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Rapid Evolution of Sperm Chromatin Remodeling Proteins in Primates

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Rapid Evolution of Sperm Chromatin Remodeling Proteins in Primates

An honors thesis presented to the
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and
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Hanna Catherine Corliss

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Abstract

Spermatogenesis requires both the remodeling and condensation of chromatin, a process facilitated by the sequential replacement of histones with sperm-specific DNA binding proteins. First, the transition nuclear proteins 1 and 2 (TNP1, TNP2) act to replace the sperm-specific histones, then they are themselves replaced by protamine 1 (PRM1) and, in some species, protamine 2 (PRM2). It has been theorized that changes to these chromatin-remodeling proteins may affect an organism's sperm formation, and thus reproductive success. While studies have found that PRM1 evolves rapidly, with evidence of positive selection on the human lineage, and that PRM2 has also evolved rapidly in some groups, the evolutionary rates of the TNPs have not been reported. Our research therefore compares the rates and patterns of evolution of the genes that encode the proteins in the protamine locus (*Prm1, Prm2, Prm3*, and *Tnp2*) and *Tnp1*, which is on a different chromosome. To do this, we have utilized NCBI databases and their BLAST tools to retrieve sequences of these five genes from diverse mammalian species, with an emphasis on the primates. We have obtained gene sequences of 25 primate species of known phylogenetic relationship, and aligned them against each other using the molecular analysis software package *MEGA7*. From these alignments, we were able to both characterize the overall consensus sequence for each protein and analyze interspecies differences. We also produced expanded alignments including other mammalian sequences, so that we may compare them to the primates. Our analyses suggest a few patterns of evolution within the genes that encode our proteins of interest. In general, the genes in the protamine locus appear to have experienced more rapid evolution than *Tnp1*, which appears to be highly conserved in most species studied, with the notable exception of the gorilla, where it appears to be an expressed pseudogene. Surprisingly, *Tnp2* has evolved so rapidly that its sequences were difficult to align across some species, even within the primates. This rapid evolution appears to be due primarily to repeat sequence expansion and contraction, rather than to simple point mutations. *Prm1* and *Prm2,* though also experiencing relatively rapid evolution (mostly at a point mutational level), exhibit conservation of certain positions, including characteristic cysteine residues and arginine stretches. Similar to *Tnp2, Prm3* shows dramatic evolution due to repeat expansions. In rodents and primates, there is a 12-nucleotide expansion that encodes a 4-amino acid repeat near the N-terminus; in addition, all mammals show a simple repeat region that encodes a stretch of glutamate residues. We note that proteins encoded at the protamine locus have evolved more rapidly in the hominoids than in the Old World monkeys. Our study of these sequences using the alignments and sequence analysis tools has led us to theorize that the evolution of the protamine locus is not only in rapid in nature, but characterized by several repeat expansion areas, indicative of non-B DNA motifs that are known to be mutagenic. We believe that the possibility of non-B DNA mutagenesis driving the rapid evolution of the protamine locus merits further study, because this implies that these proteins evolved quickly due to mutational drive, rather than to positive selection, as previously suggested by several authors. If true, this has broad implications for the study of molecular evolution, in general.

Acknowledgements

First and foremost, I would like to thank my research advisor, Dr. Caro-Beth Stewart, for warmly accepting me, along with other undergraduates, into her lab and sharing her knowledge of evolutionary bioinformatics with us. Without her guidance and practical experience as we worked through various, at times convoluted, results and their evolutionary implications, I would not have been able to complete this thesis. I feel extremely fortunate to have spent these last two years doing research with her and I will always carry with me all that she has taught us.

I would also like to acknowledge my partners, Aliza Barnett and Michael LaRocca, for their help and support on our projects. Aliza and I worked together for the first year of this project, creating our preliminary alignments and endeavoring through gorilla gene searches to present our findings about transition nuclear protein 1. Michael has partnered with me this past year and has generously provided me with his alignments on transition nuclear protein 2, which he first worked on with Yadurshini Raveendran, so that this thesis may be comprehensive of an entire genetic locus. They have both been not only great partners to work with, but have become dear friends of mine.

Finally, I would like to thank my parents, Jennifer and John, and my boyfriend, Anthony Piche, for their continued love and encouragement in all my ventures these past four years. I am who I am today because of them, and I do all that I do with them in mind.

Table of Contents

List of Figures

Introduction

Histone Replacement: An Overview

Fundamental to the mammalian life cycle are the processes of spermatogenesis and oogenesis, which create the male and female gametes that later combine to produce the embryo-forming zygote. As cell-forming processes, spermatogenesis and oogenesis are both tightly regulated and elaborate in nature, with spermatogenesis consisting of at least five different biological stages, including that of differentiation, meiosis, and maturation (Neto et al., 2016). Due to this complexity, the precise functional and evolutionary mechanisms associated with the genes and proteins that underlie some of these stages of the spermatogenesis process are not fully understood. This holds true for a crucial phase of spermatogenesis: the replacement of sperm-specific histones with protamines, a process that dramatically compacts the sperm chromatin and renders it inactive.

Early during spermatogenesis, somatic histones, basic proteins that bind to the DNA forming nucleosomes, are replaced by sperm-specific histone variants. Sperm histone replacement is thought to occur during steps 10-16 of spermiogenesis (Lévesque et al., 1998). This causes the nucleosomes to dissociate, making the chromatin more amorphous. From this point, two functionally related protein families, the transition nuclear proteins 1 and 2 (TNP1, TNP2) and protamines 1 and 2 (PRM1, PRM2), act on the chromatin. Though it is not known definitively how this occurs, it has been theorized that after histones separate, TNP1 and TNP2 function in the cell to facilitate stabilize and condense the chromatin and to aid in protamine binding (Lévesque et al., 1998). As a result of this transition, the once round histone-rich nucleus changes dramatically in shape and protein content, showing much more condensation and containing protamines as its major nuclear proteins (Meistrich et al., 2003).

The replacement of the histones with protamines is thought to affect forming spermatids in a couple of ways, both of which seem to occur as a result of the dissolution of the typical nucleosome structure of the DNA. Foremost, this dissolution allows for the once condensed, precisely assembled chromatin to undergo remodeling. During this remodeling, both nuclear elongation and condensation take place, streamlining the DNA in a way that contributes to proper sperm head formation and later functioning (Lévesque et al., 1998). In addition to this, it has also been suggested that the transition causes the cessation of chromatin transcription, suggesting that the histones' replacement not only causes a structural change in DNA, but a functional one (Meistrich et al., 2003; Lévesque et al., 1998). This, too, may be tied to the dissolution of the prior structure of the DNA, which may be needed for transcription, or possibly to repair breaks in the DNA that have occurred as a consequence of said dissolution (Meistrich et al., 2003).

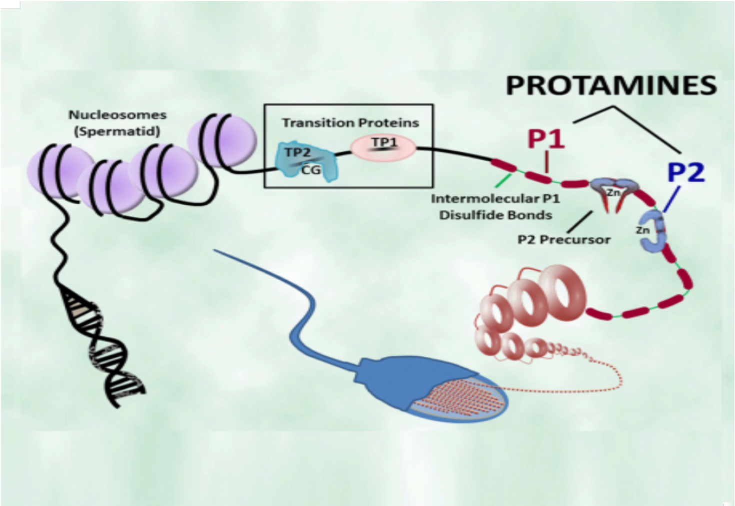

Figure 1: The transition from histones to protamines during spermatogenesis. Shown are the structural changes in chromatin during spermatogenesis, as then DNA binding proteins switch from histones to protamines (PRMs), as mediated by transition nuclear proteins (TNPs). Image from http://www.briarpatchbio.com/virtue/woocommerce/mammalian-protamines/.

Transition Nuclear Proteins (TNPs)

Our research examines evolution within the genes that encode for these proteins involved in the histone replacement process, in part so we may decipher what their amino acid conservation and changes suggest about their functioning. Whereas the TNP1 and TNP2 proteins appear to share a general function, and thus name, their two genes are quite different in their basic characteristics and evolutionary patterns. This may be partly explained by the fact that, while *Tnp1* is located on chromosome 2, *Tnp2* is located in the protamine locus on chromosome 16 in humans. While researching these genes, it has therefore been our approach to treat them as distinct entities, including *Tnp2*/TNP2more frequently with our analysis of the protamines, while examining the more slowly evolving *Tnp1/*TNP1 as a separate entity.

The *Tnp1* gene sequence, as mentioned previously, is located on chromosome 2 in humans and on chromosome 2B in non-human primates (NCBI, 2016), where it is estimated to span approximately 607 nucleotides, depending on intron length. The gene includes two exons, one intron, and the flanking non-coding 5’ and 3’ regions. The coding sequence of the first exon spans 141 nucleotides, whereas the coding region of the second exon is only about 27 nucleotides long; together these sequences compose the 168-long coding sequence of *Tnp1* in most species. The intron that divides these exons is about 200 nucleotides in length. As part of the histone replacement process, the *Tnp1* gene is typically expressed in stages 10-16 of spermiogenesis, and during these stages its expression may be modulated by kinases PKA and PKC (Lévesque et al., 1998). The expressed protein is predicted to be 55 amino acids in length in most species, and to have a molecular mass of about 6424 Daltons (TNP1 gene).

The *Tnp2* gene is found clustered with *the Prm1*, *Prm2*, and *Prm3* genes in an area of approximately 13 kb on human chromosome 16 (Hartz, 2009). The entire *Tnp2* gene takes up approximately 1,173 nucleotides and, like *Tnp1*, contains two exons, an intron, and the flanking regions (NCBI, 2016). The first exon has a coding sequence of approximately 400 nucleotides and the second has one of about 17, meaning that the entire coding region is approximately 417 nucleotides long; the intron is about 849 nucleotides (Engel et al., 1992), depending on species. Spicing this intron out of the transcript creates the *Tnp2* mRNA that encodes the TNP2 protein, which is 138 amino acids long in humans (NCBI, 2016) and most other species examined herein (see Results). Along with TNP1, TNP2 is expressed during stages 10-16 of spermiogenesis (Lévesque et al., 1998). These two proteins have been thought to be the primary proteins involved in displacement of the sperm-specific histones during the late stages of spermatogenesis, setting the stage for the deposit of the protamine proteins on the DNA of mature sperm (Meistrich et al., 2003).

Protamines (PRMs)

The protamines constitute a well-studied family of proteins [see Balhorn (2007); Braun (2001) for review] that are encoded together at chromosome 16p13.3 in humans (Engel et al., 1992). Though they are typically considered together as a locus and have some basic attributes in common, each gene and their corresponding proteins is unique.

The PRM1 protein is only about 50 amino acids long, and is about 50% arginine, making it a highly basic protein. Its 156-nucleotide coding region is derived from two exons; the first exon comprises 113 nucleotides of the coding sequence and the second 43. The *Prm2* gene, on the other hand, is longer. Its coding sequence is 309 nucleotides in length, with its first exon containing 272 of these protein-coding nucleotides and the second containing 37. The full-length PRM2 protein is 102 amino acids long, on average, and has an acidic N-terminal region and a basic C-terminal region. The N-terminal portion is cleaved off in some mammalian groups — including primates and rodents — leaving a shorter mature PRM2 protein that is highly basic, like PRM1, which is found on mature sperm in these species. Species that do not cleave off the N-terminal sequence do not have PRM2 on mature sperm, but do express the *Prm2* mRNA and the full-length PRM2 protein during sperm maturation (reviewed in Balhorn, 2007). The function of the full-length PRM2 protein variant is not known.

The protamine locus has an additional gene (originally called “gene 4”) that was recognized more recently, first an open reading frame (Nelson & Krawetz, 1994), but has been named “*Prm3*” in the genetic databases and more recent literature (see, *e.g.,* Grzmil et al., 2008). The *Prm3* gene sequence consists of one exon whose coding sequence is approximately 312 nucleotides, producing a protein sequence that is about 104 amino acids long, though the exact numbers vary depending on the species considered (Schluter & Engel, 1995; see Appendix H). Despite its name, the *Prm3* gene does not code for a protein that has true protamine-like characteristics, — that is, it does not have high levels of arginine residues, but rather is negatively-charged. The function of this protein, if any, is currently uncertain. Our analyses suggest that it might be involved in disulfide exchange with transition proteins and act as a chaperone for protamines (see Discussion).

While the PRM1 and mature PRM2 proteins are similar in their overall nature, both containing these stretches of arginine and therefore constituting highly basic proteins, PRM3 varies substantially from the two (Braun 2001). Its sequence lacks these repeated arginine stretches and instead has a glutamic acid stretch (Schluter & Engel, 1995). In fact, even though the *Prm3* gene is located between *Prm2* and *Tnp2* in the protamine locus, there has been much debate whether PRM3 can be considered a protamine (Schluter & Engel, 1995; Grzmil et al., 2008).

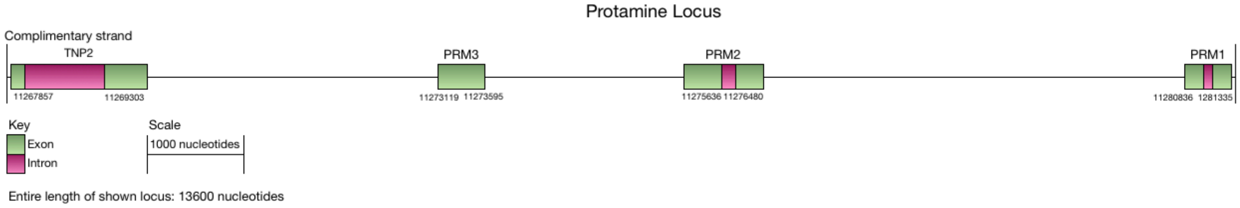

Figure 2: Illustration of the protamine locus (*Prm1, Prm2, "Prm3",* and *Tnp2* genes) on chromosome 16 of humans. [Based on references data from NCBI (2016)].

Functional relationships

Considering the central role of both TNP1 and the protamines in histone displacement during spermiogenesis, it seems plausible that evolutionary mutations that change key structural components of these proteins may influence their proper functioning, affecting reproductive fitness. In the case of TNPs, it has been suggested that complete absence or diminished expression of *Tnp1* may contribute to reduced fertility. This was supported by one study that found that when *Tnp1* is knocked out in mice, that histone displacement and chromatin condensation do still occur, but that the chromatin's structure is altered from a fine fibril to a rod-like organization (Yu et al., 2000). Ultimately, this mutation caused reduced sperm motility and fertility, leading to the conclusion that TNP1 has an important role in ensuring proper chromatin condensation, but that it may not be essential for histone displacement, as it may be compensated for partly by TNP2 (Yu et al., 2000). According to some studies, TNP2 also serves to stabilize and condense DNA, but does so more efficiently than TNP1 (Lévesque et al., 1998). Knocking out both genes produces a complete elimination of the transition nuclear proteins, and thus more severe abnormalities in terms of nuclear condensation and sterility (Braun 2001). This further suggests that the proteins function together, performing similar processes as they facilitate protamine attachment.

Similarly, the protamines' role in proper nuclear formation and sperm function is attested to by studies that ablate protein functioning. In a study where PRM1 or PRM2 expression was reduced in mice, sperm functioning was abnormal and nuclear formation was disrupted (Cho et al., 2001). When the genes were completely knocked out, male chimeras were unable to produce offspring as a result (Cho et al., 2001). Further, some studies have found positive selection occurring within the *Prm1* genes (Rooney et al., 2000; Van Den Bussche et al., 2002) towards maintaining a large amount of arginine residues, which are thought to enhance DNA binding adaptively (reviewed by Balhorn, 2007). This suggests that the maintenance of proper PRM1 and PRM2 functioning is selected for, reaffirming the idea that functional protamines are necessary for spermiogenesis. Although the functioning of PRM3 has been less studied, Grzmil et al. (2008) showed that male rats whose *Prm3* gene had been completely disrupted experienced reduced sperm motility, which was theorized to affect overall reproductive fitness. Together, these findings suggest that, at the very least, mutations in TNPs and PRMs influence reproductive fitness.

Introduction to methods and results

To better understand the nature of these chromatin remodeling proteins, we wanted to take a deeper look at the evolution of their DNA and protein sequences. We did this primarily by using the resources available through the National Center for Biotechnology Information (NCBI), which maintains searchable databases containing a vast amount of genetic data and tools to analyze them. We aligned the sequences using the software package *MEGA7* (Kumar et al. 2015), and performed tree analyses using *MacClade* (Maddison & Maddison 2005) and *PAUP**

(Swofford 2018). With these resources, we created alignments of the primate gene sequences down to the nucleotide level, so that we could examine how these genes appeared in humans and our primate relatives. From that point, we refined our alignments, producing copies where certain features — such as the coding region or intron of the gene — were highlighted, and others that included other mammalian sequences. These gene alignments allowed us to infer the respective amino acid sequences of the various proteins.

Our analyses support the notion that the protamine locus proteins have all experienced rapid evolution, seemingly through two distinct processes of mutation. The first type of mutations we saw were those of small individual changes to amino acids, apparently due to point mutations. Such point mutations commonly occur over time in DNA sequences, but they were still important to our research because they sometimes affected important areas of the proteins, such as cysteine residues that could affect the functioning of the protein. The other, more striking form of evolution we noted was the expansion and contraction of simple repeat sequences throughout some of the proteins, most notably in PRM3 but also in TNP2. We theorize that these mutations might be due to non-B DNA forming structures, which are known to be mutagenic by producing both repeat slippages and point mutations at a high rate (Kamat et al., 2016). We illustrated the influence of both of these forms of evolution in the primate lineage by comparing relative rates of amino acid replacement on a phylogenetic tree derived from the alignments. Because mutations in these sperm chromatin remodeling proteins could affect reproductive success, further study is warranted to determine if these mutational changes effect such things as mRNA structure and stability or protein structure and function.

Materials and Methods

Producing primary alignments

Our evaluation of these two functionally-related protein families, the transition nuclear proteins and protamines, has depended on the retrieval, alignment, and analysis of their mammalian nucleotide and amino acid sequences. In carrying out these processes, we have been sure to maintain consistency and order within and between data sets for the different proteins, to ensure that we may fairly compare the rates of evolution between them. For each protein, our primary mission was to produce an alignment of their respective orthologs from the same species of primates, chosen to represent the major lineages. These species are listed in Table 1. To do this, we first searched for the reference human informational page for each of the genes on NCBI. From this resource, we retrieved both the *Homo sapiens* (human) sequence, which we used as the reference sequence, and the orthologous sequences from 24 non-human primates (NHPs) for which genomic sequences have been reported on the NCBI databases. Some of the NHP genes did not have predicted mRNA records on NCBI; in these cases, we tried to find the genes using NCBI's nucleotide and protein sequence search options, or through BLAST searches of the missing species' genomes. The gene sequences for each protein were then downloaded and organized into individual folders to facilitate their later retrieval. These gene records are given in Table 1 with links to their NCBI records, so that others may access them readily.

Once we retrieved all the available primate sequences, we uploaded them onto the sequence analysis program *MEGA7* to create multiple sequence alignments for further analysis. After the sequences were added to the *MEGA 7* files, the names of the entries were simplified, with the common species names included first, and then their scientific (genus-species) names. Subsequently, the species were organized by taxonomic relationships, to facilitate easier alignment of sequences by placing species that were more closely related together.

From there, we began the alignment process. Our first step was to establish a basis of comparison for the gene to which we could align all the other primate species' sequences. We used the human gene and its corresponding mRNA sequence for this purpose, in part due to the greater confidence we have in the sequencing and annotation of human genetic material. We began by adjusting the two inputs (gene and mRNA) so that their nucleotides (A, G, T, C) matched along the entirety of their sequences, with the exception of the intronic sequences. To do this, we had to locate where the intron was within the human gene sequence, since this area would be absent from the mRNA sequence due to splicing. Locating the intron entailed first finding the area where the two sequences diverged, which is typically marked by a characteristic GT at the 5' end of the intron. From there, we were then able to insert dashes along the length of the intron into the mRNA until we found the AG at the 3' end of the intron, after which the gene and mRNA sequences began to match up again. Upon completion of this, we had two aligned reference nucleotide sequences and marked boundaries for each gene's intron for *Tnp1*, *Tnp2*, *Prm1*, and *Prm2*. *Prm3* does not have an intron, so its gene sequence was used as reference.

After aligning the gene and mRNA sequences from human, we aligned the 24 NHP orthologous nucleotide sequences against them. We did this by simply finding the location where the base pairs in the sequence of interest first started to match with the other aligned sequences and then following through the length of the sequence, checking that it matched its entire length. Wherever deletions occurred, dashes were added to the sequence of interest to compensate, and when insertions occurred dashes were added to the other sequences to ensure alignment. Once all the sequences had been aligned, we removed the noncoding, flanking regions of the sequences from them, trimming the 5' end until the starting ATG and the 3' end after the stop codon (TAA or TGA for our genes). We saved the alignments at this point, so that for each of the proteins we would have a copy of their entire, unprocessed gene sequences aligned along their entire length. After making this duplicate, we trimmed the intronic and other non-coding sequences out of the *Tnp1*, *Tnp2*, *Prm1*, and *Prm2* genes so that only the coding regions remained. Since *Prm3* does not have an intron, the above process was enough to get the coding sequence in alignment, and a duplicate file did not have to be made. This gave us the inferred protein coding sequences for the primate genes, like what is found in a processed mRNA sequence. As a final step, we saved these alignments, so that we could translate them at any point using a function in *MEGA7* to infer the amino acid sequences of the proteins. These alignments are given in the Appendices.

When we aligned the sequences for the other mammalian orthologs, we followed the same methodology, retrieving all mammal genes from the NCBI reference site (Table 2) and then aligning the sequences at nucleotide level so that the sequences matched as much as possible. We were interested to find orthologs in the genomes of marsupials and monotremes, as only *Prm1* has been studied in these groups the existence of the other genes is not known. For some more distantly-related species, who were much more divergent in sequence due to tens of millions of years of evolution, we had to adjust the process slightly by aligning the amino acid sequences first, then back-translating to the DNA sequences in *MEGA7*. To accomplish this, we first made sure all the sequences were in the proper coding frame by trimming the 5' end until we hit the start codon. From there, we utilized the translate function of *MEGA7* to give us the amino acid sequence for all the genes. This method of aligning simplified the process, because instead of having to align the often-complicated nucleotide sequence, we instead focused on the amino acids. Since the genetic code is degenerate, point mutations in the DNA sequences are sometimes silent when translated, and so amino acid sequence can be preserved even when genetic sequence is not. This made the amino acid sequences at times easier to align. Additionally, since many of the deletion and insertion mutations that occurred affected three nucleotides affected at a time, preserving the reading frame, the amino acid sequences normally did not experience a frame shift with the mutations, but instead just deletion or insertion of individual amino acids. The areas where these insertions and deletions occurred simply shifted the amino acid alignments by a single or few residues, which could easily be seen in the more simplified amino acid coding sequence. We were able to easily remedy by simply adding dashes to adjust the residues, which would also adjust the underlying nucleotide sequence by three residues per dash. Overall, with this amino acid alignment approach, we were able to produce rough alignments for distant relatives and then convert back to the nucleotide setting to fine-tune it on that level if needed. This level of manual curation of the sequence alignments was necessary, as the computerized alignment programs that we tried on these difficult datasets routinely failed to produce biologically feasible alignments.

Testing predicted mRNA variants for PRM2

While carrying out the above alignment process, it was found that PRM2 had six predicted mRNA variants listed on its NCBI informational page. Of these six variants, five were considered coding mRNAs and one was considered a noncoding mRNA. It was noted that one of these forms, the first predicted mRNA (which is the form that has been studied by other researchers in the past), was most highly expressed; we therefore used that mRNA isoform for our alignments and subsequent analyses. However, since the protamines have been well studied, it seemed unusual that these possible isoforms have only been reported in the past few years, and so we still sought to research them further. Therefore, we began investigating the validity of these mRNAs, with the goal of determining whether these predicted isoforms represent actual mRNA splice variants found within the cell.

Our primary attempt at determining the validity of these isoforms involved aligning their nucleotide sequences in a variety of ways to understand how the isoforms differed from each other and where the alleged splice sites that caused these differences in sequence were located. The initial alignment we completed was just a simple placement of these isoforms against each other and 24 primate orthologs to see if any of the nucleotide sequences for primate species better matched that of any of proposed alternative isoforms. We carried this alignment out under the belief that if some of the primate orthologous sequences did appear to match the isoforms, it would support the notion that these predicted isoforms are actually expressed. However, our sequences only seemed to match that of human isoform 1.

With our second alignment, we compared the isoforms against each other and the full-length gene to elucidate how they differed as splice variants and to ascertain the precise locations of the predicted splice sites within the gene. From doing this, we were able to clearly view the locations of the splice sites and see what bits of sequence the predicted forms thus classified as intronic. When we compared the alignment to the NCBI reference page that listed the isoforms, we were also able to see that it reflected the documented differences between the variants. Though the variants did match their given descriptions, the predicted splice sites did not all have the canonical landmarks that typically identify legitimate splice sites. For example, one variant (isoform 3) had a GC instead of a GT at the beginning of the splice site.

In order to understand how the differences in nucleotide sequence among the isoforms affects the predicted coded amino acid sequence of the PRM2 protein, we took two additional steps to analyze the six isoforms. The first of these steps was to simply translate our prepared alignment of the isoforms' nucleotide sequences so that we can analyze their inferred amino acid sequences. As a check to this measure, we additionally downloaded and aligned the predicted protein sequences given for each mRNA isoform on the NCBI reference data site. The two alignments produced identical results. We found that, while the amino acid sequences for the isoform variants were identical up until about the 76th coded amino acid, they diverged rather distinctly after that point.

If the isoforms' amino acid sequences were actual variants, their differences in protein coding could have important implications about the functioning of PRM2. Because of this, we decided to continue researching into these predicted mRNA variants. One of the methods we used to do this was to search NCBI's protein database for PRM2. In doing this, we were hoping to both check that the predicted coding isoforms were reported in their protein form and to search to see if there were other alternative variants. Our searches retrieved the reported isoforms, as well as other possible variants (named CRA-a and CRA-b) not included on the original reference site. So, we downloaded the CRA-a and CRA-b sequences, and included them in our earlier protein alignment. This revealed that CRA-a resembles isoforms 2 and 4, and CRA-b is identical to isoform 1; therefore, these records were not included in our further analyses. (Results not shown.)

After adjusting our alignment, we wanted to see if there was any actual evidence for their existence in the EST database, which contains a collection of short single-read transcripts. We did tBLASTn searches for the nucleotide sequences of the predicted mRNA variants against the *H. sapiens* EST database. From these searches, we were able to find a few matches and partial matches for the isoforms. We took the first four of the results, which reported the strongest match, for all of the isoform searches and aligned them against each other on a *MEGA7* file. This alignment illustrated that the results did not produce a compelling enough alignment in terms of strength of match to support the existence of all of the isoform variants. For this reason, we then removed most of the predicted mRNA variants from our primary alignments, choosing to solely utilize the predominant coding mRNA isoform 1, which seemed to be supported as being real by published experiments and by our alignments that include other species.

Resolving abnormal sequence alignments

Once we had our core alignments prepared, we began examining them for mutations. In doing this, we paid special attention to sequences that did not seem to align properly and aligned sequences that seemed to show exceptional evolution. Since these cases seemed unlike the other orthologous sequences, we utilized additional measures to investigate if a given sequence was accurate or if there was perhaps a better way to align it. In doing this, we sought to minimize outlying sequences, so that we might achieve better alignments for our proteins' gene sequences. Ultimately, this would enable us to isolate and analyze actual mutations occurring within the sequences rather than artifacts or inaccurate sequencing data.

For some of these outlying sequences, natural evolutionary phenomena seemed to explain their existence and effect on the alignment. For example, there were some instances where sequences exhibited mutations of either a single nucleotide or two nucleotides, causing a frameshift to occur. Frameshifts, although only slightly affecting the appearance of the gene alignment, alter the coding reading frame and the amino acids that are inserted. Because of this, they can cause a massive disruption in the protein sequence and possibly destroy protein function. For this reason, if we found a large frameshift, we opted to remove the sequence from our analysis. Frameshifts that only slightly altered the sequence, either being remedied or occurring near the end, were kept within the alignment. In another instance, two nearby deletions of one and two nucleotides were able to bring the sequence back into frame, and so we kept the sequence and combined these deletions, slightly altering nucleotide alignment for a better protein alignment.

Another set of mutations that sometimes appeared to alter our alignments significantly included those afflicting the traditional sites that we used as signals for trimming (like the beginning ATG, ending TGA, or AG that signals intron termination). While the mutations were typically only point mutations, if they changed these characteristic motifs beyond immediate recognition, they initially altered the alignment of the affected sequence significantly by making it seem out of frame. These mutations, once recognized, were typically reconciled by finding an alternative site that could provide the same function, leaving the sequence different (slightly shorter/longer, having a slightly different code) than the others, but overall a better match. The proteins they encode, while possibly not perfect matches, likely still function.

Beyond these changes, we found evidence of more drastic differences in sequence likely not due to natural genetic mutation, but instead to erroneous sequencing. These sequences can be products of either faulty sequencing work or be caused by artifacts that are byproducts of the technique used, with both sources of error being similarly disruptive to the alignment. We thought either of these possibilities might explain the few sequences within our alignments that did not match the general consensus of the alignment to an extent beyond what would seem to be reasonable if caused by mutation. To test this, we first tried to find alternative sources of sequences on NCBI, including predicted mRNAs or different sources of gene sequences from the same species. (For example, several individual gorillas have sequenced genomes and RNAseq data available in the genetic archives.) If these additional sequences did not help, or were not available, we at times attempted to conduct BLAST searches against the genome or SRA database, which has samples of collected expressed RNA sequences, to see if we could find evidence for the sequence. Ultimately, if these efforts did not produce any results and we could not reconcile apparent errors, we left out the problematic sequences from our alignments. Some of these 'problematic' DNA sequences may represent the true gene sequences from those particular species, but if so their proteins would be highly divergent.

Even after taking these steps to reduce abnormal or artefactual sequences within our alignments, two sequences remained whose alignments confounded us. Both of these sequences seemed to show that some difficulty had arisen while they were being produced, as suggested by a string of N's in their sequence and significant deletions of coding sequence. These sequences, the *Tnp1* gene for *Gorilla gorilla* (gorilla) and the *Prm2* gene for *Carlito syrichta* (tarsier), were both key elements to our initial primate alignments, representing two genera for which we had retrieved no other sequences. Because of this importance, we put extensive work into trying to achieve a better alignment for their problematic sequences, in spite of these suggestions of issues with sequencing.

We worked first on the gorilla *Tnp1* sequence. Though the sequence was given along with the other orthologs on the NCBI site, it varied substantially from their sequences when aligned. Its sequence was over 3000 nucleotides longer than the human reference sequence, and two nucleotides after the intron-exon boundary, it completely loses the coding sequence of the second intron, instead showing what appears to be a large insertion of DNA. Our attempts to possibly find alternative sequence pulled up a predicted mRNA for gorilla, but this too varied substantially from that of the reference human mRNA. The predicted gorilla mRNA, when aligned to the gorilla gene, matched up with it for a longer distance after the intron-exon boundary than the other genes do, but eventually stopped matching at a seemingly random point. The mRNA did start matching up again at the end of the large insertion, though this matched up sequence does not resemble the bit of exon that appears to be deleted.

In attempt to better understand what the large insertion of DNA actually was and if the lost exon sequence could be located, our next step was to utilize the BLAST function on NCBI to compare the sequence to genomes and other control sequences. Our searches compared the *Tnp1* sequence of the divergent gorilla segment against *G. gorilla* and *H. sapiens* genomes and the *Tnp1* sequence of *H. sapiens* (nucleotide and mRNA versions) to *G. gorilla, Pan troglodytes, Pan paniscus*, and itself. The BLAST searches comparing the human *Tnp1* gene and mRNA to the TNP1 sequences of the other primates were conducted as a control to compare the primate sequences, revealing that they were not erroneous and that our BLAST technique was sound. In theory, since the two species of *Pan* are genetically similar to both *H. sapiens* and *G. gorilla*, the same gene in all of these species should be relatively similar in sequence. The comparisons of the *H. sapiens* sequence and mRNA against *G. gorilla* were done to perhaps reveal what was causing the discrepancy in the *G. gorilla* sequence if the sequences were found to be reliable. Additionally, we conducted the other BLAST searches of the *G. gorilla* TNP1 gene sequence against the *H. sapiens* and *G. gorilla* genomes to check if the insertion could be traced back to a piece of DNA somewhere within the two other genomes. If the search results showed that there was a match between the insertion and the genomes, it would give us a sense of where the insertion originated. From there, we interpreted the implications of the BLAST results and what they meant in regards to the *G. gorilla* sequence and our alignments.

Finally, we took additional measures to determine whether or not the *Tnp1* sequence for *G. gorilla* actually produced an expressed mRNA. We conducted these searches to see if the gene, despite having an abnormal sequence, was actually being translated. If so, we wanted to see if it matched the predicted mRNA or if it perhaps matched two predicted splice variants we found while researching the gene. Our search took the spliced mutated gene, the predicted mRNA sequence, and that of the two different splice variants and ran them in a BLAST search against an input for *Gorilla* testis tissue on the SRA, a database that provides samples of mRNA that has been collected from a tissue and sequenced. As a control, we also ran the *H. sapiens* mRNA against the same entry. We then analyzed these results as we did to the previous BLAST searches, the only difference being that the sequences from the SRA database are shorter in length and represent only fragments of the mRNA sequence. This just caused a secondary consideration whether the many fragments, when considered together, aligned against the entire length of the input sequence. To ascertain this, we took results from the spliced gene mRNA search and created an alignment for them.

The *Carlito syrichta* PRM2 sequence presented us with a slightly different problem. Its sequence was not given along with the other orthologs, rather, we had to retrieve it via BLAST searches of different orthologs against the *C. syrichta* genome. The results that came back from these searches were not as concrete as others we had previously obtained. The searches had to be done with BLASTn for less similar matches than our typical methodology, which utilizes the megaBLAST. Several attempts were made to pull realistic gene matches out of the genome. We took a realistic, yet incomplete match and utilized the *C. syrichta* genome to retrieve a longer sequence with additional material surrounding them to see if a similar sequence might be found. The match within the genome contained a string of “N” sequence (indicating poor or missing sequence data), making it appear initially as if only part of the beginning of the gene, before the intron, was present. After removing this N sequence, we were able to find the later exon in the retrieved sequence. We decided to leave N's where sequence had been lost, but to otherwise align what was present.

Uncovering patterns of evolution

With our alignments refined, we were then able to analyze our sequences for patterns of evolution that occurred within a given gene or throughout the protamine locus. Our approach in doing this was to first look at the gene as a whole and to see if the sequence varied significantly between different species or orders of mammals. Since most of the sequences at this point were similar in their coding region due to the work we had done to prepare the alignments, what we were mostly looking for here were large changes in sequence, like that which occurs with expansion or contraction of repeat sequences. Expansion or contraction can be seen in a gene when areas of repeat (a singular nucleotide or a more complex repeat sequence) either grow in number or lessen in number. We noted this phenomenon particularly in PRM3, which has two separate regions undergoing apparent expansion in primates and some rodents, and spent considerable time examining the sequences involved on a nucleotide and amino acid level.

After these large regions of evolutionary change were reviewed, we began to take a closer look at the amino acid sequences themselves. In doing this, we found that many of the proteins had sites that were generally conserved across most, if not all, species; these include sites such as cysteine residues that typically occurred at a precise spot in the protein. We then became interested in the smaller point mutations that occurred at these conserved sites. Because the sites are conserved when the gene themselves are experiencing relatively rapid rates of evolution (excluding *Tnp1*), it might be inferred that they serve some function that is important enough to the protein's function to be maintained (*i.e.*, cysteine residues may be involved in disulfide bonds, catalytic sites, or zinc fingers). Thus, when mutations occur in such sites, they might impact protein form or function in the species.

Finally, we made some efforts to compare evolution between the genes. One way in which we did this was to look for similar motifs within genes. Additionally, we looked to see if changes in one gene were perhaps compensated for in another. Principally, we did this by counting the amount of a certain negative (like glutamate) or positive (like arginine) residues within protamine locus proteins to see if changes within the number of charged residues in one gene sequence was balanced by an equivalent amount of changes in another. Further research, if done, will likely continue these efforts to examine evolution within the locus.

Mapping replacements on phylogenetic trees

To characterize where evolutionary changes have occurred between orthologs, we used the coding alignments to produce phylogenetic trees for the primate sequences for each protein. This process entailed exporting the alignments into a *NEXUS* format and then uploading them into *MacClade* (Maddison & Maddison, 2005), a software program that can be used to build phylogenetic trees upon which sequence evolution can be analyzed by parsimony approaches. Using *MacClade*, we produced two types of trees: one whose branches showed nucleotide substitutions (not shown) and another showing amino acid changes (see Results). To create these trees, we manually moved the lineages to build the ‘known’ primate phylogeny. For each alignment, we next went to the settings menu and pulled up the character list, which allowed us to assign codon positions starting with the ATG start codon. For the trees showing DNA level changes, we then selected the option to trace all nucleotide changes between the sequences based on the “minimum-average-maximum” setting; this produces trees branch lengths that are an average of the most-parsimonious assignments. By selecting "display trace labeling," the amount of change between each branch was shown on the trees. We adjusted the display of these trees, showing them as a phylograms (with branches proportional to amount of change), allowing quick visualization of fast and slow lineages.

In the case of *Tnp1*, we created two trees by removing the gorilla sequences from one of them, because the predicted evolution of this gene is so extensive that it distorted the scale for the other species. This second version of the *Tnp1* alignment, without the gorilla, depicted more accurately the evolutionary rate in the gene sequences in the other primate species. The amino acid replacement tree was made in a similar process, except that after setting the codon positions we had to convert the data format to protein. We were then able to select the option to trace amino acid changes, and follow the above procedure.

These phylogenetic trees, once completed, suggested where nucleotide substitutions and amino acid replacements must have occurred along the different branches of the primate trees, illustrating the evolution of the sequences in a visually accessible way. They also enabled more direct comparison of evolutionary rates between species and between proteins, substantiating the patterns of evolution and general fast rates that we inferred from the alignment. We analyzed the evolutionary rates of the different proteins further using a program named *PAUP** (Swofford 2018), that allowed us to import the *MacClade* files (including the trees, and then perform further analyses. Such analyses included calculations of pairwise differences, patristic (reconstructed pathway) differences, amino acid composition, and homoplasy indices. In doing this, we adjusted the input data matrix to consider gaps as "new states", so that the output analyses considered the dashes (-) in our alignments as mutational events.

Table1: Primate gene sequence reference information

Family	Species	Common name	TNP1	TNP2	PRM1	PRM2	PRM3
Hominoids	Homo sapiens	Human	7141	7142	5619	5620	58531
Hominoids	Pan troglodytes	Chimpanzee	740418	467904	494139	453921	737190
Hominoids	Pan paniscus	Bonobo	100973877	100971267	100971614	100970844	100970489
Hominoids	Gorilla gorilla	Gorilla	109025868	101132169	101132528	101132898	101133753
Hominoids	Pongo abelii	Sumatran orangutan	100457411	100447013	100447749	100446402	100447377
Hominoids	Nomascus leucogenys	Northern white-cheeked gibbon	100579297	101177240	93728048-93728376	100606237	100605898
Hominoids	Hylobates lar	Lar gibbon			P35306.2	P35314.1	
Old World Monkey	Rhinopithecus bieti	Black snub-nosed monkey	108544388	108541231	108541233	108541232	108525542
Old World Monkey	Rhinopithecus roxellana	Golden snub-nosed monkey	104661612	104667709	104667706	104667707	104667708
Old World Monkey	Colobus angolensis	Angolan colobus	105504746	105525707	105525675	105525677	105525678
Old World Monkey	Piliocolobus tephrosceles	Ugandan red colobus	111546040	111555213	111555217	111555215	111555214
Old World Monkey	Papio anubis	Olive baboon	101013510	101008857	101009645	101009198	101010720
Old World Monkey	Cercocebus atys	Sooty mangabey	105587084	105572174	105572178	105572176	105572175
Old World Monkey	Mandrillus leucophaeus	Drill	105528022	105545262	105545258	105545259	105545261
Old World Monkey	Chlorocebus sabaeus	Green monkey	103217829	103228304	103228324	103228313	103228307
Old World Monkey	Macaca nemestrina	Southern pig tailed macaque	105481190	105467766	105467769	105467768	105467767
Old World Monkey	Macaca mulatta	Rhesus macaque	696593	106994950	716327	711424	711341
Old World Monkey	Macaca fascicularis	Crab eating macaque	101865270	102135039	102133914	102134321	102134688
New World Monkey	Cebus capucinus	White headed capuchin	108308899	108312173	2023915-2024410	2018902-2019582	108312174
New World Monkey	Saimiri bolivensis	Black capped squirrel monkey	101040758	101053739	32359092-32359460	101051182	101054063
New World Monkey	Aotus nancymaae	Nancy Ma's night monkey	105712758	105717843	3648450-3648956	105717858	105717844
New World Monkey	Callithrix jacchus	Common marmoset	100413199	100897054	15851618-15852126	15856569-15857256	100406387
Tarsier	Carlito (Tarsius) syrichta	Philippine tarsier	103252297	103264162	124239-124736	127495-127994	103264160
Strepsirrhine	Microcebus murinus	Gray mouse lemur	105882622	105882421	105882400	105882413	105882407
Strepsirrhine	Propithecus coquereli	Coquerel's sifaka	105825306	105813046	105813022	105813043	105813046
Strepsirrhine	Otolemur garnetti	Northern greater galago	100954886	100955396	105888098	105888096	100955088

Note: Numbers in green boxes signify gene location where we retrieved sequence from linked assemblies

Table2: Non=primate mammal gene sequence reference information

Group	Species	Common name	TNP1	TNP2	PRM1	PRM2	PRM3
Dermoptera	Galeopterus variegatus	Sunda flying lemur	709-1162	103609496	452094-452573	456258-457042	103584432
Scandentia	Tupaia chinensis	Chinese tree shrew	102473875	102499287	2361547-2362031	102498437	102498862
Rodentia	Mus musculus	House mouse	21958	21959	19118	19119	19120
Rodentia	Mus caroli	Ryukyu mouse	110298088	110311882	110311593	110311592	110311984
Rodentia	Mus pahari	Shrew mouse	110322653	110329988	110329956	110329955	110329336
Rodentia	Peromyscus maniculatus bairdii	Prairie deer mouse	102921195		102925705	102926022	102926322
Rodentia	Rattus norvegicus	Norway rat	24839	24840	24685	25345	442921
Rodentia	Dipodomys ordii	Ord's kanagaroo rat	105986781		10276116-10276342		105982084
Rodentia	Microtus ochrogaster	Prarie vole	102001940	102000407	102001258	102000976	102000694
Rodentia	Meriones unguiculatus	Mongolian gerbil	110562033	110555258	110555260	110555261	110555264
Rodentia	Mesocricetus auratus	Golden hamster	101824343	101831800	2950628-2951120	101828406	101827883
Rodentia	Cricetulus griseus	Chinese hamster	100755165		715344-715822	100689234	100769058
Rodentia	Nannospalax galili	Upper Galilee mountains blind mole rat	103727704	103731612	103731576	103731610	103731611
Rodentia	Heterocephalus glaber	Naked mole-rat	101716228			110345770	
Rodentia	Fukomys damarensis	Damara mole-rat	104853763		1425163-1425591	104852380	104852381
Rodentia	Jaculus jaculus	Lesser Egyptian jerboa	105944359	101596376	10819450-10819922	101596967	101596676
Rodentia	Castor canadensis	American beaver	109701011	109688739	391713-392184	109688724	109688723
Rodentia	Octodon degus	Degu	101583580	101574865	508282-508741	510845-511532	101581231
Rodentia	Cavia porcellus	Domestic guinea pig	100724147	101789237	100135606	101789271	100728926
Rodentia	Chinchilla lanigera	Long-tailed chinchilla	102021623	102005850	7304183-7304652	102003182	102030572
Rodentia	Marmota marmota marmota	Alpine marmot	107138681		464818-465266	107147119	107146480
Rodentia	Ictidomys tridecemlineatus	Thirteen-lined ground squirrel	101959837		9349280-9349705	9345951-9346681	101967103
Lagomorpha	Ochotona princeps	American pika	101522515	101518874	6027562-6028035	101519131	101529369
Lagomorpha	Oryctolagus cuniculus	Rabbit	100349146	100339639	4842041-4842552	4837359-4838120	100339895
Laurasiatheria	Ovis aries musimon	Sheep	101108026	101108877	100302352	511496-514161	105604855
Laurasiatheria	Capra hircus	Goat	102187724	108633918	9821753-9822144	108633871	108633320
Laurasiatheria	Pantholops hodgsonii	Chiru	102322654	102321794			102322150
Laurasiatheria	Odocoileus virginianus texanus	Texas white-tailed deer	110150370		326187-326572	110129286	110129290
Laurasiatheria	Bos taurus	Cattle	281537	281538	281423	281424	615629
Laurasiatheria	Bos indicus	Zebu cattle	109576855	109578263			109578307
Laurasiatheria	Bos mutus	Wild yak	102268027	102287295			102284194
Laurasiatheria	Bison bison bison	American bison	105003751	104996414	1540881-1541360	104996416	104996415
Laurasiatheria	Bubalus bubalis	Water buffalo	102406097	102409181	760246-760725	102415017	102415355
Laurasiatheria	Physeter catodon	Sperm whale	102981936				102992433
Laurasiatheria	Balaenoptera acutorostrata scammoni	Minke whale	103011677		1-421		103000487
Laurasiatheria	Orcinus orca	Killer whale	101273227		4437395-4437854		101289235

Note: Numbers in green boxes signify gene location where we retrieved sequence from linked assemblies

Laurasiatheria	Delphinapterus leucas	Beluga whale	111172087				111171315
Laurasiatheria	Lipotes vexillifer	Yangtze river dolphin	103090731				103069397
Laurasiatheria	Tursiops truncatus	Bottlenose dolphin	101324122		4136337-4136796		
Laurasiatheria	Sus scrofa	Pig	100513764	406180	397487	397486	100627438
Laurasiatheria	Vicugna pacos	Alpaca	102541564	102544135			102543875
Laurasiatheria	Camelus bactrianus	Bactrian camel	105063995	105074254			105074253
Laurasiatheria	Camelus ferus	Wild bactrian camel	102512380	102515117	357503-357939	102515624	102515376
Laurasiatheria	Camelus dromedarius	Arabian camel	105096066	105089045			105089044
Laurasiatheria	Felis catus	Domestic cat	101084562	101084334	35294189-35294905	35292184-35292609	101084078
Laurasiatheria	Acinonyx jubatus	Cheetah	106970078	106989294			106989363
Laurasiatheria	Panthera pardus	Leopard	109264761	109278322			109278450
Laurasiatheria	Panthera tigris altaica	Amur tiger	102951207	102962205		2936408-2937687	102966227
Laurasiatheria	Mustela putorius furo	Domestic ferret	101675765	101690918	6647774-6648234	6649732-6650400	106005594
Laurasiatheria	Enhydra lutris kenyoni	Northern sea otter	111144702		6827979-6828430	6829927-6830591	111156265
Laurasiatheria	Leptonychotes weddellii	Weddell seal	102733706	102742432	170606-171045	168193-168836	102742721
Laurasiatheria	Neomonachus schauinslandi	Hawaiian monk seal	110591953	110587830			110588044
Laurasiatheria	Odobenus rosmarus divergens	Pacific walrus	101370994	101376434			101376144
Laurasiatheria	Ursus maritimus	Polar bear	103662776	103668826			103668827
Laurasiatheria	Ailuropoda melanoleuca	Giant panda	100483816	100479927	285630-286053	287865-288522	100481683
Laurasiatheria	Canis lupus	Dog	100686780	479849	31489855-31490293	100686082	609923
Laurasiatheria	Equus przewalskii	Przewalski's horse	103550815	103565894		103565891	103565892
Laurasiatheria	Equus caballus	Horse	100630835	100189599	100036554	100056327	100056369
Laurasiatheria	Equus asinus	Ass	106838469	106836750	402755-402985	106836783	106836784
Laurasiatheria	Ceratotherium simum	Southern white rhinocerous	101405071	101387832	2317690-2317932	106803071	101407369
Laurasiatheria	Elephantulus edwardii	Cape elephant shrew	102853897				
Laurasiatheria	Myotis lucifugus	Little brown bat	102443035	102420995	1864284-1864505	338221603	1858722-1858995
Laurasiatheria	Myotis davidii	David's myotis	102775139	102772168			
Laurasiatheria	Myotis brandtii	Brandt's bat	102243337	102247954	978988-979210	982224-983983	102247665
Laurasiatheria	Hipposideros armiger	Great roundleaf bat	109380553	109387156			109387157
Laurasiatheria	Eptesicus fuscus	Big brown bat	103289327	103286294	21051981-21052202	21054139-21055526	103286292
Laurasiatheria	Rhinolophus sinicus	Chinese rufous horseshoe bat	109445105	109435891			109435890
Laurasiatheria	Rousettus aegyptiacus	Egyptian rousette	107516762	107518189	865510 to 865732	862853-864033	107518192
Laurasiatheria	Miniopterus natalensis	Natal long-fingered bat	107524746				
Laurasiatheria	Pteropus vampyrus	Large flying fox	105291076	105290962		4261271-4262354	105290927
Laurasiatheria	Pteropus alecto	Black flying fox	102888632	102890489			107195603
Laurasiatheria							
Laurasiatheria	Echinops telfairi	Small Madagascar hedgehog	101657496	101646899			101647223

Laurasiatheria	Erinaceus europaeus	Western European hedgehog	103110812				
Laurasiatheria	Condylura cristata	Star-nosed mole	101630107	101625656	14854020-14854732	101625203	101625429
Laurasiatheria	Sorex araneus	European shrew	101537955		22965902-22966389+		101542473
Afrotheria	Loxodonta africana	African savannah elephant	100665857	100663823	338221589	100663254	100663537
Sirenia	Trichechus manatus	Florida manatee	101341736	101360481	10547248-10548243	105756124	101360744
Xenathra	Dasypus novemcinctus	Nine-banded armadillo	101442860	101427865		101428736	
Pholidota	Manis javanica	Malayan pangolin	108397553				
Tubulidentata	Orycteropus afer afer	Aardvark	103213969		10816849-10817840	103196087	103196086
Marsupialia	Monodelphis domestica	Gray short tailed opossum	100011893		497042		103099847
Marsupialia	Macropus eugenii	Tammar wallaby	4300-4475, 3446-3706				
Marsupialia	Sarcophilus harrisii	Tasmanian devil	100923599				
Monotremata	Ornithorhynchus anatinus	Duck-billed platypus			Z26849.1		
Monotremata	Tachyglossidae aculeatus	Short-billed echidna			Z26848.1		

Results

Protein and gene sequence overview

The sequence alignments that we produced have allowed us to look at each of the gene and inferred amino acid sequences for many mammalian species, granting us an understanding of their individual conserved structures, as well as their evolutionary changes. Each of the three alignments we produced for the four proteins (only two alignments for PRM3, because it does not have an intron), has given us different insights into their sequences, that together combine to give a more complete understanding of these protein families. Our first alignments, which showed full-length primate gene sequences compared against each other (Appendices A, D, F, H), allowed us to determine each gene's intron boundaries, as well as gain a general sense of the conservation of the sequences throughout the gene. The second set of alignments of the spliced forms of the genes (Appendices B, C, E, G) further enabled analysis of evolution within the sequences by allowing us to infer the amino acid sequences of the proteins. And the final set of alignments (Appendices Y-BB), which consisted of the protein-coding sequences for the mammalian orthologs given on the NCBI site, gave us the ability to extrapolate these findings to other mammals and look for widespread evolutionary patterns across the various genes.

While creating our alignments, three primate species had sequences that did not align as easily to that of the other primates for their respective genes: *Gorilla gorilla* (gorilla) for *Tnp1*, *Nomascus leucogenys* (white-cheeked gibbon) for *Prm1* and *Prm2*, and *Carlito syrichta* (tarsier) for *Prm2*. Our approach towards fixing these problems varied depending on the reason behind the misalignment and the results of our methods also varied in their success. For *Nomascus,* whose *Prm1* and *Prm2* sequence contained areas of "N" sequencing flaws and did not seem to match as the others should, the solution was as easy as finding alternative sequences that worked well in the alignment. These sequences were from *Hylobates lar* (lar gibbon), a different species of gibbon that could represent the clade, and they showed none of the artifacts found in the *Nomascus* sequences. For the other two examples, the solutions were not as simple. The details of these two examples of artefactual or problematic sequences will be discussed in further detail with their respective genes.

Transition Nuclear Protein 1 (TNP1)

The alignments we produced for TNP1 and our subsequent analysis of them clearly reveal a protein that is different from the other sperm chromatin remodeling proteins. The most striking difference is that TNP1 has evolved very slowly, especially compared to TNP2. Our primary alignment of the full length *Tnp1* gene is shown in Appendix A. In this alignment, the great amount of nucleotide sequence conservation between the 25 primate sequences is almost immediately visible, especially in the protein-coding regions. Not only do the genes share remarkably similar nucleotide sequences, but they also seem to be relatively consistent in length. Most of the gene sequences are about 369 nucleotides long, with the discrepancies being small — about 6 nucleotides maximum — insertions or deletions that retain the coding frame. A striking exception to this conservation is seen in the gorilla *Tnp1* gene and inferred protein sequence. In addition to having several small mutations, the gorilla gene has an insertion of approximately 4000 nucleotides shortly after the 5' end of the intron. The gorilla *Tnp1* mRNA predicted by NCBI (XM_019021732.1) would result in a protein with 70 additional amino acids at the C-terminus. This drastic contrast between the predicted gorilla TNP1 sequence and that of the other primates suggested that the sequence warranted extensive research, the results of which are described next.

Gorilla *Tnp1*: Sorting out what happened to the *G. gorilla* sequence, which seems to have a huge insertion (3000 nucleotides+) and simultaneous exon deletion, was a complicated process that involved the utilization of many different BLAST search techniques. Some of our first searches where we compared *H. sapiens* mRNA and gene against *G. gorilla* showed that while some components of the gene and the mRNA were found in *G. gorilla* at the expected chromosome 2B, that *G. gorilla* still exhibited segments missing from the typical TNP1 gene and areas of what appeared to be repeat or overlap (Appendices R, S). Notably, there was a gap of over 3000 nucleotides on the *G. gorilla* genome between where the *H. sapiens* inputs were aligning, which seemed to explain why the Gorilla sequence on the NCBI database was over 4000 nucleotides long; the program must have included this approximately unrelated 3000-nucleotide stretch because it was located in between two elements of coding sequence. In all our subsequent control BLAST searches (described in Methods), the *H. sapiens* input sequence matched remarkably well against the genome of interest, suggesting that the results we found could be considered sound.

Now suspecting a 3000+ nucleotide insertion as possibly being the reason why the gorilla sequence did not align with its orthologs and why we could not locate elements of its exon, we attempted to realign the gorilla gene to the predicted mRNA. In so doing, we were able to find a length of 188 nucleotides of the predicted mRNA sequence that aligned to the tail-end of the nucleotide sequence. Aligning these two pieces created a rather large gap exceeding 4200 base pairs, suggesting that there was an a large insertion within the gene. When the sequence of this large intron was again run with BLAST against the *G. gorilla*, it showed evidence of a simple repeat element within the intron spanning approximately 600 nucleotides (Appendix T). In a BLAST search against the *H. sapiens* genome (Appendix U), it was determined that another part of the intron appears to have originated from DNA surrounding the gene of interest somewhere between the *Tnp1* gene and a gene for insulin-like growth factor-binding protein 5 precursor. We concluded that while the sequence looked remarkably different than its other highly conserved orthologs, that because all these different sources were supporting elements of its sequence, it could possibly really reflect a mutation in the genome. From our searches, it seems what most likely happened was that a mutational event disrupted the coding of the second exon, leaving behind a large amount of foreign sequence that has been incorporated into the gene.

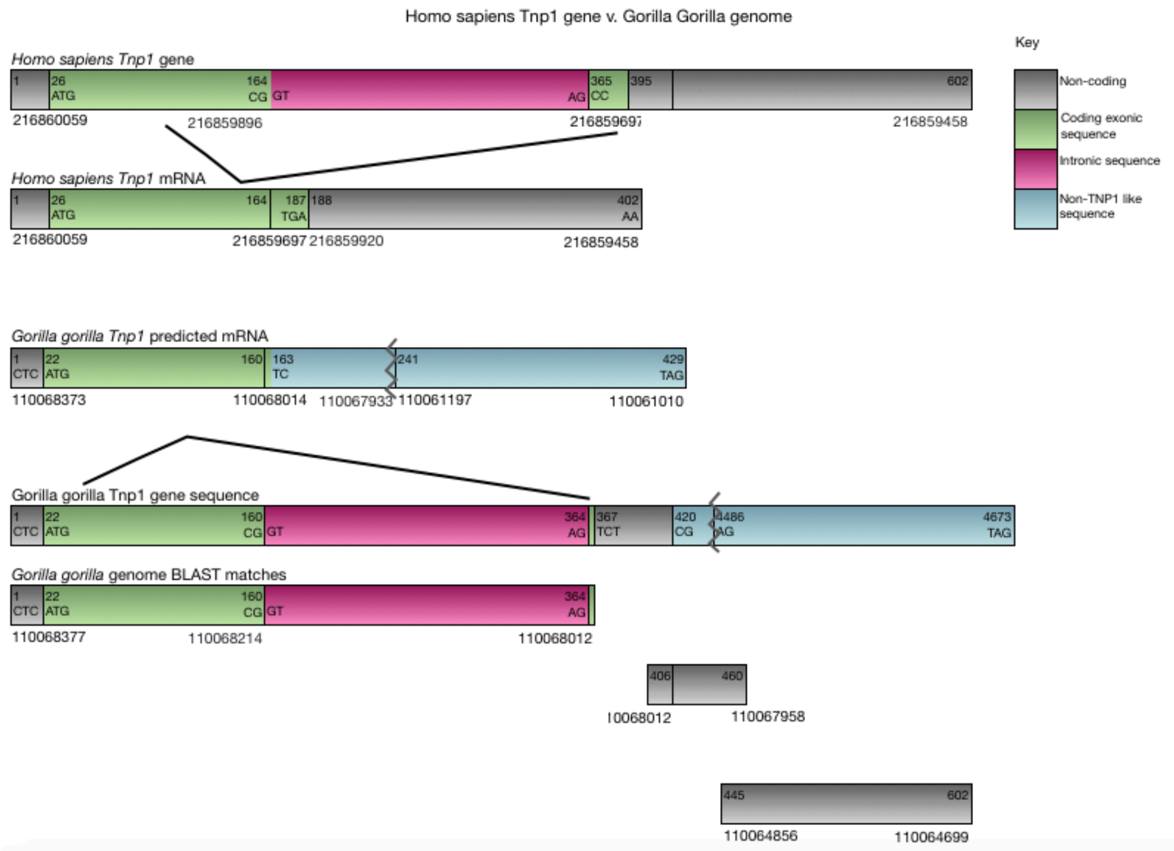

Figure 3. Tnp1 gene and mRNA structures in human (top) and gorilla (bottom). Gene and predicted mRNA variants taken from NCBI; BLAST matches derived from BLAST search of *H. sapiens* (human) gene v. *G. gorilla* (gorilla) genome.

As a final measure to check to see if the gorilla gene was expressed and if it was done so in a functionally-normal form or as a pseudogene, we also BLAST searched the SRA. Doing this gave us search results in the form of little sequences (150 nucleotides long), which we were then able to download and align against the different variants we had for the gene, including that of the predicted mRNA. Since the search results were matches from different parts of expressed RNAs, starting and stopping at different locations from each other, the alignment we produced of these pieces consisted of fragments that overlapped, gradually moving from one side of the sequence to the other (Appendix V). This step-wise alignment worked initially, until we reached a point slightly into the insertion. After this part, the sequences began to diverge in sequence, showing many different variants instead of all showing parts of a singular, uniformly expressed variant. This affirmed to us that the gene was likely an expressed pseudogene instead of one that was functionally normal. To ensure that these results were not just an artifact of our methodology, we repeated the same technique with the normally coded gorilla *Prm3* gene (Appendix W). From the search results, we constructed the entire protein coding sequence easily. In the process of doing this we also found a polymorphism with the amount of lysine residues at one point in the gene sequence. This seemed to affirm our previous findings that stated that these genes were rapidly evolving.

Removing the ~200 nucleotide intronic sequences from the *Tnp1* gene sequences gave us an alignment of the protein-coding sequences for the primate orthologs. This, our secondary alignment (shown in Appendix B), was largely similar to that of our first alignment, but with a few important differences. For one, removal of the introns produced a great sequence length change. The length of the coding sequences in this alignment resembled that of the predicted mRNA from the first, consisting of about 168 nucleotides, which is about half of their previous length. Another difference between the two alignments is that our second alignment included a predicted mRNA sequence for the *G. gorilla* sequence that was found on NCBI after research into the gorilla gene sequence. Because the gorilla gene sequence was so different, even after splicing it still constituted 4611 nucleotides, the predicted mRNA seemed necessary to produce an accurate coding sequence for gorilla, which we inferred would likely be different than that of the other primates. The predicted mRNA form had 408 nucleotides, more than twice the length of the other coding sequences. Despite this length difference, the mRNA did align with those of orthologs up until the 141-nucleotide, near the intron-exon boundary. However, beyond this point, the mRNA showed a large and significant divergence and did not match up with the end of the other sequences at any point, as we predicted. Finally, an additional difference is that translation of the gene sequences in this alignment gave the inferred protein sequence, whereas translation of the previous alignment did not due to the intron.

The translation of this second alignment produced amino acid sequences for TNP1 that were 55 amino acids in length, along with the additional stop codon (TGA). These amino acid sequences were characterized by the more frequent appearance of residues like serine, arginine, lysine, and glycine. Another defining feature was that arginine residues were almost always directly near a serine or lysine residue. Overall, these and the other amino acids seemed to be highly conserved, with relatively few point mutations occurring throughout the sequences. This was of course different for gorilla, whose amino acid sequence aligned for the first 49 amino acids before diverging. In the predicted mRNA, the amino acid sequence extended to be 135 amino acids long, while in the *Tnp1* coding sequence that we processed the amino acid sequence had a reading frame of 194 amino acids.

Transition Nuclear Protein 2 (TNP2)

Though TNP2 is similar to TNP1 in name, expression time, and suggested general functioning, the alignments of their gene sequences are very different. While both genes' sequences contain two exons and an intron, the intron sequence in *Tnp2* is much more extensive (around 850 nucleotides) and contains much more rapid evolution than that of *Tnp1*, especially when considering *Tnp2* strepsirrhines. In addition to this, the coding sequence of the exons additionally differ from that of *Tnp1* in both in terms of evolution and length. The coding sequence of the first exon is approximately 400 nucleotides long, while that of the second is only 17 nucleotides in length. Translation of these coding regions of the exons give an amino acid sequence that is about 140 residues long, a little less than three times as long as that of TNP1.

Protamine 1 (PRM1)

Starting with PRM1, we made the first full-length protamine gene sequence alignment (Appendix D). The *Prm1* gene sequences are approximately 247 nucleotides long in most primates, with the exception of the *Microcebus murinus* (mouse lemur) gene, which experienced a simple repeat expansion within the intron making this gene about 389 nucleotides long. Although this repeat expansion does not change the amino acid sequence, it should be noted as an example of repeat expansion mutation in the protamine locus.

In the second *Prm1* alignment, where the intron has been removed, this gene exhibits a coding sequence that is about 156 nucleotides long (Appendix E). Of these nucleotides, about 105 encode the first exon and the remaining 50 or so encode the second, with some differences between species. These differences largely result from deletions or insertions of one to three codons in some species. One example of this is shown by comparing the *Saimiri bolviensis* (squirrel monkey) gene to those of the other primates: it has an insertion of nine nucleotides (three codons) at site 40 of the coding sequence, as well as multiple other areas with codon deletions downstream. These more pronounced mutations, in combination with various point mutations, seem to evidence the theorized faster rate of evolution in *Prm1*, especially when comparing to that of the more conserved *Tnp1*.

Once translated, the *Prm1* gene sequences reveal inferred protein sequences that are about 50 amino acids long, that usually start with "MARY" — although the M is not present in the mature protein. One of the most pronounced characteristics of these sequences is the relatively conserved cysteine (C) residues among the eutherians present in the alignment. There are typically nine conserved cysteine, six of which occur in three pairs of cysteine residues and three single residues. These cysteine residues are found in the marsupial and monotreme sequences we retrieved from searching their genomes on NCBI, suggesting that the cysteine residues are an evolved feature of the eutherians, as previously noted (reviewed in Balhorn, 2007). Along with these cysteine residues are some highly conserved tyrosine (Y) residues and stretches of arginine (R) that typically consist of three to five sequential residues. These arginine stretches are noted even in the very distantly-related marsupial and monotreme sequences, though these sequences are otherwise rather dissimilar.

Protamine 2 (PRM2)

Prm2 is similar to *Prm1* in many respects, but also has its own individual features. The two genes have similar structures, in that they both have two exons and one intron near the later end of the sequence. The full-length *Prm2* gene is about 417 nucleotides long (Appendix F), with a coding region that is about 312 nucleotides long (Appendix G) in the predominantly-expressed mRNA variant in humans (see "*PRM2 mRNA variants*" below for details).

In contrast to *Prm1*, the *Prm2* gene codes for a protein that is about 100 amino acids long, having an acidic N-terminal segment and a basic C-terminal segment that is similar to PRM1 in that it is arginine rich. In those species that have PRM2 protamine on ejaculated sperm, the C-terminal portion is cleaved off, leaving a small basic protein similar in size and charge to PRM1. PRM2 coding sequence contains great variation in its approximately 100 amino acid length, as signified by a large area towards the 5' "MVRY" end where non-primate orthologous sequences show extensive replacements and deletions and insertions. Even with this great mutational rate, there still appear to be certain motifs that are relatively conserved within the primates like the more medial "GQEEQL" sequence. Towards the 3' end of the sequence, fewer mutations are visible, which may be due to the large number of arginine residues and three serine/cysteine pairs. For most of the primates, the alignments of the Prm2 genes were relatively straightforward, with the exception the tarsier, as explained next.

Tarsier *Prm2:* For *C. syrichta*, the decision about what to do about the apparent artifacts in the *Prm2* sequence was not so clear. Since *C. syrichta* was the only representative of the fairly-distant branch of tarsiers, we felt it was important to include it within our *Prm2* alignment. However, our BLAST searches against the genome typically only returned short matches, with only one or two being substantial in length (Appendix X). These smaller pieces typically were represented multiple times in the alignment and were found throughout the genome, suggesting that they might be a repeat element. The larger matches, though containing sequences that were similar to the *Prm2* gene from other species, referenced a piece of the genome sequencing that was contained N's. From these large N's inputs, we inferred that the *Prm2* gene in tarsier was likely improperly sequenced or overridden at least to some extent. Despite this, we decided to include this sequence from the genome and found that we could align the beginning fragment of the first exon and the second exon. While the sequence of the gene is not complete, what sequence that is available provides some sense of what the gene looks like in tarsier, and is therefore important to represent.

***PRM2 mRNA variants*:** One of the more noticeable differences between *Prm2* and the other genes was that it was reported to have six different *H. sapiens* mRNA isoforms, five of which are predicted to be coding. When researching to find evidence if these reported forms were actually expressed in human testes, we discovered reports of two other predicted mRNA isoforms on NCBI's Protein listing. Finding these recently reported isoforms was initially very surprising since the protamines have been so well characterized, but after much investigation (as described in Methods), an alignment we created of the variants made some of the predicted isoforms look implausible (Appendix J). The main reason that the variants seemed unreal from these alignments was because the predicted splice sites used to supposedly create them did not display conventional splice sites, like GT and AG.

We then expanded this alignment with results of the tBLASTn searches conducted against the dbEST database for humans (Appendices K-Q), from which we took the top four matches and aligned them. This allowed us to analyze the extent of how well the search matches aligned to the reported isoforms. From this process, we gathered that the alignment suggests that the matches are not compelling. For one, there were very few strong matches that actually came back from the results. Even though only four results were chosen for each variant, these four results were supposed to be the top matches available and they did not seem to align to the sequences of the isoforms well. Beyond this, some of the top matches for two different variants were the same sequence, meaning that the program thought that a supposed top match for one variant was similarly affective at matching a different isoform. This suggested to us that the isoforms, whose existence we already doubted, were likely not even significantly different if expressed.

Protamine 3 (PRM3)

Finally, *Prm3* is the most different gene in the protamine locus. It is approximately 312 nucleotides long and does not have an intron (Figure 1). In the aligned DNA sequences (Appendix H), there are areas of expansion and contraction of what appear to be simple repeat sequences of 12 nucleotides. These occur largely near the 5' end of the coding region, although there are additional repeats near the middle of the sequence in some species. The extent of expansion varies from species to species, with some species, such as *Callithrix jacchus* (marmoset) having less repeats than other more-extensively expanding sequences, like *Pongo abelii* (orangutan) or *Nomascus leucogenys* (gibbon). Additionally, the *Carlito syrichta* (tarsier) sequence ends with a unique extension, separate from these repeats, that was verified as matching the *C. syrichta* genome through a BLAST search (Appendix I).

Alignment of the inferred protein sequences, which are about 100 amino acids long in most species (Appendix I), reveals that the 12-nucleotide repeats result in 4-amino acid repeat motifs that expand and contract in the primates and closely-related orders of mammals, such as rodents and lagomorphs (glires). These repeats are not found in the other mammalian orders, so they arose in the ancestor of primates and glires. Further along the PRM3 sequences, there is region containing glutamate repeats that has expanded and contracted in many species; these cause the PRM3 proteins to carry negative charges. This is the opposite of the true protamines, PRM1 and PRM2, which are highly positively charged. We theorize that these glutamate residues may serve to interact with the positively charged arginine residues on PRM1 and PRM2, later mentioned in our discussion.

Non-primate mammalian sequences

Since our samples to this point only included primates, we could not say whether the trends we had observed were unique to primates, or were also found in other mammals. For that reason, we decided to include the sequences of non-primate mammals listed under the proteins' orthologs in NCBI in their respective alignments. In doing this, we wanted to include as many different species as possible for each of our proteins so as to increase our ability to extrapolate our findings. *Tnp1, Tnp2,* and *Prm3* had approximately 80 non-primate mammalian orthologs listed in NCBI, and *Prm1* and *Prm2* had about 10 and 25, respectively. Knowing that this difference in abundance of alternative species' sequences was likely due to just simple differences in the NCBI annotation of these genes within the genomes, not due to some innate quality of the protein or non-existence of the sequence data, we utilized the BLAST function to retrieve the gene sequences from the available mammalian genomes. The sequences we obtained from the reference protein pages (listed with geneID) and from BLAST searches (listed with coordinates from scaffold) for these species are included in Table 2.

For *Tnp1*, the expanded alignment including non-primate mammalian orthologs (Appendix Y) was very similar to its prior alignments. There was still a great conservation of sequence among orthologs; although there were more substitutions present, it was not beyond what would be expected when including such distant relatives. In fact, the mutation rate was relatively low when taking this into account. The alignment for *Tnp2*, on the other hand, showed such rapid evolution within the mammalian sequences that it was hard to align the sequences from different orders of mammals. For this reason, we have elected not to include the *Tnp2* alignments here. It should be noted, however, that the rate of evolution of *Tnp1* is clearly much slower than *Tnp2*. As done with our prior work, there were some species in these alignments whose sequences seemed to be unreliable or irreconcilable and were thus removed. These included for *Tnp1* the naked mole rat, sperm whale (maybe showing frameshift), pangolin (having "Ns" in its sequence), and deer.

Like *Tnp1*, the expanded mammalian alignment for *Prm1* was very similar to the primate alignments (Appendix Z). Although there were many sites of with substitutions and replacements, they mostly consisted of individual amino acid changes that spared largely conserved parts of the sequence, like the "MARY" beginning sequence or the cysteine residues. It should be noted that this was not the case for the monotremes, which represent distant relatives to the other mammals. In contrast, the additional mammalian sequences added to the *Prm2* alignment produced great variance within the alignments, as shown in Appendix AA. At the 5' end of the sequence, some sequences seemed so dissimilar from point mutations that it was difficult to know where amino acids aligned. In addition to these differences in sequence, some orders (rodents, carnivores) had large areas of either insertion or deletion in this beginning area. An example of this is found in *Myotis lucifugus,* whose sequence is about 40 nucleotides shorter than its orthologs. Beyond just these signs of rapid evolution, the patterning of motifs within some of the Prm2 sequences also seems to have changed for some species. This is demonstrated perhaps most clearly at the 3' end of the sequence, where the rodents show an expansion of a repeat encoding both cysteine and arginine residues. For these two proteins, we removed the European shrew, deer and goat (due to difficulty with the C terminus), and Brandt's bat and the

Egyptian rousette (due to problems with the N-terminus) for *Prm1* and for *Prm2* we removed the Amur tiger, American beaver, and giant panda (due to "Ns" in the sequences).

Finally, our expanded alignment of *Prm3* had perhaps the most meaningful impact on our prior alignment work (Appendix BB). Our first two alignments of Prm3 showed that gene exhibited two sites of expansion and contraction at the beginning and middle of the sequences, but were unable to give us any implication if this phenomenon was found more generally and in non-primate mammals or if it was instead limited to the primate order. When we included the additional mammalian species, we were able to see exactly how common these phenomenon were and to what extent they were represented in different clades. From the new alignment, it was clear that the initial simple repeat expansion (S_GH) at the beginning of the sequences was confined primarily to primate and rodent species, of which the former has a more dramatic presentation. We found the second expansion, that of the glutamate residues, to be more universal to the mammals. This seems especially supported when this glutamate stretch expansion is compared to the same locus in marsupials, who show much shorter stretches. While these more extreme features do command the most attention, there are also signs of evolution of individual amino acids at the 3' of the *Prm3* sequences that are occurring at a similar extent as to those in *Prm2.* The sequences we removed in the *Prm3* alignment include the cheetah ("Ns" in sequence), marmot, roundleaf bat, big brown bat, Brandt's bat, the Yangtze river dolphin, and the polar bear.

Phylogenetic tree comparisons

From the analyses that we ran using *MacClade* and *PAUP**, we created phylogenetic trees showing the most parsimonious assignment of amino acid replacements (following a PROTPARS matrix of mutational pathways) that occurred within the primate phylogeny. These trees were able to not only show on which lineages the replacements occurred, but also show relative rates of evolution for the different branches (that is, the total number of events per lineage). Although not shown here for simplification, the programs also showed what the likely specific replacements were that occurred on each lineage, and provided reconstructed ancestral H*vs* TNP2 proteins (Figure 4), and the PRM1 *vs* PRM2 (Figure 5) proteins due to their related functions, while analyzing PRM3 on its own (Figure 6).

Comparing the phylogenetic trees for each protein' amino acid sequence in this way has given us insight into the different evolutionary rates experienced by these proteins's genes and, in some cases, has revealed species that are experiencing relatively rapid evolution in most or all of the genes. Our comparison of *Tnp1* and *Tnp2* shows two proteins on the opposite sides of the evolutionary spectrum: *Tnp1* has so little mutation in some places that some branches show either a singular amino acid replacement or zero, while just the first exon of *Tnp2* shows in general more rapid evolution, with some species like tarsier and galago showing drastic changes. These findings are clearly evidenced in our original alignments, where *Tnp1* shows conservation along the entirety of its sequence and *Tnp2* shows many sites of insertion/deletion and has an intron and exon that are incredibly divergent in some of strepsirrhine species. The comparison of *Prm1* and *Prm2*, though not as clearly juxtaposed, also shows differences in evolution rate. Whereas in general the rates are comparable, in some of the strepsirrhines and platyrrhines evolution rates vary. Tarsier, galago, and marmoset show elevated amino acid replacement rates in *Prm1* when compared to *Prm2*, while squirrel monkey shows more changes in *Prm2* than *Prm1*. *Prm3* also has similar rates of evolution, with two species — marmoset and tarsier — showing higher rates of amino acid replacement than the others, although this may be due to frameshift mutations changing their N-terminal coding sequences.

From these findings, it seems that some species of the strepsirrhine and platyrrhine clades (especially tarsier, night monkey, galago, and marmoset) may be experiencing greater evolutionary rates than other primates across the genes, though it is important to note that these monkeys have at some points experienced millions of years of separation, likely factoring into this difference. Another clade, that of the hominoids, especially the African apeas, also seem to show faster rates of evolution when compared to its nearby clade the Old World monkeys for every gene. This could have important implications when it comes to the understanding of human evolution. Further analysis, examining evolution rate along the entire protamine locus, will help elucidate the mutational and selectional mechanisms underlying the evolutionary patterns of these sperm chromatin remodeling proteins.

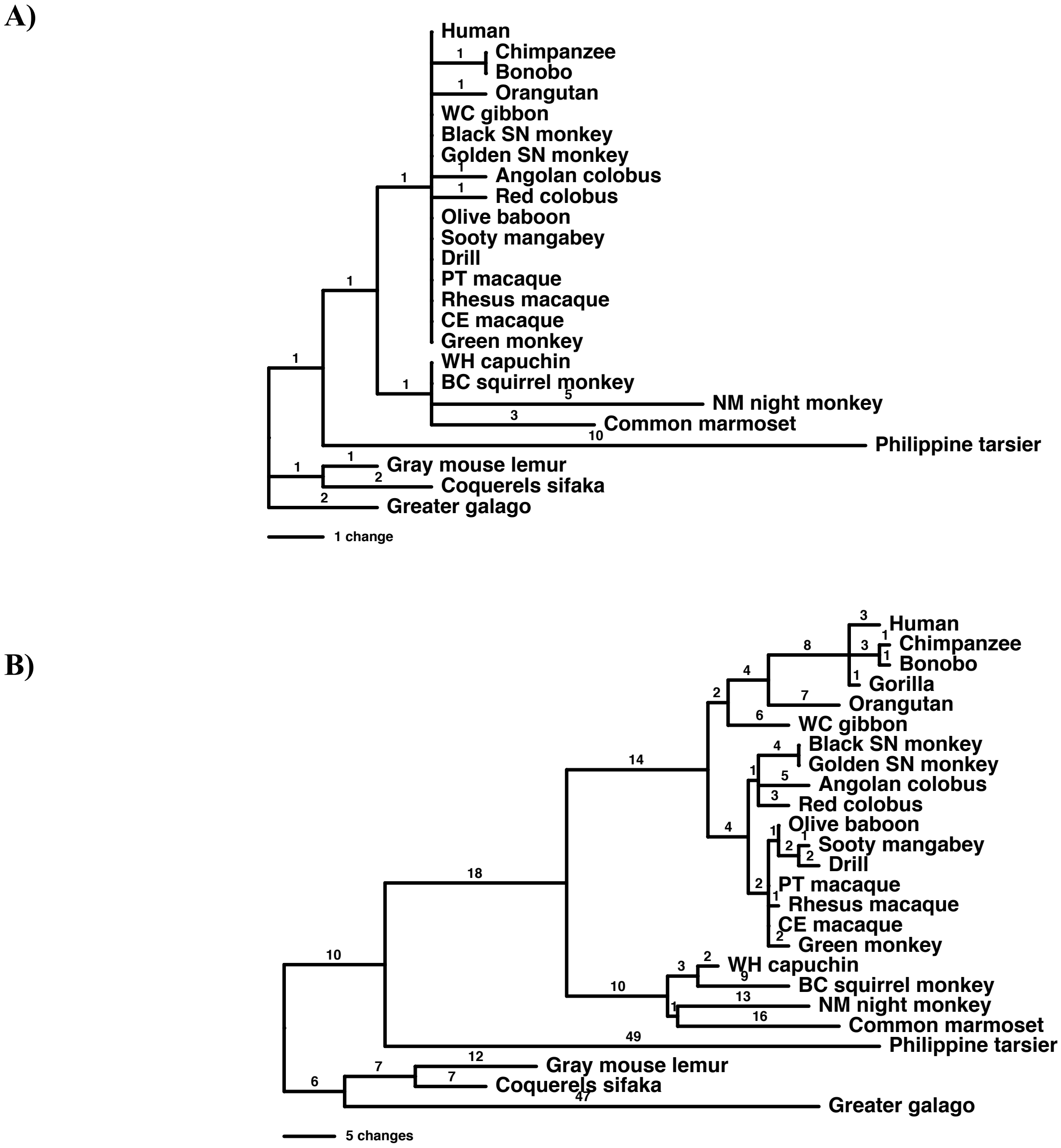

Figure 4: Comparison of phylogenetic trees for TNP1(A) and TNP2 (B), where amino acid replacements have been mapped parsimoniously on the lineages by *PAUP.** Scaled branches represent relative number of amino acid changes; for TNP1, scale bar represents 1 amino acid change, for TNP2 it represents 5. Amino acid changes were computed using a PROTPARS matrix, in which gaps are treated as states. Data taken from Appendices B and C.

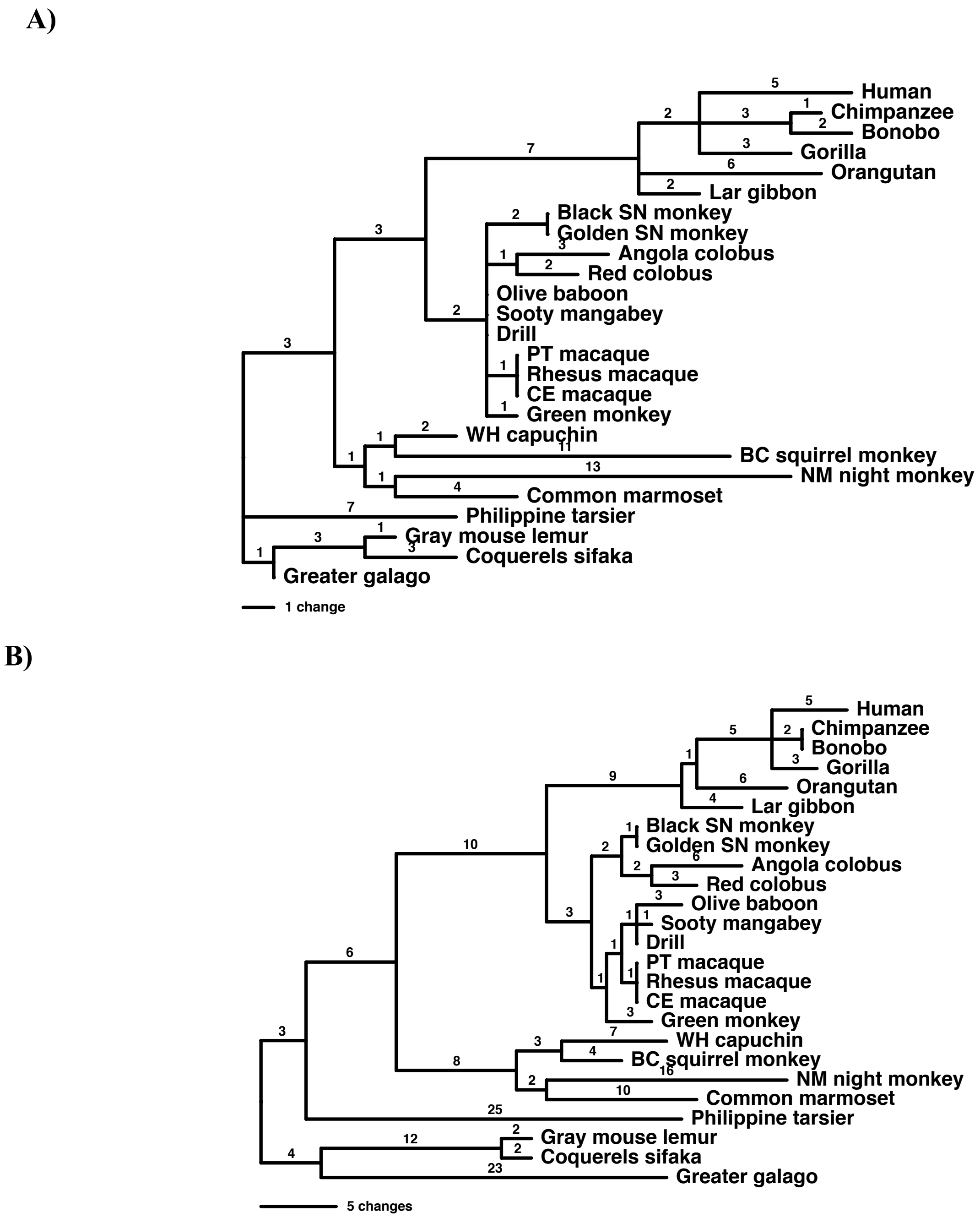

Figure 5: Phylogeny of primates' amino acid sequences for PRM1 (A) and PRM 2(B) with parsimonious amino acid replacements mapped on the lineages by *PAUP.** Branches are scaled to match the relative number of amino acid changes (scale bar is 1 amino acid change for PRM1, 5 for PRM2. Replacements computed using a PROTPARS matrix, in which gaps are treated as states, run on sequences from Appendices E and G.

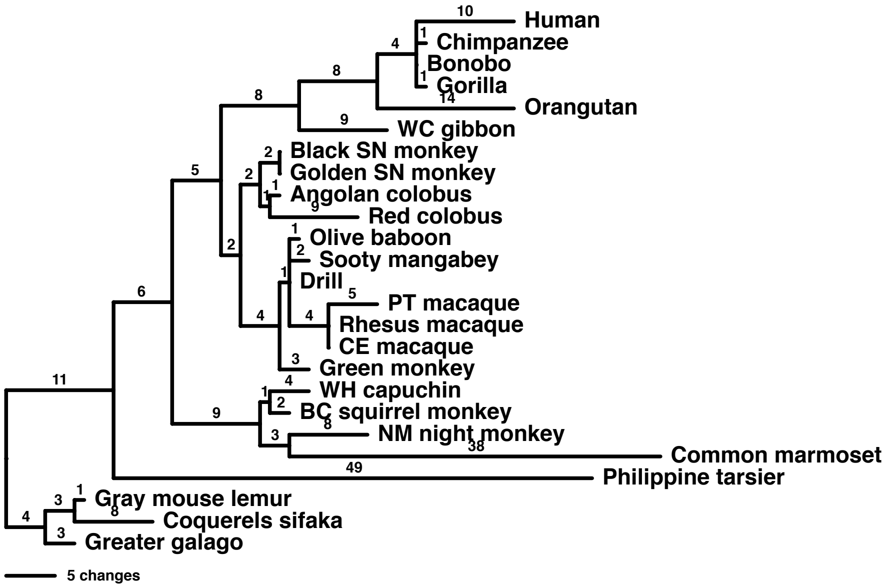

Figure 6: Phylogeny of the primates' PRM3 sequences with number of inferred amino acid replacements mapped most parsimoniously on the lineages by *PAUP.** Branches are scaled to match the relative number of amino acid changes (shown on lineages) computed using a PROTPARS matrix, in which gaps are treated as states. The scale bar equals 5 events. The sequences used in this analysis appear in Appendix H.

Discussion

One of the main conclusions that we have come to from the analysis of these alignments is that the division between TNP1 (encoded on chromosome 2 in humans) and TNP2, PRM1, PRM2, and PRM3 (encoded on chromosome 16) extends beyond their physical separation. The proteins' gene sequences, perhaps due to these different locations, vary greatly in nature, as illustrated in the alignments. Whereas the *Tnp1* gene is rather highly conserved, even when considering diverse mammals, the other genes show more rapid rates, as well as unusual patterns, of evolution. Discovering this upon inspection of the alignments caused us to consider the two groups of genes mostly separately, though the proteins are functionally related as described before. This is in line with what literature says about the protamine locus and its relatively high rates of evolution, which some have even suggested might suggest positive or sexual selection on the protamines (Wyckoff et al., 2000; Rooney et al., 2000; Van Den Bussche et al., 2002).

Understanding the evolutionary changes within the proteins' gene sequences is of upmost importance because of their influence on the amino acid sequences and repeat motifs, which we theorize might be related to functioning of the proteins. For example, cysteine residues within a sequence may interact with each other to form disulfide bonds, therefore helping to contribute to the structural integrity of the protein and enabling it to maintain function. These cysteine residues could also mark positioning of zinc fingers, which are important functional components of some proteins, including PRM2 (Balhorn, 2007). Tyrosine residues may facilitate proteins binding the DNA, with their aromatic rings inserting between bases. The arginine residues' positive charges may help the protamines bind to negatively charged DNA due to the physical force of attraction, and the negative glutamate residues in PRM2 and PRM3 may serve to counteract these positive charges during transport to the nucleus and replacement of transition proteins. If mutations were to change the amino acid sequences, they could significantly alter protein function, and thus reproductive success.

To better understand how changes in gene sequences could alter these elements within the proteins, we first located and considered the implications of amino acid conservation across the mammals. Examination of the alignments suggests selection towards maintaining arginine and cysteine residues, even when the rest of protein is undergoing changes. We theorize that this may occur to preserve these functions within the protein, thereby explaining the retention of certain positions. For this reason, we feel that changes in areas within the proteins where cysteine residues appear, as happened at the end of the rodents' PRM2 protein, should be considered for their potential importance, and further researched. After all, these cysteine residues could provide advantage for stability of PRM1 in placental mammals compared to the marsupials and monotremes, who lack these cysteine residues, as shown in the PRM1 sequence alignment and by a prior study (Retief et al., 1993).

After our examination of conserved sites, we sought to identify and quantify changes within the amino acid sequences of the proteins through lineage-based parsimony analysis in *MacClade* and *PAUP**. The phylogenetic trees created by these programs revealed that the proteins encoded at the protamine locus have indeed experienced quite rapid rates of evolution, particularly in some strepsirrhine and platyrrhine species. For all of the proteins encoded in the protamine locus, the hominoid lineages — particularly those of the African apes and humans — seem to have evolved more rapidly than the Old World monkey clade. In contrast, the TNP1 nucleotide and amino acid sequence experienced greater conservation, even showing no amino acid replacements, or even nucleotide substitutions, between in some species.

One of the most surprising signs of evolution that we have found are the large areas of expansion and contraction of repeats of amino acids that were observed throughout some of the proteins' sequences. Though these areas are especially notable in *Prm3*, they are also seen in other genes and proteins in this locus. Repeat sequences were first noted by Retief et al. (1993) in the monotreme *Prm1* sequences, but haven't been studied subsequently at this locus. These mutational changes produce proteins that can vary greatly in amino acid content and number, and likely affect function. For instance, the expansion of the glutamate sequence in PRM3 may affect its function, which we theorize might be acting as a chaperone for the positively-charged PRM1 and PRM2 proteins. The expansion and contraction of the repeat sequences is likely due to local formation of non-B DNA structures and the resultant slippage of repeats (Kamat et al., 2016), causing what would otherwise seem like unprecedented rates of mutagenesis at this locus.

Together with the observations of certain lineages experiencing rapid evolution, the findings of repeat sequence instability suggest that the interesting evolutionary patterns that occurred within the protamine locus were likely driven by unusual mutational mechanisms involving non-B DNA structures. Analysis of the entire length of this locus, conducted in a similar manner to our analyses, may reveal more about this proposed mechanism. Such analyses have been made possible by the recent sequencing of numerous mammalian genomes. The results of such studies may have wider-ranging implications for the study of rates and patterns of molecular evolution, which have primarily been based upon models involving point mutations. Future studies of rapidly-evolving proteins, like the protamines, need to consider the possibility of more rapid and expansive mutational mechanisms, such as those driven by non-B DNA structures (Kamat et al., 2016).

