 0.000000  1.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif MVKAVCV MEME-19 regular expression
--------------------------------------------------------------------
MVKAVCV
--------------------------------------------------------------------



Time 73.85 secs.

********************************************************************


********************************************************************
MOTIF WCSIDGNPKHE MEME-20    width =  11  sites =   2  llr = 60  E-
value = 2.0e+003
********************************************************************
--------------------------------------------------------------------
      Motif WCSIDGNPKHE MEME-20 Description
--------------------------------------------------------------------
Simplified        A  :5:::::::::
pos.-specific     C  :5:::::::::
probability       D  ::::5::::::
matrix            E  ::::::::::a
                  F  :::::::::::
                  G  :::::5:::::
                  H  :::::::::5:
                  I  :::5:::::::
                  K  ::::::::5::
                  L  :::::::::::
                  M  :::5:::::::
                  N  ::::::a::::
                  P  :::::5:a:::
                  Q  :::::::::::
                  R  :::::::::::
                  S  ::5:5::::5:
                  T  ::5::::::::
```

```
                  V  :::::::::::
                  W  a::::::::::
                  Y  ::::::::5::

         bits    6.4 *
                 5.7 *
                 5.1 *
                 4.5 *     **  *
Relative         3.8 ** *  *** *
Entropy          3.2 ***********
(43.3 bits)      2.5 ***********
                 1.9 ***********
                 1.3 ***********
                 0.6 ***********
                 0.0 -----------

Multilevel           WASIDGNPKHE
consensus             CTMSP  YS
sequence


--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WCSIDGNPKHE MEME-20 sites sorted by position p-value
--------------------------------------------------------------------
Sequence name             Start   P-value                Site
-------------             ----- ---------            -----------
MnSOD2_Nematostella          19  5.72e-15 LFLVLLFCDV WCSIDGNPYHE
IVKYMEEYTL
MnSOD2_Nematostella         126  4.28e-13 GGGFVNHALY WATMSPNPKSE
PRTPTGKIGD
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WCSIDGNPKHE MEME-20 block diagrams
--------------------------------------------------------------------
SEQUENCE NAME            POSITION P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
MnSOD2_Nematostella               5.7e-15  18_[20]_96_[20]_119
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WCSIDGNPKHE MEME-20 in BLOCKS format
--------------------------------------------------------------------
BL   MOTIF WCSIDGNPKHE width=11 seqs=2
MnSOD2_Nematostella      (   19) WCSIDGNPYHE  1
MnSOD2_Nematostella      (  126) WATMSPNPKSE  1
//

--------------------------------------------------------------------
```

```
--------------------------------------------------------------------
     Motif WCSIDGNPKHE MEME-20 position-specific scoring matrix
--------------------------------------------------------------------
log-odds matrix: alength= 20 w= 11 n= 7800 bayes= 11.9289 E=
2.0e+003
  -390   -336   -398   -378    -64   -470   -407   -372   -369   -
220   -216   -384   -388   -317   -286   -380   -357   -358    619
-56
   171    463   -339   -297   -218   -265   -374   -222   -295   -
248   -155   -310   -264   -259   -237   -106   -154   -150   -293
-222
  -104   -158   -229   -222   -218   -306   -286   -225   -185   -
260   -128   -118   -200   -168   -154    278    260   -221   -266
-182
  -210   -209   -369   -315    -71   -434   -366    274   -289
38    406   -321   -311   -246   -257   -266   -168     41   -210
-129
  -131   -250    308      0   -228   -212   -181   -277   -115   -
274   -175     -2   -171    -82   -118    139    -45   -266   -259
-142
   -97   -232   -174   -160   -235    191   -265   -276   -166   -
264   -183   -162    310   -147   -134   -116   -154   -247   -254
-193
  -307   -310   -148   -271   -282   -347   -151   -294   -236   -
349   -246    395   -293   -191   -228   -137   -192   -350   -280
-218
  -122   -273   -244   -196   -247   -325   -298   -279   -196   -
244   -200   -263    438   -165   -173   -148   -166   -263   -324
-243
  -138   -216   -155    -88     68   -280    -92   -169    276   -
157    -74   -122   -176    -41     56   -119   -116   -188    -33
330
   -95   -189    -80    -75    -96   -221    282   -213    -69   -
190    -93     19   -132     34    -18    165     -1   -200   -159
52
  -443   -553   -191    412   -515   -550   -491   -498   -433   -
544   -449   -399   -506   -289   -428   -462   -453   -527   -522
-457
--------------------------------------------------------------------