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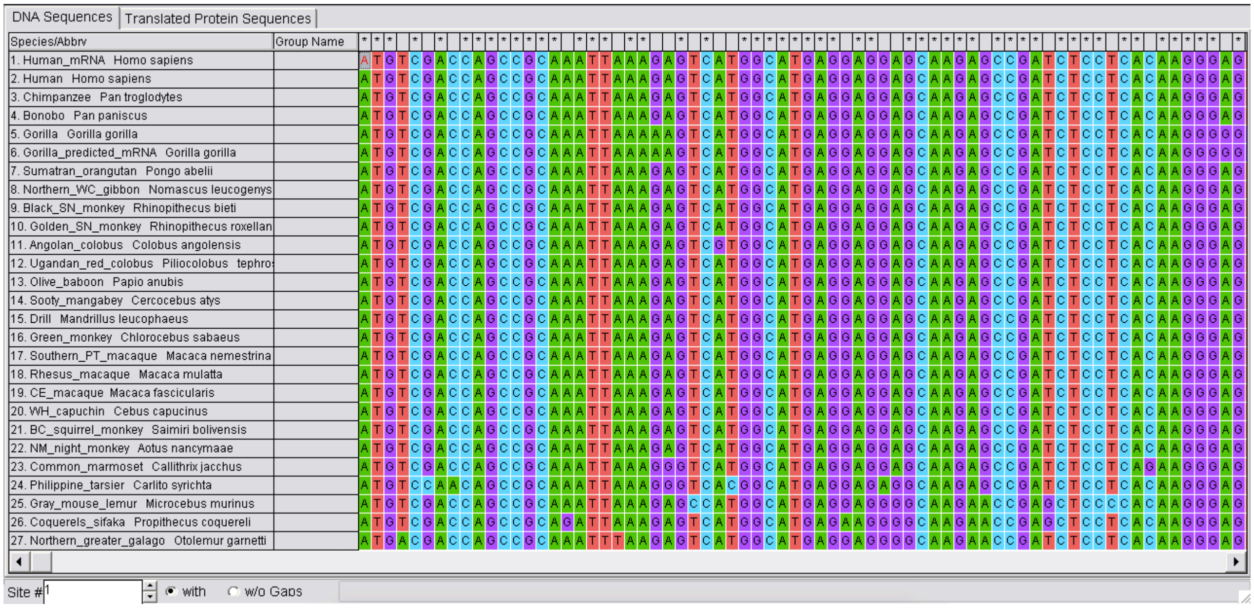
List of Appendices

Appendix A) Alignment of primate *Tnp1* full-length gene sequences



DNA Sequences | Translated Protein Sequences

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2. Human Homo sapiens		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
3. Chimpanzee Pan troglodytes		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
4. Bonobo Pan paniscus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
5. Gorilla Gorilla gorilla		ATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGGG
6. Gorilla_predicted_mRNA Gorilla gorilla		ATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGGG
7. Sumatran_orangutan Pongo abelii		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
8. Northern_WC_gibbon Nomascus leucogenys		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
9. Black_SN_monkey Rhinopithecus bieti		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
10. Golden_SN_monkey Rhinopithecus roxellan		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
11. Angolan_colobus Colobus angolensis		ATGTCGACCAGCCGCAAATTAAAGAGTCGTGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
12. Ugandan_red_colobus Piliocolobus tephro		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
13. Olive_baboon Papio anubis		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
14. Sooty_mangabey Cercocebus atys		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
15. Drill Mandrillus leucophaeus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
16. Green_monkey Chlorocebus sabaeus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
17. Southern_PT_macaque Macaca nemestrina		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
18. Rhesus_macaque Macaca mulatta		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
19. CE_macaque Macaca fascicularis		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
20. WH_capuchin Cebus capucinus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
21. BC_squirrel_monkey Saimiri bolivensis		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
22. NM_night_monkey Aotus nancymaae		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAG
23. Common_marmoset Callithrix jacchus		ATGTCGACCAGCCGCAAATTAAAGGGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCAGAAGGGAG
24. Philippine_tarsier Carlito syrichta		ATGTCCAACAGCCGCAAATTAAAGGGTCACGGCATGAGGAGAGGCAAGAGCCGATCTCCTCACAAGGGAG
25. Gray_mouse_lemur Microcebus murinus		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGAGCTCCCCACAAGGGAG
26. Coquerels_sifaka Propithecus coquereli		ATGTCGACCAGCCGCAGATTAAAGAGTCATGGCATGAGAAGGGGCAAGAACCGAGCTCCTCACAAGGGAG
27. Northern_greater_galago Otolemur garnetti		ATGACGACCAGCCGCAAATTTAAGAGTCATGGCATGAGGAGGGGCAAGAACCGATCTCCTCACAAGGGAG

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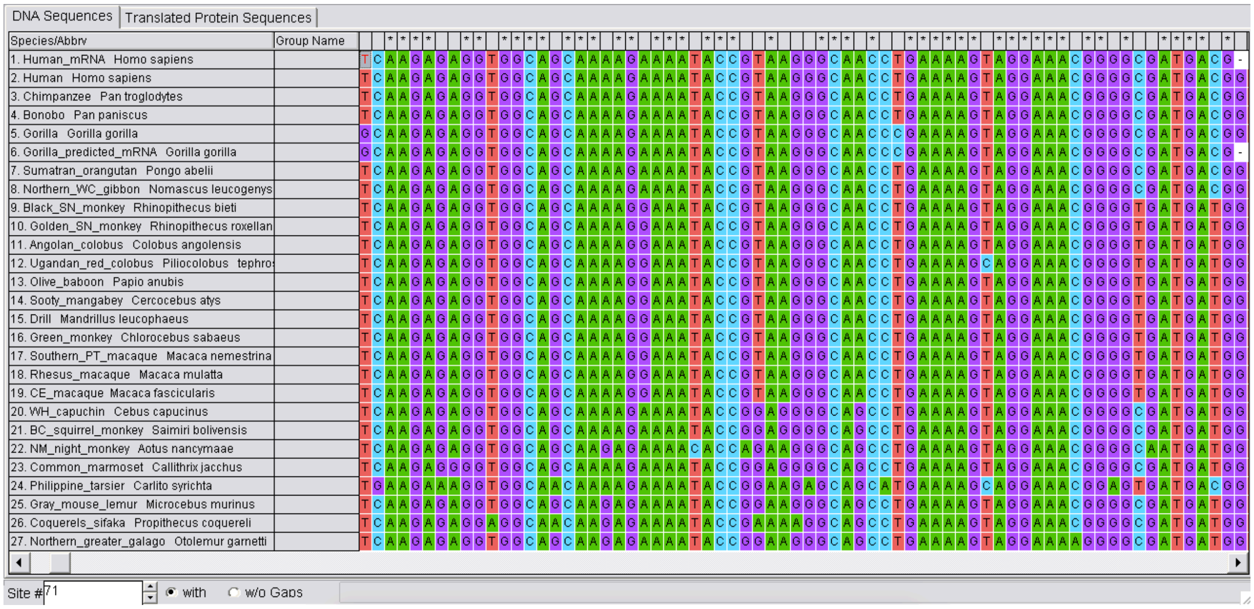

DNA Sequences | Translated Protein Sequences

Species/Abbrv	Group Name	`  ****  ** **** *** ** *** ***  *   *** *  ****** ****** ** *  **** * `
1. Human_mRNA Homo sapiens		TCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGATGACG-
2. Human Homo sapiens		TCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGATGACGG
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4. Bonobo Pan paniscus		TCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGATGACGG
5. Gorilla Gorilla gorilla		GCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCCGAAAAGTAGGAAACGGGGCGATGACGG
6. Gorilla_predicted_mRNA Gorilla gorilla		GCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCCGAAAAGTAGGAAACGGGGCGATGACG-
7. Sumatran_orangutan Pongo abelii		TCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGATGACGG
8. Northern_WC_gibbon Nomascus leucogenys		TCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGATGACGG
9. Black_SN_monkey Rhinopithecus bieti		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGATGATGG
10. Golden_SN_monkey Rhinopithecus roxellan		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGATGATGG
11. Angolan_colobus Colobus angolensis		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGATGATGG
12. Ugandan_red_colobus Piliocolobus tephro		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGCAGGAAACGGGGTGATGATGG
13. Olive_baboon Papio anubis		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGATGATGG
14. Sooty_mangabey Cercocebus atys		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGATGATGG
15. Drill Mandrillus leucophaeus		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGATGATGG
16. Green_monkey Chlorocebus sabaeus		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGATGATGG
17. Southern_PT_macaque Macaca nemestrina		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGATGATGG
18. Rhesus_macaque Macaca mulatta		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGATGATGG
19. CE_macaque Macaca fascicularis		TCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGATGATGG
20. WH_capuchin Cebus capucinus		TCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAAAGTAGGAAACGGGGCGATGATGG
21. BC_squirrel_monkey Saimiri bolivensis		TCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAAAGTAGGAAACGGGGCGATGATGG
22. NM_night_monkey Aotus nancymaae		TCAAGAGAGGTGGCAGCAAGAGAAAACACCAGAAGGGCAGCCTGAAAAGTAGGAAACGGGGCAATGATGG
23. Common_marmoset Callithrix jacchus		TCAAGAGGGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAAAGTAGGAAACGGGGCGATGATGG
24. Philippine_tarsier Carlito syrichta		TGAAGAAAGGTGGCAACAAAAGAAAATACCGGAAGAGCAGCATGAAAAGCAGGAAACGGAGTGATGACGG
25. Gray_mouse_lemur Microcebus murinus		TCAAGAGAGGTGGCAGCAAGAGAAAATACCGGAAGGGCAGCCTGAAAAGTAGGAAACGGGGCGATGATGG
26. Coquerels_sifaka Propithecus coquereli		TCAAGAGAGGAGGCAACAAGAGAAAATACCGAAAAGGCAGCCTGAAAAGTAGGAAACGGGGCGATGATGG
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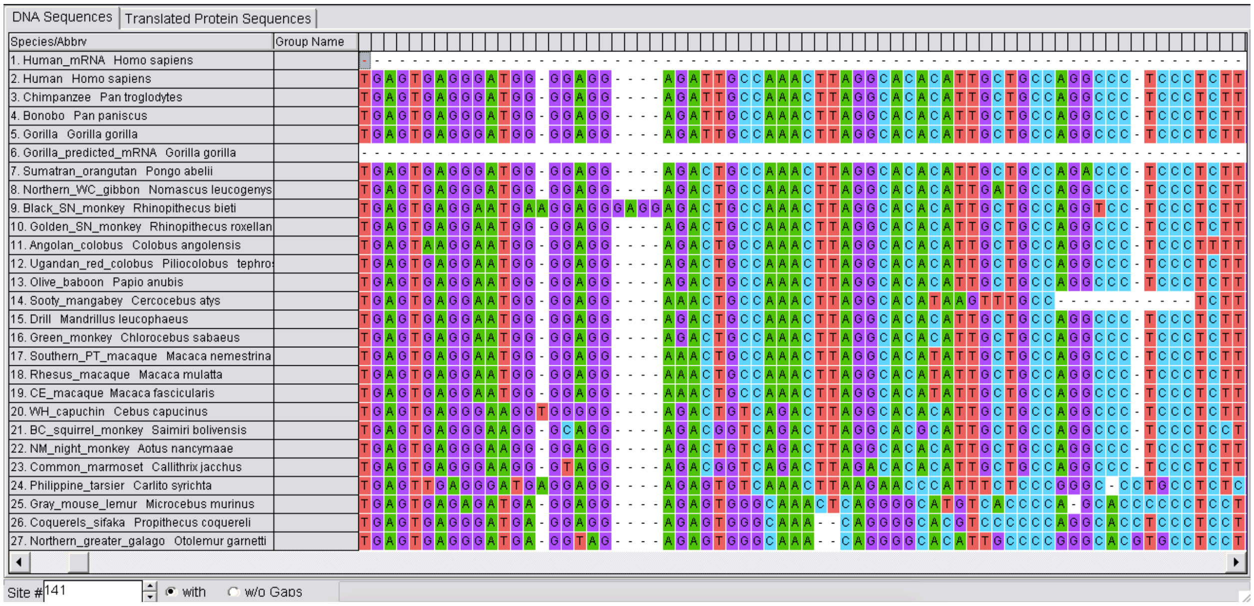

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22. NM_night_monkey  Aotus nancymaae            TGAGTGAGGGAAGG-GGAGG----AGACTGTCAGACTTAGGCACACATTGCTGCCAGGCCC-TCCCTCTT
23. Common_marmoset  Callithrix jacchus         TGAGTGAGGGAAGG-GTAGG----AGACGGTCAGACTTAGACACACATTGCTGCCAGGCCC-TCCCTCTT
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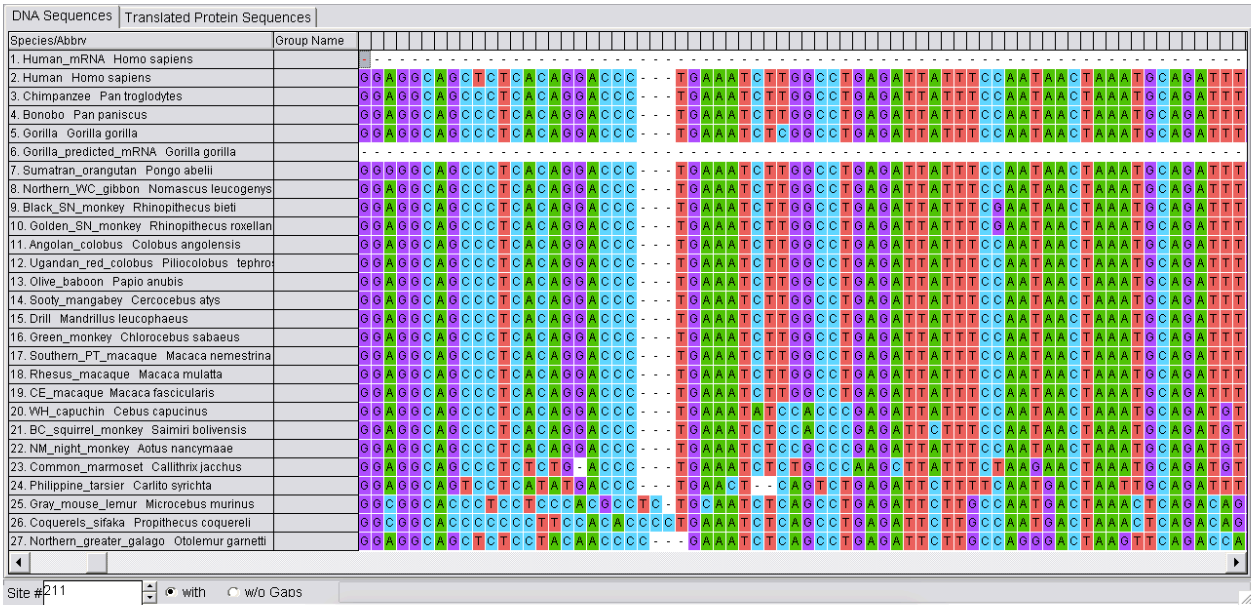

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5. Gorilla  Gorilla gorilla                      GGAGGCAGCCCTCACAGGACCC---TGAAATCTCGGCCTGAGATTATTTCCAATAACTAAATGCAGATTT
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19. CE_macaque  Macaca fascicularis             GGAGGCAGCCCTCACAGGACCC---TGAAATCTTGGCCTGAGATTATTTCCAATAACTAAATGCAGATTT
20. WH_capuchin  Cebus capucinus                GGAGGCAGCCCTCACAGGACCC---TGAAATATCCACCCGAGATTATTTCCAATAACTAAATGCAGATGT
21. BC_squirrel_monkey  Saimiri bolivensis      GGAGGCAGCCCTCACAGGACCC---TGAAATCTCCACCCGAGATTCTTTCCAATAACTAAATGCAGATGT
22. NM_night_monkey  Aotus nancymaae            GGAGGCAGCCCTCACAGGACCC---TGAAATCTCCGCCCGAGATTATTTCCAATAACTAAATGCAGATGT
23. Common_marmoset  Callithrix jacchus         GGAGGCAGCCCTCTCTG-ACCC---TGAAATCTCTGCCCAAGCTTATTTCTAAGAACTAAATGCAGATGT
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25. Gray_mouse_lemur  Microcebus murinus        GGCGGCACCCTCCTCCCACGCCTC-TGCAATCTCAGCCTGAGATTCTTGCCAATGACTAAACTCAGACAG
26. Coquerels_sifaka  Propithecus coquereli     GGCGGCACCCCCCCTTCCACACCCCTGAAATCTCAGCCTGAGATTCTTGCCAATGACTAAACTCAGACAG
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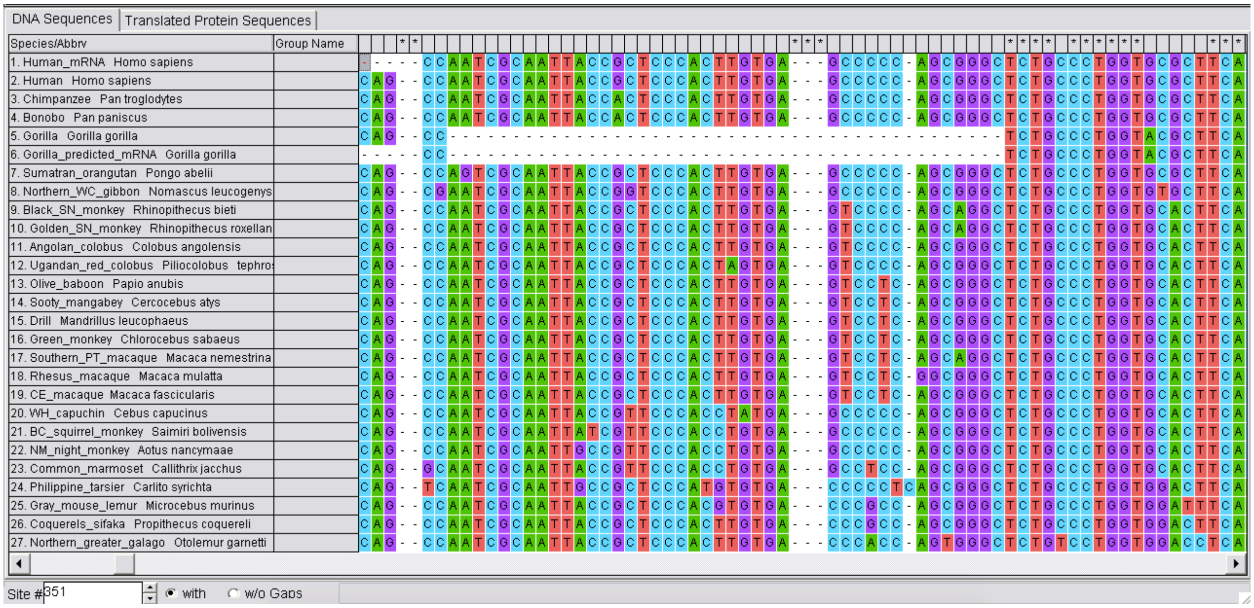

DNA Sequences | Translated Protein Sequences

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5. Gorilla  Gorilla gorilla                                CAG--CC--------------------------------------------TCTGCCCTGGTACGCTTCA
6. Gorilla_predicted_mRNA  Gorilla gorilla                 -----CC--------------------------------------------TCTGCCCTGGTACGCTTCA
7. Sumatran_orangutan  Pongo abelii                        CAG--CCAGTCGCAATTACCGCTCCCACTTGTGA---GCCCCC-AGCGGGCTCTGCCCTGGTGCGCTTCA
8. Northern_WC_gibbon  Nomascus leucogenys                 CAG--CGAATCGCAATTACCGGTCCCACTTGTGA---GCCCCC-AGCGGGCTCTGCCCTGGTGTGCTTCA
9. Black_SN_monkey  Rhinopithecus bieti                    CAG--CCAATCGCAATTACCGCTCCCACTTGTGA---GTCCCC-AGCAGGCTCTGCCCTGGTGCACTTCA
10. Golden_SN_monkey  Rhinopithecus roxellan               CAG--CCAATCGCAATTACCGCTCCCACTTGTGA---GTCCCC-AGCAGGCTCTGCCCTGGTGCACTTCA
11. Angolan_colobus  Colobus angolensis                    CAG--CCAATCGCAATTACCGCTCCCACTTGTGA---GTCCCC-AGCGGGCTCTGCCCTGGTGCACTTCA
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13. Olive_baboon  Papio anubis                             CAG--CCAATCGCAATTACCGCTCCCACTTGTGA---GTCCTC-AGCGGGCTCTGCCCTGGTGCACTTCA
14. Sooty_mangabey  Cercocebus atys                        CAG--CCAATCGCAATTACCGCTCCCACTTGTGA---GTCCTC-AGCGGGCTCTGCCCTGGTGCACTTCA
15. Drill  Mandrillus leucophaeus                          CAG--CCAATCGCAATTACCGCTCCCACTTGTGA---GTCCTC-AGCGGGCTCTGCCCTGGTGCACTTCA
16. Green_monkey  Chlorocebus sabaeus                      CAG--CCAATCGCAATTACCGCTCCCACTTGTGA---GTCCTC-AGCGGGCTCTGCCCTGGTGCACTTCA
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22. NM_night_monkey  Aotus nancymaae                       CAG--CCAATCGCAATTGCCGTTCCCACCTGTGA---GCCCCC-AGCGGGCTCTGCCCTGGTGCACTTCA
23. Common_marmoset  Callithrix jacchus                    CAG--GCAATCGCAATTACCGTTCCCACCTGTGA---GCCTCC-AGCGGGCTCTGCCCTGGTGCACTTCA
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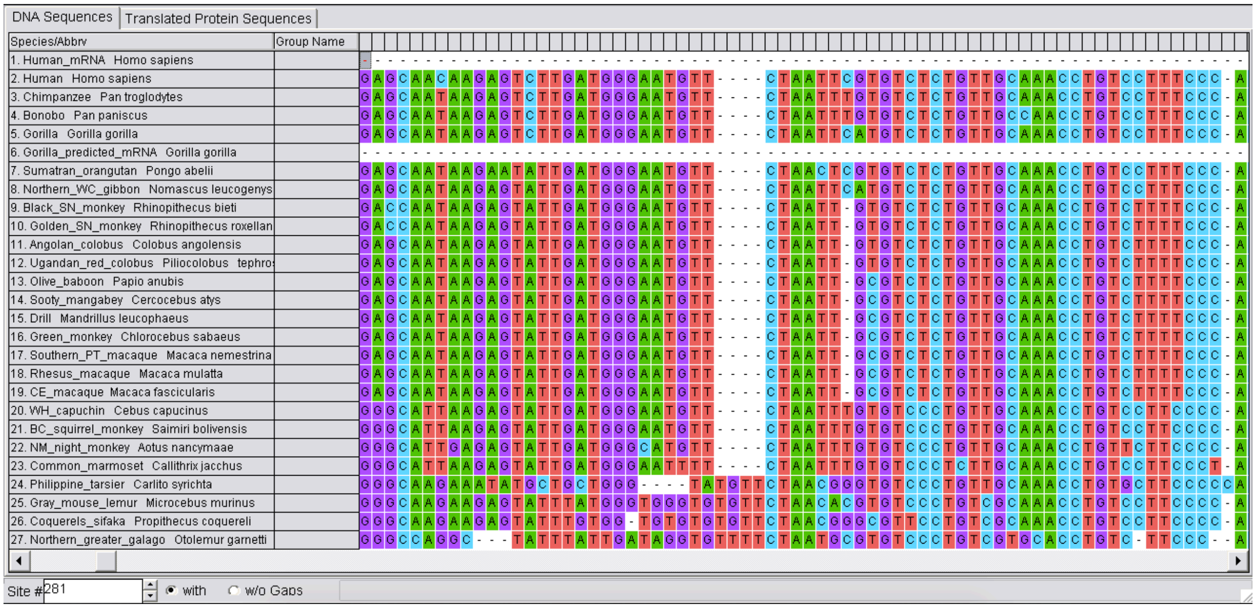

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1. Human_mRNA  Homo sapiens                                ----------------------------------------------------------------------
2. Human  Homo sapiens                                     GAGCAACAAGAGTCTTGATGGGAATGTT----CTAATTCGTGTCTCTGTTGCAAACCTGTCCTTTCCC-A
3. Chimpanzee  Pan troglodytes                             GAGCAATAAGAGTCTTGATGGGAATGTT----CTAATTTGTGTCTCTGTTGCAAACCTGTCCTTTCCC-A
4. Bonobo  Pan paniscus                                    GAGCAATAAGAGTCTTGATGGGAATGTT----CTAATTTGTGTCTCTGTTGCCAACCTGTCCTTTCCC-A
5. Gorilla  Gorilla gorilla                                GAGCAATAAGAGTCTTGATGGGAATGTT----CTAATTCATGTCTCTGTTGCAAACCTGTCCTTTCCC-A
6. Gorilla_predicted_mRNA  Gorilla gorilla                 ----------------------------------------------------------------------
7. Sumatran_orangutan  Pongo abelii                        GAGCAATAAGAATATTGATGGGAATGTT----CTAACTCGTGTCTCTGTTGCAAACCTGTCCTTTCCC-A
8. Northern_WC_gibbon  Nomascus leucogenys                 GAGCAATAAGAGTATTGATGGGAATGTT----CTAATTCATGTCTCTGTTGCAAACCTGTCCTTTCCC-A
9. Black_SN_monkey  Rhinopithecus bieti                    GACCAATAAGAGTATTGATGGGAATGTT----CTAATT-GTGTCTCTGTTGCAAACCTGTCTTTTCCC-A
10. Golden_SN_monkey  Rhinopithecus roxellan               GACCAATAAGAGTATTGATGGGAATGTT----CTAATT-GTGTCTCTGTTGCAAACCTGTCTTTTCCC-A
11. Angolan_colobus  Colobus angolensis                    GAGCAATAAGAGTATTGATGGGAATGTT----CTAATT-GTGTCTCTGTTGCAAACCTGTCTTTTCCC-A
12. Ugandan_red_colobus  Piliocolobus tephro               GAGCAATAAGAGTATTGATGGGAATGTT----CTAATT-GTGTCTCTGTTGCAAACCTGTCTTTTCCC-A
13. Olive_baboon  Papio anubis                             GAGCAATAAGAGTATTGATGGGAATGTT----CTAATT-GCGTCTCTGTTGCAAACCTGTCTTTTCCC-A
14. Sooty_mangabey  Cercocebus atys                        GAGCAATAAGAGTATTGATGGGAATGTT----CTAATT-GCGTCTCTGTTGCAAACCTGTCTTTTCCC-A
15. Drill  Mandrillus leucophaeus                          GAGCAATAAGAGTATTGATGGGAATGTT----CTAATT-GCGTCTCTGTTGCAAACCTGTCTTTTCCC-A
16. Green_monkey  Chlorocebus sabaeus                      GAGCAATAAGAGTATTGATGGGAATGTT----CTAATT-GCGTCTCTGTTGCAAACCTGTCTTTTCCC-A
17. Southern_PT_macaque  Macaca nemestrina                 GAGCAATAAGAGTATTGATGGGAATGTT----CTAATT-GCGTCTCTGTTGCAAACCTGTCTTTTCCC-A
18. Rhesus_macaque  Macaca mulatta                         GAGCAATAAGAGTATTGATGGGAATGTT----CTAATT-GCGTCTCTGTTGCAAACCTGTCTTTTCCC-A
19. CE_macaque  Macaca fascicularis                        GAGCAATAAGAGTATTGATGGGAATGTT----CTAATT-GCGTCTCTGTTGCAAACCTGTCTTTTCCC-A
20. WH_capuchin  Cebus capucinus                           GGGCATTAAGAGTATTGATGGGAATGTT----CTAATTTGTGTCCCTGTTGCAAACCTGTCCTTCCCC-A
21. BC_squirrel_monkey  Saimiri bolivensis                 GGGCATTAAGAGTATTGATGGGAATGTT----CTAATTTGTGTCCCTGTTGCAAACCTGTCCTTCCCC-A
22. NM_night_monkey  Aotus nancymaae                       GGGCATTGAGAGTATTGATGGGCATGTT----CTAATTTGTGTCCCTGTTGCAAACCTGTTCTTCCCC-A
23. Common_marmoset  Callithrix jacchus                    GGGCATTAAGAGTATTGATGGGAATTTT----CTAATTTGTGTCCCTCTTGCAAACCTGTCCTTCCCT-A
24. Philippine_tarsier  Carlito syrichta                   GGGCAAGAAATATGCTGCTGGG----TATGTTCTAACGGGTGTCCCTGTTGCAAACCTGTGCTTCCCCCA
25. Gray_mouse_lemur  Microcebus murinus                   GGGCAAGAAGAGTATTTATGGGTGGGTGTGTTCTAACACGTGTCCCTGTCGCAAACCTGTCCTTCCCC-A
26. Coquerels_sifaka  Propithecus coquereli                GGGCAAGAAGAGTATTTGTGG-TGTGTGTGTTCTAACGGGCGTTCCTGTCGCAAACCTGTCCTTCCCC-A
27. Northern_greater_galago  Otolemur garnetti             GGGCCAGGC---TATTTATTGATAGGTGTTTTCTAATGCGTGTCCCTGTCGTGCACCTGTC-TTCCC--A
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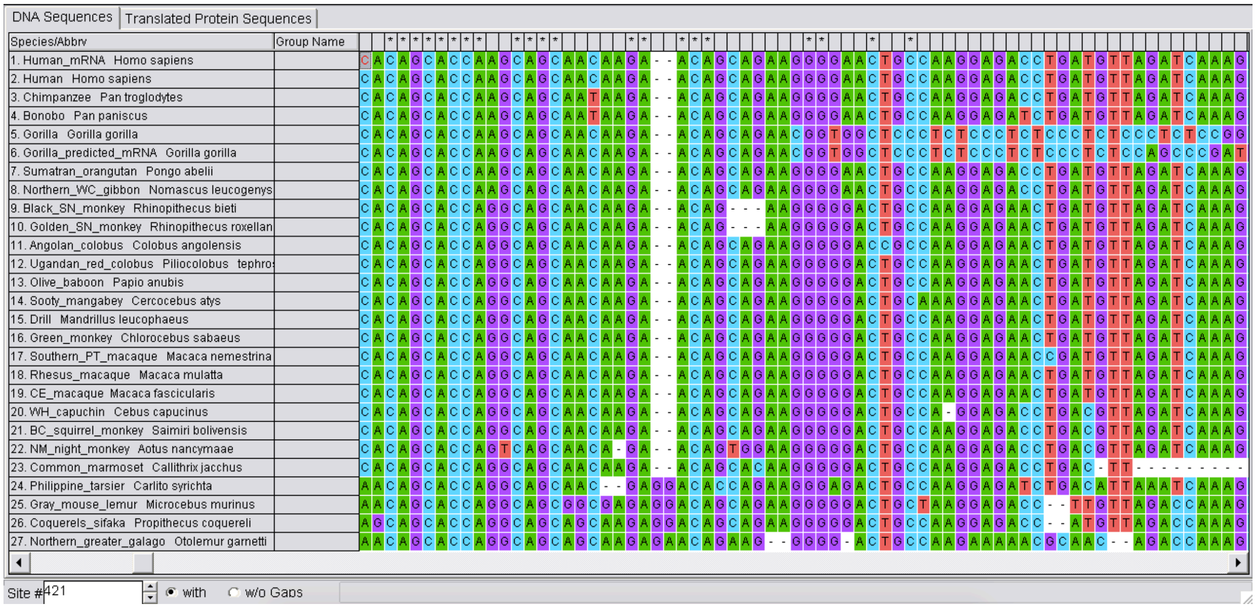
Site # 281 ● with ○ w/o Gaps



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DNA Sequences | Translated Protein Sequences
Species/Abbrv                                  Group Name    ********  ****     **  ***       **   *  *
1. Human_mRNA  Homo sapiens                                CACAGCACCAAGCAGCAACAAGA--ACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAG
2. Human  Homo sapiens                                     CACAGCACCAAGCAGCAACAAGA--ACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAG
3. Chimpanzee  Pan troglodytes                             CACAGCACCAAGCAGCAATAAGA--ACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAG
4. Bonobo  Pan paniscus                                    CACAGCACCAAGCAGCAATAAGA--ACAGCAGAAGGGGAACTGCCAAGGAGATCTGATGTTAGATCAAAG
5. Gorilla  Gorilla gorilla                                CACAGCACCAAGCAGCAACAAGA--ACAGCAGAACGGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCGG
6. Gorilla_predicted_mRNA  Gorilla gorilla                 CACAGCACCAAGCAGCAACAAGA--ACAGCAGAACGGTGGCTCCCTCTCCCTCTCCCTCTCCAGCCCGAT
7. Sumatran_orangutan  Pongo abelii                        CACAGCACCAAGCAGCAACAAGA--ACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAG
8. Northern_WC_gibbon  Nomascus leucogenys                 CACAGCACCAAGCAGCAACAAGA--ACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAG
9. Black_SN_monkey  Rhinopithecus bieti                    CACAGCACCAGGCAGCAACAAGA--ACAG---AAGGGGGACTGCCAAGGAGAACTGATGTTAGATCAAAG
10. Golden_SN_monkey  Rhinopithecus roxellan               CACAGCACCAGGCAGCAACAAGA--ACAG---AAGGGGGACTGCCAAGGAGAACTGATGTTAGATCAAAG
11. Angolan_colobus  Colobus angolensis                    CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACCGCCAAGGAGAACTGATGTTAGATCAAAG
12. Ugandan_red_colobus  Piliocolobus tephro               CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACTGCCAAGGAGAACTGATGTTAGATCAAAG
13. Olive_baboon  Papio anubis                             CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACTGCCAAGGAGAACTGATGTTAGATCAAAG
14. Sooty_mangabey  Cercocebus atys                        CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACTGCAAAGGAGAACTGATGTTAGATCAAAG
15. Drill  Mandrillus leucophaeus                          CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACTGCCAAGGAGAACTGATGTTAGATCAAAG
16. Green_monkey  Chlorocebus sabaeus                      CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACTGCCAAGGAGAACTGATGTTAGATCAAAG
17. Southern_PT_macaque  Macaca nemestrina                 CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACTGCCAAGGAGAACCGATGTTAGATCAAAG
18. Rhesus_macaque  Macaca mulatta                         CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACTGCCAAGGAGAACTGATGTTAGATCAAAG
19. CE_macaque  Macaca fascicularis                        CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACTGCCAAGGAGAACTGATGTTAGATCAAAG
20. WH_capuchin  Cebus capucinus                           CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACTGCCA-GGAGACCTGACGTTAGATCAAAG
21. BC_squirrel_monkey  Saimiri bolivensis                 CACAGCACCAGGCAGCAACAAGA--ACAGCAGAAGGGGGACTGCCAAGGAGACCTGACGTTAGATCAAAG
22. NM_night_monkey  Aotus nancymaae                       CACAGCACCAGTCAGCAACA-GA--ACAGTGGAAGGGGGACTGCCAAGGAGACCTGACGTTAGATCAAAG
23. Common_marmoset  Callithrix jacchus                    CACAGCACCAGGCAGCAACAAGA--ACAGCACAAGGGGGACTGCCAAGGAGACCTGAC-TT---------
24. Philippine_tarsier  Carlito syrichta                   AACAGCACCAGGCAGCAAC--GAGGACACCAGAAGGGAGACTGCCAAGGAGATCTGACATTAAATCAAAG
25. Gray_mouse_lemur  Microcebus murinus                   AACAGCACCAGGCAGCGGCGAGAGGACAGCAGAAGGGGGACTGCTAAGGAGACC--TTGTTAGACCAAAG
26. Coquerels_sifaka  Propithecus coquereli                AGCAGCACCAGGCAGCAGCAAGAGGACAGCAGAAGGGGGACTGCCAAGGAGACC--ATGTTAGACCAAAG
27. Northern_greater_galago  Otolemur garnetti             AACAGCACCAGGCAGCAGCAAGAGAACAGAAG--GGGG-ACTGCCAAGAAAAACGCAAC--AGACCAAAG
Site #421   ● with   ○ w/o Gaps
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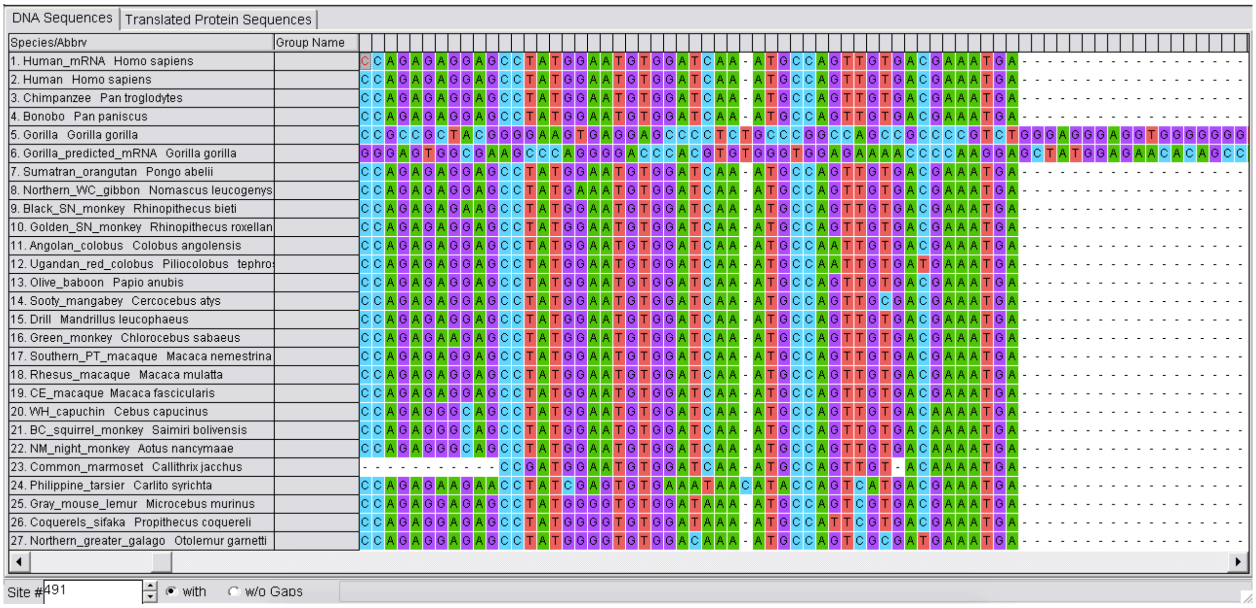

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DNA Sequences | Translated Protein Sequences
Species/Abbrv                                  Group Name
1. Human_mRNA  Homo sapiens                                CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
2. Human  Homo sapiens                                     CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
3. Chimpanzee  Pan troglodytes                             CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
4. Bonobo  Pan paniscus                                    CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
5. Gorilla  Gorilla gorilla                                CCGCCGCTACGGGGAAGTGAGGAGCCCCTCTGCCCGGCCAGCCGCCCCGTCTGGGAGGGAGGTGGGGGGG
6. Gorilla_predicted_mRNA  Gorilla gorilla                 GGGAGTGGCGAAGCCCAGGGGACCCACGTGTGGGTGGAGAAAACCCCAAGGAGCTATGGAGAACACAGCC
7. Sumatran_orangutan  Pongo abelii                        CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
8. Northern_WC_gibbon  Nomascus leucogenys                 CCAGAGAGGAGCCTATGAAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
9. Black_SN_monkey  Rhinopithecus bieti                    CCAGAGAGAAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
10. Golden_SN_monkey  Rhinopithecus roxellan               CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
11. Angolan_colobus  Colobus angolensis                    CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAATTGTGACGAAATGA------------------
12. Ugandan_red_colobus  Piliocolobus tephro               CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAATTGTGATGAAATGA------------------
13. Olive_baboon  Papio anubis                             CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
14. Sooty_mangabey  Cercocebus atys                        CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGCGACGAAATGA------------------
15. Drill  Mandrillus leucophaeus                          CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
16. Green_monkey  Chlorocebus sabaeus                      CCAGAGAAGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
17. Southern_PT_macaque  Macaca nemestrina                 CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
18. Rhesus_macaque  Macaca mulatta                         CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
19. CE_macaque  Macaca fascicularis                        CCAGAGAGGAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACGAAATGA------------------
20. WH_capuchin  Cebus capucinus                           CCAGAGGGCAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACAAAATGA------------------
21. BC_squirrel_monkey  Saimiri bolivensis                 CCAGAGGGCAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACAAAATGA------------------
22. NM_night_monkey  Aotus nancymaae                       CCAGAGGGCAGCCTATGGAATGTGGATCAA-ATGCCAGTTGTGACAAAATGA------------------
23. Common_marmoset  Callithrix jacchus                    -----------CCGATGGAATGTGGATCAA-ATGCCAGTTGT-ACAAAATGA------------------
24. Philippine_tarsier  Carlito syrichta                   CCAGAGAAGAACCTATCGAGTGTGAAATAACATACCAGTCATGACGAAATGA------------------
25. Gray_mouse_lemur  Microcebus murinus                   CCAGAGGAGAGCCTATGGGGTGTGGATAAA-ATGCCAGTCGTGACGAAATGA------------------
26. Coquerels_sifaka  Propithecus coquereli                CCAGAGGAGAGCCTATGGGGTGTGGATAAA-ATGCCATTCGTGACGAAATGA------------------
27. Northern_greater_galago  Otolemur garnetti             CCAGAGGAGAGCCTATGGGGTGTGGACAAA-ATGCCAGTCGCGATGAAATGA------------------
Site #491   ● with   ○ w/o Gaps
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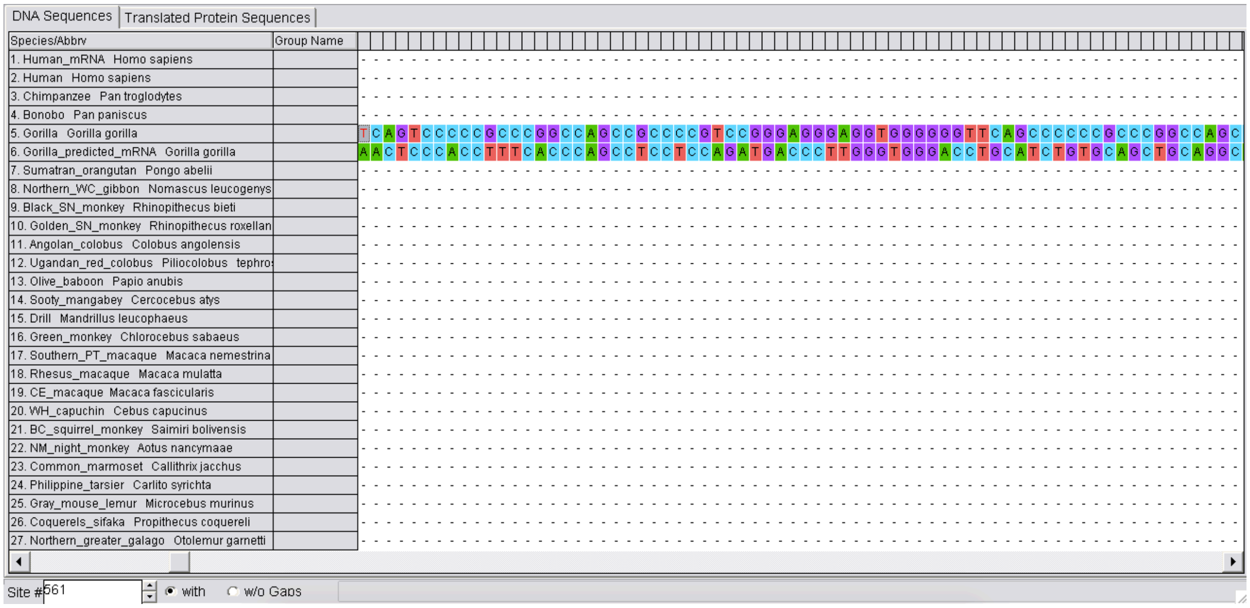
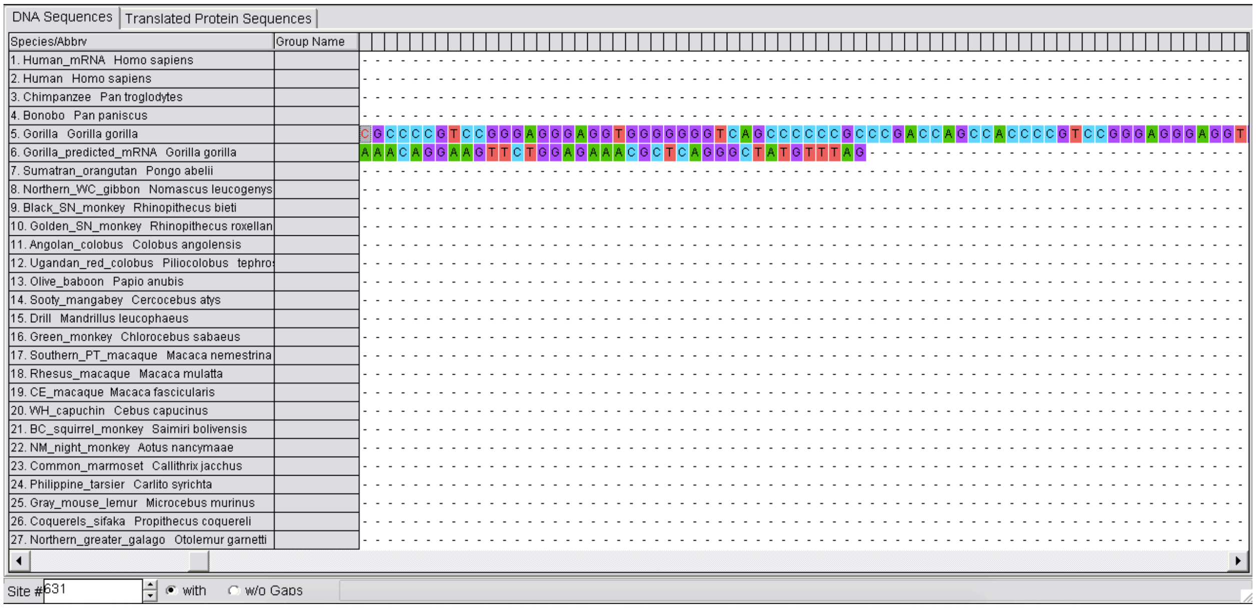


Species/Abbrv	Group Name	
1. Human_mRNA Homo sapiens		--
2. Human Homo sapiens		--
3. Chimpanzee Pan troglodytes		--
4. Bonobo Pan paniscus		--
5. Gorilla Gorilla gorilla		TCAGTCCCCCGCCCGGCCAGCCGCCCCGTCCGGGAGGGAGGTGGGGGGTTCAGCCCCCCGCCCGGCCAGC
6. Gorilla_predicted_mRNA Gorilla gorilla		AACTCCCACCTTTCACCCAGCCTCCTCCAGATGACCCTTGGGTGGGACCTGCATCTGTGCAGCTGCAGGC
7. Sumatran_orangutan Pongo abelii		--
8. Northern_WC_gibbon Nomascus leucogenys		--
9. Black_SN_monkey Rhinopithecus bieti		--
10. Golden_SN_monkey Rhinopithecus roxellan		--
11. Angolan_colobus Colobus angolensis		--
12. Ugandan_red_colobus Piliocolobus tephro		--
13. Olive_baboon Papio anubis		--
14. Sooty_mangabey Cercocebus atys		--
15. Drill Mandrillus leucophaeus		--
16. Green_monkey Chlorocebus sabaeus		--
17. Southern_PT_macaque Macaca nemestrina		--
18. Rhesus_macaque Macaca mulatta		--
19. CE_macaque Macaca fascicularis		--
20. WH_capuchin Cebus capucinus		--
21. BC_squirrel_monkey Saimiri bolivensis		--
22. NM_night_monkey Aotus nancymaae		--
23. Common_marmoset Callithrix jacchus		--
24. Philippine_tarsier Carlito syrichta		--
25. Gray_mouse_lemur Microcebus murinus		--
26. Coquerels_sifaka Propithecus coquereli		--
27. Northern_greater_galago Otolemur garnetti		--

Site # 561 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
1. Human_mRNA Homo sapiens		--
2. Human Homo sapiens		--
3. Chimpanzee Pan troglodytes		--
4. Bonobo Pan paniscus		--
5. Gorilla Gorilla gorilla		CGCCCCGTCCGGGAGGGAGGTGGGGGGGTCAGCCCCCCGCCCGACCAGCCACCCCGTCCGGGAGGGAGGT
6. Gorilla_predicted_mRNA Gorilla gorilla		AAACAGGAAGTTCTGGAGAAACGCTCAGGGCTATGTTTAG------------------------------
7. Sumatran_orangutan Pongo abelii		--
8. Northern_WC_gibbon Nomascus leucogenys		--
9. Black_SN_monkey Rhinopithecus bieti		--
10. Golden_SN_monkey Rhinopithecus roxellan		--
11. Angolan_colobus Colobus angolensis		--
12. Ugandan_red_colobus Piliocolobus tephro		--
13. Olive_baboon Papio anubis		--
14. Sooty_mangabey Cercocebus atys		--
15. Drill Mandrillus leucophaeus		--
16. Green_monkey Chlorocebus sabaeus		--
17. Southern_PT_macaque Macaca nemestrina		--
18. Rhesus_macaque Macaca mulatta		--
19. CE_macaque Macaca fascicularis		--
20. WH_capuchin Cebus capucinus		--
21. BC_squirrel_monkey Saimiri bolivensis		--
22. NM_night_monkey Aotus nancymaae		--
23. Common_marmoset Callithrix jacchus		--
24. Philippine_tarsier Carlito syrichta		--
25. Gray_mouse_lemur Microcebus murinus		--
26. Coquerels_sifaka Propithecus coquereli		--
27. Northern_greater_galago Otolemur garnetti		--

Site # 631 ● with ○ w/o Gaps

Appendix B1) Alignment of primate *Tnp1* coding exon nucleotide sequences

Species/Abbrv	Group Name	
1. Human Homo sapiens		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
2. Chimpanzee Pan troglodytes		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
3. Bonobo Pan paniscus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
4. Gorilla Gorilla gorilla		ATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
5. Gorilla_predicted_mRNA Gorilla gorilla		ATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
6. Sumatran_orangutan Pongo abelii		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
7. Northen_WC_gibbon Nomascus leucogenys		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
8. Black_SN_monkey Rhinopithecus bieti		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
9. Golden_SN_monkey Rhinopithecus roxellana		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
10. Angolan_colobus Colobus angolensis palliatus		ATGTCGACCAGCCGCAAATTAAAGAGTCGTGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
11. Ugandan_red_colobus Piliocolobus tephrosceles		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
12. Olive_baboon Papio anubis		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
13. Sooty_mangabey Cercocebus atys		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
14. Drill Mandrillus leucophaeus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
15. Green_monkey Chlorocebus sabaeus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
16. Southern_PT_macaque Macaca nemestrina		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
17. Rhesus_macaque Macaca mulatta		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
18. CE_macaque Macaca fascicularis		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
19. WH_capuchin Cebus capucinus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
21. NM_night_monkey Aotus nancymaae		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCACAAGG
22. Common_marmoset Callithrix jacchus		ATGTCGACCAGCCGCAAATTAAAGGGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCAGAAGG
23. Philippine_tarsier Tarsius syrichta		ATGTCCAACAGCCGCAAATTAAAGGGTCACGGCATGAGGAGAGGCAAGAGCCGATCTCCTCACAAGG
24. Gray_mouse_lemur Microcebus murinus		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGAGCTCCCCACAAGG
25. Coquerels_sifaka Propithecus coquereli		ATGTCGACCAGCCGCAGATTAAAGAGTCATGGCATGAGAAGGGGCAAGAACCGAGCTCCTCACAAGG
26. Northern_greater_galago Otolemur garnettii		ATGACGACCAGCCGCAAATTTAAGAGTCATGGCATGAGGAGGGGCAAGAACCGATCTCCTCACAAGG

Site # 1 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
1. Human Homo sapiens		GAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGA
2. Chimpanzee Pan troglodytes		GAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGA
3. Bonobo Pan paniscus		GAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGA
4. Gorilla Gorilla gorilla		GGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCCGAAAAGTAGGAAACGGGGCGA
5. Gorilla_predicted_mRNA Gorilla gorilla		GGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCCGAAAAGTAGGAAACGGGGCGA
6. Sumatran_orangutan Pongo abelii		GAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGA
7. Northen_WC_gibbon Nomascus leucogenys		GAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGA
8. Black_SN_monkey Rhinopithecus bieti		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGA
9. Golden_SN_monkey Rhinopithecus roxellana		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGA
10. Angolan_colobus Colobus angolensis palliatus		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGA
11. Ugandan_red_colobus Piliocolobus tephrosceles		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGCAGGAAACGGGGTGA
12. Olive_baboon Papio anubis		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGA
13. Sooty_mangabey Cercocebus atys		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGA
14. Drill Mandrillus leucophaeus		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGA
15. Green_monkey Chlorocebus sabaeus		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGA
16. Southern_PT_macaque Macaca nemestrina		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGA
17. Rhesus_macaque Macaca mulatta		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGA
18. CE_macaque Macaca fascicularis		GAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAAACGGGGTGA
19. WH_capuchin Cebus capucinus		GAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAAAGTAGGAAACGGGGCGA
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		GAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAAAGTAGGAAACGGGGCGA
21. NM_night_monkey Aotus nancymaae		GAGTCAAGAGAGGTGGCAGCAAGAGAAAACACCAGAAGGGCAGCCTGAAAAGTAGGAAACGGGGCAA
22. Common_marmoset Callithrix jacchus		GAGTCAAGAGGGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAAAGTAGGAAACGGGGCGA
23. Philippine_tarsier Tarsius syrichta		GAGTGAAGAAAGGTGGCAACAAAAGAAAATACCGGAAGAGCAGCATGAAAAGCAGGAAACGGAGTGA
24. Gray_mouse_lemur Microcebus murinus		GAGTCAAGAGAGGTGGCAGCAAGAGAAAATACCGGAAGGGCAGCCTGAAAAGTAGGAAACGGGGCGA
25. Coquerels_sifaka Propithecus coquereli		GAGTCAAGAGAGGAGGCAACAAGAGAAAATACCGAAAAGGCAGCCTGAAAAGTAGGAAACGGGGCGA
26. Northern_greater_galago Otolemur garnettii		GAGTCAAGAGAGGTGGCAGCAAGAGAAAATACCGGAAGGGCAGCCTGAAAAGTAGGAAAAGGGGCGA

Site # 68 ● with ○ w/o Gaps

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Species/Abbrv                                          Group Name  *** *    *  *      *  * *
1. Human  Homo sapiens                                             TGACGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
2. Chimpanzee  Pan troglodytes                                     TGACGCCAATCGCAATTACCACTCCCACTTGTGA----------------------------------
3. Bonobo  Pan paniscus                                            TGACGCCAATCGCAATTACCACTCCCACTTGTGA----------------------------------
4. Gorilla  Gorilla gorilla                                        TGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAACGGTGGCTCC
5. Gorilla_predicted_mRNA  Gorilla gorilla                         TGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAACGGTGGCTCC
6. Sumatran_orangutan  Pongo abelii                               TGACGCCAGTCGCAATTACCGCTCCCACTTGTGA----------------------------------
7. Northen_WC_gibbon  Nomascus leucogenys                         TGACGCGAATCGCAATTACCGGTCCCACTTGTGA----------------------------------
8. Black_SN_monkey  Rhinopithecus bieti                           TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
9. Golden_SN_monkey  Rhinopithecus roxellana                      TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
10. Angolan_colobus  Colobus angolensis palliatus                 TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
11. Ugandan_red_colobus  Piliocolobus tephrosceles                TGATGCCAATCGCAATTACCGCTCCCACTAGTGA----------------------------------
12. Olive_baboon  Papio anubis                                    TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
13. Sooty_mangabey  Cercocebus atys                               TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
14. Drill  Mandrillus leucophaeus                                 TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
15. Green_monkey  Chlorocebus sabaeus                             TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
16. Southern_PT_macaque  Macaca nemestrina                        TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
17. Rhesus_macaque  Macaca mulatta                                TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
18. CE_macaque  Macaca  fascicularis                              TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
19. WH_capuchin  Cebus capucinus                                  TGATGCCAATCGCAATTACCGTTCCCACCTATGA----------------------------------
20. BC_squirrel_monkey  Saimiri boliviensis boliviensi            TGATGCCAATCGCAATTATCGTTCCCACCTGTGA----------------------------------
21. NM_night_monkey  Aotus nancymaae                              TGATGCCAATCGCAATTGCCGTTCCCACCTGTGA----------------------------------
22. Common_marmoset  Callithrix jacchus                           TGATGGCAATCGCAATTACCGTTCCCACCTGTGA----------------------------------
23. Philippine_tarsier  Tarsius syrichta                          TGACGTCAATCGCAATTGCCGCTCCCATGTGTGA----------------------------------
24. Gray_mouse_lemur  Microcebus murinus                          TGATGCCAATCGCAATTACCGCTCCCACGTGTGA----------------------------------
25. Coquerels_sifaka  Propithecus coquereli                       TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
26. Northern_greater_galago  Otolemur garnettii                   TGATGCCAATCGCAATTACCGCTCCCACTTGTGA----------------------------------
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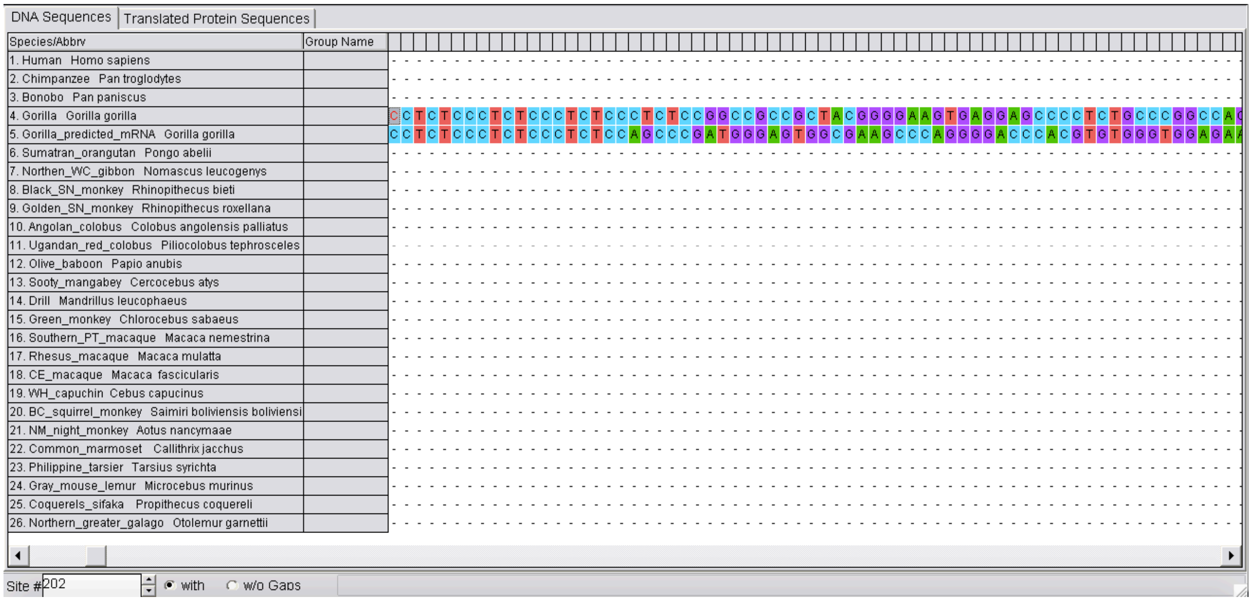
Site # 135 ● with ○ w/o Gaps



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Species/Abbrv                                          Group Name
1. Human  Homo sapiens                                             --------------------------------------------------------------------
2. Chimpanzee  Pan troglodytes                                     --------------------------------------------------------------------
3. Bonobo  Pan paniscus                                            --------------------------------------------------------------------
4. Gorilla  Gorilla gorilla                                        CCTCTCCCTCTCCCTCTCCCTCTCCGGCCGCCGCTACGGGGAAGTGAGGAGCCCCTCTGCCCGGCCAC
5. Gorilla_predicted_mRNA  Gorilla gorilla                         CCTCTCCCTCTCCCTCTCCAGCCCGATGGGAGTGGCGAAGCCCAGGGGACCCACGTGTGGGTGGAGAA
6. Sumatran_orangutan  Pongo abelii                               --------------------------------------------------------------------
7. Northen_WC_gibbon  Nomascus leucogenys                         --------------------------------------------------------------------
8. Black_SN_monkey  Rhinopithecus bieti                           --------------------------------------------------------------------
9. Golden_SN_monkey  Rhinopithecus roxellana                      --------------------------------------------------------------------
10. Angolan_colobus  Colobus angolensis palliatus                 --------------------------------------------------------------------
11. Ugandan_red_colobus  Piliocolobus tephrosceles                --------------------------------------------------------------------
12. Olive_baboon  Papio anubis                                    --------------------------------------------------------------------
13. Sooty_mangabey  Cercocebus atys                               --------------------------------------------------------------------
14. Drill  Mandrillus leucophaeus                                 --------------------------------------------------------------------
15. Green_monkey  Chlorocebus sabaeus                             --------------------------------------------------------------------
16. Southern_PT_macaque  Macaca nemestrina                        --------------------------------------------------------------------
17. Rhesus_macaque  Macaca mulatta                                --------------------------------------------------------------------
18. CE_macaque  Macaca  fascicularis                              --------------------------------------------------------------------
19. WH_capuchin  Cebus capucinus                                  --------------------------------------------------------------------
20. BC_squirrel_monkey  Saimiri boliviensis boliviensi            --------------------------------------------------------------------
21. NM_night_monkey  Aotus nancymaae                              --------------------------------------------------------------------
22. Common_marmoset  Callithrix jacchus                           --------------------------------------------------------------------
23. Philippine_tarsier  Tarsius syrichta                          --------------------------------------------------------------------
24. Gray_mouse_lemur  Microcebus murinus                          --------------------------------------------------------------------
25. Coquerels_sifaka  Propithecus coquereli                       --------------------------------------------------------------------
26. Northern_greater_galago  Otolemur garnettii                   --------------------------------------------------------------------
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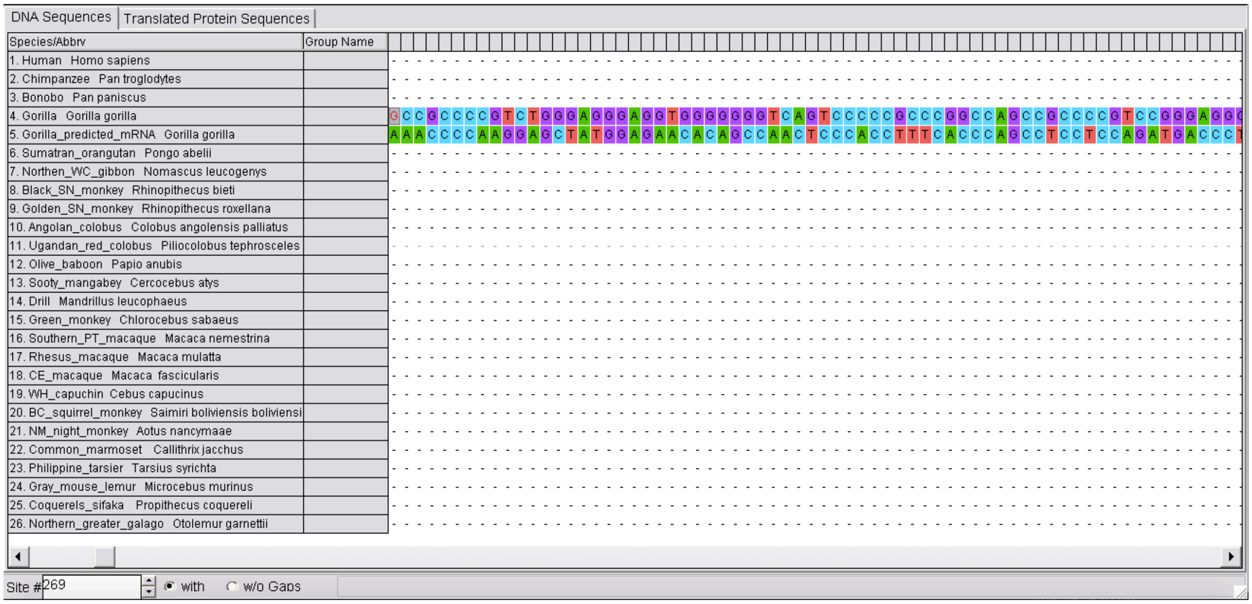
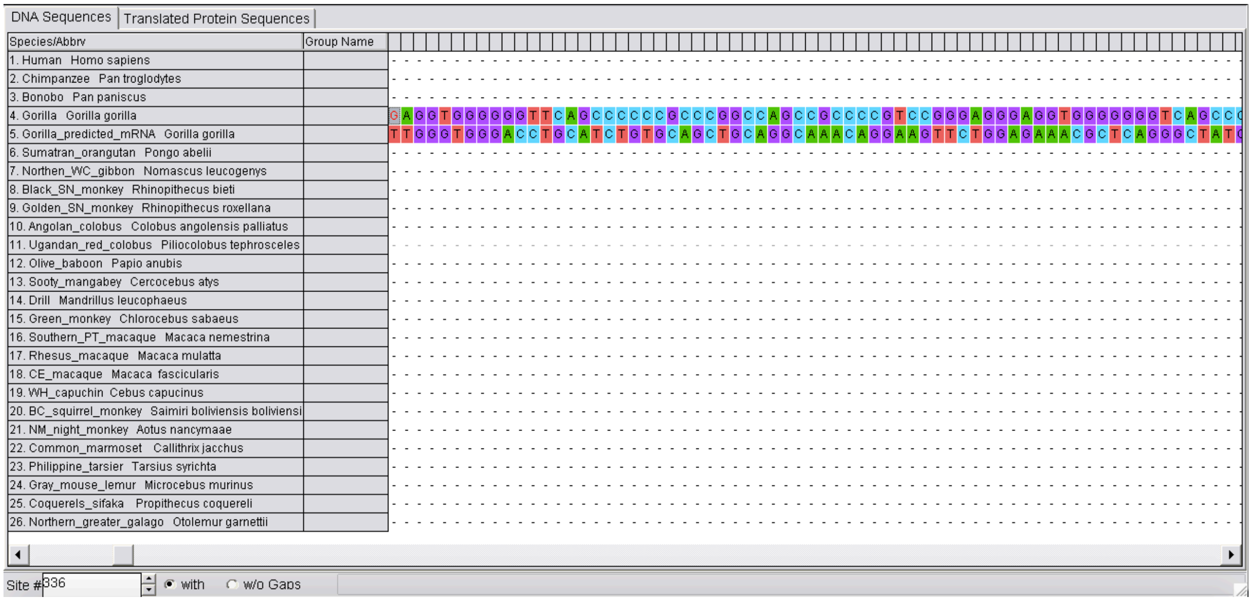
Site # 202 ● with ○ w/o Gaps



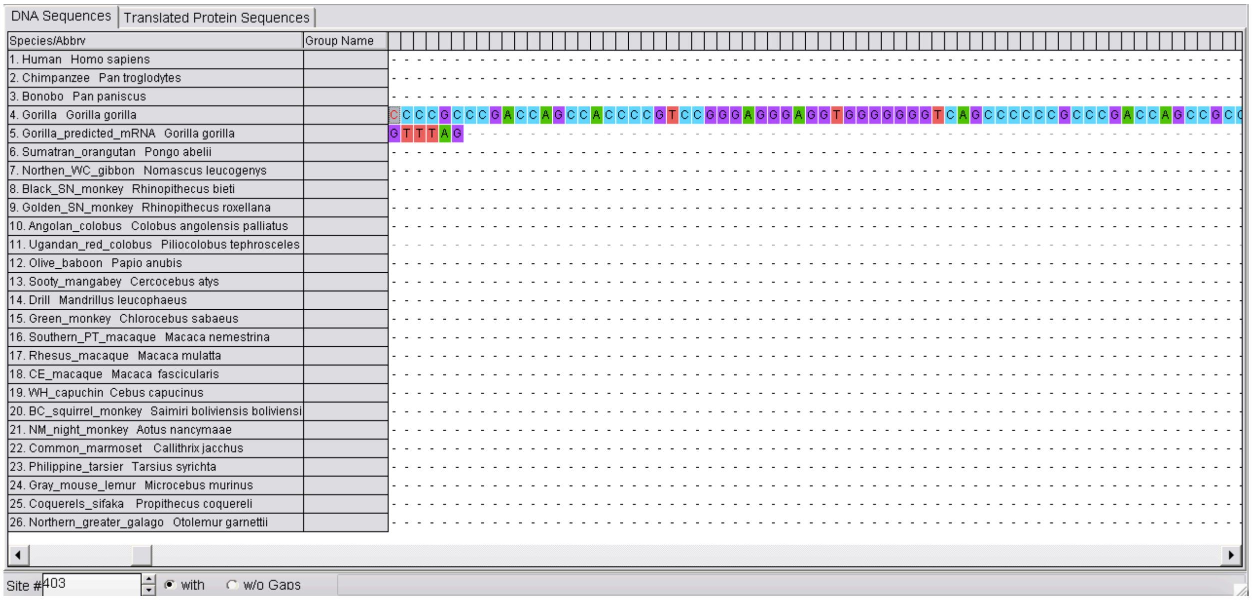
Species/Abbrv	Group Name	
1. Human Homo sapiens		
2. Chimpanzee Pan troglodytes		
3. Bonobo Pan paniscus		
4. Gorilla Gorilla gorilla		GCCGCCCCGTCTGGGAGGGAGGTGGGGGGTCAGTCCCCCGCCCGGCCAGCCGCCCCGTCCGGGAGG
5. Gorilla_predicted_mRNA Gorilla gorilla		AAACCCCAAGGAGCTATGGAGAACACAGCCAACTCCCACCTTTCACCCAGCCTCCTCCAGATGACCC
6. Sumatran_orangutan Pongo abelii		
7. Northen_WC_gibbon Nomascus leucogenys		
8. Black_SN_monkey Rhinopithecus bieti		
9. Golden_SN_monkey Rhinopithecus roxellana		
10. Angolan_colobus Colobus angolensis palliatus		
11. Ugandan_red_colobus Piliocolobus tephrosceles		
12. Olive_baboon Papio anubis		
13. Sooty_mangabey Cercocebus atys		
14. Drill Mandrillus leucophaeus		
15. Green_monkey Chlorocebus sabaeus		
16. Southern_PT_macaque Macaca nemestrina		
17. Rhesus_macaque Macaca mulatta		
18. CE_macaque Macaca fascicularis		
19. WH_capuchin Cebus capucinus		
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		
21. NM_night_monkey Aotus nancymaae		
22. Common_marmoset Callithrix jacchus		
23. Philippine_tarsier Tarsius syrichta		
24. Gray_mouse_lemur Microcebus murinus		
25. Coquerels_sifaka Propithecus coquereli		
26. Northern_greater_galago Otolemur garnettii		

Site # 269 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
1. Human Homo sapiens		
2. Chimpanzee Pan troglodytes		
3. Bonobo Pan paniscus		
4. Gorilla Gorilla gorilla		GAGGTGGGGGGTTCAGCCCCCCGCCCGGCCAGCCGCCCCGTCCGGGAGGGAGGTGGGGGGTCAGCC
5. Gorilla_predicted_mRNA Gorilla gorilla		TTGGGTGGGACCTGCATCTGTGCAGCTGCAGGCAAACAGGAAGTTCTGGAGAAACGCTCAGGGCTAT
6. Sumatran_orangutan Pongo abelii		
7. Northen_WC_gibbon Nomascus leucogenys		
8. Black_SN_monkey Rhinopithecus bieti		
9. Golden_SN_monkey Rhinopithecus roxellana		
10. Angolan_colobus Colobus angolensis palliatus		
11. Ugandan_red_colobus Piliocolobus tephrosceles		
12. Olive_baboon Papio anubis		
13. Sooty_mangabey Cercocebus atys		
14. Drill Mandrillus leucophaeus		
15. Green_monkey Chlorocebus sabaeus		
16. Southern_PT_macaque Macaca nemestrina		
17. Rhesus_macaque Macaca mulatta		
18. CE_macaque Macaca fascicularis		
19. WH_capuchin Cebus capucinus		
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		
21. NM_night_monkey Aotus nancymaae		
22. Common_marmoset Callithrix jacchus		
23. Philippine_tarsier Tarsius syrichta		
24. Gray_mouse_lemur Microcebus murinus		
25. Coquerels_sifaka Propithecus coquereli		
26. Northern_greater_galago Otolemur garnettii		

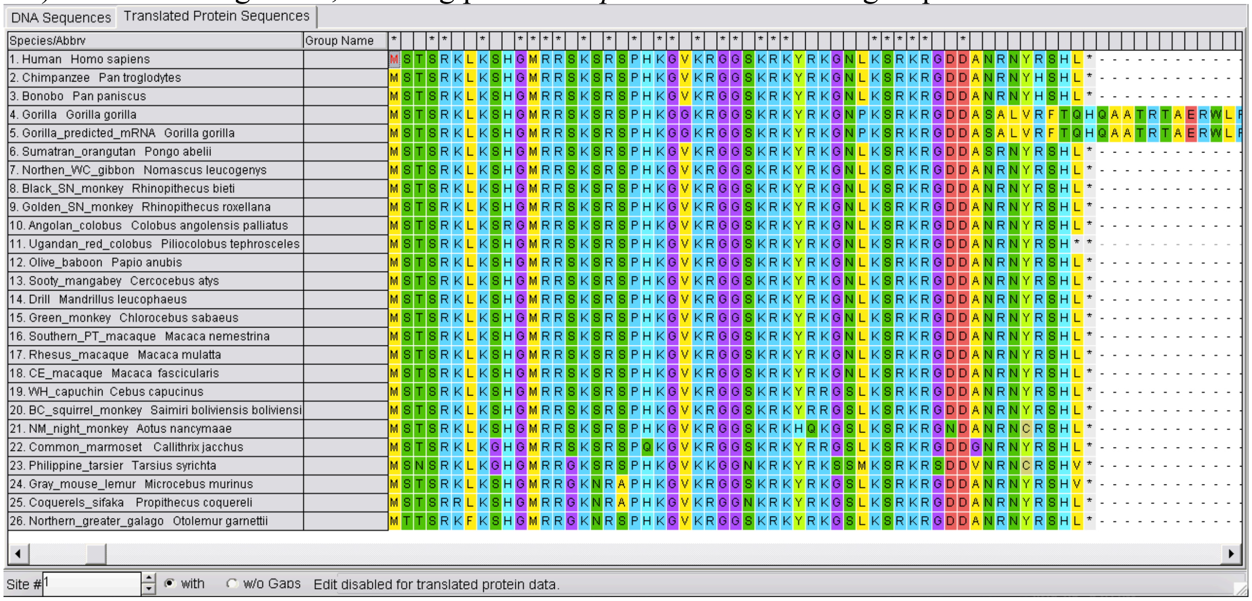
Site # 336 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
1. Human Homo sapiens		
2. Chimpanzee Pan troglodytes		
3. Bonobo Pan paniscus		
4. Gorilla Gorilla gorilla		CCCCGCCCGACCAGCCACCCCGTCCGGGAGGGAGGTGGGGGGTCAGCCCCCCGCCCGACCAGCCGCC
5. Gorilla_predicted_mRNA Gorilla gorilla		GTTTAG
6. Sumatran_orangutan Pongo abelii		
7. Northen_WC_gibbon Nomascus leucogenys		
8. Black_SN_monkey Rhinopithecus bieti		
9. Golden_SN_monkey Rhinopithecus roxellana		
10. Angolan_colobus Colobus angolensis palliatus		
11. Ugandan_red_colobus Piliocolobus tephrosceles		
12. Olive_baboon Papio anubis		
13. Sooty_mangabey Cercocebus atys		
14. Drill Mandrillus leucophaeus		
15. Green_monkey Chlorocebus sabaeus		
16. Southern_PT_macaque Macaca nemestrina		
17. Rhesus_macaque Macaca mulatta		
18. CE_macaque Macaca fascicularis		
19. WH_capuchin Cebus capucinus		
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		
21. NM_night_monkey Aotus nancymaae		
22. Common_marmoset Callithrix jacchus		
23. Philippine_tarsier Tarsius syrichta		
24. Gray_mouse_lemur Microcebus murinus		
25. Coquerels_sifaka Propithecus coquereli		
26. Northern_greater_galago Otolemur garnettii		

Site # 403 ● with ○ w/o Gaps

B2) Translated alignment, showing primate *Tnp1* amino acid coding sequences



Species/Abbrv	Group Name	
1. Human Homo sapiens		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
2. Chimpanzee Pan troglodytes		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYHSHL*
3. Bonobo Pan paniscus		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYHSHL*
4. Gorilla Gorilla gorilla		MSTSRKLKSHGMRRSKSRSPHKGGKRGGSKRKYRKGNPKSRKRGDDASALVRFTQHQAATRTAERWL
5. Gorilla_predicted_mRNA Gorilla gorilla		MSTSRKLKSHGMRRSKSRSPHKGGKRGGSKRKYRKGNPKSRKRGDDASALVRFTQHQAATRTAERWL
6. Sumatran_orangutan Pongo abelii		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDASRNYRSHL*
7. Northen_WC_gibbon Nomascus leucogenys		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
8. Black_SN_monkey Rhinopithecus bieti		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
9. Golden_SN_monkey Rhinopithecus roxellana		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
10. Angolan_colobus Colobus angolensis palliatus		MSTSRKLKSRGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
11. Ugandan_red_colobus Piliocolobus tephrosceles		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSH**
12. Olive_baboon Papio anubis		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
13. Sooty_mangabey Cercocebus atys		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
14. Drill Mandrillus leucophaeus		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
15. Green_monkey Chlorocebus sabaeus		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
16. Southern_PT_macaque Macaca nemestrina		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
17. Rhesus_macaque Macaca mulatta		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
18. CE_macaque Macaca fascicularis		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*
19. WH_capuchin Cebus capucinus		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRRGSLKSRKRGDDANRNYRSHL*
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRRGSLKSRKRGDDANRNYRSHL*
21. NM_night_monkey Aotus nancymaae		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKHQKGSLKSRKRGNDANRNCRSHL*
22. Common_marmoset Callithrix jacchus		MSTSRKLKGHGMRRSKSRSPQKGVKRGGSKRKYRRGSLKSRKRGDDGNRNYRSHL*
23. Philippine_tarsier Tarsius syrichta		MSNSRKLKGHGMRRGKSRSPHKGVKKGGNKRKYRKSSMKSRKRSDDVNRNCRSHV*
24. Gray_mouse_lemur Microcebus murinus		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHV*
25. Coquerels_sifaka Propithecus coquereli		MSTSRRLKSHGMRRGKNRAPHKGVKRGGNKRKYRKGSLKSRKRGDDANRNYRSHL*
26. Northern_greater_galago Otolemur garnettii		MTTSRKFKSHGMRRGKNRSPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHL*

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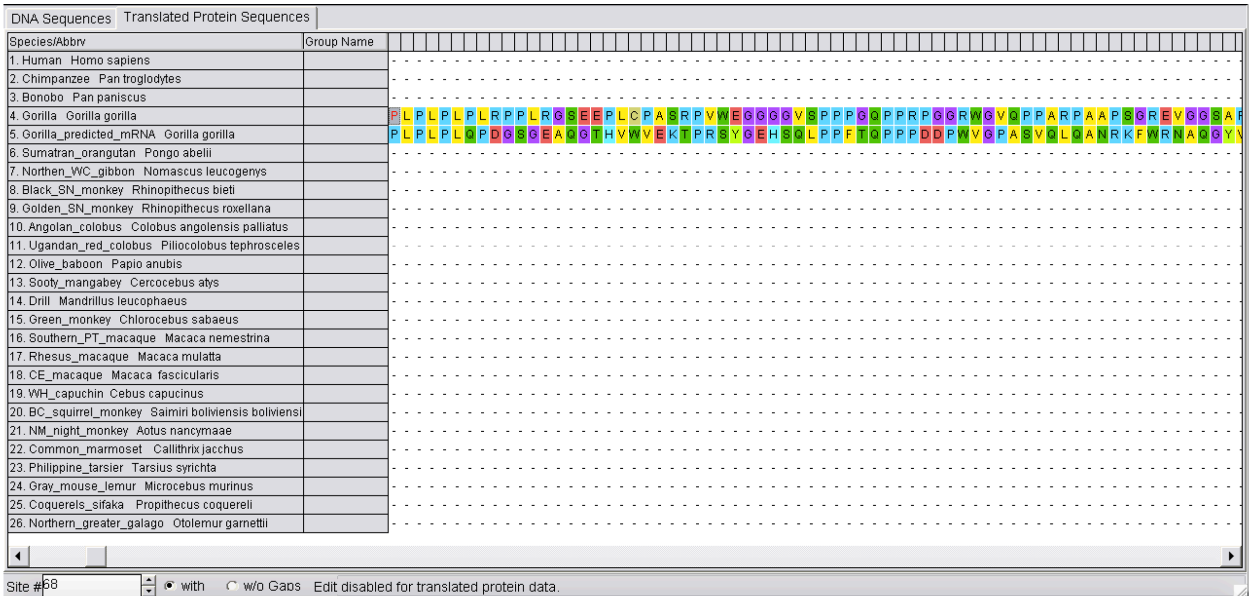

Species/Abbrv	Group Name	
1. Human Homo sapiens		---
2. Chimpanzee Pan troglodytes		---
3. Bonobo Pan paniscus		---
4. Gorilla Gorilla gorilla		PLPLPLPLRPPLRGSEEPLCPASRPVWEGGGGVSPPPGQPPRPGGRWGVQPPARPAAPSGREVGGSA
5. Gorilla_predicted_mRNA Gorilla gorilla		PLPLPLQPDGSGEAQGTHVWVEKTPRSYGEHSQLPPFTQPPPDDPWVGPASVQLQANRKFWRNAQGY
6. Sumatran_orangutan Pongo abelii		---
7. Northen_WC_gibbon Nomascus leucogenys		---
8. Black_SN_monkey Rhinopithecus bieti		---
9. Golden_SN_monkey Rhinopithecus roxellana		---
10. Angolan_colobus Colobus angolensis palliatus		---
11. Ugandan_red_colobus Piliocolobus tephrosceles		---
12. Olive_baboon Papio anubis		---
13. Sooty_mangabey Cercocebus atys		---
14. Drill Mandrillus leucophaeus		---
15. Green_monkey Chlorocebus sabaeus		---
16. Southern_PT_macaque Macaca nemestrina		---
17. Rhesus_macaque Macaca mulatta		---
18. CE_macaque Macaca fascicularis		---
19. WH_capuchin Cebus capucinus		---
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		---
21. NM_night_monkey Aotus nancymaae		---
22. Common_marmoset Callithrix jacchus		---
23. Philippine_tarsier Tarsius syrichta		---
24. Gray_mouse_lemur Microcebus murinus		---
25. Coquerels_sifaka Propithecus coquereli		---
26. Northern_greater_galago Otolemur garnettii		---

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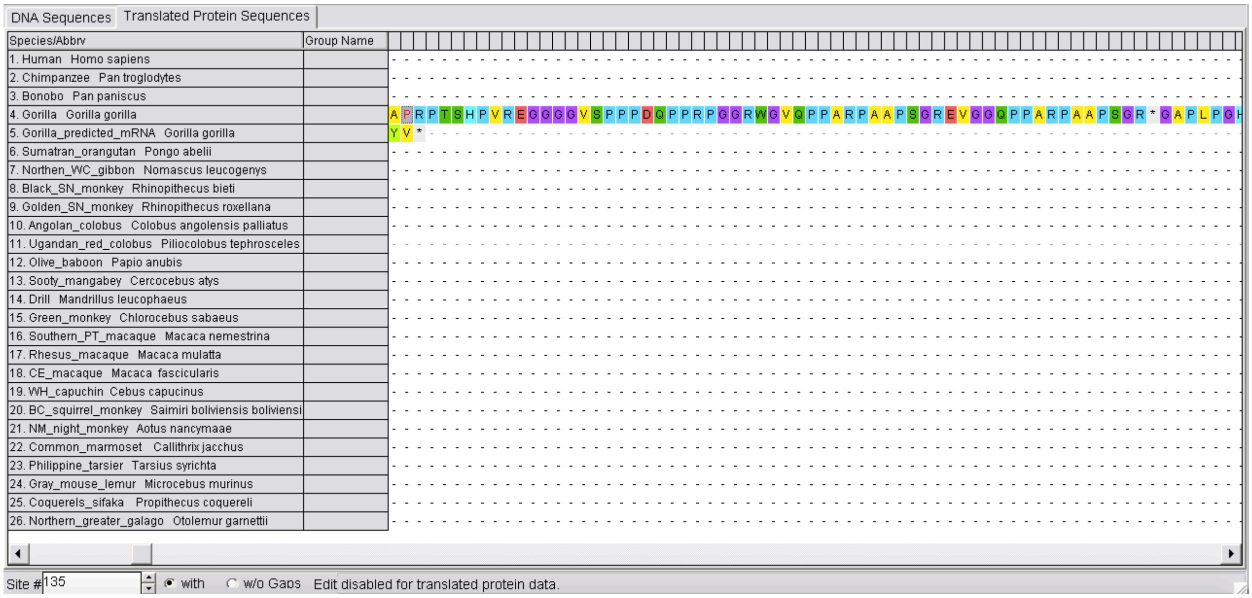
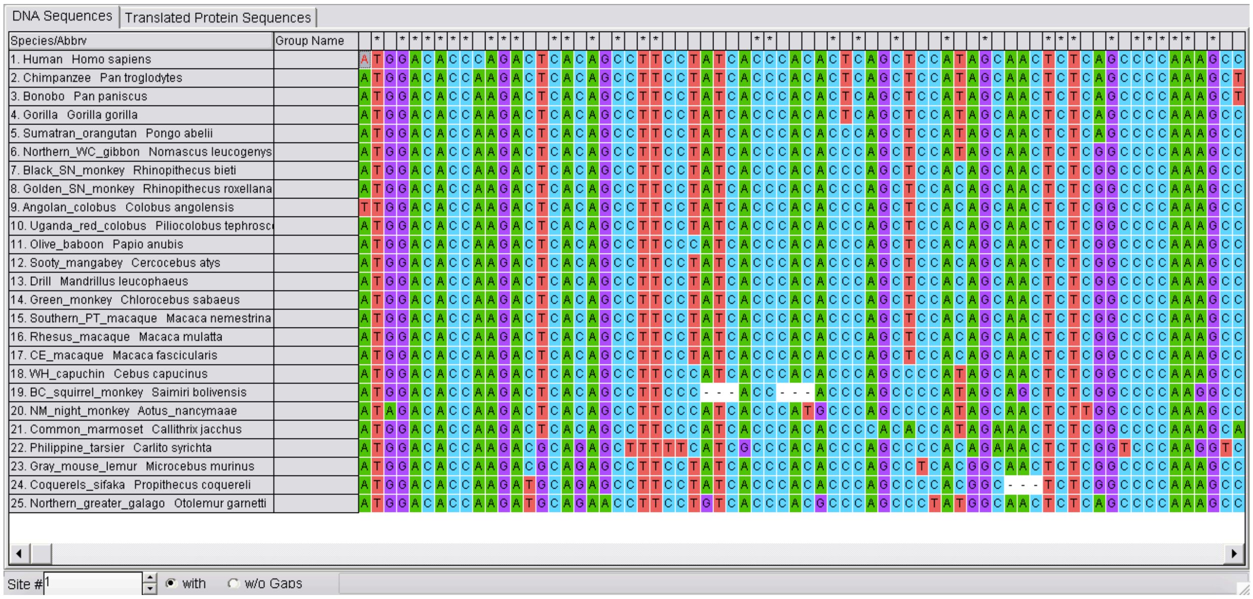


Species/Abbrv	Group Name	
1. Human Homo sapiens		---
2. Chimpanzee Pan troglodytes		---
3. Bonobo Pan paniscus		---
4. Gorilla Gorilla gorilla		APRPTSHPVREGGGGVSPPPDQPPRPGGRWGVQPPARPAAPSGREVGGQPPARPAAPSGR*GAPLPG
5. Gorilla_predicted_mRNA Gorilla gorilla		YV*--
6. Sumatran_orangutan Pongo abelii		---
7. Northen_WC_gibbon Nomascus leucogenys		---
8. Black_SN_monkey Rhinopithecus bieti		---
9. Golden_SN_monkey Rhinopithecus roxellana		---
10. Angolan_colobus Colobus angolensis palliatus		---
11. Ugandan_red_colobus Piliocolobus tephrosceles		---
12. Olive_baboon Papio anubis		---
13. Sooty_mangabey Cercocebus atys		---
14. Drill Mandrillus leucophaeus		---
15. Green_monkey Chlorocebus sabaeus		---
16. Southern_PT_macaque Macaca nemestrina		---
17. Rhesus_macaque Macaca mulatta		---
18. CE_macaque Macaca fascicularis		---
19. WH_capuchin Cebus capucinus		---
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		---
21. NM_night_monkey Aotus nancymaae		---
22. Common_marmoset Callithrix jacchus		---
23. Philippine_tarsier Tarsius syrichta		---
24. Gray_mouse_lemur Microcebus murinus		---
25. Coquerels_sifaka Propithecus coquereli		---
26. Northern_greater_galago Otolemur garnettii		---

Site # 135 ● with ○ w/o Gaps Edit disabled for translated protein data.

Appendix C1) Alignment of primate *Tnp2* coding exon nucleotide sequences



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Species/Abbrv                                  Group Name   * ****** ***  ** * * **       **    * *  *   *  *    ***  * ***** *  
1. Human  Homo sapiens                                     ATGGACACCCAGACTCACAGCCTTCCTATCACCCACACTCAGCTCCATAGCAACTCTCAGCCCCAAAGCC
2. Chimpanzee  Pan troglodytes                             ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACTCAGCTCCATAGCAACTCTCAGCCCCAAAGCT
3. Bonobo  Pan paniscus                                    ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACTCAGCTCCATAGCAACTCTCAGCCCCAAAGCT
4. Gorilla  Gorilla gorilla                                ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACTCAGCTCCATAGCAACTCTCAGCCCCAAAGCC
5. Sumatran_orangutan  Pongo abelii                        ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCATAGCAACTCTCAGCCCCAAAGCC
6. Northern_WC_gibbon  Nomascus leucogenys                 ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCATAGCAACTCTCGGCCCCAAAGCC
7. Black_SN_monkey  Rhinopithecus bieti                    ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
8. Golden_SN_monkey  Rhinopithecus roxellana               ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
9. Angolan_colobus  Colobus angolensis                     TTGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
10. Uganda_red_colobus  Piliocolobus tephrosc               ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
11. Olive_baboon  Papio anubis                             ATGGACACCAAGACTCACAGCCTTCCCATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
12. Sooty_mangabey  Cercocebus atys                        ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
13. Drill  Mandrillus leucophaeus                          ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
14. Green_monkey  Chlorocebus sabaeus                      ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
15. Southern_PT_macaque  Macaca nemestrina                 ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
16. Rhesus_macaque  Macaca mulatta                         ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
17. CE_macaque  Macaca fascicularis                        ATGGACACCAAGACTCACAGCCTTCCTATCACCCACACCCAGCTCCACAGCAACTCTCGGCCCCAAAGCC
18. WH_capuchin  Cebus capucinus                          ATGGACACCAAGACTCACAGCCTTCCCATCACCCACACCCAGCCCCATAGCAACTCTCGGCCCCAAAGCC
19. BC_squirrel_monkey  Saimiri bolivensis                 ATGGACACCAAGACTCACAGCCTTCCC---ACC---ACCCAGCCCCATAGCAGCTCTCGGCCCCAAGGCC
20. NM_night_monkey  Aotus_nancymaae                       ATAGACACCAAGACTCACAGCCTTCCCATCACCCATGCCCAGCCCCATAGCAACTCTTGGCCCCAAAGCC
21. Common_marmoset  Callithrix jacchus                    ATGGACACCAAGACTCACAGCCTTCCCATCACCCACACCCCACACCATAGAAACTCTCGGCCCCAAAGCA
22. Philippine_tarsier  Carlito syrichta                   ATGGACACCAAGACGCAGAGCTTTTTCATCGCCCACACCCAGCCCCACAGAAACTCTCGGTCCCAAGGTC
23. Gray_mouse_lemur  Microcebus murinus                   ATGGACACCAAGACGCAGAGCCTTCCTATCACCCACACCCAGCCTCACGGCAACTCTCGGCCCCAAAGCC
24. Coquerels_sifaka  Propithecus coquereli                ATGGACACCAAGATGCAGAGCCTTCCTATCACCCACACCCAGCCCCACGGC---TCTCGGCCCCAAAGCC
25. Northern_greater_galago  Otolemur garnetti             ATGGACACCAAGATGCAGAACCTTCCTGTCACCCACGCCCAGCCCTATGGCAACTCTCAGCCCCAAAGCC
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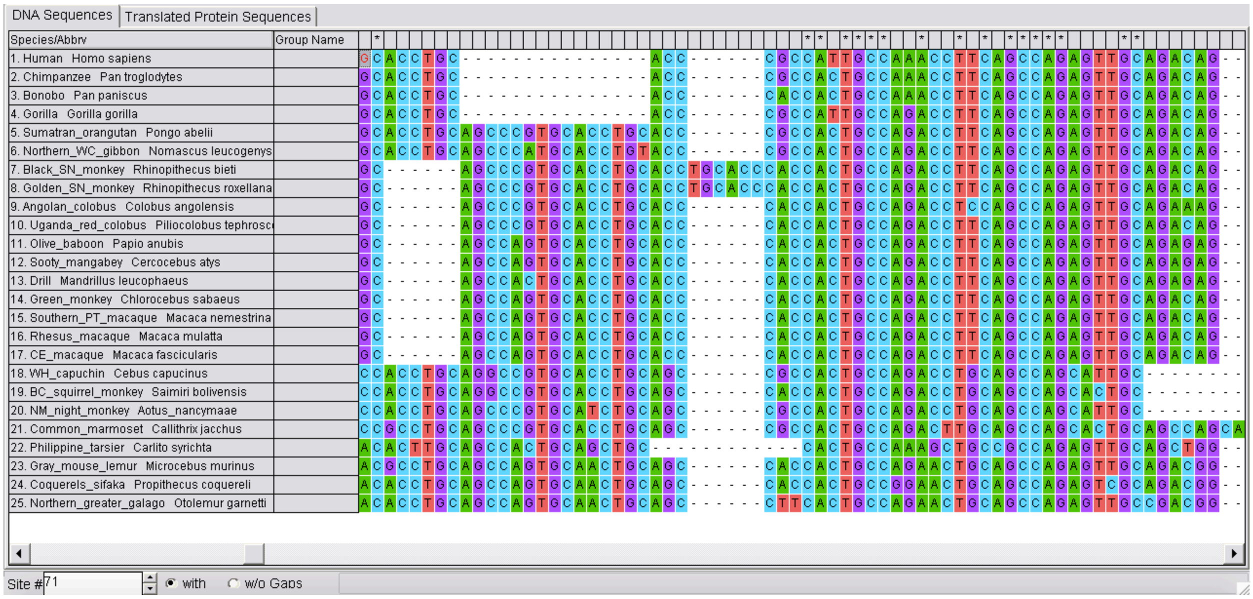

```
Species/Abbrv                                  Group Name   *                                 ** ****  *  * * *****    **        
1. Human  Homo sapiens                                     GCACCTGC---------------ACC------CGCCATTGCCAAACCTTCAGCCAGAGTTGCAGACAG--
2. Chimpanzee  Pan troglodytes                             GCACCTGC---------------ACC------CGCCACTGCCAAACCTTCAGCCAGAGTTGCAGACAG--
3. Bonobo  Pan paniscus                                    GCACCTGC---------------ACC------CACCACTGCCAAACCTTCAGCCAGAGTTGCAGACAG--
4. Gorilla  Gorilla gorilla                                GCACCTGC---------------ACC------CGCCATTGCCAGACCTTCAGCCAGAGTTGCAGACAG--
5. Sumatran_orangutan  Pongo abelii                        GCACCTGCAGCCCGTGCACCTGCACC------CGCCACTGCCAGACCTTCAGCCAGAGTTGCAGACAG--
6. Northern_WC_gibbon  Nomascus leucogenys                 GCACCTGCAGCCCATGCACCTGTACC------CGCCACTGCCAGACCTTCAGCCAGAGTTGCAGACAG--
7. Black_SN_monkey  Rhinopithecus bieti                    GC------AGCCCGTGCACCTGCACCTGCACCCACCACTGCCAGACCTTCAGCCAGAGTTGCAGACAG--
8. Golden_SN_monkey  Rhinopithecus roxellana               GC------AGCCCGTGCACCTGCACCTGCACCCACCACTGCCAGACCTTCAGCCAGAGTTGCAGACAG--
9. Angolan_colobus  Colobus angolensis                     GC------AGCCCGTGCACCTGCACC------CACCACTGCCAGACCTCCAGCCAGAGTTGCAGAAAG--
10. Uganda_red_colobus  Piliocolobus tephrosc               GC------AGCCCGTGCACCTGCACC------CACCACTGCCAGACCTTCAGCCAGAGTTGCAGACAG--
11. Olive_baboon  Papio anubis                             GC------AGCCAGTGCACCTGCACC------CACCACTGCCAGACCTTCAGCCAGAGTTGCAGAGAG--
12. Sooty_mangabey  Cercocebus atys                        GC------AGCCAGTGCACCTGCACC------CACCACTGCCAGACCTTCAGCCAGAGTTGCAGAGAG--
13. Drill  Mandrillus leucophaeus                          GC------AGCCACTGCACCTGCACC------CACCACTGCCAGACCTTCAGCCAGAGTTGCAGAGAG--
14. Green_monkey  Chlorocebus sabaeus                      GC------AGCCAGTGCACCTGCACC------CACCACTGCCAGACCTTCAGCCAGAGTTGCAGACAG--
15. Southern_PT_macaque  Macaca nemestrina                 GC------AGCCAGTGCACCTGCACC------CACCACTGCCAGACCTTCAGCCAGAGTTGCAGACAG--
16. Rhesus_macaque  Macaca mulatta                         GC------AGCCAGTGCACCTGCACC------CACCACTGCCAGACCTTCAGCCAGAGTTGCAGACAG--
17. CE_macaque  Macaca fascicularis                        GC------AGCCAGTGCACCTGCACC------CACCACTGCCAGACCTTCAGCCAGAGTTGCAGACAG--
18. WH_capuchin  Cebus capucinus                          CCACCTGCAGGCCGTGCACCTGCAGC------CGCCACTGCCAGACCTGCAGCCAGCATTGC--------
19. BC_squirrel_monkey  Saimiri bolivensis                 CCACCTGCAGGCCGTGCACCTGCAGC------CACCACTGCCAGACCTGCAGCCAGCACTGC--------
20. NM_night_monkey  Aotus_nancymaae                       CCACCTGCAGCCCGTGCATCTGCAGC------CGCCACTGCCAGACCTGCAGCCAGCATTGC--------
21. Common_marmoset  Callithrix jacchus                    CCGCCTGCAGCCCGTGCACCTGCAGC------CGCCACTGCCAGACTTGCAGCCAGCACTGCAGCCAGCA
22. Philippine_tarsier  Carlito syrichta                   ACACTTGCAGCCACTGCAGCTGC------------CACTGCCAAAGCTGCCGCCAGAGTTGCAGCTGG--
23. Gray_mouse_lemur  Microcebus murinus                   ACGCCTGCAGCCAGTGCAACTGCAGC------CACCACTGCCAGAACTGCAGCCAGAGTTGCAGACGG--
24. Coquerels_sifaka  Propithecus coquereli                ACACCTGCAGCCAGTGCAACTGCAGC------CACCACTGCCGGAACTGCAGCCAGAGTCGCAGACGG--
25. Northern_greater_galago  Otolemur garnetti             ACACCTGCAGCCAGTGCAACTGCAGC------CTTCACTGCCAGAACTGCAGCCAGAGTTGCCGACGG--
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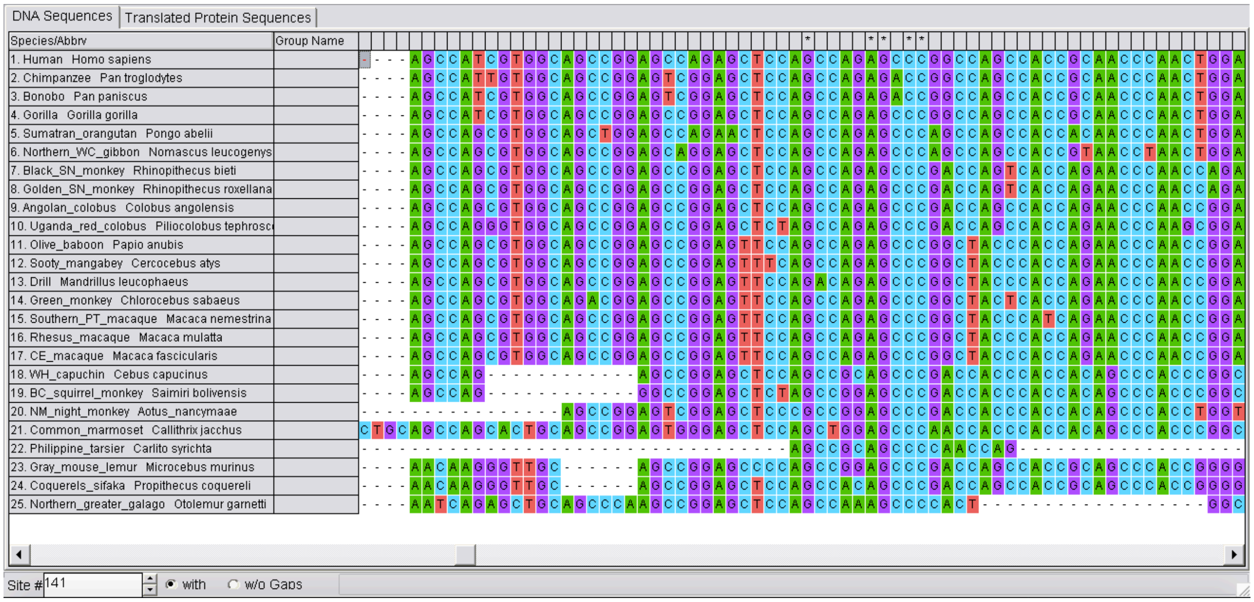

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Species/Abbrv                                  Group Name                                    *    ** **
1. Human  Homo sapiens                                     ----AGCCATCGTGGCAGCCGGAGCCAGAGCTCCAGCCAGAGCCCGGCCAGCCACCGCAACCCAACTGGA
2. Chimpanzee  Pan troglodytes                             ----AGCCATTGTGGCAGCCGGAGTCGGAGCTCCAGCCAGAGACCGGCCAGCCACCGCAACCCAACTGGA
3. Bonobo  Pan paniscus                                    ----AGCCATCGTGGCAGCCGGAGTCGGAGCTCCAGCCAGAGACCGGCCAGCCACCGCAACCCAACTGGA
4. Gorilla  Gorilla gorilla                                ----AGCCATCGTGGCAGCCGGAGCCGGAGCTCCAGCCAGAGCCCGGCCAGCCACCGCAACCCAACTGGA
5. Sumatran_orangutan  Pongo abelii                        ----AGCCAGCGTGGCAGCTGGAGCCAGAACTCCAGCCAGAGCCCAGCCAGCCACCACAACCCAACTGGA
6. Northern_WC_gibbon  Nomascus leucogenys                 ----AGCCAGCGTGGCAGCCGGAGCAGGAGCTCCAGCCAGAGCCCAGCCAGCCACCGTAACCTAACTGGA
7. Black_SN_monkey  Rhinopithecus bieti                    ----AGCCAGCGTGGCAGCCGGAGCCGGAGCTCCAGCCAGAGCCCGACCAGTCACCAGAACCCAACCAGA
8. Golden_SN_monkey  Rhinopithecus roxellana               ----AGCCAGCGTGGCAGCCGGAGCCGGAGCTCCAGCCAGAGCCCGACCAGTCACCAGAACCCAACCAGA
9. Angolan_colobus  Colobus angolensis                     ----AGCCAGCGTGGCAGCCGGAGCCGGAGCTCCAGCCAGAGCCCGACCAGCCACCAGAACCCAACCGGA
10. Uganda_red_colobus  Piliocolobus tephrosc              ----AGCCAGGGTGGCAGCCGGAGCCGGAGCTCTAGCCAGAGCCCGACCAGCCACCAGAACCCAAGCGGA
11. Olive_baboon  Papio anubis                             ----AGCCAGCGTGGCAGCCGGAGCCGGAGTTCCAGCCAGAGCCCGGCTACCCACCAGAACCCAACCGGA
12. Sooty_mangabey  Cercocebus atys                        ----AGCCAGCGTGGCAGCCGGAGCCGGAGTTTCAGCCAGAGCCCGGCTACCCACCAGAACCCAACCGGA
13. Drill  Mandrillus leucophaeus                          ----AGCCAGCGTGGCAGCCGGAGCCGGAGTTCCAGACAGAGCCCGGCTACCCACCAGAACCCAACCGGA
14. Green_monkey  Chlorocebus sabaeus                      ----AGCCAGCGTGGCAGACGGAGCCGGAGTTCCAGCCAGAGCCCGGCTACTCACCAGAACCCAACCGGA
15. Southern_PT_macaque  Macaca nemestrina                 ----AGCCAGCGTGGCAGCCGGAGCCGGAGTTCCAGCCAGAGCCCGGCTACCCATCAGAACCCAACCGGA
16. Rhesus_macaque  Macaca mulatta                         ----AGCCAGCGTGGCAGCCGGAGCCGGAGTTCCAGCCAGAGCCCGGCTACCCACCAGAACCCAACCGGA
17. CE_macaque  Macaca fascicularis                        ----AGCCAGCGTGGCAGCCGGAGCCGGAGTTCCAGCCAGAGCCCGGCTACCCACCAGAACCCAACCGGA
18. WH_capuchin  Cebus capucinus                           ----AGCCAG------------AGCCGGAGCTCCAGCCGCAGCCCGACCACCCACCACAGCCCACCCGGC
19. BC_squirrel_monkey  Saimiri bolivensis                 ----AGCCAG------------GGCCGGAGCTCTAGCCGGAGCCCGACCACCCACCACAGCCCACCCGGC
20. NM_night_monkey  Aotus_nancymaae                       ----------------AGCCGGAGTCGGAGCTCCCGCCGGAGCCCGACCACCCACCACAGCCCACCTGGT
21. Common_marmoset  Callithrix jacchus                    CTGCAGCCAGCACTGCAGCCGGAGTGGGAGCTCCAGCTGGAGCCCAACCACCCACCACAGCCCACCCGGC
22. Philippine_tarsier  Carlito syrichta                   ----------------------------------AGCCGCAGCCCCAACCAG------------------
23. Gray_mouse_lemur  Microcebus murinus                   ----AACAAGGGTTGC------AGCCGGAGCCCCAGCCGGAGCCCGACCAGCCACCGCAGCCCACCGGGG
24. Coquerels_sifaka  Propithecus coquereli                ----AACAAGGGTTGC------AGCCGGAGCTCCAGCCACAGCCCGACCAGCCACCGCAGCCCACCGGGG
25. Northern_greater_galago  Otolemur garnetti             ----AATCAGAGCTGCAGCCCAAGCCGGAGCTCCAGCCAAAGCCCCACT------------------GGC
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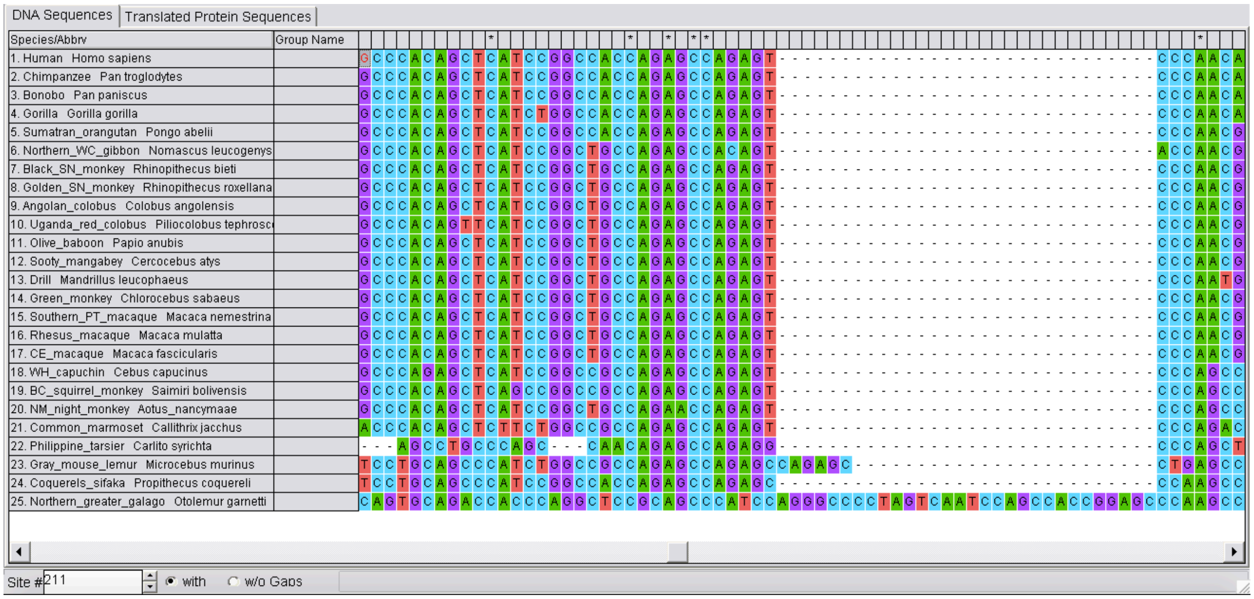
Site # 141 ● with ○ w/o Gaps



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Species/Abbrv                                  Group Name            *          *  * **                                      *
1. Human  Homo sapiens                                     GCCCACAGCTCATCCGGCCACCAGAGCCAGAGT------------------------------CCCAACA
2. Chimpanzee  Pan troglodytes                             GCCCACAGCTCATCCGGCCACCAGAGCCAGAGT------------------------------CCCAACA
3. Bonobo  Pan paniscus                                    GCCCACAGCTCATCCGGCCACCAGAGCCAGAGT------------------------------CCCAACA
4. Gorilla  Gorilla gorilla                                GCCCACAGCTCATCTGGCCACCAGAGCCAGAGT------------------------------CCCAACA
5. Sumatran_orangutan  Pongo abelii                        GCCCACAGCTCATCCGGCCACCAGAGCCAGAGT------------------------------CCCAACG
6. Northern_WC_gibbon  Nomascus leucogenys                 GCCCACAGCTCATCCGGCTGCCAGAGCCACAGT------------------------------ACCAACG
7. Black_SN_monkey  Rhinopithecus bieti                    GCCCACAGCTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAACG
8. Golden_SN_monkey  Rhinopithecus roxellana               GCCCACAGCTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAACG
9. Angolan_colobus  Colobus angolensis                     GCCCACAGCTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAACG
10. Uganda_red_colobus  Piliocolobus tephrosc              GCCCACAGTTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAACG
11. Olive_baboon  Papio anubis                             GCCCACAGCTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAACG
12. Sooty_mangabey  Cercocebus atys                        GCCCACAGCTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAACG
13. Drill  Mandrillus leucophaeus                          GCCCACAGCTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAATG
14. Green_monkey  Chlorocebus sabaeus                      GCCCACAGCTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAACG
15. Southern_PT_macaque  Macaca nemestrina                 GCCCACAGCTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAACG
16. Rhesus_macaque  Macaca mulatta                         GCCCACAGCTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAACG
17. CE_macaque  Macaca fascicularis                        GCCCACAGCTCATCCGGCTGCCAGAGCCAGAGT------------------------------CCCAACG
18. WH_capuchin  Cebus capucinus                           GCCCAGAGCTCATCCGGCCGCCAGAGCCAGAGT------------------------------CCCAGCC
19. BC_squirrel_monkey  Saimiri bolivensis                 GCCCACAGCTCAGCCGGCCGCCAGAGCCAGAGT------------------------------CCCAGCC
20. NM_night_monkey  Aotus_nancymaae                       GCCCACAGCTCATCCGGCTGCCAGAACCAGAGT------------------------------CCCAGCC
21. Common_marmoset  Callithrix jacchus                    ACCCACAGCTCTTCTGGCCGCCAGAGCCAGAGT------------------------------CCCAGAC
22. Philippine_tarsier  Carlito syrichta                   ---AGCCTGCCCAGC---CAACAGAGCCAGAGG------------------------------CCCAGCT
23. Gray_mouse_lemur  Microcebus murinus                   TCCTGCAGCCCATCTGGCCGCCAGAGCCAGAGCCAGAGC------------------------CTGAGCC
24. Coquerels_sifaka  Propithecus coquereli                TCCTGCAGCCCATCCGGCCACCAGAGCCAGAGC------------------------------CCAAGCC
25. Northern_greater_galago  Otolemur garnetti             CAGTGCAGACCACCCAGGCTCCGCAGCCCATCCAGGGCCCCTAGTCAATCCAGCCACCGGAGCCCAAGCC
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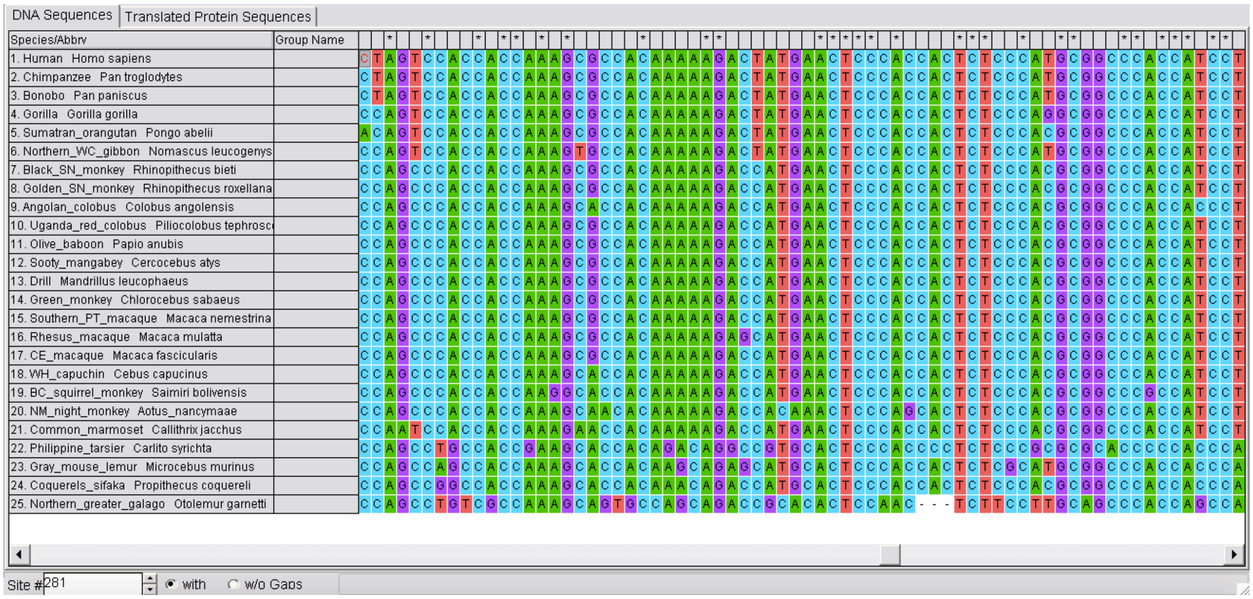
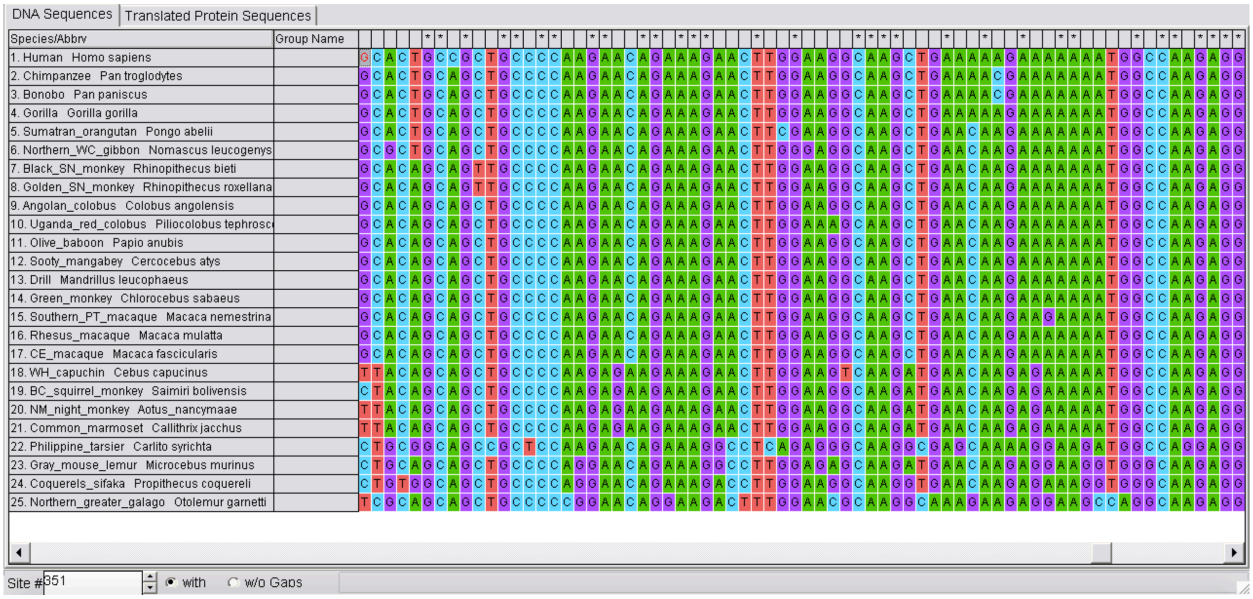
Site # 211 ● with ○ w/o Gaps



DNA Sequences | Translated Protein Sequences

Species/Abbrv	Group Name	`  *  *   * ** * *     *    **       ***** *    ***  *  **   ** *** ** `
1. Human Homo sapiens		CTAGTCCACCACCAAAGCGCCACAAAAAGACTATGAACTCCCACCACTCTCCCATGCGGCCCACCATCCT
2. Chimpanzee Pan troglodytes		CTAGTCCACCACCAAAGCGCCACAAAAAGACTATGAACTCCCACCACTCTCCCATGCGGCCCACCATCCT
3. Bonobo Pan paniscus		CTAGTCCACCACCAAAGCGCCACAAAAAGACTATGAACTCCCACCACTCTCCCATGCGGCCCACCATCCT
4. Gorilla Gorilla gorilla		CCAGTCCACCACCAAAGCGCCACAAAAAGACTATGAACTCCCACCACTCTCCCAGGCGGCCCACCATCCT
5. Sumatran_orangutan Pongo abelii		ACAGTCCACCACCAAAGCGCCACAAAAAGACTATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
6. Northern_WC_gibbon Nomascus leucogenys		CCAGTCCACCACCAAAGTGCCACAAAAAGACTATGAACTCCCACCACTCTCCCATGCGGCCCACCATCCT
7. Black_SN_monkey Rhinopithecus bieti		CCAGCCCACCACCAAAGCGCCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
8. Golden_SN_monkey Rhinopithecus roxellana		CCAGCCCACCACCAAAGCGCCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
9. Angolan_colobus Colobus angolensis		CCAGCCCACCACCAAAGCACCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCACCCT
10. Uganda_red_colobus Piliocolobus tephrosc		CCAGCCCACCACCAAAGCGCCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
11. Olive_baboon Papio anubis		CCAGCCCACCACCAAAGCGCCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
12. Sooty_mangabey Cercocebus atys		CCAGCCCACCACCAAAGCGCCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
13. Drill Mandrillus leucophaeus		CCAGCCCACCACCAAAGCGCCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
14. Green_monkey Chlorocebus sabaeus		CCAGCCCACCACCAAAGCGCCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
15. Southern_PT_macaque Macaca nemestrina		CCAGCCCACCACCAAAGCGCCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
16. Rhesus_macaque Macaca mulatta		CCAGCCCACCACCAAAGCGCCACAAAAAGAGCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
17. CE_macaque Macaca fascicularis		CCAGCCCACCACCAAAGCGCCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
18. WH_capuchin Cebus capucinus		CCAGCCCACCACCAAAGCACCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
19. BC_squirrel_monkey Saimiri bolivensis		CCAGCCCACCACCAAGGCACCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCGCCATCCT
20. NM_night_monkey Aotus_nancymaae		CCAGCCCACCACCAAAGCAACACAAAAAGACCACAAACTCCCAGCACTCTCCCACGCGGCCCACCATCCT
21. Common_marmoset Callithrix jacchus		CCAATCCACCACCAAAGAACCACAAAAAGACCATGAACTCCCACCACTCTCCCACGCGGCCCACCATCCT
22. Philippine_tarsier Carlito syrichta		CCAGCCTGCCACCGAAGCACCACAGACAGGCCGTGCACTCCCACCCCTCTCCCGCGCGCACCCCCACCCA
23. Gray_mouse_lemur Microcebus murinus		CCAGCCAGCCACCAAAGCACCACAAGCAGAGCATGCACTCCCACCACTCTCGCATGCGGCCCACCACCCA
24. Coquerels_sifaka Propithecus coquereli		CCAGCCGGCCACCAAAGCACCACAAACAGACCATGCACTCCCACCACTCTCCCACGCGGCCCACCACCCA
25. Northern_greater_galago Otolemur garnetti		CCAGCCTGTCGCCAAAGCAGTGCCAGCAGACCGCACACTCCAAC---TCTTCCTTGCAGCCCACCAGCCA

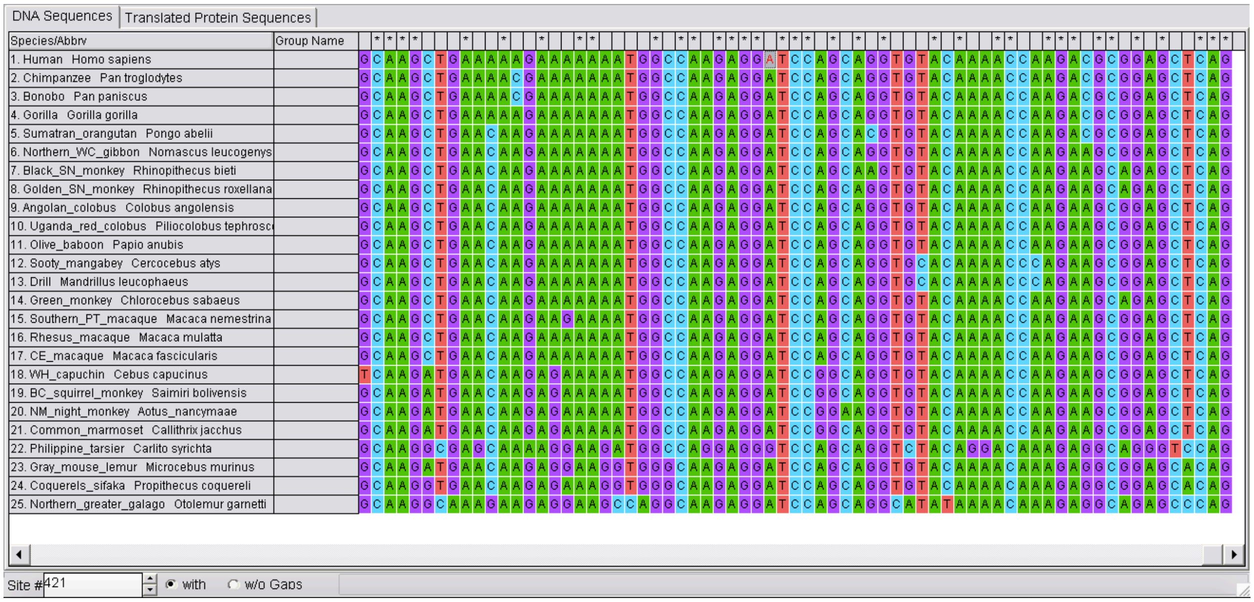
Site # 281 ● with ○ w/o Gaps



DNA Sequences | Translated Protein Sequences

Species/Abbrv	Group Name	`     ** *  ** **  **  ** ***   *  *    ****   *  *  *  **    * ** ****`
1. Human Homo sapiens		GCACTGCCGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAAAAAGAAAAAAATGGCCAAGAGG
2. Chimpanzee Pan troglodytes		GCACTGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAAAACGAAAAAAATGGCCAAGAGG
3. Bonobo Pan paniscus		GCACTGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAAAACGAAAAAAATGGCCAAGAGG
4. Gorilla Gorilla gorilla		GCACTGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAAAAAGAAAAAAATGGCCAAGAGG
5. Sumatran_orangutan Pongo abelii		GCACTGCAGCTGCCCCAAGAACAGAAAGAACTTCGAAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
6. Northern_WC_gibbon Nomascus leucogenys		GCGCTGCAGCTGCCCCAAGAACAGAAAGAACTTGGGAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
7. Black_SN_monkey Rhinopithecus bieti		GCACAGCAGTTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
8. Golden_SN_monkey Rhinopithecus roxellana		GCACAGCAGTTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
9. Angolan_colobus Colobus angolensis		GCACAGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
10. Uganda_red_colobus Piliocolobus tephrosc		GCACAGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAAGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
11. Olive_baboon Papio anubis		GCACAGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
12. Sooty_mangabey Cercocebus atys		GCACAGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
13. Drill Mandrillus leucophaeus		GCACAGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
14. Green_monkey Chlorocebus sabaeus		GCACAGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
15. Southern_PT_macaque Macaca nemestrina		GCACAGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAACAAGAAGAAAATGGCCAAGAGG
16. Rhesus_macaque Macaca mulatta		GCACAGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
17. CE_macaque Macaca fascicularis		GCACAGCAGCTGCCCCAAGAACAGAAAGAACTTGGAAGGCAAGCTGAACAAGAAAAAAATGGCCAAGAGG
18. WH_capuchin Cebus capucinus		TTACAGCAGCTGCCCCAAGAGAAGAAAGAACTTGGAAGTCAAGATGAACAAGAGAAAAATGGCCAAGAGG
19. BC_squirrel_monkey Saimiri bolivensis		CTACAGCAGCTGCCCCAAGAGAAGAAAGAACTTGGAAGGCAAGATGAACAAGAGAAAAATGGCCAAGAGG
20. NM_night_monkey Aotus_nancymaae		TTACAGCAGCTGCCCCAAGAGAAGAAAGAACTTGGAAGGCAAGATGAACAAGAGAAAAATGGCCAAGAGG
21. Common_marmoset Callithrix jacchus		TTACAGCAGCTGCCCCAAGAGAAGAAAGAACTTGGAAGGCAAGATGAACAAGAGAAAAATGGCCAAGAGG
22. Philippine_tarsier Carlito syrichta		CTGCGGCAGCCGCTCCAAGAACAGAAAGGCCTCAGAGGGCAAGGCGAGCAAAAGGAAGATGGCCAGGAGG
23. Gray_mouse_lemur Microcebus murinus		CTGCAGCAGCTGCCCCAGGAACAGAAAGGCCTTGGAGAGCAAGATGAACAAGAGGAAGGTGGGCAAGAGG
24. Coquerels_sifaka Propithecus coquereli		CTGTGGCAGCTGCCCCAGGAACAGAAAGACCTTGGAAGGCAAGGTGAACAAGAGAAAGGTGGGCAAGAGG
25. Northern_greater_galago Otolemur garnetti		TCGCAGCAGCTGCCCCCGGAACAGGAAGACTTTGGAACGCAAGGCAAAGAAGAGGAAGCCAGGCAAGAGG

Site # 351 ● with ○ w/o Gaps



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Species/Abbrv  Group Name                          ****   *  *  *  **    * ** **** *** * * *   * *  **  *** ** * *  ***
1. Human  Homo sapiens                            GCAAGCTGAAAAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGACGCGGAGCTCAG
2. Chimpanzee  Pan troglodytes                    GCAAGCTGAAAACGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGACGCGGAGCTCAG
3. Bonobo  Pan paniscus                           GCAAGCTGAAAACGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGACGCGGAGCTCAG
4. Gorilla  Gorilla gorilla                       GCAAGCTGAAAAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGACGCGGAGCTCAG
5. Sumatran_orangutan  Pongo abelii               GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCACGTGTACAAAACCAAGACGCGGAGCTCAG
6. Northern_WC_gibbon  Nomascus leucogenys        GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGAAGCGGAGCTCAG
7. Black_SN_monkey  Rhinopithecus bieti           GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAAGTGTACAAAACCAAGAAGCAGAGCTCAG
8. Golden_SN_monkey  Rhinopithecus roxellana      GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGAAGCAGAGCTCAG
9. Angolan_colobus  Colobus angolensis            GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGAAGCGGAGCTCAG
10. Uganda_red_colobus  Piliocolobus tephrosc     GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGAAGCGGAGCTCAG
11. Olive_baboon  Papio anubis                    GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGAAGCGGAGCTCAG
12. Sooty_mangabey  Cercocebus atys               GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGCACAAAACCCAGAAGCGGAGCTCAG
13. Drill  Mandrillus leucophaeus                 GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGCACAAAACCCAGAAGCGGAGCTCAG
14. Green_monkey  Chlorocebus sabaeus             GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGAAGCAGAGCTCAG
15. Southern_PT_macaque  Macaca nemestrina        GCAAGCTGAACAAGAAGAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGAAGCGGAGCTCAG
16. Rhesus_macaque  Macaca mulatta                GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGAAGCGGAGCTCAG
17. CE_macaque  Macaca fascicularis               GCAAGCTGAACAAGAAAAAAATGGCCAAGAGGATCCAGCAGGTGTACAAAACCAAGAAGCGGAGCTCAG
18. WH_capuchin  Cebus capucinus                  TCAAGATGAACAAGAGAAAAATGGCCAAGAGGATCCGGCAGGTGTACAAAACCAAGAAGCGGAGCTCAG
19. BC_squirrel_monkey  Saimiri bolivensis        GCAAGATGAACAAGAGAAAAATGGCCAAGAGGATCCGGCAGGTGTACAAAACCAAGAAGCGGAGCTCAG
20. NM_night_monkey  Aotus_nancymaae              GCAAGATGAACAAGAGAAAAATGGCCAAGAGGATCCGGAAGGTGTACAAAACCAAGAAGCGGAGCTCAG
21. Common_marmoset  Callithrix jacchus           GCAAGATGAACAAGAGAAAAATGGCCAAGAGGATCCGGCAGGTGTACAAAACCAAGAAGCGGAGCTCAG
22. Philippine_tarsier  Carlito syrichta          GCAAGGCGAGCAAAAGGAAGATGGCCAGGAGGGTCCAGCAGGTCTACAGGACAAAGAGGCAGGGTCCAG
23. Gray_mouse_lemur  Microcebus murinus          GCAAGATGAACAAGAGGAAGGTGGGCAAGAGGATCCAGCAGGTGTACAAAACAAAGAGGCGGAGCACAG
24. Coquerels_sifaka  Propithecus coquereli       GCAAGGTGAACAAGAGAAAGGTGGGCAAGAGGATCCAGCAGGTGTACAAAACAAAGAGGCGGAGCACAG
25. Northern_greater_galago  Otolemur garnetti    GCAAGGCAAAGAAGAGGAAGCCAGGCAAGAGGATCCAGCAGGCATATAAAACAAAGAGGCAGAGCCCAG
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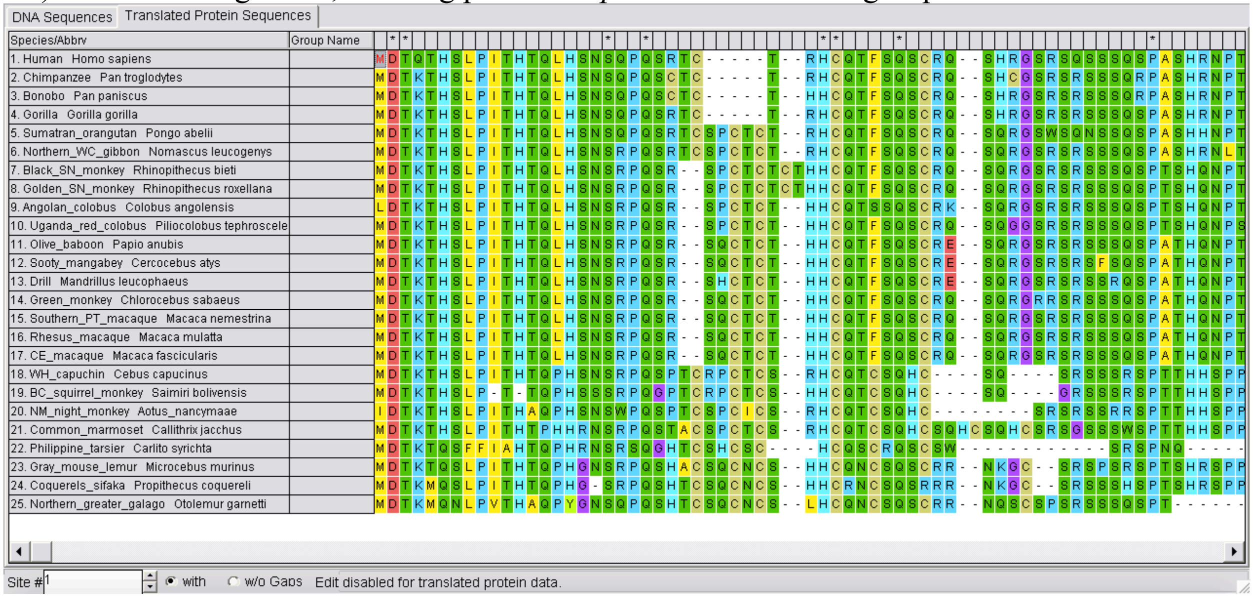
Site #421 ● with ○ w/o Gaps

Exon 2 occurs after this point, but due to difficulty aligning the intron that therefore caused an inability to locate the exon sequence, it is not shown here

C2) Translated alignment, showing primate *Tnp2* amino acid coding sequences



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Species/Abbrv  Group Name                          **               *  *             **    *                   *
1. Human  Homo sapiens                            MDTQTHSLPITHTQLHSNSQPQSRTC-----T--RHCQTFSQSCRQ--SHRGSRSQSSSQSPASHRNPT
2. Chimpanzee  Pan troglodytes                    MDTKTHSLPITHTQLHSNSQPQSCTC-----T--RHCQTFSQSCRQ--SHCGSRSRSSSQRPASHRNPT
3. Bonobo  Pan paniscus                           MDTKTHSLPITHTQLHSNSQPQSCTC-----T--HHCQTFSQSCRQ--SHRGSRSRSSSQRPASHRNPT
4. Gorilla  Gorilla gorilla                       MDTKTHSLPITHTQLHSNSQPQSRTC-----T--RHCQTFSQSCRQ--SHRGSRSRSSSQSPASHRNPT
5. Sumatran_orangutan  Pongo abelii               MDTKTHSLPITHTQLHSNSQPQSRTCSPCTCT--RHCQTFSQSCRQ--SQRGSWSQNSSQSPASHHNPT
6. Northern_WC_gibbon  Nomascus leucogenys        MDTKTHSLPITHTQLHSNSRPQSRTCSPCTCT--RHCQTFSQSCRQ--SQRGSRSRSSSQSPASHRNLT
7. Black_SN_monkey  Rhinopithecus bieti           MDTKTHSLPITHTQLHSNSRPQSR--SPCTCTCTHHCQTFSQSCRQ--SQRGSRSRSSSQSPTSHQNPT
8. Golden_SN_monkey  Rhinopithecus roxellana      MDTKTHSLPITHTQLHSNSRPQSR--SPCTCTCTHHCQTFSQSCRQ--SQRGSRSRSSSQSPTSHQNPT
9. Angolan_colobus  Colobus angolensis            LDTKTHSLPITHTQLHSNSRPQSR--SPCTCT--HHCQTSSQSCRK--SQRGSRSRSSSQSPTSHQNPT
10. Uganda_red_colobus  Piliocolobus tephroscele  MDTKTHSLPITHTQLHSNSRPQSR--SPCTCT--HHCQTFSQSCRQ--SQGGSRSRSSSQSPTSHQNPS
11. Olive_baboon  Papio anubis                    MDTKTHSLPITHTQLHSNSRPQSR--SQCTCT--HHCQTFSQSCRE--SQRGSRSRSSSQSPATHQNPT
12. Sooty_mangabey  Cercocebus atys               MDTKTHSLPITHTQLHSNSRPQSR--SQCTCT--HHCQTFSQSCRE--SQRGSRSRSFSQSPATHQNPT
13. Drill  Mandrillus leucophaeus                 MDTKTHSLPITHTQLHSNSRPQSR--SHCTCT--HHCQTFSQSCRE--SQRGSRSRSSRQSPATHQNPT
14. Green_monkey  Chlorocebus sabaeus             MDTKTHSLPITHTQLHSNSRPQSR--SQCTCT--HHCQTFSQSCRQ--SQRGRRSRSSSQSPATHQNPT
15. Southern_PT_macaque  Macaca nemestrina        MDTKTHSLPITHTQLHSNSRPQSR--SQCTCT--HHCQTFSQSCRQ--SQRGSRSRSSSQSPATHQNPT
16. Rhesus_macaque  Macaca mulatta                MDTKTHSLPITHTQLHSNSRPQSR--SQCTCT--HHCQTFSQSCRQ--SQRGSRSRSSSQSPATHQNPT
17. CE_macaque  Macaca fascicularis               MDTKTHSLPITHTQLHSNSRPQSR--SQCTCT--HHCQTFSQSCRQ--SQRGSRSRSSSQSPATHQNPT
18. WH_capuchin  Cebus capucinus                  MDTKTHSLPITHTQPHSNSRPQSPTCRPCTCS--RHCQTCSQHC----SQ----SRSSSRSPTTHHSPP
19. BC_squirrel_monkey  Saimiri bolivensis        MDTKTHSLP-T-TQPHSSSRPQGPTCRPCTCS--HHCQTCSQHC----SQ----GRSSSRSPTTHHSPP
20. NM_night_monkey  Aotus_nancymaae              IDTKTHSLPITHAQPHSNSWPQSPTCSPCICS--RHCQTCSQHC--------SRSRSSRRSPTTHHSPP
21. Common_marmoset  Callithrix jacchus           MDTKTHSLPITHTPHHRNSRPQSTACSPCTCS--RHCQTCSQHCSQHCSQHCSRSGSSSWSPTTHHSPP
22. Philippine_tarsier  Carlito syrichta          MDTKTQSFFIAHTQPHRNSRSQGHTCSHCSC----HCQSCRQSCSW------------SRSPNQ-----
23. Gray_mouse_lemur  Microcebus murinus          MDTKTQSLPITHTQPHGNSRPQSHACSQCNCS--HHCQNCSQSCRR--NKGC--SRSPSRSPTSHRSPP
24. Coquerels_sifaka  Propithecus coquereli       MDTKMQSLPITHTQPHG-SRPQSHTCSQCNCS--HHCRNCSQSRRR--NKGC--SRSSSHSPTSHRSPP
25. Northern_greater_galago  Otolemur garnetti    MDTKMQNLPVTHAQPYGNSQPQSHTCSQCNCS--LHCQNCSQSCRR--NQSCSPSRSSSQSPT------
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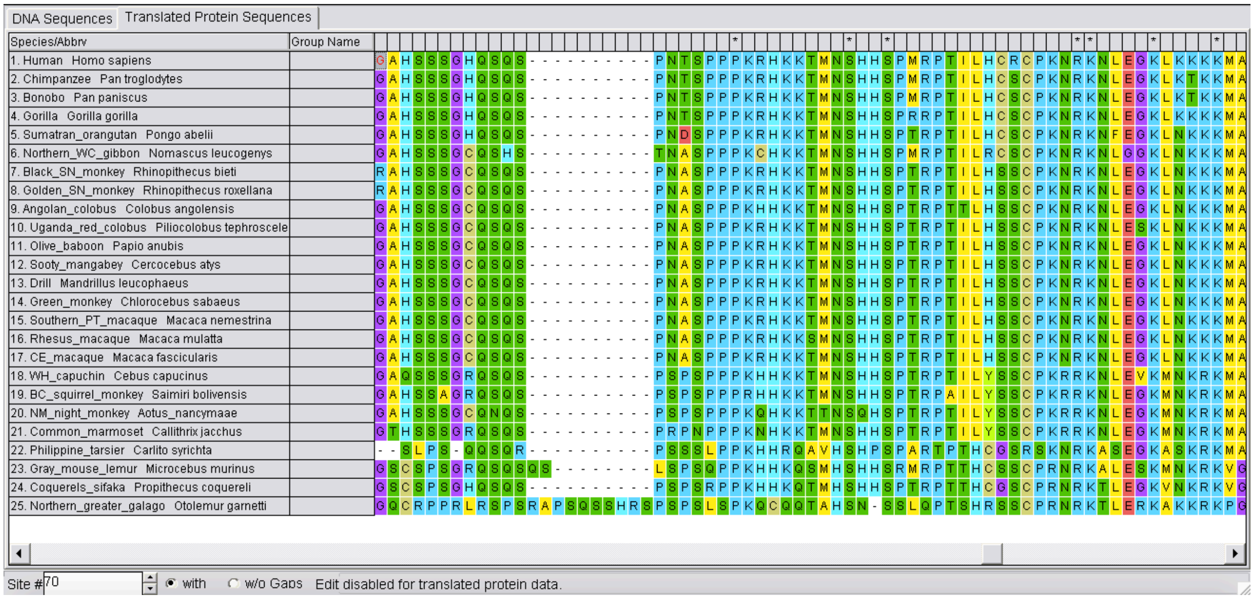

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Species/Abbrv                                     Group Name                              *        *  *              **    *    *
1. Human  Homo sapiens                                        GAHSSSGHQSQS----------PNTSPPPKRHKKTMNSHHSPMRPTILHCRCPKNRKNLEGKLKKKKMA
2. Chimpanzee  Pan troglodytes                                GAHSSSGHQSQS----------PNTSPPPKRHKKTMNSHHSPMRPTILHCSCPKNRKNLEGKLKTKKMA
3. Bonobo  Pan paniscus                                       GAHSSSGHQSQS----------PNTSPPPKRHKKTMNSHHSPMRPTILHCSCPKNRKNLEGKLKTKKMA
4. Gorilla  Gorilla gorilla                                   GAHSSSGHQSQS----------PNTSPPPKRHKKTMNSHHSPRRPTILHCSCPKNRKNLEGKLKKKKMA
5. Sumatran_orangutan  Pongo abelii                           GAHSSSGHQSQS----------PNDSPPPKRHKKTMNSHHSPTRPTILHCSCPKNRKNFEGKLNKKKMA
6. Northern_WC_gibbon  Nomascus leucogenys                    GAHSSSGCQSHS----------TNASPPPKCHKKTMNSHHSPMRPTILRCSCPKNRKNLGGKLNKKKMA
7. Black_SN_monkey  Rhinopithecus bieti                       RAHSSSGCQSQS----------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMA
8. Golden_SN_monkey  Rhinopithecus roxellana                  RAHSSSGCQSQS----------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMA
9. Angolan_colobus  Colobus angolensis                        GAHSSSGCQSQS----------PNASPPPKHHKKTMNSHHSPTRPTTLHSSCPKNRKNLEGKLNKKKMA
10. Uganda_red_colobus  Piliocolobus tephroscele              GAHSSSGCQSQS----------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLESKLNKKKMA
11. Olive_baboon  Papio anubis                                GAHSSSGCQSQS----------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMA
12. Sooty_mangabey  Cercocebus atys                           GAHSSSGCQSQS----------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMA
13. Drill  Mandrillus leucophaeus                             GAHSSSGCQSQS----------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMA
14. Green_monkey  Chlorocebus sabaeus                         GAHSSSGCQSQS----------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMA
15. Southern_PT_macaque  Macaca nemestrina                    GAHSSSGCQSQS----------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMA
16. Rhesus_macaque  Macaca mulatta                            GAHSSSGCQSQS----------PNASPPPKRHKKSMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMA
17. CE_macaque  Macaca fascicularis                           GAHSSSGCQSQS----------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMA
18. WH_capuchin  Cebus capucinus                              GAQSSSGRQSQS----------PSPSPPPKHHKKTMNSHHSPTRPTILYSSCPKRRKNLEVKMNKRKMA
19. BC_squirrel_monkey  Saimiri bolivensis                    GAHSSAGRQSQS----------PSPSPPPRHHKKTMNSHHSPTRPAILYSSCPKRRKNLEGKMNKRKMA
20. NM_night_monkey  Aotus_nancymaae                          GAHSSSGCQNQS----------PSPSPPPKQHKKTTNSQHSPTRPTILYSSCPKRRKNLEGKMNKRKMA
21. Common_marmoset  Callithrix jacchus                       GTHSSSGRQSQS----------PRPNPPPKNHKKTMNSHHSPTRPTILYSSCPKRRKNLEGKMNKRKMA
22. Philippine_tarsier  Carlito syrichta                      --SLPS-QQSQR----------PSSSLPPKHHRQAVHSHPSPARTPTHCGSRSKNRKASEGKASKRKMA
23. Gray_mouse_lemur  Microcebus murinus                      GSCSPSGRQSQSQS--------LSPSQPPKHHKQSMHSHHSRMRPTTHCSSCPRNRKALESKMNKRKVG
24. Coquerels_sifaka  Propithecus coquereli                   GSCSPSGHQSQS----------PSPSRPPKHHKQTMHSHHSPTRPTTHCGSCPRNRKTLEGKVNKRKVG
25. Northern_greater_galago  Otolemur garnetti                GQCRPPRLRSPSRAPSQSSHRSPSPSLSPKQCQQTAHSN-SSLQPTSHRSSCPRNRKTLERKAKKRKPG
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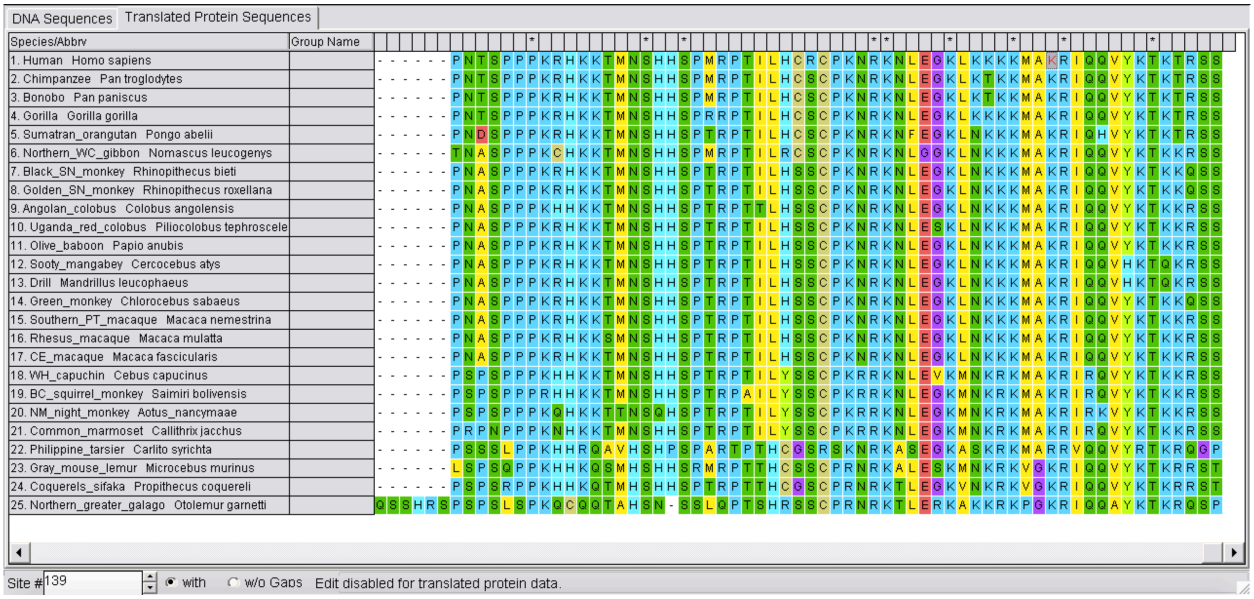

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Species/Abbrv                                     Group Name              *        *  *              **    *    *   *      *
1. Human  Homo sapiens                                        ------PNTSPPPKRHKKTMNSHHSPMRPTILHCRCPKNRKNLEGKLKKKKMAKRIQQVYKTKTRSS
2. Chimpanzee  Pan troglodytes                                ------PNTSPPPKRHKKTMNSHHSPMRPTILHCSCPKNRKNLEGKLKTKKMAKRIQQVYKTKTRSS
3. Bonobo  Pan paniscus                                       ------PNTSPPPKRHKKTMNSHHSPMRPTILHCSCPKNRKNLEGKLKTKKMAKRIQQVYKTKTRSS
4. Gorilla  Gorilla gorilla                                   ------PNTSPPPKRHKKTMNSHHSPRRPTILHCSCPKNRKNLEGKLKKKKMAKRIQQVYKTKTRSS
5. Sumatran_orangutan  Pongo abelii                           ------PNDSPPPKRHKKTMNSHHSPTRPTILHCSCPKNRKNFEGKLNKKKMAKRIQHVYKTKTRSS
6. Northern_WC_gibbon  Nomascus leucogenys                    ------TNASPPPKCHKKTMNSHHSPMRPTILRCSCPKNRKNLGGKLNKKKMAKRIQQVYKTKKRSS
7. Black_SN_monkey  Rhinopithecus bieti                       ------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMAKRIQQVYKTKKQSS
8. Golden_SN_monkey  Rhinopithecus roxellana                  ------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMAKRIQQVYKTKKQSS
9. Angolan_colobus  Colobus angolensis                        ------PNASPPPKHHKKTMNSHHSPTRPTTLHSSCPKNRKNLEGKLNKKKMAKRIQQVYKTKKRSS
10. Uganda_red_colobus  Piliocolobus tephroscele              ------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLESKLNKKKMAKRIQQVYKTKKRSS
11. Olive_baboon  Papio anubis                                ------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMAKRIQQVYKTKKRSS
12. Sooty_mangabey  Cercocebus atys                           ------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMAKRIQQVHKTQKRSS
13. Drill  Mandrillus leucophaeus                             ------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMAKRIQQVHKTQKRSS
14. Green_monkey  Chlorocebus sabaeus                         ------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMAKRIQQVYKTKKQSS
15. Southern_PT_macaque  Macaca nemestrina                    ------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMAKRIQQVYKTKKRSS
16. Rhesus_macaque  Macaca mulatta                            ------PNASPPPKRHKKSMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMAKRIQQVYKTKKRSS
17. CE_macaque  Macaca fascicularis                           ------PNASPPPKRHKKTMNSHHSPTRPTILHSSCPKNRKNLEGKLNKKKMAKRIQQVYKTKKRSS
18. WH_capuchin  Cebus capucinus                              ------PSPSPPPKHHKKTMNSHHSPTRPTILYSSCPKRRKNLEVKMNKRKMAKRIRQVYKTKKRSS
19. BC_squirrel_monkey  Saimiri bolivensis                    ------PSPSPPPRHHKKTMNSHHSPTRPAILYSSCPKRRKNLEGKMNKRKMAKRIRQVYKTKKRSS
20. NM_night_monkey  Aotus_nancymaae                          ------PSPSPPPKQHKKTTNSQHSPTRPTILYSSCPKRRKNLEGKMNKRKMAKRIRKVYKTKKRSS
21. Common_marmoset  Callithrix jacchus                       ------PRPNPPPKNHKKTMNSHHSPTRPTILYSSCPKRRKNLEGKMNKRKMAKRIRQVYKTKKRSS
22. Philippine_tarsier  Carlito syrichta                      ------PSSSLPPKHHRQAVHSHPSPARTPTHCGSRSKNRKASEGKASKRKMARRVQQVYRTKRQGP
23. Gray_mouse_lemur  Microcebus murinus                      ------LSPSQPPKHHKQSMHSHHSRMRPTTHCSSCPRNRKALESKMNKRKVGKRIQQVYKTKRRST
24. Coquerels_sifaka  Propithecus coquereli                   ------PSPSRPPKHHKQTMHSHHSPTRPTTHCGSCPRNRKTLEGKVNKRKVGKRIQQVYKTKRRST
25. Northern_greater_galago  Otolemur garnetti                QSSHRSPSPSLSPKQCQQTAHSN-SSLQPTSHRSSCPRNRKTLERKAKKRKPGKRIQQAYKTKRQSP
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Site # 139 ● with ○ w/o Gaps Edit disabled for translated protein data.

Appendix D: Alignment of primate *Prm1* full-length gene sequences

```
Species/Abbrv                                            Group Name  ********  *******  * *  **       *  **    *****      *****    **
1. Human_mRNA  Homo sapiens                                          ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATATTACCGCCAGAGACAAA
2. Human  Homo sapiens                                               ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATATTACCGCCAGAGACAAA
3. Chimpanzee  Pan troglodytes                                       ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGTTACCGCCAGAGACAAA
4. Bonobo  Pan paniscus                                              ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGTTACCGCCAGAGAC---
5. Gorilla  Gorilla gorilla gorilla                                  ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGTTACCGCCAGAGACAAA
6. Lar_gibbon  Hylobates lar                                         ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGTTACCGCCGGGGACAAA
7. Sumatran_orangutan  Pongo abelii                                  ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCAGAGCAGATGTTGCCGCCGGAGACAAA
8. Black_SN_monkey  Rhinopithecus bieti                              ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGCTGCCGCCCGAGACGAA
9. Golden_SN_monkey  Rhinopithecus roxellana                         ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGCTGCCGCCCGAGACGAA
10. Angolan_colobus  Colobus angolensis palliatus                    ATGGCCAGGTACAGATGCCGTCGCAGC------CAGAGCCGGAGCAGATGCTGCCGCCAGAGACGAA
11. Ugandan_red_colobus  Piliocolobus tephrosceles                   ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGCTGCCGCCAGAGACAAA
12. Olive_baboon  Papio anubis                                       ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGCTGCCGCCAGAGACGAA
13. Sooty_mangabey  Cercocebus atys                                  ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGCTGCCGCCAGAGACGAA
14. Drill  Mandrillus leucophaeus                                    ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGCTGCCGCCAGAGACGAA
15. Green_monkey  Chlorocebus sabaeus                                ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGAAGCAGATGCTGCCGCCAGAGACGAA
16. Southern_PT_macaque  Macaca nemestrina                           ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGCTGCCGCCGGAGACGAA
17. Rhesus_macaque  Macaca mulatta                                   ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGCTGCCGCCGGAGACGAA
18. CE_macaque  Macaca fascicularis                                  ATGGCCAGGTACAGATGCTGTCGCAGC------CAGAGCCGGAGCAGATGCTGCCGCCGGAGACGAA
19. WH_capuchin  Cebus_capucinus                                     ATGGCCAGGTACAGATGCTGCCGCAGC------CGGAGCCGGAGCAGATGCTACCGCCAAAGACGAA
20. BC_squirrel_monkey  Saimiri boliviensis boliviensis              ATGGCCAGGTACAGATGCTGCCGCAGC------CGGAGCCGGAGCAGATGCTACCGCCGAAGACGAA
21. NM_night_monkey  Aotus nancymaae                                 ATGGCCAGGCACAGATGCTGCCGTAGCCGTAGCCAGAGCCGGAGCAGACGCGACCGCCAAAAACGAA
22. Common_marmoset  Callithrix jacchus                              ATGGCCAGGTACAGATGCTGCCGCAGC------CAGAGCCGGAGCAGATGCTACCGCCAAAGACGAA
23. Philippine_tarsier  Carlito syrichta                             ATGGCCAGATACAGATGCTGCCTCAGT------CCAAGTCGGAGCAGATGCCGCCGCCGGAGACGCA
24. Gray_mouse_lemur  Microcebus murinus                             ATGGCCAGATACAGATGTTGCCGCAGC------CAAAGCAGGAGCAGATGCCGCCGCCGGAGACGAA
25. Coquerels_sifaka  Propithecus coquereli                          ATGGCCAGATACAGATGTTGCCGTAGC------CAAAGCAGGAGCAGGTGCCGCCGCCGGAGACAAA
26. Northern_greater_galago  Otolemur garnettii                      ATGGCCAGATACAGATGTTGCCGCAGC------CAAAGCAGGAGCAGGTGCCGCCGCCGGAGACGAA
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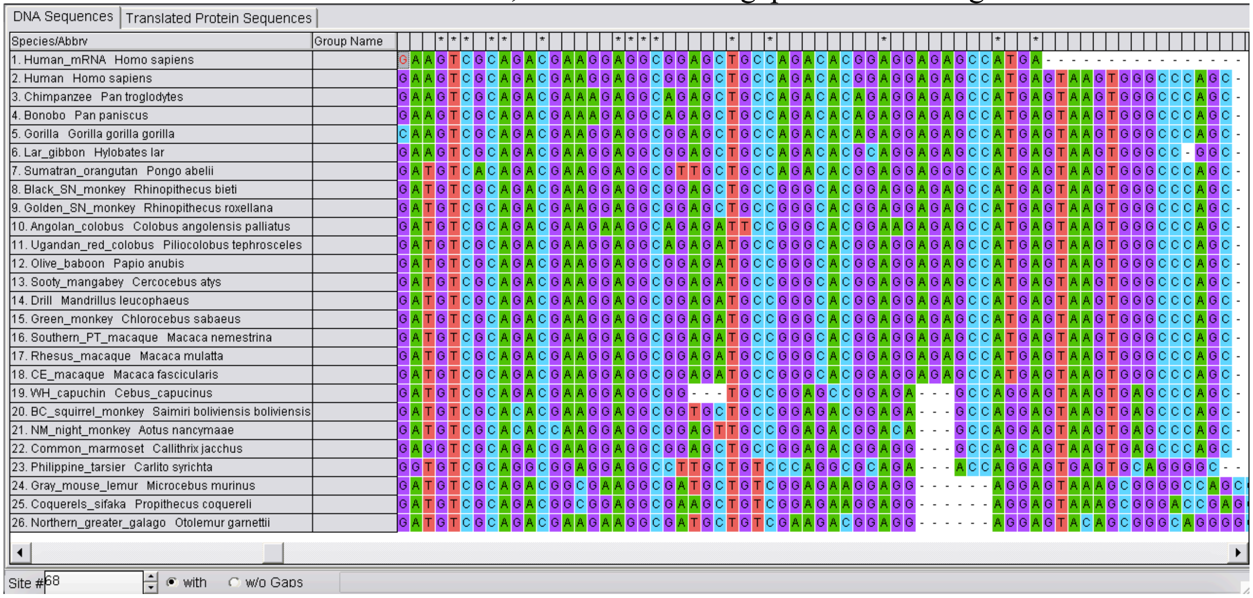
Site # 1 ● with ○ w/o Gaps

The intron occurs at nucleotide site 119, site 112 without gaps added for alignment



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Species/Abbrv                                            Group Name     *** **  *     ****     *  *        *        *  *
1. Human_mRNA  Homo sapiens                                          GAAGTCGCAGACGAAGGAGGCGGAGCTGCCAGACACGGAGGAGAGCCATGA----------------
2. Human  Homo sapiens                                               GAAGTCGCAGACGAAGGAGGCGGAGCTGCCAGACACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
3. Chimpanzee  Pan troglodytes                                       GAAGTCGCAGACGAAAGAGGCAGAGCTGCCAGACACAGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
4. Bonobo  Pan paniscus                                              GAAGTCGCAGACGAAAGAGGCAGAGCTGCCAGACACAGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
5. Gorilla  Gorilla gorilla gorilla                                  CAAGTCGCAGACGAAGGAGGCGGAGCTGCCAGACACAGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
6. Lar_gibbon  Hylobates lar                                         GAAGTCGCAGACGAAGGAGGCGGAGCTGCCAGACACGCAGGAGAGCCATGAGTAAGTGGGCC-GGC-
7. Sumatran_orangutan  Pongo abelii                                  GATGTCACAGACGAAGGAGGCGTTGCTGCCAGACACGGAGGAGGGCCATGAGTAAGTGGGCCCAGC-
8. Black_SN_monkey  Rhinopithecus bieti                              GATGTCGCAGACGAAGGAGGCGGAGCTGCCGGGCACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
9. Golden_SN_monkey  Rhinopithecus roxellana                         GATGTCGCAGACGAAGGAGGCGGAGCTGCCGGGCACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
10. Angolan_colobus  Colobus angolensis palliatus                    GATGTCGCAGACGAAGAAGGCAGAGATTCCGGGCACGGAAGAGAGCCATGAGTAAGTGGGCCCAGC-
11. Ugandan_red_colobus  Piliocolobus tephrosceles                   GATGTCGCAGACGAAGGAGGCAGAGATGCCGGGCACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
12. Olive_baboon  Papio anubis                                       GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
13. Sooty_mangabey  Cercocebus atys                                  GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
14. Drill  Mandrillus leucophaeus                                    GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
15. Green_monkey  Chlorocebus sabaeus                                GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
16. Southern_PT_macaque  Macaca nemestrina                           GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
17. Rhesus_macaque  Macaca mulatta                                   GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
18. CE_macaque  Macaca fascicularis                                  GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGTAAGTGGGCCCAGC-
19. WH_capuchin  Cebus_capucinus                                     GATGTCGCAGACGAAGGAGGCGG---TGCCGGAGCCGGAGA---GCCAGGAGTAAGTGAGCCCAGC-
20. BC_squirrel_monkey  Saimiri boliviensis boliviensis              GATGTCGCACACGAAGGAGGCGGTGCTGCCGGAGACGGAGA---GCCAGGAGTAAGTGAGCCCAGC-
21. NM_night_monkey  Aotus nancymaae                                 GATGTCGCACACCAAGGAGGCGGAGTTGCCGGAGACGGACA---GCCAGGAGTAAGTGAGCCCAGC-
22. Common_marmoset  Callithrix jacchus                              GAGGTCGCAGACGAAGGAGGCGGAGCTGCCGGAGACGGAGG---GCCAGCAGTAAGTGAGCCCAGC-
23. Philippine_tarsier  Carlito syrichta                             GGTGTCGCAGGCGGAGGAGGCCTTGCTGTCCCAGGCGCAGA---ACCAGGAGTGAGTGCAGGGGC--
24. Gray_mouse_lemur  Microcebus murinus                             GATGTCGCAGACGGCGAAGGCGATGCTGTCGGAGAAGGAGG------AGGAGTAAAGCGGGGCCAGC
25. Coquerels_sifaka  Propithecus coquereli                          GATGTCGCAGACGGCGGAGGCGAAGCTGTCGGAGAAGGAGG------AGGAGTAAAGCGGGACCGAG
26. Northern_greater_galago  Otolemur garnettii                      GATGTCGCAGACGAAGAAGGCGATGCTGTCGAAGACGGAGG------AGGAGTACAGCGGGCAGGGG
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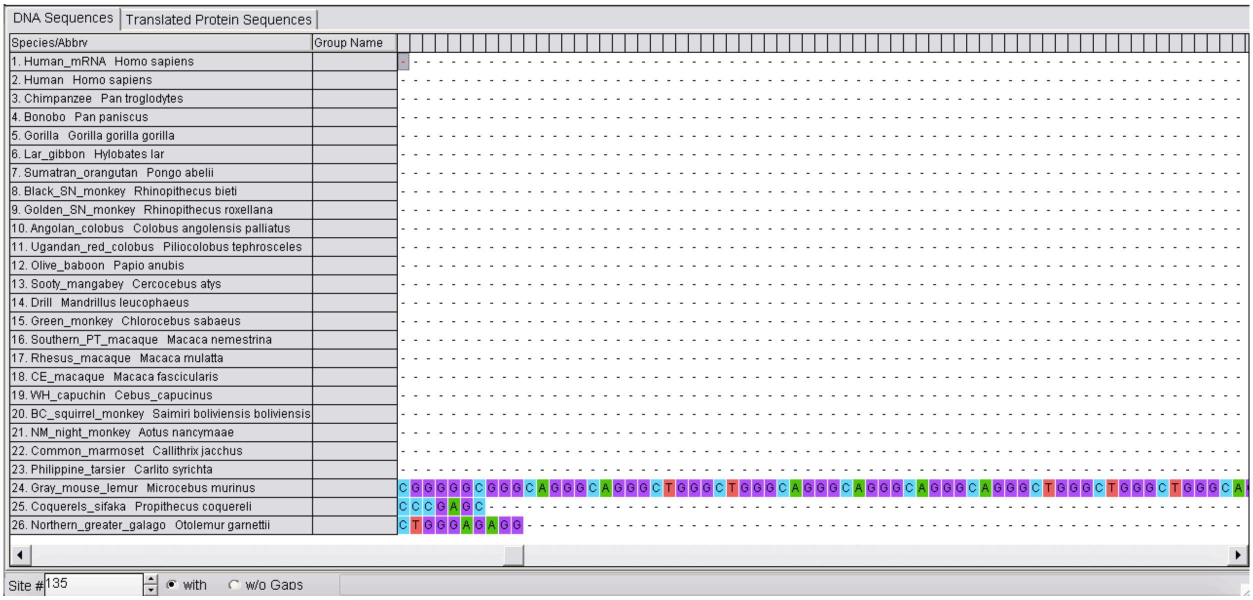
Site # 68 ● with ○ w/o Gaps



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Species/Abbrv                                        Group Name
1. Human_mRNA  Homo sapiens                                     -------------------------------------------------------------------
2. Human  Homo sapiens                                          -------------------------------------------------------------------
3. Chimpanzee  Pan troglodytes                                  -------------------------------------------------------------------
4. Bonobo  Pan paniscus                                         -------------------------------------------------------------------
5. Gorilla  Gorilla gorilla gorilla                             -------------------------------------------------------------------
6. Lar_gibbon  Hylobates lar                                    -------------------------------------------------------------------
7. Sumatran_orangutan  Pongo abelii                             -------------------------------------------------------------------
8. Black_SN_monkey  Rhinopithecus bieti                         -------------------------------------------------------------------
9. Golden_SN_monkey  Rhinopithecus roxellana                    -------------------------------------------------------------------
10. Angolan_colobus  Colobus angolensis palliatus               -------------------------------------------------------------------
11. Ugandan_red_colobus  Piliocolobus tephrosceles              -------------------------------------------------------------------
12. Olive_baboon  Papio anubis                                  -------------------------------------------------------------------
13. Sooty_mangabey  Cercocebus atys                             -------------------------------------------------------------------
14. Drill  Mandrillus leucophaeus                               -------------------------------------------------------------------
15. Green_monkey  Chlorocebus sabaeus                           -------------------------------------------------------------------
16. Southern_PT_macaque  Macaca nemestrina                      -------------------------------------------------------------------
17. Rhesus_macaque  Macaca mulatta                              -------------------------------------------------------------------
18. CE_macaque  Macaca fascicularis                             -------------------------------------------------------------------
19. WH_capuchin  Cebus_capucinus                                -------------------------------------------------------------------
20. BC_squirrel_monkey  Saimiri boliviensis boliviensis         -------------------------------------------------------------------
21. NM_night_monkey  Aotus nancymaae                            -------------------------------------------------------------------
22. Common_marmoset  Callithrix jacchus                         -------------------------------------------------------------------
23. Philippine_tarsier  Carlito syrichta                        -------------------------------------------------------------------
24. Gray_mouse_lemur  Microcebus murinus                        CGGGGGCGGGCAGGGCAGGGCTGGGCTGGGCAGGGCAGGGCAGGGCAGGGCTGGGCTGGGCTGGGCA
25. Coquerels_sifaka  Propithecus coquereli                     CCCGAGC------------------------------------------------------------
26. Northern_greater_galago  Otolemur garnettii                 CTGGGAGAGG---------------------------------------------------------
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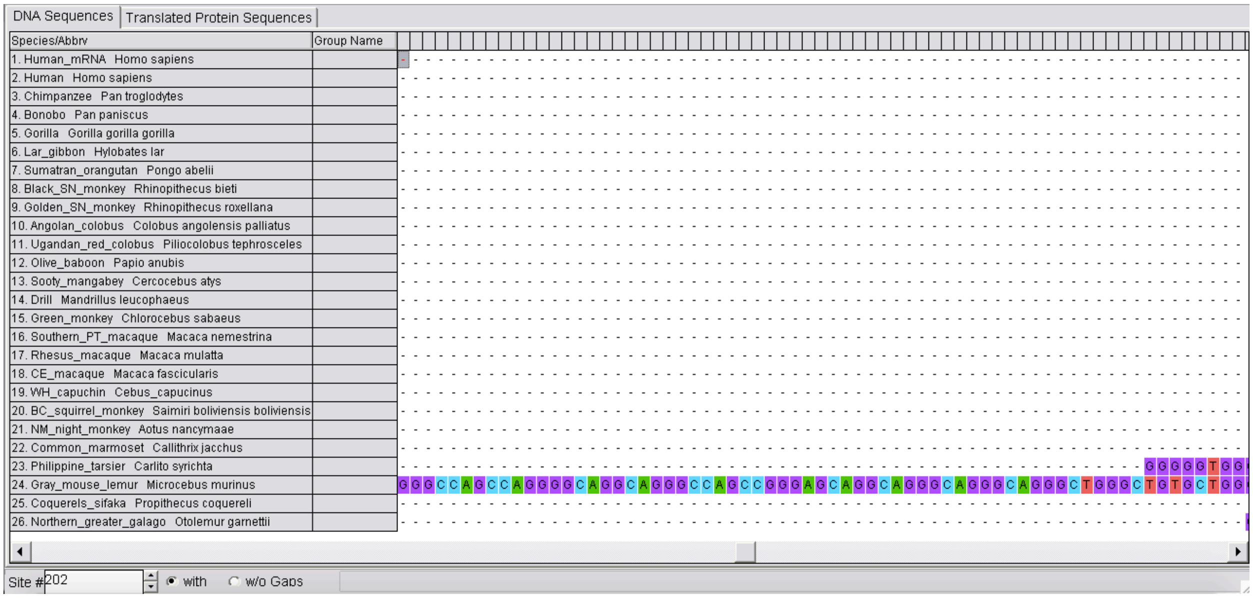
Site # 135 ● with ○ w/o Gaps



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Species/Abbrv                                        Group Name
1. Human_mRNA  Homo sapiens                                     -------------------------------------------------------------------
2. Human  Homo sapiens                                          -------------------------------------------------------------------
3. Chimpanzee  Pan troglodytes                                  -------------------------------------------------------------------
4. Bonobo  Pan paniscus                                         -------------------------------------------------------------------
5. Gorilla  Gorilla gorilla gorilla                             -------------------------------------------------------------------
6. Lar_gibbon  Hylobates lar                                    -------------------------------------------------------------------
7. Sumatran_orangutan  Pongo abelii                             -------------------------------------------------------------------
8. Black_SN_monkey  Rhinopithecus bieti                         -------------------------------------------------------------------
9. Golden_SN_monkey  Rhinopithecus roxellana                    -------------------------------------------------------------------
10. Angolan_colobus  Colobus angolensis palliatus               -------------------------------------------------------------------
11. Ugandan_red_colobus  Piliocolobus tephrosceles              -------------------------------------------------------------------
12. Olive_baboon  Papio anubis                                  -------------------------------------------------------------------
13. Sooty_mangabey  Cercocebus atys                             -------------------------------------------------------------------
14. Drill  Mandrillus leucophaeus                               -------------------------------------------------------------------
15. Green_monkey  Chlorocebus sabaeus                           -------------------------------------------------------------------
16. Southern_PT_macaque  Macaca nemestrina                      -------------------------------------------------------------------
17. Rhesus_macaque  Macaca mulatta                              -------------------------------------------------------------------
18. CE_macaque  Macaca fascicularis                             -------------------------------------------------------------------
19. WH_capuchin  Cebus_capucinus                                -------------------------------------------------------------------
20. BC_squirrel_monkey  Saimiri boliviensis boliviensis         -------------------------------------------------------------------
21. NM_night_monkey  Aotus nancymaae                            -------------------------------------------------------------------
22. Common_marmoset  Callithrix jacchus                         -------------------------------------------------------------------
23. Philippine_tarsier  Carlito syrichta                        -----------------------------------------------------------GGGGGTGG
24. Gray_mouse_lemur  Microcebus murinus                        GGGCCAGCCAGGGGCAGGCAGGGCCAGCCGGGAGCAGGCAGGGCAGGGCAGGGCTGGGCTGTGCTGG
25. Coquerels_sifaka  Propithecus coquereli                     -------------------------------------------------------------------
26. Northern_greater_galago  Otolemur garnettii                 -------------------------------------------------------------------
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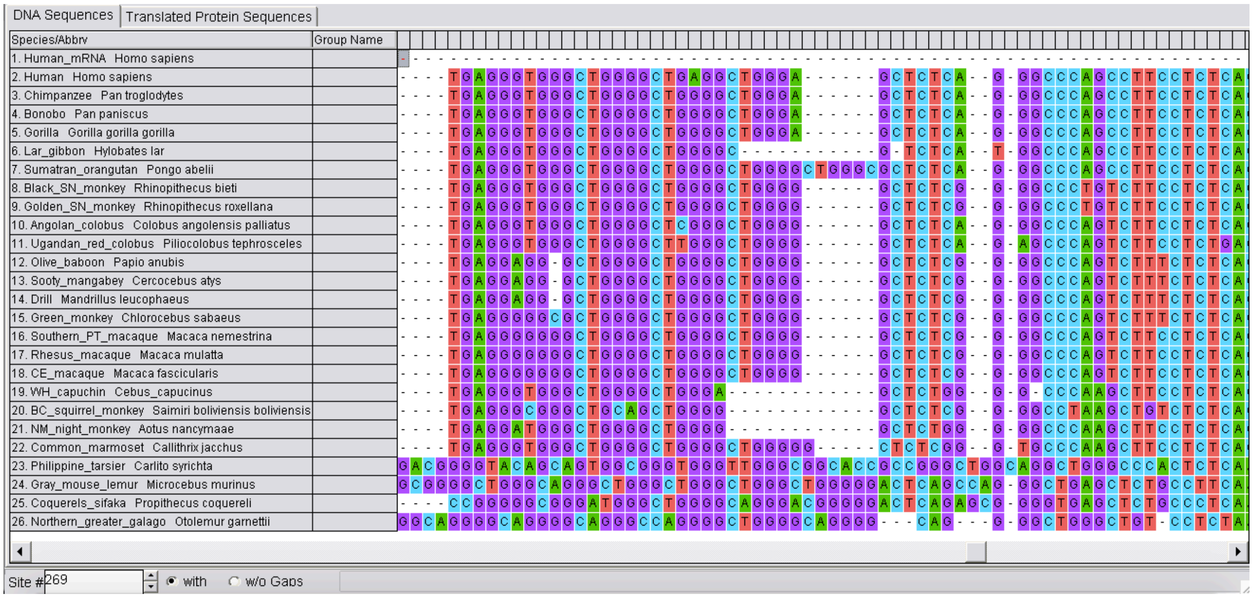
Site # 202 ● with ○ w/o Gaps



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DNA Sequences  Translated Protein Sequences
Species/Abbrv                                            Group Name
1. Human_mRNA  Homo sapiens                                          -------------------------------------------------------------------
2. Human  Homo sapiens                                               ----TGAGGGTGGGCTGGGGCTGAGGCTGGGA------GCTCTCA--G-GGCCCAGCCTTCCTCTCA
3. Chimpanzee  Pan troglodytes                                       ----TGAGGGTGGGCTGGGGCTGGGGCTGGGA------GCTCTCA--G-GGCCCAGCCTTCCTCTCA
4. Bonobo  Pan paniscus                                              ----TGAGGGTGGGCTGGGGCTGGGGCTGGGA------GCTCTCA--G-GGCCCAGCCTTCCTCTCA
5. Gorilla  Gorilla gorilla gorilla                                  ----TGAGGGTGGGCTGGGGCTGGGGCTGGGA------GCTCTCA--G-GGCCCAGCCTTCCTCTCA
6. Lar_gibbon  Hylobates lar                                         ----TGAGGGTGGGCTGGGGCTGGGGC-----------G-TCTCA--T-GGCCCAGCCTTCCTCTCA
7. Sumatran_orangutan  Pongo abelii                                  ----TGAGGGTGGGCTGGGGCTGGGGCTGGGGCTGGGCGCTCTCA--G-GGCCCAGCCTTCCTCTCA
8. Black_SN_monkey  Rhinopithecus bieti                              ----TGAGGGTGGGCTGGGGCTGGGGCTGGGG------GCTCTCG--G-GGCCCTGTCTTCCTCTCA
9. Golden_SN_monkey  Rhinopithecus roxellana                         ----TGAGGGTGGGCTGGGGCTGGGGCTGGGG------GCTCTCG--G-GGCCCTGTCTTCCTCTCA
10. Angolan_colobus  Colobus angolensis palliatus                    ----TGAGGGTGGGCTGGGGCTCGGGCTGGGG------GCTCTCA--G-GGCCCAGTCTTCCTCTCA
11. Ugandan_red_colobus  Piliocolobus tephrosceles                   ----TGAGGGTGGGCTGGGGCTTGGGCTGGGG------GCTCTCA--G-AGCCCAGTCTTCCTCTGA
12. Olive_baboon  Papio anubis                                       ----TGAGGAGG-GCTGGGGCTGGGGCTGGGG------GCTCTCG--G-GGCCCAGTCTTTCTCTCA
13. Sooty_mangabey  Cercocebus atys                                  ----TGAGGAGG-GCTGGGGCTGGGGCTGGGG------GCTCTCG--G-GGCCCAGTCTTTCTCTCA
14. Drill  Mandrillus leucophaeus                                    ----TGAGGAGG-GCTGGGGCTGGGGCTGGGG------GCTCTCG--G-GGCCCAGTCTTTCTCTCA
15. Green_monkey  Chlorocebus sabaeus                                ----TGAGGGGGCGCTGGGGCTGGGGCTGGGG------GCTCTCG--G-GGCCCAGTCTTTCTCTCA
16. Southern_PT_macaque  Macaca nemestrina                           ----TGAGGGGGGGCTGGGGCTGGGGCTGGGG------GCTCTCG--G-GGCCCAGTCTTCCTCTCA
17. Rhesus_macaque  Macaca mulatta                                   ----TGAGGGGGGGCTGGGGCTGGGGCTGGGG------GCTCTCG--G-GGCCCAGTCTTCCTCTCA
18. CE_macaque  Macaca fascicularis                                  ----TGAGGGGGGGCTGGGGCTGGGGCTGGGG------GCTCTCG--G-GGCCCAGTCTTCCTCTCA
19. WH_capuchin  Cebus_capucinus                                     ----TGAGGGTGGGCTGGGGCTGGGA------------GCTCTGG--G-G-CCCAAGCTTCCTCTCA
20. BC_squirrel_monkey  Saimiri boliviensis boliviensis              ----TGAGGGCGGGCTGCAGCTGGGG------------GCTCTCG--G-GGCCTAAGCTGTCTCTCA
21. NM_night_monkey  Aotus nancymaae                                 ----TGAGGATGGGCTGGGGCTGGGG------------GCTCTGG--G-GGCCCAAGCTTCCTCTCA
22. Common_marmoset  Callithrix jacchus                              ----TGAGGGTGGGCTGGGGCTGGGGCTGGGGG-----CTCTCGG--G-TGCCCAAGCTTCCTCTCA
23. Philippine_tarsier  Carlito syrichta                             GACGGGGTACAGCAGTGGCGGGTGGGTTGGGCGGCACCGCCGGGCTGGCAGGCTGGGCCCACTCTCA
24. Gray_mouse_lemur  Microcebus murinus                             GCGGGGCTGGGCAGGGCTGGGCTGGGCTGGGCTGGGGGACTCAGCCAG-GGCTGAGCTCTGCCTTCA
25. Coquerels_sifaka  Propithecus coquereli                          ----CCGGGGGCGGGATGGGCTGGGGCAGGGACGGGGGACTCAGAGCG-GGGTGAGCTCTGCCCTCA
26. Northern_greater_galago  Otolemur garnettii                      GGCAGGGGCAGGGGCAGGGCCAGGGGCTGGGGCAGGGG---CAG---G-GGCTGGGCTGT-CCTCTA
Site # 269   ● with   ○ w/o Gaps
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DNA Sequences  Translated Protein Sequences
Species/Abbrv                                            Group Name                          ** *   **** *                * **   * *** *
1. Human_mRNA  Homo sapiens                                          -----------------------GGTGCTGCCGCCCCAGGTACAGACCGCGATGTAGAAGACACTAA
2. Human  Homo sapiens                                               CCACTTTTCTTGGTCTC-ACCAGGGTGCTGCCGCCCCAGGTACAGACCGCGATGTAGAAGACACTAA
3. Chimpanzee  Pan troglodytes                                       CCACTTTTTTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTCCAGAATGAGACGTAGAAGACACTAA
4. Bonobo  Pan paniscus                                              CCACTTTTTTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTCCAGACTGAGACGTAGAAGACACTAA
5. Gorilla  Gorilla gorilla gorilla                                  CCACTTTTCTTGGTCTC-ACCAGGGTGCTGTCGCCGCAGGAACAGACTGAGACGTAGAAAACACTAA
6. Lar_gibbon  Hylobates lar                                         CCACTTTTCTTGGTCTC-ACCAGGGTGCTGCCGCCCCAGGTACAGGCTGAGACGTAGAAGACACTAA
7. Sumatran_orangutan  Pongo abelii                                  CCACTTTTCTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAGACTGAGATGTAGAAGACACTAA
8. Black_SN_monkey  Rhinopithecus bieti                              CTACCTTTTTTGGTCTC-ATCAGGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
9. Golden_SN_monkey  Rhinopithecus roxellana                         CTACCTTTTTTGGTCTC-ATCAGGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
10. Angolan_colobus  Colobus angolensis palliatus                    CTACCTTTTTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
11. Ugandan_red_colobus  Piliocolobus tephrosceles                   CTACCTTTTTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAGGCGGAGGTGTAGAAGATACTAA
12. Olive_baboon  Papio anubis                                       CCACCTTTCTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
13. Sooty_mangabey  Cercocebus atys                                  CCACCTTTCTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
14. Drill  Mandrillus leucophaeus                                    CCACCTTTCTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
15. Green_monkey  Chlorocebus sabaeus                                CCACCTTTCTTGGTCTC-ACCAGAGTACTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
16. Southern_PT_macaque  Macaca nemestrina                           CCACCTTTCTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
17. Rhesus_macaque  Macaca mulatta                                   CCACCTTTCTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
18. CE_macaque  Macaca fascicularis                                  CCACCTTTCTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
19. WH_capuchin  Cebus_capucinus                                     CCACCTTTCTTGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAGACTGAGGTGTAGAAGATACTAA
20. BC_squirrel_monkey  Saimiri boliviensis boliviensis              CCACCTCTCTCGGTCTC-CCCAGGGTGCTGCCGCCGCAGGTACAAGCTGAGGTGTAGAAGATACTAA
21. NM_night_monkey  Aotus nancymaae                                 CCACCTTTTTTGGTCTC-ACCAGGGTGCGGCCGCCGCAGGTATAAGCCGCGGTGTAGAAGAAACTAA
22. Common_marmoset  Callithrix jacchus                              CCACCTTTCATGGTCTC-ACCAGGGTGCTGCCGCCGCAGGTACAAGCTGCCATGTAGAAGATACTAA
23. Philippine_tarsier  Carlito syrichta                             A-GCCTCT----GTCCC--CCAGGGTGCTGCCGCCGCTCCTTCCGGCTGAGGTGTAGAAGATACTGA
24. Gray_mouse_lemur  Microcebus murinus                             ACGCCCCTCTCGTTCCCCGCCAGGGTGCTGCCGCCGCAGGTACAGGTGTAGAAGAAGAAGATACTAA
25. Coquerels_sifaka  Propithecus coquereli                          ACGCCTTTCTCCTTCCCCGCCAGGGTGCTACCGCCGCAGGTACAGGTGTAGAAGAAG---ATACTAA
26. Northern_greater_galago  Otolemur garnettii                      ACACCTTCCTTGTTCCCTGCCAGGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGATACTAA
Site # 336   ● with   ○ w/o Gaps
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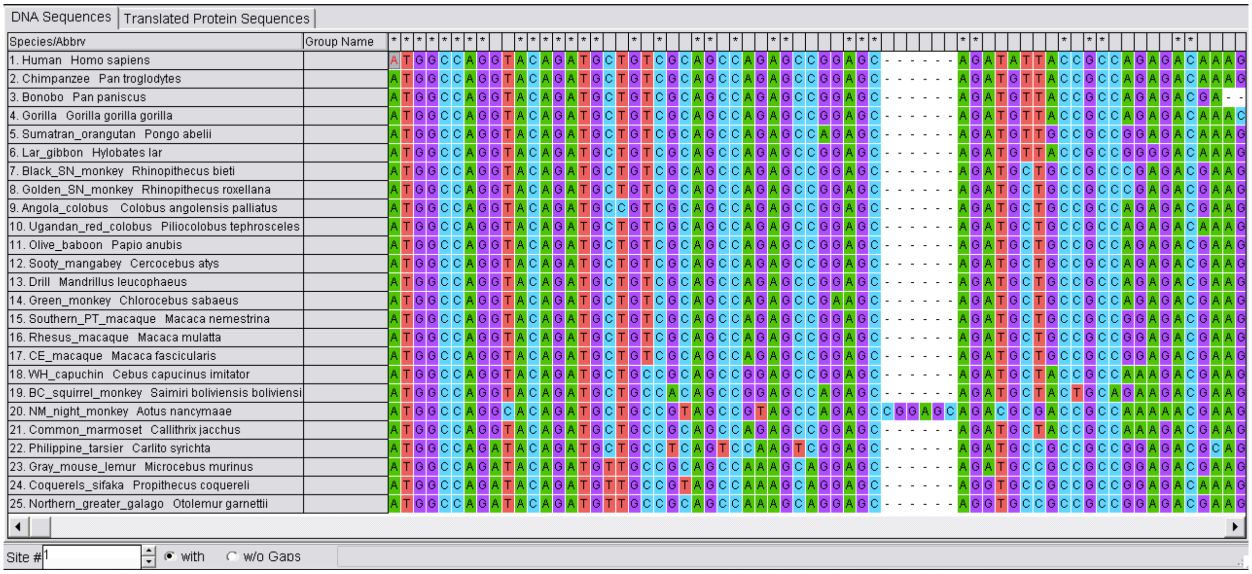
Appendix E1) Alignment of primate *Prm1* coding exon nucleotide sequences



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Species/Abbrv                                           Group Name  ********  *******  * *  ** *  **    ***      **      * **     **
1. Human  Homo sapiens                                              ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATATTACCGCCAGAGACAAAG
2. Chimpanzee  Pan troglodytes                                      ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGTTACCGCCAGAGACAAAG
3. Bonobo  Pan paniscus                                             ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGTTACCGCCAGAGACGA--
4. Gorilla  Gorilla gorilla gorilla                                 ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGTTACCGCCAGAGACAAAC
5. Sumatran_orangutan  Pongo abelii                                 ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCAGAGC------AGATGTTGCCGCCGGAGACAAAG
6. Lar_gibbon  Hylobates lar                                        ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGTTACCGCCGGGGACAAAG
7. Black_SN_monkey  Rhinopithecus bieti                             ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCCGAGACGAAG
8. Golden_SN_monkey  Rhinopithecus roxellana                        ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCCGAGACGAAG
9. Angola_colobus  Colobus angolensis palliatus                     ATGGCCAGGTACAGATGCCGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCAGAGACGAAG
10. Ugandan_red_colobus  Piliocolobus tephrosceles                  ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCAGAGACAAAG
11. Olive_baboon  Papio anubis                                      ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCAGAGACGAAG
12. Sooty_mangabey  Cercocebus atys                                 ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCAGAGACGAAG
13. Drill  Mandrillus leucophaeus                                   ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCAGAGACGAAG
14. Green_monkey  Chlorocebus sabaeus                               ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGAAGC------AGATGCTGCCGCCAGAGACGAAG
15. Southern_PT_macaque  Macaca nemestrina                          ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCGGAGACGAAG
16. Rhesus_macaque  Macaca mulatta                                  ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCGGAGACGAAG
17. CE_macaque  Macaca fascicularis                                 ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCGGAGACGAAG
18. WH_capuchin  Cebus capucinus imitator                           ATGGCCAGGTACAGATGCTGCCGCAGCCGGAGCCGGAGC------AGATGCTACCGCCAAAGACGAAG
19. BC_squirrel_monkey  Saimiri boliviensis boliviensi              ATGGCCAGGTACAGATGCTGCCACAGCCGGAGCCAGAGC------AGATGCTACTGCAGAAGACGAAG
20. NM_night_monkey  Aotus nancymaae                                ATGGCCAGGCACAGATGCTGCCGTAGCCGTAGCCAGAGCCGGAGCAGACGCGACCGCCAAAAACGAAG
21. Common_marmoset  Callithrix jacchus                             ATGGCCAGGTACAGATGCTGCCGCAGCCAGAGCCGGAGC------AGATGCTACCGCCAAAGACGAAG
22. Philippine_tarsier  Carlito syrichta                            ATGGCCAGATACAGATGCTGCCTCAGTCCAAGTCGGAGC------AGATGCCGCCGCCGGAGACGCAG
23. Gray_mouse_lemur  Microcebus murinus                            ATGGCCAGATACAGATGTTGCCGCAGCCAAAGCAGGAGC------AGATGCCGCCGCCGGAGACGAAG
24. Coquerels_sifaka  Propithecus coquereli                         ATGGCCAGATACAGATGTTGCCGTAGCCAAAGCAGGAGC------AGGTGCCGCCGCCGGAGACAAAG
25. Northern_greater_galago  Otolemur garnettii                     ATGGCCAGATACAGATGTTGCCGCAGCCAAAGCAGGAGC------AGGTGCCGCCGCCGGAGACGAAG
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Site # 1 ● with ○ w/o Gaps