--------------------------------------------------------------------
     Motif WCSIDGNPKHE MEME-20 position-specific probability matrix
--------------------------------------------------------------------
letter-probability matrix: alength= 20 w= 11 nsites= 2 E= 2.0e+003
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
 0.500000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
```

```
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.500000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.500000  0.000000  0.000000  0.500000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.500000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  1.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  1.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.500000
 0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.500000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.500000  0.000000  0.000000  0.000000  0.000000
 0.000000  0.000000  0.000000  1.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000
--------------------------------------------------------------------

--------------------------------------------------------------------
      Motif WCSIDGNPKHE MEME-20 regular expression
--------------------------------------------------------------------
W[AC][ST][IM][DS][GP]NP[KY][HS]E
--------------------------------------------------------------------




Time 76.18 secs.

********************************************************************


********************************************************************
SUMMARY OF MOTIFS
********************************************************************

--------------------------------------------------------------------
      Combined block diagrams: non-overlapping sites with p-value <
0.0001
--------------------------------------------------------------------
```

```
SEQUENCE NAME            COMBINED P-VALUE  MOTIF DIAGRAM
-------------            ----------------  -------------
CCS_Homo                        2.52e-156  11_[11(2.82e-
16)]_6_[9(7.15e-36)]_4_\
    [15(2.38e-11)]_5_[10(6.16e-13)]_[16(2.37e-09)]_[1(3.80e-28)]_2_\
    [5(1.23e-23)]_[4(2.64e-31)]_[8(3.36e-11)]_2_[12(9.30e-23)]_18
CuZnSOD1_Homo                    4.83e-89  [14(5.77e-
13)]_3_[10(1.43e-11)]_9_\
    [1(1.89e-30)]_2_[5(5.97e-28)]_3_[4(1.84e-33)]_[8(6.06e-12)]_1
MnSOD_Homo                      6.05e-178  [14(4.99e-
08)]_11_[3(3.54e-53)]_2_\
    [6(4.30e-47)]_1_[7(1.10e-42)]_6_[2(4.00e-51)]_[13(1.61e-17)]_3
CuZnSOD2_Homo                    1.70e-48  33_[18(2.59e-
09)]_38_[10(1.65e-09)]_\
    13_[1(3.93e-22)]_27_[4(1.42e-28)]_[8(9.49e-10)]_27
CCS_Ciona                       3.69e-143  4_[11(2.88e-
18)]_5_[9(1.11e-30)]_5_\
    [15(1.04e-10)]_4_[10(4.83e-10)]_[16(7.44e-09)]_[1(1.68e-27)]_2_\
    [5(1.50e-23)]_[4(2.65e-29)]_[8(6.25e-06)]_2_[12(4.10e-22)]_15