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Species/Abbrv                                           Group Name     **  **  *     ***      *  *        *        *  **** *   * ** *
1. Human  Homo sapiens                                              GAAGTCGCAGACGAAGGAGGCGGAGCTGCCAGACACGGAGGAGAGCCATGAGGTGCTGCCGCCCCAGG
2. Chimpanzee  Pan troglodytes                                      GAAGTCGCAGACGAAAGAGGCAGAGCTGCCAGACACAGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
3. Bonobo  Pan paniscus                                             --AGTCGCAGACGAAAGAGGCAGAGCTGCCAGACACAGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
4. Gorilla  Gorilla gorilla gorilla                                 CAAGTCGCAGACGAAGGAGGCGGAGCTGCCAGACACAGAGGAGAGCCATGAGGTGCTGTCGCCGCAGG
5. Sumatran_orangutan  Pongo abelii                                 GATGTCACAGACGAAGGAGGCGTTGCTGCCAGACACGGAGGAGGGCCATGAGGTGCTGCCGCCGCAGG
6. Lar_gibbon  Hylobates lar                                        GAAGTCGCAGACGAAGGAGGCGGAGCTGCCAGACACGCAGGAGAGCCATGAGGTGCTGCCGCCCCAGG
7. Black_SN_monkey  Rhinopithecus bieti                             GATGTCGCAGACGAAGGAGGCGGAGCTGCCGGGCACGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
8. Golden_SN_monkey  Rhinopithecus roxellana                        GATGTCGCAGACGAAGGAGGCGGAGCTGCCGGGCACGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
9. Angola_colobus  Colobus angolensis palliatus                     GATGTCGCAGACGAAGAAGGCAGAGATTCCGGGCACGGAAGAGAGCCATGAGGTGCTGCCGCCGCAGG
10. Ugandan_red_colobus  Piliocolobus tephrosceles                  GATGTCGCAGACGAAGGAGGCAGAGATGCCGGGCACGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
11. Olive_baboon  Papio anubis                                      GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
12. Sooty_mangabey  Cercocebus atys                                 GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
13. Drill  Mandrillus leucophaeus                                   GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
14. Green_monkey  Chlorocebus sabaeus                               GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGGTACTGCCGCCGCAGG
15. Southern_PT_macaque  Macaca nemestrina                          GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
16. Rhesus_macaque  Macaca mulatta                                  GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
17. CE_macaque  Macaca fascicularis                                 GATGTCGCAGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGG
18. WH_capuchin  Cebus capucinus imitator                           GATGTCGCAGACGAAGGAGGCGG---TGCCGGAGCCGGAGA---GCCAGGAGGTGCTGCCGCCGCAGG
19. BC_squirrel_monkey  Saimiri boliviensis boliviensi              GATGTGGCACACGAAGGAGGTGGTGCTGCCGGAGACAGAGA---GCCACGAGGTGCTGCCACCGCAGG
20. NM_night_monkey  Aotus nancymaae                                GATGTCGCACACCAAGGAGGCGGAGTTGCCGGAGACGGACA---GCCAGGAGGTGCGGCCGCCGCAGG
21. Common_marmoset  Callithrix jacchus                             GAGGTCGCAGACGAAGGAGGCGGAGCTGCCGGAGACGGAGG---GCCAGCAGGTGCTGCCGCCGCAGG
22. Philippine_tarsier  Carlito syrichta                            GGTGTCGCAGGCGGAGGAGGCCTTGCTGTCCCAGGCGCAGA---ACCAGGAGGTGCTGCCGCCGCTCC
23. Gray_mouse_lemur  Microcebus murinus                            GATGTCGCAGACGGCGAAGGCGATGCTGTCGGAGAAGGAGG------AGGAGGTGCTGCCGCCGCAGG
24. Coquerels_sifaka  Propithecus coquereli                         GATGTCGCAGACGGCGGAGGCGAAGCTGTCGGAGAAGGAGG------AGGAGGTGCTACCGCCGCAGG
25. Northern_greater_galago  Otolemur garnettii                     GATGTCGCAGACGAAGAAGGCGATGCTGTCGAAGACGGAGG------AGGAGGTGCTGCCGCCGCAGG
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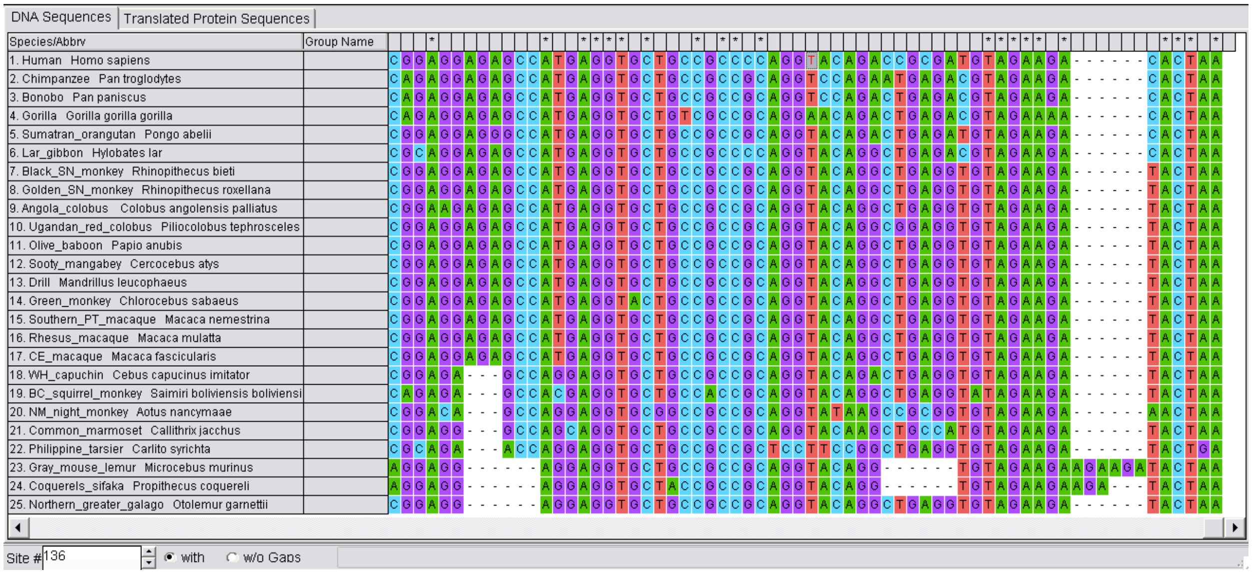
Site # 68 ● with ○ w/o Gaps



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Species/Abbrv                                           Group Name
                                                                   *        *  **** *   * ** *                 ***** *       *** *
1. Human  Homo sapiens                                            CGGAGGAGAGCCATGAGGTGCTGCCGCCCCAGGTACAGACCGCGATGTAGAAGA------CACTAA
2. Chimpanzee  Pan troglodytes                                    CAGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTCCAGAATGAGACGTAGAAGA------CACTAA
3. Bonobo  Pan paniscus                                           CAGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTCCAGACTGAGACGTAGAAGA------CACTAA
4. Gorilla  Gorilla gorilla gorilla                               CAGAGGAGAGCCATGAGGTGCTGTCGCCGCAGGAACAGACTGAGACGTAGAAAA------CACTAA
5. Sumatran_orangutan  Pongo abelii                               CGGAGGAGGGCCATGAGGTGCTGCCGCCGCAGGTACAGACTGAGATGTAGAAGA------CACTAA
6. Lar_gibbon  Hylobates lar                                      CGCAGGAGAGCCATGAGGTGCTGCCGCCCCAGGTACAGGCTGAGACGTAGAAGA------CACTAA
7. Black_SN_monkey  Rhinopithecus bieti                           CGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
8. Golden_SN_monkey  Rhinopithecus roxellana                      CGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
9. Angola_colobus  Colobus angolensis palliatus                   CGGAAGAGAGCCATGAGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
10. Ugandan_red_colobus  Piliocolobus tephrosceles                CGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTACAGGCGGAGGTGTAGAAGA------TACTAA
11. Olive_baboon  Papio anubis                                    CGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
12. Sooty_mangabey  Cercocebus atys                               CGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
13. Drill  Mandrillus leucophaeus                                 CGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
14. Green_monkey  Chlorocebus sabaeus                             CGGAGGAGAGCCATGAGGTACTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
15. Southern_PT_macaque  Macaca nemestrina                        CGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
16. Rhesus_macaque  Macaca mulatta                                CGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
17. CE_macaque  Macaca fascicularis                               CGGAGGAGAGCCATGAGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
18. WH_capuchin  Cebus capucinus imitator                         CGGAGA---GCCAGGAGGTGCTGCCGCCGCAGGTACAGACTGAGGTGTAGAAGA------TACTAA
19. BC_squirrel_monkey  Saimiri boliviensis boliviensi            CAGAGA---GCCACGAGGTGCTGCCACCGCAGGTACAGGCTGAGGTATAGAAGA------TACTAA
20. NM_night_monkey  Aotus nancymaae                              CGGACA---GCCAGGAGGTGCGGCCGCCGCAGGTATAAGCCGCGGTGTAGAAGA------AACTAA
21. Common_marmoset  Callithrix jacchus                           CGGAGG---GCCAGCAGGTGCTGCCGCCGCAGGTACAAGCTGCCATGTAGAAGA------TACTAA
22. Philippine_tarsier  Carlito syrichta                          CGCAGA---ACCAGGAGGTGCTGCCGCCGCTCCTTCCGGCTGAGGTGTAGAAGA------TACTGA
23. Gray_mouse_lemur  Microcebus murinus                          AGGAGG------AGGAGGTGCTGCCGCCGCAGGTACAGG------TGTAGAAGAAGAAGATACTAA
24. Coquerels_sifaka  Propithecus coquereli                       AGGAGG------AGGAGGTGCTACCGCCGCAGGTACAGG------TGTAGAAGAAGA---TACTAA
25. Northern_greater_galago  Otolemur garnettii                   CGGAGG------AGGAGGTGCTGCCGCCGCAGGTACAGGCTGAGGTGTAGAAGA------TACTAA
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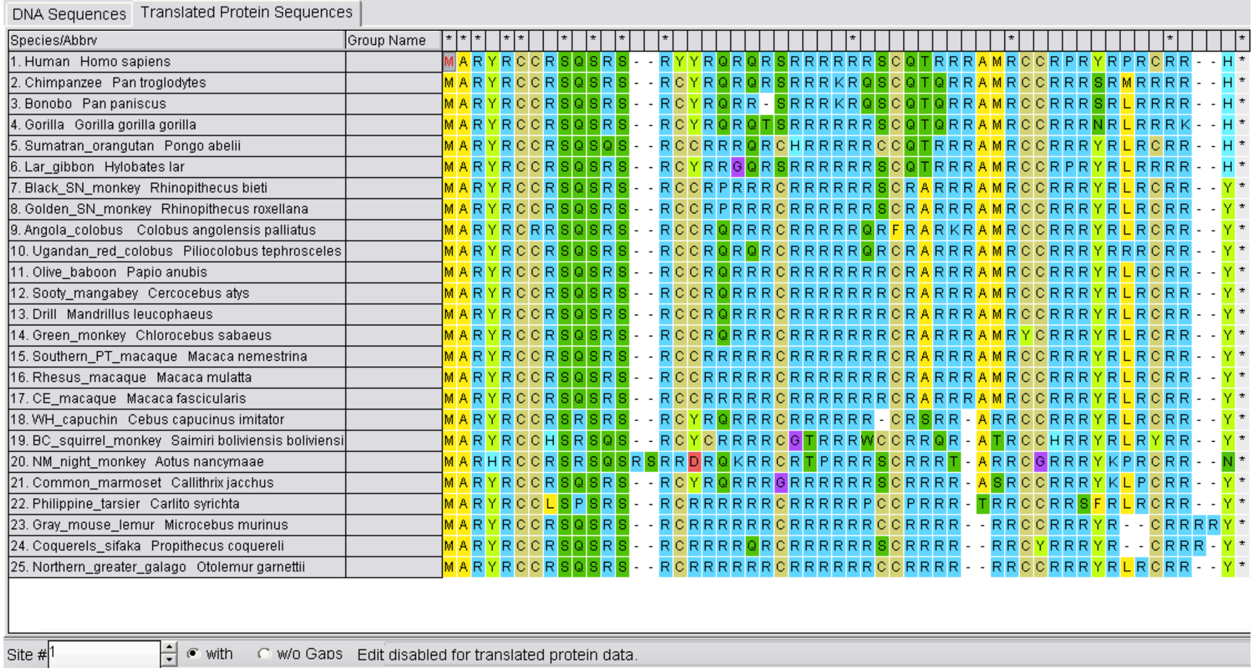
Site # 136 ● with ○ w/o Gaps

E2) Translated alignment, showing primate *Prm1* amino acid coding sequences



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Species/Abbrv                                           Group Name
                                                                  *** **  * * *  *            *          *          *    *
1. Human  Homo sapiens                                            MARYRCCRSQSRS--RYYRQRQRSRRRRRRSCQTRRRAMRCCRPRYRPRCRR--H*
2. Chimpanzee  Pan troglodytes                                    MARYRCCRSQSRS--RCYRQRQRSRRRKRQSCQTQRRAMRCCRRRSRMRRRR--H*
3. Bonobo  Pan paniscus                                           MARYRCCRSQSRS--RCYRQRR-SRRRKRQSCQTQRRAMRCCRRRSRLRRRR--H*
4. Gorilla  Gorilla gorilla gorilla                               MARYRCCRSQSRS--RCYRQRQTSRRRRRRSCQTQRRAMRCCRRRNRLRRRK--H*
5. Sumatran_orangutan  Pongo abelii                               MARYRCCRSQSQS--RCCRRRQRCHRRRRRCCQTRRRAMRCCRRRYRLRCRR--H*
6. Lar_gibbon  Hylobates lar                                      MARYRCCRSQSRS--RCYRRGQRSRRRRRRSCQTRRRAMRCCRPRYRLRRRR--H*
7. Black_SN_monkey  Rhinopithecus bieti                           MARYRCCRSQSRS--RCCRPRRRCRRRRRRSCRARRRAMRCCRRRYRLRCRR--Y*
8. Golden_SN_monkey  Rhinopithecus roxellana                      MARYRCCRSQSRS--RCCRPRRRCRRRRRRSCRARRRAMRCCRRRYRLRCRR--Y*
9. Angola_colobus  Colobus angolensis palliatus                   MARYRCRRSQSRS--RCCRQRRRCRRRRRQRFRARKRAMRCCRRRYRLRCRR--Y*
10. Ugandan_red_colobus  Piliocolobus tephrosceles                MARYRCCRSQSRS--RCCRQRQRCRRRRRQRCRARRRAMRCCRRRYRRRCRR--Y*
11. Olive_baboon  Papio anubis                                    MARYRCCRSQSRS--RCCRQRRRCRRRRRRRCRARRRAMRCCRRRYRLRCRR--Y*
12. Sooty_mangabey  Cercocebus atys                               MARYRCCRSQSRS--RCCRQRRRCRRRRRRRCRARRRAMRCCRRRYRLRCRR--Y*
13. Drill  Mandrillus leucophaeus                                 MARYRCCRSQSRS--RCCRQRRRCRRRRRRRCRARRRAMRCCRRRYRLRCRR--Y*
14. Green_monkey  Chlorocebus sabaeus                             MARYRCCRSQSRS--RCCRQRRRCRRRRRRRCRARRRAMRYCRRRYRLRCRR--Y*
15. Southern_PT_macaque  Macaca nemestrina                        MARYRCCRSQSRS--RCCRRRRRCRRRRRRRCRARRRAMRCCRRRYRLRCRR--Y*
16. Rhesus_macaque  Macaca mulatta                                MARYRCCRSQSRS--RCCRRRRRCRRRRRRRCRARRRAMRCCRRRYRLRCRR--Y*
17. CE_macaque  Macaca fascicularis                               MARYRCCRSQSRS--RCCRRRRRCRRRRRRRCRARRRAMRCCRRRYRLRCRR--Y*
18. WH_capuchin  Cebus capucinus imitator                         MARYRCCRSRSRS--RCYRQRRRCRRRRRR-CRSRR-ARRCCRRRYRLRCRR--Y*
19. BC_squirrel_monkey  Saimiri boliviensis boliviensi            MARYRCCHSRSQS--RCYCRRRRCGTRRRWCCRRQR-ATRCCHRRYRLRYRR--Y*
20. NM_night_monkey  Aotus nancymaae                              MARHRCCRSRSQSRSRRDRQKRRCRTPRRRSCRRRT-ARRCGRRRYKPRCRR--N*
21. Common_marmoset  Callithrix jacchus                           MARYRCCRSQSRS--RCYRQRRRGRRRRRRSCRRRR-ASRCCRRRYKLPCRR--Y*
22. Philippine_tarsier  Carlito syrichta                          MARYRCCLSPSRS--RCRRRRRRCRRRRRPCCPRRR-TRRCCRRSFRLRCRR--Y*
23. Gray_mouse_lemur  Microcebus murinus                          MARYRCCRSQSRS--RCRRRRRRCRRRRRRCCRRRR--RRCCRRRYR--CRRRRY*
24. Coquerels_sifaka  Propithecus coquereli                       MARYRCCRSQSRS--RCRRRRQRCRRRRRRSCRRRR--RRCYRRRYR--CRRR-Y*
25. Northern_greater_galago  Otolemur garnettii                   MARYRCCRSQSRS--RCRRRRRRCRRRRRRCCRRRR--RRCCRRRYRLRCRR--Y*
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Site # 1 ● with ○ w/o Gaps Edit disabled for translated protein data.

Appendix F) Alignment of primate *Prm2* full-length gene sequences

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Species/Abbrv                                        Group Name  ********   *      ** ****  *** * *                   *  *          
1. Human_mRNA  Homo sapiens                                      ATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGAGGTGTACAGGCAGCAGTTGCATG
2. Human  Homo sapiens                                           ATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGAGGTGTACAGGCAGCAGTTGCATG
3. Chimpanzee  Pan troglodytes                                   ATGGTCCGATACCGCGTGAGGAGCCCGAGCGAACCCTCGCACGAGGTGTACAGGCAGCAGTTGCATG
4. Bonobo  Pan paniscus                                          ATGGTCCGATACCGCGTGAGGAGCCCGAGCGAACCCTCGCACGAGGTGTACAGGCAGCAGTTGCATG
5. Gorilla  Gorilla gorilla gorilla                              ATGGTCCGACGCCGCGTGAGGAGCCCGAGCGAACGCTCGCACGAGGTGTACAGGCAGCAGTTGCATG
6. Sumatran_orangutan  Pongo abelii                             ATGGTCCGATACTGTGTGAGGAGCCTGAGCGAACGCTCGCACGAGGTGTACGGGCAGCAGTTGCATG
7. Lar_gibbon  Hylobates lar                                     ATGGTCCGATACTGCGTGAGGAGCCTGAGCGAACGCTCGCACGAGGTGTACGGGCAGCAGTTGCGTG
8. Black_SN_monkey  Rhinopithecus bieti                          ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
9. Golden_SN_monkey  Rhinopithecus roxellana                     ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCATGGGCAGCAGGTGCATG
10. Angolan_colobus  Colobus angolensis palliatus                ATGGTCCGATACCACATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACAGGCAGCAGGTGCATG
11. Ugandan_red_colobus  Piliocolobus tephrosceles               ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCAGGAGGTGCACGGGCAGCAGCTGCATG
12. Olive_baboon  Papio anubis                                   ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCG---------CACGGGCAGCAGGTGCATG
13. Sooty_mangabey  Cercocebus atys                              ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
14. Drill  Mandrillus leucophaeus                                ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
15. Green_monkey  Chlorocebus sabaeus                            ATGGTCCGATACCGCACCAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCACG
16. Southern_PT_macaque  Macaca nemestrina                       ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
17. Rhesus_macaque  Macaca mulatta                               ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
18. CE_macaque  Macaca fascicularis                              ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
19. WH_capuchin  Cebus capucinus                                 ATGGTCCGATGCCGCTTGAGGAGCCCGAGCGAACGCCCACACGAGGAGTACAGGCAGCTGGTGAACG
20. BC_squirrel_monkey  Saimiri boliviensis boliviensi            ATGGTCCGATACCGCTTGAGGAGCCCGAGCGAACGCCCACACGAGGAGTACAGGCAGCTGGTGAACA
21. NM_night_monkey  Aotus nancymaae                             ATGGTCCGATACCACGGGAGGAGCCCGAGCGAACGCCTCTACGAGGAGCACAGGCAGCTGGTGAACA
22. Common_marmoset  Callithrix jacchus                          ATGGTCCGATACCGCGTGAGGAGCCCGAGCGAACGCCCACACGAGGAGTACAGGCAGCTGGTGAACT
23. Philippine_tarsier  Carlito syrichta                         ATGGTCCGCCACCGCGGGAGCAGCCCGAGCCAGCACCCCGCCCCAGGGCTCCCAGGTGCAGGGCCATA
24. Gray_mouse_lemur  Microcebus murinus                         ATGGTCCGGTACCGGGAGAGGAGCCCCAGCGAGCGCCCGCACCAGGGGTATAGGCAGCAAGGGCACG
25. Coquerels_sifaka  Propithecus coquereli                      ATGGTCCGGTACCGCGAGAGGAGCCCCAGCGAACGCCCGCACCAGGGGTACAGGCAGCAAGGGCACG
26. Northern_greater_galago  Otolemur garnettii                  ATGGTCCGGTACCGTGTGAGGAGCCCCAGCGAACATGCGAACCAGGGGTTGAGGCAGGAAGGGCATG
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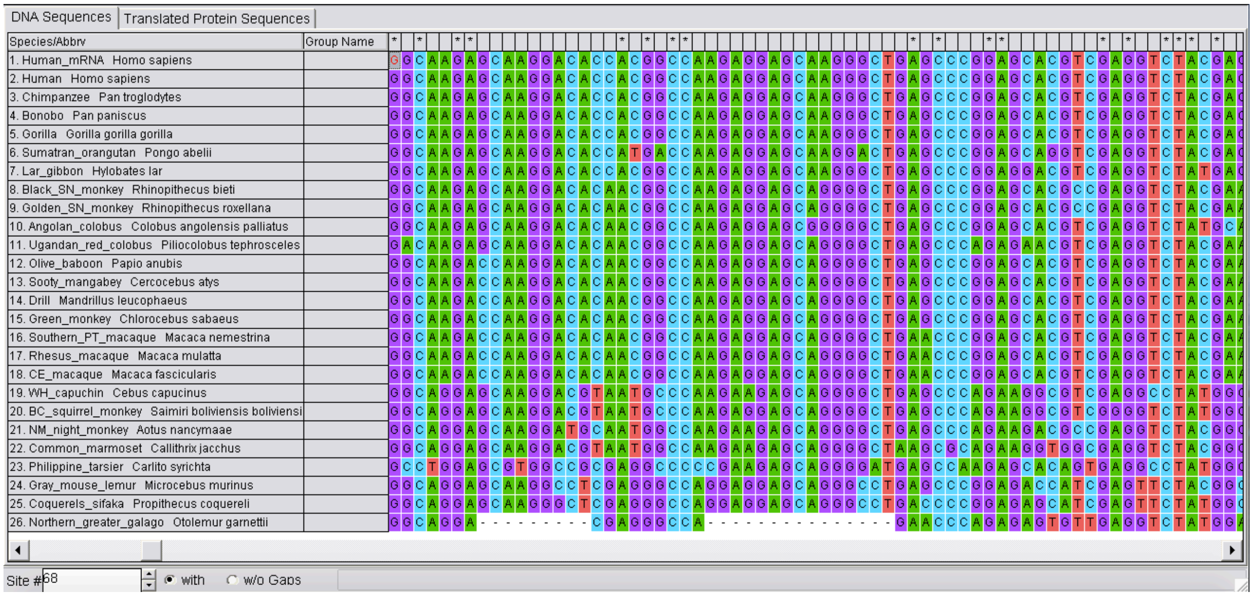

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Species/Abbrv                                        Group Name  * *  **           * * **                 * *   **       * *  *** * 
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2. Human  Homo sapiens                                           GGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
3. Chimpanzee  Pan troglodytes                                   GGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
4. Bonobo  Pan paniscus                                          GGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
5. Gorilla  Gorilla gorilla gorilla                              GGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
6. Sumatran_orangutan  Pongo abelii                             GGCAAGAGCAAGGACACCATGACCAAGAGGAGCAAGGACTGAGCCCGGAGCAGGTCGAGGTCTACGA
7. Lar_gibbon  Hylobates lar                                     GGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGGACGTCGAGGTCTATGA
8. Black_SN_monkey  Rhinopithecus bieti                          GGCAAGAGCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGCCGAGGTCTACGA
9. Golden_SN_monkey  Rhinopithecus roxellana                     GGCAAGAGCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGCCGAGGTCTACGA
10. Angolan_colobus  Colobus angolensis palliatus                GGCAAGAGCAAGGACACAACGGCCAAGAGGAGCGGGGGCTGAGCCCGGAGCACGTCGAGGTCTATGC
11. Ugandan_red_colobus  Piliocolobus tephrosceles               GACAAGAGCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCAGAGAACGTCGAGGTCTACGA
12. Olive_baboon  Papio anubis                                   GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
13. Sooty_mangabey  Cercocebus atys                              GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
14. Drill  Mandrillus leucophaeus                                GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
15. Green_monkey  Chlorocebus sabaeus                            GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
16. Southern_PT_macaque  Macaca nemestrina                       GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAACCCGGAGCACGTCGAGGTCTACGA
17. Rhesus_macaque  Macaca mulatta                               GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAACCCGGAGCACGTCGAGGTCTACGA
18. CE_macaque  Macaca fascicularis                              GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAACCCGGAGCACGTCGAGGTCTACGA
19. WH_capuchin  Cebus capucinus                                 GGCAGGAGCAAGGACGTAATGCCCAAGAAGAGCAGGGGCTGAGCCCAGAAGGCGTCGAGGCCTATGG
20. BC_squirrel_monkey  Saimiri boliviensis boliviensi            GGCAGGAGCAAGGACGTAATGCCCAAGAGGAGCAGGGGCTGAGCCCAGAAGGCGTCGGGGTCTATGG
21. NM_night_monkey  Aotus nancymaae                             GGCAGGAGCAAGGATGCAATGGCCAAGAAGAGCAGGGGCTGAGCCCAGAAGACGCCGAGGTCTACGG
22. Common_marmoset  Callithrix jacchus                          GGCAGGAGCAAGGACGTAATGGCCAAGAAGAGCAGGGGCTAAGCGCAGAAGGTGGCGAGGTCTACGG
23. Philippine_tarsier  Carlito syrichta                         GCCTGGAGCGTGGCCGCGAGGCCCCCGAAGAGCAGGGGATGAGCCAAGAGCACAGTGAGGCCTATGG
24. Gray_mouse_lemur  Microcebus murinus                         GGCAGGAGCAAGGCCTCGAGGGCCAGGAGGAGCAGGGCCTGAGCCCGGAGACCATCGAGTTCTACGG
25. Coquerels_sifaka  Propithecus coquereli                      GGCAGGAGCAAGGGCTCGAGGGCCAGGAGGAGCAGGGCCTGACCCCGGAGAGCATCGAGTTCTATGG
26. Northern_greater_galago  Otolemur garnettii                  GGCAGGA---------CGAGGGCCA---------------GAACCCAGAGAGTGTTGAGGTCTATGG
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Species/Abbrv	Group Name	` **   * *               *                 *****`
1. Human_mRNA Homo sapiens		GAGGACCCAT---GGCCAGTCTCACTATAGGCGCAGA---CACTGCTCTCGAAGGAGGCTGCACCGGA
2. Human Homo sapiens		GAGGACCCAT---GGCCAGTCTCACTATAGGCGCAGA---CACTGCTCTCGAAGGAGGCTGCACCGGA
3. Chimpanzee Pan troglodytes		GAGGACCCAC---GGCCATTCTCACTATAGGCGCAGA---CACTGCTCTCGAAGGAGGCTGCGTCGGA
4. Bonobo Pan paniscus		GAGGACCCAC---GGCCATTCTCACTATAGGCGCAGA---CACTGCTCTCGAAGGAGGCTGCGCCGGA
5. Gorilla Gorilla gorilla gorilla		GAGGACCCAC---GGCCATTCTCACTATAGGCGCAGA---CACTGCTCTCAAAGGAGGCTGCGCCGGA
6. Sumatran_orangutan Pongo abelii		GAGGACCCAG---GGCCATTCTCACTATAGACGCAGG---CACTGCTCTCGAAGGAGGCTGCACCGGA
7. Lar_gibbon Hylobates lar		GAGGACCCAC---GGCCATTCTCACTATAGGCGCAGG---CACTGCTCTCGAAGGAGGCTGCACCGGA
8. Black_SN_monkey Rhinopithecus bieti		AAGGACCCACCAAGGCTACTCTCACCATAGGCGCAGG---CGCTGCTCTCGAAGGAGGCTGCACCGGA
9. Golden_SN_monkey Rhinopithecus roxellana		AAGGACCCACCAAGGCTACTCTCACCATAGGCGCAGG---CGCTGCTCTCGAAGGAGGCTGCACCGGA
10. Angolan_colobus Colobus angolensis palliatus		AAGGACCCACCGAGGCTACTCTCACCATAGGAGCAGG---AGCTGCTCTCGAAGGAGGCTGCACCGGA
11. Ugandan_red_colobus Piliocolobus tephrosceles		AAGGACCCACCAAGGCTACTCTCACCATAGGAGCAGG---CGCTGCTCTCGAAGGAGGCTGCACCGGA
12. Olive_baboon Papio anubis		AAGGACCCACCGAGGCCACTCTTACCATAGGCGCAGG---CGCTGCTCTCGAAGGAGGCTGCACCGGA
13. Sooty_mangabey Cercocebus atys		AAGGACCCACCGAGGCCACTCTTACCATAGGCGCAGG---CGCTGCTCTCGAAGGAGGCTGCACCGGA
14. Drill Mandrillus leucophaeus		AAGGACCCACCGAGGCCACTCTTACCATAGGCGCAGG---CGCTGCTCTCGAAGGAGGCTGCACCGGA
15. Green_monkey Chlorocebus sabaeus		AAGGACCCACCGAGGCCACTCTCCCCATAGGCGCAGG---CGCTGCTCTCGAAGGAGGCTGCACCGGA
16. Southern_PT_macaque Macaca nemestrina		AAGGACCCACCGAGGCCACTCTCACCATAGGCGCAGG---CGCTGCTCTCGAAGGAGGCTGCACCGGA
17. Rhesus_macaque Macaca mulatta		AAGGACCCACCGAGGCCACTCTCACCATAGGCGCAGG---CGCTGCTCTCGAAGGAGGCTGCACCGGA
18. CE_macaque Macaca fascicularis		AAGGACCCACCGAGGCCACTCTCACCATAGGCGCAGG---CGCTGCTCTCGAAGGAGGCTGCACCGGA
19. WH_capuchin Cebus capucinus		GAGGAGCCACCGAGTCTGCTATCGCTACAGGCGCAGG---CGCTGCTCTCGCAGACGGCTGTACCGGA
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		GAGAACCCACCGAACCTGCTATCGCCACAGGCGCAGG---CGCTGCTCTCGCAGGAGGCTGTACCGGA
21. NM_night_monkey Aotus nancymaae		GAGGACCCAGCGAGGCTGCTATCGCTATAGGCGCAGG---AGCTGCTCTCGCAGGAGGTTGAACCGGA
22. Common_marmoset Callithrix jacchus		GAGGACCCACCAAGGCTACTCTAGCTATAGGCGCAGG---CGCTGCTCTCGCAGGAGGCGGTACCGGA
23. Philippine_tarsier Carlito syrichta		GAGGGTCCACAGGGGTGGC---CACCGCTCCCGGCAACGGCGCTGCTNNNNNNNNNNNNNNNNNNNNN
24. Gray_mouse_lemur Microcebus murinus		CAGGACCTACCGAGGCCGC---CGCTGCAGGCGCAGGCGGCGCTGCTCTCGGAGGAGGCTGTGCCGGA
25. Coquerels_sifaka Propithecus coquereli		CAGGACCTACCAAGGCCGC---CGCTGTAGGCGCAGG---CGCTGCTCTCGGAGGAGGCTGTGCCGGA
26. Northern_greater_galago Otolemur garnettii		AAGGACCTACCGAGGCCAC---CACCGTAGGCACAGG---CACTGCTCTCGGAGGAGACTGTACCGGA

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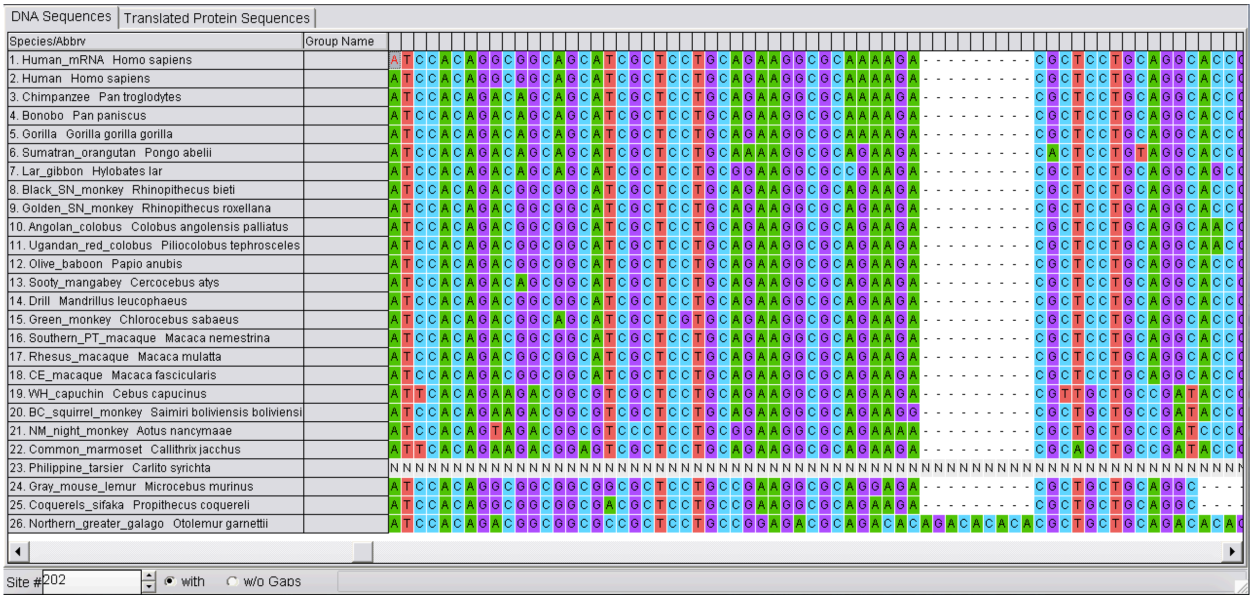

Species/Abbrv	Group Name	
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2. Human Homo sapiens		ATCCACAGGCGGCAGCATCGCTCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACC
3. Chimpanzee Pan troglodytes		ATCCACAGACAGCAGCATCGCTCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACC
4. Bonobo Pan paniscus		ATCCACAGACAGCAGCATCGCTCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACC
5. Gorilla Gorilla gorilla gorilla		ATCCACAGACAGCAGCATCGCTCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACC
6. Sumatran_orangutan Pongo abelii		ATCCACAGACAGCAGCATCGCTCCTGCAAAAGGCGCAGAAGA---------CACTCCTGTAGGCACC
7. Lar_gibbon Hylobates lar		ATCCACAGACAGCAGCATCGCTCCTGCGGAAGGCGCCGAAGA---------CGCTCCTGCAGGCAGC
8. Black_SN_monkey Rhinopithecus bieti		ATCCACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACC
9. Golden_SN_monkey Rhinopithecus roxellana		ATCCACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACC
10. Angolan_colobus Colobus angolensis palliatus		ATCCACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCAAC
11. Ugandan_red_colobus Piliocolobus tephrosceles		ATCCACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCAAC
12. Olive_baboon Papio anubis		ATCCACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACC
13. Sooty_mangabey Cercocebus atys		ATCCACAGACAGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACC
14. Drill Mandrillus leucophaeus		ATCCACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACC
15. Green_monkey Chlorocebus sabaeus		ATCCACAGACGGCAGCATCGCTCGTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACC
16. Southern_PT_macaque Macaca nemestrina		ATCCACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACC
17. Rhesus_macaque Macaca mulatta		ATCCACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACC
18. CE_macaque Macaca fascicularis		ATCCACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACC
19. WH_capuchin Cebus capucinus		ATTCACAGAAGACGGCGTCGCTCCTGCAGAAGGCGCAGAAGA---------CGTTGCTGCCGATACC
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		ATCCACAGAAGACGGCGTCGCTCCTGCAGAAGGCGCAGAAGG---------CGCTGCTGCCGATACC
21. NM_night_monkey Aotus nancymaae		ATCCACAGTAGACGGCGTCCCTCCTGCGGAAGGCGCAGAAAA---------CGCTGCTGCCGATCCC
22. Common_marmoset Callithrix jacchus		ATTCACAGAAGACGGAGTCGCTCCTGCAGAAGGCGCAGAAGA---------CGCAGCTGCCGATACC
23. Philippine_tarsier Carlito syrichta		NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
24. Gray_mouse_lemur Microcebus murinus		ATCCACAGGCGGCGGCGGCGCTCCTGCCGAAGGCGCAGGAGA---------CGCTGCTGCAGGC----
25. Coquerels_sifaka Propithecus coquereli		ATCCACAGGCGGCGGCGACGCTCCTGCCGAAGGCGCAGAAGA---------CGCTGCTGCAGGC----
26. Northern_greater_galago Otolemur garnettii		ATCCACAGACGGCGGCGCCGCTCCTGCCGGAGACGCAGACACAGACACACACGCTGCTGCAGACACA

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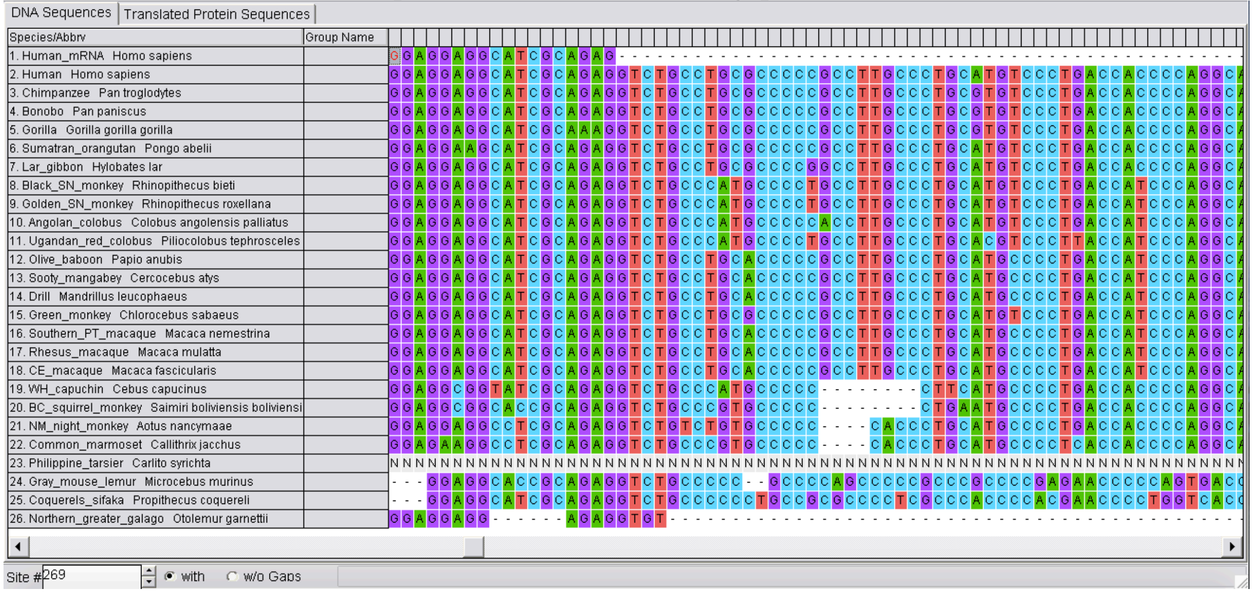

Species/Abbrv	Group Name	
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2. Human Homo sapiens		GGAGGAGGCATCGCAGAGGTCTGCCTGCGCCCCCGCCTTGCCCTGCATGTCCCTGACCACCCCAGGCA
3. Chimpanzee Pan troglodytes		GGAGGAGGCATCGCAGAGGTCTGCCTGCGCCCCCGCCTTGCCCTGCGTGTCCCTGACCACCCCAGGCA
4. Bonobo Pan paniscus		GGAGGAGGCATCGCAGAGGTCTGCCTGCGCCCCCGCCTTGCCCTGCGTGTCCCTGACCACCCCAGGCA
5. Gorilla Gorilla gorilla gorilla		GGAGGAGGCATCGCAAAGGTCTGCCTGCGCCCCCGCCTTGCCCTGCGTGTCCCTGACCACCCCAGGCA
6. Sumatran_orangutan Pongo abelii		GGAGGAAGCATCGCAGAGGTCTGCCTGCGCCCCCGCCTTGCCCTGCATGTCCCTGACCACCCCAGGCA
7. Lar_gibbon Hylobates lar		GGAGGAGGCATCGCAGAGGTCTGCCTGCGCCCCGGCCTTGCCCTGCATGTCCCTGACCACCCCAGGCA
8. Black_SN_monkey Rhinopithecus bieti		GGAGGAGGCATCGCAGAGGTCTGCCCATGCCCCTGCCTTGCCCTGCATGTCCCTGACCATCCCAGGCA
9. Golden_SN_monkey Rhinopithecus roxellana		GGAGGAGGCATCGCAGAGGTCTGCCCATGCCCCTGCCTTGCCCTGCATGTCCCTGACCATCCCAGGCA
10. Angolan_colobus Colobus angolensis palliatus		GGAGGAGGCATCGCAGAGGTCTGCCCATGCCCCCACCTTGCCCTGCATGTCCCTGACCATCCCAGGCA
11. Ugandan_red_colobus Piliocolobus tephrosceles		GGAGGAGGCATCGCAGAGGTCTGCCCATGCCCCTGCCTTGCCCTGCACGTCCCTTACCATCCCAGGCA
12. Olive_baboon Papio anubis		GGAGGAGGCATCGCAGAGGTCTGCCTGCACCCCCGCCTTGCCCTGCATGCCCCTGACCATCCCAGGCA
13. Sooty_mangabey Cercocebus atys		GGAGGAGGCATCGCAGAGGTCTGCCTGCACCCCCGCCTTGCCCTGCATGCCCCTGACCATCCCAGGCA
14. Drill Mandrillus leucophaeus		GGAGGAGGCATCGCAGAGGTCTGCCTGCACCCCCGCCTTGCCCTGCATGCCCCTGACCATCCCAGGCA
15. Green_monkey Chlorocebus sabaeus		GGAGGAGGCATCGCAGAGGTCTGCCTGCGCCCCCGCCTTGCCCTGCATGTCCCTGACCATCCCAGGCA
16. Southern_PT_macaque Macaca nemestrina		GGAGGAGGCATCGCAGAGGTCTGCCTGCACCCCCGCCTTGCCCTGCATGCCCCTGACCATCCCAGGCA
17. Rhesus_macaque Macaca mulatta		GGAGGAGGCATCGCAGAGGTCTGCCTGCACCCCCGCCTTGCCCTGCATGCCCCTGACCATCCCAGGCA
18. CE_macaque Macaca fascicularis		GGAGGAGGCATCGCAGAGGTCTGCCTGCACCCCCGCCTTGCCCTGCATGCCCCTGACCATCCCAGGCA
19. WH_capuchin Cebus capucinus		GGAGGCGGTATCGCAGAGGTCTGCCCATGCCCCC--------CTTCATGCCCCTGACCACCCCAGGCA
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		GGAGGCGGCACCGCAGAGGTCTGCCCGTGCCCCC--------CTGAATGCCCCTGACCACCCCAGGCA
21. NM_night_monkey Aotus nancymaae		GGAGGAGGCCTCGCAGAGGTCTGTCTGTGCCCCC----CACCCTGCATGCCCCTGACCACCCCAGGCA
22. Common_marmoset Callithrix jacchus		GGAGAAGGCCTCGCAGAGGTCTGCCCGTGCCCCC----CACCCTGCATGCCCCTCACCACCCCAGGCA
23. Philippine_tarsier Carlito syrichta		NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
24. Gray_mouse_lemur Microcebus murinus		---GGAGGCACCGCAGAGGTCTGCCCCC--GCCCCAGCCCCCGCCCGCCCCGAGAACCCCCAGTGACC
25. Coquerels_sifaka Propithecus coquereli		---GGAGGCATCGCAGAGGTCTGCCCCCCTGCCGCGCCCCTCGCCCACCCCACGAACCCCTGGTCACC
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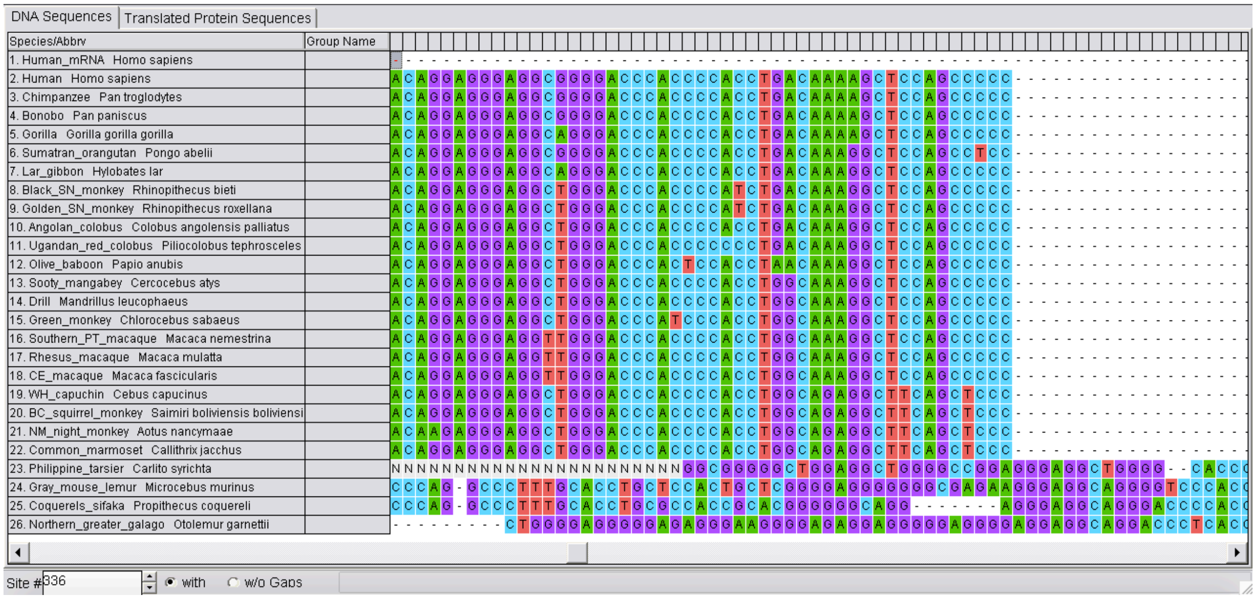

Species/Abbrv	Group Name	
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2. Human Homo sapiens		ACAGGAGGGAGGCGGGGACCCACCCCACCTGACAAAAGCTCCAGCCCCC-------------------
3. Chimpanzee Pan troglodytes		ACAGGAGGGAGGCGGGGACCCACCCCACCTGACAAAAGCTCCAGCCCCC-------------------
4. Bonobo Pan paniscus		ACAGGAGGGAGGCGGGGACCCACCCCACCTGACAAAAGCTCCAGCCCCC-------------------
5. Gorilla Gorilla gorilla gorilla		ACAGGAGGGAGGCAGGGACCCACCCCACCTGACAAAAGCTCCAGCCCCC-------------------
6. Sumatran_orangutan Pongo abelii		ACAGGAGGGAGGCGGGGACCCACCCCACCTGACAAAGGCTCCAGCCTCC-------------------
7. Lar_gibbon Hylobates lar		ACAGGAGGGAGGCAGGGACCCACCCCACCTGACAAAGGCTCCAGCCCCC-------------------
8. Black_SN_monkey Rhinopithecus bieti		ACAGGAGGGAGGCTGGGACCCACCCCATCTGACAAAGGCTCCAGCCCCC-------------------
9. Golden_SN_monkey Rhinopithecus roxellana		ACAGGAGGGAGGCTGGGACCCACCCCATCTGACAAAGGCTCCAGCCCCC-------------------
10. Angolan_colobus Colobus angolensis palliatus		ACAGGAGGGAGGCTGGGACCCACCCCACCTGACAAAGGCTCCAGCCCCC-------------------
11. Ugandan_red_colobus Piliocolobus tephrosceles		ACAGGAGGGAGGCTGGGACCCACCCCCCCTGACAAAGGCTCCAGCCCCC-------------------
12. Olive_baboon Papio anubis		ACAGGAGGGAGGCTGGGACCCACTCCACCTAACAAAGGCTCCAGCCCCC-------------------
13. Sooty_mangabey Cercocebus atys		ACAGGAGGGAGGCTGGGACCCACCCCACCTGGCAAAGGCTCCAGCCCCC-------------------
14. Drill Mandrillus leucophaeus		ACAGGAGGGAGGCTGGGACCCACCCCACCTGGCAAAGGCTCCAGCCCCC-------------------
15. Green_monkey Chlorocebus sabaeus		ACAGGAGGGAGGCTGGGACCCATCCCACCTGGCAAAGGCTCCAGCCCCC-------------------
16. Southern_PT_macaque Macaca nemestrina		ACAGGAGGGAGGTTGGGACCCACCCCACCTGGCAAAGGCTCCAGCCCCC-------------------
17. Rhesus_macaque Macaca mulatta		ACAGGAGGGAGGTTGGGACCCACCCCACCTGGCAAAGGCTCCAGCCCCC-------------------
18. CE_macaque Macaca fascicularis		ACAGGAGGGAGGTTGGGACCCACCCCACCTGGCAAAGGCTCCAGCCCCC-------------------
19. WH_capuchin Cebus capucinus		ACAGGAGGGAGGCTGGGACCCACCCCACCTGGCAGAGGCTTCAGCTCCC-------------------
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		ACAGGAGGGAGGCTGGGACCCACCCCACCTGGCAGAGGCTTCAGCTCCC-------------------
21. NM_night_monkey Aotus nancymaae		ACAAGAGGGAGGCTGGGACCCACCCCACCTGGCAGAGGCTTCAGCTCCC-------------------
22. Common_marmoset Callithrix jacchus		ACAGGAGGGAGGCTGGGACCCACCCCACCTGGCAGAGGCTTCAGCTCCC-------------------
23. Philippine_tarsier Carlito syrichta		NNNNNNNNNNNNNNNNNNNNNNNGGCGGGGGCTGGAGGCTGGGGCCGGAGGGAGGCTGGGG--CACCC
24. Gray_mouse_lemur Microcebus murinus		CCCAG-GCCCTTTGCACCTGCTCCACTGCTCGGGGAGGGGGGGCGAGAAGGGAGGCAGGGGTCCCACC
25. Coquerels_sifaka Propithecus coquereli		CCCAG-GCCCTTTGCACCTGCGCCACCGCACGGGGGGCAGG-------AGGGAGGCAGGGACCCCACC
26. Northern_greater_galago Otolemur garnettii		---------CTGGGGAGGGGGAGAGGGAAGGGGAGAGGAGGGGGAGGGGAGGAGGCAGGACCCTCACC

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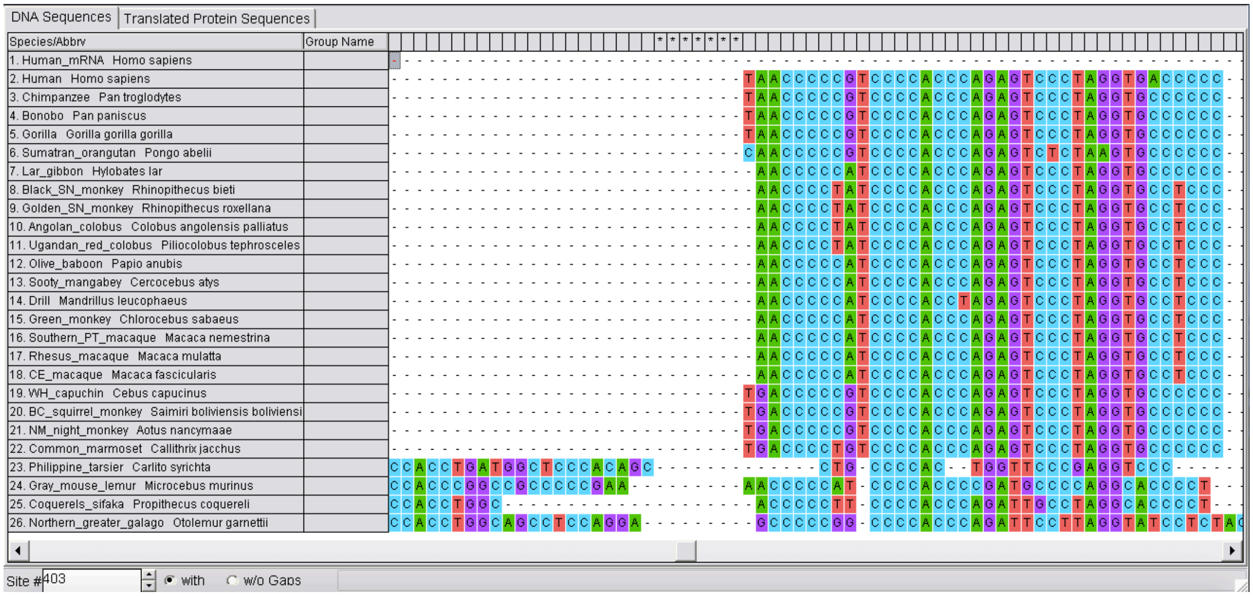

DNA Sequences | Translated Protein Sequences

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Species/Abbrv                                          Group Name                      *******                                        
1. Human_mRNA  Homo sapiens                                       --------------------------------------------------------------------
2. Human  Homo sapiens                                            ----------------------------TAACCCCCGTCCCCACCCAGAGTCCCTAGGTGACCCCC--
3. Chimpanzee  Pan troglodytes                                    ----------------------------TAACCCCCGTCCCCACCCAGAGTCCCTAGGTGCCCCCC--
4. Bonobo  Pan paniscus                                           ----------------------------TAACCCCCGTCCCCACCCAGAGTCCCTAGGTGCCCCCC--
5. Gorilla  Gorilla gorilla gorilla                               ----------------------------TAACCCCCGTCCCCACCCAGAGTCCCTAGGTGCCCCCC--
6. Sumatran_orangutan  Pongo abelii                               ----------------------------CAACCCCCGTCCCCACCCAGAGTCTCTAAGTGCCCCCC--
7. Lar_gibbon  Hylobates lar                                      -----------------------------AACCCCCATCCCCACCCAGAGTCCCTAGGTGCCCCCC--
8. Black_SN_monkey  Rhinopithecus bieti                           -----------------------------AACCCCTATCCCCACCCAGAGTCCCTAGGTGCCTCCC--
9. Golden_SN_monkey  Rhinopithecus roxellana                      -----------------------------AACCCCTATCCCCACCCAGAGTCCCTAGGTGCCTCCC--
10. Angolan_colobus  Colobus angolensis palliatus                 -----------------------------AACCCCTATCCCCACCCAGAGTCCCTAGGTGCCTCCC--
11. Ugandan_red_colobus  Piliocolobus tephrosceles                -----------------------------AACCCCTATCCCCACCCAGAGTCCCTAGGTGCCTCCC--
12. Olive_baboon  Papio anubis                                    -----------------------------AACCCCCATCCCCACCCAGAGTCCCTAGGTGCCTCCC--
13. Sooty_mangabey  Cercocebus atys                               -----------------------------AACCCCCATCCCCACCCAGAGTCCCTAGGTGCCTCCC--
14. Drill  Mandrillus leucophaeus                                 -----------------------------AACCCCCATCCCCACCTAGAGTCCCTAGGTGCCTCCC--
15. Green_monkey  Chlorocebus sabaeus                             -----------------------------AACCCCCATCCCCACCCAGAGTCCCTAGGTGCCTCCC--
16. Southern_PT_macaque  Macaca nemestrina                        -----------------------------AACCCCCATCCCCACCCAGAGTCCCTAGGTGCCTCCC--
17. Rhesus_macaque  Macaca mulatta                                -----------------------------AACCCCCATCCCCACCCAGAGTCCCTAGGTGCCTCCC--
18. CE_macaque  Macaca fascicularis                               -----------------------------AACCCCCATCCCCACCCAGAGTCCCTAGGTGCCTCCC--
19. WH_capuchin  Cebus capucinus                                  ----------------------------TGACCCCCGTCCCCACCCAGAGTCCCTAGGTGCCCCCC--
20. BC_squirrel_monkey  Saimiri boliviensis boliviensi            ----------------------------TGACCCCCGTCCCCACCCAGAGTCCCTAGGTGCCCCCC--
21. NM_night_monkey  Aotus nancymaae                              ----------------------------TGACCCCCGTCCCCACCCAGAGTCCCTAGGTGCCCCCC--
22. Common_marmoset  Callithrix jacchus                            ----------------------------TGACCCCTGTCCCCACCCAGAGTCCCTAGGTGCCCCCC--
23. Philippine_tarsier  Carlito syrichta                          CCACCTGATGGCTCCCACAGC-------------CTG-CCCCAC--TGGTTCCCGAGGTCCC------
24. Gray_mouse_lemur  Microcebus murinus                          CCACCCGGCCGCCCCCGAA---------AACCCCCAT-CCCCACCCCGATGCCCCAGGCACCCCT---
25. Coquerels_sifaka  Propithecus coquereli                       CCACCTGGC--------------------ACCCCCTT-CCCCACCCAGATTGCCTAGGCACCCCT---
26. Northern_greater_galago  Otolemur garnettii                   CCACCTGGCAGCCTCCAGGA---------GCCCCCGG-CCCCACCCAGATTCCTTAGGTATCCTCTAC
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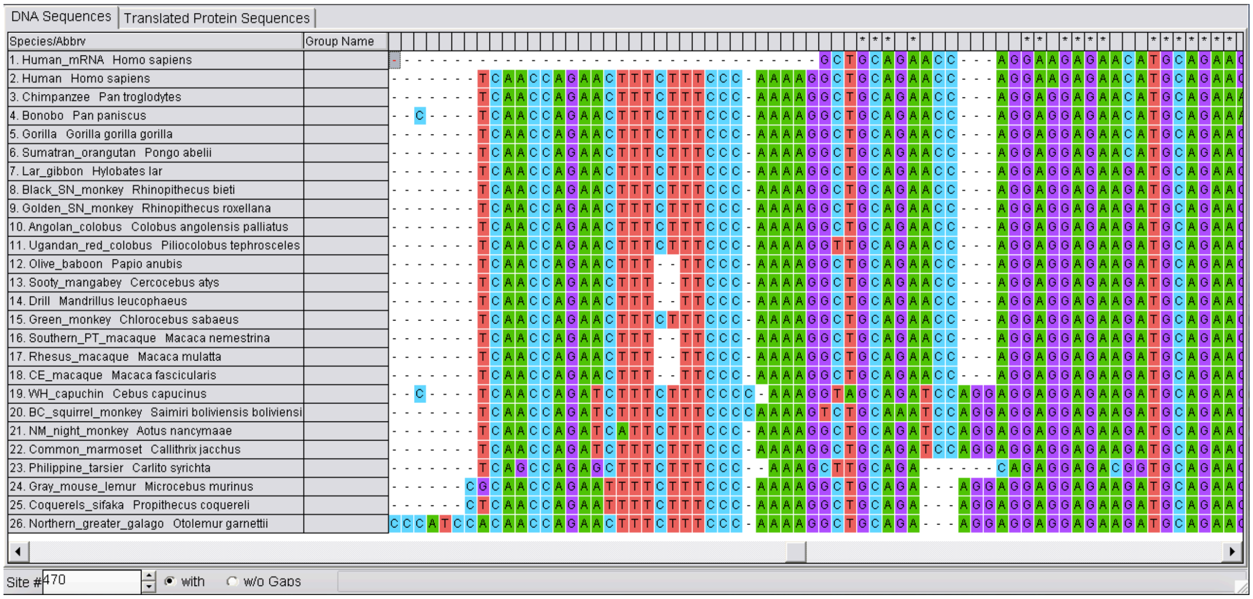
Site # 403 ● with ○ w/o Gaps



DNA Sequences | Translated Protein Sequences

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Species/Abbrv                                          Group Name                                        *** *        ** ****   ******* 
1. Human_mRNA  Homo sapiens                                       ----------------------------------GCTGCAGAACC---AGGAAGAGAACATGCAGAAC
2. Human  Homo sapiens                                            -------TCAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAAGAGAACATGCAGAAC
3. Chimpanzee  Pan troglodytes                                    -------TCAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAA
4. Bonobo  Pan paniscus                                           --C----TCAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAA
5. Gorilla  Gorilla gorilla gorilla                               -------TCAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAC
6. Sumatran_orangutan  Pongo abelii                               -------TCAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAC
7. Lar_gibbon  Hylobates lar                                      -------TCAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
8. Black_SN_monkey  Rhinopithecus bieti                           -------TCAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
9. Golden_SN_monkey  Rhinopithecus roxellana                      -------TCAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
10. Angolan_colobus  Colobus angolensis palliatus                 -------TCAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
11. Ugandan_red_colobus  Piliocolobus tephrosceles                -------TCAACCAGAACTTTCTTTCCC-AAAAGGTTGCAGAACC---AGGAGGAGAAGATGCAGAAC
12. Olive_baboon  Papio anubis                                    -------TCAACCAGAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
13. Sooty_mangabey  Cercocebus atys                               -------TCAACCAGAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
14. Drill  Mandrillus leucophaeus                                 -------TCAACCAGAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
15. Green_monkey  Chlorocebus sabaeus                             -------TCAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
16. Southern_PT_macaque  Macaca nemestrina                        -------TCAACCAGAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
17. Rhesus_macaque  Macaca mulatta                                -------TCAACCAGAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
18. CE_macaque  Macaca fascicularis                               -------TCAACCAGAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAC
19. WH_capuchin  Cebus capucinus                                  --C----TCAACCAGATCTTTCTTTCCCC-AAAGGTAGCAGATCCAGGAGGAGGAGAAGATGCAGAAC
20. BC_squirrel_monkey  Saimiri boliviensis boliviensi            -------TCAACCAGATCTTTCTTTCCCCAAAAGTCTGCAAATCCAGGAGGAGGAGAAGATGCAGAAC
21. NM_night_monkey  Aotus nancymaae                              -------TCAACCAGATCATTCTTTCCC-AAAAGGCTGCAGATCCAGGAGGAGGAGAAGATGCAGAAC
22. Common_marmoset  Callithrix jacchus                            -------TCAACCAGATCTTTCTTTCCC-AAAAGGCTGCAGATCCAGGAGGAGGAGAAGATGCAGAAC
23. Philippine_tarsier  Carlito syrichta                          -------TCAGCCAGAGCTTTCTTTCCC--AAAGCTTGCAGA------CAGAGGAGACGGTGCAGAAC
24. Gray_mouse_lemur  Microcebus murinus                          ------CGCAACCAGAATTTTCTTTCCC-AAAAGGCTGCAGA---AGGAGGAGGAGAAGATGCAGAAC
25. Coquerels_sifaka  Propithecus coquereli                       ------CTCAACCAGAATTTTCTTTCCC-AAAAGGCTGCAGA---AGGAGGAGGAGAAGATGCAGAAC
26. Northern_greater_galago  Otolemur garnettii                   CCCATCCACAACCAGAACTTTCTTTCCC-AAAAGGCTGCAGA---AGGAGGAGGAGAAGATGCAGAAC
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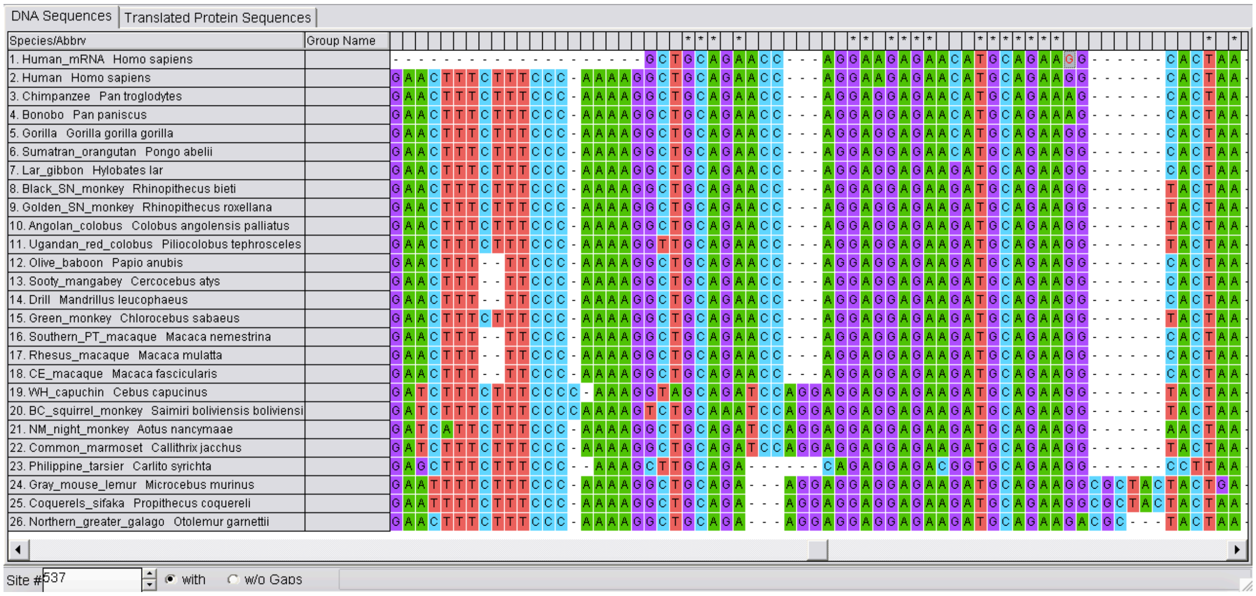
Site # 470 ● with ○ w/o Gaps



Species/Abbrv	Group Name	`                       *** *        ** ****   *******           * * `
1. Human_mRNA Homo sapiens		`--------------------GCTGCAGAACC---AGGAAGAGAACATGCAGAAGG------CACTAA-`
2. Human Homo sapiens		`GAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAAGAGAACATGCAGAAGG------CACTAA-`
3. Chimpanzee Pan troglodytes		`GAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAAG------CACTAA-`
4. Bonobo Pan paniscus		`GAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAAG------CACTAA-`
5. Gorilla Gorilla gorilla gorilla		`GAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAGG------CACTAA-`
6. Sumatran_orangutan Pongo abelii		`GAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAGG------CACTAA-`
7. Lar_gibbon Hylobates lar		`GAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA-`
8. Black_SN_monkey Rhinopithecus bieti		`GAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------TACTAA-`
9. Golden_SN_monkey Rhinopithecus roxellana		`GAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------TACTAA-`
10. Angolan_colobus Colobus angolensis palliatus		`GAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------TACTAA-`
11. Ugandan_red_colobus Piliocolobus tephrosceles		`GAACTTTCTTTCCC-AAAAGGTTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------TACTAA-`
12. Olive_baboon Papio anubis		`GAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA-`
13. Sooty_mangabey Cercocebus atys		`GAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA-`
14. Drill Mandrillus leucophaeus		`GAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA-`
15. Green_monkey Chlorocebus sabaeus		`GAACTTTCTTTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------TACTAA-`
16. Southern_PT_macaque Macaca nemestrina		`GAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA-`
17. Rhesus_macaque Macaca mulatta		`GAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA-`
18. CE_macaque Macaca fascicularis		`GAACTTT--TTCCC-AAAAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA-`
19. WH_capuchin Cebus capucinus		`GATCTTTCTTTCCCC-AAAGGTAGCAGATCCAGGAGGAGGAGAAGATGCAGAAGG------TACTAA-`
20. BC_squirrel_monkey Saimiri boliviensis boliviensi		`GATCTTTCTTTCCCCAAAAGTCTGCAAATCCAGGAGGAGGAGAAGATGCAGAAGG------TACTAA-`
21. NM_night_monkey Aotus nancymaae		`GATCATTCTTTCCC-AAAAGGCTGCAGATCCAGGAGGAGGAGAAGATGCAGAAGG------AACTAA-`
22. Common_marmoset Callithrix jacchus		`GATCTTTCTTTCCC-AAAAGGCTGCAGATCCAGGAGGAGGAGAAGATGCAGAAGG------TACTAA-`
23. Philippine_tarsier Carlito syrichta		`GAGCTTTCTTTCCC--AAAGCTTGCAGA------CAGAGGAGACGGTGCAGAAGG------CCTTAA-`
24. Gray_mouse_lemur Microcebus murinus		`GAATTTTCTTTCCC-AAAAGGCTGCAGA---AGGAGGAGGAGAAGATGCAGAAGGCGCTACTACTGA-`
25. Coquerels_sifaka Propithecus coquereli		`GAATTTTCTTTCCC-AAAAGGCTGCAGA---AGGAGGAGGAGAAGATGCAGAAGGCGCTACTACTAA-`
26. Northern_greater_galago Otolemur garnettii		`GAACTTTCTTTCCC-AAAAGGCTGCAGA---AGGAGGAGGAGAAGATGCAGAAGACGC---TACTAA-`

Site #537 ● with ○ w/o Gaps

Appendix G1) Alignment of primate *Prm1* coding exon nucleotide sequences

Species/Abbrv	Group Name	******** * ** **** *** * * * *
1. Human Homo sapiens		ATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGAGGTGTACAGGCAGCAGTTGCATG
2. Chimpanzee Pan troglodytes		ATGGTCCGATACCGCGTGAGGAGCCCGAGCGAACCCTCGCACGAGGTGTACAGGCAGCAGTTGCATG
3. Bonobo Pan paniscus		ATGGTCCGATACCGCGTGAGGAGCCCGAGCGAACCCTCGCACGAGGTGTACAGGCAGCAGTTGCATG
4. Gorilla Gorilla gorilla gorilla		ATGGTCCGACGCCGCGTGAGGAGCCCGAGCGAACGCTCGCACGAGGTGTACAGGCAGCAGTTGCATG
5. Sumatran_orangutan Pongo abelii		ATGGTCCGATACTGTGTGAGGAGCCTGAGCGAACGCTCGCACGAGGTGTACGGGCAGCAGTTGCATG
6. Lar_gibbon Hylobates lar		ATGGTCCGATACTGCGTGAGGAGCCTGAGCGAACGCTCGCACGAGGTGTACGGGCAGCAGTTGCGTG
7. Black_SN_monkey Rhinopithecus bieti		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
8. Golden_SN_monkey Rhinopithecus roxellana		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCATGGGCAGCAGGTGCATG
9. Angola_colobus Colobus angolensis palliatus		ATGGTCCGATACCACATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACAGGCAGCAGGTGCATG
10. Ugandan_red_colobus Piliocolobus tephrosceles		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCAGGAGGTGCACGGGCAGCAGCTGCATG
11. Olive_baboon Papio anubis		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCAC---------GGGCAGCAGGTGCATG
12. Sooty_mangabey Cercocebus atys		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
13. Drill Mandrillus leucophaeus		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
14. Green_monkey Chlorocebus sabaeus		ATGGTCCGATACCGCACCAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCACG
15. Southern_PT_macaque Macaca nemestrina		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
16. Rhesus_macaque Macaca mulatta		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
17. CE_macaque Macaca fascicularis		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGTGCATG
18. WH_capuchin Cebus capucinus imitator		ATGGTCCGATGCCGCTTGAGGAGCCCGAGCGAACGCCCACACGAGGAGTACAGGCAGCTGGTGAACG
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		ATGGTCCGATACCGCTTGAGGAGCCCGAGCGAACGCCCACACGAGGAGTACAGGCAGCTGGTGAACA
20. NM_night_monkey Aotus nancymaae		ATGGTCCGATACCACGGGAGGAGCCCGAGCGAACGCCTCTACGAGGAGCACAGGCAGCTGGTGAACA
21. Common_marmoset Callithrix jacchus		ATGGTCCGATACCGCGTGAGGAGCCCGAGCGAACGCCCACACGAGGAGTACAGGCAGCTGGTGAACT
22. Philippine_tarsier Carlito syrichta		ATGGTCCGCCACCGCGGGAGCAGCCCGAGCCAGCACCCGCCCCAGGGCTCCCAGGTGCAGGGCCATA
23. Gray_mouse_lemur Microcebus murinus		ATGGTCCGGTACCGGGAGAGGAGCCCCAGCGAGCGCCCGCACCAGGGGTATAGGCAGCAAGGGCACG
24. Coquerels_sifaka Propithecus coquereli		ATGGTCCGGTACCGCGAGAGGAGCCCCAGCGAACGCCCGCACCAGGGGTACAGGCAGCAAGGGCACG
25. Northern_greater_galago Otolemur garnettii		ATGGTCCGGTACCGTGTGAGGAGCCCCAGCGAACATGCGAACCAGGGGTTGAGGCAGGAAGGGCATG

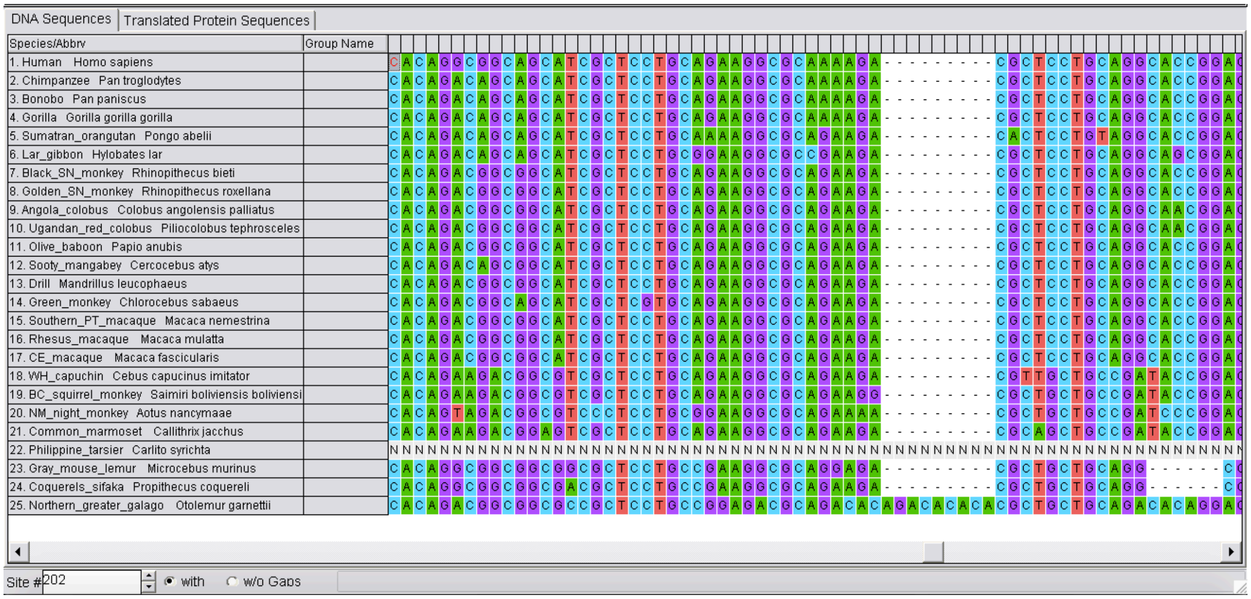
Site # 1   ● with   ○ w/o Gaps

Species/Abbrv	Group Name	* * ** ** * ** * * *** *
1. Human Homo sapiens		GGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
2. Chimpanzee Pan troglodytes		GGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
3. Bonobo Pan paniscus		GGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
4. Gorilla Gorilla gorilla gorilla		GGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
5. Sumatran_orangutan Pongo abelii		GGCAAGAGCAAGGACACCATGACCAAGAGGAGCAAGGACTGAGCCCGGAGCAGGTCGAGGTCTACGA
6. Lar_gibbon Hylobates lar		GGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGGACGTCGAGGTCTATGA
7. Black_SN_monkey Rhinopithecus bieti		GGCAAGAGCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGCCGAGGTCTACGA
8. Golden_SN_monkey Rhinopithecus roxellana		GGCAAGAGCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGCCGAGGTCTACGA
9. Angola_colobus Colobus angolensis palliatus		GGCAAGAGCAAGGACACAACGGCCAAGAGGAGCGGGGGCTGAGCCCGGAGCACGTCGAGGTCTATGC
10. Ugandan_red_colobus Piliocolobus tephrosceles		GACAAGAGCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCAGAGAACGTCGAGGTCTACGA
11. Olive_baboon Papio anubis		GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
12. Sooty_mangabey Cercocebus atys		GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
13. Drill Mandrillus leucophaeus		GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
14. Green_monkey Chlorocebus sabaeus		GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAGCCCGGAGCACGTCGAGGTCTACGA
15. Southern_PT_macaque Macaca nemestrina		GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAACCCGGAGCACGTCGAGGTCTACGA
16. Rhesus_macaque Macaca mulatta		GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAACCCGGAGCACGTCGAGGTCTACGA
17. CE_macaque Macaca fascicularis		GGCAAGACCAAGGACACAACGGCCAAGAGGAGCAGGGGCTGAACCCGGAGCACGTCGAGGTCTACGA
18. WH_capuchin Cebus capucinus imitator		GGCAGGAGCAAGGACGTAATGCCCAAGAAGAGCAGGGGCTGAGCCCAGAAGGCGTCGAGGCCTATGG
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		GGCAGGAGCAAGGACGTAATGCCCAAGAGGAGCAGGGGCTGAGCCCAGAAGGCGTCGGGGTCTATGG
20. NM_night_monkey Aotus nancymaae		GGCAGGAGCAAGGATGCAATGGCCAAGAAGAGCAGGGGCTGAGCCCAGAAGACGCCGAGGTCTACGG
21. Common_marmoset Callithrix jacchus		GGCAGGAGCAAGGACGTAATGGCCAAGAAGAGCAGGGGCTAAGCGCAGAAGGTGGCGAGGTCTACGG
22. Philippine_tarsier Carlito syrichta		GCCTGGAGCGTGGCCGCGAGGCCCCCGAAGAGCAGGGGATGAGCCAAGAGCACAGTGAGGCCTATGG
23. Gray_mouse_lemur Microcebus murinus		GGCAGGAGCAAGGCCTCGAGGGCCAGGAGGAGCAGGGCCTGAGCCCGGAGACCATCGAGTTCTACGG
24. Coquerels_sifaka Propithecus coquereli		GGCAGGAGCAAGGGCTCGAGGGCCAGGAGGAGCAGGGCCTGACCCCGGAGAGCATCGAGTTCTATGG
25. Northern_greater_galago Otolemur garnettii		GGCAGGACGAGGGCCAGAAC------------------------CCAGAGAGTGTTGAGGTCTATGG

Site # 68   ● with   ○ w/o Gaps

Species/Abbrv	Group Name	` **   * *                          *   *****`
1. Human Homo sapiens		GAGGACCCAT---GGCCAGTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCACCGGATCC
2. Chimpanzee Pan troglodytes		GAGGACCCAC---GGCCATTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCGTCGGATCC
3. Bonobo Pan paniscus		GAGGACCCAC---GGCCATTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCGCCGGATCC
4. Gorilla Gorilla gorilla gorilla		GAGGACCCAC---GGCCATTCTCACTATAGGCGCAGACACTGCTCTCAAAGGAGGCTGCGCCGGATCC
5. Sumatran_orangutan Pongo abelii		GAGGACCCAG---GGCCATTCTCACTATAGACGCAGGCACTGCTCTCGAAGGAGGCTGCACCGGATCC
6. Lar_gibbon Hylobates lar		GAGGACCCAC---GGCCATTCTCACTATAGGCGCAGGCACTGCTCTCGAAGGAGGCTGCACCGGATCC
7. Black_SN_monkey Rhinopithecus bieti		AAGGACCCACCAAGGCTACTCTCACCATAGGCGCAGGCGCTGCTCTCGAAGGAGGCTGCACCGGATCC
8. Golden_SN_monkey Rhinopithecus roxellana		AAGGACCCACCAAGGCTACTCTCACCATAGGCGCAGGCGCTGCTCTCGAAGGAGGCTGCACCGGATCC
9. Angola_colobus Colobus angolensis palliatus		AAGGACCCACCGAGGCTACTCTCACCATAGGAGCAGGAGCTGCTCTCGAAGGAGGCTGCACCGGATCC
10. Ugandan_red_colobus Piliocolobus tephrosceles		AAGGACCCACCAAGGCTACTCTCACCATAGGAGCAGGCGCTGCTCTCGAAGGAGGCTGCACCGGATCC
11. Olive_baboon Papio anubis		AAGGACCCACCGAGGCCACTCTTACCATAGGCGCAGGCGCTGCTCTCGAAGGAGGCTGCACCGGATCC
12. Sooty_mangabey Cercocebus atys		AAGGACCCACCGAGGCCACTCTTACCATAGGCGCAGGCGCTGCTCTCGAAGGAGGCTGCACCGGATCC
13. Drill Mandrillus leucophaeus		AAGGACCCACCGAGGCCACTCTTACCATAGGCGCAGGCGCTGCTCTCGAAGGAGGCTGCACCGGATCC
14. Green_monkey Chlorocebus sabaeus		AAGGACCCACCGAGGCCACTCTCCCCATAGGCGCAGGCGCTGCTCTCGAAGGAGGCTGCACCGGATCC
15. Southern_PT_macaque Macaca nemestrina		AAGGACCCACCGAGGCCACTCTCACCATAGGCGCAGGCGCTGCTCTCGAAGGAGGCTGCACCGGATCC
16. Rhesus_macaque Macaca mulatta		AAGGACCCACCGAGGCCACTCTCACCATAGGCGCAGGCGCTGCTCTCGAAGGAGGCTGCACCGGATCC
17. CE_macaque Macaca fascicularis		AAGGACCCACCGAGGCCACTCTCACCATAGGCGCAGGCGCTGCTCTCGAAGGAGGCTGCACCGGATCC
18. WH_capuchin Cebus capucinus imitator		GAGGAGCCACCGAGTCTGCTATCGCTACAGGCGCAGGCGCTGCTCTCGCAGACGGCTGTACCGGATTC
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		GAGAACCCACCGAACCTGCTATCGCCACAGGCGCAGGCGCTGCTCTCGCAGGAGGCTGTACCGGATCC
20. NM_night_monkey Aotus nancymaae		GAGGACCCAGCGAGGCTGCTATCGCTATAGGCGCAGGAGCTGCTCTCGCAGGAGGTTGAACCGGATCC
21. Common_marmoset Callithrix jacchus		GAGGACCCACCAAGGCTACTCTAGCTATAGGCGCAGGCGCTGCTCTCGCAGGAGGCGGTACCGGATTC
22. Philippine_tarsier Carlito syrichta		GAGGGTCCACAGGGGTGGCCACCGCTCCCGGCAACGGCGCTGCTNNNNNNNNNNNNNNNNNNNNNNNN
23. Gray_mouse_lemur Microcebus murinus		CAGGACCTACCGAGGCCGCCGCTGCAGGCGCAGGCGGCGCTGCTCTCGGAGGAGGCTGTGCCGGATCC
24. Coquerels_sifaka Propithecus coquereli		CAGGACCTACCAAGGCCGCCGCTGTAGGCGC---AGGCGCTGCTCTCGGAGGAGGCTGTGCCGGATCC
25. Northern_greater_galago Otolemur garnettii		AAGGACCTACCGAGGCCACCACCGTAGGCAC---AGGCACTGCTCTCGGAGGAGACTGTACCGGATCC

Site # 135   ● with   ○ w/o Gaps



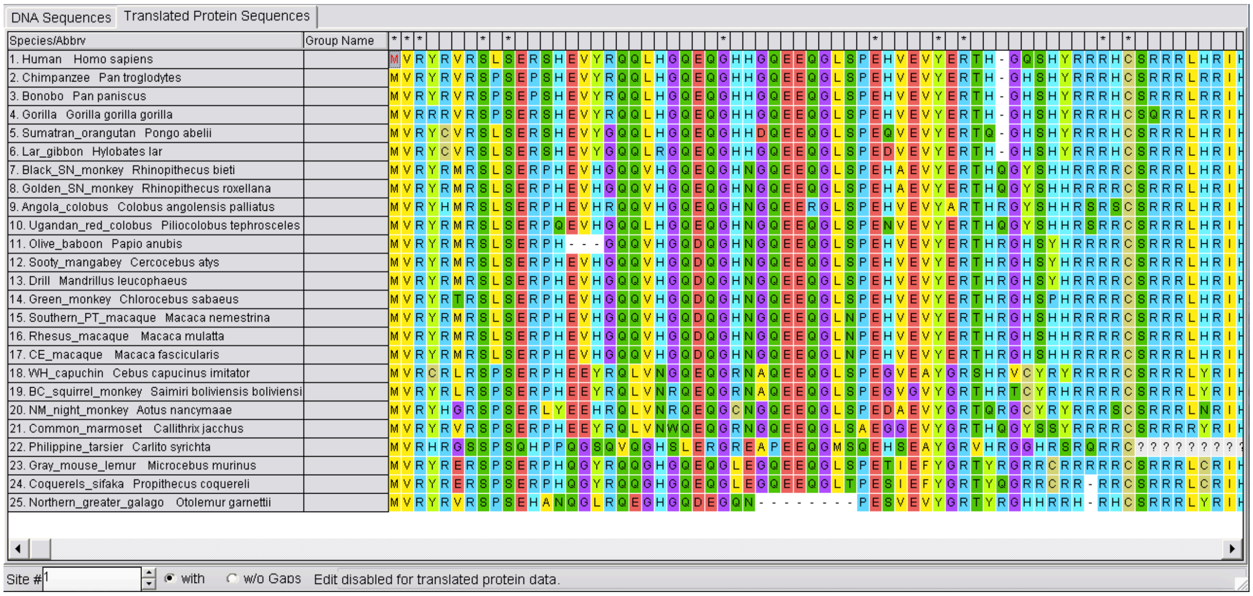
Species/Abbrv	Group Name	
1. Human Homo sapiens		CACAGGCGGCAGCATCGCTCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACCGGAG
2. Chimpanzee Pan troglodytes		CACAGACAGCAGCATCGCTCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACCGGAG
3. Bonobo Pan paniscus		CACAGACAGCAGCATCGCTCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACCGGAG
4. Gorilla Gorilla gorilla gorilla		CACAGACAGCAGCATCGCTCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACCGGAG
5. Sumatran_orangutan Pongo abelii		CACAGACAGCAGCATCGCTCCTGCAAAAGGCGCAGAAGA---------CACTCCTGTAGGCACCGGAG
6. Lar_gibbon Hylobates lar		CACAGACAGCAGCATCGCTCCTGCGGAAGGCGCCGAAGA---------CGCTCCTGCAGGCAGCGGAG
7. Black_SN_monkey Rhinopithecus bieti		CACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAG
8. Golden_SN_monkey Rhinopithecus roxellana		CACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAG
9. Angola_colobus Colobus angolensis palliatus		CACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCAACGGAG
10. Ugandan_red_colobus Piliocolobus tephrosceles		CACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCAACGGAG
11. Olive_baboon Papio anubis		CACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAG
12. Sooty_mangabey Cercocebus atys		CACAGACAGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAG
13. Drill Mandrillus leucophaeus		CACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAG
14. Green_monkey Chlorocebus sabaeus		CACAGACGGCAGCATCGCTCGTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAG
15. Southern_PT_macaque Macaca nemestrina		CACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAG
16. Rhesus_macaque Macaca mulatta		CACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAG
17. CE_macaque Macaca fascicularis		CACAGACGGCGGCATCGCTCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAG
18. WH_capuchin Cebus capucinus imitator		CACAGAAGACGGCGTCGCTCCTGCAGAAGGCGCAGAAGA---------CGTTGCTGCCGATACCGGAG
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		CACAGAAGACGGCGTCGCTCCTGCAGAAGGCGCAGAAGG---------CGCTGCTGCCGATACCGGAG
20. NM_night_monkey Aotus nancymaae		CACAGTAGACGGCGTCCCTCCTGCGGAAGGCGCAGAAAA---------CGCTGCTGCCGATCCCGGAG
21. Common_marmoset Callithrix jacchus		CACAGAAGACGGAGTCGCTCCTGCAGAAGGCGCAGAAGA---------CGCAGCTGCCGATACCGGAG
22. Philippine_tarsier Carlito syrichta		NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
23. Gray_mouse_lemur Microcebus murinus		CACAGGCGGCGGCGGCGCTCCTGCCGAAGGCGCAGGAGA---------CGCTGCTGCAGG------CC
24. Coquerels_sifaka Propithecus coquereli		CACAGGCGGCGGCGACGCTCCTGCCGAAGGCGCAGAAGA---------CGCTGCTGCAGG------CC
25. Northern_greater_galago Otolemur garnettii		CACAGACGGCGGCGCCGCTCCTGCCGGAGACGCAGACACAGACACACACGCTGCTGCAGACACAGGAG

Site # 202   ● with   ○ w/o Gaps

Species/Abbrv	Group Name	`                      *** *        ** ****   *******           * *`
1. Human Homo sapiens		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAAGAGAACATGCAGAAGG------CACTAA
2. Chimpanzee Pan troglodytes		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAAG------CACTAA
3. Bonobo Pan paniscus		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAAG------CACTAA
4. Gorilla Gorilla gorilla gorilla		CGGAGGAGGCATCGCAAAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAGG------CACTAA
5. Sumatran_orangutan Pongo abelii		CGGAGGAAGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAACATGCAGAAGG------CACTAA
6. Lar_gibbon Hylobates lar		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA
7. Black_SN_monkey Rhinopithecus bieti		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------TACTAA
8. Golden_SN_monkey Rhinopithecus roxellana		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------TACTAA
9. Angola_colobus Colobus angolensis palliatus		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------TACTAA
10. Ugandan_red_colobus Piliocolobus tephrosceles		CGGAGGAGGCATCGCAGAGGTTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------TACTAA
11. Olive_baboon Papio anubis		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA
12. Sooty_mangabey Cercocebus atys		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA
13. Drill Mandrillus leucophaeus		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA
14. Green_monkey Chlorocebus sabaeus		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------TACTAA
15. Southern_PT_macaque Macaca nemestrina		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA
16. Rhesus_macaque Macaca mulatta		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA
17. CE_macaque Macaca fascicularis		CGGAGGAGGCATCGCAGAGGCTGCAGAACC---AGGAGGAGAAGATGCAGAAGG------CACTAA
18. WH_capuchin Cebus capucinus imitator		CGGAGGCGGTATCGCAGAGGTAGCAGATCCAGGAGGAGGAGAAGATGCAGAAGG------TACTAA
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		CGGAGGCGGCACCGCAGAGTCTGCAAATCCAGGAGGAGGAGAAGATGCAGAAGG------TACTAA
20. NM_night_monkey Aotus nancymaae		CGGAGGAGGCCTCGCAGAGGCTGCAGATCCAGGAGGAGGAGAAGATGCAGAAGG------AACTAA
21. Common_marmoset Callithrix jacchus		CGGAGAAGGCCTCGCAGAGGCTGCAGATCCAGGAGGAGGAGAAGATGCAGAAGG------TACTAA
22. Philippine_tarsier Carlito syrichta		NNNNNNNNNNNNNNNNNNNCTTGCAGA------CAGAGGAGACGGTGCAGAAGG------CCTTAA
23. Gray_mouse_lemur Microcebus murinus		---CGGAGGCACCGCAGAGGCTGCAGA---AGGAGGAGGAGAAGATGCAGAAGGCGCTACTACTGA
24. Coquerels_sifaka Propithecus coquereli		---CGGAGGCATCGCAGAGGCTGCAGA---AGGAGGAGGAGAAGATGCAGAAGGCGCTACTACTAA
25. Northern_greater_galago Otolemur garnettii		AGGAGG------AGGAGAGGCTGCAGA---AGGAGGAGGAGAAGATGCAGAAGACGC---TACTAA

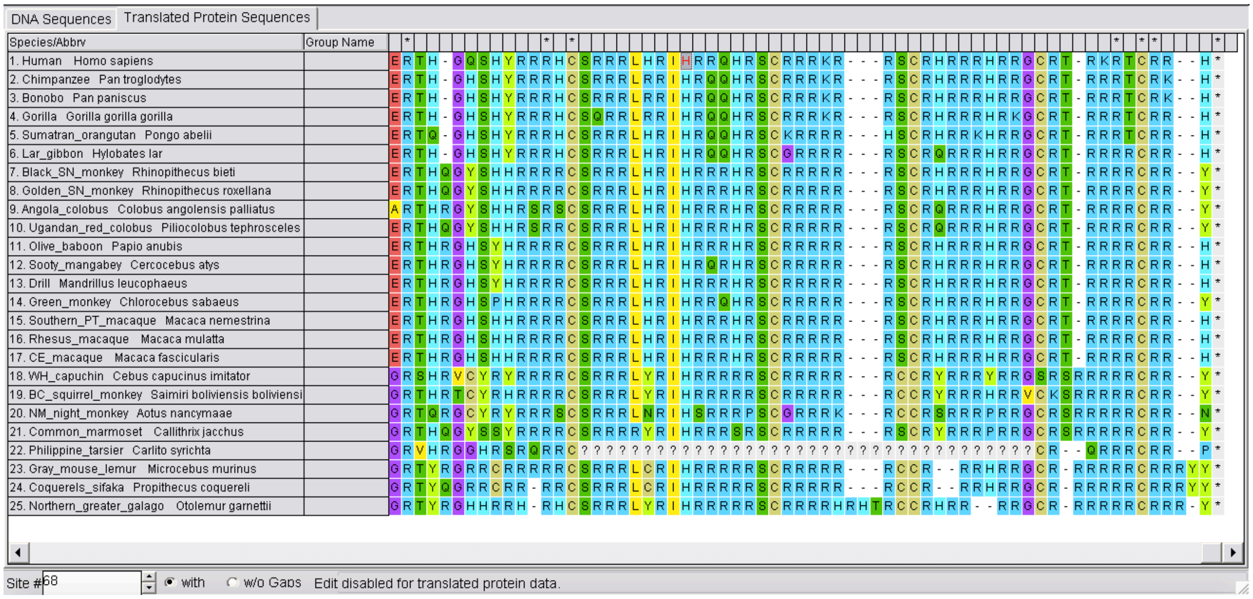
Site # 269 ● with ○ w/o Gaps

G2) Translated alignment, showing primate *Prm2* amino acid coding sequences



Species/Abbrv	Group Name	`***    * *                *           *    * *          * *`
1. Human Homo sapiens		MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTH-GQSHYRRRHCSRRRLHRIH
2. Chimpanzee Pan troglodytes		MVRYRVRSPSEPSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTH-GHSHYRRRHCSRRRLRRIH
3. Bonobo Pan paniscus		MVRYRVRSPSEPSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTH-GHSHYRRRHCSRRRLRRIH
4. Gorilla Gorilla gorilla gorilla		MVRRRVRSPSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTH-GHSHYRRRHCSQRRLRRIH
5. Sumatran_orangutan Pongo abelii		MVRYCVRSLSERSHEVYGQQLHGQEQGHHDQEEQGLSPEQVEVYERTQ-GHSHYRRRHCSRRRLHRIH
6. Lar_gibbon Hylobates lar		MVRYCVRSLSERSHEVYGQQLRGQEQGHHGQEEQGLSPEDVEVYERTH-GHSHYRRRHCSRRRLHRIH
7. Black_SN_monkey Rhinopithecus bieti		MVRYRMRSLSERPHEVHGQQVHGQEQGHNGQEEQGLSPEHAEVYERTHQGYSHHRRRRCSRRRLHRIH
8. Golden_SN_monkey Rhinopithecus roxellana		MVRYRMRSLSERPHEVHGQQVHGQEQGHNGQEEQGLSPEHAEVYERTHQGYSHHRRRRCSRRRLHRIH
9. Angola_colobus Colobus angolensis palliatus		MVRYHMRSLSERPHEVHRQQVHGQEQGHNGQEERGLSPEHVEVYARTHRGYSHHRSRSCSRRRLHRIH
10. Ugandan_red_colobus Piliocolobus tephrosceles		MVRYRMRSLSERPQEVHGQQLHGQEQGHNGQEEQGLSPENVEVYERTHQGYSHHRSRRCSRRRLHRIH
11. Olive_baboon Papio anubis		MVRYRMRSLSERPH---GQQVHGQDQGHNGQEEQGLSPEHVEVYERTHRGHSYHRRRRCSRRRLHRIH
12. Sooty_mangabey Cercocebus atys		MVRYRMRSLSERPHEVHGQQVHGQDQGHNGQEEQGLSPEHVEVYERTHRGHSYHRRRRCSRRRLHRIH
13. Drill Mandrillus leucophaeus		MVRYRMRSLSERPHEVHGQQVHGQDQGHNGQEEQGLSPEHVEVYERTHRGHSYHRRRRCSRRRLHRIH
14. Green_monkey Chlorocebus sabaeus		MVRYRTRSLSERPHEVHGQQVHGQDQGHNGQEEQGLSPEHVEVYERTHRGHSPHRRRRCSRRRLHRIH
15. Southern_PT_macaque Macaca nemestrina		MVRYRMRSLSERPHEVHGQQVHGQDQGHNGQEEQGLNPEHVEVYERTHRGHSHHRRRRCSRRRLHRIH
16. Rhesus_macaque Macaca mulatta		MVRYRMRSLSERPHEVHGQQVHGQDQGHNGQEEQGLNPEHVEVYERTHRGHSHHRRRRCSRRRLHRIH
17. CE_macaque Macaca fascicularis		MVRYRMRSLSERPHEVHGQQVHGQDQGHNGQEEQGLNPEHVEVYERTHRGHSHHRRRRCSRRRLHRIH
18. WH_capuchin Cebus capucinus imitator		MVRCRLRSPSERPHEEYRQLVNGQEQGRNAQEEQGLSPEGVEAYGRSHRVCYRYRRRRCSRRRLYRIH
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		MVRYRLRSPSERPHEEYRQLVNRQEQGRNAQEEQGLSPEGVGVYGRTHRTCYRHRRRRCSRRRLYRIH
20. NM_night_monkey Aotus nancymaae		MVRYHGRSPSERLYEEHRQLVNRQEQGCNGQEEQGLSPEDAEVYGRTQRGCYRYRRRSCSRRRLNRIH
21. Common_marmoset Callithrix jacchus		MVRYRVRSPSERPHEEYRQLVNWQEQGRNGQEEQGLSAEGGEVYGRTHQGYSSYRRRRCSRRRRYRIH
22. Philippine_tarsier Carlito syrichta		MVRHRGSSPSQHPPQGSQVQGHSLERGREAPEEQGMSQEHSEAYGRVHRGGHRSRQRRC?????????
23. Gray_mouse_lemur Microcebus murinus		MVRYRERSPSERPHQGYRQQGHGQEQGLEGQEEQGLSPETIEFYGRTYRGRRCRRRRRCSRRRLCRIH
24. Coquerels_sifaka Propithecus coquereli		MVRYRERSPSERPHQGYRQQGHGQEQGLEGQEEQGLTPESIEFYGRTYQGRRCRR-RRCSRRRLCRIH
25. Northern_greater_galago Otolemur garnettii		MVRYRVRSPSEHANQGLRQEGHGQDEGQN--------PESVEVYGRTYRGHHRRH-RHCSRRRLYRIH

Site # 1 ● with ○ w/o Gaps Edit disabled for translated protein data.

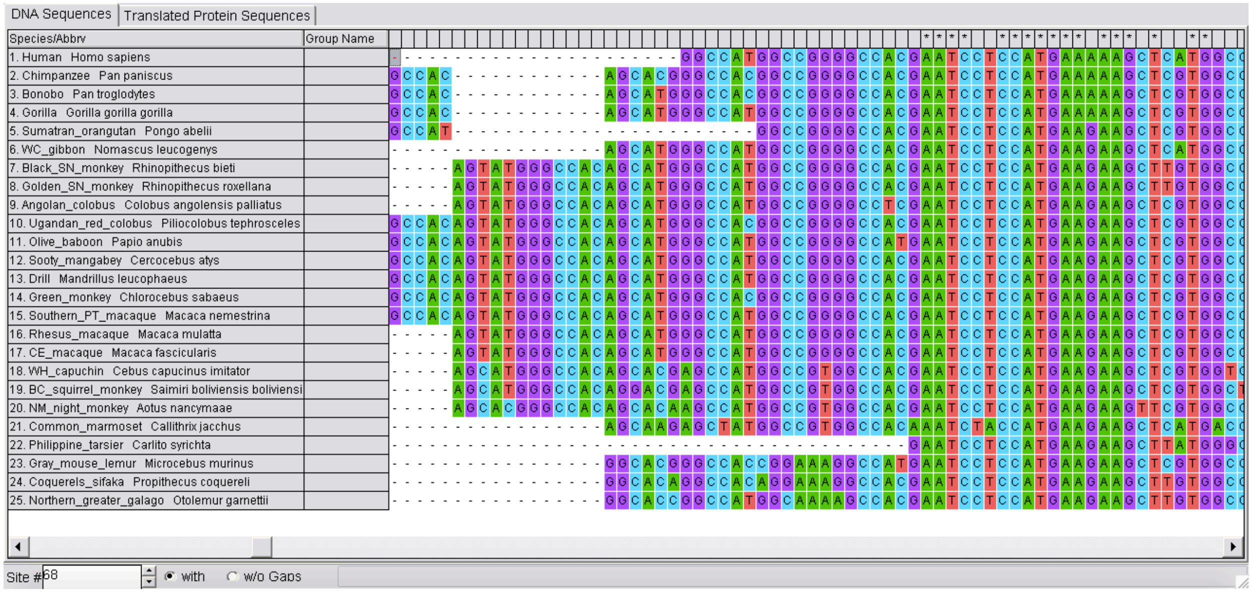


Species/Abbrv	Group Name	` *          * *                                          * **    *`
1. Human Homo sapiens		ERTH-GQSHYRRRHCSRRRLHRIHRRQHRSCRRRKR---RSCRHRRRHRRGCRT-RKRTCRR--H*
2. Chimpanzee Pan troglodytes		ERTH-GHSHYRRRHCSRRRLRRIHRQQHRSCRRRKR---RSCRHRRRHRRGCRT-RRRTCRK--H*
3. Bonobo Pan paniscus		ERTH-GHSHYRRRHCSRRRLRRIHRQQHRSCRRRKR---RSCRHRRRHRRGCRT-RRRTCRK--H*
4. Gorilla Gorilla gorilla gorilla		ERTH-GHSHYRRRHCSQRRLRRIHRQQHRSCRRRKR---RSCRHRRRHRKGCRT-RRRTCRR--H*
5. Sumatran_orangutan Pongo abelii		ERTQ-GHSHYRRRHCSRRRLHRIHRQQHRSCKRRRR---HSCRHRRKHRRGCRT-RRRTCRR--H*
6. Lar_gibbon Hylobates lar		ERTH-GHSHYRRRHCSRRRLHRIHRQQHRSCGRRRR---RSCRQRRRHRRGCRT-RRRRCRR--H*
7. Black_SN_monkey Rhinopithecus bieti		ERTHQGYSHHRRRRCSRRRLHRIHRRRHRSCRRRRR---RSCRHRRRHRRGCRT-RRRRCRR--Y*
8. Golden_SN_monkey Rhinopithecus roxellana		ERTHQGYSHHRRRRCSRRRLHRIHRRRHRSCRRRRR---RSCRHRRRHRRGCRT-RRRRCRR--Y*
9. Angola_colobus Colobus angolensis palliatus		ARTHRGYSHHRSRSCSRRRLHRIHRRRHRSCRRRRR---RSCRQRRRHRRGCRT-RRRRCRR--Y*
10. Ugandan_red_colobus Piliocolobus tephrosceles		ERTHQGYSHHRSRRCSRRRLHRIHRRRHRSCRRRRR---RSCRQRRRHRRGCRT-RRRRCRR--Y*
11. Olive_baboon Papio anubis		ERTHRGHSYHRRRRCSRRRLHRIHRRRHRSCRRRRR---RSCRHRRRHRRGCRT-RRRRCRR--H*
12. Sooty_mangabey Cercocebus atys		ERTHRGHSYHRRRRCSRRRLHRIHRQRHRSCRRRRR---RSCRHRRRHRRGCRT-RRRRCRR--H*
13. Drill Mandrillus leucophaeus		ERTHRGHSYHRRRRCSRRRLHRIHRRRHRSCRRRRR---RSCRHRRRHRRGCRT-RRRRCRR--H*
14. Green_monkey Chlorocebus sabaeus		ERTHRGHSPHRRRRCSRRRLHRIHRRQHRSCRRRRR---RSCRHRRRHRRGCRT-RRRRCRR--Y*
15. Southern_PT_macaque Macaca nemestrina		ERTHRGHSHHRRRRCSRRRLHRIHRRRHRSCRRRRR---RSCRHRRRHRRGCRT-RRRRCRR--H*
16. Rhesus_macaque Macaca mulatta		ERTHRGHSHHRRRRCSRRRLHRIHRRRHRSCRRRRR---RSCRHRRRHRRGCRT-RRRRCRR--H*
17. CE_macaque Macaca fascicularis		ERTHRGHSHHRRRRCSRRRLHRIHRRRHRSCRRRRR---RSCRHRRRHRRGCRT-RRRRCRR--H*
18. WH_capuchin Cebus capucinus imitator		GRSHRVCYRYRRRRCSRRRLYRIHRRRRRSCRRRRR---RCCRYRRRYRRGSRSRRRRRCRR--Y*
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		GRTHRTCYRHRRRRCSRRRLYRIHRRRRRSCRRRRR---RCCRYRRRHRRVCKSRRRRRCRR--Y*
20. NM_night_monkey Aotus nancymaae		GRTQRGCYRYRRRSCSRRRLNRIHSRRRPSCGRRRK---RCCRSRRRPRRGCRSRRRRRCRR--N*
21. Common_marmoset Callithrix jacchus		GRTHQGYSSYRRRRCSRRRRYRIHRRRSRSCRRRRR---RSCRYRRRPRRGCRSRRRRRCRR--Y*
22. Philippine_tarsier Carlito syrichta		GRVHRGGHRSRQRRC????????????????????????????????????CR--QRRRCRR--P*
23. Gray_mouse_lemur Microcebus murinus		GRTYRGRRCRRRRRCSRRRLCRIHRRRRRSCRRRRR---RCCR--RRHRRGCR-RRRRRCRRRYY*
24. Coquerels_sifaka Propithecus coquereli		GRTYQGRRCRR-RRCSRRRLCRIHRRRRRSCRRRRR---RCCR--RRHRRGCR-RRRRRCRRRYY*
25. Northern_greater_galago Otolemur garnettii		GRTYRGHHRRH-RHCSRRRLYRIHRRRRRSCRRRRHRHTRCCRHRR--RRGCR-RRRRRCRRR-Y*

Site # 68 ● with ○ w/o Gaps Edit disabled for translated protein data.

The translated coding sequence

Appendix H) Alignment of primate *Prm3* gene sequences



```
Species/Abbrv                                           Group Name                                            ****  ******* *** *  **
1. Human  Homo sapiens                                              -----------------------GGCCATGGCCGGGGCCACGAATCCTCCATGAAAAAGCTCATGGC
2. Chimpanzee  Pan paniscus                                         GCCAC------------AGCACGGGCCACGGCCGGGGCCACGAATCCTCCATGAAAAAGCTCGTGGC
3. Bonobo  Pan troglodytes                                          GCCAC------------AGCATGGGCCACGGCCGGGGCCACGAATCCTCCATGAAAAAGCTCGTGGC
4. Gorilla  Gorilla gorilla gorilla                                 GCCAC------------AGCATGGGCCATGGCCGGGGCCACGAATCCTCCATGAAAAAGCTCGTGGC
5. Sumatran_orangutan  Pongo abelii                                 GCCAT------------------------GGCCGGGGCCACGAATCCTCCATGAAGAAGCTCGTGGC
6. WC_gibbon  Nomascus leucogenys                                   -----------------AGCATGGGCCATGGCCGGGGCCACGAATCCTCCATGAAGAAGCTCATGGC
7. Black_SN_monkey  Rhinopithecus bieti                             -----AGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCATGAAGAAGCTTGTGGC
8. Golden_SN_monkey  Rhinopithecus roxellana                        -----AGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCATGAAGAAGCTTGTGGC
9. Angolan_colobus  Colobus angolensis palliatus                    -----AGTATGGGCCACAGCATGGGCCATGGCCGGGGCCTCGAATCCTCCATGAAGAAGCTCGTGGC
10. Ugandan_red_colobus  Piliocolobus tephrosceles                  GCCACAGTATGGGCCACAGCATGGGCCACGGCCGGGGCCACGAATCCTCCATGAAGAAGCTCGTGGC
11. Olive_baboon  Papio anubis                                      GCCACAGTATGGGCCACAGCATGGGCCATGGCCGGGGCCATGAATCCTCCATGAAGAAGCTCGTGGC
12. Sooty_mangabey  Cercocebus atys                                 GCCACAGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCATGAAGAAGCTCGTGGC
13. Drill  Mandrillus leucophaeus                                   GCCACAGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCATGAAGAAGCTCGTGGC
14. Green_monkey  Chlorocebus sabaeus                               GCCACAGTATGGGCCACAGCATGGGCCACGGCCGGGGCCACGAATCCTCCATGAAGAAGCTCGTGGC
15. Southern_PT_macaque  Macaca nemestrina                          GCCACAGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCATGAAGAAGCTCGTGGC
16. Rhesus_macaque  Macaca mulatta                                  -----AGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCATGAAGAAGCTCGTGGC
17. CE_macaque  Macaca fascicularis                                 -----AGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCATGAAGAAGCTCGTGGC
18. WH_capuchin  Cebus capucinus imitator                           -----AGCATGGGCCACAGCACGAGCCATGGCCGTGGCCACGAATCCTCCATGAAGAAGCTCGTGGT
19. BC_squirrel_monkey  Saimiri boliviensis boliviensi              -----AGCATGGGCCACAGGACGAGCCATGGCCGTGGCCACGAATCCTCCATGAAGAAGCTCGTGGC
20. NM_night_monkey  Aotus nancymaae                                -----AGCACGGGCCACAGCACAAGCCATGGCCGTGGCCACGAATCCTCCATGAAGAAGTTCGTGGC
21. Common_marmoset  Callithrix jacchus                             -----------------AGCAAGAGCTATGGCCGTGGCCACAAATCTACCATGAAGAAGCTCATGAC
22. Philippine_tarsier  Carlito syrichta                            -----------------------------------------GAATCCTCCATGAAGAAGCTTATGGG
23. Gray_mouse_lemur  Microcebus murinus                            -----------------GGCACGGGCCACCGGAAAGGCCATGAATCCTCCATGAAGAAGCTCGTGGC
24. Coquerels_sifaka  Propithecus coquereli                         -----------------GGCACAGGCCACAGGAAAGGCCACGAATCCTCCATGAAGAAGCTTGTGGC
25. Northern_greater_galago  Otolemur garnettii                     -----------------GGCACCGGCCATGGCAAAAGCCACGAATCCTCCATGAAGAAGCTTGTGGC
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Species/Abbrv                                           Group Name  ***** **** ************** ***  * ** ***      **       ******
1. Human  Homo sapiens                                              ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAGAGCCCAGGCCACAGCCCAGGCCACAGCACG-
2. Chimpanzee  Pan paniscus                                         ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGG
3. Bonobo  Pan troglodytes                                          ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCACGGGCCACAGCACGG
4. Gorilla  Gorilla gorilla gorilla                                 ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGG
5. Sumatran_orangutan  Pongo abelii                                 ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCGGCCACAC---CCAGGCCACAGCACGG
6. WC_gibbon  Nomascus leucogenys                                   ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCACAGGCCAC-------
7. Black_SN_monkey  Rhinopithecus bieti                             ATGGGTTCCCACTGTGCCAAGCTCAACACAGGTCACAGCCCAGGCCACAGCACGGGCCAC-------
8. Golden_SN_monkey  Rhinopithecus roxellana                        ATGGGTTCCCACTGTGCCAAGCTCAACACAGGTCACAGCCCAGGCCACAGCACGGGCCAC-------
9. Angolan_colobus  Colobus angolensis palliatus                    ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCCCGGGCCAC-------
10. Ugandan_red_colobus  Piliocolobus tephrosceles                  ATGGGTTCCCGCTGTGCCAAGCTCAACACATGCCACAGCCCAGGCCACGGCCCAGGCCACAGCACAG
11. Olive_baboon  Papio anubis                                      ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACAG
12. Sooty_mangabey  Cercocebus atys                                 ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCACAGGCCACAGCACAGGCCACAGCACAG
13. Drill  Mandrillus leucophaeus                                   ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACAG
14. Green_monkey  Chlorocebus sabaeus                               ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCCCAGGCCACAGCACAG
15. Southern_PT_macaque  Macaca nemestrina                          ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCCCAGGCCACAGCACAG
16. Rhesus_macaque  Macaca mulatta                                  ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCACAGGCCAC-------
17. CE_macaque  Macaca fascicularis                                 ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCACAGCCCAGGCCACAGCACAGGCCAC-------
18. WH_capuchin  Cebus capucinus imitator                           ATGGGTTCCCGCTGTGCCAAGCTCAGCACAGGCCACAGCCCGGGCCATAGCACTGGCCAC-------
19. BC_squirrel_monkey  Saimiri boliviensis boliviensi              ATGGGTTCCCACTGTGCCAAGCTCAGCACAGGCCACAGCCCGGGCCATAGCACTGGCCAC-------
20. NM_night_monkey  Aotus nancymaae                                ATGGGTTCCCACTGTGCCAAGCTCAGCACAGGCCACAGCCCGGGCCATAGCACTGGCCAC-------
21. Common_marmoset  Callithrix jacchus                             ATGGGTTCCCACTGTGCCAAGCTCAGCACAGGCCACAGCCTGGGCCATAGCACCGGCCAC-------
22. Philippine_tarsier  Carlito syrichta                            ATGGGATCCCACTGTGCCAAGCTCAGCACCGGCCACAGCACAGGCCACGGCCAGGGCCAC-------
23. Gray_mouse_lemur  Microcebus murinus                            ATGGGCTCCCGCTGTGCCAAGCTCAGCACAGGCCACAGCTCGGGCCACGGCACGGGCCAC-------
24. Coquerels_sifaka  Propithecus coquereli                         ATGGGTTCCCGCTGTGCCAAGCTCAGCACGGGCCACAGCTCAGGCCACGGCACGGGCCAC-------
25. Northern_greater_galago  Otolemur garnettii                     ATGGGTTCCCGCTGTGCCAAGCTCAGCACGGGCCACAGCACAGGCCATGGCACAGGCCAC-------
```
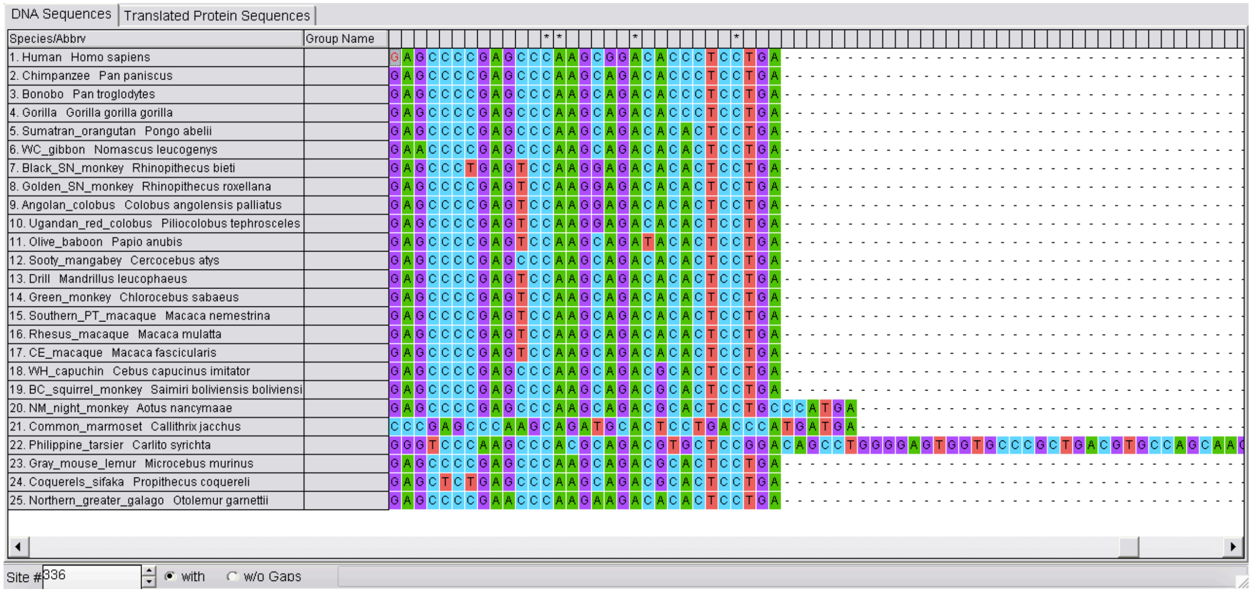

Species/Abbrv	Group Name	`                                                   ** *  **  ******`
1. Human Homo sapiens		`GGGGAAGAGGAGGAG---------------------------AAAGAAGAGCTGCCGGTGCAGGGCA`
2. Chimpanzee Pan paniscus		`GGGGAAGAGGAGGAG---------------------------AAAGAAGAGCTGCCAGTGCAGGGCA`
3. Bonobo Pan troglodytes		`GGGGAAGAGGAGGAG---------------------------AAAGAAGAGCTGCCAGTGCAGGGCA`
4. Gorilla Gorilla gorilla gorilla		`GGGGAAGAGGAGGAG---------------------------AAAGAAGAGCTGCCAGTGCAGGGCA`
5. Sumatran_orangutan Pongo abelii		`---------------------------------------GAGAAAGAGGAACTGCCGGTGCAGGGCA`
6. WC_gibbon Nomascus leucogenys		`GGGGAAGAGGAGGAAGAGGAGGAGGAGGGGGAAGAGGAGGAGAAAGAGGAGCTGCCGGTGCAGGGCA`
7. Black_SN_monkey Rhinopithecus bieti		`GGGGAAGAGGAGGAGGAAGAGGAG---------------------------CTGCCAGTGCAGGGCA`
8. Golden_SN_monkey Rhinopithecus roxellana		`GGGGAAGAGGAGGAGGAAGAGGAG---------------------------CTGCCAGTACAGGGCA`
9. Angolan_colobus Colobus angolensis palliatus		`GGGGAAGAGGAGGAGGAAGAGGAG---------------------------CTGCCAGTGCAGGGCA`
10. Ugandan_red_colobus Piliocolobus tephrosceles		`GGGGAAGAGGAGGAGGAAGAGGAG---------------------------CTGCCAGTGCAGGGCA`
11. Olive_baboon Papio anubis		`GGGGAAGAGGAGGAGGAAGAAGAG---------------------------CTGCCAGTGCAGGGCA`
12. Sooty_mangabey Cercocebus atys		`GGGGAAGAGGAGGAGGAAGAAGAG---------------------------CTGCCAGTGCAGGGCA`
13. Drill Mandrillus leucophaeus		`GGGGAAGAGGAGGAGGAAGAAGAG---------------------------CTGCCAGTGCAGGGCA`
14. Green_monkey Chlorocebus sabaeus		`GGGGAAGAGGAGGAGGAAGAAGAG---------------------------CTGCCAGTGCAGGGCA`
15. Southern_PT_macaque Macaca nemestrina		`GGGGAAGAGGAGGAGGAAGAAGAG---------------------------CTGCCAGTGCAGGGCA`
16. Rhesus_macaque Macaca mulatta		`GGGGAAGAGGAGGAGGAAGAAGAG---------------------------CTGCCAGTGCAGGGCA`
17. CE_macaque Macaca fascicularis		`GGGGAAGAGGAGGAGGAAGAAGAG---------------------------CTGCCAGTGCAGGGCA`
18. WH_capuchin Cebus capucinus imitator		`GAAGATGAGGAGGAAGAGGAG------------------------------CTGCTGGTCCAGGGCA`
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		`GAAGATGAGGAGGAAGAGGAG------------------------------CTGCCGGTCCAGGGCA`
20. NM_night_monkey Aotus nancymaae		`GAAGACGAGGAAGAAGAGGAG------------------------------CTGCCGGTCAAGGGCA`
21. Common_marmoset Callithrix jacchus		`GGAGAAGATAAGGAGGAAGAGGAG---------------------------CTGCCGGTCCAGGGCA`
22. Philippine_tarsier Carlito syrichta		`GGGCAGGAGGAGGAGGAG---------------------------------CTTCCGGTGCAGGGCA`
23. Gray_mouse_lemur Microcebus murinus		`GAGGAGGAGGAGGAAGAGGAGGAGGAGGAGGAG------------------CTCCCGGTTCAGGGCA`
24. Coquerels_sifaka Propithecus coquereli		`GAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAGGAGGAGGAAGAGGAG---CTCCCGGTTCAGGGCA`
25. Northern_greater_galago Otolemur garnettii		`GAAGAGGAGGAAGAGGAAGAGGAGGAAGAGGAG------------------CTCCCAGTGCAGGGCA`

Site # 202 ● with ○ w/o Gaps

Species/Abbrv	Group Name	` **  * **    **  **   *   **** ** *     ** ** ** ***         **`
1. Human Homo sapiens		`CTGTGTGAGTCAGGATAACTTCTCCTTGTCATCAGCGGGCGAGGAAGAGGAGGAAGAGGAGGAGGAG`
2. Chimpanzee Pan paniscus		`CTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGCGGGCGAGGAAGAGGAGGAAGAGGAGGAGGAG`
3. Bonobo Pan troglodytes		`CTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGCGGGCGAGGAAGAGGAGGAAGAGGAGGAGGAG`
4. Gorilla Gorilla gorilla gorilla		`CTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGCGGGCGAGGAAGAGGAGGAAGAGGAGGAGAAG`
5. Sumatran_orangutan Pongo abelii		`CTGTGTGAGCCAGGATAACTTCTCCTTGTCATCAGAGGGCGAGGAAGAGGAGGAAGAGGAGGAGGAG`
6. WC_gibbon Nomascus leucogenys		`CTGTGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGCGAGGAAGAGGAGGAAGAGGAGGAGGAG`
7. Black_SN_monkey Rhinopithecus bieti		`CTGCTTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGTGAGGAAGAGGAGGAAGAGGAGGAGGAA`
8. Golden_SN_monkey Rhinopithecus roxellana		`CTGCTTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGTGAGGAAGAGGAGGAAGAGGAGGAGGAA`
9. Angolan_colobus Colobus angolensis palliatus		`CTGCGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGTGAGGAAGAGGAGGAAGAGGAGGAGGAA`
10. Ugandan_red_colobus Piliocolobus tephrosceles		`CTGCGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGTGAGGAAGAGGAG---------GAGGAA`
11. Olive_baboon Papio anubis		`CTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAGGGTGAGGAGGAGGAGGAAGAGGAGGAGGAA`
12. Sooty_mangabey Cercocebus atys		`CTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAGGGTGAGGAAGAGGAGGAAGAGGAGGAGGAA`
13. Drill Mandrillus leucophaeus		`CTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAGGGTGAGGAGGAGGAGGAAGAGGAGGAGGAA`
14. Green_monkey Chlorocebus sabaeus		`CTGTGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGTGAGGAAGAGGAGGAAGAGGAGGAGGAA`
15. Southern_PT_macaque Macaca nemestrina		`CTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAGGGTGAGGAAGAGGAGGAAGAGGAGGAGGAA`
16. Rhesus_macaque Macaca mulatta		`CTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAAGGTGAGGAAGAGGAGGAAGAGGAGGAGGAA`
17. CE_macaque Macaca fascicularis		`CTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAGGGTGAGGAAGAGGAGGAAGAGGAGGAGGAA`
18. WH_capuchin Cebus capucinus imitator		`CTGCGTGAGTCAGGATAACTTCTCCCTGTCATCAGAGGGCGAGGAAGACGAGGAGGAGAAAGAGGAA`
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		`TTGCGTGAGTCAGGATAACTTCTCCCTGTCATCAGAGGGCGAGGAAGACGAGGAGGAGAAAGAGGAA`
20. NM_night_monkey Aotus nancymaae		`CTGCGTGAGTCAGGACAAC---TCCCTGTCATCAGAGAGCGAGGAAGACGAGGAG---AAAGAGGAA`
21. Common_marmoset Callithrix jacchus		`CTGCATGAGTCAGGATAACTTCTGTCTGTCATCAGAGGGCGAAGAAGATGAGGAGGAGAAAGAGGAA`
22. Philippine_tarsier Carlito syrichta		`CTGCGTGAGCCGAGATGACTTCTCCTTGTCGTCGGAG---GAGGAAGAGGAGGAAGAGGAGGAA---`
23. Gray_mouse_lemur Microcebus murinus		`CTGTGTGAGTCAGGATAACTTCTCCCTGTCGTCGGAGGGCGAGGAAGATGAGGAGGAGGAGGAGGAA`
24. Coquerels_sifaka Propithecus coquereli		`CTGTGTAAGTCAGGATAACTTCTCCCTGTCATCAGAGGGTGAGGAAGATGAGGAGGAGGAGGAGGAA`
25. Northern_greater_galago Otolemur garnettii		`CTGTGTGAGTCAGGATAACTTCTCCCTGTCGTCAGAGGGCGAGGAAGACGAGGAGGAGGAGGAGGAG`

Site # 135 ● with ○ w/o Gaps

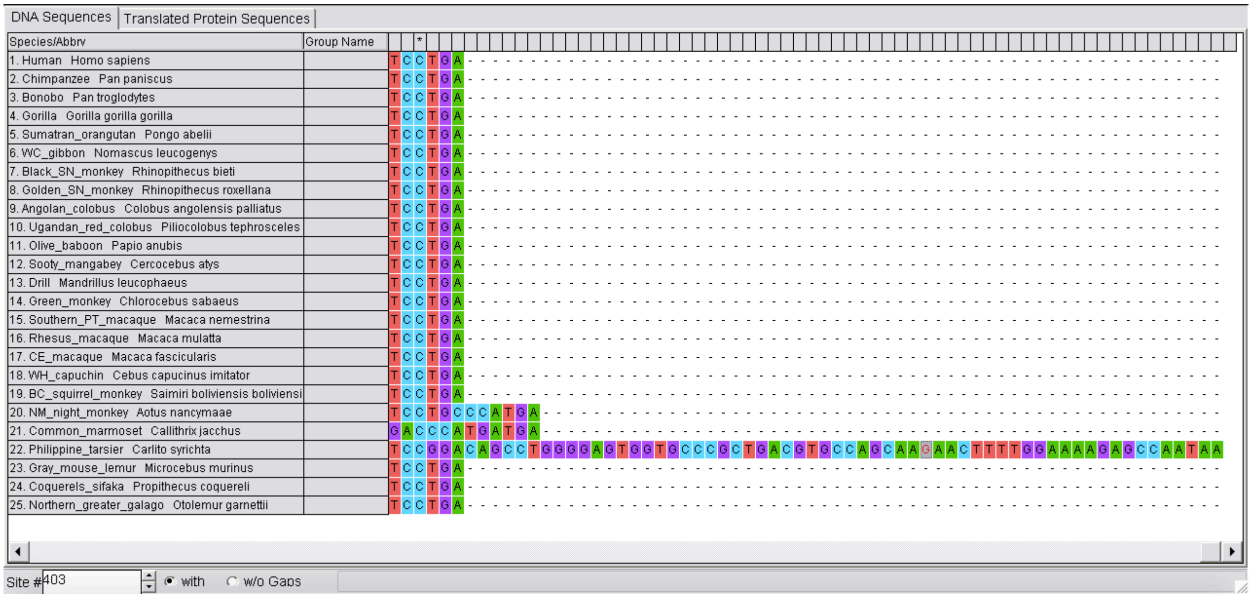


Species/Abbrv	Group Name	`            **     *       *`
1. Human Homo sapiens		`GAGCCCCGAGCCCAAGCGGACACCCTCCTGA------------------------------------`
2. Chimpanzee Pan paniscus		`GAGCCCCGAGCCCAAGCAGACACCCTCCTGA------------------------------------`
3. Bonobo Pan troglodytes		`GAGCCCCGAGCCCAAGCAGACACCCTCCTGA------------------------------------`
4. Gorilla Gorilla gorilla gorilla		`GAGCCCCGAGCCCAAGCAGACACCCTCCTGA------------------------------------`
5. Sumatran_orangutan Pongo abelii		`GAGCCCCGAGCCCAAGCAGACACACTCCTGA------------------------------------`
6. WC_gibbon Nomascus leucogenys		`GAACCCCGAGCCCAAGCAGACACACTCCTGA------------------------------------`
7. Black_SN_monkey Rhinopithecus bieti		`GAGCCCTGAGTCCAAGGAGACACACTCCTGA------------------------------------`
8. Golden_SN_monkey Rhinopithecus roxellana		`GAGCCCCGAGTCCAAGGAGACACACTCCTGA------------------------------------`
9. Angolan_colobus Colobus angolensis palliatus		`GAGCCCCGAGTCCAAGGAGACACACTCCTGA------------------------------------`
10. Ugandan_red_colobus Piliocolobus tephrosceles		`GAGCCCCGAGTCCAAGGAGACACACTCCTGA------------------------------------`
11. Olive_baboon Papio anubis		`GAGCCCCGAGTCCAAGCAGATACACTCCTGA------------------------------------`
12. Sooty_mangabey Cercocebus atys		`GAGCCCCGAGCCCAAGCAGACACACTCCTGA------------------------------------`
13. Drill Mandrillus leucophaeus		`GAGCCCCGAGTCCAAGCAGACACACTCCTGA------------------------------------`
14. Green_monkey Chlorocebus sabaeus		`GAGCCCCGAGTCCAAGCAGACACACTCCTGA------------------------------------`
15. Southern_PT_macaque Macaca nemestrina		`GAGCCCCGAGTCCAAGCAGACACACTCCTGA------------------------------------`
16. Rhesus_macaque Macaca mulatta		`GAGCCCCGAGTCCAAGCAGACACACTCCTGA------------------------------------`
17. CE_macaque Macaca fascicularis		`GAGCCCCGAGTCCAAGCAGACACACTCCTGA------------------------------------`
18. WH_capuchin Cebus capucinus imitator		`GAGCCCCGAGCCCAAGCAGACGCACTCCTGA------------------------------------`
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		`GAGCCCCGAGCCCAAGCAGACGCACTCCTGA------------------------------------`
20. NM_night_monkey Aotus nancymaae		`GAGCCCCGAGCCCAAGCAGACGCACTCCTGCCCATGA------------------------------`
21. Common_marmoset Callithrix jacchus		`CCCGAGCCCAAGCAGATGCACTCCTGACCCATGATGA------------------------------`
22. Philippine_tarsier Carlito syrichta		`GGGTCCCAAGCCCACGCAGACGTGCTCCGGACAGCCTGGGGAGTGGTGCCCGCTGACGTGCCAGCAA`
23. Gray_mouse_lemur Microcebus murinus		`GAGCCCCGAGCCCAAGCAGACGCACTCCTGA------------------------------------`
24. Coquerels_sifaka Propithecus coquereli		`GAGCTCTGAGCCCAAGCAGACGCACTCCTGA------------------------------------`
25. Northern_greater_galago Otolemur garnettii		`GAGCCCCGAACCCAAGAAGACACACTCCTGA------------------------------------`

Site # 336 ● with ○ w/o Gaps

Species/Abbrv	Group Name	`**** ** *** **   ***   ***    *  * * *         *             *`
1. Human Homo sapiens		`AGCTGCTGCTGCTG---GAGCCTGAGCGGCAGGAGGAGGGCCACAAGGACAACGCCGAGGCCCAGCA`
2. Chimpanzee Pan paniscus		`AGCTGCTGCTGCTG---GAGCCTGAGCGGCAGGAGGAGGGCCAGAAGGACAACGCCGAGGCCCAGCA`
3. Bonobo Pan troglodytes		`AGCTGCTGCTGCTG---GAGCCTGAGCGGCAGGAGGAGGGCCAGAAGGACAACGCCGAGGCCCAGCA`
4. Gorilla Gorilla gorilla gorilla		`AGCTGCTGCTGCTG---GAGCCTGAGCGGCAGGAGGAGGGCCAGAAGGACAACGCCGAGGCCCAGCA`
5. Sumatran_orangutan Pongo abelii		`AGCTGCTGCTGCTGTTGGAGCCTGAGCGGCAGGAGGAGGGCCAGAAGGACAACGCTGAGGCCCAGCA`
6. WC_gibbon Nomascus leucogenys		`AGCTGCTGCTGATG---GAGCGTGAGCGGCAGGAGGAGGGCCAG---GACAATGCCGAGGCCCAGCA`
7. Black_SN_monkey Rhinopithecus bieti		`AGCTGCTGCTGATG---GAGCCTGAGCGGCAGGAGGAGGCCCAGGAGGACAACGCCGAGGCCCAGCA`
8. Golden_SN_monkey Rhinopithecus roxellana		`AGCTGCTGCTGATG---GAGCCTGAGCGGCAGGAGGAGGCCCAGGAGGACAACGCTGAGGCCCAGCA`
9. Angolan_colobus Colobus angolensis palliatus		`AGCTGCTGCTGATG---GAGCCTGAGAGGCAGGAGGAGGCCCAGGAGGACAATGCCGAGGCCCAGCA`
10. Ugandan_red_colobus Piliocolobus tephrosceles		`AGCTGCTGCTGATG---GAGCCTGAGCGGCAGGAGGAGGCCCAGGAGGACAACGCCGAGGCCCAGCA`
11. Olive_baboon Papio anubis		`AGCTGCTGCTGATG---GAGCCTGAGCGGCAGGAGGAGGGCCAGGAGGACAACGCCGAGGCCCAGAA`
12. Sooty_mangabey Cercocebus atys		`AGCTGCTGCTGATG---GAGCCTGAGCGGCAGGAGGAGGGCCAGGAGGACAACGCCGAGGCCCAGAA`
13. Drill Mandrillus leucophaeus		`AGCTGCTGCTGATG---GAGCCTGAGCGGCAGGAGGAGGGCCAGGAGGACAACGCCGAGGCCCAGAA`
14. Green_monkey Chlorocebus sabaeus		`AGCTGCTGCTGATG---GAGCCTGAGCGGCACGAGGAGGACCAGGAGGACAACGCCGAGGCCCAGCA`
15. Southern_PT_macaque Macaca nemestrina		`AGCTGCTGCTGATG---GAGCCTGAGCGGCAGGAGGAGGGCCAGGAGGACAACGCTGAGGCCCAGAA`
16. Rhesus_macaque Macaca mulatta		`AGCTGCTGCTGATG---GAGCCTGAGCGGCAGGAGGAGGGCCAGGAGGACAACGCTGAGGCCCAGAA`
17. CE_macaque Macaca fascicularis		`AGCTGCTGCTGATG---GAGCCTGAGCGGCAGGAGGAGGGCCAGGAGGACAACGCTGAGGCCCAGAA`
18. WH_capuchin Cebus capucinus imitator		`AGCTGCTACTGATG---GAGTCGGAGCGGCAGGAAGAG---GATGAGGACAGTGCCAAGGCCAAGCA`
19. BC_squirrel_monkey Saimiri boliviensis boliviensi		`AGCTGCTACTGATG---GAGCCGGAGCGGCAGGAAGAG------GAGGACAGTGCCAAGGCCAAGCA`
20. NM_night_monkey Aotus nancymaae		`AGCTGCTGCTGATG---GAGCCGGAGCGGCAGAAAGAG---GATGAGGACAGTGCCAAAGCCAAGCA`
21. Common_marmoset Callithrix jacchus		`AGCTGCTACTGATG---GAGCCGGAGCAGCAGGAAGGGATGAGGACAGTGCCAAGGACAAGCAGAAC`
22. Philippine_tarsier Carlito syrichta		`AGCTGCTTCTGATG---GAGCCCGAGTGGAAGGAGGAGAGCACAGTGGACAACCCCATGACCCAGCA`
23. Gray_mouse_lemur Microcebus murinus		`AGCTGCTACTGATG---GAGTCGGAGCAGCAGGAGGCGGCGGCCGAGGACAGCCCCGTGGCCCAGCA`
24. Coquerels_sifaka Propithecus coquereli		`AGCTGCTACTGATG---GAGCCTGAGCAGCAGGAGGAGACGGCCGAAGACAGCCCCGTGGCCCAGCA`
25. Northern_greater_galago Otolemur garnettii		`AGCTACTGCTGATG---GAGTCTGAGCAACAGGAAGAGGAGGCCGAAGATAGCCCCGCAGCCCAGCA`

Site # 269 ● with ○ w/o Gaps



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Species/Abbrv                                          Group Name   *
1. Human  Homo sapiens                                            TCCTGA------------------------------------------------------------
2. Chimpanzee  Pan paniscus                                       TCCTGA------------------------------------------------------------
3. Bonobo  Pan troglodytes                                        TCCTGA------------------------------------------------------------
4. Gorilla  Gorilla gorilla gorilla                               TCCTGA------------------------------------------------------------
5. Sumatran_orangutan  Pongo abelii                               TCCTGA------------------------------------------------------------
6. WC_gibbon  Nomascus leucogenys                                 TCCTGA------------------------------------------------------------
7. Black_SN_monkey  Rhinopithecus bieti                           TCCTGA------------------------------------------------------------
8. Golden_SN_monkey  Rhinopithecus roxellana                      TCCTGA------------------------------------------------------------
9. Angolan_colobus  Colobus angolensis palliatus                  TCCTGA------------------------------------------------------------
10. Ugandan_red_colobus  Piliocolobus tephrosceles                TCCTGA------------------------------------------------------------
11. Olive_baboon  Papio anubis                                    TCCTGA------------------------------------------------------------
12. Sooty_mangabey  Cercocebus atys                               TCCTGA------------------------------------------------------------
13. Drill  Mandrillus leucophaeus                                 TCCTGA------------------------------------------------------------
14. Green_monkey  Chlorocebus sabaeus                             TCCTGA------------------------------------------------------------
15. Southern_PT_macaque  Macaca nemestrina                        TCCTGA------------------------------------------------------------
16. Rhesus_macaque  Macaca mulatta                                TCCTGA------------------------------------------------------------
17. CE_macaque  Macaca fascicularis                               TCCTGA------------------------------------------------------------
18. WH_capuchin  Cebus capucinus imitator                         TCCTGA------------------------------------------------------------
19. BC_squirrel_monkey  Saimiri boliviensis boliviensi            TCCTGA------------------------------------------------------------
20. NM_night_monkey  Aotus nancymaae                              TCCTGCCCATGA------------------------------------------------------
21. Common_marmoset  Callithrix jacchus                           GACCCATGATGA------------------------------------------------------
22. Philippine_tarsier  Carlito syrichta                          TCCGGACAGCCTGGGGAGTGGTGCCCGCTGACGTGCCAGCAAGAACTTTTGGAAAAGAGCCAATAA
23. Gray_mouse_lemur  Microcebus murinus                          TCCTGA------------------------------------------------------------
24. Coquerels_sifaka  Propithecus coquereli                       TCCTGA------------------------------------------------------------
25. Northern_greater_galago  Otolemur garnettii                   TCCTGA------------------------------------------------------------
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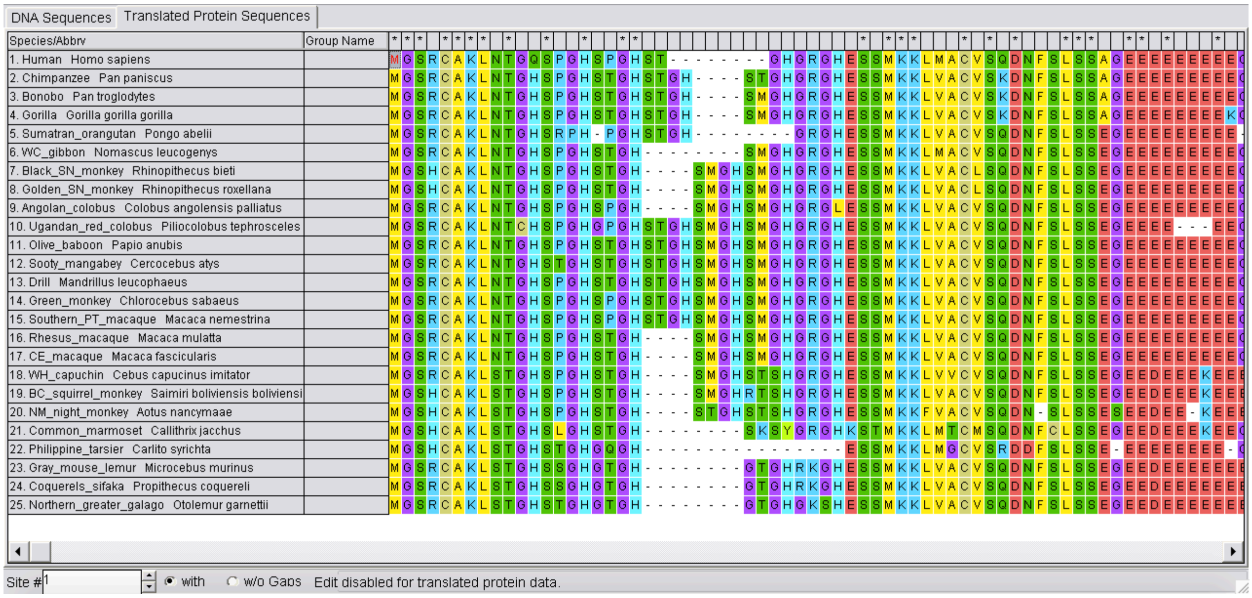
Site # 403   ● with   ○ w/o Gaps



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Species/Abbrv                                          Group Name *** **** *  *  *  **                 * ***   * * *   ***  ** *   *
1. Human  Homo sapiens                                            MGSRCAKLNTGQSPGHSPGHST--------GHGRGHESSMKKLMACVSQDNFSLSSAGEEEEEEEEE
2. Chimpanzee  Pan paniscus                                       MGSRCAKLNTGHSPGHSTGHSTGH----STGHGRGHESSMKKLVACVSKDNFSLSSAGEEEEEEEEE
3. Bonobo  Pan troglodytes                                        MGSRCAKLNTGHSPGHSTGHSTGH----SMGHGRGHESSMKKLVACVSKDNFSLSSAGEEEEEEEEE
4. Gorilla  Gorilla gorilla gorilla                               MGSRCAKLNTGHSPGHSTGHSTGH----SMGHGRGHESSMKKLVACVSKDNFSLSSAGEEEEEEEEK
5. Sumatran_orangutan  Pongo abelii                               MGSRCAKLNTGHSRPH-PGHSTGH--------GRGHESSMKKLVACVSQDNFSLSSEGEEEEEEEEE
6. WC_gibbon  Nomascus leucogenys                                 MGSRCAKLNTGHSPGHSTGH--------SMGHGRGHESSMKKLMACVSQDNFSLSSEGEEEEEEEEE
7. Black_SN_monkey  Rhinopithecus bieti                           MGSHCAKLNTGHSPGHSTGH----SMGHSMGHGRGHESSMKKLVACLSQDNFSLSSEGEEEEEEEEE
8. Golden_SN_monkey  Rhinopithecus roxellana                      MGSHCAKLNTGHSPGHSTGH----SMGHSMGHGRGHESSMKKLVACLSQDNFSLSSEGEEEEEEEEE
9. Angolan_colobus  Colobus angolensis palliatus                  MGSRCAKLNTGHSPGHSPGH----SMGHSMGHGRGLESSMKKLVACVSQDNFSLSSEGEEEEEEEEE
10. Ugandan_red_colobus  Piliocolobus tephrosceles                MGSRCAKLNTCHSPGHGPGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEEEE---EE
11. Olive_baboon  Papio anubis                                    MGSRCAKLNTGHSPGHSTGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEEEEEEEEE
12. Sooty_mangabey  Cercocebus atys                               MGSRCAKLNTGHSTGHSTGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEEEEEEEEE
13. Drill  Mandrillus leucophaeus                                 MGSRCAKLNTGHSPGHSTGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEEEEEEEEE
14. Green_monkey  Chlorocebus sabaeus                             MGSRCAKLNTGHSPGHSPGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEEEEEEEEE
15. Southern_PT_macaque  Macaca nemestrina                        MGSRCAKLNTGHSPGHSPGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEEEEEEEEE
16. Rhesus_macaque  Macaca mulatta                                MGSRCAKLNTGHSPGHSTGH----SMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEEEEEEEEE
17. CE_macaque  Macaca fascicularis                               MGSRCAKLNTGHSPGHSTGH----SMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEEEEEEEEE
18. WH_capuchin  Cebus capucinus imitator                         MGSRCAKLSTGHSPGHSTGH----SMGHSTSHGRGHESSMKKLVVCVSQDNFSLSSEGEEDEEEKEE
19. BC_squirrel_monkey  Saimiri boliviensis boliviensi            MGSHCAKLSTGHSPGHSTGH----SMGHRTSHGRGHESSMKKLVACVSQDNFSLSSEGEEDEEEKEE
20. NM_night_monkey  Aotus nancymaae                              MGSHCAKLSTGHSPGHSTGH----STGHSTSHGRGHESSMKKFVACVSQDN-SLSSESEEDEE-KEE
21. Common_marmoset  Callithrix jacchus                           MGSHCAKLSTGHSLGHSTGH--------SKSYGRGHKSTMKKLMTCMSQDNFCLSSEGEEDEEEKEE
22. Philippine_tarsier  Carlito syrichta                          MGSHCAKLSTGHSTGHGQGH----------------ESSMKKLMGCVSRDDFSLSSE-EEEEEEEE-
23. Gray_mouse_lemur  Microcebus murinus                          MGSRCAKLSTGHSSGHGTGH--------GTGHRKGHESSMKKLVACVSQDNFSLSSEGEEDEEEEEE
24. Coquerels_sifaka  Propithecus coquereli                       MGSRCAKLSTGHSSGHGTGH--------GTGHRKGHESSMKKLVACVSQDNFSLSSEGEEDEEEEEE
25. Northern_greater_galago  Otolemur garnettii                   MGSRCAKLSTGHSTGHGTGH--------GTGHGKSHESSMKKLVACVSQDNFSLSSEGEEDEEEEEE
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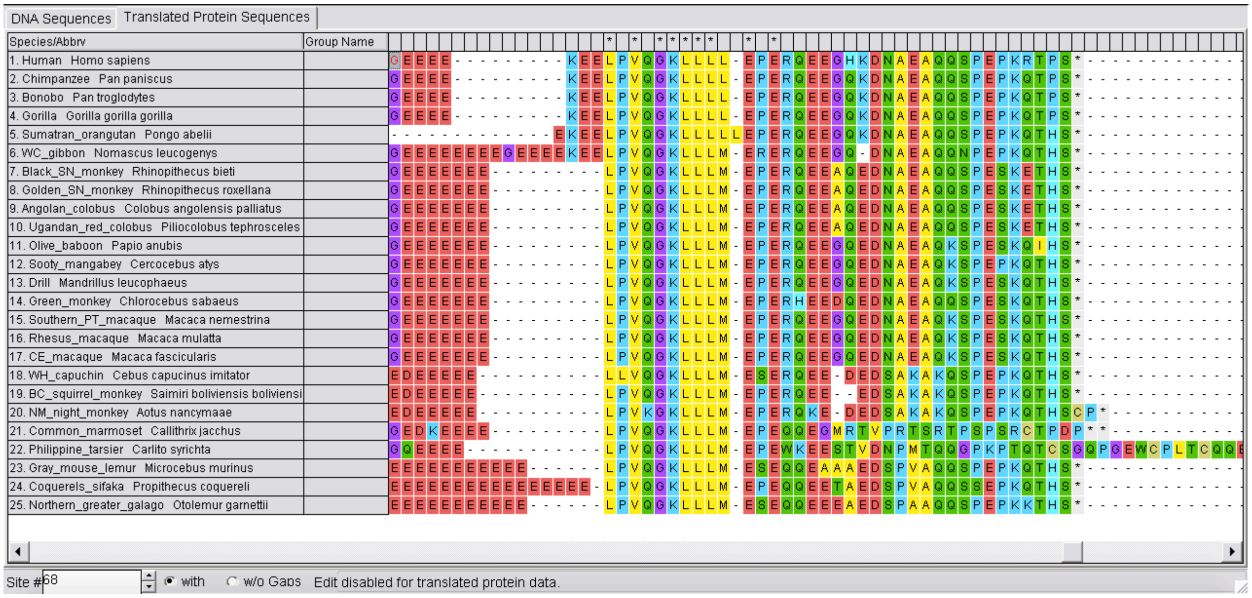

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Species/Abbrv                                Group Name                   * * *****  * *
1. Human  Homo sapiens                                  GEEEE---------KEELPVQGKLLLL-EPERQEEGHKDNAEAQQSPEPKRTPS*-------------
2. Chimpanzee  Pan paniscus                             GEEEE---------KEELPVQGKLLLL-EPERQEEGQKDNAEAQQSPEPKQTPS*-------------
3. Bonobo  Pan troglodytes                              GEEEE---------KEELPVQGKLLLL-EPERQEEGQKDNAEAQQSPEPKQTPS*-------------
4. Gorilla  Gorilla gorilla gorilla                     GEEEE---------KEELPVQGKLLLL-EPERQEEGQKDNAEAQQSPEPKQTPS*-------------
5. Sumatran_orangutan  Pongo abelii                     -------------EKEELPVQGKLLLLLEPERQEEGQKDNAEAQQSPEPKQTHS*-------------
6. WC_gibbon  Nomascus leucogenys                       GEEEEEEEEGEEEEKEELPVQGKLLLM-ERERQEEGQ-DNAEAQQNPEPKQTHS*-------------
7. Black_SN_monkey  Rhinopithecus bieti                 GEEEEEEE---------LPVQGKLLLM-EPERQEEAQEDNAEAQQSPESKETHS*-------------
8. Golden_SN_monkey  Rhinopithecus roxellana            GEEEEEEE---------LPVQGKLLLM-EPERQEEAQEDNAEAQQSPESKETHS*-------------
9. Angolan_colobus  Colobus angolensis palliatus        GEEEEEEE---------LPVQGKLLLM-EPERQEEAQEDNAEAQQSPESKETHS*-------------
10. Ugandan_red_colobus  Piliocolobus tephrosceles      GEEEEEEE---------LPVQGKLLLM-EPERQEEAQEDNAEAQQSPESKETHS*-------------
11. Olive_baboon  Papio anubis                          GEEEEEEE---------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPESKQIHS*-------------
12. Sooty_mangabey  Cercocebus atys                     GEEEEEEE---------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPEPKQTHS*-------------
13. Drill  Mandrillus leucophaeus                       GEEEEEEE---------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPESKQTHS*-------------
14. Green_monkey  Chlorocebus sabaeus                   GEEEEEEE---------LPVQGKLLLM-EPERHEEDQEDNAEAQQSPESKQTHS*-------------
15. Southern_PT_macaque  Macaca nemestrina              GEEEEEEE---------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPESKQTHS*-------------
16. Rhesus_macaque  Macaca mulatta                      GEEEEEEE---------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPESKQTHS*-------------
17. CE_macaque  Macaca fascicularis                     GEEEEEEE---------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPESKQTHS*-------------
18. WH_capuchin  Cebus capucinus imitator               EDEEEEE----------LLVQGKLLLM-ESERQEE-DEDSAKAKQSPEPKQTHS*-------------
19. BC_squirrel_monkey  Saimiri boliviensis boliviensi  EDEEEEE----------LPVQGKLLLM-EPERQEE--EDSAKAKQSPEPKQTHS*-------------
20. NM_night_monkey  Aotus nancymaae                    EDEEEEE----------LPVKGKLLLM-EPERQKE-DEDSAKAKQSPEPKQTHSCP*-----------
21. Common_marmoset  Callithrix jacchus                 GEDKEEEE---------LPVQGKLLLM-EPEQQEGMRTVPRTSRTPSPSRCTPDP**-----------
22. Philippine_tarsier  Carlito syrichta                GQEEEE-----------LPVQGKLLLM-EPEWKEESTVDNPMTQQGPKPTQTCSGQPGEWCPLTCQQE
23. Gray_mouse_lemur  Microcebus murinus                EEEEEEEEEEE------LPVQGKLLLM-ESEQQEAAAEDSPVAQQSPEPKQTHS*-------------
24. Coquerels_sifaka  Propithecus coquereli             EEEEEEEEEEEEEEEE-LPVQGKLLLM-EPEQQEETAEDSPVAQQSSEPKQTHS*-------------
25. Northern_greater_galago  Otolemur garnettii         EEEEEEEEEEE------LPVQGKLLLM-ESEQQEEEAEDSPAAQQSPEPKKTHS*-------------

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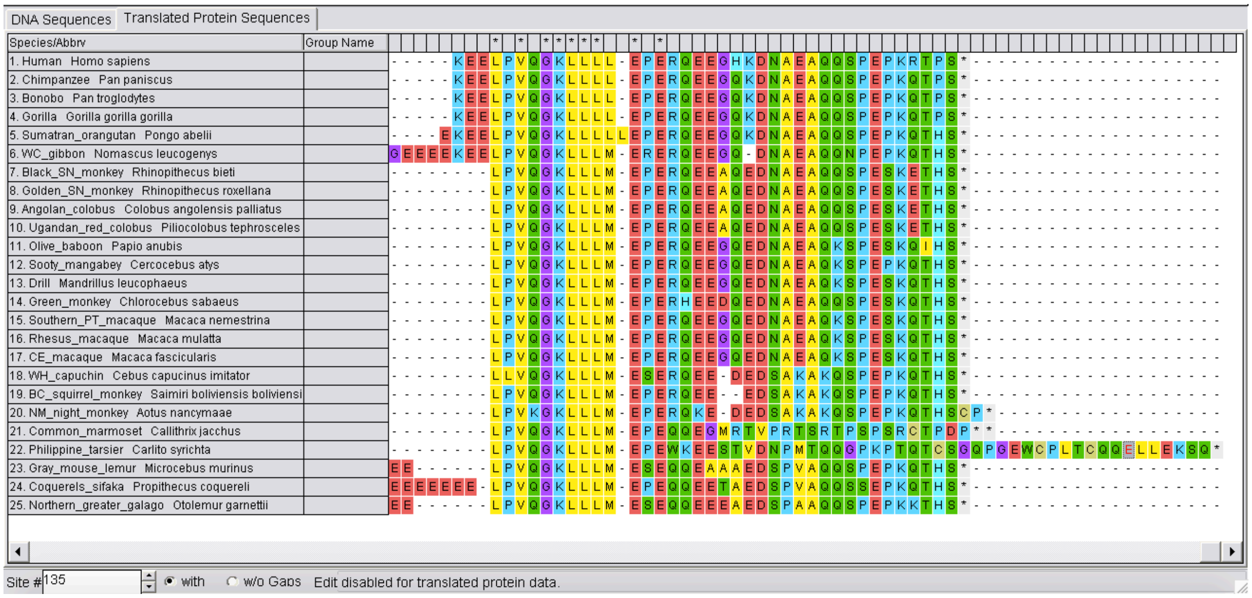

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Species/Abbrv                                Group Name          * * *****  * *
1. Human  Homo sapiens                                  -----KEELPVQGKLLLL-EPERQEEGHKDNAEAQQSPEPKRTPS*--------------------
2. Chimpanzee  Pan paniscus                             -----KEELPVQGKLLLL-EPERQEEGQKDNAEAQQSPEPKQTPS*--------------------
3. Bonobo  Pan troglodytes                              -----KEELPVQGKLLLL-EPERQEEGQKDNAEAQQSPEPKQTPS*--------------------
4. Gorilla  Gorilla gorilla gorilla                     -----KEELPVQGKLLLL-EPERQEEGQKDNAEAQQSPEPKQTPS*--------------------
5. Sumatran_orangutan  Pongo abelii                     ----EKEELPVQGKLLLLLEPERQEEGQKDNAEAQQSPEPKQTHS*--------------------
6. WC_gibbon  Nomascus leucogenys                       GEEEEKEELPVQGKLLLM-ERERQEEGQ-DNAEAQQNPEPKQTHS*--------------------
7. Black_SN_monkey  Rhinopithecus bieti                 --------LPVQGKLLLM-EPERQEEAQEDNAEAQQSPESKETHS*--------------------
8. Golden_SN_monkey  Rhinopithecus roxellana            --------LPVQGKLLLM-EPERQEEAQEDNAEAQQSPESKETHS*--------------------
9. Angolan_colobus  Colobus angolensis palliatus        --------LPVQGKLLLM-EPERQEEAQEDNAEAQQSPESKETHS*--------------------
10. Ugandan_red_colobus  Piliocolobus tephrosceles      --------LPVQGKLLLM-EPERQEEAQEDNAEAQQSPESKETHS*--------------------
11. Olive_baboon  Papio anubis                          --------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPESKQIHS*--------------------
12. Sooty_mangabey  Cercocebus atys                     --------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPEPKQTHS*--------------------
13. Drill  Mandrillus leucophaeus                       --------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPESKQTHS*--------------------
14. Green_monkey  Chlorocebus sabaeus                   --------LPVQGKLLLM-EPERHEEDQEDNAEAQQSPESKQTHS*--------------------
15. Southern_PT_macaque  Macaca nemestrina              --------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPESKQTHS*--------------------
16. Rhesus_macaque  Macaca mulatta                      --------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPESKQTHS*--------------------
17. CE_macaque  Macaca fascicularis                     --------LPVQGKLLLM-EPERQEEGQEDNAEAQKSPESKQTHS*--------------------
18. WH_capuchin  Cebus capucinus imitator               --------LLVQGKLLLM-ESERQEE-DEDSAKAKQSPEPKQTHS*--------------------
19. BC_squirrel_monkey  Saimiri boliviensis boliviensi  --------LPVQGKLLLM-EPERQEE--EDSAKAKQSPEPKQTHS*--------------------
20. NM_night_monkey  Aotus nancymaae                    --------LPVKGKLLLM-EPERQKE-DEDSAKAKQSPEPKQTHSCP*------------------
21. Common_marmoset  Callithrix jacchus                 --------LPVQGKLLLM-EPEQQEGMRTVPRTSRTPSPSRCTPDP**------------------
22. Philippine_tarsier  Carlito syrichta                --------LPVQGKLLLM-EPEWKEESTVDNPMTQQGPKPTQTCSGQPGEWCPLTCQQELLEKSQ*
23. Gray_mouse_lemur  Microcebus murinus                EE------LPVQGKLLLM-ESEQQEAAAEDSPVAQQSPEPKQTHS*--------------------
24. Coquerels_sifaka  Propithecus coquereli             EEEEEEE-LPVQGKLLLM-EPEQQEETAEDSPVAQQSSEPKQTHS*--------------------
25. Northern_greater_galago  Otolemur garnettii         EE------LPVQGKLLLM-ESEQQEEEAEDSPAAQQSPEPKKTHS*--------------------

Site # 135   ● with   ○ w/o Gaps   Edit disabled for translated protein data.
```

BLAST ® » blastn suite » RID-22Z6XB6N015

BLAST Results

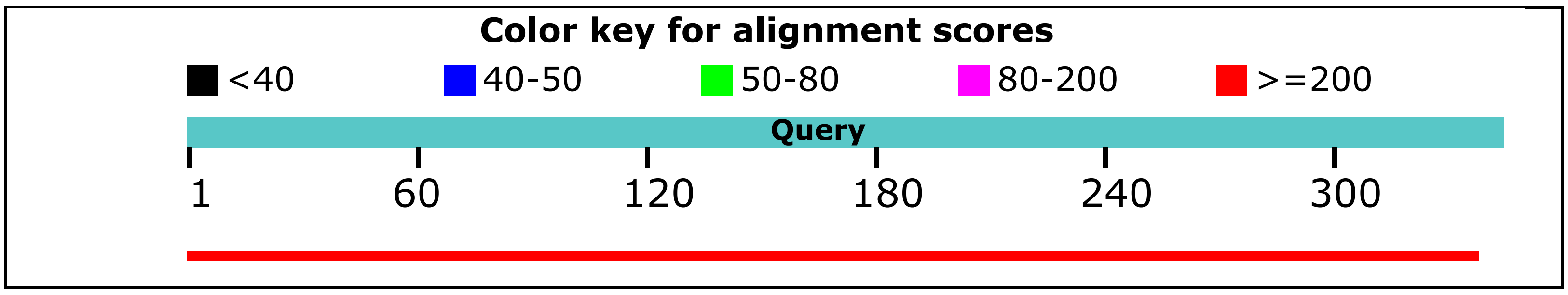
Appendix I: NCBI Blast Carlito syrichta Prm3 v. Carlito syrichta genome

Job title: NW_007249715.1:129292-129627 Carlito syrichta

RID	22Z6XB6N015 (Expires on 12-02 23:01 pm)		
Query ID	lcl|Query_160503	**Database Name**	Genome (Tarsius_syrichta-2.0.1 reference Annotation Release 101)
Description	NW_007249715.1:129292-129627 Carlito syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold305619, whole genome shotgun sequence	**Description**	Carlito syrichta Tarsius_syrichta-2.0.1 [GCF_000164805.1] chromosomes plus unplaced and unlocalized scaffolds (reference assembly in Annotation Release 101)
Molecule type	nucleic acid		
Query Length	336	**Program**	BLASTN 2.7.1+

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Carlito syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold305619	621	621	100%	8e-176	100%	NW_007249715.1

Alignments

Carlito syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold305619

Sequence ID: **NW_007249715.1** Length: 506769 Number of Matches: 1
Range 1: 129292 to 129627

Score	Expect	Identities	Gaps	Strand	Frame
621 bits(336)	8e-176()	336/336(100%)	0/336(0%)	Plus/Plus	

Features:

```
Query  1       ATGGGATCCCACTGTGCCAAGCTCAGCACCGGCCACAGCACAGGCCACGGCCAGGGCCAC  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129292  ATGGGATCCCACTGTGCCAAGCTCAGCACCGGCCACAGCACAGGCCACGGCCAGGGCCAC  129351

Query  61      GAATCCTCCATGAAGAAGCTTATGGGCTGCGTGAGCCGAGATGACTTCTCCTTGTCGtcg  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129352  GAATCCTCCATGAAGAAGCTTATGGGCTGCGTGAGCCGAGATGACTTCTCCTTGTCGTCG  129411

Query  121     gaggaggaagaggaggaagaggaggaagggcaggaggaggaggagcttcCGGTGCAGGGC  180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129412  GAGGAGGAAGAGGAGGAAGAGGAGGAAGGGCAGGAGGAGGAGGAGCTTCCGGTGCAGGGC  129471

Query  181     AAGCTGCTTCTGATGGAGCCCGAGTGGAAGGAGGAGAGCACAGTGGACAACCCCATGACC  240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129472  AAGCTGCTTCTGATGGAGCCCGAGTGGAAGGAGGAGAGCACAGTGGACAACCCCATGACC  129531

Query  241     CAGCAGGGTCCCAAGCCCACGCAGACGTGCTCCGGACAGCCTGGGGAGTGGTGCCCGCTG  300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129532  CAGCAGGGTCCCAAGCCCACGCAGACGTGCTCCGGACAGCCTGGGGAGTGGTGCCCGCTG  129591

Query  301     ACGTGCCAGCAAGAACTTTTGGAAAAGAGCCAATAA  336
               ||||||||||||||||||||||||||||||||||||
Sbjct  129592  ACGTGCCAGCAAGAACTTTTGGAAAAGAGCCAATAA  129627
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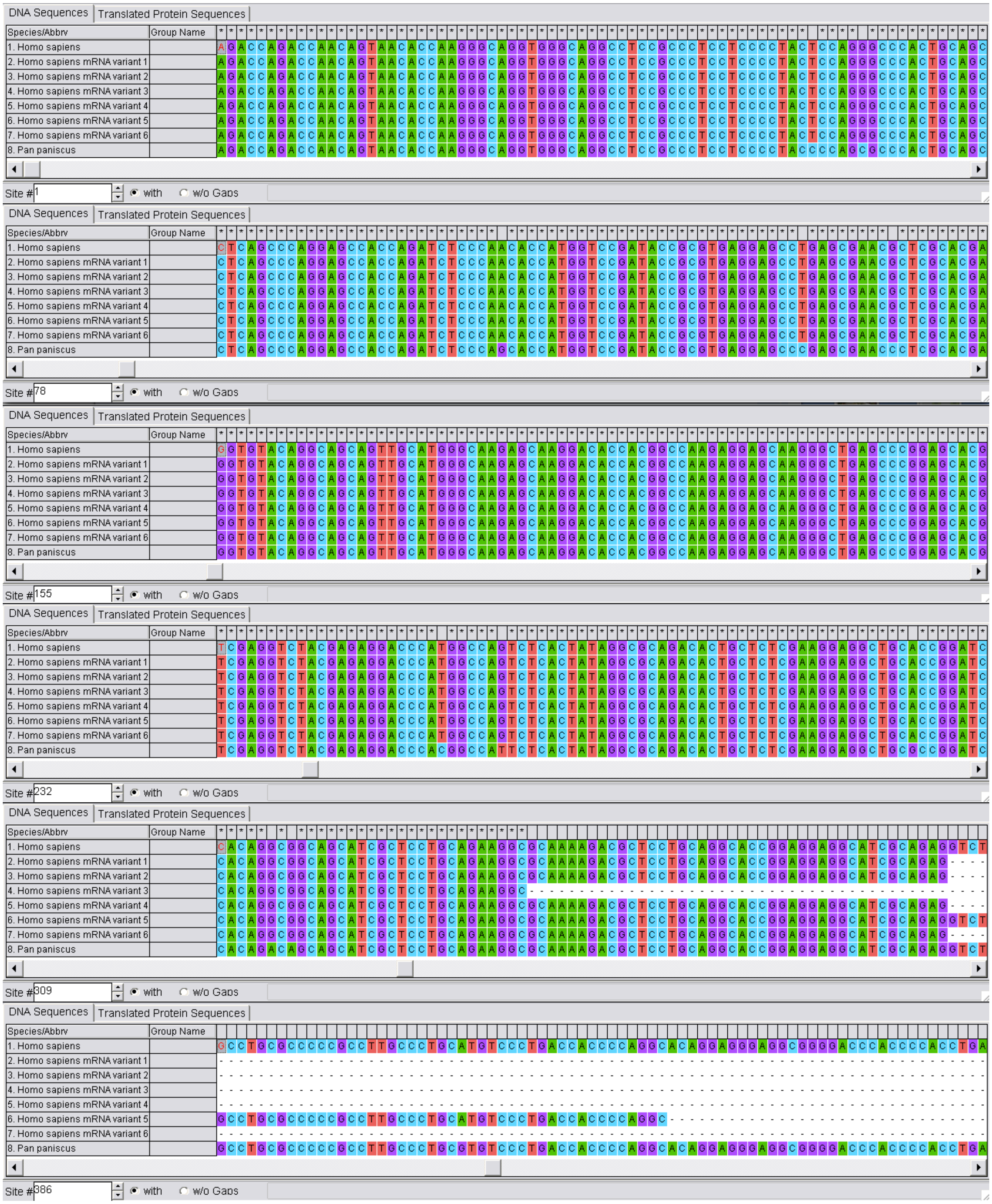
Appendix J) *Prm2* predicted mRNA isoforms alignment



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Species/Abbrv                  Group Name  *********************************************************** **** ************
1. Homo sapiens                            AGACCAGACCAACAGTAACACCAAGGGCAGGTGGGCAGGCCTCCGCCCTCCTCCCCTACTCCAGGGCCCACTGCAGC
2. Homo sapiens mRNA variant 1             AGACCAGACCAACAGTAACACCAAGGGCAGGTGGGCAGGCCTCCGCCCTCCTCCCCTACTCCAGGGCCCACTGCAGC
3. Homo sapiens mRNA variant 2             AGACCAGACCAACAGTAACACCAAGGGCAGGTGGGCAGGCCTCCGCCCTCCTCCCCTACTCCAGGGCCCACTGCAGC
4. Homo sapiens mRNA variant 3             AGACCAGACCAACAGTAACACCAAGGGCAGGTGGGCAGGCCTCCGCCCTCCTCCCCTACTCCAGGGCCCACTGCAGC
5. Homo sapiens mRNA variant 4             AGACCAGACCAACAGTAACACCAAGGGCAGGTGGGCAGGCCTCCGCCCTCCTCCCCTACTCCAGGGCCCACTGCAGC
6. Homo sapiens mRNA variant 5             AGACCAGACCAACAGTAACACCAAGGGCAGGTGGGCAGGCCTCCGCCCTCCTCCCCTACTCCAGGGCCCACTGCAGC
7. Homo sapiens mRNA variant 6             AGACCAGACCAACAGTAACACCAAGGGCAGGTGGGCAGGCCTCCGCCCTCCTCCCCTACTCCAGGGCCCACTGCAGC
8. Pan paniscus                            AGACCAGACCAACAGTAACACCAAGGGCAGGTGGGCAGGCCTCCGCCCTCCTCCCCTACCCCAGCGCCCACTGCAGC
Site # 1   ● with   ○ w/o Gaps

Species/Abbrv                  Group Name  **************************** ***************************** ******** *********
1. Homo sapiens                            CTCAGCCCAGGAGCCACCAGATCTCCCAACACCATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGA
2. Homo sapiens mRNA variant 1             CTCAGCCCAGGAGCCACCAGATCTCCCAACACCATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGA
3. Homo sapiens mRNA variant 2             CTCAGCCCAGGAGCCACCAGATCTCCCAACACCATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGA
4. Homo sapiens mRNA variant 3             CTCAGCCCAGGAGCCACCAGATCTCCCAACACCATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGA
5. Homo sapiens mRNA variant 4             CTCAGCCCAGGAGCCACCAGATCTCCCAACACCATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGA
6. Homo sapiens mRNA variant 5             CTCAGCCCAGGAGCCACCAGATCTCCCAACACCATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGA
7. Homo sapiens mRNA variant 6             CTCAGCCCAGGAGCCACCAGATCTCCCAACACCATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGA
8. Pan paniscus                            CTCAGCCCAGGAGCCACCAGATCTCCCAGCACCATGGTCCGATACCGCGTGAGGAGCCCGAGCGAACCCTCGCACGA
Site # 78   ● with   ○ w/o Gaps

Species/Abbrv                  Group Name  *****************************************************************************
1. Homo sapiens                            GGTGTACAGGCAGCAGTTGCATGGGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACG
2. Homo sapiens mRNA variant 1             GGTGTACAGGCAGCAGTTGCATGGGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACG
3. Homo sapiens mRNA variant 2             GGTGTACAGGCAGCAGTTGCATGGGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACG
4. Homo sapiens mRNA variant 3             GGTGTACAGGCAGCAGTTGCATGGGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACG
5. Homo sapiens mRNA variant 4             GGTGTACAGGCAGCAGTTGCATGGGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACG
6. Homo sapiens mRNA variant 5             GGTGTACAGGCAGCAGTTGCATGGGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACG
7. Homo sapiens mRNA variant 6             GGTGTACAGGCAGCAGTTGCATGGGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACG
8. Pan paniscus                            GGTGTACAGGCAGCAGTTGCATGGGCAAGAGCAAGGACACCACGGCCAAGAGGAGCAAGGGCTGAGCCCGGAGCACG
Site # 155   ● with   ○ w/o Gaps

Species/Abbrv                  Group Name  ********************** ***** **************************************** *******
1. Homo sapiens                            TCGAGGTCTACGAGAGGACCCATGGCCAGTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCACCGGATC
2. Homo sapiens mRNA variant 1             TCGAGGTCTACGAGAGGACCCATGGCCAGTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCACCGGATC
3. Homo sapiens mRNA variant 2             TCGAGGTCTACGAGAGGACCCATGGCCAGTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCACCGGATC
4. Homo sapiens mRNA variant 3             TCGAGGTCTACGAGAGGACCCATGGCCAGTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCACCGGATC
5. Homo sapiens mRNA variant 4             TCGAGGTCTACGAGAGGACCCATGGCCAGTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCACCGGATC
6. Homo sapiens mRNA variant 5             TCGAGGTCTACGAGAGGACCCATGGCCAGTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCACCGGATC
7. Homo sapiens mRNA variant 6             TCGAGGTCTACGAGAGGACCCATGGCCAGTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCACCGGATC
8. Pan paniscus                            TCGAGGTCTACGAGAGGACCCACGGCCATTCTCACTATAGGCGCAGACACTGCTCTCGAAGGAGGCTGCGCCGGATC
Site # 232   ● with   ○ w/o Gaps

Species/Abbrv                  Group Name  ***** * ***********************
1. Homo sapiens                            CACAGGCGGCAGCATCGCTCCTGCAGAAGGCGCAAAAGACGCTCCTGCAGGCACCGGAGGAGGCATCGCAGAGGTCT
2. Homo sapiens mRNA variant 1             CACAGGCGGCAGCATCGCTCCTGCAGAAGGCGCAAAAGACGCTCCTGCAGGCACCGGAGGAGGCATCGCAGAG----
3. Homo sapiens mRNA variant 2             CACAGGCGGCAGCATCGCTCCTGCAGAAGGCGCAAAAGACGCTCCTGCAGGCACCGGAGGAGGCATCGCAGAG----
4. Homo sapiens mRNA variant 3             CACAGGCGGCAGCATCGCTCCTGCAGAAGGC----------------------------------------------
5. Homo sapiens mRNA variant 4             CACAGGCGGCAGCATCGCTCCTGCAGAAGGCGCAAAAGACGCTCCTGCAGGCACCGGAGGAGGCATCGCAGAG----
6. Homo sapiens mRNA variant 5             CACAGGCGGCAGCATCGCTCCTGCAGAAGGCGCAAAAGACGCTCCTGCAGGCACCGGAGGAGGCATCGCAGAGGTCT
7. Homo sapiens mRNA variant 6             CACAGGCGGCAGCATCGCTCCTGCAGAAGGCGCAAAAGACGCTCCTGCAGGCACCGGAGGAGGCATCGCAGAG----
8. Pan paniscus                            CACAGACAGCAGCATCGCTCCTGCAGAAGGCGCAAAAGACGCTCCTGCAGGCACCGGAGGAGGCATCGCAGAGGTCT
Site # 309   ● with   ○ w/o Gaps

Species/Abbrv                  Group Name
1. Homo sapiens                            GCCTGCGCCCCCGCCTTGCCCTGCATGTCCCTGACCACCCCAGGCACAGGAGGGAGGCGGGGACCCACCCCACCTGA
2. Homo sapiens mRNA variant 1             -----------------------------------------------------------------------------
3. Homo sapiens mRNA variant 2             -----------------------------------------------------------------------------
4. Homo sapiens mRNA variant 3             -----------------------------------------------------------------------------
5. Homo sapiens mRNA variant 4             -----------------------------------------------------------------------------
6. Homo sapiens mRNA variant 5             GCCTGCGCCCCCGCCTTGCCCTGCATGTCCCTGACCACCCCAGGC--------------------------------
7. Homo sapiens mRNA variant 6             -----------------------------------------------------------------------------
8. Pan paniscus                            GCCTGCGCCCCCGCCTTGCCCTGCGTGTCCCTGACCACCCCAGGCACAGGAGGGAGGCGGGGACCCACCCCACCTGA
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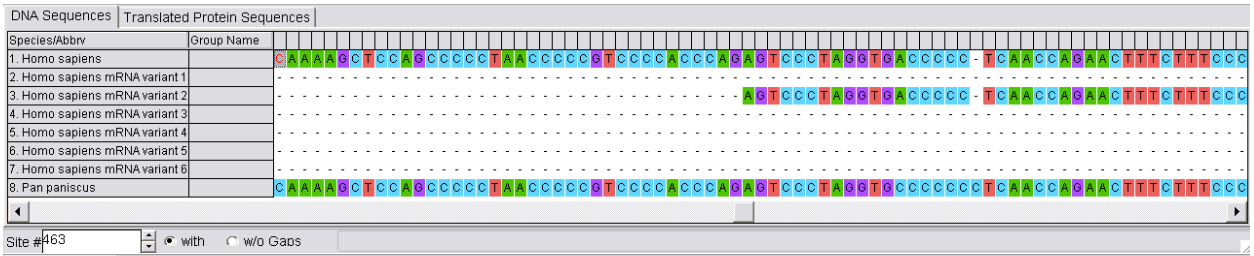

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Species/Abbrv                 Group Name
1. Homo sapiens                           CAAAAGCTCCAGCCCCCTAACCCCCGTCCCCACCCAGAGTCCCTAGGTGACCCCC-TCAACCAGAACTTTCTTTCCC
2. Homo sapiens mRNA variant 1            -----------------------------------------------------------------------------
3. Homo sapiens mRNA variant 2            -------------------------------------AGTCCCTAGGTGACCCCC-TCAACCAGAACTTTCTTTCCC
4. Homo sapiens mRNA variant 3            -----------------------------------------------------------------------------
5. Homo sapiens mRNA variant 4            -----------------------------------------------------------------------------
6. Homo sapiens mRNA variant 5            -----------------------------------------------------------------------------
7. Homo sapiens mRNA variant 6            -----------------------------------------------------------------------------
8. Pan paniscus                           CAAAAGCTCCAGCCCCCTAACCCCCGTCCCCACCCAGAGTCCCTAGGTGCCCCCCCTCAACCAGAACTTTCTTTCCC
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Site # 463 ● with ○ w/o Gaps

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Species/Abbrv                 Group Name                                        ***************************************
1. Homo sapiens                           AAAAGGCTGCAGAACCAGGAAGAGAACATGCAGAAGGCACTAAGCTTCCTGGGCCCCTCACCCCCAGCTGGAAATTA
2. Homo sapiens mRNA variant 1            -----GCTGCAGAACCAGGAAGAGAACATGCAGAAGGCACTAAGCTTCCTGGGCCCCTCACCCCCAGCTGGAAATTA
3. Homo sapiens mRNA variant 2            AAAAGGCTGCAGAACCAGGAAGAGAACATGCAGAAGGCACTAAGCTTCCTGGGCCCCTCACCCCCAGCTGGAAATTA
4. Homo sapiens mRNA variant 3            --------------------------------------ACTAAGCTTCCTGGGCCCCTCACCCCCAGCTGGAAATTA
5. Homo sapiens mRNA variant 4            ------------AACCAGGAAGAGAACATGCAGAAGGCACTAAGCTTCCTGGGCCCCTCACCCCCAGCTGGAAATTA
6. Homo sapiens mRNA variant 5            -------TGCAGAACCAGGAAGAGAACATGCAGAAGGCACTAAGCTTCCTGGGCCCCTCACCCCCAGCTGGAAATTA
7. Homo sapiens mRNA variant 6            -----GCTGCAGAACCAGGAAGAGAACATGCAGAAGGCACTAAGCTTCCTGGGCCCCTCACCCCCAGCTGGAAATTA
8. Pan paniscus                           AAAAGGCTGCAGAACCAGGAGGAGAACATGCAGAAAGCACTAAGCTTCCTGGGCCCCTCACCCCCAGCTGGAAATTA
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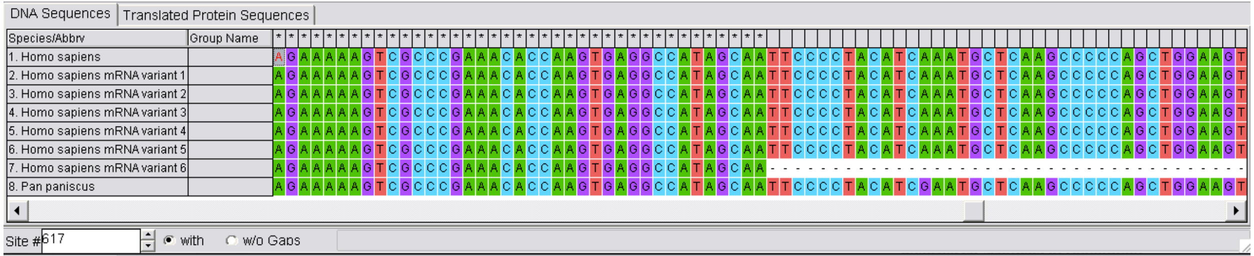
Site # 540 ● with ○ w/o Gaps



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Species/Abbrv                 Group Name  ***************************************
1. Homo sapiens                           AGAAAAAGTCGCCCGAAACACCAAGTGAGGCCATAGCAATTCCCCTACATCAAATGCTCAAGCCCCCAGCTGGAAGT
2. Homo sapiens mRNA variant 1            AGAAAAAGTCGCCCGAAACACCAAGTGAGGCCATAGCAATTCCCCTACATCAAATGCTCAAGCCCCCAGCTGGAAGT
3. Homo sapiens mRNA variant 2            AGAAAAAGTCGCCCGAAACACCAAGTGAGGCCATAGCAATTCCCCTACATCAAATGCTCAAGCCCCCAGCTGGAAGT
4. Homo sapiens mRNA variant 3            AGAAAAAGTCGCCCGAAACACCAAGTGAGGCCATAGCAATTCCCCTACATCAAATGCTCAAGCCCCCAGCTGGAAGT
5. Homo sapiens mRNA variant 4            AGAAAAAGTCGCCCGAAACACCAAGTGAGGCCATAGCAATTCCCCTACATCAAATGCTCAAGCCCCCAGCTGGAAGT
6. Homo sapiens mRNA variant 5            AGAAAAAGTCGCCCGAAACACCAAGTGAGGCCATAGCAATTCCCCTACATCAAATGCTCAAGCCCCCAGCTGGAAGT
7. Homo sapiens mRNA variant 6            AGAAAAAGTCGCCCGAAACACCAAGTGAGGCCATAGCAA--------------------------------------
8. Pan paniscus                           AGAAAAAGTCGCCCGAAACACCAAGTGAGGCCATAGCAATTCCCCTACATCGAATGCTCAAGCCCCCAGCTGGAAGT
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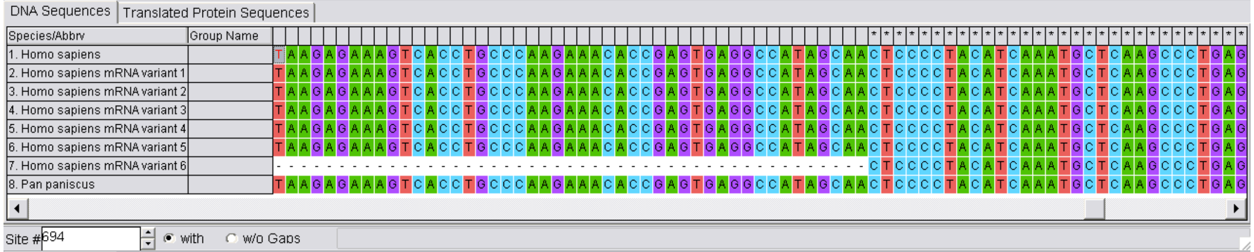
Site # 617 ● with ○ w/o Gaps



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Species/Abbrv                 Group Name                                                 ******************************
1. Homo sapiens                           TAAGAGAAAGTCACCTGCCCAAGAAACACCGAGTGAGGCCATAGCAACTCCCCTACATCAAATGCTCAAGCCCTGAG
2. Homo sapiens mRNA variant 1            TAAGAGAAAGTCACCTGCCCAAGAAACACCGAGTGAGGCCATAGCAACTCCCCTACATCAAATGCTCAAGCCCTGAG
3. Homo sapiens mRNA variant 2            TAAGAGAAAGTCACCTGCCCAAGAAACACCGAGTGAGGCCATAGCAACTCCCCTACATCAAATGCTCAAGCCCTGAG
4. Homo sapiens mRNA variant 3            TAAGAGAAAGTCACCTGCCCAAGAAACACCGAGTGAGGCCATAGCAACTCCCCTACATCAAATGCTCAAGCCCTGAG
5. Homo sapiens mRNA variant 4            TAAGAGAAAGTCACCTGCCCAAGAAACACCGAGTGAGGCCATAGCAACTCCCCTACATCAAATGCTCAAGCCCTGAG
6. Homo sapiens mRNA variant 5            TAAGAGAAAGTCACCTGCCCAAGAAACACCGAGTGAGGCCATAGCAACTCCCCTACATCAAATGCTCAAGCCCTGAG
7. Homo sapiens mRNA variant 6            -----------------------------------------------CTCCCCTACATCAAATGCTCAAGCCCTGAG
8. Pan paniscus                           TAAGAGAAAGTCACCTGCCCAAGAAACACCGAGTGAGGCCATAGCAACTCCCCTACATCAAATGCTCAAGCCCTGAG
```

Site # 694 ● with ○ w/o Gaps

```
Species/Abbrv                 Group Name  ********************************** *****************************************
1. Homo sapiens                           TTGCCGCCGAGAAGCCCACAAGATCTGAGTGAAACGAGCAAAAGTCACCTGCCCAATAAAGCTTGACAAGACACTC
2. Homo sapiens mRNA variant 1            TTGCCGCCGAGAAGCCCACAAGATCTGAGTGAAATGAGCAAAAGTCACCTGCCCAATAAAGCTTGACAAGACACTC
3. Homo sapiens mRNA variant 2            TTGCCGCCGAGAAGCCCACAAGATCTGAGTGAAATGAGCAAAAGTCACCTGCCCAATAAAGCTTGACAAGACACTC
4. Homo sapiens mRNA variant 3            TTGCCGCCGAGAAGCCCACAAGATCTGAGTGAAATGAGCAAAAGTCACCTGCCCAATAAAGCTTGACAAGACACTC
5. Homo sapiens mRNA variant 4            TTGCCGCCGAGAAGCCCACAAGATCTGAGTGAAATGAGCAAAAGTCACCTGCCCAATAAAGCTTGACAAGACACTC
6. Homo sapiens mRNA variant 5            TTGCCGCCGAGAAGCCCACAAGATCTGAGTGAAATGAGCAAAAGTCACCTGCCCAATAAAGCTTGACAAGACACTC
7. Homo sapiens mRNA variant 6            TTGCCGCCGAGAAGCCCACAAGATCTGAGTGAAATGAGCAAAAGTCACCTGCCCAATAAAGCTTGACAAGACACTC
8. Pan paniscus                           TTGCCGCCGAGAAGCCCACAAGATCTGAGTGAAATGAGCAAAAGTCACCTGCCCAATAAAGCTTGACAAGACACTC
```

Site # 771 ● with ○ w/o Gaps

BLAST ® » tblastn » RID-ZJ6T120K015

BLAST Results

Appendix K: NCBI tBlastn NP_002753.2 PRM2 isoform 1 v. Homo sapiens EST

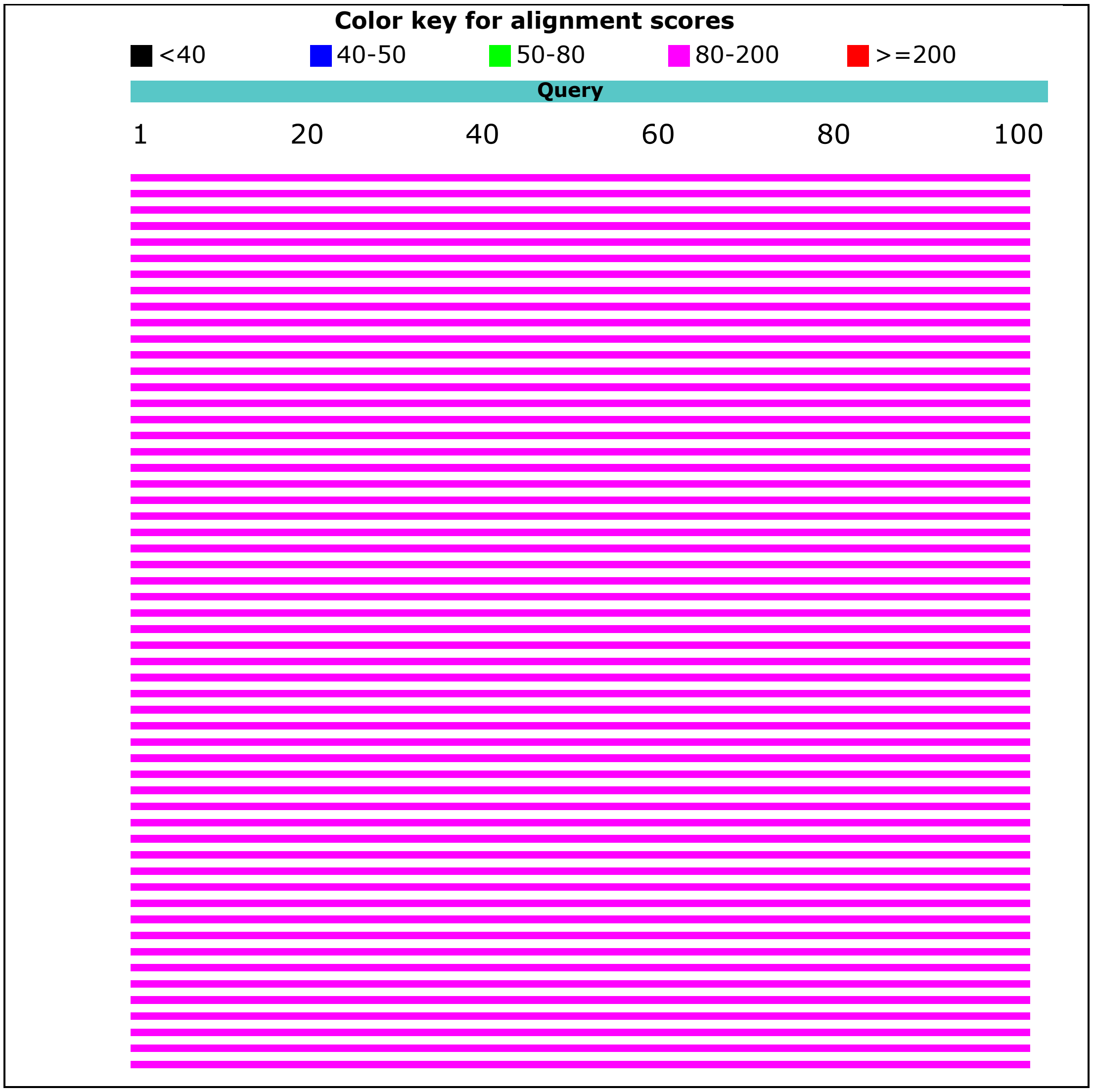
Job title: NP_002753.2 protamine-2 isoform 1 [Homo

RID ZJ6T120K015 (Expires on 11-02 08:53 am)

Query ID	lcl|Query_69089	**Database Name**	est
Description	NP_002753.2 protamine-2 isoform 1 [Homo sapiens]	**Description**	Database of GenBank+EMBL+DDBJ sequences from EST Divisions
Molecule type	amino acid	**Program**	TBLASTN 2.7.1+
Query Length	102		

Graphic Summary

Distribution of the top 100 Blast Hits on 696 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
HY041193 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence	186	186	100%	2e-60	100%	HY041193.1
HY037781 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131P10, mRNA sequence	186	186	100%	2e-60	100%	HY037781.1
HY019058 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064M11, mRNA sequence	186	186	100%	2e-60	100%	HY019058.1
HY031628 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D109I23, mRNA sequence	186	186	100%	2e-60	100%	HY031628.1
HY018995 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064I07, mRNA sequence	186	186	100%	2e-60	100%	HY018995.1
DB081917 TESTI4 Homo sapiens cDNA clone TESTI4028124 5', mRNA sequence	186	186	100%	2e-60	100%	DB081917.1
DB026406 TESTI2 Homo sapiens cDNA clone TESTI2008597 5', mRNA sequence	186	186	100%	2e-60	100%	DB026406.1
HY021923 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D074G19, mRNA sequence	186	186	100%	2e-60	100%	HY021923.1
5540 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC005303, mRNA sequence	186	186	100%	2e-60	100%	CV027318.1
HY017578 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D059K21, mRNA sequence	186	186	100%	2e-60	100%	HY017578.1
HY007196 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024L20, mRNA sequence	186	186	100%	2e-60	100%	HY007196.1
HY006973 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024A03, mRNA sequence	186	186	100%	2e-60	100%	HY006973.1
AGENCOURT_10399420 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6614218 5', mRNA sequence	186	186	100%	3e-60	100%	BU567583.1
AGENCOURT_10404024 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6613910 5', mRNA sequence	186	186	100%	3e-60	100%	BU567345.1
AGENCOURT_7838474 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6101594 5', mRNA sequence	186	186	100%	3e-60	100%	BQ438663.1
HY023254 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D079H16, mRNA sequence	186	186	100%	3e-60	100%	HY023254.1
DB075497 TESTI4 Homo sapiens cDNA clone TESTI4019393 5', mRNA sequence	186	186	100%	3e-60	100%	DB075497.1
DB453196 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H013060K24 5', mRNA sequence	186	186	100%	3e-60	100%	DB453196.1

Descriptions carry on for over 30 pages, not shown here.

clone H04D003C07, mRNA sequence

Alignments

HY041193 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence.

Sequence ID: **HY041193.1** Length: 431 Number of Matches: 1
Range 1: 112 to 417

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+1

Features:

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Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  292  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  417
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HY037781 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131P10, mRNA sequence.

Sequence ID: **HY037781.1** Length: 451 Number of Matches: 1
Range 1: 112 to 417

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  292  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  417
```

HY019058 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064M11, mRNA sequence.