CuZnSOD_Ciona                    8.27e-83  [14(3.29e-
11)]_3_[10(2.00e-11)]_9_\
    [1(7.28e-30)]_2_[5(7.79e-22)]_3_[4(8.76e-34)]_[8(8.67e-13)]_1
MnSOD_Ciona                     1.18e-163  19_[3(1.62e-
55)]_2_[6(2.32e-40)]_1_\
    [7(3.64e-38)]_6_[2(2.35e-51)]_[13(4.85e-14)]_1
CuZnSOD1_Biomphalaria            1.58e-62  5_[1(2.74e-
32)]_2_[5(6.42e-25)]_3_\
    [4(1.86e-24)]_3_[8(4.07e-11)]_5
CuZnSOD2_Biomphalaria            2.75e-86  [19(7.89e-
10)]_8_[10(1.06e-10)]_9_\
    [1(3.82e-32)]_2_[5(5.70e-27)]_3_[4(5.00e-36)]_[8(2.37e-12)]_1
CuZnSOD3_Biomphalaria            6.82e-57  43_[10(1.17e-
09)]_18_[1(9.89e-23)]_\
    2_[5(1.20e-16)]_3_[4(9.65e-30)]_[8(2.99e-10)]_1
MnSOD_Biomphalaria              1.09e-153  21_[3(3.29e-
51)]_2_[6(2.96e-43)]_1_\
    [7(3.94e-34)]_6_[2(4.71e-49)]_[13(3.17e-13)]_5
CCS_Crassostrea                 1.51e-109  9_[11(7.52e-
17)]_6_[9(5.65e-39)]_20_\
    [10(1.07e-09)]_[16(7.44e-10)]_[1(1.20e-19)]_21_[17(6.30e-
33)]_3_\
    [8(8.64e-09)]_3_[12(3.02e-19)]_12
CuZnSOD_Crassostrea              5.03e-96  2_[14(1.29e-
10)]_3_[10(5.00e-12)]_9_\
    [1(4.50e-32)]_2_[5(2.39e-28)]_3_[4(1.68e-38)]_[8(8.67e-13)]_1
MnSOD_Crassostrea               4.23e-160  25_[3(2.36e-
61)]_2_[6(4.00e-38)]_2_\
    [7(2.59e-33)]_6_[2(1.82e-50)]_[13(1.39e-15)]_2
CCS_Drosophila                  3.29e-112  3_[11(5.36e-
10)]_5_[9(5.95e-32)]_19_\
    [10(6.30e-08)]_2_[16(7.60e-06)]_[1(4.06e-27)]_4_[5(2.18e-17)]_\
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    [4(3.79e-25)]_[8(1.26e-10)]_2_[12(2.77e-23)]_12
CuZnSOD_Drosophila               9.92e-84  [19(7.89e-
10)]_4_[10(1.28e-11)]_9_\
    [1(4.55e-31)]_2_[5(7.13e-22)]_3_[4(5.33e-38)]_[8(7.22e-11)]_2
MnSOD_Drosophila                 3.87e-66  9_[3(3.93e-
55)]_2_[6(7.71e-35)]_27
CuZnSOD2_Drosophila              3.33e-78  4_[10(2.00e-
11)]_9_[1(5.26e-31)]_2_\
    [5(4.42e-24)]_3_[4(8.74e-37)]_[8(7.22e-11)]_2
CuZnSOD_Caenorhabditis           1.25e-75  22_[14(1.18e-
08)]_2_[10(5.28e-10)]_\
    1_[16(2.40e-05)]_[1(3.82e-32)]_2_[5(8.94e-25)]_3_[4(1.45e-
24)]_3_\
    [8(1.80e-10)]_3
MnSOD_Caenorhabditis            7.97e-154  22_[3(1.35e-
52)]_2_[6(4.15e-36)]_\
    [7(2.59e-35)]_6_[2(1.41e-51)]_[13(7.13e-17)]_3
CCS_Hydra                       3.93e-111  5_[11(5.72e-
14)]_6_[9(2.30e-40)]_3_\
    [15(2.67e-10)]_5_[10(5.78e-10)]_[16(4.21e-05)]_1_[1(8.30e-
23)]_25_\
    [4(2.05e-18)]_7_[12(3.31e-20)]_5
CuZn_Hydra                       6.05e-81  [14(2.26e-
10)]_1_[10(7.55e-10)]_9_\
    [1(2.49e-30)]_2_[5(1.85e-25)]_3_[4(1.69e-34)]_[8(5.98e-11)]_1
MnSOD_Hydra                     3.58e-156  20_[3(4.80e-
49)]_2_[6(1.98e-44)]_1_\
    [7(4.70e-38)]_6_[2(3.14e-48)]_[13(3.96e-15)]_2
CCS_Acropora                    2.10e-129  7_[11(2.88e-
18)]_6_[9(5.92e-36)]_6_\
    [15(5.11e-11)]_4_[10(2.53e-10)]_[16(3.72e-08)]_[1(1.20e-27)]_2_\
    [5(6.37e-26)]_[4(3.96e-29)]_2
CuZnSOD_Acropora                 3.44e-84  23_[14(8.67e-