Sequence ID: **HY019058.1** Length: 456 Number of Matches: 1
Range 1: 111 to 416

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  291  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  416
```

HY031628 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D109I23, mRNA sequence.

Sequence ID: **HY031628.1** Length: 453 Number of Matches: 1
Range 1: 112 to 417

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
```

```
Sbjct  112   MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61    RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
             RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  292   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  417
```

HY018995 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064I07, mRNA sequence.

Sequence ID: **HY018995.1** Length: 462 Number of Matches: 1
Range 1: 111 to 416

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+3

Features:

```
Query  1     MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
             MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111   MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61    RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
             RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  291   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  416
```

DB081917 TESTI4 Homo sapiens cDNA clone TESTI4028124 5', mRNA sequence.

Sequence ID: **DB081917.1** Length: 463 Number of Matches: 1
Range 1: 111 to 416

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+3

Features:

```
Query  1     MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
             MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111   MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61    RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
             RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  291   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  416
```

DB026406 TESTI2 Homo sapiens cDNA clone TESTI2008597 5', mRNA sequence.

Sequence ID: **DB026406.1** Length: 464 Number of Matches: 1
Range 1: 111 to 416

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+3

Features:

```
Query  1     MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
             MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111   MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61    RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
             RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  291   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  416
```

HY021923 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D074G19, mRNA sequence.

Sequence ID: **HY021923.1** Length: 453 Number of Matches: 1
Range 1: 112 to 417

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+1

Features:

```
Query  1     MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
             MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
```

Alignments go on for over 50 pages, not shown here.

BLAST ® » tblastn » RID-ZJ92K4AY014

BLAST Results

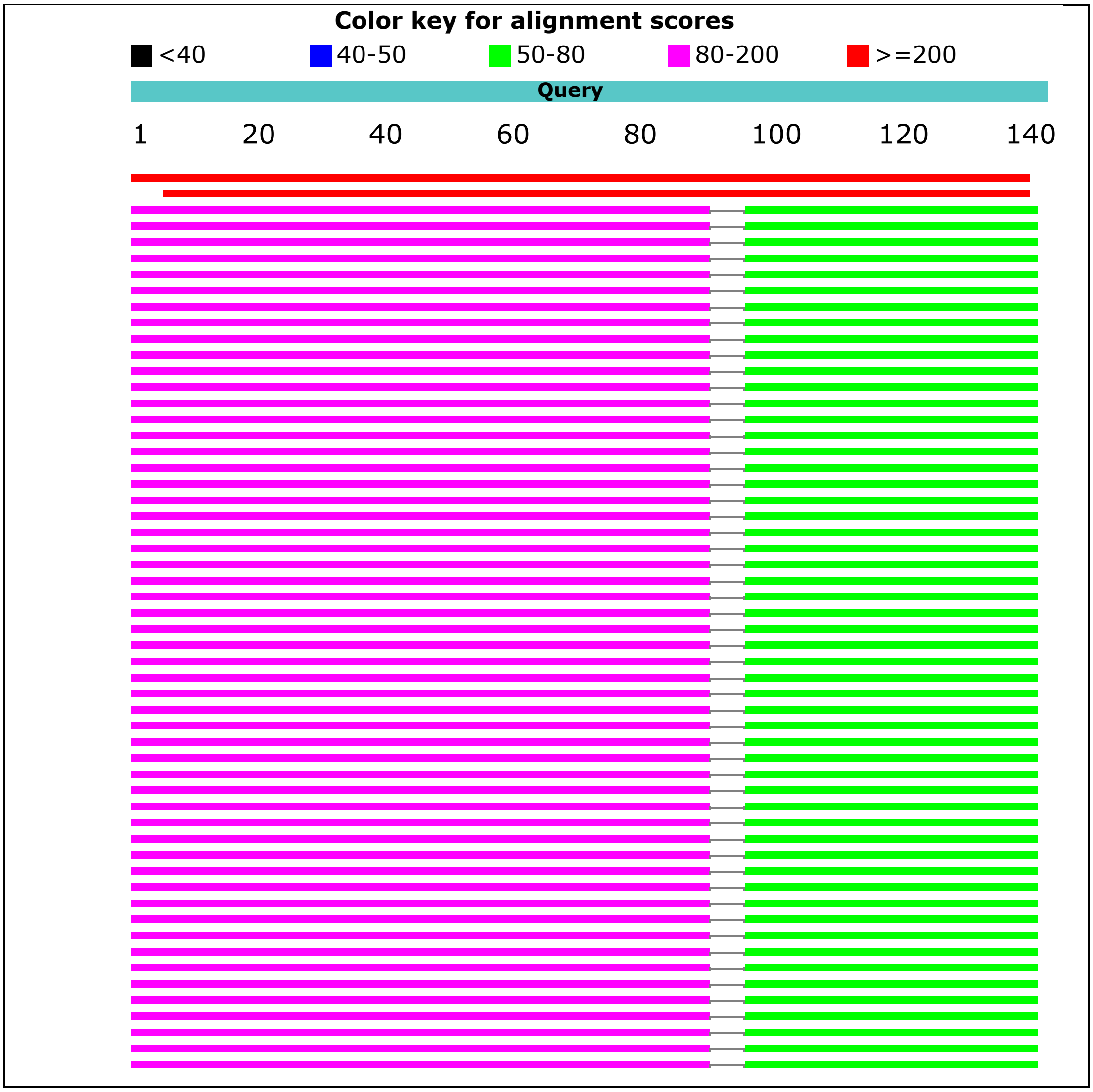
Appendix L: NCBI tBlastn NP_001273285.1 PRM2 isoform 2 v. Homo sapiens EST

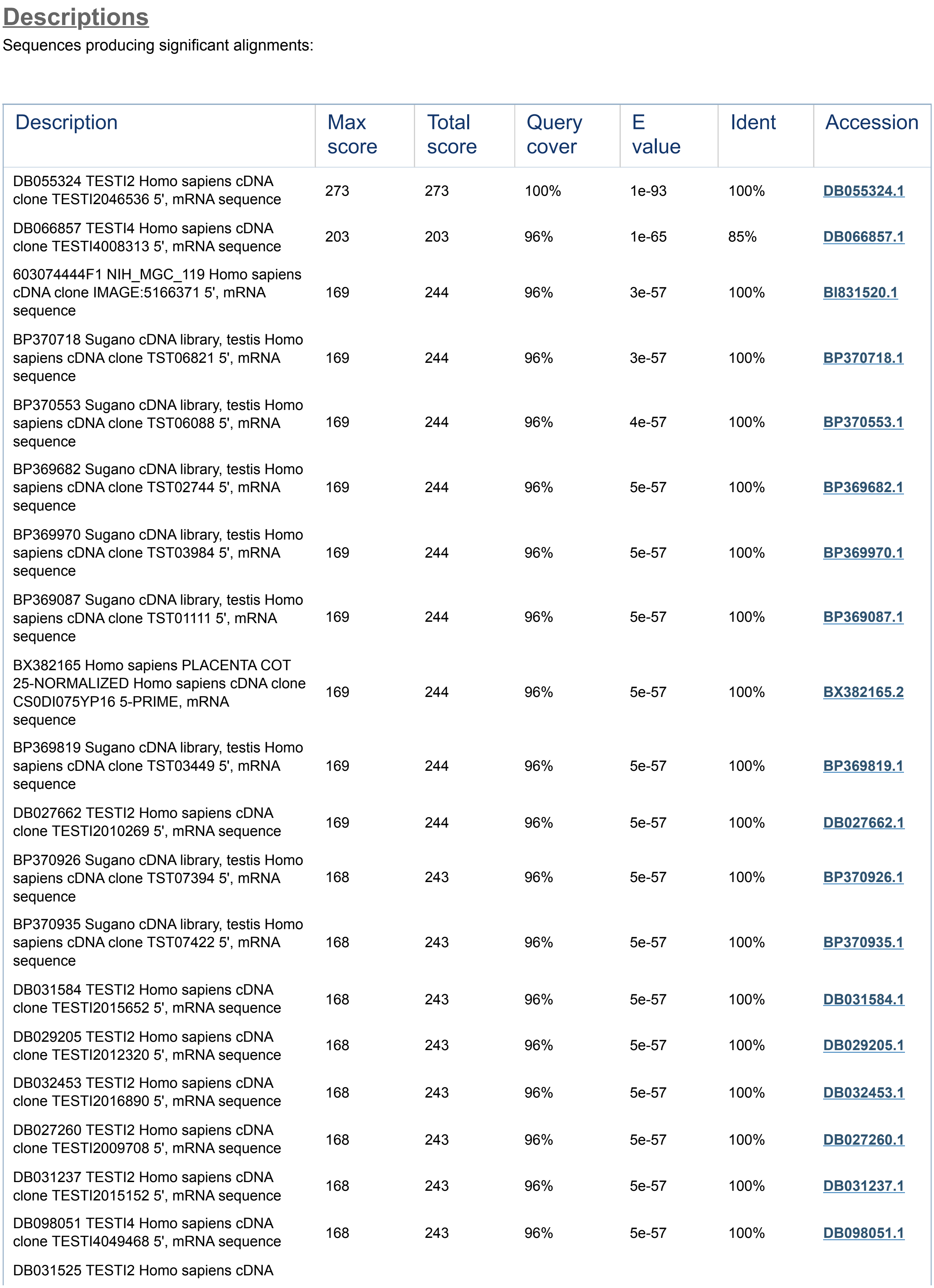
Job title: NP_001273285.1 protamine-2 isoform 2 [Homo

RID	ZJ92K4AY014 (Expires on 11-02 09:33 am)		
Query ID	lcl|Query_172351	**Database Name**	est
Description	NP_001273285.1 protamine-2 isoform 2 [Homo sapiens]	**Description**	Database of GenBank+EMBL+DDBJ sequences from EST Divisions
Molecule type	amino acid	**Program**	TBLASTN 2.7.1+
Query Length	140		

Graphic Summary

Distribution of the top 198 Blast Hits on 718 subject sequences





Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
DB055324 TESTI2 Homo sapiens cDNA clone TESTI2046536 5', mRNA sequence	273	273	100%	1e-93	100%	DB055324.1
DB066857 TESTI4 Homo sapiens cDNA clone TESTI4008313 5', mRNA sequence	203	203	96%	1e-65	85%	DB066857.1
603074444F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5166371 5', mRNA sequence	169	244	96%	3e-57	100%	BI831520.1
BP370718 Sugano cDNA library, testis Homo sapiens cDNA clone TST06821 5', mRNA sequence	169	244	96%	3e-57	100%	BP370718.1
BP370553 Sugano cDNA library, testis Homo sapiens cDNA clone TST06088 5', mRNA sequence	169	244	96%	4e-57	100%	BP370553.1
BP369682 Sugano cDNA library, testis Homo sapiens cDNA clone TST02744 5', mRNA sequence	169	244	96%	5e-57	100%	BP369682.1
BP369970 Sugano cDNA library, testis Homo sapiens cDNA clone TST03984 5', mRNA sequence	169	244	96%	5e-57	100%	BP369970.1
BP369087 Sugano cDNA library, testis Homo sapiens cDNA clone TST01111 5', mRNA sequence	169	244	96%	5e-57	100%	BP369087.1
BX382165 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI075YP16 5-PRIME, mRNA sequence	169	244	96%	5e-57	100%	BX382165.2
BP369819 Sugano cDNA library, testis Homo sapiens cDNA clone TST03449 5', mRNA sequence	169	244	96%	5e-57	100%	BP369819.1
DB027662 TESTI2 Homo sapiens cDNA clone TESTI2010269 5', mRNA sequence	169	244	96%	5e-57	100%	DB027662.1
BP370926 Sugano cDNA library, testis Homo sapiens cDNA clone TST07394 5', mRNA sequence	168	243	96%	5e-57	100%	BP370926.1
BP370935 Sugano cDNA library, testis Homo sapiens cDNA clone TST07422 5', mRNA sequence	168	243	96%	5e-57	100%	BP370935.1
DB031584 TESTI2 Homo sapiens cDNA clone TESTI2015652 5', mRNA sequence	168	243	96%	5e-57	100%	DB031584.1
DB029205 TESTI2 Homo sapiens cDNA clone TESTI2012320 5', mRNA sequence	168	243	96%	5e-57	100%	DB029205.1
DB032453 TESTI2 Homo sapiens cDNA clone TESTI2016890 5', mRNA sequence	168	243	96%	5e-57	100%	DB032453.1
DB027260 TESTI2 Homo sapiens cDNA clone TESTI2009708 5', mRNA sequence	168	243	96%	5e-57	100%	DB027260.1
DB031237 TESTI2 Homo sapiens cDNA clone TESTI2015152 5', mRNA sequence	168	243	96%	5e-57	100%	DB031237.1
DB098051 TESTI4 Homo sapiens cDNA clone TESTI4049468 5', mRNA sequence	168	243	96%	5e-57	100%	DB098051.1
DB031525 TESTI2 Homo sapiens cDNA						

Descriptions go on for over 30 pages, not shown here.

mRNA sequence						
RST21724 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence	32.3	32.3	16%	8.0	56%	BG202367.1

Alignments

DB055324 TESTI2 Homo sapiens cDNA clone TESTI2046536 5', mRNA sequence.

Sequence ID: **DB055324.1** Length: 555 Number of Matches: 1
Range 1: 111 to 530

Score	Expect	Method	Identities	Positives	Gaps	Frame
273 bits(699)	1e-93()	Compositional matrix adjust.	140/140(100%)	140/140(100%)	0/140(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRESLGDPLNQNFLSQKAAEPGREHAEGTKLP  120
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRESLGDPLNQNFLSQKAAEPGREHAEGTKLP
Sbjct  291  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRESLGDPLNQNFLSQKAAEPGREHAEGTKLP  470

Query  121  GPLTPSWKLRKSRPKHQVRP  140
            GPLTPSWKLRKSRPKHQVRP
Sbjct  471  GPLTPSWKLRKSRPKHQVRP  530
```

DB066857 TESTI4 Homo sapiens cDNA clone TESTI4008313 5', mRNA sequence.

Sequence ID: **DB066857.1** Length: 579 Number of Matches: 1
Range 1: 127 to 483

Score	Expect	Method	Identities	Positives	Gaps	Frame
203 bits(516)	1e-65()	Compositional matrix adjust.	115/136(85%)	115/136(84%)	18/136(13%)	+1

Features:

```
Query  6    VRSLS-ERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLH  64
            VRSLS  R  EVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLH
Sbjct  127  VRSLSRTRRTEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLH  306

Query  65   RIHRRQHRSCRRRKRRSCRHRRRHRRESLGDPLNQNFLSQKAAEPGREHAEGTKLPGPLT  124
            RIHRRQHRSCRRRKRRSCRHRRRHRR                 EPGREHAEGTKLPGPLT
Sbjct  307  RIHRRQHRSCRRRKRRSCRHRRRHRR-----------------EPGREHAEGTKLPGPLT  435

Query  125  PSWKLRKSRPKHQVRP  140
            PSWKLRKSRPKHQVRP
Sbjct  436  PSWKLRKSRPKHQVRP  483
```

603074444F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5166371 5', mRNA sequence.

Sequence ID: **BI831520.1** Length: 677 Number of Matches: 2
Range 1: 90 to 359

Score	Expect	Method	Identities	Positives	Gaps	Frame
169 bits(429)	3e-57(2)	Compositional matrix adjust.	90/90(100%)	90/90(100%)	0/90(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  90   MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  269

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  90
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR
Sbjct  270  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  359
```

Range 2: 331 to 465

Score	Expect	Method	Identities	Positives	Gaps	Frame

75.1 bits(183)	3e-57(2)	Compositional matrix adjust.	36/45(80%)	37/45(82%)	0/45(0%)	+1

Features:

```
Query  96   PLNQNFLSQKAAEPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  140
            P        +AAEPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP
Sbjct  331  PAGTGGGIAEAAEPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  465
```

BP370718 Sugano cDNA library, testis Homo sapiens cDNA clone TST06821 5', mRNA sequence.

Sequence ID: **BP370718.1** Length: 561 Number of Matches: 2
Range 1: 111 to 380

Score	Expect	Method	Identities	Positives	Gaps	Frame
169 bits(428)	3e-57(2)	Compositional matrix adjust.	90/90(100%)	90/90(100%)	0/90(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  90
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR
Sbjct  291  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  380
```

Range 2: 352 to 486

Score	Expect	Method	Identities	Positives	Gaps	Frame
75.1 bits(183)	3e-57(2)	Compositional matrix adjust.	36/45(80%)	37/45(82%)	0/45(0%)	+1

Features:

```
Query  96   PLNQNFLSQKAAEPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  140
            P        +AAEPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP
Sbjct  352  PAGTGGGIAEAAEPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  486
```

BP370553 Sugano cDNA library, testis Homo sapiens cDNA clone TST06088 5', mRNA sequence.

Sequence ID: **BP370553.1** Length: 558 Number of Matches: 2
Range 1: 108 to 377

Score	Expect	Method	Identities	Positives	Gaps	Frame
169 bits(427)	4e-57(2)	Compositional matrix adjust.	90/90(100%)	90/90(100%)	0/90(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  108  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  287

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  90
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR
Sbjct  288  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  377
```

Range 2: 349 to 483

Score	Expect	Method	Identities	Positives	Gaps	Frame
75.1 bits(183)	4e-57(2)	Compositional matrix adjust.	36/45(80%)	37/45(82%)	0/45(0%)	+1

Features:

```
Query  96   PLNQNFLSQKAAEPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  140
            P        +AAEPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP
Sbjct  349  PAGTGGGIAEAAEPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  483
```

BP369682 Sugano cDNA library, testis Homo sapiens cDNA clone TST02744 5', mRNA sequence.

Sequence ID: **BP369682.1** Length: 571 Number of Matches: 2
Range 1: 108 to 377

Alignments go on and are not shown here.

BLAST Results

Appendix M: NCBI tBlastn NP_001273286.1 PRM2 isoform 3 v. Homo sapiens EST

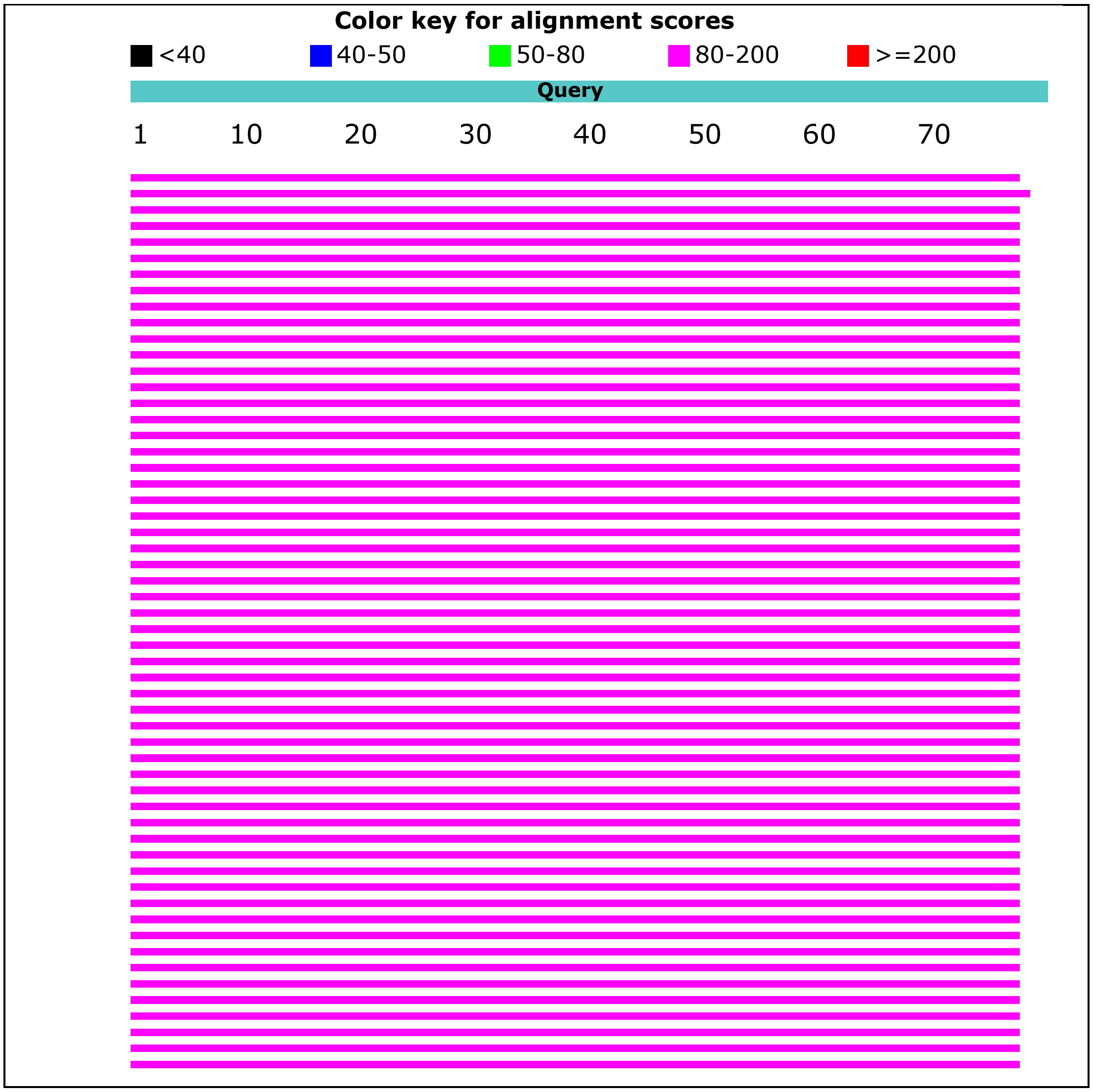
Job title: NP_001273286.1 protamine-2 isoform 3 [Homo

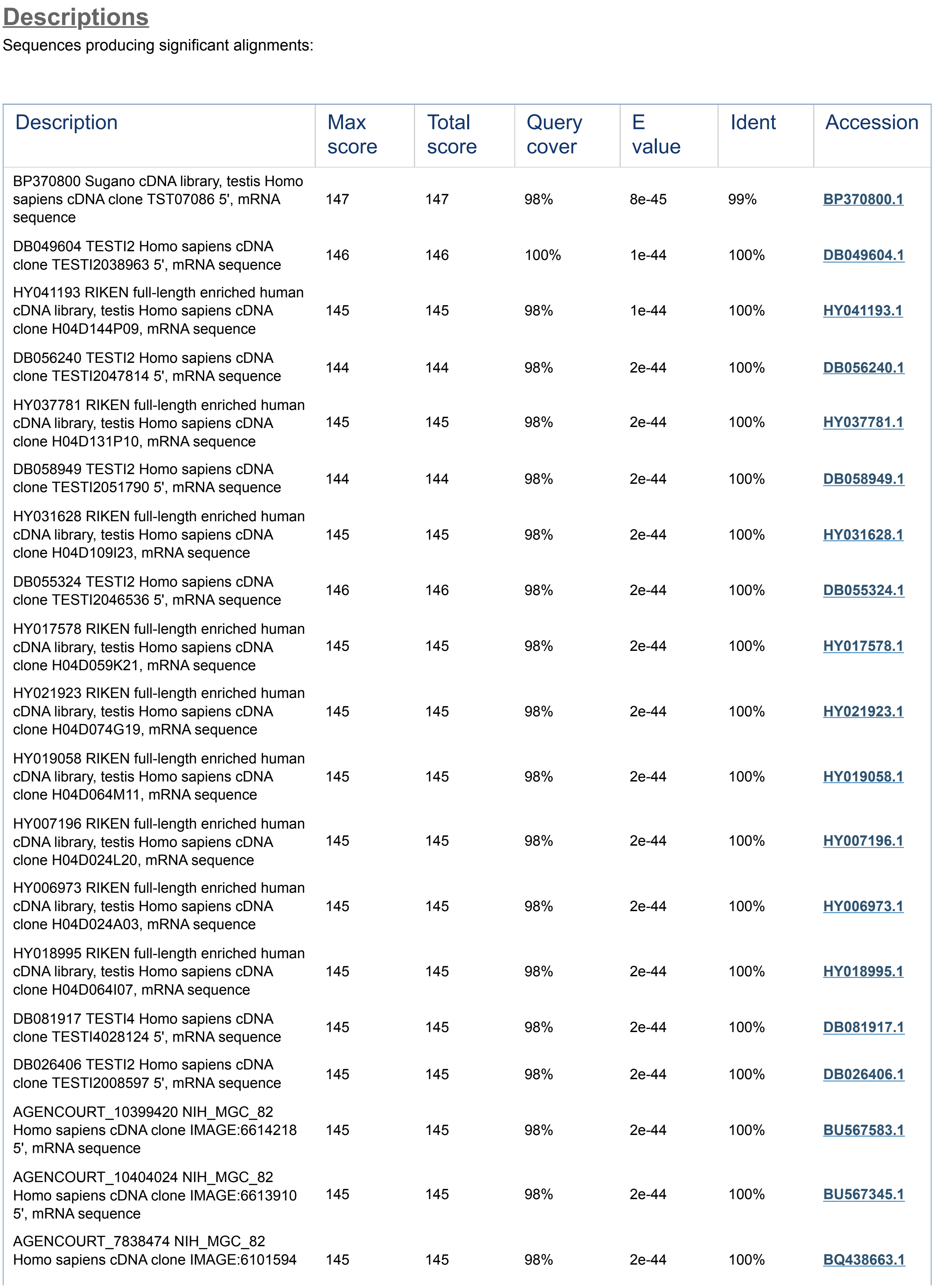
RID ZJ9511TV014 (Expires on 11-02 09:34 am)

Query ID	lcl|Query_216703	**Database Name**	est
Description	NP_001273286.1 protamine-2 isoform 3 [Homo sapiens]	**Description**	Database of GenBank+EMBL+DDBJ sequences from EST Divisions
Molecule type	amino acid	**Program**	TBLASTN 2.7.1+
Query Length	77		

Graphic Summary

Distribution of the top 100 Blast Hits on 686 subject sequences





Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
BP370800 Sugano cDNA library, testis Homo sapiens cDNA clone TST07086 5', mRNA sequence	147	147	98%	8e-45	99%	BP370800.1
DB049604 TESTI2 Homo sapiens cDNA clone TESTI2038963 5', mRNA sequence	146	146	100%	1e-44	100%	DB049604.1
HY041193 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence	145	145	98%	1e-44	100%	HY041193.1
DB056240 TESTI2 Homo sapiens cDNA clone TESTI2047814 5', mRNA sequence	144	144	98%	2e-44	100%	DB056240.1
HY037781 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131P10, mRNA sequence	145	145	98%	2e-44	100%	HY037781.1
DB058949 TESTI2 Homo sapiens cDNA clone TESTI2051790 5', mRNA sequence	144	144	98%	2e-44	100%	DB058949.1
HY031628 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D109I23, mRNA sequence	145	145	98%	2e-44	100%	HY031628.1
DB055324 TESTI2 Homo sapiens cDNA clone TESTI2046536 5', mRNA sequence	146	146	98%	2e-44	100%	DB055324.1
HY017578 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D059K21, mRNA sequence	145	145	98%	2e-44	100%	HY017578.1
HY021923 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D074G19, mRNA sequence	145	145	98%	2e-44	100%	HY021923.1
HY019058 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064M11, mRNA sequence	145	145	98%	2e-44	100%	HY019058.1
HY007196 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024L20, mRNA sequence	145	145	98%	2e-44	100%	HY007196.1
HY006973 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024A03, mRNA sequence	145	145	98%	2e-44	100%	HY006973.1
HY018995 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064I07, mRNA sequence	145	145	98%	2e-44	100%	HY018995.1
DB081917 TESTI4 Homo sapiens cDNA clone TESTI4028124 5', mRNA sequence	145	145	98%	2e-44	100%	DB081917.1
DB026406 TESTI2 Homo sapiens cDNA clone TESTI2008597 5', mRNA sequence	145	145	98%	2e-44	100%	DB026406.1
AGENCOURT_10399420 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6614218 5', mRNA sequence	145	145	98%	2e-44	100%	BU567583.1
AGENCOURT_10404024 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6613910 5', mRNA sequence	145	145	98%	2e-44	100%	BU567345.1
AGENCOURT_7838474 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6101594	145	145	98%	2e-44	100%	BQ438663.1

Descriptions go on, not shown here.

HY195250 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D038M02, mRNA sequence	34.7	34.7	23%	0.19	100%	HY195250.1
HY205168 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D074G19, mRNA sequence	34.7	34.7	23%	0.20	100%	HY205168.1
AGENCOURT_10617460 NIH_MGC_141 Homo sapiens cDNA clone IMAGE:6732965 5', mRNA sequence	34.3	34.3	57%	0.42	52%	BU958638.1
AGENCOURT_10617591 NIH_MGC_141 Homo sapiens cDNA clone IMAGE:6732826 5', mRNA sequence	34.3	34.3	57%	0.42	52%	BU958533.1
AGENCOURT_10545241 NIH_MGC_107 Homo sapiens cDNA clone IMAGE:6728653 5', mRNA sequence	34.3	34.3	57%	0.42	52%	BU944388.1
AGENCOURT_10545424 NIH_MGC_107 Homo sapiens cDNA clone IMAGE:6728497 5', mRNA sequence	33.9	33.9	57%	0.47	52%	BU944248.1
BP369069 Sugano cDNA library, testis Homo sapiens cDNA clone TST01048 5', mRNA sequence	33.1	33.1	22%	1.0	94%	BP369069.1
HY211883 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D095B14, mRNA sequence	32.7	32.7	22%	1.2	100%	HY211883.1
TC106758 Human bone marrow, large insert, pCMV expression library Homo sapiens cDNA clone TC106758 5' similar to Homo sapiens cyclin B1 (CCNB1), mRNA sequence	31.6	31.6	49%	2.8	41%	DN999008.1
K-EST0033024 S10SNU1 Homo sapiens cDNA clone S10SNU1-7-C01 5', mRNA sequence	30.4	30.4	53%	6.6	38%	BM755303.1

Alignments

BP370800 Sugano cDNA library, testis Homo sapiens cDNA clone TST07086 5', mRNA sequence.

Sequence ID: **BP370800.1** Length: 573 Number of Matches: 1
Range 1: 111 to 338

Score	Expect	Method	Identities	Positives	Gaps	Frame
147 bits(371)	8e-45()	Compositional matrix adjust.	75/76(99%)	75/76(98%)	0/76(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQL GQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111  MVRYRVRSLSERSHEVYRQQLGGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61   RRLHRIHRRQHRSCRR  76
            RRLHRIHRRQHRSCRR
Sbjct  291  RRLHRIHRRQHRSCRR  338
```

DB049604 TESTI2 Homo sapiens cDNA clone TESTI2038963 5', mRNA sequence.

Sequence ID: **DB049604.1** Length: 565 Number of Matches: 1
Range 1: 111 to 341

Score	Expect	Method	Identities	Positives	Gaps	Frame
146 bits(369)	1e-44()	Compositional matrix adjust.	77/77(100%)	77/77(100%)	0/77(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
```

```
                MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111   MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61    RRLHRIHRRQHRSCRRH  77
             RRLHRIHRRQHRSCRRH
Sbjct  291   RRLHRIHRRQHRSCRRH  341
```

HY041193 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence.

Sequence ID: **HY041193.1** Length: 431 Number of Matches: 1
Range 1: 112 to 339

Score	Expect	Method	Identities	Positives	Gaps	Frame
145 bits(365)	1e-44()	Compositional matrix adjust.	76/76(100%)	76/76(100%)	0/76(0%)	+1

Features:

```
Query  1     MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
             MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112   MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61    RRLHRIHRRQHRSCRR  76
             RRLHRIHRRQHRSCRR
Sbjct  292   RRLHRIHRRQHRSCRR  339
```

DB056240 TESTI2 Homo sapiens cDNA clone TESTI2047814 5', mRNA sequence.

Sequence ID: **DB056240.1** Length: 378 Number of Matches: 1
Range 1: 111 to 338

Score	Expect	Method	Identities	Positives	Gaps	Frame
144 bits(363)	2e-44()	Compositional matrix adjust.	76/76(100%)	76/76(100%)	0/76(0%)	+3

Features:

```
Query  1     MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
             MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111   MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61    RRLHRIHRRQHRSCRR  76
             RRLHRIHRRQHRSCRR
Sbjct  291   RRLHRIHRRQHRSCRR  338
```

HY037781 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131P10, mRNA sequence.

Sequence ID: **HY037781.1** Length: 451 Number of Matches: 1
Range 1: 112 to 339

Score	Expect	Method	Identities	Positives	Gaps	Frame
145 bits(365)	2e-44()	Compositional matrix adjust.	76/76(100%)	76/76(100%)	0/76(0%)	+1

Features:

```
Query  1     MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
             MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112   MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61    RRLHRIHRRQHRSCRR  76
             RRLHRIHRRQHRSCRR
Sbjct  292   RRLHRIHRRQHRSCRR  339
```

DB058949 TESTI2 Homo sapiens cDNA clone TESTI2051790 5', mRNA sequence.

Sequence ID: **DB058949.1** Length: 373 Number of Matches: 1
Range 1: 106 to 333

Score	Expect	Method	Identities	Positives	Gaps	Frame
144 bits(363)	2e-44()	Compositional matrix adjust.	76/76(100%)	76/76(100%)	0/76(0%)	+1

Features:

```
Query  1     MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
```

Alignments go on, not shown here.

BLAST ® » tblastn » RID-ZJ95NR8M014

BLAST Results

Appendix N: NCBI tBlastn NP_001273287.1 PRM2 isoform 4 v. Homo sapiens EST

Job title: NP_001273287.1 protamine-2 isoform 4 [Homo

RID	ZJ95NR8M014 (Expires on 11-02 09:34 am)		
Query ID	lcl|Query_161987	**Database Name**	est
Description	NP_001273287.1 protamine-2 isoform 4 [Homo sapiens]	**Description**	Database of GenBank+EMBL+DDBJ sequences from EST Divisions
Molecule type	amino acid	**Program**	TBLASTN 2.7.1+
Query Length	123		

Graphic Summary

Distribution of the top 197 Blast Hits on 716 subject sequences

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
DB055324 TESTI2 Homo sapiens cDNA clone TESTI2046536 5', mRNA sequence	225	225	100%	8e-75	88%	DB055324.1
DB066922 TESTI4 Homo sapiens cDNA clone TESTI4008395 5', mRNA sequence	212	212	95%	1e-69	87%	DB066922.1
DB066857 TESTI4 Homo sapiens cDNA clone TESTI4008313 5', mRNA sequence	211	211	95%	2e-69	97%	DB066857.1
603074444F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5166371 5', mRNA sequence	167	239	100%	1e-55	100%	BI831520.1
BP370718 Sugano cDNA library, testis Homo sapiens cDNA clone TST06821 5', mRNA sequence	167	239	100%	1e-55	100%	BP370718.1
BP370553 Sugano cDNA library, testis Homo sapiens cDNA clone TST06088 5', mRNA sequence	167	238	100%	2e-55	100%	BP370553.1
BP370825 Sugano cDNA library, testis Homo sapiens cDNA clone TST07157 5', mRNA sequence	167	238	100%	2e-55	100%	BP370825.1
DB030627 TESTI2 Homo sapiens cDNA clone TESTI2014285 5', mRNA sequence	167	238	100%	2e-55	100%	DB030627.1
BP369970 Sugano cDNA library, testis Homo sapiens cDNA clone TST03984 5', mRNA sequence	167	238	100%	2e-55	100%	BP369970.1
602688764F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4821351 5', mRNA sequence	167	238	100%	2e-55	100%	BG704546.1
BP369682 Sugano cDNA library, testis Homo sapiens cDNA clone TST02744 5', mRNA sequence	167	238	100%	2e-55	100%	BP369682.1
BP371030 Sugano cDNA library, testis Homo sapiens cDNA clone TST07680 5', mRNA sequence	167	238	100%	2e-55	100%	BP371030.1
BP369697 Sugano cDNA library, testis Homo sapiens cDNA clone TST02790 5', mRNA sequence	167	238	100%	2e-55	100%	BP369697.1
BP369206 Sugano cDNA library, testis Homo sapiens cDNA clone TST01381 5', mRNA sequence	167	238	100%	2e-55	100%	BP369206.1
BP369495 Sugano cDNA library, testis Homo sapiens cDNA clone TST02180 5', mRNA sequence	167	238	100%	2e-55	100%	BP369495.1
BP368798 Sugano cDNA library, testis Homo sapiens cDNA clone TST00232 5', mRNA sequence	167	238	100%	2e-55	100%	BP368798.1
BP369087 Sugano cDNA library, testis Homo sapiens cDNA clone TST01111 5', mRNA sequence	167	238	100%	2e-55	100%	BP369087.1
BP369819 Sugano cDNA library, testis Homo sapiens cDNA clone TST03449 5', mRNA sequence	167	238	100%	2e-55	100%	BP369819.1

Descriptions go on, not shown here.

Alignments

DB055324 TESTI2 Homo sapiens cDNA clone TESTI2046536 5', mRNA sequence.

Sequence ID: **DB055324.1** Length: 555 Number of Matches: 1
Range 1: 111 to 530

Score	Expect	Method	Identities	Positives	Gaps	Frame
225 bits(573)	8e-75()	Compositional matrix adjust.	123/140(88%)	123/140(87%)	17/140(12%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR-----------------EPGREHAEGTKLP  103
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR                 EPGREHAEGTKLP
Sbjct  291  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRESLGDPLNQNFLSQKAAEPGREHAEGTKLP  470

Query  104  GPLTPSWKLRKSRPKHQVRP  123
            GPLTPSWKLRKSRPKHQVRP
Sbjct  471  GPLTPSWKLRKSRPKHQVRP  530
```

DB066922 TESTI4 Homo sapiens cDNA clone TESTI4008395 5', mRNA sequence.

Sequence ID: **DB066922.1** Length: 559 Number of Matches: 1
Range 1: 127 to 534

Score	Expect	Method	Identities	Positives	Gaps	Frame
212 bits(539)	1e-69()	Compositional matrix adjust.	118/136(87%)	118/136(86%)	18/136(13%)	+1

Features:

```
Query  6    VRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLHR  65
            VRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLHR
Sbjct  127  VRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLHR  306

Query  66   IHRRQHRSCRRRKRRSCRHRRRHRR------------------EPGREHAEGTKLPGPLT  107
            IHRRQHRSCRRRKRRSCRHRRRHRR                  EPGREHAEGTKLPGPLT
Sbjct  307  IHRRQHRSCRRRKRRSCRHRRRHRRGLPAPPPCPPCP*PPQAAEPGREHAEGTKLPGPLT  486

Query  108  PSWKLRKSRPKHQVRP  123
            PSWKLRKSRPKHQVRP
Sbjct  487  PSWKLRKSRPKHQVRP  534
```

DB066857 TESTI4 Homo sapiens cDNA clone TESTI4008313 5', mRNA sequence.

Sequence ID: **DB066857.1** Length: 579 Number of Matches: 1
Range 1: 127 to 483

Score	Expect	Method	Identities	Positives	Gaps	Frame
211 bits(538)	2e-69()	Compositional matrix adjust.	115/119(97%)	115/119(96%)	1/119(0%)	+1

Features:

```
Query  6    VRSLS-ERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLH  64
            VRSLS  R  EVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLH
Sbjct  127  VRSLSRTRRTEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLH  306

Query  65   RIHRRQHRSCRRRKRRSCRHRRRHRREPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  123
            RIHRRQHRSCRRRKRRSCRHRRRHRREPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP
Sbjct  307  RIHRRQHRSCRRRKRRSCRHRRRHRREPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  483
```

603074444F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5166371 5', mRNA sequence.

Sequence ID: **BI831520.1** Length: 677 Number of Matches: 2
Range 1: 90 to 359

Score	Expect	Method	Identities	Positives	Gaps	Frame
167 bits(424)	1e-55(2)	Compositional matrix adjust.	90/90(100%)	90/90(100%)	0/90(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  90   MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  269

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  90
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR
Sbjct  270  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  359
```

Range 2: 367 to 465

Score	Expect	Method	Identities	Positives	Gaps	Frame
71.6 bits(174)	1e-55(2)	Compositional matrix adjust.	33/33(100%)	33/33(100%)	0/33(0%)	+1

Features:

```
Query  91   EPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  123
            EPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP
Sbjct  367  EPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  465
```

BP370718 Sugano cDNA library, testis Homo sapiens cDNA clone TST06821 5', mRNA sequence.
Sequence ID: **BP370718.1** Length: 561 Number of Matches: 2
Range 1: 111 to 380

Score	Expect	Method	Identities	Positives	Gaps	Frame
167 bits(423)	1e-55(2)	Compositional matrix adjust.	90/90(100%)	90/90(100%)	0/90(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  90
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR
Sbjct  291  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  380
```

Range 2: 388 to 486

Score	Expect	Method	Identities	Positives	Gaps	Frame
71.6 bits(174)	1e-55(2)	Compositional matrix adjust.	33/33(100%)	33/33(100%)	0/33(0%)	+1

Features:

```
Query  91   EPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  123
            EPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP
Sbjct  388  EPGREHAEGTKLPGPLTPSWKLRKSRPKHQVRP  486
```

BP370553 Sugano cDNA library, testis Homo sapiens cDNA clone TST06088 5', mRNA sequence.
Sequence ID: **BP370553.1** Length: 558 Number of Matches: 2
Range 1: 108 to 377

Score	Expect	Method	Identities	Positives	Gaps	Frame
167 bits(422)	2e-55(2)	Compositional matrix adjust.	90/90(100%)	90/90(100%)	0/90(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  108  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  287

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  90
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR
Sbjct  288  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR  377
```

Range 2: 385 to 483

Alignments go on, not shown
here.

BLAST ® » tblastn » RID-ZJ98FW6R01N

BLAST Results

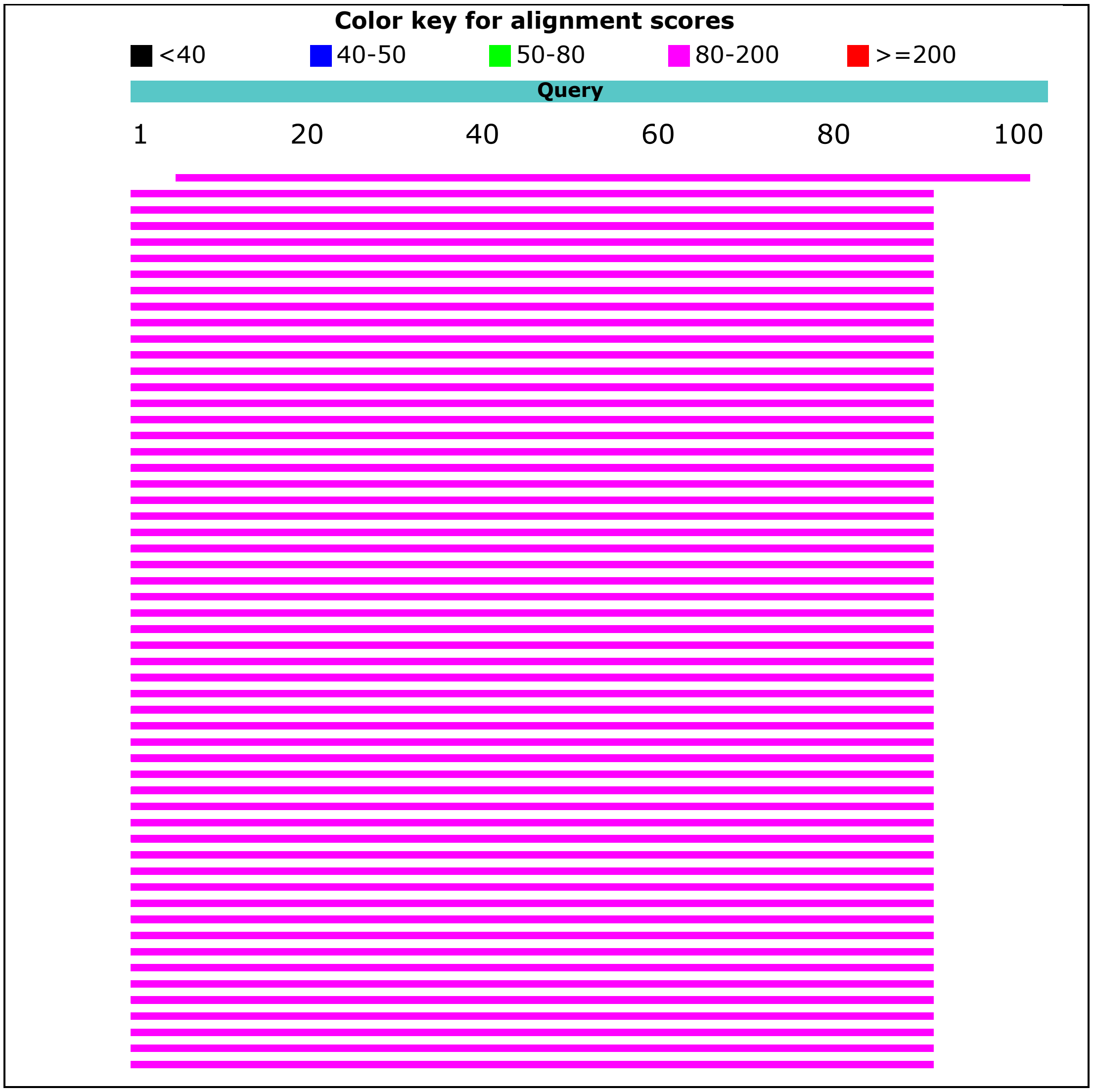
Appendix O: NCBI tBlastn NP_001273288.1 PRM2 isoform 5 v. Homo sapiens EST

Job title: NP_001273288.1 protamine-2 isoform 5 [Homo

RID	ZJ98FW6R01N (Expires on 11-02 09:36 am)		
Query ID	lcl|Query_172495	**Database Name**	est
Description	NP_001273288.1 protamine-2 isoform 5 [Homo sapiens]	**Description**	Database of GenBank+EMBL+DDBJ sequences from EST Divisions
Molecule type	amino acid	**Program**	TBLASTN 2.7.1+
Query Length	102		

Graphic Summary

Distribution of the top 100 Blast Hits on 695 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
DB066922 TESTI4 Homo sapiens cDNA clone TESTI4008395 5', mRNA sequence	180	180	95%	1e-57	99%	DB066922.1
HY041193 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence	167	167	89%	7e-53	100%	HY041193.1
HY037781 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131P10, mRNA sequence	167	167	89%	9e-53	100%	HY037781.1
HY031628 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D109I23, mRNA sequence	167	167	89%	9e-53	100%	HY031628.1
HY017578 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D059K21, mRNA sequence	167	167	89%	1e-52	100%	HY017578.1
HY019058 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064M11, mRNA sequence	167	167	89%	1e-52	100%	HY019058.1
HY007196 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024L20, mRNA sequence	167	167	89%	1e-52	100%	HY007196.1
HY006973 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024A03, mRNA sequence	167	167	89%	1e-52	100%	HY006973.1
HY021923 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D074G19, mRNA sequence	167	167	89%	1e-52	100%	HY021923.1
HY018995 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064I07, mRNA sequence	167	167	89%	1e-52	100%	HY018995.1
DB081917 TESTI4 Homo sapiens cDNA clone TESTI4028124 5', mRNA sequence	167	167	89%	1e-52	100%	DB081917.1
DB026406 TESTI2 Homo sapiens cDNA clone TESTI2008597 5', mRNA sequence	167	167	89%	1e-52	100%	DB026406.1
BP370301 Sugano cDNA library, testis Homo sapiens cDNA clone TST05305 5', mRNA sequence	168	168	89%	1e-52	100%	BP370301.1
HY023254 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D079H16, mRNA sequence	167	167	89%	1e-52	100%	HY023254.1
AGENCOURT_10399420 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6614218 5', mRNA sequence	167	167	89%	1e-52	100%	BU567583.1
AGENCOURT_10404024 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6613910 5', mRNA sequence	167	167	89%	1e-52	100%	BU567345.1
AGENCOURT_7838474 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6101594 5', mRNA sequence	167	167	89%	1e-52	100%	BQ438663.1
5540 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC005303, mRNA sequence	167	167	89%	1e-52	100%	CV027318.1

Descriptions go on, not shown here.

Alignments

DB066922 TESTI4 Homo sapiens cDNA clone TESTI4008395 5', mRNA sequence.
Sequence ID: **DB066922.1** Length: 559 Number of Matches: 1
Range 1: 127 to 417

Score	Expect	Method	Identities	Positives	Gaps	Frame
180 bits(457)	1e-57()	Compositional matrix adjust.	96/97(99%)	96/97(98%)	0/97(0%)	+1

Features:

```
Query  6    VRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLHR  65
            VRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLHR
Sbjct  127  VRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLHR  306

Query  66   IHRRQHRSCRRRKRRSCRHRRRHRRGLPAPPPCPACP  102
            IHRRQHRSCRRRKRRSCRHRRRHRRGLPAPPPCP CP
Sbjct  307  IHRRQHRSCRRRKRRSCRHRRRHRRGLPAPPPCPPCP  417
```

HY041193 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence.
Sequence ID: **HY041193.1** Length: 431 Number of Matches: 1
Range 1: 112 to 384

Score	Expect	Method	Identities	Positives	Gaps	Frame
167 bits(422)	7e-53()	Compositional matrix adjust.	91/91(100%)	91/91(100%)	0/91(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  91
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG
Sbjct  292  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  384
```

HY037781 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131P10, mRNA sequence.
Sequence ID: **HY037781.1** Length: 451 Number of Matches: 1
Range 1: 112 to 384

Score	Expect	Method	Identities	Positives	Gaps	Frame
167 bits(422)	9e-53()	Compositional matrix adjust.	91/91(100%)	91/91(100%)	0/91(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  91
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG
Sbjct  292  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  384
```

HY031628 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D109I23, mRNA sequence.
Sequence ID: **HY031628.1** Length: 453 Number of Matches: 1
Range 1: 112 to 384

Score	Expect	Method	Identities	Positives	Gaps	Frame
167 bits(422)	9e-53()	Compositional matrix adjust.	91/91(100%)	91/91(100%)	0/91(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  91
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG
Sbjct  292  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  384
```

HY017578 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D059K21, mRNA sequence.

Sequence ID: **HY017578.1** Length: 462 Number of Matches: 1
Range 1: 112 to 384

Score	Expect	Method	Identities	Positives	Gaps	Frame
167 bits(422)	1e-52()	Compositional matrix adjust.	91/91(100%)	91/91(100%)	0/91(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  91
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG
Sbjct  292  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  384
```

HY019058 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064M11, mRNA sequence.

Sequence ID: **HY019058.1** Length: 456 Number of Matches: 1
Range 1: 111 to 383

Score	Expect	Method	Identities	Positives	Gaps	Frame
167 bits(422)	1e-52()	Compositional matrix adjust.	91/91(100%)	91/91(100%)	0/91(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  91
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG
Sbjct  291  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  383
```

HY007196 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024L20, mRNA sequence.

Sequence ID: **HY007196.1** Length: 472 Number of Matches: 1
Range 1: 113 to 385

Score	Expect	Method	Identities	Positives	Gaps	Frame
167 bits(422)	1e-52()	Compositional matrix adjust.	91/91(100%)	91/91(100%)	0/91(0%)	+2

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  113  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  292

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  91
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG
Sbjct  293  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  385
```

HY006973 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024A03, mRNA sequence.

Sequence ID: **HY006973.1** Length: 472 Number of Matches: 1
Range 1: 113 to 385

Score	Expect	Method	Identities	Positives	Gaps	Frame
167 bits(422)	1e-52()	Compositional matrix adjust.	91/91(100%)	91/91(100%)	0/91(0%)	+2

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  113  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  292

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  91
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG
Sbjct  293  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  385
```

Alignments go on, not shown here.

BLAST Results

Appendix P: NCBI tBlastn EAW85158.1 PRM2 isoform CRA_a v. Homo sapiens EST

Job title: EAW85158.1 protamine 2, isoform CRA_a,

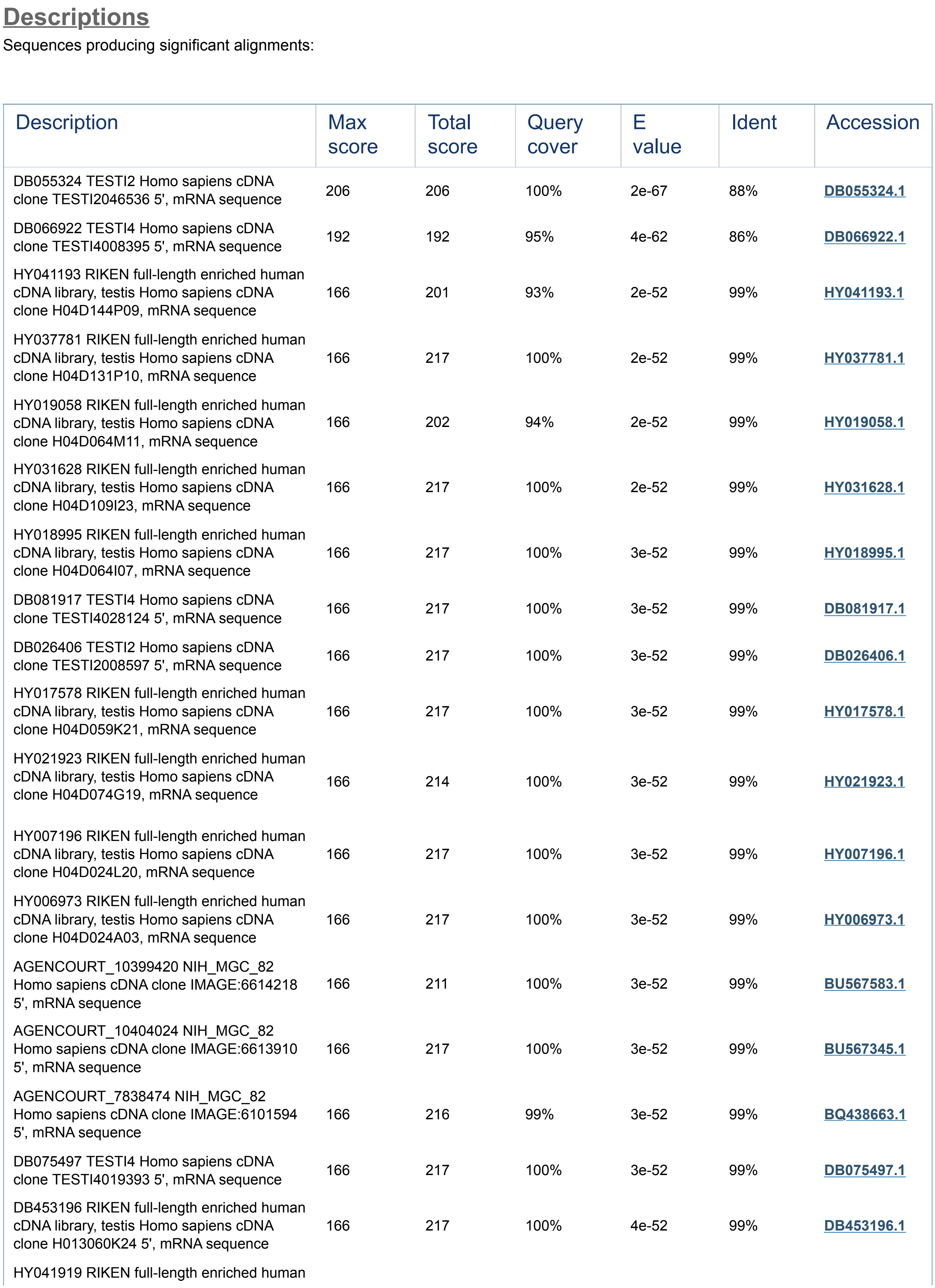
RID ZJ9RGSZ0014 (Expires on 11-02 09:44 am)

Query ID lcl|Query_144251
Description EAW85158.1 protamine 2, isoform CRA_a, partial [Homo sapiens]
Molecule type amino acid
Query Length 112

Database Name est
Description Database of GenBank+EMBL+DDBJ sequences from EST Divisions
Program TBLASTN 2.7.1+

Graphic Summary

Distribution of the top 195 Blast Hits on 711 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
DB055324 TESTI2 Homo sapiens cDNA clone TESTI2046536 5', mRNA sequence	206	206	100%	2e-67	88%	DB055324.1
DB066922 TESTI4 Homo sapiens cDNA clone TESTI4008395 5', mRNA sequence	192	192	95%	4e-62	86%	DB066922.1
HY041193 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence	166	201	93%	2e-52	99%	HY041193.1
HY037781 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131P10, mRNA sequence	166	217	100%	2e-52	99%	HY037781.1
HY019058 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064M11, mRNA sequence	166	202	94%	2e-52	99%	HY019058.1
HY031628 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D109I23, mRNA sequence	166	217	100%	2e-52	99%	HY031628.1
HY018995 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064I07, mRNA sequence	166	217	100%	3e-52	99%	HY018995.1
DB081917 TESTI4 Homo sapiens cDNA clone TESTI4028124 5', mRNA sequence	166	217	100%	3e-52	99%	DB081917.1
DB026406 TESTI2 Homo sapiens cDNA clone TESTI2008597 5', mRNA sequence	166	217	100%	3e-52	99%	DB026406.1
HY017578 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D059K21, mRNA sequence	166	217	100%	3e-52	99%	HY017578.1
HY021923 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D074G19, mRNA sequence	166	214	100%	3e-52	99%	HY021923.1
HY007196 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024L20, mRNA sequence	166	217	100%	3e-52	99%	HY007196.1
HY006973 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024A03, mRNA sequence	166	217	100%	3e-52	99%	HY006973.1
AGENCOURT_10399420 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6614218 5', mRNA sequence	166	211	100%	3e-52	99%	BU567583.1
AGENCOURT_10404024 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6613910 5', mRNA sequence	166	217	100%	3e-52	99%	BU567345.1
AGENCOURT_7838474 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6101594 5', mRNA sequence	166	216	99%	3e-52	99%	BQ438663.1
DB075497 TESTI4 Homo sapiens cDNA clone TESTI4019393 5', mRNA sequence	166	217	100%	3e-52	99%	DB075497.1
DB453196 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H013060K24 5', mRNA sequence	166	217	100%	4e-52	99%	DB453196.1
HY041919 RIKEN full-length enriched human						

Descriptions go on, not shown here

cDNA library, testis Homo sapiens cDNA clone H04D012E22, mRNA sequence	51.6	51.6	19%	2e-07	100%	HY186934.1
HY227731 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence	51.6	51.6	19%	3e-07	100%	HY227731.1
EST95513 Testis I Homo sapiens cDNA 5' end similar to protamine 2, mRNA sequence	50.4	50.4	19%	4e-07	100%	AA382302.1
EST96416 Testis I Homo sapiens cDNA 5' end similar to protamine 2, mRNA sequence	50.4	50.4	19%	4e-07	100%	AA383080.1
AGENCOURT_10444665 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6619365 5', mRNA sequence	51.2	51.2	19%	4e-07	100%	BU852822.1
BP370920 Sugano cDNA library, testis Homo sapiens cDNA clone TST07381 5', mRNA sequence	50.8	50.8	19%	5e-07	100%	BP370920.1
DB341880 TESTI4 Homo sapiens cDNA clone TESTI4049883 3', mRNA sequence	50.4	50.4	19%	1e-06	100%	DB341880.1
HY185973 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D009E02, mRNA sequence	49.7	49.7	19%	1e-06	95%	HY185973.1
DB041421 TESTI2 Homo sapiens cDNA clone TESTI2028489 5', mRNA sequence	48.5	48.5	19%	6e-06	95%	DB041421.1
CM0-TN0033-290700-482-f12 TN0033 Homo sapiens cDNA, mRNA sequence	46.6	46.6	19%	7e-06	91%	BE843346.1
HY189610 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D020G09, mRNA sequence	45.8	45.8	19%	3e-05	95%	HY189610.1
DB024173 TESTI2 Homo sapiens cDNA clone TESTI2005620 5', mRNA sequence	46.2	46.2	26%	5e-05	77%	DB024173.1
603080587F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5172309 5', mRNA sequence	45.8	45.8	41%	1e-04	60%	BI831316.1
ob16c11.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1323860 3' similar to gb:X07862 Human mRNA for protamine 2 (HUMAN);, mRNA sequence	36.6	67.4	41%	2e-04	83%	AA903972.1
HY202211 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064I07, mRNA sequence	42.7	42.7	19%	3e-04	86%	HY202211.1
DB097798 TESTI4 Homo sapiens cDNA clone TESTI4049158 5', mRNA sequence	39.3	39.3	36%	0.005	54%	DB097798.1
DB510139 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H013018L11 3', mRNA sequence	32.7	32.7	11%	1.6	100%	DB510139.1

Alignments

DB055324 TESTI2 Homo sapiens cDNA clone TESTI2046536 5', mRNA sequence.

Sequence ID: **DB055324.1** Length: 555 Number of Matches: 1
Range 1: 111 to 494

Score	Expect	Method	Identities	Positives	Gaps	Frame
206 bits(524)	2e-67()	Compositional matrix adjust.	112/128(88%)	112/128(87%)	16/128(12%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR----------------AEPGREHAEGTKLP  104
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR                AEPGREHAEGTKLP
Sbjct  291  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRESLGDPLNQNFLSQKAAEPGREHAEGTKLP  470

Query  105  GPLTPSWK  112
            GPLTPSWK
Sbjct  471  GPLTPSWK  494
```

DB066922 TESTI4 Homo sapiens cDNA clone TESTI4008395 5', mRNA sequence.

Sequence ID: **DB066922.1** Length: 559 Number of Matches: 1

Range 1: 127 to 498

Score	Expect	Method	Identities	Positives	Gaps	Frame
192 bits(489)	4e-62()	Compositional matrix adjust.	107/124(86%)	107/124(86%)	17/124(13%)	+1

Features:

```
Query  6    VRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLHR  65
            VRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLHR
Sbjct  127  VRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSRRRLHR  306

Query  66   IHRRQHRSCRRRKRRSCRHRRRHRR-----------------AEPGREHAEGTKLPGPLT  108
            IHRRQHRSCRRRKRRSCRHRRRHRR                 AEPGREHAEGTKLPGPLT
Sbjct  307  IHRRQHRSCRRRKRRSCRHRRRHRRGLPAPPPCPPCP*PPQAAEPGREHAEGTKLPGPLT  486

Query  109  PSWK  112
            PSWK
Sbjct  487  PSWK  498
```

HY041193 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence.

Sequence ID: **HY041193.1** Length: 431 Number of Matches: 2

Range 1: 112 to 384

Score	Expect	Method	Identities	Positives	Gaps	Frame
166 bits(421)	2e-52()	Compositional matrix adjust.	90/91(99%)	90/91(98%)	0/91(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRA  91
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRR
Sbjct  292  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRG  384
```

Range 2: 386 to 430

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.3 bits(77)	0.82()	Compositional matrix adjust.	15/15(100%)	15/15(100%)	0/15(0%)	+2

Features:

```
Query  91   AEPGREHAEGTKLPG  105
            AEPGREHAEGTKLPG
Sbjct  386  AEPGREHAEGTKLPG  430
```

HY037781 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131P10, mRNA sequence.

Sequence ID: **HY037781.1** Length: 451 Number of Matches: 2

Range 1: 112 to 384

Score	Expect	Method	Identities	Positives	Gaps	Frame
166 bits(421)	2e-52()	Compositional matrix adjust.	90/91(99%)	90/91(98%)	0/91(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
```

Alignments go on, not shown here.

BLAST Results

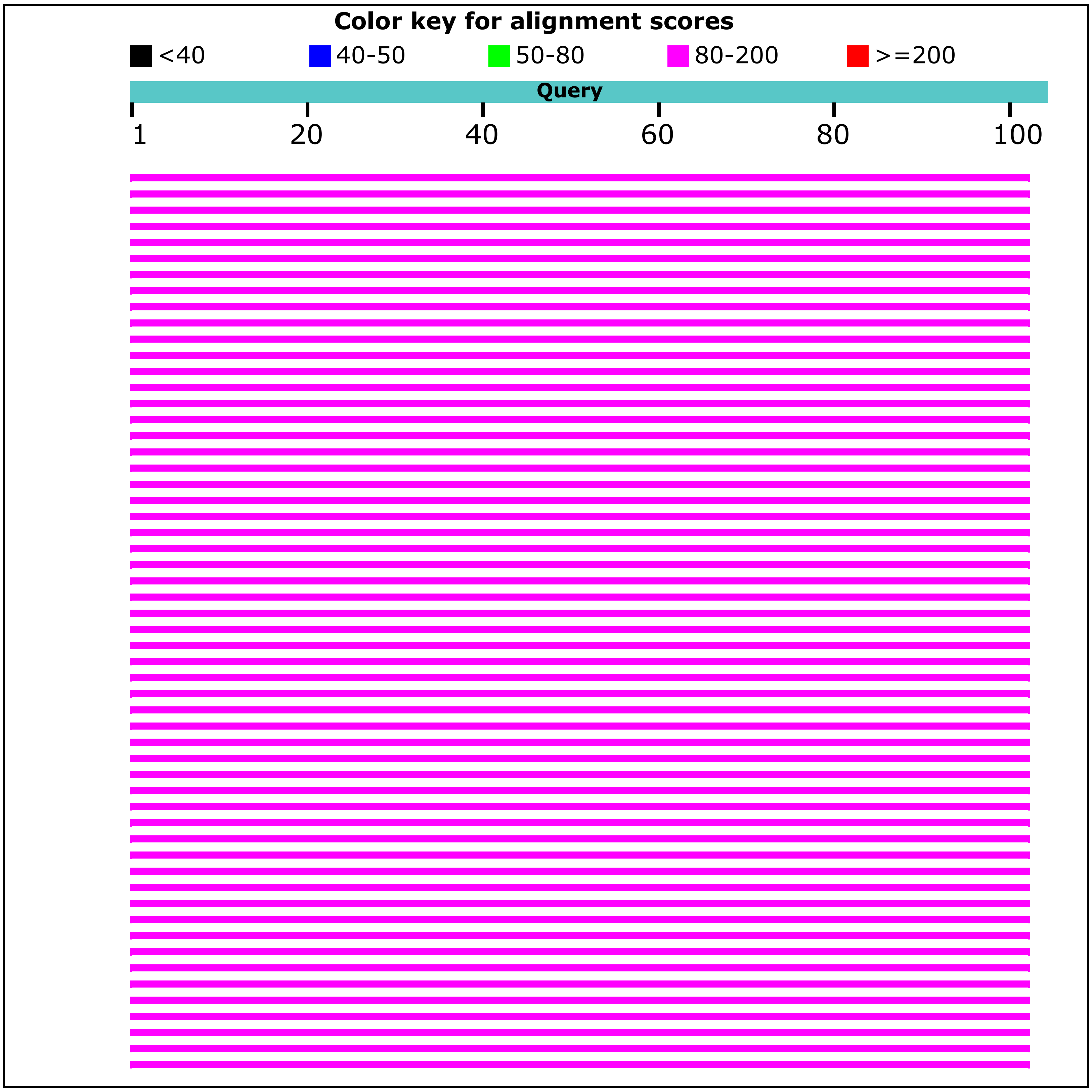
Alignment Q: NCBI tBlastn EAW85159.1 PRM2 isoform CRA_b v. Homo sapiens EST

Job title: EAW85159.1 protamine 2, isoform CRA_b [Homo

RID	ZJ9SBVZT014 (Expires on 11-02 09:44 am)		
Query ID	lcl|Query_155587	**Database Name**	est
Description	EAW85159.1 protamine 2, isoform CRA_b [Homo sapiens]	**Description**	Database of GenBank+EMBL+DDBJ sequences from EST Divisions
Molecule type	amino acid	**Program**	TBLASTN 2.7.1+
Query Length	102		

Graphic Summary

Distribution of the top 100 Blast Hits on 696 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
HY041193 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence	186	186	100%	2e-60	100%	HY041193.1
HY037781 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131P10, mRNA sequence	186	186	100%	2e-60	100%	HY037781.1
HY019058 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064M11, mRNA sequence	186	186	100%	2e-60	100%	HY019058.1
HY031628 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D109I23, mRNA sequence	186	186	100%	2e-60	100%	HY031628.1
HY018995 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064I07, mRNA sequence	186	186	100%	2e-60	100%	HY018995.1
DB081917 TESTI4 Homo sapiens cDNA clone TESTI4028124 5', mRNA sequence	186	186	100%	2e-60	100%	DB081917.1
DB026406 TESTI2 Homo sapiens cDNA clone TESTI2008597 5', mRNA sequence	186	186	100%	2e-60	100%	DB026406.1
HY021923 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D074G19, mRNA sequence	186	186	100%	2e-60	100%	HY021923.1
5540 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC005303, mRNA sequence	186	186	100%	2e-60	100%	CV027318.1
HY017578 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D059K21, mRNA sequence	186	186	100%	2e-60	100%	HY017578.1
HY007196 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024L20, mRNA sequence	186	186	100%	2e-60	100%	HY007196.1
HY006973 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D024A03, mRNA sequence	186	186	100%	2e-60	100%	HY006973.1
AGENCOURT_10399420 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6614218 5', mRNA sequence	186	186	100%	3e-60	100%	BU567583.1
AGENCOURT_10404024 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6613910 5', mRNA sequence	186	186	100%	3e-60	100%	BU567345.1
AGENCOURT_7838474 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6101594 5', mRNA sequence	186	186	100%	3e-60	100%	BQ438663.1
HY023254 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D079H16, mRNA sequence	186	186	100%	3e-60	100%	HY023254.1
DB075497 TESTI4 Homo sapiens cDNA clone TESTI4019393 5', mRNA sequence	186	186	100%	3e-60	100%	DB075497.1
DB453196 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H013060K24 5', mRNA sequence	186	186	100%	3e-60	100%	DB453196.1

Descriptions continue, not shown here.

HY183988 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D003C07, mRNA sequence	38.1	38.1	37%	0.025	89%	HY183988.1

Alignments

HY041193 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D144P09, mRNA sequence.
Sequence ID: **HY041193.1** Length: 431 Number of Matches: 1
Range 1: 112 to 417

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  292  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  417
```

HY037781 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131P10, mRNA sequence.
Sequence ID: **HY037781.1** Length: 451 Number of Matches: 1
Range 1: 112 to 417

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  292  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  417
```

HY019058 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064M11, mRNA sequence.
Sequence ID: **HY019058.1** Length: 456 Number of Matches: 1
Range 1: 111 to 416

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  291  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  416
```

HY031628 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D109I23, mRNA sequence.
Sequence ID: **HY031628.1** Length: 453 Number of Matches: 1
Range 1: 112 to 417

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+1

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  112  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  291

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  292  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  417
```

HY018995 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D064I07, mRNA sequence.

Sequence ID: **HY018995.1** Length: 462 Number of Matches: 1
Range 1: 111 to 416

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	2e-60()	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+3

Features:

```
Query  1    MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  60
            MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR
Sbjct  111  MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQEEQGLSPEHVEVYERTHGQSHYRRRHCSR  290

Query  61   RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  102
            RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH
Sbjct  291  RRLHRIHRRQHRSCRRRKRRSCRHRRRHRRGCRTRKRTCRRH  416
```

BLAST ® » blastn suite » RID-4J6P1VZ9014

BLAST Results

Appendix R: NCBI BLAST Homo sapiens TNP1 mRNA v. Gorilla gorilla genome

Nucleotide Sequence (415 letters)

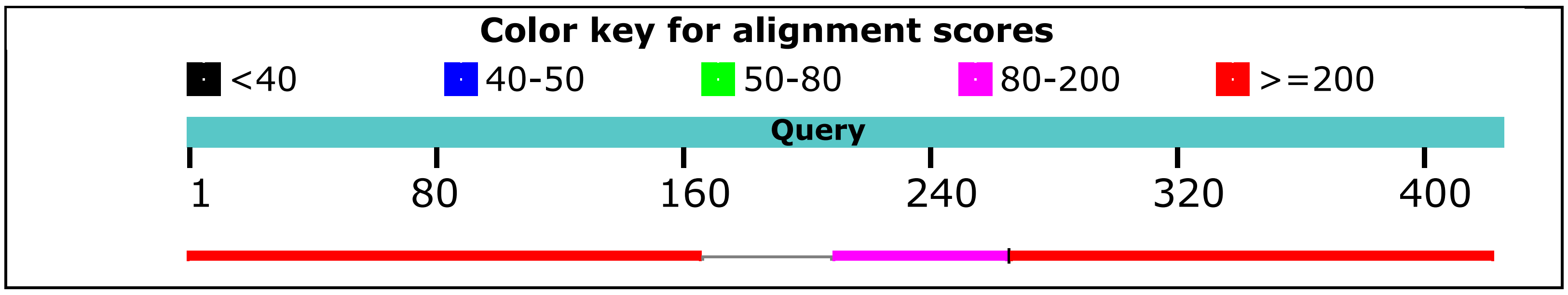
RID 4J6P1VZ9014 (Expires on 12-09 15:33 pm)

Query ID lcl|Query_240161
Description None
Molecule type nucleic acid
Query Length 415

Database Name Genome (gorGor4 reference Annotation Release 101)
Description Gorilla gorilla gorGor4 [GCF_000151905.2] chromosomes plus unplaced and unlocalized scaffolds (reference assembly in Annotation Release 101)
Program BLASTN 2.6.0+

⊖ Graphic Summary

Distribution of 4 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Gorilla gorilla gorilla chromosome 2B, gorGor4	305	961	90%	1e-80	99%	NC_018426.2

Alignments

Gorilla gorilla gorilla chromosome 2B, gorGor4
Sequence ID: **NC_018426.2** Length: 135448346 Number of Matches: 4
Range 1: 1189477 to 1189647

Score	Expect	Identities	Gaps	Strand	Frame
305 bits(165)	1e-80()	169/171(99%)	0/171(0%)	Plus/Minus	

Features:

```
Query  245      AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAGCCAGAGAGGAG  304
                ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  1189647  AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGAGCAAAGCCAGAGAGGAG  1189588

Query  305      CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAGGAATGTATATGTTGGCTGT  364
                |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  1189587  CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAAGAATGTATATGTTGGCTGT  1189528

Query  365      TTTTCCCCAACATCTCAATAAAActttgaaagcagaaaaaaaaaaaaaaaaa  415
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1189527  TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAAAAAAAAAAAAAAAA  1189477
```

Range 2: 110064699 to 110064856

Score	Expect	Identities	Gaps	Strand	Frame
281 bits(152)	2e-73()	156/158(99%)	0/158(0%)	Plus/Minus	

Features:

```
Query  245        AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAGCCAGAGAGGAG  304
                  ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  110064856  AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGAGCAAAGCCAGAGAGGAG  110064797

Query  305        CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAGGAATGTATATGTTGGCTGT  364
                  |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  110064796  CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAAGAATGTATATGTTGGCTGT  110064737

Query  365        TTTTCCCCAACATCTCAATAAAActttgaaagcagaaa  402
                  ||||||||||||||||||||||||||||||||||||||
Sbjct  110064736  TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAA  110064699
```

Range 3: 110068214 to 110068377

Score	Expect	Identities	Gaps	Strand	Frame
281 bits(152)	2e-73()	160/164(98%)	0/164(0%)	Plus/Minus	

Features:

```
Query  1          GCCCCTCATTTTGGCAGAACTTACCATGTCGACCAGCCGCAAATTAAAGAGTCATGGCAT  60
                  |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  110068377  GCCCCTCATTTTGGCAGAACTTACCATGTCGACCAGCCGCAAATTAAAAAGTCATGGCAT  110068318

Query  61         GAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAGTCAAGAGAGgtggcagcaaaagaaa  120
                  ||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||
Sbjct  110068317  GAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAA  110068258

Query  121        ataccGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGATGACG  164
                  ||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  110068257  ATACCGTAAGGGCAACCCGAAAAGTAGGAAACGGGGCGATGACG  110068214
```

Range 4: 110067958 to 110068012

Score	Expect	Identities	Gaps	Strand	Frame
91.6 bits(49)	3e-16()	53/55(96%)	0/55(0%)	Plus/Minus	

Features:

```
Query  206        CTCTGCCCTGGTGCGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAGGG  260
                  |||||||||||| ||||||||||||||||||||||||||||||||||||||| ||
Sbjct  110068012  CTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAACGG  110067958
```

BLAST ® » blastn suite » RID-4J74W88T014

BLAST Results

Appendix S: NCBI BLAST Homo sapiens TNP1 gene v. Gorilla gorilla genome

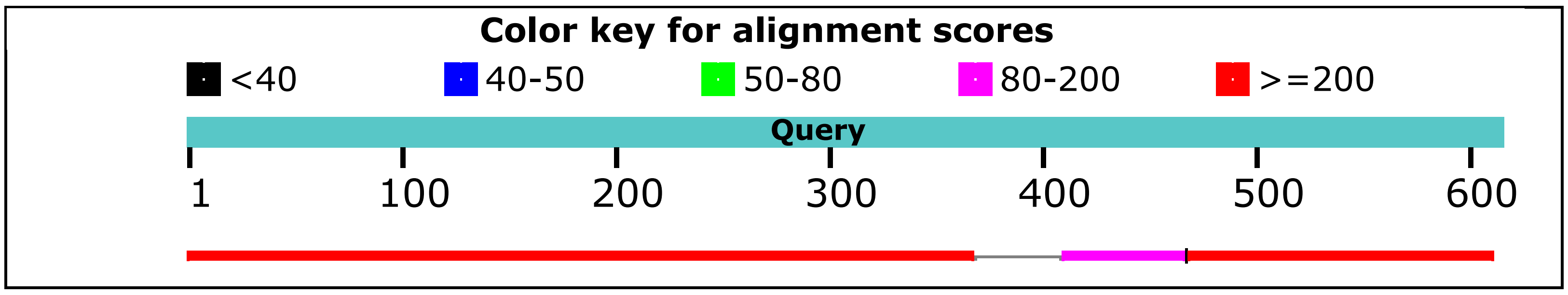
Nucleotide Sequence (602 letters)

RID	4J74W88T014 (Expires on 12-09 15:41 pm)
Query ID	lcl|Query_157133
Description	None
Molecule type	nucleic acid
Query Length	602

Database Name	Genome (gorGor4 reference Annotation Release 101)
Description	Gorilla gorilla gorGor4 [GCF_000151905.2] chromosomes plus unplaced and unlocalized scaffolds (reference assembly in Annotation Release 101)
Program	BLASTN 2.6.0+

Graphic Summary

Distribution of 4 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Gorilla gorilla gorilla chromosome 2B, gorGor4	632	1287	93%	6e-179	98%	NC_018426.2

Alignments

Gorilla gorilla gorilla chromosome 2B, gorGor4
Sequence ID: **NC_018426.2** Length: 135448346 Number of Matches: 4
Range 1: 110068012 to 110068377

Score	Expect	Identities	Gaps	Strand	Frame
632 bits(342)	6e-179()	358/366(98%)	0/366(0%)	Plus/Minus	

Features:

```
Query  1          GCCCCTCATTTTGGCAGAACTTACCATGTCGACCAGCCGCAAATTAAAGAGTCATGGCAT  60
                  |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  110068377  GCCCCTCATTTTGGCAGAACTTACCATGTCGACCAGCCGCAAATTAAAAAGTCATGGCAT  110068318

Query  61         GAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGAGTCAAGAGAGgtggcagcaaaagaaa  120
                  ||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||
Sbjct  110068317  GAGGAGGAGCAAGAGCCGATCTCCTCACAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAA  110068258

Query  121        ataccGTAAGGGCAACCTGAAAAGTAGGAAACGGGGCGATGACGGTGAGTGAGGGATGGG  180
                  ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  110068257  ATACCGTAAGGGCAACCCGAAAAGTAGGAAACGGGGCGATGACGGTGAGTGAGGGATGGG  110068198

Query  181        GAGGAGATTGCCAAACTTAGGCACACATTGCTGCCAGGCCCTCCCTCTTGGAGGCAGCTC  240
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  110068197  GAGGAGATTGCCAAACTTAGGCACACATTGCTGCCAGGCCCTCCCTCTTGGAGGCAGCCC  110068138

Query  241        TCACAGGACCCTGAAATCTTGGCCTGAGATTATTTCCAATAACTAAATGCAGATTTGAGC  300
                  ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  110068137  TCACAGGACCCTGAAATCTCGGCCTGAGATTATTTCCAATAACTAAATGCAGATTTGAGC  110068078

Query  301        AACAAGAGTCTTGATGGGAATGTTCTAATTCGTGTCTCTGTTGCAAACCTGTCCTTTCCC  360
                  || |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  110068077  AATAAGAGTCTTGATGGGAATGTTCTAATTCATGTCTCTGTTGCAAACCTGTCCTTTCCC  110068018

Query  361        ACAGCC  366
                  ||||||
Sbjct  110068017  ACAGCC  110068012
```

Range 2: 1189490 to 1189647

Score	Expect	Identities	Gaps	Strand	Frame
281 bits(152)	3e-73()	156/158(99%)	0/158(0%)	Plus/Minus	

Features:

```
Query  445      AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAGCCAGAGAGGAG  504
                ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  1189647  AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGAGCAAAGCCAGAGAGGAG  1189588

Query  505      CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAGGAATGTATATGTTGGCTGT  564
                |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  1189587  CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAAGAATGTATATGTTGGCTGT  1189528

Query  565      TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAA  602
                ||||||||||||||||||||||||||||||||||||||
Sbjct  1189527  TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAA  1189490
```

Range 3: 110064699 to 110064856

Score	Expect	Identities	Gaps	Strand	Frame

281 bits(152)	3e-73()	156/158(99%)	0/158(0%)	Plus/Minus	

Features:

```
Query  445        AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAGCCAGAGAGGAG  504
                  ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  110064856  AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGAGCAAAGCCAGAGAGGAG  110064797
Query  505        CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAGGAATGTATATGTTGGCTGT  564
                  |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  110064796  CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAAGAATGTATATGTTGGCTGT  110064737
Query  565        TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAA  602
                  ||||||||||||||||||||||||||||||||||||||
Sbjct  110064736  TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAA  110064699
```

Range 4: 110067958 to 110068012

Score	Expect	Identities	Gaps	Strand	Frame
91.6 bits(49)	5e-16()	53/55(96%)	0/55(0%)	Plus/Minus	

Features:

```
Query  406        CTCTGCCCTGGTGCGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAGGG  460
                  |||||||||||| ||||||||||||||||||||||||||||||||||||||| ||
Sbjct  110068012  CTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAACGG  110067958
```

BLAST ® » blastn suite » RID-4P61V4ZH01R

BLAST Results

Appendix T: NCBI BLAST Gorilla gorilla TNP1 insertion v. Gorilla gorilla genome

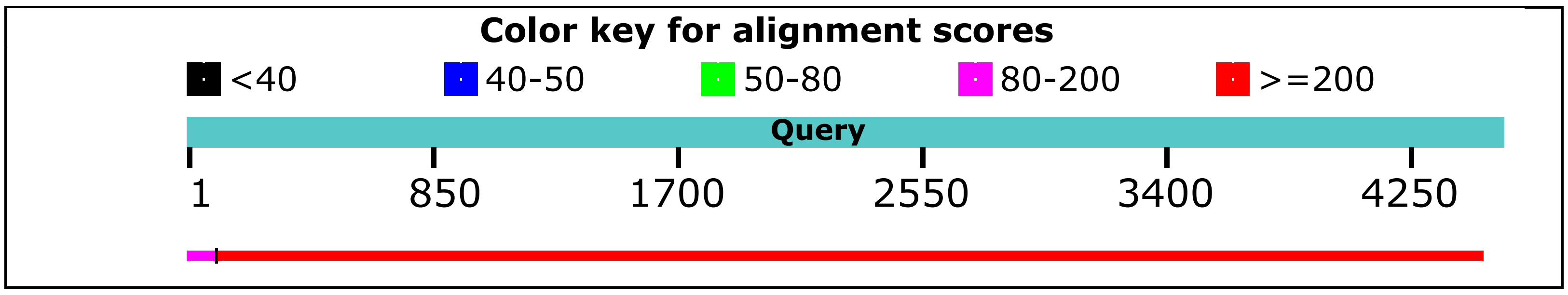
Nucleotide Sequence (4470 letters)

RID 4P61V4ZH01R (Expires on 12-11 03:46 am)

Query ID	lcl|Query_41537	**Database Name**	Genome (gorGor4 reference Annotation Release 101)
Description	None	**Description**	Gorilla gorilla gorGor4 [GCF_000151905.2] chromosomes plus unplaced and unlocalized scaffolds (reference assembly in Annotation Release 101)
Molecule type	nucleic acid	**Program**	BLASTN 2.5.1+
Query Length	4470		

Graphic Summary

Distribution of the top 3 Blast Hits on 1 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Gorilla gorilla gorilla chromosome 2B, gorGor4	8102	8889	100%	0.0	100%	NC_018426.2

Alignments

Gorilla gorilla gorilla chromosome 2B, gorGor4
Sequence ID: **NC_018426.2** Length: 135448346 Number of Matches: 3
Range 1: 110061010 to 110065396

Score	Expect	Identities	Gaps	Strand	Frame
8102 bits(4387)	0.0()	4387/4387(100%)	0/4387(0%)	Plus/Minus	

Features:

```
Query  84         ccggcCGCCGCTAcggggaagtgaggagcccctctgcccggccagccgccccgtctggga  143
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110065396  CCGGCCGCCGCTACGGGGAAGTGAGGAGCCCCTCTGCCCGGCCAGCCGCCCCGTCTGGGA  110065337
Query  144        gggaggtgggggggtcagtcccccgcccggccagccgccccgtccgggagggaggtgggg  203
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110065336  GGGAGGTGGGGGGGTCAGTCCCCCGCCCGGCCAGCCGCCCCGTCCGGGAGGGAGGTGGGG  110065277
Query  204        ggttcagcccccgcccggccagccgccccgtccgggagggaggtgggggggtcagcccc  263
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110065276  GGTTCAGCCCCCCGCCCGGCCAGCCGCCCCGTCCGGGAGGGAGGTGGGGGGGTCAGCCCC  110065217
Query  264        ccgcccgaccagccaccccgtccgggagggaggtgggggggtcagcccccgcccgacca  323
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110065216  CCGCCCGACCAGCCACCCCGTCCGGGAGGGAGGTGGGGGGGTCAGCCCCCCGCCCGACCA  110065157
Query  324        gccgccccgtccgggagggaggtgggggggttcagcccccgcccggccagccgccccgtc  383
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110065156  GCCGCCCCGTCCGGGAGGGAGGTGGGGGGTTCAGCCCCCCGCCCGGCCAGCCGCCCCGTC  110065097
Query  384        cgggagggaggtgggggggtcagccccccgcccggccagccgccccgtccgggaggtgagg  443
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110065096  CGGGAGGGAGGTGGGGGGTCAGCCCCCCGCCCGGCCAGCCGCCCCGTCCGGGAGGTGAGG  110065037
Query  444        ggcgcctctgcccggccacccctactgggaagtgaggagcccctctgcccggccagccgc  503
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110065036  GGCGCCTCTGCCCGGCCACCCCTACTGGGAAGTGAGGAGCCCCTCTGCCCGGCCAGCCGC  110064977
Query  504        cccgtccgggagggaggtgggggggtcctatgtcctatgaccctgccaaatccccctttg  563
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064976  CCCGTCCGGGAGGGAGGTGGGGGGGTCCTATGTCCTATGACCCTGCCAAATCCCCCTTTG  110064917
Query  564        cgagaaacacccaagaatgatcaataaataaataaataaataaataaaaagaataaaaaa  623
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064916  CGAGAAACACCCAAGAATGATCAATAAATAAATAAATAAATAAATAAAAAGAATAAAAAA  110064857
Query  624        aagaacagcagaaGGGGAACTGCCAAGGAGACCTGATGTTAGAGCAAAGCCAGAGAGGAG  683
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064856  AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGAGCAAAGCCAGAGAGGAG  110064797
Query  684        CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAAGAATGTATATGTTGGCTGT  743
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064796  CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAAGAATGTATATGTTGGCTGT  110064737
Query  744        TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAATGTTTACTTTGATCTTTTGGTT  803
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064736  TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAATGTTTACTTTGATCTTTTGGTT  110064677
Query  804        GGAAGGACTTGAGTTCCTGAGCTAGGTGGGTTTGGGGAAGAATTGGCCAGTATGAAACCA  863
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064676  GGAAGGACTTGAGTTCCTGAGCTAGGTGGGTTTGGGGAAGAATTGGCCAGTATGAAACCA  110064617
Query  864        TTAAATGTGACTTGGAAAATATCAAAAGTAATTTGTCCTCCAATTCCCTCCCACGGTGGT  923
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064616  TTAAATGTGACTTGGAAAATATCAAAAGTAATTTGTCCTCCAATTCCCTCCCACGGTGGT  110064557
Query  924        CCTACTCTGGCCACACACTATTGCCGTATTTGTCTTCATCCCAGTGTGCTGTCTCTCTCC  983
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064556  CCTACTCTGGCCACACACTATTGCCGTATTTGTCTTCATCCCAGTGTGCTGTCTCTCTCC  110064497
```

```
Query  984        TCAAcatggaaagggagaagagataAAAAAGGGAGAAATGCATTCATTAGCATTAACCAA  1043
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064496  TCAACATGGAAAGGGAGAAGAGATAAAAAAGGGAGAAATGCATTCATTAGCATTAACCAA  110064437

Query  1044       AGGATTCAAGCTGTTTCTGTTAGAGCTTAAACCAAAGGATGCAAGCTGTTTTTGTCAGAG  1103
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064436  AGGATTCAAGCTGTTTCTGTTAGAGCTTAAACCAAAGGATGCAAGCTGTTTTTGTCAGAG  110064377

Query  1104       CTTATAGCATAGAGGTGTTGAAAGCTAAACTAAAGACTTGGCCCGGAGATAGAGATCACC  1163
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064376  CTTATAGCATAGAGGTGTTGAAAGCTAAACTAAAGACTTGGCCCGGAGATAGAGATCACC  110064317

Query  1164       TGAAGGAGCTCTTAGAAGCTCTTAATTCATTGATCATATGGGCAGGATTAGCAGGCTAAG  1223
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064316  TGAAGGAGCTCTTAGAAGCTCTTAATTCATTGATCATATGGGCAGGATTAGCAGGCTAAG  110064257

Query  1224       AGATGGGAACACCTTCTGAACAGAGACCAACATGTTCTTTGTAAAGGATCCTATTAGTAA  1283
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064256  AGATGGGAACACCTTCTGAACAGAGACCAACATGTTCTTTGTAAAGGATCCTATTAGTAA  110064197

Query  1284       CAGTGGAAGTGATGAGAGTTTAGATTTCTTTAGGTTATTTTGGTAGCTATGTTGGGCTTG  1343
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064196  CAGTGGAAGTGATGAGAGTTTAGATTTCTTTAGGTTATTTTGGTAGCTATGTTGGGCTTG  110064137

Query  1344       AGGTGGGCAAGACTGAAGAATGGGATATTGCCTCGTAGCATGCCATAAGCCTTAGTCCAG  1403
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064136  AGGTGGGCAAGACTGAAGAATGGGATATTGCCTCGTAGCATGCCATAAGCCTTAGTCCAG  110064077

Query  1404       TGTGCCTAGAAGTAGGAATTGTCTCAATCTGAGTATTGATCATTTGACAGAGAACTGACT  1463
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064076  TGTGCCTAGAAGTAGGAATTGTCTCAATCTGAGTATTGATCATTTGACAGAGAACTGACT  110064017

Query  1464       TTAGGGATAGAGCTGGTTCTGCTCATTTAGGAAATTCCTAAGCCCTCACTTTACCTTGTC  1523
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110064016  TTAGGGATAGAGCTGGTTCTGCTCATTTAGGAAATTCCTAAGCCCTCACTTTACCTTGTC  110063957

Query  1524       CCTGAGTTGTAACACAATTTATGATGTCTCTGGTCAAGGATATGACATTCACCCACTCAG  1583
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063956  CCTGAGTTGTAACACAATTTATGATGTCTCTGGTCAAGGATATGACATTCACCCACTCAG  110063897

Query  1584       AGGTGGATAGTATTTTTCTTGTGTTTCCTGTTGCCTCAGAGGTAGCTCCAGGGTAGAAAT  1643
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063896  AGGTGGATAGTATTTTTCTTGTGTTTCCTGTTGCCTCAGAGGTAGCTCCAGGGTAGAAAT  110063837

Query  1644       GAGACTCATATTTAAACTCAAGAACCAACCACCCACGTGGTTTCTGGGGAAGTAACCAGG  1703
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063836  GAGACTCATATTTAAACTCAAGAACCAACCACCCACGTGGTTTCTGGGGAAGTAACCAGG  110063777

Query  1704       AAAGGGTATAAGCAGGAAGGAATGAGGGGGCATGAGGTTAGACACGAAGTTTCCAGCAGT  1763
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063776  AAAGGGTATAAGCAGGAAGGAATGAGGGGGCATGAGGTTAGACACGAAGTTTCCAGCAGT  110063717

Query  1764       CAGGGGTGTGAGACATGGGAAGAGGACACTATTAAGTCTGAGCGTCATGCAAATGTGTGG  1823
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063716  CAGGGGTGTGAGACATGGGAAGAGGACACTATTAAGTCTGAGCGTCATGCAAATGTGTGG  110063657

Query  1824       GTACCAGGATGTTGGTCCTATTAAGGGGTGGCAAGGGGTGTTCCTGTGGGTCAGAATcta  1883
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063656  GTACCAGGATGTTGGTCCTATTAAGGGGTGGCAAGGGGTGTTCCTGTGGGTCAGAATCTA  110063597

Query  1884       gaaatgcaataaaaaagcatgttcatttttcagataagtTATTTCACTTGttggggtaaa  1943
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063596  GAAATGCAATAAAAAAGCATGTTCATTTTTCAGATAAGTTATTTCACTTGTTGGGGTAAA  110063537

Query  1944       atatttcaaGTCCTCACTCTTCCATAACCCTAAGAATGAGCATGCTGATTCAGAGCTGTT  2003
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063536  ATATTTCAAGTCCTCACTCTTCCATAACCCTAAGAATGAGCATGCTGATTCAGAGCTGTT  110063477

Query  2004       TTCAAGTTCATGTGAAAAACATCTCTCCTTACCATCAGGCACACAGATACTTCAAAGTTT  2063
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063476  TTCAAGTTCATGTGAAAAACATCTCTCCTTACCATCAGGCACACAGATACTTCAAAGTTT  110063417

Query  2064       TCCATTGTCAGTTTCCCTTTTTGTCAAATGGAGGATAGGGATAGGGAAAATGCTTCATAA  2123
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063416  TCCATTGTCAGTTTCCCTTTTTGTCAAATGGAGGATAGGGATAGGGAAAATGCTTCATAA  110063357

Query  2124       CCCTCATCCTCCATGGTTGTGTCTATTTTACCTCCTAAATGTGACTTTTGTTTGTCTTTG  2183
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063356  CCCTCATCCTCCATGGTTGTGTCTATTTTACCTCCTAAATGTGACTTTTGTTTGTCTTTG  110063297

Query  2184       CCTCTCTAACCAAACTCAAGTTAGTCTCAAATAATCCTATATGTGTCCGTAGTGTCACTG  2243
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063296  CCTCTCTAACCAAACTCAAGTTAGTCTCAAATAATCCTATATGTGTCCGTAGTGTCACTG  110063237

Query  2244       AACGAAGCTCTAACTTCTTAGAAGTTTGCACACATATCTGATCTGGATTCCCTCCTTCAA  2303
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063236  AACGAAGCTCTAACTTCTTAGAAGTTTGCACACATATCTGATCTGGATTCCCTCCTTCAA  110063177

Query  2304       ATCTCTGAAAGAACTCATCAGCCATGGCTCTCACCCTGCTCTCATGCCTCCTGGGACTTC  2363
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063176  ATCTCTGAAAGAACTCATCAGCCATGGCTCTCACCCTGCTCTCATGCCTCCTGGGACTTC  110063117

Query  2364       CTCTGCCtctgtataaaatataaacacactttgcaacacatgaaatctataaaataaatc  2423
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063116  CTCTGCCTCTGTATAAAATATAAACACACTTTGCAACACATGAAATCTATAAAATAAATC  110063057
```

```
Query  2424       caaaaagtaaaaattgtttaattattttaatgtgcttttgCTGCTCTTGCTGTAAATTCT  2483
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110063056  CAAAAAGTAAAAATTGTTTAATTATTTTAATGTGCTTTTGCTGCTCTTGCTGTAAATTCT  110062997

Query  2484       TTTAAACTTAGCCTCATAGGTTGGGTTCTCAGGGAGTGGAGATGGAGTTTGAATGCAAGA  2543
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062996  TTTAAACTTAGCCTCATAGGTTGGGTTCTCAGGGAGTGGAGATGGAGTTTGAATGCAAGA  110062937

Query  2544       TGTTTATTAGAGGTCAGTACTTGAAGAGGGAGCTGAACAAACCATCAGGCAGTATAGCCA  2603
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062936  TGTTTATTAGAGGTCAGTACTTGAAGAGGGAGCTGAACAAACCATCAGGCAGTATAGCCA  110062877

Query  2604       GGCCTTTATACCATTTATACCCCACCTGGCTGGGCTGCGCCAGTAAGACATGGCATTTCC  2663
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062876  GGCCTTTATACCATTTATACCCCACCTGGCTGGGCTGCGCCAGTAAGACATGGCATTTCC  110062817

Query  2664       CTGCTGAGGCAGACTCAGAAGGGAGCATCAGCTGGAGGTTCCTTGGTGGACCACACACCC  2723
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062816  CTGCTGAGGCAGACTCAGAAGGGAGCATCAGCTGGAGGTTCCTTGGTGGACCACACACCC  110062757

Query  2724       ACAATCTGAGCAGCTCACCTCGGTGTCTATTACAATTGCTCTCTGGATGATCTGTATCTT  2783
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062756  ACAATCTGAGCAGCTCACCTCGGTGTCTATTACAATTGCTCTCTGGATGATCTGTATCTT  110062697

Query  2784       TTCTCAGCCTCTGGTCCCCATCTTCCCCTTAAGCCTCTTCACAGCTTGCTGCCTTGCCAC  2843
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062696  TTCTCAGCCTCTGGTCCCCATCTTCCCCTTAAGCCTCTTCACAGCTTGCTGCCTTGCCAC  110062637

Query  2844       TTCCTGCTGTGACTGTGTGTCATGAGTCTTCAAATGCTCTTGTGCACAGCTCACTTCTTG  2903
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062636  TTCCTGCTGTGACTGTGTGTCATGAGTCTTCAAATGCTCTTGTGCACAGCTCACTTCTTG  110062577

Query  2904       TGGATTGCCAATTTGCACAAAGATGACCTCTCCCATAGGACAAAGTCAACAGTCAGGAAC  2963
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062576  TGGATTGCCAATTTGCACAAAGATGACCTCTCCCATAGGACAAAGTCAACAGTCAGGAAC  110062517

Query  2964       AAACTAGAATACCGTGATGCTGAGTGTGCAACATTTACTTCCCTCAGGAAACTTGTTATG  3023
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062516  AAACTAGAATACCGTGATGCTGAGTGTGCAACATTTACTTCCCTCAGGAAACTTGTTATG  110062457

Query  3024       ATTAGGGAGCCACAGATCCCTGCAGATGGTCCAAATGAAGACTTTGTCAAAGGGATTATT  3083
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062456  ATTAGGGAGCCACAGATCCCTGCAGATGGTCCAAATGAAGACTTTGTCAAAGGGATTATT  110062397

Query  3084       TACAGAGGACAGACACCTAGAGCCTACCAATGAGGTCTTCAGACCCTTAGGACTGAGAAG  3143
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062396  TACAGAGGACAGACACCTAGAGCCTACCAATGAGGTCTTCAGACCCTTAGGACTGAGAAG  110062337

Query  3144       GCAAAAGGGCAAAATAGCACAACAGGAGCCCATTGACAGCCAAAACTGTGTGTGGGAAGG  3203
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062336  GCAAAAGGGCAAAATAGCACAACAGGAGCCCATTGACAGCCAAAACTGTGTGTGGGAAGG  110062277

Query  3204       AATGGTTGTGAATGGACCTCCTGGTAAAATCTGTACTAGGAGGATCGCAGCTGTTGTCAG  3263
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062276  AATGGTTGTGAATGGACCTCCTGGTAAAATCTGTACTAGGAGGATCGCAGCTGTTGTCAG  110062217

Query  3264       GCTCAGACACAGGGAGGAAACGTTCCATCATTTATCTAATCTCCTGCTGCTGCTCTCATT  3323
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062216  GCTCAGACACAGGGAGGAAACGTTCCATCATTTATCTAATCTCCTGCTGCTGCTCTCATT  110062157

Query  3324       GGCGAAATTCAGAAGTCAACAGACAAGAGACCCCAGGTGACACAGAGCATAAGGGCCAGC  3383
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062156  GGCGAAATTCAGAAGTCAACAGACAAGAGACCCCAGGTGACACAGAGCATAAGGGCCAGC  110062097

Query  3384       CCCCTGGGGCATCAAAGAGCAGAGAATGTTGGATAAAATCTCCAAAATCCAACAGTGATA  3443
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062096  CCCCTGGGGCATCAAAGAGCAGAGAATGTTGGATAAAATCTCCAAAATCCAACAGTGATA  110062037

Query  3444       TCTGACACAACTTTGCAGACAAAATTCTTCTTTCCTGGACTCCTTAGAAGTTTGTCACTT  3503
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110062036  TCTGACACAACTTTGCAGACAAAATTCTTCTTTCCTGGACTCCTTAGAAGTTTGTCACTT  110061977

Query  3504       TATCAACCTGCTTATCTCCTCCCTTATGCTGTCATGGACCAAAGTCCCTTCAGAAGCAAA  3563
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061976  TATCAACCTGCTTATCTCCTCCCTTATGCTGTCATGGACCAAAGTCCCTTCAGAAGCAAA  110061917

Query  3564       TTGTAGAGAGATAGAGTGAGGAGAGAGTTACACAGGGCTCCTGAACCCTCACCTTAAAAA  3623
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061916  TTGTAGAGAGATAGAGTGAGGAGAGAGTTACACAGGGCTCCTGAACCCTCACCTTAAAAA  110061857

Query  3624       GCTTGTTTTCATGTTATTTGCTTGACAGTATTATCCCCAAACCAATACAACGCAATGTTC  3683
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061856  GCTTGTTTTCATGTTATTTGCTTGACAGTATTATCCCCAAACCAATACAACGCAATGTTC  110061797

Query  3684       TAATGCAGTGCTATATCTTCACAATACTCTAAACACTGAAACAATCTAATTAATCATCAG  3743
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061796  TAATGCAGTGCTATATCTTCACAATACTCTAAACACTGAAACAATCTAATTAATCATCAG  110061737

Query  3744       GACAGGCATGTGGTGAACAGCCCAAGACTAGCCACGGCAGACAGATCCTCGCCTGGTGac  3803
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061736  GACAGGCATGTGGTGAACAGCCCAAGACTAGCCACGGCAGACAGATCCTCGCCTGGTGAC  110061677

Query  3804       ttcagcctctgccttcttAGACAGGTTGTGAAGGAATGGTAGCCGCCCGGAAAACTCTAC  3863
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061676  TTCAGCCTCTGCCTTCTTAGACAGGTTGTGAAGGAATGGTAGCCGCCCGGAAAACTCTAC  110061617

Query  3864       TTTGCACTGGGAACATTTTCCAGACCCACATATTGGAAGTTTTTCAACACTGGCATTGAT  3923
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061616  TTTGCACTGGGAACATTTTCCAGACCCACATATTGGAAGTTTTTCAACACTGGCATTGAT  110061557

Query  3924       GTAGTCTCTGTACCCCAGGAATATTCATTCTGTCCCTCTGTTTACAGTTCCTATAGGCCC  3983
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061556  GTAGTCTCTGTACCCCAGGAATATTCATTCTGTCCCTCTGTTTACAGTTCCTATAGGCCC  110061497

Query  3984       AGCACCTACAAGGCACGCGTAGGGGTCTTTGACCATGGGGACTCTCTTTCAGAAAACCCA  4043
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061496  AGCACCTACAAGGCACGCGTAGGGGTCTTTGACCATGGGGACTCTCTTTCAGAAAACCCA  110061437

Query  4044       AAGGCCTCACCCCCTGTGtgctttttctccatctcccTAACCAAGGAGGACTTTGTTTCC  4103
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061436  AAGGCCTCACCCCCTGTGTGCTTTTTCTCCATCTCCCTAACCAAGGAGGACTTTGTTTCC  110061377

Query  4104       CTCCCCAGTTTTCTCCAGAACGCTATGTCCTAAAGTCATCACTTGTTTAGACTtttggaa  4163
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061376  CTCCCCAGTTTTCTCCAGAACGCTATGTCCTAAAGTCATCACTTGTTTAGACTTTTGGAA  110061317

Query  4164       aagtgaaaaaaaaaaaaaaaaaaaaaaaatgaaggatctTGGCCACAAGCCCTTTTGGG  4223
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061316  AAGTGAAAAAAAAAAAAAAAAAAAAAAAATGAAGGATCTTGGCCACAAGCCCTTTTGGG  110061257

Query  4224       TCACCTTGACCTTCATGTGAGCTGACTTGGATATGGGGCCTCTGCTCCACTGGCATCAGA  4283
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061256  TCACCTTGACCTTCATGTGAGCTGACTTGGATATGGGGCCTCTGCTCCACTGGCATCAGA  110061197

Query  4284       GCCCGATGGGAGTGGCGAAGCCCAGGGGACCCACGTGTGGGTGGAGAAAACCCCAAGGAG  4343
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061196  GCCCGATGGGAGTGGCGAAGCCCAGGGGACCCACGTGTGGGTGGAGAAAACCCCAAGGAG  110061137

Query  4344       CTATGGAGAACACAGCCAACTCCCACCTTTCACCCAGCCTCCTCCAGATGACCCTTGGGT  4403
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061136  CTATGGAGAACACAGCCAACTCCCACCTTTCACCCAGCCTCCTCCAGATGACCCTTGGGT  110061077

Query  4404       GGGACCTGCATCTGTGCAGCTGCAGGCAAACAGGAAGTTCTGGAGAAACGCTCAGGGCTA  4463
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110061076  GGGACCTGCATCTGTGCAGCTGCAGGCAAACAGGAAGTTCTGGAGAAACGCTCAGGGCTA  110061017

Query  4464       TGTTTAG  4470
                  |||||||
Sbjct  110061016  TGTTTAG  110061010
```

Range 2: 1189490 to 1189970

Score	Expect	Identities	Gaps	Strand	Frame
632 bits(342)	5e-178()	448/496(90%)	20/496(4%)	Plus/Minus	

Features:

```
Query  291      gggaggtgggggggtcagccccccgcccgaccagccgccccgtccgggagggaggtgggg  350
                ||||||||||||||| ||||||||||||| ||||||||||| ||||||||||||||||||
Sbjct  1189970  GGGAGGTGGGGGGGTTAGCCCCCCGCCCGGCCAGCCGCCCCTTCCGGGAGGGAGGTGGGG  1189911

Query  351      ggttcagccccccgcccggccagccgccccgtccgggagggaggtggggggtcagccccc  410
                ||||||||||||||||||||||||||||||||||||||||    || |||| | | |   
Sbjct  1189910  GGTTCAGCCCCCCGCCCGGCCAGCCGCCCCGTCCGGGAGG----TGAGGGG-C-G-CTTT  1189858

Query  411      cgcccggccagccgccccgtccgggaggtgaggggcgcctctgcccggcca--c-cccta  467
                 |||||||||    ||||  | |||| |||||| || | | | ||||||||||  | ||| |
Sbjct  1189857  TGCCCGGCCA----CCCCTACTGGGAAGTGAGGAGCCCTTTTGCCCGGCCAGCCGCCCCA  1189802

Query  468      -ctgggaagtgaggagcccctctgcccggccagccgccccgtccgggagggaggtggggg  526
                 | ||| |  | ||||| |     |  |||||||||||||||||||||||||| |||||||
Sbjct  1189801  GCCGGG-A--G-GGAGGCGGGGGGGTCGGCCAGCCGCCCCGTCCGGGAGGGAAGTGGGGG  1189746

Query  527      ggtcctatgtcctatgaccctgccaaatcccccttgcgagaaacacccaagaatgatca  586
                |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  1189745  GGTCCTATGTCCTATGACCCTGCCAAATCCCCCTCTGCGAGAAACACCCAAGAATGATCA  1189686

Query  587      ataaataaataaataaataaataaaaagaataaaaaaaa-gaacagcagaaGGGGAACTG  645
                ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  1189685  ATAAATAAATAAATAAATAAATAAAAAGAATAAAAAAAAAGAACAGCAGAAGGGGAACTG  1189626

Query  646      CCAAGGAGACCTGATGTTAGAGCAAAGCCAGAGAGGAGCCTATGGAATGTGGATCAAATG  705
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1189625  CCAAGGAGACCTGATGTTAGAGCAAAGCCAGAGAGGAGCCTATGGAATGTGGATCAAATG  1189566

Query  706      CCAGTTGTGACGAAATGAAGAATGTATATGTTGGCTGTTTTTCCCCAACATCTCAATAAA  765
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1189565  CCAGTTGTGACGAAATGAAGAATGTATATGTTGGCTGTTTTTCCCCAACATCTCAATAAA  1189506

Query  766      ACTTTGAAAGCAGAAA  781
                ||||||||||||||||
Sbjct  1189505  ACTTTGAAAGCAGAAA  1189490
```

Range 3: 110067929 to 110068011

Score	Expect	Identities	Gaps	Strand	Frame

154 bits(83)	5e-34()	83/83(100%)	0/83(0%)	Plus/Minus

Features:

```
Query  1          TCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAACGgtggctc  60
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110068011  TCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAACGGTGGCTC  110067952

Query  61         cctctccctctccctctccctct  83
                  |||||||||||||||||||||||
Sbjct  110067951  CCTCTCCCTCTCCCTCTCCCTCT  110067929
```

BLAST Results

Appendix U: NCBI BLAST Gorilla gorilla TNP1 insertion v. Homo sapiens genome

Nucleotide Sequence (4470 letters)

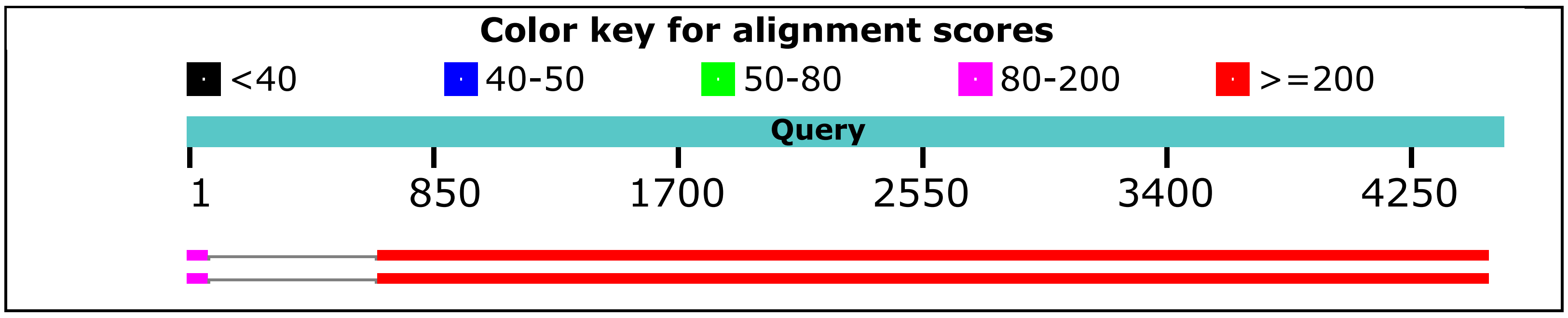
RID 4P683WKT01R (Expires on 12-11 03:50 am)

Query ID lcl|Query_119147
Description None
Molecule type nucleic acid
Query Length 4470

Database Name Genome (all assemblies top-level)
Description Homo sapiens all assemblies [GCF_000001405.33 GCF_000306695.2] chromosomes plus unplaced and unlocalized scaffolds in Annotation Release 108
Program BLASTN 2.5.1+

Graphic Summary

Distribution of the top 4 Blast Hits on 2 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens chromosome 2, alternate assembly CHM1_1.1	6495	6585	87%	0.0	97%	NC_018913.2
Homo sapiens chromosome 2, GRCh38.p7 Primary Assembly	6495	6585	87%	0.0	97%	NC_000002.12

Alignments

Homo sapiens chromosome 2, alternate assembly CHM1_1.1

Sequence ID: **NC_018913.2** Length: 243205335 Number of Matches: 2

Range 1: 217726504 to 217730392

Score	Expect	Identities	Gaps	Strand	Frame
6495 bits(3517)	0.0()	3787/3904(97%)	72/3904(1%)	Plus/Minus	

Features:

160853 bp at 5' side: insulin-like growth factor-binding protein 5 precursor52 bp at 3' side: spermatid nuclear transition protein 1

```
Query  624        aaGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGAGCAAAGCCAGAGAGGAG  683
                  ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  217730392  AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAGCCAGAGAGGAG  217730333

Query  684        CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAAGAATGTATATGTTGGCTGT  743
                  |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  217730332  CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAGGAATGTATATGTTGGCTGT  217730273

Query  744        TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAATGTTTACTTTGATCTTTTGGTT  803
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217730272  TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAATGTTTACTTTGATCTTTTGGTT  217730213

Query  804        GGAAGGACTTGAGTTCCTGAGCTAGGTGGGTTTGGGGAAGAATTGGCCAGTATGAAACCA  863
                  |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217730212  GGAAAGACTTGAGTTCCTGAGCTAGGTGGGTTTGGGGAAGAATTGGCCAGTATGAAACCA  217730153

Query  864        TTAAATGTGACTTGGAAAATATCAAAAGTAATTTGTCCTCCAATTCCCTCCCAC------  917
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217730152  TTAAATGTGACTTGGAAAATATCAAAAGTAATTTGTCCTCCAATTCCCTCCCACCACCGT  217730093

Query  918        ----GGTGGTCCTACTCTGGCCACACACTATTGCCGTATTTGTCTTCATCCCAGTGTGCT  973
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217730092  GGGAGGTGGTCCTACTCTGGCCACACACTATTGCCGTATTTGTCTTCATCCCAGTGTGCT  217730033

Query  974        GTCTCTCTCCTCAACATGGAAAGGGAGAAGAGATAAAAAAGGGAGAAATGCATTCATTAG  1033
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217730032  GTCTCTCTCCTCAACATGGAAAGGGAGAAGAGATAAAAAAGGGAGAAATGCATTCATTAG  217729973

Query  1034       CATTAACCAAAGGATTCAAGCTGTTTCTGTTAGAGCTTAAACCAAAGGATGCAAGCTGTT  1093
                  |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  217729972  CATTAACCAAAGGATTCAAGCTGTTTTTGTTAGAGCTTAAACCAAAGGATGCAAGCTGTT  217729913

Query  1094       TTTGTCAGAGCTTATAGCATAGAGGTGTTGAAAGCTAAACTAAA------GACTTGGCCC  1147
                  || |||||||||||||||||||||||||||||||||||||||||      ||||||||||
Sbjct  217729912  TTCGTCAGAGCTTATAGCATAGAGGTGTTGAAAGCTAAACTAAATCTAAAGACTTGGCCC  217729853

Query  1148       GGAGATAGAGATCACCTGAAGGAGCTCTTAGAAGCTCTTAATTCATTGATCATATGGGCA  1207
                  |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  217729852  GGAGATAGAGATCACCTGGAGGAGCTCTTAGAAGCTCTTAATTCATTGATCATATGGGCA  217729793

Query  1208       GGATTAGCAGGCTAAGAGATGGGAACACCTTCTGAACAGAGACCAACATGTTCTTTGTAA  1267
                  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217729792  GTATTAGCAGGCTAAGAGATGGGAACACCTTCTGAACAGAGACCAACATGTTCTTTGTAA  217729733

Query  1268       AGGATCCTATTAGTAACAGTGGAAGTGATGAGAGTTTAGATTTCTTTAGGTTATTTTGGT  1327
                  ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217729732  AGGATCCTATTGGTAACAGTGGAAGTGATGAGAGTTTAGATTTCTTTAGGTTATTTTGGT  217729673

Query  1328       AGCTATGTTGGGCTTGAGGTGGGCAAGACTGAAGAATGGGATATTGCCTCGTAGCATGCC  1387
                  |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  217729672  AGCTATGTTGGGCTTGAGGTGGGCAAGACTGAAGAGTGGGATATTGCCTCGTAGCATGCC  217729613

Query  1388       ATAAGCCTTAGTCCAGTGTGCCTAGAAGTAGGAATTGTCTCAATCTGAGTATTGATCATT  1447
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  217729612  ATAAGCCTTAGTCCAGTGTGCCTAGAAGTAGGAATTGTCTCAATCTGAGTATTGATCATT  217729553

Query  1448       TGACAGAGA------------ACTGACTTTAGGGATAGAGCTGGTTCTGCTCATTTAGGA  1495
                  |||||||||            |||||||||||||||||||||||||||||||||||||||
Sbjct  217729552  TGACAGAGAGAGAGAGAGAGAACTGACTTTAGGGATAGAGCTGGTTCTGCTCATTTAGGA  217729493

Query  1496       AATTCCTAAGCCCTCACTTTACCTTGTCCCTGAGTTGTAACACAATTTATGATGTCTCTG  1555
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217729492  AATTCCTAAGCCCTCACTTTACCTTGTCCCTGAGTTGTAACACAATTTATGATGTCTCTG  217729433

Query  1556       GTCAAGGATATGACATTCACCCACTCAGAGGTGGATAGTATTTTTCTTGTGTTTCCTGTT  1615
                  |||||||||||||||||||||||||||||||||||| |||||||||||||  ||||||||
Sbjct  217729432  GTCAAGGATATGACATTCACCCACTCAGAGGTGGATCGTATTTTTCTTGT--TTCCTGTT  217729375

Query  1616       GCCTCAGAGGTAGCTCCAGGGTAGAAATGAGACTCATATTTAAACTCAAGAACCAACCAC  1675
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217729374  GCCTCAGAGGTAGCTCCAGGGTAGAAATGAGACTCATATTTAAACTCAAGAACCAACCAC  217729315

Query  1676       CCACGTGGTTTCTGGGGAAGTAACCAGGAAAGGGTATAAGCAGGAAGGAATGAGGGGGCA  1735
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217729314  CCACGTGGTTTCTGGGGAAGTAACCAGGAAAGGGTATAAGCAGGAAGGAATGAGGGGGCA  217729255

Query  1736       TGAGGTTAGACACGAAGTTTCCAGCAGTCAGGGGTGTGAGACATGGGAAGAGGACACTAT  1795
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217729254  TGAGGTTAGACACGAAGTTTCCAGCAGTCAGGGGTGTGAGACATGGGAAGAGGACACTAT  217729195

Query  1796       TAAGTCTGAGCGTCATGCAAATGTGTGGGTACCAGGATGTTGGTCCTATTAAGGGGTGGC  1855
                  ||||||||||| ||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  217729194  TAAGTCTGAGCCTCATGCAAATGTGTGGGTACCAGGATGTTGGTCCTAT-AAGGGGTGGC  217729136

Query  1856       AAGGGGTGTTCCTGTGGGTCAGAATCTAGAAATGCAATAAAAAA--GCATGTTCATTTTT  1913
                  ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Sbjct  217729135  AAGGGGTGTTCCTGTGGGTCAGAATCTAGAAATGCAATAAAAAAAAGCATGTTCATTTTT  217729076

Query  1914       CAGATAAGTTATTTCACTTGTTGGGGTAAAATATTTCAAGTCCTCACTCTTCCATAACCC  1973
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217729075  CAGATAAGTTATTTCACTTGTTGGGGTAAAATATTTCAAGTCCTCACTCTTCCATAACCC  217729016

Query  1974       TAAGAATGAGCATGCTGATTCAGAGCTGTTTTCAAGTTCATGTGAAAAACATCTCTCCTT  2033
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217729015  TAAGAATGAGCATGCTGATTCAGAGCTGTTTTCAAGTTCATGTGAAAAACATCTCTCCTT  217728956

Query  2034       ACCATCAGGCACACAGATACTTCAAAGTTTTCCATTGTCAGTTTCCCTTTTTGTCAAATG  2093
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  217728955  ACCATCAGGCACACAGATACTTCAAAGTTTTCCATTGTCAGTTTCCCTTTTTGTTAAATG  217728896

Query  2094       GAGGATAGGGATAGGGAAAATGCTTCATAACCCTCATCCTCCATGGTTGTGTCTATTTTA  2153
                  |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  217728895  GAGGATAGGGATAGGGAAAATGCTTCATAACCCTCATCCTCCATGGTTGTGTATATTTTA  217728836

Query  2154       CCTCCTAAATGTGACTTTTGTTTGTCTTTGCCTCTCTAACCAAACTCAAGTTAGTCTCAA  2213
                  ||||||||||||||||||||||||||||||| ||||||||||||||||  ||||||||||
Sbjct  217728835  CCTCCTAAATGTGACTTTTGTTTGTCTTTGCTTCTCTAACCAAACTCAGATTAGTCTCAA  217728776

Query  2214       ATAATCCTATATGTGTCCGTAGTGTCACTGAACGAAGCTCTAACTTCTTAGAAGTTTGCA  2273
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217728775  ATAATCCTATATGTGTCCGTAGTGTCACTGAACGAAGCTCTAACTTCTTAGAAGTTTGCA  217728716

Query  2274       CACATATCTGATCTGGATTCCCTCCTTCAAATCTCTGAAAGAACTCATCAGCCATGGCTC  2333
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217728715  CACATATCTGATCTGGATTCCCTCCTTCAAATCTCTGAAAGAACTCATCAGCCATGGCTC  217728656

Query  2334       TCACCCTGCTCTCATGCCTCCTGGGACTTCCTCTGCCTCTGTataaaatataaacacact  2393
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217728655  TCACCCTGCTCTCATGCCTCCTGGGACTTCCTCTGCCTCTGTATAAAATATAAACACACT  217728596

Query  2394       ttgcaacacatgaaatctataaaataaatccaaaaagtaaaaatTGTTTAATTATTTTAA  2453
                  ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  217728595  TTGCAACACATGAAATCTAGAAAATAAATCCAAAAAGTAAAAATTGTTTAATTATTTTAA  217728536

Query  2454       TGTGCTTTTGCTGCTCTTGCTGTAAATTCTTTTAAACTTAGCCTCATAGGTTGGGTTCTC  2513
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217728535  TGTGCTTTTGCTGCTCTTGCTGTAAATTCTTTTAAACTTAGCCTCATAGGTTGGGTTCTC  217728476

Query  2514       AGGGAGTGGAGATGGAGTTTGAATGCAAGATGTTTATTAGAGGTCAGTACTTGAAGAGGG  2573
                  ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  217728475  AGGGAGTGGAGATGGAGCTTGAATGCAAGATGTTTATTAGAGGTCAGTACTTGAAGAGGG  217728416

Query  2574       AG-CTG-A------------------------ACAAACCATCAGGCAGTATAGCCAGGCC  2607
                  || ||| |                        ||||||||||||||||||||||||||||
Sbjct  217728415  AGGCTGCAGGGTCGTACAGAAGAAGGAGCTGCACAAACCATCAGGCAGTATAGCCAGGCC  217728356

Query  2608       TTTATACCATTTATACCCCACCTGGCTGGGCTGCGCCAGTAAGACATGGCATTTCCCTGC  2667
                  ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  217728355  TTTATACCATTTATACCCCCCCTGGCTGGGCTGCGCCAGTAAGACATGGCATTTCCCTGC  217728296

Query  2668       TGAGGCAGACTCAGAAGGGAGCATCAGCTGGAGGTTCCTTGGTGGACCACACACCCACAA  2727
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217728295  TGAGGCAGACTCAGAAGGGAGCATCAGCTGGAGGTTCCTTGGTGGACCACACACCCACAA  217728236

Query  2728       TCTGAGCAGCTCACCTCGGTGTCTATTACAATTGCTCTCTGGATGATCTGTATCTTTTCT  2787
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217728235  TCTGAGCAGCTCACCTCGGTGTCTATTACAATTGCTCTCTGGATGATCTGTATCTTTTCT  217728176

Query  2788       CAGCCTCTGGTCCCCATCTTCCCCTTAAGCCTCTTCACAGCTTGCTGCCTTGCCACTTCC  2847
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217728175  CAGCCTCTGGTCCCCATCTTCCCCTTAAGCCTCTTCACAGCTTGCTGCCTTGCCACTTCC  217728116
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Query  2848       TGCTGTGACTGTGTGTCATGAGTCTTCAAATGCTCTTGTGCACAGCTCACTTCTTGTGGA  2907
                  |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217728115  TGCTATGACTGTGTGTCATGAGTCTTCAAATGCTCTTGTGCACAGCTCACTTCTTGTGGA  217728056

Query  2908       TTGCCAATTTGCACAAAGATGACCTCTCCCATAGGACAAAGTCAACAGTCAGGAACAAAC  2967
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217728055  TTGCCAATTTGCACAAAGATGACCTCTCCCATAGGACAAAGTCAACAGTCAGGAACAAAC  217727996

Query  2968       TAGAATACCGTGATGCTGAGTGTGCAACATTTACTTCCCTCAGGAAACTTGTTATGATTA  3027
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727995  TAGAATACCGTGATGCTGAGTGTGCAACATTTACTTCCCTCAGGAAACTTGTTATGATTA  217727936

Query  3028       GGGAGCCACAGATCCCTGCAGATGGTCCAAATGAAGACTTTGTCAAAGGGATTATTTACA  3087
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727935  GGGAGCCACAGATCCCTGCAGATGGTCCAAATGAAGACTTTGTCAAAGGGATTATTTACA  217727876

Query  3088       GAGGACAGACACCTAGAGCCTACCAATGAGGTCTTCAGACCCTTAGGACTGAGAAGGCAA  3147
                  ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727875  GAGGAGAGACACCTAGAGCCTACCAATGAGGTCTTCAGACCCTTAGGACTGAGAAGGCAA  217727816

Query  3148       AAGGGCAAAATAGCACAACAGGAGCCCATTGACAGCCAAAACTGTGTGTGGGAAGGAATG  3207
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727815  AAGGGCAAAATAGCACAACAGGAGCCCATTGACAGCCAAAACTGTGTGTGGGAAGGAATG  217727756

Query  3208       GTTGTGAATGGACCTCCTGGTAAAATCTGTACTAGGAGGATCGCAGCTGTTGTCAGGCTC  3267
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727755  GTTGTGAATGGACCTCCTGGTAAAATCTGTACTAGGAGGATCGCAGCTGTTGTCAGGCTC  217727696

Query  3268       AGACACAGGGAGGAAACGTTCCATCATTTATCTAATCTCCTGCTGCTGCTCTCATTGGCG  3327
                  ||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727695  AGACACAGGGAAGAAACATTCCATCATTTATCTAATCTCCTGCTGCTGCTCTCATTGGCG  217727636

Query  3328       AAATTCAGAAGTCAACAGACAAGAGACCCCAGGTGACACAGAGCATAAGGGCCAGCCCCC  3387
                  |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727635  AAATTCAGAAGTCAGCAGACAAGAGACCCCAGGTGACACAGAGCATAAGGGCCAGCCCCC  217727576

Query  3388       TGGGGCATCAAAGAGCAGAGAATGTTGGATAAAATCTCCAAAATCCAACAGTGATATCTG  3447
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727575  TGGGGCATCAAAGAGCAGAGAATGTTGGATAAAATCTCCAAAATCCAACAGTGATATCTG  217727516

Query  3448       ACACAACTTTGCAGACAAAATTCTTCTTTCC-TGGACTCCTTAGAAGTTTGTCACTTTAT  3506
                  ||||||||||| ||||||||||||||||||| ||||||||||||||||||| ||||||||
Sbjct  217727515  ACACAACTTTGTAGACAAAATTCTTCTTTCCCTGGACTCCTTAGAAGTTTGCCACTTTAT  217727456

Query  3507       CAACCTGCTTATCTCCTCCCTTATGCTGTCATGGACCAAAGTCCCTTCAGAAGCAAATTG  3566
                  ||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||||||
Sbjct  217727455  CAACCTGCTTATCTCCTCCCTTATGTTGTCATGGACCGAAGTCCCTTCAGAAGCAAATTG  217727396

Query  3567       TAGAGAGATAGAGTGAGGAGAGAGTTACACAGGGCTCCTGAACCCTCACCTTAAAAAGCT  3626
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727395  TAGAGAGATAGAGTGAGGAGAGAGTTACACAGGGCTCCTGAACCCTCACCTTAAAAAGCT  217727336

Query  3627       TGTTTTCATGTTATTTGCTTGACAGTATTATCCCCAAACCAATACAACGCAATGTTCTAA  3686
                  |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  217727335  TGTTTTCATGTTATTTGCATGACAGTATTATCCCCAAACCAATACAACGCAATGTTCTAA  217727276

Query  3687       TGCAGTGCTATATCTTCACAATACTCTAAACACTGAAACAATCTAATTAATCATCAGGAC  3746
                  || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727275  TGTAGTGCTATATCTTCACAATACTCTAAACACTGAAACAATCTAATTAATCATCAGGAC  217727216

Query  3747       AGGCATGTGGTGAACAGCCCAAGACTAGCCACGGCAGACAGATCCTCGCCTGGTGACTTC  3806
                  |||| ||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  217727215  AGGCCTGTGGTGAACAGCCCAAGACTAGCCACGGCAGACAGATCTTCGCCTGGTGACTTC  217727156

Query  3807       AGCCTCTGCCTTCTTAGACAGGTTGTGAAGGAATGGTAGCCGCCCGGAAAACTCTACTTT  3866
                  |||||||||| |||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  217727155  AGCCTCTGCCCTCTTAGACAGGTTGTGAAGGAATGGTAGCCGCCCGGAAAACTCTGCTTT  217727096

Query  3867       GCACTGGAACATTTTCCAGACCCACATATTGGAAGTTTTTCAACACTGGCATTGATGTA  3926
                  |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217727095  GCACTGGAACTTTTTCCAGACCCACATATTGGAAGTTTTTCAACACTGGCATTGATGTA  217727036

Query  3927       GTCTCTGTACCCCAGGAATATTCATTCTGTCCCTCTGTTTACAGTTCCTATAGGCCCAGC  3986
                  ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  217727035  GTCTCTGTACCCCAGGAATATTCATTCTGTCCCTCTGTTTACAGTTCCTGTAGGCCCAGC  217726976

Query  3987       ACCTACAAGGCACGCGTAGGGGTCTTTGACCATGGGGACTCTCTTTCAGAAAACCCAAAG  4046
                  |||| ||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217726975  ACCTGCAAGGCACGTGTAGGGGTCTTTGACCATGGGGACTCTCTTTCAGAAAACCCAAAG  217726916

Query  4047       GCCTCACCCCCTGTGTGCTTTTTCTCCATCTCCCTAACCAAGGAGGACTTTGTTTCCCTC  4106
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  217726915  GCCTCACCCCCTGTGTGCTTTTTCTCCATCTCCCTAACCAAGGAGGACTTTGTTTCCCTC  217726856

Query  4107       CCCAGTTTTCTCCAGAACGCTATGTCCTAAAGTCATCACTTGTTTAGACTTTTGGaaaag  4166
                  |||||||||||||||||||||||||||||||||||||||||||||        |||||||
Sbjct  217726855  CCCAGTTTTCTCCAGAACGCTATGTCCTAAAGTCATCACTTGTTT--------GGAAAAG  217726804

Query  4167       tgaaaaaaaaaaaaaaaaaaaaaaaaaTGAAGGATCTTGGCCACAAGCCCTTTTGGGTCA  4226
                  |||||||  ||||||||||||||    |||||||||||||||||||||||||||||||||
Sbjct  217726803  TGAAAAATCAAAAAAAAAAAAAA----TGAAGGATCTTGGCCACAAGCCCTTTTGGGTCA  217726748

Query  4227       CCTTGACCTTCATGTGAGCTGACTTGGATATGGGGCCTCTGCTCCACTGGCATCAGAGCC  4286
                  |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  217726747  CCTTGACCTTCATGTGAGCTGACTTGGATATGGGGCCTCTGCTCCACTGGCCTCAGAGCC  217726688
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Query  4287       CGATGGAGTGGCGAAGCCCAGGGGACCCACGTGTGGGTGGAGAAAACCCCAAGGAGCTA  4346
                  |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  217726687  CGATGGAGTGGCGAAGCCCAGGGGACCCACATGTGGGTGGAGAAAACCCCAAGGAGCTA  217726628
Query  4347       TGGAGAACACAGCCAACTCCCACCTTTCACCCAGCCTCCTCCAGATGACCCTTGGGTGGG  4406
                  |||||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||
Sbjct  217726627  TGGAGAACACAGCCAACTCCCAACTTTCACCCAGCCTCCTCCGGATGACCCTTGGGTGGG  217726568
Query  4407       ACCTGCATCTGTGCAGCTGCAGGCAAACAGGAAGTTCTGGAGAAACGCTCAGGGCTATGT  4466
                  ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  217726567  ACCTGCATCTGTGCAGCTGCAGGCAAACAGGAAGTTCTGGAGAAATGCTCAGGGCTATGT  217726508
Query  4467       TTAG  4470
                  ||||
Sbjct  217726507  TTAG  217726504
```

Range 2: 217730377 to 217730430

Score	Expect	Identities	Gaps	Strand	Frame
89.8 bits(48)	3e-14()	52/54(96%)	0/54(0%)	Plus/Minus	

Features:
164726 bp at 5' side: insulin-like growth factor-binding protein 5 precursor14 bp at 3' side: spermatid nuclear transition protein 1

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Query  1          TCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAACGG  54
                  ||||||||||| ||||||||||||||||||||||||||||||||||||||| ||
Sbjct  217730430  TCTGCCCTGGTGCGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAGGG  217730377
```

Homo sapiens chromosome 2, GRCh38.p7 Primary Assembly
Sequence ID: **NC_000002.12** Length: 242193529 Number of Matches: 2
Range 1: 216855727 to 216859615

Score	Expect	Identities	Gaps	Strand	Frame
6495 bits(3517)	0.0()	3787/3904(97%)	72/3904(1%)	Plus/Minus	

Features:
160952 bp at 5' side: insulin-like growth factor-binding protein 5 precursor52 bp at 3' side: spermatid nuclear transition protein 1

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Query  624        aaGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGAGCAAAGCCAGAGAGGAG  683
                  ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  216859615  AAGAACAGCAGAAGGGGAACTGCCAAGGAGACCTGATGTTAGATCAAAGCCAGAGAGGAG  216859556
Query  684        CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAAGAATGTATATGTTGGCTGT  743
                  |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  216859555  CCTATGGAATGTGGATCAAATGCCAGTTGTGACGAAATGAGGAATGTATATGTTGGCTGT  216859496
Query  744        TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAATGTTTACTTTGATCTTTTGGTT  803
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216859495  TTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAATGTTTACTTTGATCTTTTGGTT  216859436
Query  804        GGAAGGACTTGAGTTCCTGAGCTAGGTGGGTTTGGGGAAGAATTGGCCAGTATGAAACCA  863
                  |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216859435  GGAAAGACTTGAGTTCCTGAGCTAGGTGGGTTTGGGGAAGAATTGGCCAGTATGAAACCA  216859376
Query  864        TTAAATGTGACTTGGAAAATATCAAAAGTAATTTGTCCTCCAATTCCCTCCCAC------  917
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216859375  TTAAATGTGACTTGGAAAATATCAAAAGTAATTTGTCCTCCAATTCCCTCCCACCACCGT  216859316
Query  918        ----GGTGGTCCTACTCTGGCCACACACTATTGCCGTATTTGTCTTCATCCCAGTGTGCT  973
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216859315  GGGAGGTGGTCCTACTCTGGCCACACACTATTGCCGTATTTGTCTTCATCCCAGTGTGCT  216859256
Query  974        GTCTCTCTCCTCAACATGGAAAGGGAGAAGAGATAAAAAAGGGAGAAATGCATTCATTAG  1033
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216859255  GTCTCTCTCCTCAACATGGAAAGGGAGAAGAGATAAAAAAGGGAGAAATGCATTCATTAG  216859196
Query  1034       CATTAACCAAAGGATTCAAGCTGTTTCTGTTAGAGCTTAAACCAAAGGATGCAAGCTGTT  1093
                  |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  216859195  CATTAACCAAAGGATTCAAGCTGTTTTTGTTAGAGCTTAAACCAAAGGATGCAAGCTGTT  216859136
Query  1094       TTTGTCAGAGCTTATAGCATAGAGGTGTTGAAAGCTAAACTAAA------GACTTGGCCC  1147
                  || |||||||||||||||||||||||||||||||||||||||||      ||||||||||
Sbjct  216859135  TTCGTCAGAGCTTATAGCATAGAGGTGTTGAAAGCTAAACTAAATCTAAAGACTTGGCCC  216859076
Query  1148       GGAGATAGAGATCACCTGAAGGAGCTCTTAGAAGCTCTTAATTCATTGATCATATGGGCA  1207
                  |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  216859075  GGAGATAGAGATCACCTGGAGGAGCTCTTAGAAGCTCTTAATTCATTGATCATATGGGCA  216859016
Query  1208       GGATTAGCAGGCTAAGAGATGGGAACACCTTCTGAACAGAGACCAACATGTTCTTTGTAA  1267
                  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216859015  GTATTAGCAGGCTAAGAGATGGGAACACCTTCTGAACAGAGACCAACATGTTCTTTGTAA  216858956
Query  1268       AGGATCCTATTAGTAACAGTGGAAGTGATGAGAGTTTAGATTTCTTTAGGTTATTTTGGT  1327
                  ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216858955  AGGATCCTATTGGTAACAGTGGAAGTGATGAGAGTTTAGATTTCTTTAGGTTATTTTGGT  216858896
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Query  1328       AGCTATGTTGGGCTTGAGGTGGGCAAGACTGAAGAATGGGATATTGCCTCGTAGCATGCC  1387
                  ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  216858895  AGCTATGTTGGGCTTGAGGTGGGCAAGACTGAAGAGTGGGATATTGCCTCGTAGCATGCC  216858836

Query  1388       ATAAGCCTTAGTCCAGTGTGCCTAGAAGTAGGAATTGTCTCAATCTGAGTATTGATCATT  1447
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216858835  ATAAGCCTTAGTCCAGTGTGCCTAGAAGTAGGAATTGTCTCAATCTGAGTATTGATCATT  216858776

Query  1448       TGACAGAGA------------ACTGACTTTAGGGATAGAGCTGGTTCTGCTCATTTAGGA  1495
                  |||||||||            |||||||||||||||||||||||||||||||||||||||
Sbjct  216858775  TGACAGAGAGAGAGAGAGAGAACTGACTTTAGGGATAGAGCTGGTTCTGCTCATTTAGGA  216858716

Query  1496       AATTCCTAAGCCCTCACTTTACCTTGTCCCTGAGTTGTAACACAATTTATGATGTCTCTG  1555
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216858715  AATTCCTAAGCCCTCACTTTACCTTGTCCCTGAGTTGTAACACAATTTATGATGTCTCTG  216858656

Query  1556       GTCAAGGATATGACATTCACCCACTCAGAGGTGGATAGTATTTTTCTTGTGTTTCCTGTT  1615
                  |||||||||||||||||||||||||||||||||||| |||||||||||||  ||||||||
Sbjct  216858655  GTCAAGGATATGACATTCACCCACTCAGAGGTGGATCGTATTTTTCTTGT--TTCCTGTT  216858598

Query  1616       GCCTCAGAGGTAGCTCCAGGGTAGAAATGAGACTCATATTTAAACTCAAGAACCAACCAC  1675
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216858597  GCCTCAGAGGTAGCTCCAGGGTAGAAATGAGACTCATATTTAAACTCAAGAACCAACCAC  216858538

Query  1676       CCACGTGGTTTCTGGGGAAGTAACCAGGAAAGGGTATAAGCAGGAAGGAATGAGGGGGCA  1735
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216858537  CCACGTGGTTTCTGGGGAAGTAACCAGGAAAGGGTATAAGCAGGAAGGAATGAGGGGGCA  216858478

Query  1736       TGAGGTTAGACACGAAGTTTCCAGCAGTCAGGGGTGTGAGACATGGGAAGAGGACACTAT  1795
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  216858477  TGAGGTTAGACACGAAGTTTCCAGCAGTCAGGGGTGTGAGACATGGGAAGAGGACACTAT  216858418

Query  1796       TAAGTCTGAGCGTCATGCAAATGTGTGGGTACCAGGATGTTGGTCCTATTAAGGGGTGGC  1855
                  ||||||||||| ||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  216858417  TAAGTCTGAGCCTCATGCAAATGTGTGGGTACCAGGATGTTGGTCCTAT-AAGGGGTGGC  216858359

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Query  1914       CAGATAAGTTATTTCACTTGTTGGGGTAAAATATTTCAAGTCCTCACTCTTCCATAACCC  1973
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Sbjct  216858298  CAGATAAGTTATTTCACTTGTTGGGGTAAAATATTTCAAGTCCTCACTCTTCCATAACCC  216858239

Query  1974       TAAGAATGAGCATGCTGATTCAGAGCTGTTTTCAAGTTCATGTGAAAAACATCTCTCCTT  2033
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Sbjct  216858238  TAAGAATGAGCATGCTGATTCAGAGCTGTTTTCAAGTTCATGTGAAAAACATCTCTCCTT  216858179

Query  2034       ACCATCAGGCACACAGATACTTCAAAGTTTTCCATTGTCAGTTTCCCTTTTTGTCAAATG  2093
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Sbjct  216858178  ACCATCAGGCACACAGATACTTCAAAGTTTTCCATTGTCAGTTTCCCTTTTTGTTAAATG  216858119

Query  2094       GAGGATAGGGATAGGGAAAATGCTTCATAACCCTCATCCTCCATGGTTGTGTCTATTTTA  2153
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Query  2154       CCTCCTAAATGTGACTTTTGTTTGTCTTTGCCTCTCTAACCAAACTCAAGTTAGTCTCAA  2213
                  ||||||||||||||||||||||||||||||| ||||||||||||||||  ||||||||||
Sbjct  216858058  CCTCCTAAATGTGACTTTTGTTTGTCTTTGCTTCTCTAACCAAACTCAGATTAGTCTCAA  216857999

Query  2214       ATAATCCTATATGTGTCCGTAGTGTCACTGAACGAAGCTCTAACTTCTTAGAAGTTTGCA  2273
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Query  2274       CACATATCTGATCTGGATTCCCTCCTTCAAATCTCTGAAAGAACTCATCAGCCATGGCTC  2333
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Query  2334       TCACCCTGCTCTCATGCCTCCTGGGACTTCCTCTGCCTCTGTataaaatataaacacact  2393
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Query  2394       ttgcaacacatgaaatctataaaataaatccaaaaagtaaaaatTGTTTAATTATTTTAA  2453
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Query  2454       TGTGCTTTTGCTGCTCTTGCTGTAAATTCTTTTAAACTTAGCCTCATAGGTTGGGTTCTC  2513
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Query  2574       AG-CTG-A------------------------ACAAACCATCAGGCAGTATAGCCAGGCC  2607
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Query  2608       TTTATACCATTTATACCCCACCTGGCTGGGCTGCGCCAGTAAGACATGGCATTTCCCTGC  2667
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Query  2668       TGAGGCAGACTCAGAAGGGAGCATCAGCTGGAGGTTCCTTGGTGGACCACACACCCACAA  2727
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Sbjct  216857518  TGAGGCAGACTCAGAAGGGAGCATCAGCTGGAGGTTCCTTGGTGGACCACACACCCACAA  216857459
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Query  2728       TCTGAGCAGCTCACCTCGGTGTCTATTACAATTGCTCTCTGGATGATCTGTATCTTTTCT  2787
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Query  2788       CAGCCTCTGGTCCCCATCTTCCCCTTAAGCCTCTTCACAGCTTGCTGCCTTGCCACTTCC  2847
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Query  2848       TGCTGTGACTGTGTGTCATGAGTCTTCAAATGCTCTTGTGCACAGCTCACTTCTTGTGGA  2907
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Query  2908       TTGCCAATTTGCACAAAGATGACCTCTCCCATAGGACAAAGTCAACAGTCAGGAACAAAC  2967
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Sbjct  216857278  TTGCCAATTTGCACAAAGATGACCTCTCCCATAGGACAAAGTCAACAGTCAGGAACAAAC  216857219

Query  2968       TAGAATACCGTGATGCTGAGTGTGCAACATTTACTTCCCTCAGGAAACTTGTTATGATTA  3027
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Query  3028       GGGAGCCACAGATCCCTGCAGATGGTCCAAATGAAGACTTTGTCAAAGGGATTATTTACA  3087
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Query  3448       ACACAACTTTGCAGACAAAATTCTTCTTTCC-TGGACTCCTTAGAAGTTTGTCACTTTAT  3506
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Query  3507       CAACCTGCTTATCTCCTCCCTTATGCTGTCATGGACCAAAGTCCCTTCAGAAGCAAATTG  3566
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Sbjct  216856618  TAGAGAGATAGAGTGAGGAGAGAGTTACACAGGGCTCCTGAACCCTCACCTTAAAAAGCT  216856559

Query  3627       TGTTTTCATGTTATTTGCTTGACAGTATTATCCCCAAACCAATACAACGCAATGTTCTAA  3686
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Query  3747       AGGCATGTGGTGAACAGCCCAAGACTAGCCACGGCAGACAGATCCTCGCCTGGTGACTTC  3806
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Sbjct  216856378  AGCCTCTGCCCTCTTAGACAGGTTGTGAAGGAATGGTAGCCGCCCGGAAAACTCTGCTTT  216856319

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Query  4107       CCCAGTTTTCTCCAGAACGCTATGTCCTAAAGTCATCACTTGTTTAGACTTTTGGaaaag  4166
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Query  4167       tgaaaaaaaaaaaaaaaaaaaaaaaaaaTGAAGGATCTTGGCCACAAGCCCTTTTGGGTCA  4226
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Query  4467       TTAG  4470
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Sbjct  216855730  TTAG  216855727
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Range 2: 216859600 to 216859653

Score	Expect	Identities	Gaps	Strand	Frame
89.8 bits(48)	3e-14()	52/54(96%)	0/54(0%)	Plus/Minus	

Features:
164825 bp at 5' side: insulin-like growth factor-binding protein 5 precursor14 bp at 3' side: spermatid nuclear transition protein 1

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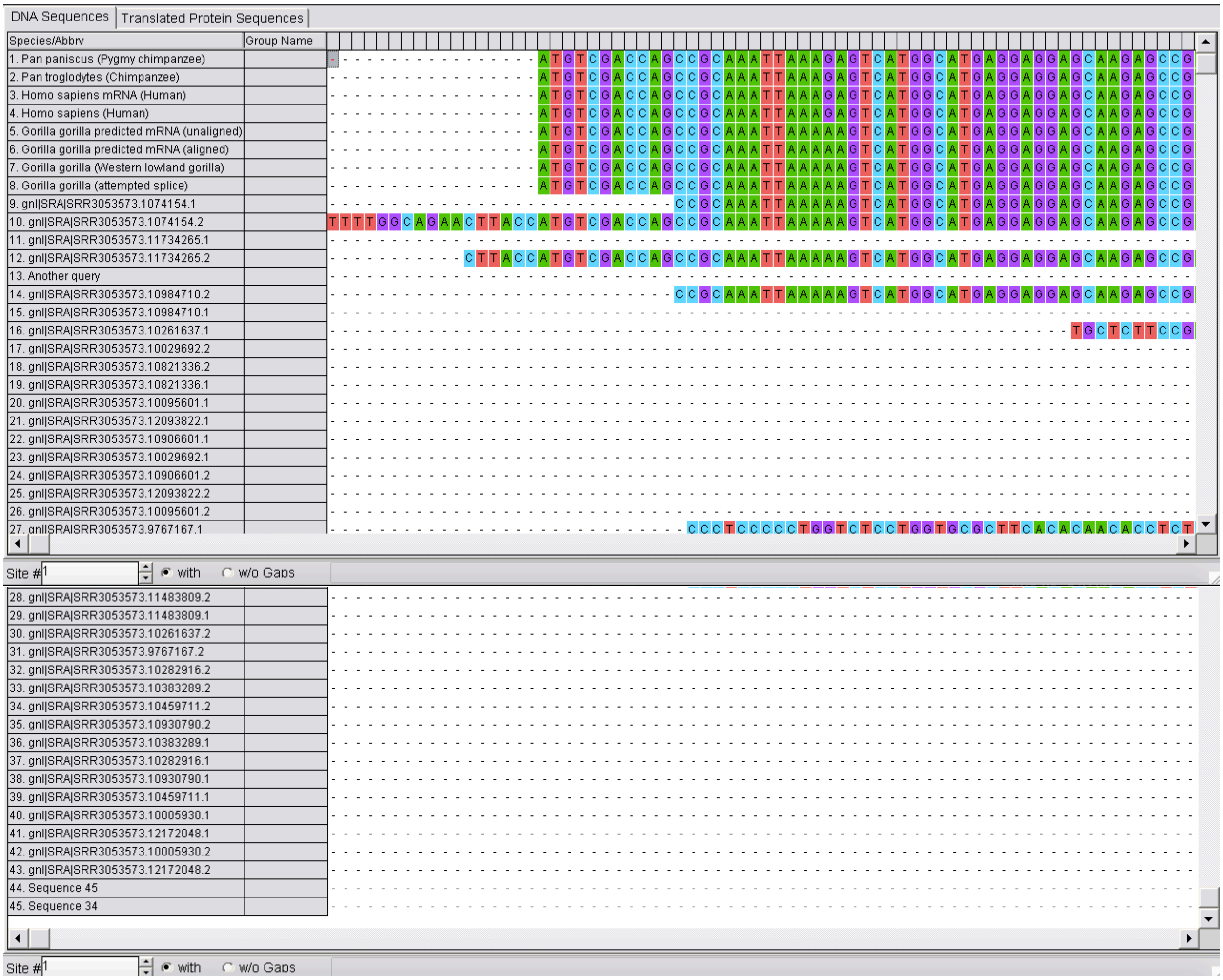
Appendix V) Alignment of resulting gnls from Gorilla *Tnp1* v. SRX1486509 BLAST



Species/Abbrv	Group Name	
1. Pan paniscus (Pygmy chimpanzee)		-----------------ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCG
2. Pan troglodytes (Chimpanzee)		-----------------ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCG
3. Homo sapiens mRNA (Human)		-----------------ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCG
4. Homo sapiens (Human)		-----------------ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCG
5. Gorilla gorilla predicted mRNA (unaligned)		-----------------ATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCG
6. Gorilla gorilla predicted mRNA (aligned)		-----------------ATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCG
7. Gorilla gorilla (Western lowland gorilla)		-----------------ATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCG
8. Gorilla gorilla (attempted splice)		-----------------ATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCG
9. gnl|SRA|SRR3053573.1074154.1		----------------------------CCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCG
10. gnl|SRA|SRR3053573.1074154.2		TTTTGGCAGAACTTACCATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCG
11. gnl|SRA|SRR3053573.11734265.1		--
12. gnl|SRA|SRR3053573.11734265.2		-----------CTTACCATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCG
13. Another query		--
14. gnl|SRA|SRR3053573.10984710.2		----------------------------CCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCG
15. gnl|SRA|SRR3053573.10984710.1		--
16. gnl|SRA|SRR3053573.10261637.1		--TGCTCTTCCG
17. gnl|SRA|SRR3053573.10029692.2		--
18. gnl|SRA|SRR3053573.10821336.2		--
19. gnl|SRA|SRR3053573.10821336.1		--
20. gnl|SRA|SRR3053573.10095601.1		--
21. gnl|SRA|SRR3053573.12093822.1		--
22. gnl|SRA|SRR3053573.10906601.1		--
23. gnl|SRA|SRR3053573.10029692.1		--
24. gnl|SRA|SRR3053573.10906601.2		--
25. gnl|SRA|SRR3053573.12093822.2		--
26. gnl|SRA|SRR3053573.10095601.2		--
27. gnl|SRA|SRR3053573.9767167.1		-----------------------------CCCTCCCCCTGGTCTCCTGGTGCGCTTCACACAACACCTCT
28. gnl|SRA|SRR3053573.11483809.2		--
29. gnl|SRA|SRR3053573.11483809.1		--
30. gnl|SRA|SRR3053573.10261637.2		--
31. gnl|SRA|SRR3053573.9767167.2		--
32. gnl|SRA|SRR3053573.10282916.2		--
33. gnl|SRA|SRR3053573.10383289.2		--
34. gnl|SRA|SRR3053573.10459711.2		--
35. gnl|SRA|SRR3053573.10930790.2		--
36. gnl|SRA|SRR3053573.10383289.1		--
37. gnl|SRA|SRR3053573.10282916.1		--
38. gnl|SRA|SRR3053573.10930790.1		--
39. gnl|SRA|SRR3053573.10459711.1		--
40. gnl|SRA|SRR3053573.10005930.1		--
41. gnl|SRA|SRR3053573.12172048.1		--
42. gnl|SRA|SRR3053573.10005930.2		--
43. gnl|SRA|SRR3053573.12172048.2		--
44. Sequence 45		--
45. Sequence 34		--

Species/Abbrv	Group Name	
1. Pan paniscus (Pygmy chimpanzee)		ATCTCCTCACAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
2. Pan troglodytes (Chimpanzee)		ATCTCCTCACAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
3. Homo sapiens mRNA (Human)		ATCTCCTCACAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
4. Homo sapiens (Human)		ATCTCCTCACAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
5. Gorilla gorilla predicted mRNA (unaligned)		ATCTCCTCACAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCCGAAAAGTAGG
6. Gorilla gorilla predicted mRNA (aligned)		ATCTCCTCACAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCCGAAAAGTAGG
7. Gorilla gorilla (Western lowland gorilla)		ATCTCCTCACAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCCGAAAAGTAGG
8. Gorilla gorilla (attempted splice)		ATCTCCTCACAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCCGAAAAGTAGG
9. gnl|SRA|SRR3053573.1074154.1		ATCTCCTCACAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
10. gnl|SRA|SRR3053573.1074154.2		ATCTCCTCACAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
11. gnl|SRA|SRR3053573.11734265.1		-----------------GCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
12. gnl|SRA|SRR3053573.11734265.2		ATCTCCTCACAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
13. Another query		--
14. gnl|SRA|SRR3053573.10984710.2		ATCTCCTCACAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
15. gnl|SRA|SRR3053573.10984710.1		-------------------------GGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
16. gnl|SRA|SRR3053573.10261637.1		ATCT---GGGCAACCTGAAAAGTAGG
17. gnl|SRA|SRR3053573.10029692.2		--GGCAACCTGAAAAGTAGG
18. gnl|SRA|SRR3053573.10821336.2		--
19. gnl|SRA|SRR3053573.10821336.1		--
20. gnl|SRA|SRR3053573.10095601.1		----------------------------ATTCTGACATGTGACTGGAGTTCAGACGTGTGCTCTTCCGAT
21. gnl|SRA|SRR3053573.12093822.1		---TGGAGTTCAGACGTGTGCTCTTCCGAT
22. gnl|SRA|SRR3053573.10906601.1		--TGTGCTCTTCCGAT
23. gnl|SRA|SRR3053573.10029692.1		--
24. gnl|SRA|SRR3053573.10906601.2		--
25. gnl|SRA|SRR3053573.12093822.2		--
26. gnl|SRA|SRR3053573.10095601.2		--TCTCCGTCCCCCTC
27. gnl|SRA|SRR3053573.9767167.1		CCCTCTCCCTCTCCCTCGTCTCCTGGTGCGCTTCCCACAGCCCCTCTCCCTCTC----------------

Site # 71 ● with ○ w/o Gaps

28. gnl|SRA|SRR3053573.11483809.2		--------CTCTCCCTCGTCTCCTGGTGCGCTTCACACAGCACCTCTCCCTCTCCCTCTCCGTCCCCCTC
29. gnl|SRA|SRR3053573.11483809.1		---CTCCCTCTCCGTCCCCCTC
30. gnl|SRA|SRR3053573.10261637.2		---GGGCAACCTGAAAAGTAGG
31. gnl|SRA|SRR3053573.9767167.2		---AAAAGTAGG
32. gnl|SRA|SRR3053573.10282916.2		--------------------------GTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGG
33. gnl|SRA|SRR3053573.10383289.2		------------------------------CAGCAAAAGTAAATACCGTAAGGGCAACCTGAAAAGTAGG
34. gnl|SRA|SRR3053573.10459711.2		--------------------------------------GAAAATACCGTAAGGGCAACCTGAAAAGTAGG
35. gnl|SRA|SRR3053573.10930790.2		--CTGAAAAGTAGG
36. gnl|SRA|SRR3053573.10383289.1		---AAGGGCAACCTGAAAAGTAGT
37. gnl|SRA|SRR3053573.10282916.1		--CTGAAAAGTAGG
38. gnl|SRA|SRR3053573.10930790.1		---GTAGG
39. gnl|SRA|SRR3053573.10459711.1		--TAGG
40. gnl|SRA|SRR3053573.10005930.1		--GACGTGTGCTCTTCCGAT
41. gnl|SRA|SRR3053573.12172048.1		----------------------------------ACATGTGACTGGAATTCAGACGTGTGCTCTTCCGAT
42. gnl|SRA|SRR3053573.10005930.2		--
43. gnl|SRA|SRR3053573.12172048.2		--
44. Sequence 45		--
45. Sequence 34		--

Site # 71 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
1. Pan paniscus (Pygmy chimpanzee)		AAACGGGGCGATGACGCCAATCGCAATTACCACTCCCACTTGTGA-------------------------
2. Pan troglodytes (Chimpanzee)		AAACGGGGCGATGACGCCAATCGCAATTACCACTCCCACTTGTGA-------------------------
3. Homo sapiens mRNA (Human)		AAACGGGGCGATGACGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------------
4. Homo sapiens (Human)		AAACGGGGCGATGACGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------------
5. Gorilla gorilla predicted mRNA (unaligned)		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
6. Gorilla gorilla predicted mRNA (aligned)		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
7. Gorilla gorilla (Western lowland gorilla)		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
8. Gorilla gorilla (attempted splice)		AAACGGGGCGATGACGCCTCTGCCCTGCCTATGGAATTTGTGA---------------------------
9. gnl|SRA|SRR3053573.1074154.1		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCAN--------------------------------
10. gnl|SRA|SRR3053573.1074154.2		AAACGGGGCG--
11. gnl|SRA|SRR3053573.11734265.1		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
12. gnl|SRA|SRR3053573.11734265.2		AAACGGGGCGATGACGCCTCT---
13. Another query		--AGCACCAAGCAGCAACAAGAACAGCAGAAC
14. gnl|SRA|SRR3053573.10984710.2		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCAC-------------------------------
15. gnl|SRA|SRR3053573.10984710.1		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
16. gnl|SRA|SRR3053573.10261637.1		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
17. gnl|SRA|SRR3053573.10029692.2		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
18. gnl|SRA|SRR3053573.10821336.2		--------------CGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
19. gnl|SRA|SRR3053573.10821336.1		----------------CCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
20. gnl|SRA|SRR3053573.10095601.1		CTTCTCCGTCCCCCTCCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
21. gnl|SRA|SRR3053573.12093822.1		CT-----------------------------GCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
22. gnl|SRA|SRR3053573.10906601.1		CT------------------------------CTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
23. gnl|SRA|SRR3053573.10029692.1		-------------------------TGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
24. gnl|SRA|SRR3053573.10906601.2		--------------------------------CTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
25. gnl|SRA|SRR3053573.12093822.2		-------------------------------GCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
26. gnl|SRA|SRR3053573.10095601.2		CC----------------TCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
27. gnl|SRA|SRR3053573.9767167.1		--------CCCTCTCCCTCGTCTCCTGGTGTGCTTCACACAGCACC------------------------

28. gnl|SRA|SRR3053573.11483809.2		CCTCTCCCTCCTCTCCCCCGTCTCCTGGTGCGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
29. gnl|SRA|SRR3053573.11483809.1		CCTCTCCCTCCTCTCCCTCGTCTCCTGGTGCGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
30. gnl|SRA|SRR3053573.10261637.2		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
31. gnl|SRA|SRR3053573.9767167.2		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
32. gnl|SRA|SRR3053573.10282916.2		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
33. gnl|SRA|SRR3053573.10383289.2		AAACGGGGCGATGACGCCTCTGCCCTTGAACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAG
34. gnl|SRA|SRR3053573.10459711.2		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
35. gnl|SRA|SRR3053573.10930790.2		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
36. gnl|SRA|SRR3053573.10383289.1		AAACGGGGTGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
37. gnl|SRA|SRR3053573.10282916.1		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
38. gnl|SRA|SRR3053573.10930790.1		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
39. gnl|SRA|SRR3053573.10459711.1		AAACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
40. gnl|SRA|SRR3053573.10005930.1		CT------------CGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
41. gnl|SRA|SRR3053573.12172048.1		CT---------------------------------CACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
42. gnl|SRA|SRR3053573.10005930.2		--------------CGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
43. gnl|SRA|SRR3053573.12172048.2		-----------------------------------CACACAGCACCAAGCAGCAACAAGAACAGCAGAAC
44. Sequence 45		--
45. Sequence 34		--

```
Species/Abbrv                                   Group Name
1. Pan paniscus (Pygmy chimpanzee)              ----------------------------------------------------------------------
2. Pan troglodytes (Chimpanzee)                 ----------------------------------------------------------------------
3. Homo sapiens mRNA (Human)                    ----------------------------------------------------------------------
4. Homo sapiens (Human)                         ----------------------------------------------------------------------
5. Gorilla gorilla predicted mRNA (unaligned)   GGTGGCTCCCTCTCCCTCTCCCTCTCCAGCCCGATGGGAGTGGCGAAGCCCAGGGGACCCACGTGTGGGT
6. Gorilla gorilla predicted mRNA (aligned)     GGTGGCTCCCTCTCCCTCTCCCTCTCC-------------------------------------------
7. Gorilla gorilla (Western lowland gorilla)    GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCGGCCGCCGCTACGGGGAAGTGAGGAGCCCCTCTGCCC
8. Gorilla gorilla (attempted splice)           ----------------------------------------------------------------------
9. gnl|SRA|SRR3053573.1074154.1                 ----------------------------------------------------------------------
10. gnl|SRA|SRR3053573.1074154.2                ----------------------------------------------------------------------
11. gnl|SRA|SRR3053573.11734265.1               GGTGGCTCCCTCTCCCTCTCCCTCTCC-------------------------------------------
12. gnl|SRA|SRR3053573.11734265.2               ----------------------------------------------------------------------
13. Another query                               GGTGGCTCCCTCTCCCTCTCCCTCTCC-------------------------------------------
14. gnl|SRA|SRR3053573.10984710.2               ----------------------------------------------------------------------
15. gnl|SRA|SRR3053573.10984710.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCT-----------------------------------
16. gnl|SRA|SRR3053573.10261637.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCT-----------------------
17. gnl|SRA|SRR3053573.10029692.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCCCCCCCCCCCCCCCCC--------
18. gnl|SRA|SRR3053573.10821336.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCTCGCCTCCCCCTCCCCCTCCCCCC
19. gnl|SRA|SRR3053573.10821336.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCTCTCCTCCCTCTCCCTCTCCCTCC
20. gnl|SRA|SRR3053573.10095601.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCT--------------------------------
21. gnl|SRA|SRR3053573.12093822.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTACCTCCTCTCCTCCCTCTCCCTCTCCCTCC
22. gnl|SRA|SRR3053573.10906601.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCTCTCCTCCCTCTCCCTCTCCCTCC
23. gnl|SRA|SRR3053573.10029692.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCTCTCCTCCCTCTCCCTCTCCCTCC
24. gnl|SRA|SRR3053573.10906601.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCCTCCCCGCCGCTCCCCCCCCCCCC
25. gnl|SRA|SRR3053573.12093822.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCCCTCTCCTCCCCCCCCCTCCCCCCCCT
26. gnl|SRA|SRR3053573.10095601.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCT---------AGATCGGAAGAGCG---------
27. gnl|SRA|SRR3053573.9767167.1                ----------TCTCCCTCTCCCTCTCCG------------------------------------------
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Site # 211 ● with ○ w/o Gaps

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28. gnl|SRA|SRR3053573.11483809.2               GGTGGCTCCCTCTCCCTC----------------------------------------------------
29. gnl|SRA|SRR3053573.11483809.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCTCTCCTCCCTCTCCC---------
30. gnl|SRA|SRR3053573.10261637.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCTAGATCGGAAGAGCG---------
31. gnl|SRA|SRR3053573.9767167.2                GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCTCCGTCTTGCCCTTCTCCGTCTCCCTTTCCC
32. gnl|SRA|SRR3053573.10282916.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCC----------------------------------
33. gnl|SRA|SRR3053573.10383289.2               GGGGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTGC------------------------------
34. gnl|SRA|SRR3053573.10459711.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCC----------CGCGCAGCGCC------------
35. gnl|SRA|SRR3053573.10930790.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTTGTAGGTAACGCGCGTAGCTCTCTCCGCTC--
36. gnl|SRA|SRR3053573.10383289.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCACCTCTCCCTCCTCTCCTCCCTCTCCCTCTC-----------
37. gnl|SRA|SRR3053573.10282916.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCTCTCCTCCCTCTCCCTCTCCCTCCTCTC--
38. gnl|SRA|SRR3053573.10930790.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCTCTCCTCCCTCTCCCTCTCCCTCCTCTCCC
39. gnl|SRA|SRR3053573.10459711.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCTCTCCTCCCTCTCCCTCTCCCTCCTCTCCC
40. gnl|SRA|SRR3053573.10005930.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCACTCCCACCTCTCCTCCCTCTCCCTCTCCCTCCTCTCCC
41. gnl|SRA|SRR3053573.12172048.1               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTCCTCTCCTCCCTCTCCCTCTCCCTCCTCTCCC
42. gnl|SRA|SRR3053573.10005930.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCTTTACGGGGACTCCTCCGCCCCCGCCCGCCGCC
43. gnl|SRA|SRR3053573.12172048.2               GGTGGCTCCCTCTCCCTCTCCCTCTCCCTCCTCTCCCCCGCCCTGTCCCCCCACCTCCCCCCCCATCCCC
44. Sequence 45                                 ----------------------------------------------------------------------
45. Sequence 34                                 ----------------------------------------------------------------------
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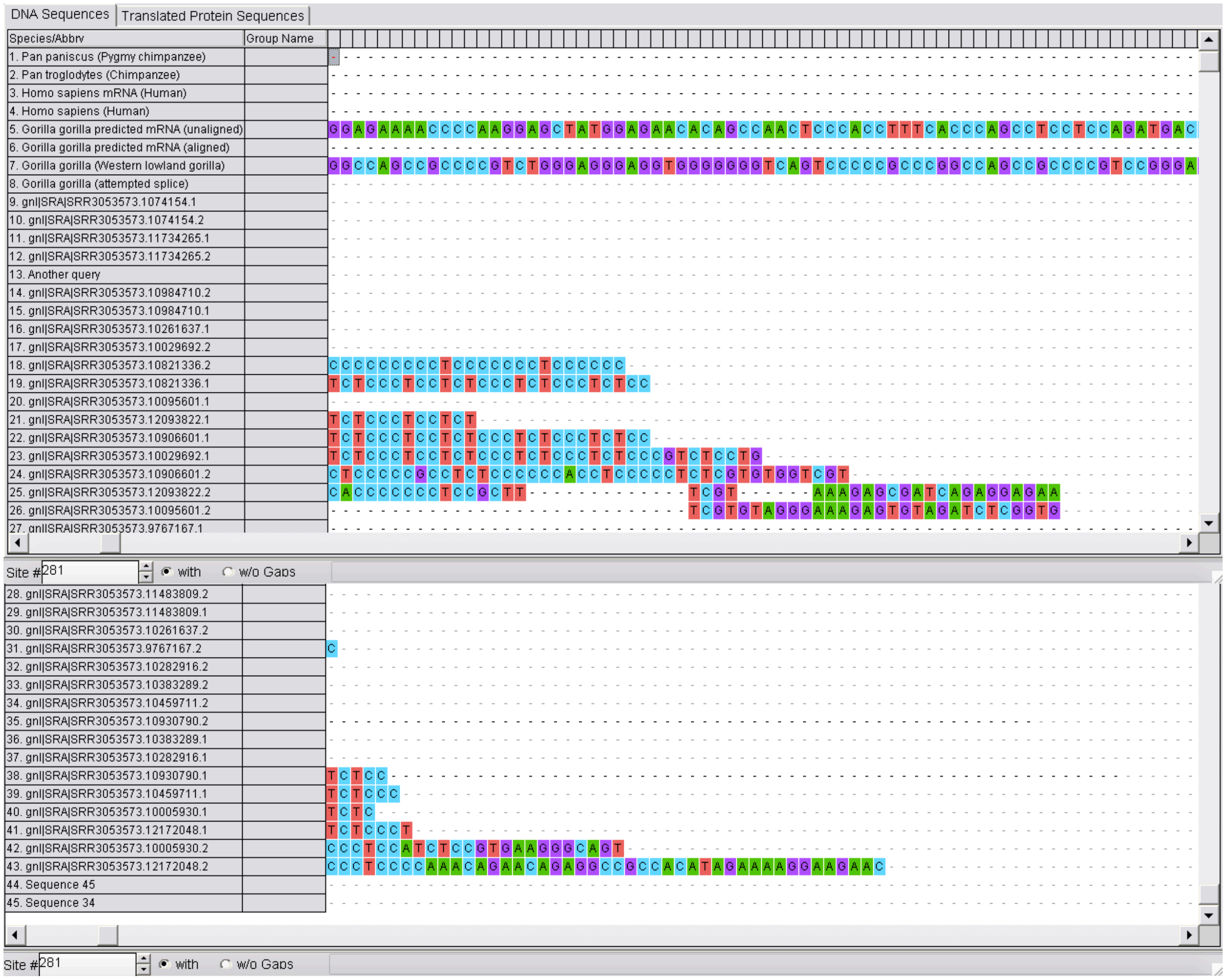
Site # 211 ● with ○ w/o Gaps



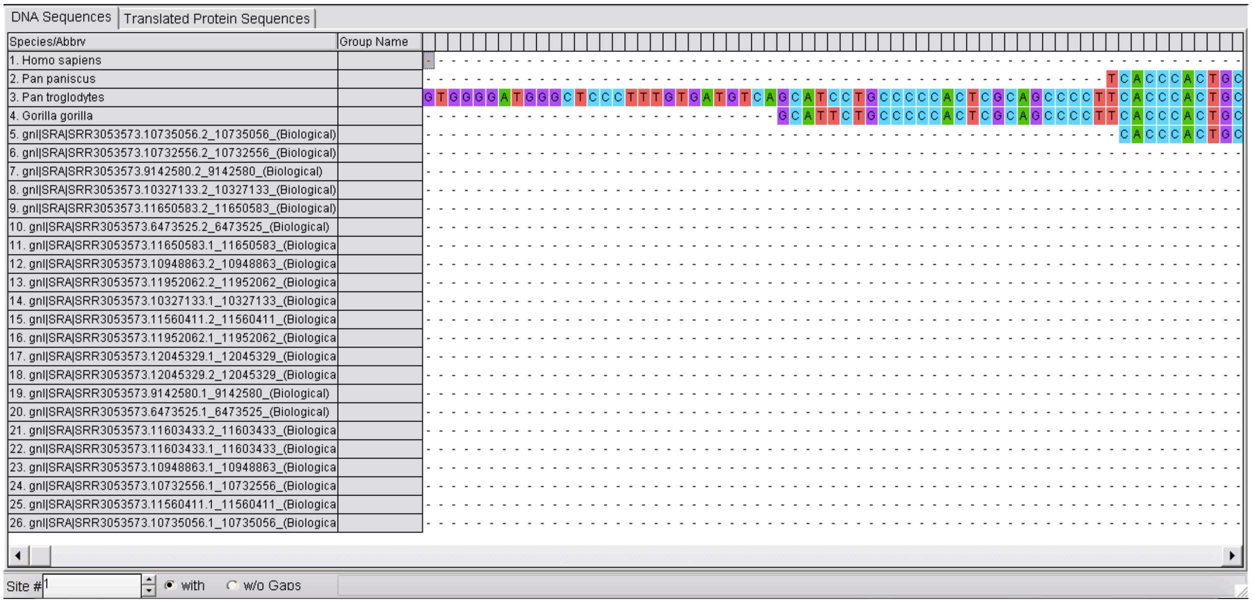
Species/Abbrv	Group Name	
1. Pan paniscus (Pygmy chimpanzee)		
2. Pan troglodytes (Chimpanzee)		
3. Homo sapiens mRNA (Human)		
4. Homo sapiens (Human)		
5. Gorilla gorilla predicted mRNA (unaligned)		GGAGAAAACCCCAAGGAGCTATGGAGAACACAGCCAACTCCCACCTTTCACCCAGCCTCCTCCAGATGAC
6. Gorilla gorilla predicted mRNA (aligned)		
7. Gorilla gorilla (Western lowland gorilla)		GGCCAGCCGCCCCGTCTGGGAGGGAGGTGGGGGGGTCAGTCCCCCGCCCGGCCAGCCGCCCCGTCCGGGA
8. Gorilla gorilla (attempted splice)		
9. gnl|SRA|SRR3053573.1074154.1		
10. gnl|SRA|SRR3053573.1074154.2		
11. gnl|SRA|SRR3053573.11734265.1		
12. gnl|SRA|SRR3053573.11734265.2		
13. Another query		
14. gnl|SRA|SRR3053573.10984710.2		
15. gnl|SRA|SRR3053573.10984710.1		
16. gnl|SRA|SRR3053573.10261637.1		
17. gnl|SRA|SRR3053573.10029692.2		
18. gnl|SRA|SRR3053573.10821336.2		CCCCCCCCCTCCCCCCCTCCCCCC
19. gnl|SRA|SRR3053573.10821336.1		TCTCCCTCCTCTCCCTCTCCCTCTCC
20. gnl|SRA|SRR3053573.100095601.1		
21. gnl|SRA|SRR3053573.12093822.1		TCTCCCTCCTCT
22. gnl|SRA|SRR3053573.10906601.1		TCTCCCTCCTCTCCCTCTCCCTCTCC
23. gnl|SRA|SRR3053573.10029692.1		TCTCCCTCCTCTCCCTCTCCCTCTCCCGTCTCCTG
24. gnl|SRA|SRR3053573.10906601.2		CTCCCCCGCCTCTCCCCCCACCTCCCCCTCTCGTGTGGTCGT
25. gnl|SRA|SRR3053573.12093822.2		CACCCCCCCTCCGCTT------------TCGT------AAAGAGCGATCAGAGGAGAA
26. gnl|SRA|SRR3053573.10095601.2		----------------------------TCGTGTAGGGAAAGAGTGTAGATCTCGGTG
27. gnl|SRA|SRR3053573.9767167.1		

Site # 281 ● with ○ w/o Gaps

28. gnl|SRA|SRR3053573.11483809.2		
29. gnl|SRA|SRR3053573.11483809.1		
30. gnl|SRA|SRR3053573.10261637.2		
31. gnl|SRA|SRR3053573.9767167.2		C
32. gnl|SRA|SRR3053573.10282916.2		
33. gnl|SRA|SRR3053573.10383289.2		
34. gnl|SRA|SRR3053573.10459711.2		
35. gnl|SRA|SRR3053573.10930790.2		
36. gnl|SRA|SRR3053573.10383289.1		
37. gnl|SRA|SRR3053573.10282916.1		
38. gnl|SRA|SRR3053573.10930790.1		TCTCC
39. gnl|SRA|SRR3053573.10459711.1		TCTCCC
40. gnl|SRA|SRR3053573.10005930.1		TCTC
41. gnl|SRA|SRR3053573.12172048.1		TCTCCCT
42. gnl|SRA|SRR3053573.10005930.2		CCCTCCATCTCCGTGAAGGGCAGT
43. gnl|SRA|SRR3053573.12172048.2		CCCTCCCCAAACAGAACAGAGGCCGCCACATAGAAAAGGAAGAAC
44. Sequence 45		
45. Sequence 34		

Site # 281 ● with ○ w/o Gaps

Appendix W) Alignment of resulting gnls from Gorilla *Prm3* v. SRX1486509 BLAST



DNA Sequences | Translated Protein Sequences

```
Species/Abbrv                                              Group Name
1. Homo sapiens                                                       -----------------------------------------------------------------
2. Pan paniscus                                                       ------------------------------------------------------TCACCCACTGC
3. Pan troglodytes                                                    GTGGGGATGGGCTCCCTTTGTGATGTCAGCATCCTGCCCCCACTCGCAGCCCCTTCACCCACTGC
4. Gorilla gorilla                                                    ----------------------------GCATTCTGCCCCCACTCGCAGCCCCTTCACCCACTGC
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological)                -------------------------------------------------------CACCCACTGC
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological)                -----------------------------------------------------------------
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)                  -----------------------------------------------------------------
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological)                -----------------------------------------------------------------
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological)                -----------------------------------------------------------------
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)                 -----------------------------------------------------------------
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica                 -----------------------------------------------------------------
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica                 -----------------------------------------------------------------
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica                 -----------------------------------------------------------------
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica                 -----------------------------------------------------------------
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica                 -----------------------------------------------------------------
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica                 -----------------------------------------------------------------
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica                 -----------------------------------------------------------------
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica                 -----------------------------------------------------------------
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)                 -----------------------------------------------------------------
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)                 -----------------------------------------------------------------
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica                 -----------------------------------------------------------------
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica                 -----------------------------------------------------------------
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica                 -----------------------------------------------------------------
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica                 -----------------------------------------------------------------
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica                 -----------------------------------------------------------------
26. gnl|SRA|SRR3053573.10735056.1_10735056_(Biologica                 -----------------------------------------------------------------
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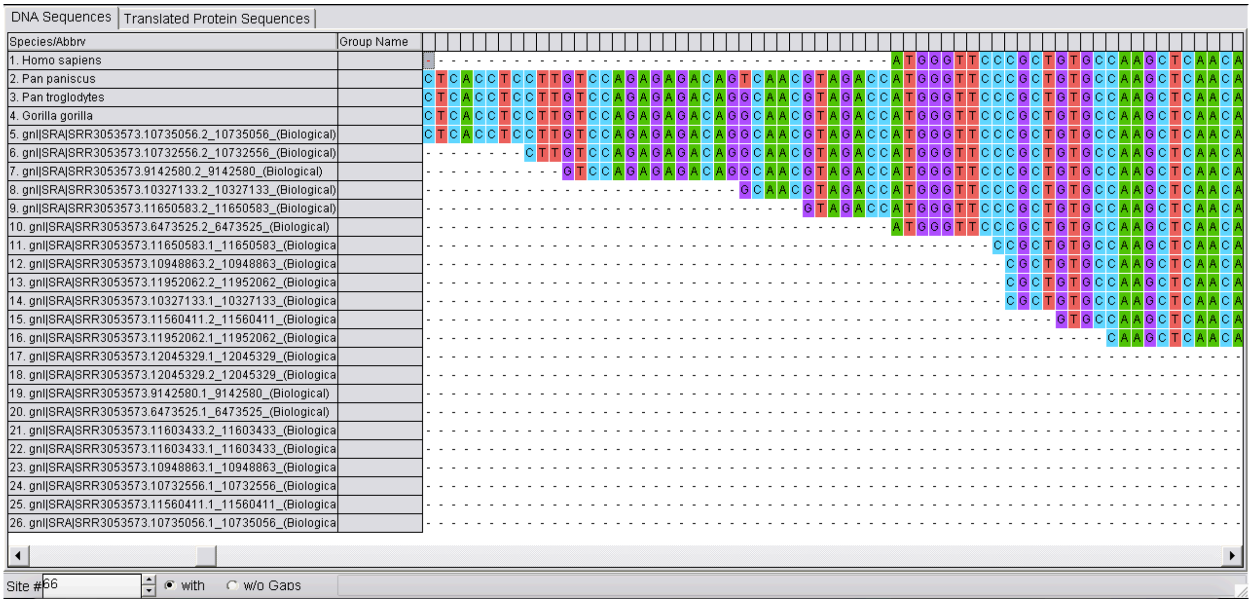
Site # 1 ● with ○ w/o Gaps



DNA Sequences | Translated Protein Sequences

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Species/Abbrv                                              Group Name
1. Homo sapiens                                                       -------------------------------------ATGGGTTCCCGCTGTGCCAAGCTCAACA
2. Pan paniscus                                                       CTCACCTCCTTGTCCAGAGAGACAGTCAACGTAGACCATGGGTTCCCGCTGTGCCAAGCTCAACA
3. Pan troglodytes                                                    CTCACCTCCTTGTCCAGAGAGACAGGCAACGTAGACCATGGGTTCCCGCTGTGCCAAGCTCAACA
4. Gorilla gorilla                                                    CTCACCTCCTTGTCCAGAGAGACAGGCAACGTAGACCATGGGTTCCCGCTGTGCCAAGCTCAACA
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological)                CTCACCTCCTTGTCCAGAGAGACAGGCAACGTAGACCATGGGTTCCCGCTGTGCCAAGCTCAACA
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological)                --------CTTGTCCAGAGAGACAGGCAACGTAGACCATGGGTTCCCGCTGTGCCAAGCTCAACA
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)                  -----------GTCCAGAGAGACAGGCAACGTAGACCATGGGTTCCCGCTGTGCCAAGCTCAACA
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological)                -------------------------GCAACGTAGACCATGGGTTCCCGCTGTGCCAAGCTCAACA
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological)                ------------------------------GTAGACCATGGGTTCCCGCTGTGCCAAGCTCAACA
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)                 -------------------------------------ATGGGTTCCCGCTGTGCCAAGCTCAACA
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica                 ---------------------------------------------CCGCTGTGCCAAGCTCAACA
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica                 ----------------------------------------------CGCTGTGCCAAGCTCAACA
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica                 ----------------------------------------------CGCTGTGCCAAGCTCAACA
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica                 ----------------------------------------------CGCTGTGCCAAGCTCAACA
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica                 --------------------------------------------------GTGCCAAGCTCAACA
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica                 ------------------------------------------------------CAAGCTCAACA
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica                 -----------------------------------------------------------------
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica                 -----------------------------------------------------------------
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)                 -----------------------------------------------------------------
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)                 -----------------------------------------------------------------
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica                 -----------------------------------------------------------------
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica                 -----------------------------------------------------------------
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica                 -----------------------------------------------------------------
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica                 -----------------------------------------------------------------
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica                 -----------------------------------------------------------------
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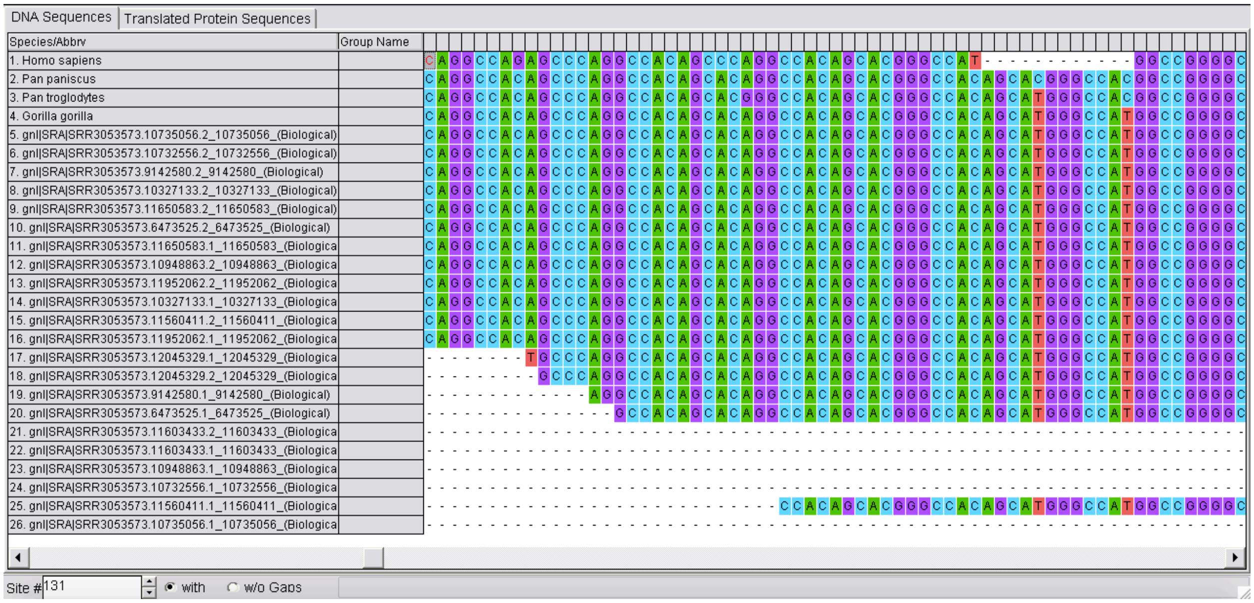
Site # 66 ● with ○ w/o Gaps

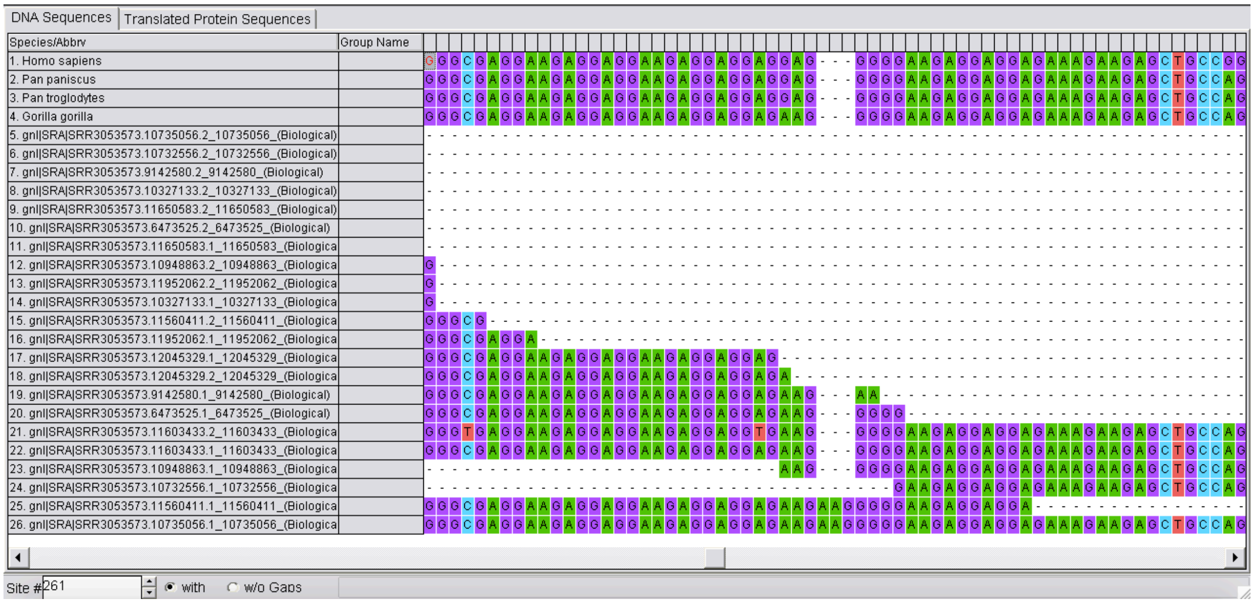


Species/Abbrv	Group Name	
1. Homo sapiens		CAGGCCAGAGCCCAGGCCACAGCCCAGGCCACAGCACGGGCCAT------------GGCCGGGGC
2. Pan paniscus		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCACGGGCCACGGCCGGGGC
3. Pan troglodytes		CAGGCCACAGCCCAGGCCACAGCACGGGCCACAGCACGGGCCACAGCATGGGCCACGGCCGGGGC
4. Gorilla gorilla		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological)		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological)		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological)		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological)		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica		CAGGCCACAGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica		--------TGCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica		---------GCCCAGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)		-------------AGGCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)		---------------GCCACAGCACAGGCCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica		---
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica		---
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica		---
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica		---
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica		----------------------------CCACAGCACGGGCCACAGCATGGGCCATGGCCGGGGC
26. gnl|SRA|SRR3053573.10735056.1_10735056_(Biologica		---

Site # 131 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
1. Homo sapiens		CACGAATCCTCCATGAAAAAGCTCATGGCCTGTGTGAGTCAGGATAACTTCTCCTTGTCATCAGC
2. Pan paniscus		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
3. Pan troglodytes		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
4. Gorilla gorilla		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological)		CACGAATCCT---
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological)		CACGAATCCTCCATGAAAAAGCTCGTGG-------------------------------------
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)		CACGAATCCTCCATGAAAAAGCTCGTGGCCT----------------------------------
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological)		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGAT--------------------
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological)		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTT---------------
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTG--------
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica		---------------------CTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica		----------------------TCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica		---
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica		---
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica		CACGAATCCTCCATGAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC
26. gnl|SRA|SRR3053573.10735056.1_10735056_(Biologica		------------------------GTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGC

Site # 196 ● with ○ w/o Gaps