08)]_5_[10(1.73e-10)]_\
    7_[1(2.31e-32)]_2_[5(1.11e-24)]_3_[4(1.14e-34)]_[8(8.67e-13)]_1
MnSOD_Acropora                   5.10e-62  25_[3(7.81e-
46)]_2_[6(3.27e-38)]_8
CCS_Amphimedon                  1.03e-115  3_[11(6.99e-
19)]_5_[9(4.44e-36)]_7_\
    [15(7.57e-09)]_5_[10(1.39e-09)]_[16(1.85e-09)]_1_[1(5.40e-
19)]_28_\
    [17(2.11e-29)]_5_[8(1.51e-10)]_2_[12(3.67e-22)]_5
CuZnSOD_Amphimedon               4.55e-74  12_[14(6.59e-
08)]_3_[10(1.39e-09)]_\
    8_[1(3.40e-29)]_2_[5(2.58e-18)]_2_[4(2.31e-35)]_[8(1.20e-11)]_3
MnSOD_Amphimedon                1.16e-144  25_[3(6.56e-
47)]_2_[6(3.86e-37)]_1_\
    [7(8.60e-42)]_6_[2(2.39e-52)]_14
CCS_Trichoplax                  3.83e-123  4_[11(1.39e-
18)]_6_[9(9.20e-30)]_6_\
    [15(7.94e-11)]_4_[10(9.96e-14)]_[16(4.25e-08)]_[1(9.89e-23)]_2_\
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    [5(2.04e-16)]_[4(5.14e-16)]_4_[12(1.05e-22)]_10
CuZnSOD_Trichoplax               5.53e-93  [14(4.81e-
13)]_2_[10(4.72e-11)]_9_\
    [1(6.21e-32)]_2_[5(5.64e-26)]_3_[4(1.39e-37)]_[8(2.09e-12)]_2
MnSOD_Trichoplax                1.39e-157  24_[3(2.25e-
53)]_2_[6(1.61e-38)]_1_\
    [7(9.86e-39)]_6_[2(1.03e-50)]_[13(4.88e-12)]_3
CCS_Capsaspora                  2.63e-108  4_[11(3.09e-
14)]_12_[9(1.32e-32)]_4_\
    [15(4.26e-09)]_7_[10(2.56e-13)]_[16(1.44e-08)]_[1(1.35e-24)]_5_\
    [5(2.01e-07)]_[4(2.19e-22)]_[8(9.05e-06)]_2_[12(2.76e-19)]_46
CuZnSOD_Capsaspora               1.08e-84  [19(4.06e-
05)]_6_[10(7.26e-08)]_7_\
    [1(1.22e-34)]_2_[5(2.80e-29)]_3_[4(1.14e-34)]_[8(1.94e-11)]_1
FeMnSOD_Capsaspora              1.34e-154  27_[3(3.62e-
57)]_2_[6(2.44e-34)]_2_\
    [7(1.32e-35)]_6_[2(2.35e-47)]_[13(7.13e-17)]_4
CCS_Nematostella                2.62e-169  10_[11(7.84e-
20)]_6_[9(5.65e-39)]_8_\
    [15(3.89e-11)]_4_[10(5.80e-11)]_[16(7.44e-10)]_[1(4.50e-32)]_2_\
    [5(1.16e-25)]_[4(8.78e-36)]_[8(5.87e-10)]_2_[12(9.97e-24)]_7
CuZnSOD3_Nematostella            1.62e-32  14_[1(3.73e-
05)]_3_[5(1.06e-18)]_3_\
    [4(1.76e-25)]_3_[8(8.10e-10)]
CuZnSOD2_Nematostella            6.96e-88  [14(6.61e-
11)]_3_[10(6.04e-14)]_1_\
    [16(3.19e-05)]_[1(1.66e-28)]_2_[5(1.64e-25)]_3_[4(8.78e-
36)]_[8(8.67e-13)]_\
    3
CuZnSOD1_Nematostella            3.78e-89  [14(3.55e-
10)]_3_[10(4.43e-12)]_9_\
    [1(2.74e-32)]_2_[5(3.45e-26)]_3_[4(5.00e-36)]_[8(1.20e-11)]_1
MnSOD1_Nematostella             7.98e-173  21_[3(7.46e-
56)]_2_[6(1.35e-43)]_1_\
    [7(5.18e-44)]_6_[2(9.43e-52)]_[13(2.67e-14)]_3
MnSOD2_Nematostella              4.32e-68  18_[20(5.72e-
15)]_4_[3(7.23e-34)]_\
    42_[20(4.28e-13)]_7_[7(2.95e-23)]_5_[2(2.97e-12)]_[13(3.22e-
11)]_10
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Stopped because requested number of motifs (20) found.
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CPU: meme-server

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