```
1. Homo sapiens                                      GGGCGAGGAAGAGGAGGAAGAGGAGGAGGAG---GGGGAAGAGGAGGAGAAAGAAGAGCTGCCGG
2. Pan paniscus                                      GGGCGAGGAAGAGGAGGAAGAGGAGGAGGAG---GGGGAAGAGGAGGAGAAAGAAGAGCTGCCAG
3. Pan troglodytes                                   GGGCGAGGAAGAGGAGGAAGAGGAGGAGGAG---GGGGAAGAGGAGGAGAAAGAAGAGCTGCCAG
4. Gorilla gorilla                                   GGGCGAGGAAGAGGAGGAAGAGGAGGAGAAG---GGGGAAGAGGAGGAGAAAGAAGAGCTGCCAG
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological) -----------------------------------------------------------------
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological) -----------------------------------------------------------------
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)   -----------------------------------------------------------------
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological) -----------------------------------------------------------------
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological) -----------------------------------------------------------------
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)  -----------------------------------------------------------------
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica  -----------------------------------------------------------------
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica  G----------------------------------------------------------------
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica  G----------------------------------------------------------------
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica  G----------------------------------------------------------------
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica  GGGCG------------------------------------------------------------
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica  GGGCGAGGA--------------------------------------------------------
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica  GGGCGAGGAAGAGGAGGAAGAGGAGGAG-------------------------------------
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica  GGGCGAGGAAGAGGAGGAAGAGGAGGAGA------------------------------------
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)  GGGCGAGGAAGAGGAGGAAGAGGAGGAGAAG---AA-----------------------------
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)  GGGCGAGGAAGAGGAGGAAGAGGAGGAGAAG---GGGG---------------------------
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica  GGGTGAGGAAGAGGAGGAAGAGGAGGTGAAG---GGGGAAGAGGAGGAGAAAGAAGAGCTGCCAG
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica  GGGCGAGGAAGAGGAGGAAGAGGAGGAGAAG---GGGGAAGAGGAGGAGAAAGAAGAGCTGCCAG
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica  ----------------------------AAG---GGGGAAGAGGAGGAGAAAGAAGAGCTGCCAG
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica  -------------------------------------GAAGAGGAGGAGAAAGAAGAGCTGCCAG
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica  GGGCGAGGAAGAGGAGGAAGAGGAGGAGAAGAAGGGGGAAGAGGAGGA-----------------
26. gnl|SRA|SRR3053573.10735056.1_10735056_(Biologica  GGGCGAGGAAGAGGAGGAAGAGGAGGAGAAGAAGGGGGAAGAGGAGGAGAAAGAAGAGCTGCCAG
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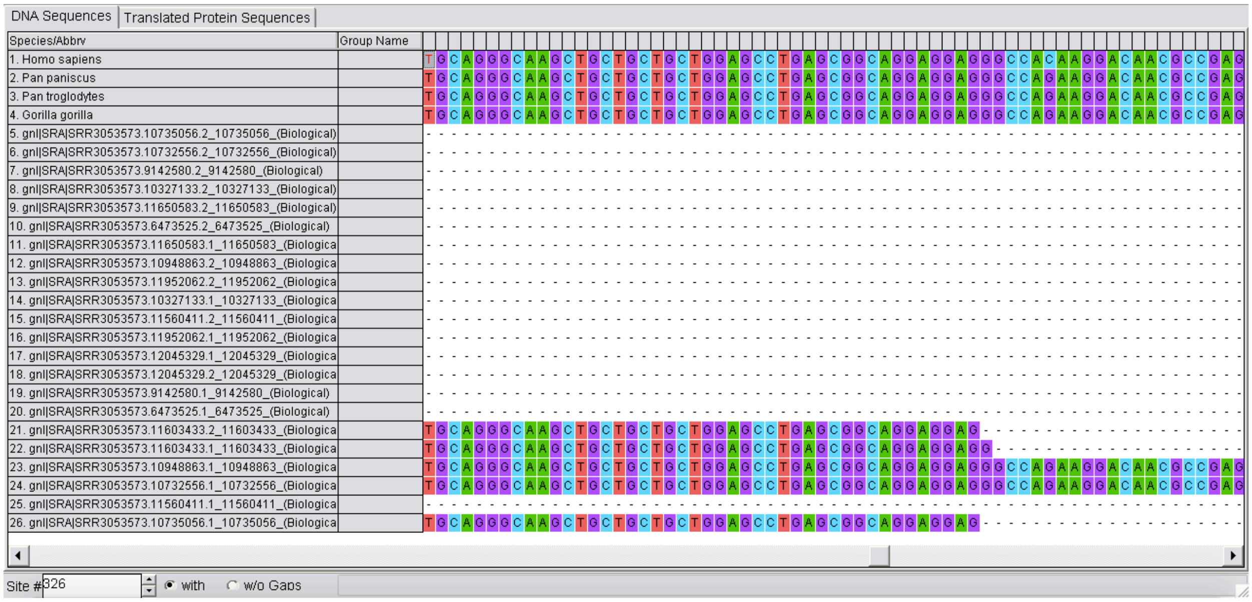
Site # 261 ● with ○ w/o Gaps



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1. Homo sapiens                                      TGCAGGGCAAGCTGCTGCTGCTGGAGCCTGAGCGGCAGGAGGAGGGCCACAAGGACAACGCCGAG
2. Pan paniscus                                      TGCAGGGCAAGCTGCTGCTGCTGGAGCCTGAGCGGCAGGAGGAGGGCCAGAAGGACAACGCCGAG
3. Pan troglodytes                                   TGCAGGGCAAGCTGCTGCTGCTGGAGCCTGAGCGGCAGGAGGAGGGCCAGAAGGACAACGCCGAG
4. Gorilla gorilla                                   TGCAGGGCAAGCTGCTGCTGCTGGAGCCTGAGCGGCAGGAGGAGGGCCAGAAGGACAACGCCGAG
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological) -----------------------------------------------------------------
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological) -----------------------------------------------------------------
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)   -----------------------------------------------------------------
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological) -----------------------------------------------------------------
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological) -----------------------------------------------------------------
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)  -----------------------------------------------------------------
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica  -----------------------------------------------------------------
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica  -----------------------------------------------------------------
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica  -----------------------------------------------------------------
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica  -----------------------------------------------------------------
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica  -----------------------------------------------------------------
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica  -----------------------------------------------------------------
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica  -----------------------------------------------------------------
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica  -----------------------------------------------------------------
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)  -----------------------------------------------------------------
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)  -----------------------------------------------------------------
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica  TGCAGGGCAAGCTGCTGCTGCTGGAGCCTGAGCGGCAGGAGGAG---------------------
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica  TGCAGGGCAAGCTGCTGCTGCTGGAGCCTGAGCGGCAGGAGGAGG--------------------
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica  TGCAGGGCAAGCTGCTGCTGCTGGAGCCTGAGCGGCAGGAGGAGGGCCAGAAGGACAACGCCGAG
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica  TGCAGGGCAAGCTGCTGCTGCTGGAGCCTGAGCGGCAGGAGGAGGGCCAGAAGGACAACGCCGAG
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica  -----------------------------------------------------------------
26. gnl|SRA|SRR3053573.10735056.1_10735056_(Biologica  TGCAGGGCAAGCTGCTGCTGCTGGAGCCTGAGCGGCAGGAGGAG---------------------
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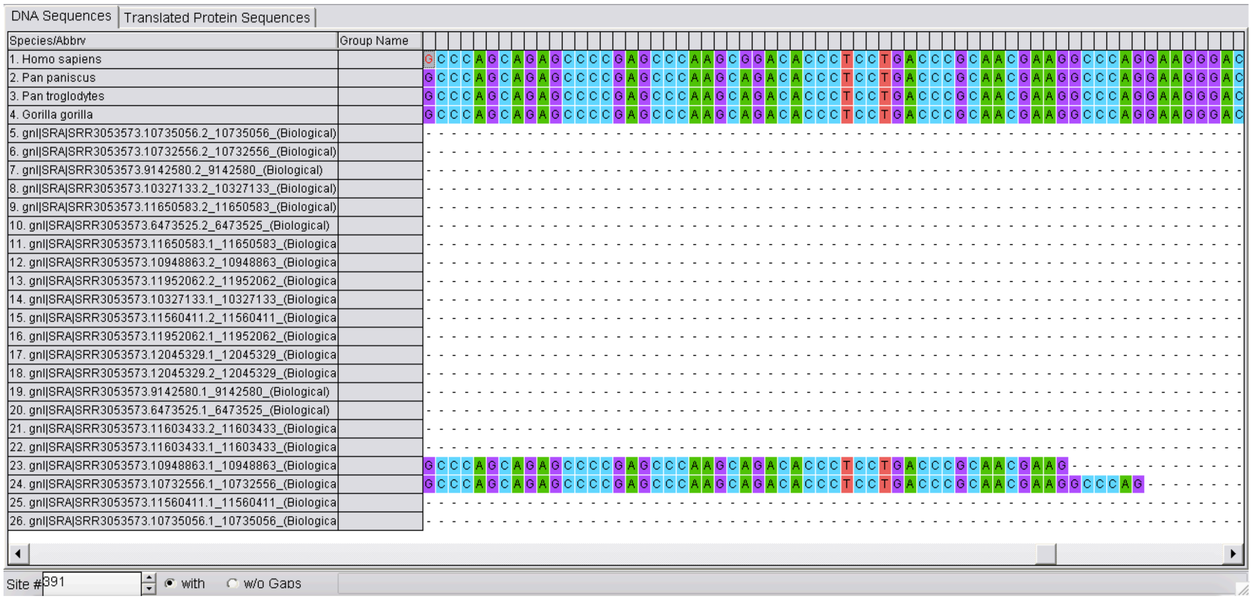
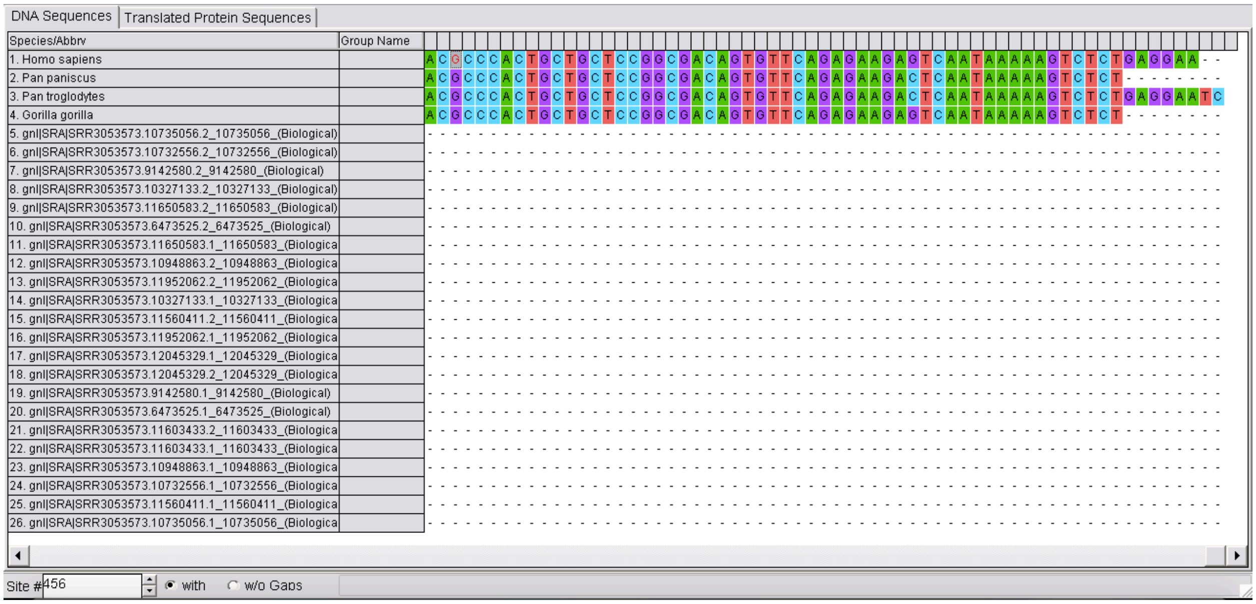
Site # 326 ● with ○ w/o Gaps



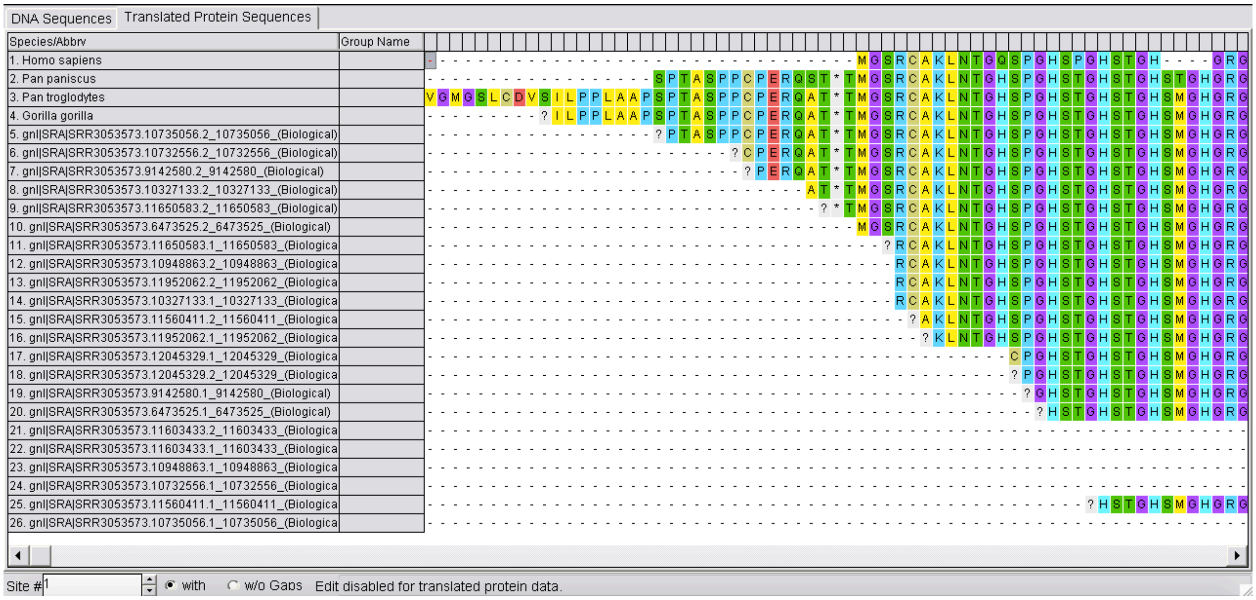
Species/Abbrv	Group Name	
1. Homo sapiens		GCCCAGCAGAGCCCCGAGCCCAAGCGGACACCCTCCTGACCCGCAACGAAGGCCCAGGAAGGGAC
2. Pan paniscus		GCCCAGCAGAGCCCCGAGCCCAAGCAGACACCCTCCTGACCCGCAACGAAGGCCCAGGAAGGGAC
3. Pan troglodytes		GCCCAGCAGAGCCCCGAGCCCAAGCAGACACCCTCCTGACCCGCAACGAAGGCCCAGGAAGGGAC
4. Gorilla gorilla		GCCCAGCAGAGCCCCGAGCCCAAGCAGACACCCTCCTGACCCGCAACGAAGGCCCAGGAAGGGAC
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological)		---
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological)		---
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)		---
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological)		---
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological)		---
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)		---
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica		---
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica		---
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica		---
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica		---
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica		---
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica		---
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica		---
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica		---
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)		---
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)		---
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica		---
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica		---
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica		GCCCAGCAGAGCCCCGAGCCCAAGCAGACACCCTCCTGACCCGCAACGAAG--------------
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica		GCCCAGCAGAGCCCCGAGCCCAAGCAGACACCCTCCTGACCCGCAACGAAGGCCCAG--------
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica		---
26. gnl|SRA|SRR3053573.10735056.1_10735056_(Biologica		---

Site # 391 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
1. Homo sapiens		ACGCCCACTGCTGCTCCGGCGACAGTGTTCAGAGAAGAGTCAATAAAAAGTCTCTGAGGAA--
2. Pan paniscus		ACGCCCACTGCTGCTCCGGCGACAGTGTTCAGAGAAGACTCAATAAAAAGTCTCT--------
3. Pan troglodytes		ACGCCCACTGCTGCTCCGGCGACAGTGTTCAGAGAAGACTCAATAAAAAGTCTCTGAGGAATC
4. Gorilla gorilla		ACGCCCACTGCTGCTCCGGCGACAGTGTTCAGAGAAGAGTCAATAAAAAGTCTCT--------
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological)		---
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological)		---
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)		---
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological)		---
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological)		---
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)		---
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica		---
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica		---
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica		---
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica		---
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica		---
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica		---
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica		---
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica		---
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)		---
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)		---
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica		---
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica		---
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica		---
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica		---
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica		---
26. gnl|SRA|SRR3053573.10735056.1_10735056_(Biologica		---

Site # 456 ● with ○ w/o Gaps



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Species/Abbrv                                     Group Name
1. Homo sapiens                                               ----------------------------------MGSRCAKLNTGQSPGHSPGHSTGH----GRG
2. Pan paniscus                                               ------------------SPTASPPCPERQST*TMGSRCAKLNTGHSPGHSTGHSTGHSTGHGRG
3. Pan troglodytes                                            VGMGSLCDVSILPPLAAPSPTASPPCPERQAT*TMGSRCAKLNTGHSPGHSTGHSTGHSMGHGRG
4. Gorilla gorilla                                            ---------?ILPPLAAPSPTASPPCPERQAT*TMGSRCAKLNTGHSPGHSTGHSTGHSMGHGRG
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological)        ------------------?PTASPPCPERQAT*TMGSRCAKLNTGHSPGHSTGHSTGHSMGHGRG
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological)        ------------------------?CPERQAT*TMGSRCAKLNTGHSPGHSTGHSTGHSMGHGRG
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)          -------------------------?PERQAT*TMGSRCAKLNTGHSPGHSTGHSTGHSMGHGRG
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological)        ------------------------------AT*TMGSRCAKLNTGHSPGHSTGHSTGHSMGHGRG
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological)        -------------------------------?*TMGSRCAKLNTGHSPGHSTGHSTGHSMGHGRG
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)         ----------------------------------MGSRCAKLNTGHSPGHSTGHSTGHSMGHGRG
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica         ------------------------------------?RCAKLNTGHSPGHSTGHSTGHSMGHGRG
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica         -------------------------------------RCAKLNTGHSPGHSTGHSTGHSMGHGRG
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica         -------------------------------------RCAKLNTGHSPGHSTGHSTGHSMGHGRG
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica         -------------------------------------RCAKLNTGHSPGHSTGHSTGHSMGHGRG
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica         --------------------------------------?AKLNTGHSPGHSTGHSTGHSMGHGRG
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica         ---------------------------------------?KLNTGHSPGHSTGHSTGHSMGHGRG
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica         ----------------------------------------------CPGHSTGHSTGHSMGHGRG
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica         ----------------------------------------------?PGHSTGHSTGHSMGHGRG
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)         -----------------------------------------------?GHSTGHSTGHSMGHGRG
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)         ------------------------------------------------?HSTGHSTGHSMGHGRG
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica         -----------------------------------------------------------------
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica         -----------------------------------------------------------------
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica         -----------------------------------------------------------------
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica         -----------------------------------------------------------------
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica         ----------------------------------------------------?HSTGHSMGHGRG
26. gnl|SRA|SRR3053573.10735056.1_10735056_(Biologica         -----------------------------------------------------------------
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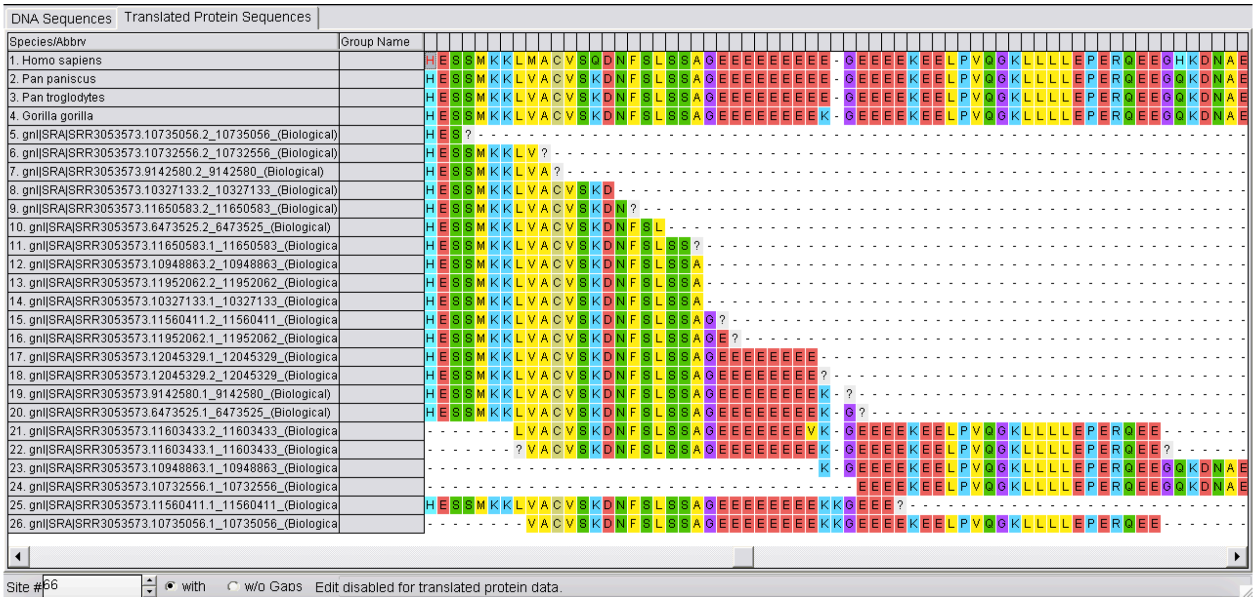

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Species/Abbrv                                     Group Name
1. Homo sapiens                                               HESSMKKLMACVSQDNFSLSSAGEEEEEEEEEE-GEEEEKEELPVQGKLLLLEPERQEEGHKDNAE
2. Pan paniscus                                               HESSMKKLVACVSKDNFSLSSAGEEEEEEEEEE-GEEEEKEELPVQGKLLLLEPERQEEGQKDNAE
3. Pan troglodytes                                            HESSMKKLVACVSKDNFSLSSAGEEEEEEEEEE-GEEEEKEELPVQGKLLLLEPERQEEGQKDNAE
4. Gorilla gorilla                                            HESSMKKLVACVSKDNFSLSSAGEEEEEEEEEK-GEEEEKEELPVQGKLLLLEPERQEEGQKDNAE
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological)        HES?--------------------------------------------------------------
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological)        HESSMKKLV?--------------------------------------------------------
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)          HESSMKKLVA?-------------------------------------------------------
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological)        HESSMKKLVACVSKD---------------------------------------------------
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological)        HESSMKKLVACVSKDN?-------------------------------------------------
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)         HESSMKKLVACVSKDNFSL-----------------------------------------------
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica         HESSMKKLVACVSKDNFSLSS?--------------------------------------------
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica         HESSMKKLVACVSKDNFSLSSA--------------------------------------------
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica         HESSMKKLVACVSKDNFSLSSA--------------------------------------------
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica         HESSMKKLVACVSKDNFSLSSA--------------------------------------------
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica         HESSMKKLVACVSKDNFSLSSAG?------------------------------------------
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica         HESSMKKLVACVSKDNFSLSSAGE?-----------------------------------------
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica         HESSMKKLVACVSKDNFSLSSAGEEEEEEEEE----------------------------------
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica         HESSMKKLVACVSKDNFSLSSAGEEEEEEEEE?---------------------------------
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)         HESSMKKLVACVSKDNFSLSSAGEEEEEEEEEK-?-------------------------------
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)         HESSMKKLVACVSKDNFSLSSAGEEEEEEEEEK-G?------------------------------
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica         -------LVACVSKDNFSLSSAGEEEEEEEEVK-GEEEEKEELPVQGKLLLLEPERQEE-------
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica         -------?VACVSKDNFSLSSAGEEEEEEEEEK-GEEEEKEELPVQGKLLLLEPERQEE?------
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica         --------------------------------K-GEEEEKEELPVQGKLLLLEPERQEEGQKDNAE
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica         -----------------------------------EEEEKEELPVQGKLLLLEPERQEEGQKDNAE
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica         HESSMKKLVACVSKDNFSLSSAGEEEEEEEEEKKGEEE?---------------------------
26. gnl|SRA|SRR3053573.10735056.1_10735056_(Biologica         --------VACVSKDNFSLSSAGEEEEEEEEEKKGEEEEKEELPVQGKLLLLEPERQEE-------
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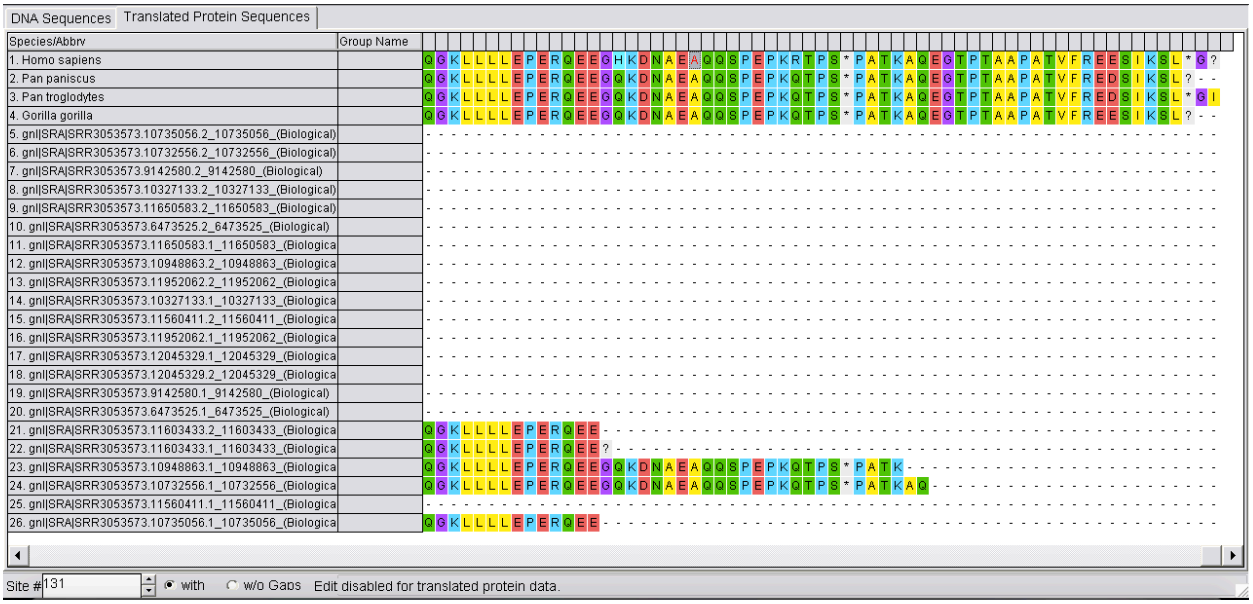
The translated alignment, which shows that the coding sequence is covered by the gnl results



Species/Abbrv	Group Name	
1. Homo sapiens		QGKLLLLEPERQEEGHKDNAEAQQSPEPKRTPS*PATKAQEGTPTAAPATVFREESIKSL*G?
2. Pan paniscus		QGKLLLLEPERQEEGQKDNAEAQQSPEPKQTPS*PATKAQEGTPTAAPATVFREDSIKSL?--
3. Pan troglodytes		QGKLLLLEPERQEEGQKDNAEAQQSPEPKQTPS*PATKAQEGTPTAAPATVFREDSIKSL*GI
4. Gorilla gorilla		QGKLLLLEPERQEEGQKDNAEAQQSPEPKQTPS*PATKAQEGTPTAAPATVFREESIKSL?--
5. gnl|SRA|SRR3053573.10735056.2_10735056_(Biological)		---
6. gnl|SRA|SRR3053573.10732556.2_10732556_(Biological)		---
7. gnl|SRA|SRR3053573.9142580.2_9142580_(Biological)		---
8. gnl|SRA|SRR3053573.10327133.2_10327133_(Biological)		---
9. gnl|SRA|SRR3053573.11650583.2_11650583_(Biological)		---
10. gnl|SRA|SRR3053573.6473525.2_6473525_(Biological)		---
11. gnl|SRA|SRR3053573.11650583.1_11650583_(Biologica		---
12. gnl|SRA|SRR3053573.10948863.2_10948863_(Biologica		---
13. gnl|SRA|SRR3053573.11952062.2_11952062_(Biologica		---
14. gnl|SRA|SRR3053573.10327133.1_10327133_(Biologica		---
15. gnl|SRA|SRR3053573.11560411.2_11560411_(Biologica		---
16. gnl|SRA|SRR3053573.11952062.1_11952062_(Biologica		---
17. gnl|SRA|SRR3053573.12045329.1_12045329_(Biologica		---
18. gnl|SRA|SRR3053573.12045329.2_12045329_(Biologica		---
19. gnl|SRA|SRR3053573.9142580.1_9142580_(Biological)		---
20. gnl|SRA|SRR3053573.6473525.1_6473525_(Biological)		---
21. gnl|SRA|SRR3053573.11603433.2_11603433_(Biologica		QGKLLLLEPERQEE---
22. gnl|SRA|SRR3053573.11603433.1_11603433_(Biologica		QGKLLLLEPERQEE?--
23. gnl|SRA|SRR3053573.10948863.1_10948863_(Biologica		QGKLLLLEPERQEEGQKDNAEAQQSPEPKQTPS*PATK-------------------------
24. gnl|SRA|SRR3053573.10732556.1_10732556_(Biologica		QGKLLLLEPERQEEGQKDNAEAQQSPEPKQTPS*PATKAQ-----------------------
25. gnl|SRA|SRR3053573.11560411.1_11560411_(Biologica		---
26. gnl|SRA|SRR3053573.10735056.1_10735056_(Biologica		QGKLLLLEPERQEE---

Site # 131 ● with ○ w/o Gaps Edit disabled for translated protein data.

BLAST® » blastn suite » RID-F0Y284B4015

BLAST Results

Questions/comments

Appendix X: Search for Prm2 in Carlito syrichta by Samiri bolivensis probe BLAST

Job title: NW_003943634.1:c18022769-18022020 Saimiri

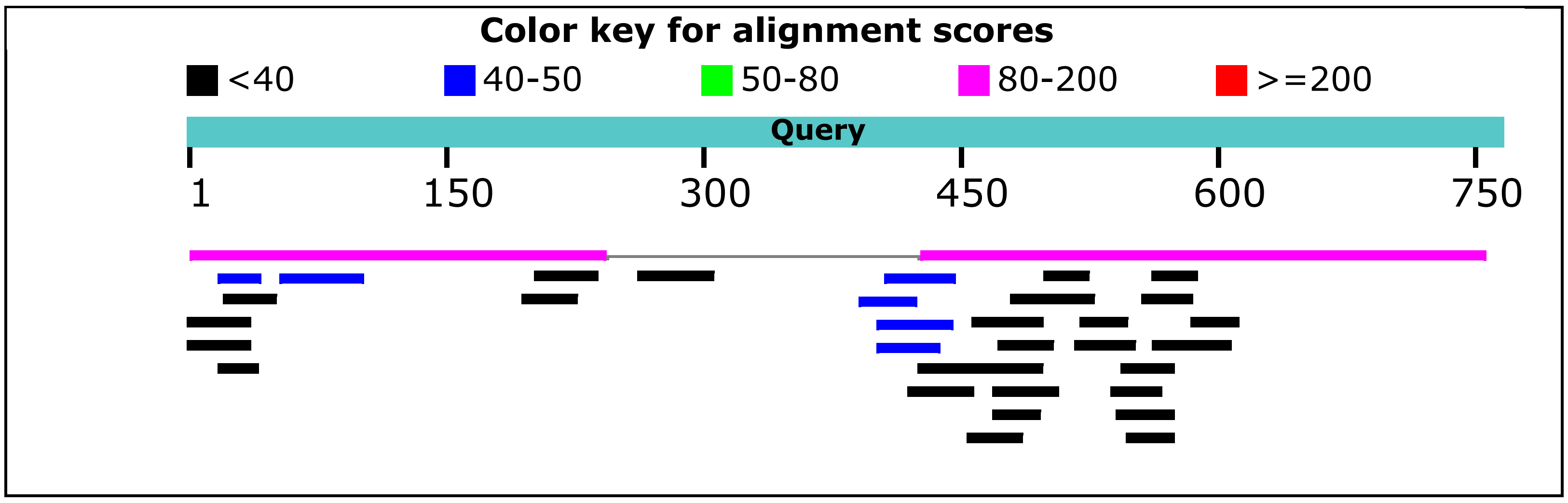
RID F0Y284B4015 (Expires on 05-09 00:01 am)

Query ID lcl|Query_37561
Description NW_003943634.1:c18022769-18022020 Saimiri boliviensis boliviensis isolate 3227 unplaced genomic scaffold, SaiBol1.0 scaffold00031, whole genome shotgun sequence
Molecule type nucleic acid
Query Length 750

Database Name GPIPE/9478/100/ref_top_level
Description Tarsius syrichta Tarsius_syrichta-2.0.1 [GCF_000164805.1] chromosomes plus unplaced and unlocalized scaffolds (reference assembly in Annotation Release 100)
Program BLASTN 2.8.0+

⊟ Graphic Summary

Distribution of the top 34 Blast Hits on 33 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold305619	136	235	75%	2e-29	71%	NW_007249715.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold314713	48.2	48.2	5%	0.008	87%	NW_007258809.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold143404	42.8	42.8	6%	0.33	80%	NW_007087500.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold304335	42.8	42.8	4%	0.33	90%	NW_007248431.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold305073	42.8	42.8	5%	0.33	84%	NW_007249169.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold115602	41.0	41.0	2%	1.2	100%	NW_007059698.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold303129	41.0	41.0	4%	1.2	86%	NW_007247225.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold78724	39.2	39.2	3%	4.0	96%	NW_007022820.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold92604	39.2	39.2	3%	4.0	92%	NW_007036700.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold102065	39.2	39.2	4%	4.0	86%	NW_007046161.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold120636	39.2	39.2	9%	4.0	73%	NW_007064732.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold123307	39.2	39.2	3%	4.0	96%	NW_007067403.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold135706	39.2	39.2	6%	4.0	78%	NW_007079802.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold138808	39.2	39.2	4%	4.0	83%	NW_007082904.1

Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold142933	39.2	39.2	5%	4.0	84%	NW_007087029.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold169162	39.2	39.2	3%	4.0	92%	NW_007113258.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold169693	39.2	39.2	3%	4.0	92%	NW_007113789.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold191702	39.2	39.2	3%	4.0	93%	NW_007135798.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold283083	39.2	39.2	4%	4.0	85%	NW_007227179.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold288207	39.2	39.2	4%	4.0	85%	NW_007232303.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold288366	39.2	39.2	2%	4.0	100%	NW_007232462.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold300787	39.2	39.2	5%	4.0	82%	NW_007244883.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold301878	39.2	39.2	3%	4.0	90%	NW_007245974.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold302600	39.2	39.2	3%	4.0	92%	NW_007246696.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold302862	39.2	39.2	4%	4.0	87%	NW_007246958.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold303061	39.2	39.2	4%	4.0	83%	NW_007247157.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold303111	39.2	39.2	4%	4.0	88%	NW_007247207.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold303726	39.2	39.2	3%	4.0	92%	NW_007247822.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold303727	39.2	39.2	4%	4.0	90%	NW_007247823.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1	39.2	39.2	4%	4.0	86%	NW_007248560.1

Scaffold304464						
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold304668	39.2	39.2	3%	4.0	92%	NW_007248764.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold309834	39.2	39.2	5%	4.0	81%	NW_007253930.1
Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold314085	39.2	39.2	4%	4.0	90%	NW_007258181.1

Alignments

Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold305619
Sequence ID: **NW_007249715.1** Length: 506769 Number of Matches: 2
Range 1: 127870 to 128164

Score	Expect	Identities	Gaps	Strand	Frame
136 bits(150)	2e-29()	234/329(71%)	37/329(11%)	Plus/Plus	

Features:

```
Query  423     GGAGGGAGGCTGGGACCCACCCCACCTGGCAGAGGCTTCAGCTCCCTGACCCCCGTCCCC  482
               |||||||||||||| |  ||||||||||    | |     ||||||  ||  ||  ||||
Sbjct  127870  GGAGGGAGGCTGGGGC--ACCCCACCTG----ATG-----GCTCCC--ACAGCCTGCCCC  127916

Query  483     ACCCAGAGTCCCTAGGTGCCCCCCTCAACCAGATCTTTCTTTCCCCAAAAGTCTGCAAAT  542
               ||   |  |||| ||||    |||||| ||||| ||||||||||||||  ||||  |||| | 
Sbjct  127917  ACT--GGTTCCCGAGGT----CCCTCAGCCAGAGCTTTCTTTCCC--AAAGCTTGCAGA-  127967

Query  543     CCAGGAGGAGGAGAAGATGCAGAAGGTACTAAGCTTCCTGGGCCCCTCGCCCCCTG-CTG  601
                |||    |||||| | |||||||||   |||  ||||||  ||| ||||||  || | |
Sbjct  127968  -CAG----AGGAGACGGTGCAGAAGGCCTTAAAGTTCCTGCTCCC-TCGCCCTGTGGCCG  128021

Query  602     GAAAGTAAAAGTCACCTGCCTGAGAAACACCAAGTGAGGCCATAGCAACACCCCT--ACA  659
                  || | |||| ||| ||| || | |||   |  |||||||| ||| ||||   |||
Sbjct  128022  CTGAGGAGAAGTAACCAGCCTAAGGAGCAC---GCCAGGCCATAGTAACTCCCCACAACA  128078

Query  660     TCAAATGCTCAAGCCCTGAATTGCTGCTGAGAAGCTCACAAGATCTGAGTGAAATGTGCC  719
                || | ||||  || ||||   ||| |  |||| | |||||||||||||||| ||| | || 
Sbjct  128079  ACAGACGCTCTTGCTCTGA---GCTTCCAAGAACCCCACAAGATCTGAGTAAAAGGAGCA  128135

Query  720     AAAGTCACCTGCCCAATAAAGCTTGACAA  748
               ||||||||||||| |||||||||||||||
Sbjct  128136  AAAGTCACCTGCCAAATAAAGCTTGACAA  128164
```

Range 2: 127404 to 127631

Score	Expect	Identities	Gaps	Strand	Frame
98.7 bits(108)	5e-18()	167/239(70%)	11/239(4%)	Plus/Plus	

Features:

```
Query  3       CCAACACTAACACCAAGGGCAGGTGGGCAGGCCCcagccctcctcccccaccccagggcc  62
               ||||||||||||||||  ||||||||||||||| | |||||| |||||||     ||| |
Sbjct  127404  CCAACACTAACACCAAACGCAGGTGGGCAGGCCTC-GCCCTCTTCCCCCA-----GGGTC  127457

Query  63      cactgcagcctcagcccaggAGCCACCGGATCTCCCAACACCATGGTCCGATACCGCTTG  122
               | |  ||||||||| |    |||| | |   | ||   ||||||||||||  |||||  |
Sbjct  127458  CCCA-CAGCCTCAGTC----AGCCCCAGCCCCGCCTTGCACCATGGTCCGCCACCGCGGG  127512

Query  123     AGGAGCCCGAGCGAACGCCCACACGAGGAGTACAGGCAGCTGGTGAACAGGCAGGAGCAA  182
               || ||||||||| | | ||| | | |||  | |  |  || ||   | || | |||||  
Sbjct  127513  AGCAGCCCGAGCCAGCACCCGCCCCAGGGCTCCCAGGTGCAGGGCCATAGCCTGGAGCGT  127572

Query  183     GGACGTAATGCCCAAGAGGAGCAGGGGCTGAGCCCAGAAGGCGTCGGGGTCTATGGGAG  241
               || ||  | ||||  || |||||||| ||||||| |||   |   | || |||||||||
Sbjct  127573  GGCCGCGAGGCCCCCGAAGAGCAGGGGATGAGCCAAGAGCACAGTGAGGCCTATGGGAG  127631
```

Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold314713
Sequence ID: **NW_007258809.1** Length: 1611238 Number of Matches: 1
Range 1: 896641 to 896679

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.008()	34/39(87%)	0/39(0%)	Plus/Plus	

Features:

```
Query  396     TGAATGCCCCTGACCACCCCAGGCACAGGAGGGAGGCTG  434
               |||||||||  |||||||||||||| |||||| | ||||
Sbjct  896641  TGAATGCCCTGGACCACCCCAGGCAGAGGAGGCATGCTG  896679
```

Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold143404
Sequence ID: **NW_007087500.1** Length: 661 Number of Matches: 1
Range 1: 83 to 128

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	0.33()	37/46(80%)	0/46(0%)	Plus/Plus	

Features:

```
Query  52   accccagggcccactgcagcctcagcccaggAGCCACCGGATCTCC  97
            ||||  |||||||  |||||| | |||||| ||  |||||||||||
Sbjct  83   ACCCAGGGGCCCAGAGCAGCCACGGCCCAGCAGGGACCGGATCTCC  128
```

Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold304335
Sequence ID: **NW_007248431.1** Length: 984681 Number of Matches: 1
Range 1: 495311 to 495341

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	0.33()	28/31(90%)	0/31(0%)	Plus/Minus	

Features:

```
Query  387     GTGCCCCCCTGAATGCCCCTGACCACCCCAG  417
               ||||||||||| ||||||||| ||||| |||
Sbjct  495341  GTGCCCCCCTGGATGCCCCTGTCCACCTCAG  495311
```

Tarsius syrichta isolate Samal-C Ts95f unplaced genomic scaffold, Tarsius_syrichta-2.0.1 Scaffold305073
Sequence ID: **NW_007249169.1** Length: 578577 Number of Matches: 1
Range 1: 304117 to 304159

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	0.33()	36/43(84%)	1/43(2%)	Plus/Minus	

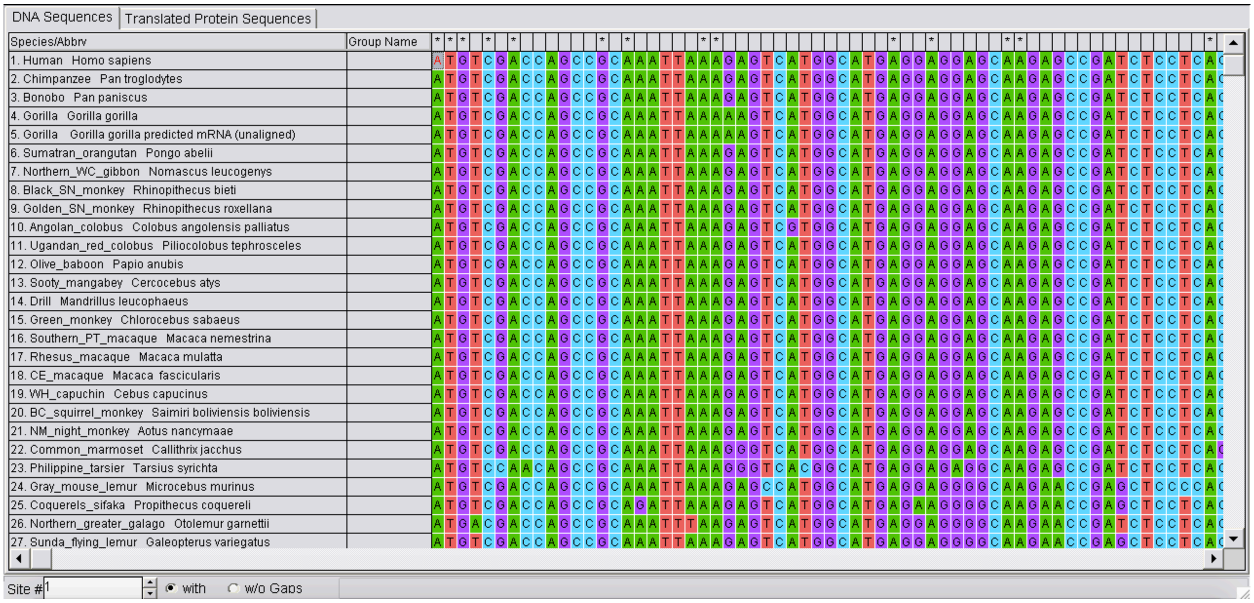
Features:

```
Query  400     TGCCCCTGACCACCCCAGGCACAG-GAGGGAGGCTGGGACCCA  441
               |||||||||||||||||| |   | || |||| ||||||||||
Sbjct  304159  TGCCCCTGACCACCCCAGTCCTTGTGACGGAGTCTGGGACCCA  304117
```

Support center Mailing list YouTube

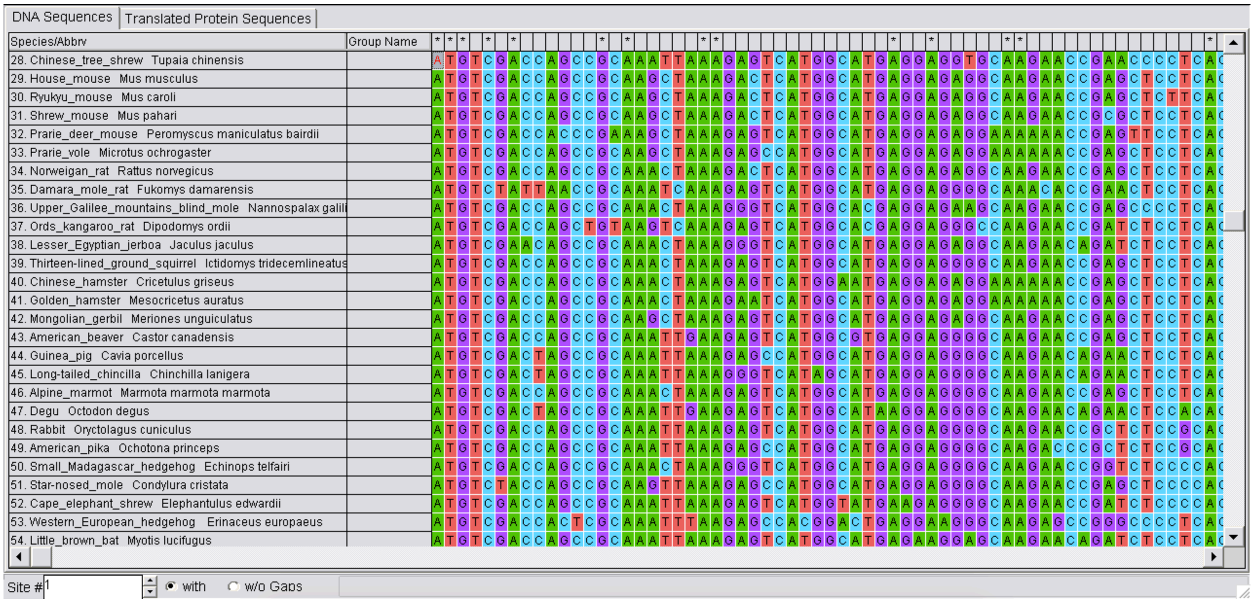
- National Library Of Medicine

Appendix Y) Alignment of mammalian *Tnp1* coding exon sequences



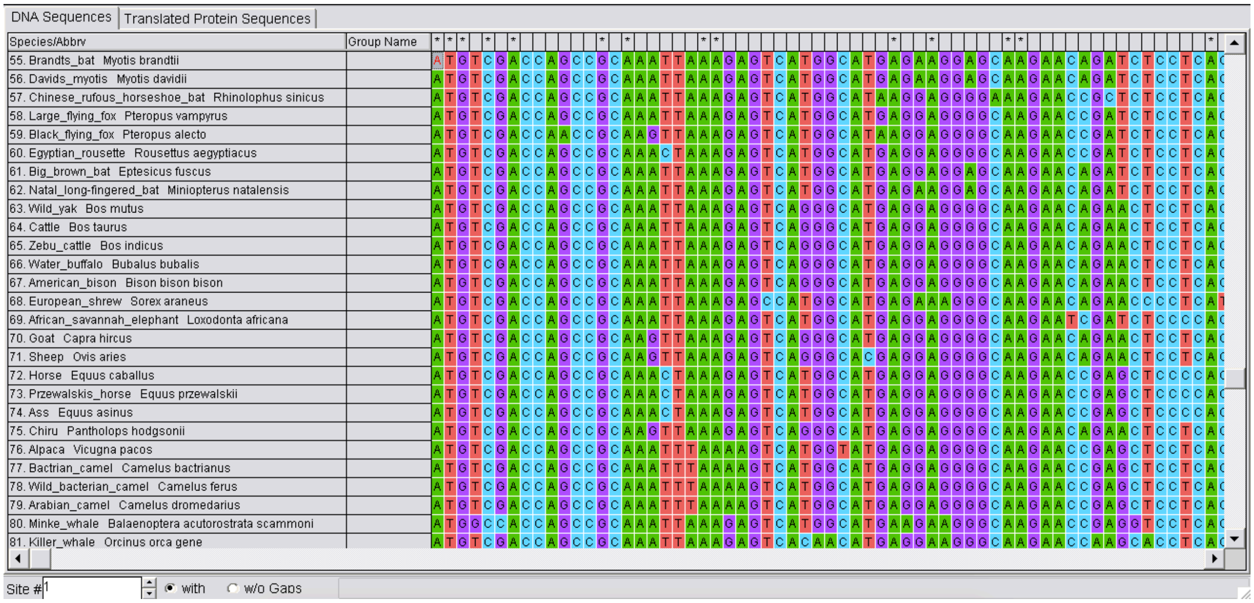
Species/Abbrv	Group Name	`*** * *      * *     **             *  *     **              *`
1. Human Homo sapiens		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
2. Chimpanzee Pan troglodytes		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
3. Bonobo Pan paniscus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
4. Gorilla Gorilla gorilla		ATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
5. Gorilla Gorilla gorilla predicted mRNA (unaligned)		ATGTCGACCAGCCGCAAATTAAAAAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
6. Sumatran_orangutan Pongo abelii		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
7. Northern_WC_gibbon Nomascus leucogenys		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
8. Black_SN_monkey Rhinopithecus bieti		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
9. Golden_SN_monkey Rhinopithecus roxellana		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
10. Angolan_colobus Colobus angolensis palliatus		ATGTCGACCAGCCGCAAATTAAAGAGTCGTGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
11. Ugandan_red_colobus Piliocolobus tephrosceles		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
12. Olive_baboon Papio anubis		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
13. Sooty_mangabey Cercocebus atys		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
14. Drill Mandrillus leucophaeus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
15. Green_monkey Chlorocebus sabaeus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
16. Southern_PT_macaque Macaca nemestrina		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
17. Rhesus_macaque Macaca mulatta		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
18. CE_macaque Macaca fascicularis		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
19. WH_capuchin Cebus capucinus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
20. BC_squirrel_monkey Saimiri boliviensis boliviensis		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
21. NM_night_monkey Aotus nancymaae		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
22. Common_marmoset Callithrix jacchus		ATGTCGACCAGCCGCAAATTAAAGGGTCATGGCATGAGGAGGAGCAAGAGCCGATCTCCTCA
23. Philippine_tarsier Tarsius syrichta		ATGTCCAACAGCCGCAAATTAAAGGGTCACGGCATGAGGAGAGGCAAGAGCCGATCTCCTCA
24. Gray_mouse_lemur Microcebus murinus		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGAGCTCCCCA
25. Coquerels_sifaka Propithecus coquereli		ATGTCGACCAGCCGCAGATTAAAGAGTCATGGCATGAGAAGGGGCAAGAACCGAGCTCCTCA
26. Northern_greater_galago Otolemur garnettii		ATGACGACCAGCCGCAAATTTAAGAGTCATGGCATGAGGAGGGGCAAGAACCGATCTCCTCA
27. Sunda_flying_lemur Galeopterus variegatus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCA

Site # 1 ● with ○ w/o Gaps



Species/Abbrv	Group Name	`*** * *      * *     **             *  *     **              *`
28. Chinese_tree_shrew Tupaia chinensis		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGTGCAAGAACCGAACCCCTCA
29. House_mouse Mus musculus		ATGTCGACCAGCCGCAAGCTAAAGACTCATGGCATGAGGAGAGGCAAGAACCGAGCTCCTCA
30. Ryukyu_mouse Mus caroli		ATGTCGACCAGCCGCAAGCTAAAGACTCATGGCATGAGGAGAGGCAAGAACCGAGCTCTTCA
31. Shrew_mouse Mus pahari		ATGTCGACCAGCCGCAAGCTAAAGACTCATGGCATGAGGAGAGGCAAGAACCGCGCTCCTCA
32. Prarie_deer_mouse Peromyscus maniculatus bairdii		ATGTCGACCACCCGAAAGCTAAAGAGTCATGGCATGAGGAGAGGAAAAAACCGAGTTCCTCA
33. Prarie_vole Microtus ochrogaster		ATGTCGACCAGCCGCAAGCTAAAGAGCCATGGCATGAGGAGAGGAAAAAACCGAGCTCCTCA
34. Norweigan_rat Rattus norvegicus		ATGTCGACCAGCCGCAAACTAAAGACTCATGGCATGAGGAGAGGCAAGAACCGAGCTCCTCA
35. Damara_mole_rat Fukomys damarensis		ATGTCTATTAACCGCAAATCAAAGAGTCATGGCATGAGGAGGGGCAAACACCGAACTCCTCA
36. Upper_Galilee_mountains_blind_mole Nannospalax galili		ATGTCGACCAGCCGCAAACTAAAGGGTCATGGCACGAGGAGAAGCAAGAACCGAGCCCCTCA
37. Ords_kangaroo_rat Dipodomys ordii		ATGTCGACCAGCTGTAAGTCAAAGAGTCATGGCACGAGGAGGGCCAAGAACCGATCTCCTCA
38. Lesser_Egyptian_jerboa Jaculus jaculus		ATGTCGAACAGCCGCAAACTAAAGGGTCATGGCATGAGGAGAGGCAAGAACAGATCTCCTCA
39. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		ATGTCGACCAGCCGCAAACTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCA
40. Chinese_hamster Cricetulus griseus		ATGTCGACCAGCCGCAAACTAAAGAGTCATGGAATGAGGAGAGGAAAAAACCGAGCTCCTCA
41. Golden_hamster Mesocricetus auratus		ATGTCGACCAGCCGCAAACTAAAGAATCATGGCATGAGGAGAGGAAAAAACCGAGCTCCTCA
42. Mongolian_gerbil Meriones unguiculatus		ATGTCGACCAGCCGCAAGCTAAAGAGTCATGGCATGAGGAGAGGCAAGAACCGAGCTCCTCA
43. American_beaver Castor canadensis		ATGTCGACCAGCCGCAAATTGAAGAGTCATGGCGTGAGGAGGGGCAAGAACCGAGCTCCTCA
44. Guinea_pig Cavia porcellus		ATGTCGACTAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAACAGAACTCCTCA
45. Long-tailed_chincilla Chinchilla lanigera		ATGTCGACTAGCCGCAAATTAAAGGGTCATAGCATGAGGAGGGGCAAGAACAGAACTCCTCA
46. Alpine_marmot Marmota marmota marmota		ATGTCGACCAGCCGCAAACTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCA
47. Degu Octodon degus		ATGTCGACTAGCCGCAAATTGAAGAGTCATGGCATAAGGAGGGGCAAGAACAGAACTCCACA
48. Rabbit Oryctolagus cuniculus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGCTCTCCGCA
49. American_pika Ochotona princeps		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGACCCGCTCTCCGCA
50. Small_Madagascar_hedgehog Echinops telfairi		ATGTCGACCAGCCGCAAACTAAAGGGTCATGGCATGAGGAGGGGCAAGAACCGGTCTCCCCA
51. Star-nosed_mole Condylura cristata		ATGTCTACCAGCCGCAAGTTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGAGCTCCCCA
52. Cape_elephant_shrew Elephantulus edwardii		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGTATGAAGAGGGGCAAGAACCGATCTCCCCA
53. Western_European_hedgehog Erinaceus europaeus		ATGTCGACCACTCGCAAATTTAAGAGCCACGGACTGAGGAAGGGCAAGAGCCGGGCCCCTCA
54. Little_brown_bat Myotis lucifugus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGAAGGAGCAAGAACAGATCTCCTCA

Site # 1 ● with ○ w/o Gaps



Species/Abbrv	Group Name	*** * * * * ** * * ** *
55. Brandts_bat Myotis brandtii		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGAAGGAGCAAGAACAGATCTCCTCAC
56. Davids_myotis Myotis davidii		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGAAGGAGCAAGAACAGATCTCCTCAC
57. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATAAGGAGGGGAAAGAACCGCTCTCCTCAC
58. Large_flying_fox Pteropus vampyrus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGATCTCCTCAC
59. Black_flying_fox Pteropus alecto		ATGTCGACCAACCGCAAGTTAAAGAGTCATGGCATAAGGAGGGGCAAGAACCGATCTCCTCAC
60. Egyptian_rousette Rousettus aegyptiacus		ATGTCGACCAGCCGCAAACTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGATCTCCTCAC
61. Big_brown_bat Eptesicus fuscus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGAGCAAGAACAGATCTCCTCAC
62. Natal_long-fingered_bat Miniopterus natalensis		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGAAGGAGCAAGAACAGATCTCCTCAC
63. Wild_yak Bos mutus		ATGTCGACCAGCCGCAAATTAAAGAGTCAGGGCATGAGGAGGGGCAAGAACAGAACTCCTCAC
64. Cattle Bos taurus		ATGTCGACCAGCCGCAAATTAAAGAGTCAGGGCATGAGGAGGGGCAAGAACAGAACTCCTCAC
65. Zebu_cattle Bos indicus		ATGTCGACCAGCCGCAAATTAAAGAGTCAGGGCATGAGGAGGGGCAAGAACAGAACTCCTCAC
66. Water_buffalo Bubalus bubalis		ATGTCGACCAGCCGCAAATTAAAGAGTCAGGGCATGAGGAGGGGCAAGAACAGAACTCCTCAC
67. American_bison Bison bison bison		ATGTCGACCAGCCGCAAATTAAAGAGTCAGGGCATGAGGAGGGGCAAGAACAGAACTCCTCAC
68. European_shrew Sorex araneus		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGAAAGGGCAAGAACAGAACCCCTCAT
69. African_savannah_elephant Loxodonta africana		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGGGCAAGAATCGATCTCCCCAC
70. Goat Capra hircus		ATGTCGACCAGCCGCAAGTTAAAGAGTCAGGGCATGAGGAGGGGCAAGAACAGAACTCCTCAC
71. Sheep Ovis aries		ATGTCGACCAGCCGCAAGTTAAAGAGTCAGGGCACGAGGAGGGGCAAGAACAGAACTCCTCAC
72. Horse Equus caballus		ATGTCGACCAGCCGCAAACTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCCCAC
73. Przewalskis_horse Equus przewalskii		ATGTCGACCAGCCGCAAACTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCCCAC
74. Ass Equus asinus		ATGTCGACCAGCCGCAAACTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCCCAC
75. Chiru Pantholops hodgsonii		ATGTCGACCAGCCGCAAGTTAAAGAGTCAGGGCATGAGGAGGGGCAAGAACAGAACTCCTCAC
76. Alpaca Vicugna pacos		ATGTCGACCAGCCGCAAATTTAAAAGTCATGGTATGAGGAGGGGCAAGAACCGAGCTCCTCAC
77. Bactrian_camel Camelus bactrianus		ATGTCGACCAGCCGCAAATTTAAAAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
78. Wild_bacterian_camel Camelus ferus		ATGTCGACCAGCCGCAAATTTAAAAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
79. Arabian_camel Camelus dromedarius		ATGTCGACCAGCCGCAAATTTAAAAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
80. Minke_whale Balaenoptera acutorostrata scammoni		ATGGCCACCAGCCGCAAATTAAAGAGTCATGGCATGAAGAAGGGCAAGAACCGAGGTCCTCAC
81. Killer_whale Orcinus orca gene		ATGTCGACCAGCCGCAAATTAAAGAGTCACAACATGAGGAAGGGCAAGAACCAAGCACCTCAC

Site # 1 ● with ○ w/o Gaps

Species/Abbrv	Group Name	*** * * * * ** * * ** *
82. Bottlenose_dolphin Tursiops truncatus		ATGTCGACCAGCCGCAAATTAAAGGGTCACAGCATGAGGAAGGGCAAGAACCAAGCACCTCAC
83. Beluga_whale Delphinapterus leucas		ATGTCAACCAGCCGCAAATTAAAGAGTCACAGCATGAGGAAGGGCAAGAACCAAGCACCTCAC
84. Yangtze_river_dolphin Lipotes vexillifer		ATGTCGACCAGCCGCAAATTAAAGAGTCCCAGCATGAGGAAGGGCAAGAACCAAGCTCCTCAC
85. Northern_sea_otter Enhydra lutris kenyoni		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
86. Pacific_walrus Odobenus rosmarus divergens		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGTCAAGAACCGAGCTCCTCAC
87. Weddell_seal Leptonychotes weddellii		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
88. Hawaiian_monk_seal Neomonachus schauinslandi		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
89. Florida_manatee Trichechus manatus latirostris		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGATCTCCCCAC
90. Domestic_ferret Mustela putorius furo		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
91. Aardvark Orycteropus afer afer		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGATCTCCTCAT
92. Polar_bear Ursus maritimus		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
93. Pig Sus scrofa		ATGTCGACCAGCCGCAAGTTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGCGCTCCTCAC
94. Dog Canis lupus		ATGTCTACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
95. Domestic_cat Felis catus		ATGTCGACCGGCCGCAAATTCAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
96. Cheetah Acinonyx jubatus		ATGTCGACCAGCCGCAAATTCAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
97. Leopard Panthera pardus		ATGTCGACCAACCGCAAATTCAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
98. Amur_tiger Panthera tigris altaica		ATGTCGACCAACCGCAAATTCAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCTCAC
99. Giant_panda Ailuropoda melanoleuca		ATGTCGACCAGCCGCAAATTAAAGAGCCATGGCATGAGGAGGGGCAAGAATCGAGCTCCCCAC
100. Nine-banded_armadillo Dasypus novemcinctus		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCT---CAC
101. Southern_white_rhinocerous Ceratotherium simum simu		ATGTCGACCAGCCGCAAATTAAAGAGTCATGGCATGAGGAGGGGCAAGAACCGAGCTCCCTAC
102. Gray_short_tailed_opossum Monodelphis domestica		ATGTCTACCAACAGGAGGATGAAAAGCAAAGGAGGGAGGAGAAATAAGAGCAGAGCTCCTCAC
103. Tasmanian_devil Sarcophilus harrisii		ATGTCTACCAACAGGAGAATGAAGAGCCAAAGCGGGAGGAGAAACAAGAGCAGATCTCCCCAT
104. Tammar_wallaby Macropus eugenii		ATGTCTACCAACAGGAGAATGAAAAGCCGAGGCGGGAGGAGAAACAAGAGCAGATCTCCTCAC

Site # 1 ● with ○ w/o Gaps

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Species/Abbrv                                          Group Name   ** ** *  *              **    *     *              *     ** **
1. Human  Homo sapiens                                              CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
2. Chimpanzee  Pan troglodytes                                      CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
3. Bonobo  Pan paniscus                                             CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
4. Gorilla  Gorilla gorilla                                         CAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCCGAAAAGTAGGAA
5. Gorilla  Gorilla gorilla predicted mRNA (unaligned)              CAAGGGGGGCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCCGAAAAGTAGGAA
6. Sumatran_orangutan  Pongo abelii                                 CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
7. Northern_WC_gibbon  Nomascus leucogenys                          CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
8. Black_SN_monkey  Rhinopithecus bieti                             CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
9. Golden_SN_monkey  Rhinopithecus roxellana                        CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
10. Angolan_colobus  Colobus angolensis palliatus                   CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
11. Ugandan_red_colobus  Piliocolobus tephrosceles                  CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGCAGGAA
12. Olive_baboon  Papio anubis                                      CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
13. Sooty_mangabey  Cercocebus atys                                CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
14. Drill  Mandrillus leucophaeus                                   CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
15. Green_monkey  Chlorocebus sabaeus                               CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
16. Southern_PT_macaque  Macaca nemestrina                         CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
17. Rhesus_macaque  Macaca mulatta                                 CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
18. CE_macaque  Macaca fascicularis                                CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGTAAGGGCAACCTGAAAAGTAGGAA
19. WH_capuchin  Cebus capucinus                                   CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAAAGTAGGAA
20. BC_squirrel_monkey  Saimiri boliviensis boliviensis            CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAAAGTAGGAA
21. NM_night_monkey  Aotus nancymaae                               CAAGGGAGTCAAGAGAGGTGGCAGCAAGAGAAAACACCAGAAGGGCAGCCTGAAAAGTAGGAA
22. Common_marmoset  Callithrix jacchus                            GAAGGGAGTCAAGAGGGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAAAGTAGGAA
23. Philippine_tarsier  Tarsius syrichta                           CAAGGGAGTGAAGAAAGGTGGCAACAAAAGAAAATACCGGAAGAGCAGCATGAAAAGCAGGAA
24. Gray_mouse_lemur  Microcebus murinus                           CAAGGGAGTCAAGAGAGGTGGCAGCAAGAGAAAATACCGGAAGGGCAGCCTGAAAAGTAGGAA
25. Coquerels_sifaka  Propithecus coquereli                        CAAGGGAGTCAAGAGAGGAGGCAACAAGAGAAAATACCGAAAAGGCAGCCTGAAAAGTAGGAA
26. Northern_greater_galago  Otolemur garnettii                    CAAGGGAGTCAAGAGAGGTGGCAGCAAGAGAAAATACCGGAAGGGCAGCCTGAAAAGTAGGAA
27. Sunda_flying_lemur  Galeopterus variegatus                     CAAGGGAGTCAAGAGAGGAGGCAGCAAAAGAAAATACCGGAAGGGCAGTCTGAAGAGTAGGAA
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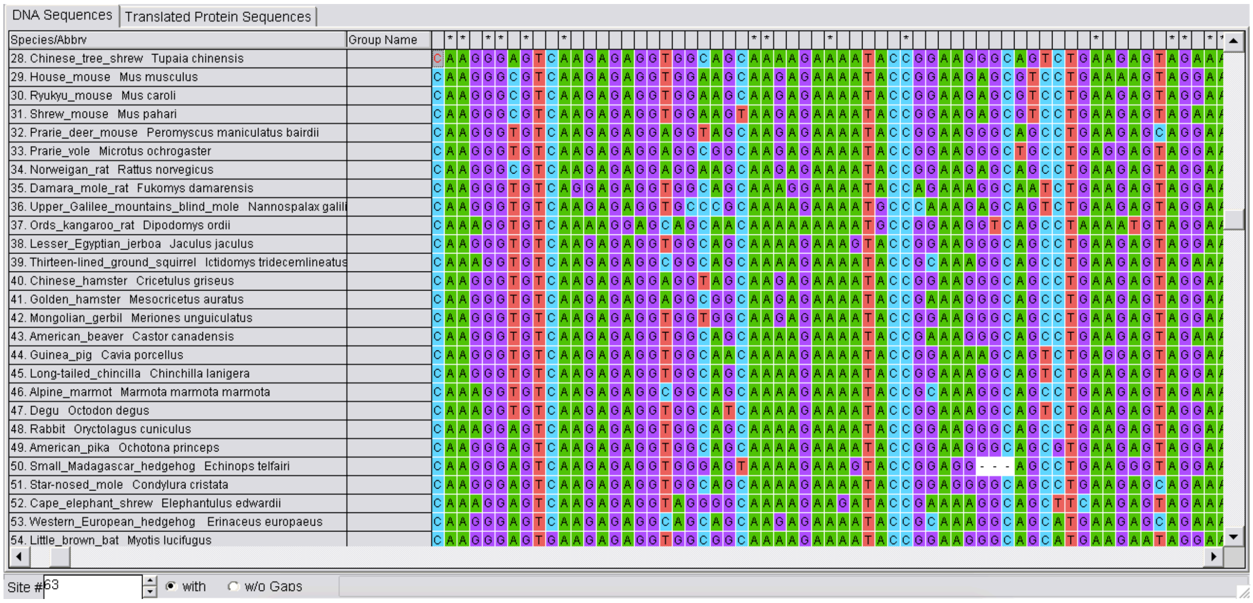
Site # 63   ● with   ○ w/o Gaps



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Species/Abbrv                                          Group Name   ** ** *  *              **    *     *              *     ** **
28. Chinese_tree_shrew  Tupaia chinensis                            CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGTCTGAAGAGTAGAAA
29. House_mouse  Mus musculus                                       CAAGGGCGTCAAGAGAGGTGGAAGCAAGAGAAAATACCGGAAGAGCGTCCTGAAAAGTAGGAA
30. Ryukyu_mouse  Mus caroli                                        CAAGGGCGTCAAGAGAGGTGGAAGCAAGAGAAAATACCGGAAGAGCGTCCTGAAGAGTAGGAA
31. Shrew_mouse  Mus pahari                                         CAAGGGCGTCAAGAGAGGTGGAAGTAAGAGAAAATACCGGAAGAGCGTCCTGAAGAGTAGAAA
32. Prarie_deer_mouse  Peromyscus maniculatus bairdii              CAAGGGTGTCAAGAGAGGAGGTAGCAAGAGAAAATACCGGAAGGGCAGCCTGAAGAGCAGGAA
33. Prarie_vole  Microtus ochrogaster                               CAAGGGTGTCAAGAGAGGAGGCGGCAAGAGAAAATACCGGAAGGGCTGCCTGAGGAGTAGGAA
34. Norweigan_rat  Rattus norvegicus                                CAAGGGCGTCAAGAGAGGAGGAAGCAAGAGAAAATACCGGAAGAGCAGCCTGAAGAGTAGGAA
35. Damara_mole_rat  Fukomys damarensis                             CAAGGGTGTCAGGAGAGGTGGCAGCAAAGGAAAATACCAGAAAGGCAATCTGAAGAGTAGGAA
36. Upper_Galilee_mountains_blind_mole  Nannospalax galili          CAAGGGTGTCAAGAGAGGTGCCCGCAAAAGAAAATGCCCAAAGAGCAGTCTGAAGAGTAGGAA
37. Ords_kangaroo_rat  Dipodomys ordii                              CAAAGGTGTCAAAAGGAGCAGCAACAAAAAAAAATGCCGGAAGGTCAGCCTAAAATGTAGGAA
38. Lesser_Egyptian_jerboa  Jaculus jaculus                         CAAGGGTGTCAAGAGAGGTGGCAGCAAAAGAAAGTACCGGAAGGGCAGCCTGAAGAGTAGGAA
39. Thirteen-lined_ground_squirrel  Ictidomys tridecemlineatus     CAAAGGTGTCAAGAGAGGCGGCAGCAAAAGAAAATACCGCAAAGGCAGCCTGAAGAGTAGAAA
40. Chinese_hamster  Cricetulus griseus                             CAAGGGTGTCAAGAGAGGAGGTAGCAAGAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGGAA
41. Golden_hamster  Mesocricetus auratus                            CAAGGGTGTCAAGAGAGGAGGCGGCAAGAGAAAATACCGAAAGGGCAGCCTGAAGAGTAGGAA
42. Mongolian_gerbil  Meriones unguiculatus                         CAAGGGTGTCAAGAGAGGTGGTGGCAAGAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGGAA
43. American_beaver  Castor canadensis                              CAAGGGTGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGAAAGGGCAGCCTGAAGAGTAGAAA
44. Guinea_pig  Cavia porcellus                                     CAAGGGTGTCAAGAGAGGTGGCAACAAAAGAAAATACCGGAAAAGCAGTCTGAGGAGTAGGAA
45. Long-tailed_chincilla  Chinchilla lanigera                      CAAGGGTGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAAGGCAGTCTGAAGAGTAGGAA
46. Alpine_marmot  Marmota marmota marmota                          CAAAGGTGTCAAGAGAGGCGGCAGCAAAAGAAAATACCGCAAAGGCAGCCTGAAGAGTAGAAA
47. Degu  Octodon degus                                             CAAAGGTGTCAAGAGAGGTGGCATCAAAAGAAAATACCGGAAAGGCAGTCTGAAGAGTAGGAA
48. Rabbit  Oryctolagus cuniculus                                   CAAAGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGGAA
49. American_pika  Ochotona princeps                                CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCGTGAAGAGTAGGAA
50. Small_Madagascar_hedgehog  Echinops telfairi                    CAAGGGAGTCAAGAGAGGTGGGAGTAAAAGAAAGTACCGGAGG---AGCCTGAAGGGTAGGAA
51. Star-nosed_mole  Condylura cristata                             CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAGAGCAGAAA
52. Cape_elephant_shrew  Elephantulus edwardii                      CAAAGGAGTCAAGAGAGGTAGGGGCAAAAGAAGATACCGAAAAGGCAGCTTCAAGAGTAGAAA
53. Western_European_hedgehog  Erinaceus europaeus                  CAAGGGAGTCAAGAGAGGCAGCAGCAAGAGAAAATACCGCAAAGGCAGCATGAAGAGCAGAAA
54. Little_brown_bat  Myotis lucifugus                              CAAGGGAGTGAAGAGAGGTGGCGGCAAAAGAAAATACCGGAAGGGCAGCATGAAGAATAGGAA
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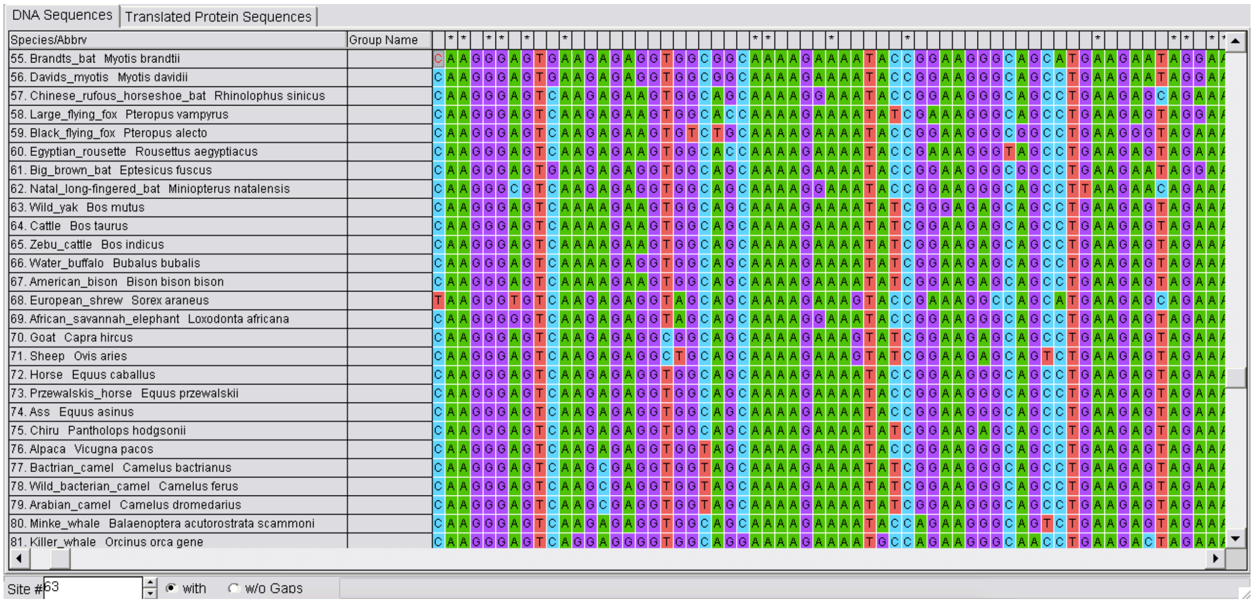
Site # 63   ● with   ○ w/o Gaps



Species/Abbrv	Group Name	
55. Brandts_bat Myotis brandtii		CAAGGGAGTGAAGAGAGGTGGCGGCAAAAGAAAATACCGGAAGGGCAGCATGAAGAATAGGAA
56. Davids_myotis Myotis davidii		CAAGGGAGTGAAGAGAGGTGGCGGCAAAAGAAAATACCGGAAGGGCAGCCTGAAGAATAGGAA
57. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		CAAGGGAGTCAAGAGAAGTGGCAGCAAAAGGAAATACCGGAAGGGCAGCCTGAAGAGCAGAAA
58. Large_flying_fox Pteropus vampyrus		CAAGGGAGTCAAGAGAAGTGGCACCAAAAGAAAATATCGAAAGGGCAGCCTGAAGAGTAGGAA
59. Black_flying_fox Pteropus alecto		CAAGGGAGTCAAGAGAAGTGTCTGCAAAAGAAAATACCGGAAGGGCGGCCTGAAGGGTAGAAA
60. Egyptian_rousette Rousettus aegyptiacus		CAAGGGAGTCAAGAGAAGTGGCACCAAAAGAAAATACCGAAAGGGTAGCCTGAAGAGTAGAAA
61. Big_brown_bat Eptesicus fuscus		CAAGGGAGTGAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCGGCCTGAAGAATAGGAA
62. Natal_long-fingered_bat Miniopterus natalensis		CAAGGGCGTCAAGAGAGGTGGCAGCAAAAGGAAATACCGGAAGGGCAGCCTTAAGAACAGAAA
63. Wild_yak Bos mutus		CAAGGGAGTCAAAAGAAGTGGCAGCAAAAGAAAATATCGGGAGAGCAGCCTGAAGAGTAGAAA
64. Cattle Bos taurus		CAAGGGAGTCAAAAGAAGTGGCAGCAAAAGAAAATATCGGAAGAGCAGCCTGAAGAGTAGAAA
65. Zebu_cattle Bos indicus		CAAGGGAGTCAAAAGAAGTGGCAGCAAAAGAAAATATCGGAAGAGCAGCCTGAAGAGTAGAAA
66. Water_buffalo Bubalus bubalis		CAAGGGAGTCAAAAGAGGTGGCAGCAAAAGAAAATATCGGAAGAGCAGCCTGAAGAGTAGAAA
67. American_bison Bison bison bison		CAAGGGAGTCAAAAGAAGTGGCAGCAAAAGAAAATATCGGAAGAGCAGCCTGAAGAGTAGAAA
68. European_shrew Sorex araneus		TAAGGGTGTCAAGAGAGGTAGCAGCAAAAGAAAGTACCGAAAGGCCAGCATGAAGAGCAGAAA
69. African_savannah_elephant Loxodonta africana		CAAGGGGGTCAAGAGAGGTAGCAGCAAAAGGAAATACCGGAAGGGCAGCCTGAAGAGTAGAAA
70. Goat Capra hircus		CAAGGGAGTCAAGAGAGGCGGCAGCAAAAGAAAGTATCGGAAGAGCAGCCTGAAGAGTAGAAA
71. Sheep Ovis aries		CAAGGGAGTCAAGAGAGGCTGCAGCAAAAGAAAGTATCGGAAGAGCAGTCTGAAGAGTAGAAA
72. Horse Equus caballus		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGAAA
73. Przewalskis_horse Equus przewalskii		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGAAA
74. Ass Equus asinus		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGAAA
75. Chiru Pantholops hodgsonii		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATATCGGAAGAGCAGCCTGAAGAGTAGAAA
76. Alpaca Vicugna pacos		CAAGGGAGTCAAGAGAGGTGGTAGCAAAAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGAAA
77. Bactrian_camel Camelus bactrianus		CAAGGGAGTCAAGCGAGGTGGTAGCAAAAGAAAATATCGGAAGGGCAGCCTGAAGAGTAGAAA
78. Wild_bacterian_camel Camelus ferus		CAAGGGAGTCAAGCGAGGTGGTAGCAAAAGAAAATATCGGAAGGGCAGCCTGAAGAGTAGAAA
79. Arabian_camel Camelus dromedarius		CAAGGGAGTCAAGCGAGGTGGTAGCAAAAGAAAATATCGGAAGGGCAGCCTGAAGAGTAGAAA
80. Minke_whale Balaenoptera acutorostrata scammoni		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCAGAAGGGCAGTCTGAAGAGTAGAAA
81. Killer_whale Orcinus orca gene		CAAGGGAGTCAGGAGGGGTGGCAGGAAAAGAAAATGCCAGAAGGGCAACCTGAAGACTAGAAA

Site # 63 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
82. Bottlenose_dolphin Tursiops truncatus		CAAGGGAGTCAAGAGAGGTGGCAGGAAAAGAAAATACCAGAAGGGCAACATGAAGAGTAGAAA
83. Beluga_whale Delphinapterus leucas		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCAGAAGGGCAACCTGAAGAGTAGAAA
84. Yangtze_river_dolphin Lipotes vexillifer		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCAGAAGGGCAGCCTGAAGAGTAGCAA
85. Northern_sea_otter Enhydra lutris kenyoni		CAAGGGAGTGAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAAGGAAGCTTGAAGAGTAGGAA
86. Pacific_walrus Odobenus rosmarus divergens		CAAGGGAGTGAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCCTAAAGAGTAGGAA
87. Weddell_seal Leptonychotes weddellii		CAAGGGAGTGAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCCTAAAGAGTAGGAA
88. Hawaiian_monk_seal Neomonachus schauinslandi		CAAGGGAGTGAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCCTAAAGAGTAGGAA
89. Florida_manatee Trichechus manatus latirostris		CAAGGGGGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGTCTGAAGAGTAGAAA
90. Domestic_ferret Mustela putorius furo		CAAGGGAGTGAAGAGAGGTGGCAGCAAGAGAAAATACCGGAAAGGAAGCTTGAAGAGTAGGAA
91. Aardvark Orycteropus afer afer		TAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAGGGGCAGCCTGAAGAGTAGGAA
92. Polar_bear Ursus maritimus		CAAGGGAGTGAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGGAA
93. Pig Sus scrofa		CAAGGGAGTTAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGAAA
94. Dog Canis lupus		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGCGTGAAGAGTAGGAA
95. Domestic_cat Felis catus		CAAGGGAGTCAAGAGAGGGGGCAGCAAAAGAAAATACCGGAAGGGCAGTCCGAAGAGTAGAAA
96. Cheetah Acinonyx jubatus		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGTCTGAAGAGTAGAAA
97. Leopard Panthera pardus		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATACCGGAAGGGCAGTCTGAAGAGTAGAAA
98. Amur_tiger Panthera tigris altaica		CAAGGGAGTCAAGAGAGGTGGCAGTAAAAGAAAATACCGGAAGGGCAGTCTGAAGAGTAGAAA
99. Giant_panda Ailuropoda melanoleuca		CAAGGGAGTGAAGAGAGGTGGCAACAAAAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGGAA
100. Nine-banded_armadillo Dasypus novemcinctus		CAAGGGAGTCAAGAGAGGTGGCAGCAAAAGAAAATATCGGAAGTGTGGCCTGAAGAGTAGAAA
101. Southern_white_rhinocerous Ceratotherium simum simu		CAAGGGAGTCAAGAGAGGTGGCGGCAAAAGAAAATACCGGAAGGGCAGCCTGAAGAGTAGAAA
102. Gray_short_tailed_opossum Monodelphis domestica		CAAGGGGGTGAAAAGAGCTGGTTCTAAAAGGAAATATCGTAAGACTGGGCTGAAGAGCAGAAA
103. Tasmanian_devil Sarcophilus harrisii		TAAGGGGGTCAAAAGAGCTGGAGCTAAAAGGAAATATCGGAAGGCTGGGCTGAAGAGCAGAAA
104. Tammar_wallaby Macropus eugenii		CAAGGGGGTCAAAAGAGCTGGAGCTAAAAGGAAATACCGGAAGGCTGGGCTGAAGAGCAGAAA

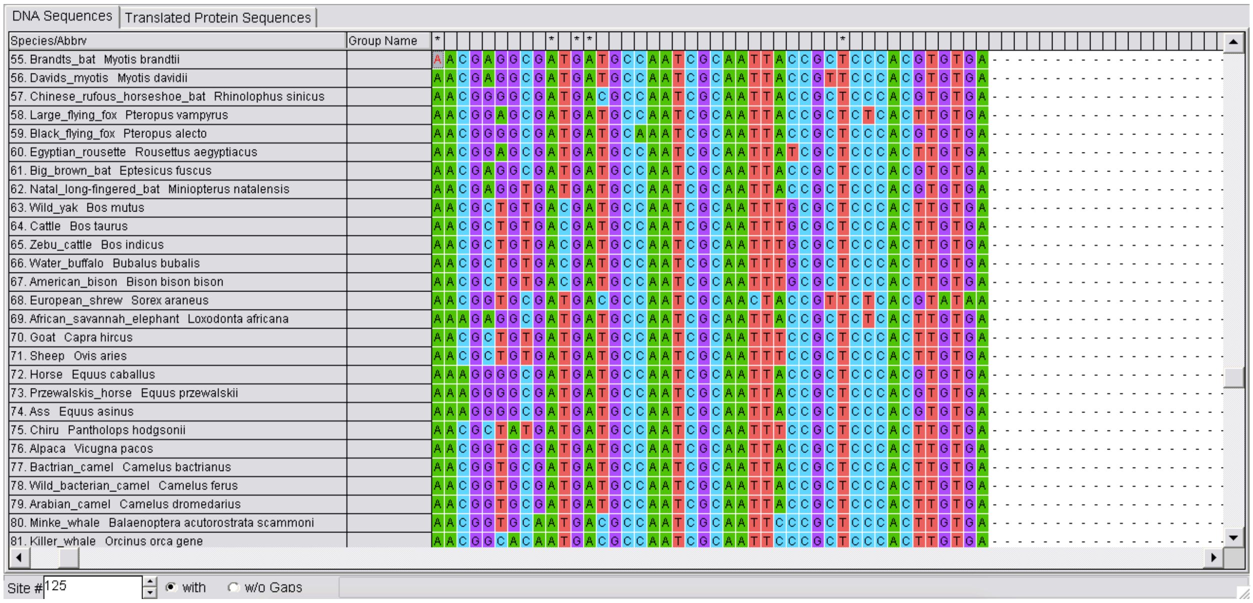
Site # 63 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
1. Human Homo sapiens		AACGGGGCGATGACGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
2. Chimpanzee Pan troglodytes		AACGGGGCGATGACGCCAATCGCAATTACCACTCCCACTTGTGA-------------------
3. Bonobo Pan paniscus		AACGGGGCGATGACGCCAATCGCAATTACCACTCCCACTTGTGA-------------------
4. Gorilla Gorilla gorilla		AACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACA
5. Gorilla Gorilla gorilla predicted mRNA (unaligned)		AACGGGGCGATGACGCCTCTGCCCTGGTACGCTTCACACAGCACCAAGCAGCAACAAGAACA
6. Sumatran_orangutan Pongo abelii		AACGGGGCGATGACGCCAGTCGCAATTACCGCTCCCACTTGTGA-------------------
7. Northern_WC_gibbon Nomascus leucogenys		AACGGGGCGATGACGCGAATCGCAATTACCGGTCCCACTTGTGA-------------------
8. Black_SN_monkey Rhinopithecus bieti		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
9. Golden_SN_monkey Rhinopithecus roxellana		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
10. Angolan_colobus Colobus angolensis palliatus		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
11. Ugandan_red_colobus Piliocolobus tephrosceles		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTAGTGA-------------------
12. Olive_baboon Papio anubis		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
13. Sooty_mangabey Cercocebus atys		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
14. Drill Mandrillus leucophaeus		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
15. Green_monkey Chlorocebus sabaeus		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
16. Southern_PT_macaque Macaca nemestrina		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
17. Rhesus_macaque Macaca mulatta		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
18. CE_macaque Macaca fascicularis		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
19. WH_capuchin Cebus capucinus		AACGGGGCGATGATGCCAATCGCAATTACCGTTCCCACCTATGA-------------------
20. BC_squirrel_monkey Saimiri boliviensis boliviensis		AACGGGGCGATGATGCCAATCGCAATTATCGTTCCCACCTGTGA-------------------
21. NM_night_monkey Aotus nancymaae		AACGGGGCAATGATGCCAATCGCAATTGCCGTTCCCACCTGTGA-------------------
22. Common_marmoset Callithrix jacchus		AACGGGGCGATGATGGCAATCGCAATTACCGTTCCCACCTGTGA-------------------
23. Philippine_tarsier Tarsius syrichta		AACGGAGTGATGACGTCAATCGCAATTGCCGCTCCCATGTGTGA-------------------
24. Gray_mouse_lemur Microcebus murinus		AACGGGGCGATGATGCCAATCGCAATTACCGCTCCCACGTGTGA-------------------
25. Coquerels_sifaka Propithecus coquereli		AACGGGGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
26. Northern_greater_galago Otolemur garnettii		AAAGGGGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
27. Sunda_flying_lemur Galeopterus variegatus		AACGGGGTGATGATGCCAATCGCAGTTACCGCTCCCACATGTGA-------------------

Site # 125 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
28. Chinese_tree_shrew Tupaia chinensis		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
29. House_mouse Mus musculus		AACGGGGCGATGATGCAAGTCGCAATTACCGATCCCACTTGTGA-------------------
30. Ryukyu_mouse Mus caroli		AACGGGGCGATGATGCAAGTCGCAATTACCGATCCCACTTGTGA-------------------
31. Shrew_mouse Mus pahari		AACGGGGCGATGATGCAAGTCGCAACTACCGATCCCACTTGTGA-------------------
32. Prarie_deer_mouse Peromyscus maniculatus bairdii		AACGGGGCGATGATGCAAGTCGCACTTACCGCTCCCACTTGTGA-------------------
33. Prarie_vole Microtus ochrogaster		AACGGGGCGATGACGCAAGTCGCAATTACCGCTCCCACTTGTGA-------------------
34. Norweigan_rat Rattus norvegicus		AACGGGGCGATGATGCAAGTCGCAATTACCGATCCCACTTGTAA-------------------
35. Damara_mole_rat Fukomys damarensis		AACGGGTCAAAGATGCCAATCGCAATTACCGCTCCCACTGTTGA-------------------
36. Upper_Galilee_mountains_blind_mole Nannospalax galili		AAAGGGGCAATGATGCCAGCCGCAATTATGGTTCCCACTTATGA-------------------
37. Ords_kangaroo_rat Dipodomys ordii		AACATGGTGATGATGGCCATCACAAGCATCGCTCCCATTTGTGA-------------------
38. Lesser_Egyptian_jerboa Jaculus jaculus		AGCGGTACGATGACGCCAGTCGCAGCTACCGTTCCCACTTGTGA-------------------
39. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		AACGGGGCGATGATGCCAATCGCAGTTACCGCTCCCACTTGTGA-------------------
40. Chinese_hamster Cricetulus griseus		AACGGGGCGATGATGCAAGTCGCAGTTACCGCTCCCACTTGTGA-------------------
41. Golden_hamster Mesocricetus auratus		AACGGGGCGATGATGCAAGTCGCAGTTACCGCTCCCACTTGTGA-------------------
42. Mongolian_gerbil Meriones unguiculatus		AACGGAGCGATGATGCAAGTCGCAATTACCGCTCCCACTTGTGA-------------------
43. American_beaver Castor canadensis		AACGGGGCGATGACGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
44. Guinea_pig Cavia porcellus		AAAGGAGCGATGACGCCAACCGCAATTTTCGCTCCCATGTTTGA-------------------
45. Long-tailed_chincilla Chinchilla lanigera		AACGGAGCGATGATGCCAATCGCACTTGCCGCTCCCACTTTTGA-------------------
46. Alpine_marmot Marmota marmota marmota		AACGGGGCGATGATGCCAATCGCAGTTACCGCTCCCACTTGTGA-------------------
47. Degu Octodon degus		AACGGGGTGATGATGCCAATCGTACTTATCGCTCCCACATTTGA-------------------
48. Rabbit Oryctolagus cuniculus		AAAGGAGCGATGATGCCAACCGCAATTACCGCTCCCACTTGTGA-------------------
49. American_pika Ochotona princeps		AACGGAGCGATGATGCCAATCGCAATTACCGCTCTCACTTGTGA-------------------
50. Small_Madagascar_hedgehog Echinops telfairi		AACGGGGCGATGATGCCAATCGCAATTACCGCTCACACTTGTGA-------------------
51. Star-nosed_mole Condylura cristata		AACGGTCTGACGATGCCAATCGCAATTACCGCTCCCACTTGTGA-------------------
52. Cape_elephant_shrew Elephantulus edwardii		AACGGGGTGATGATGCCACTCGTAGTCACCGCTCACACTTGTAA-------------------
53. Western_European_hedgehog Erinaceus europaeus		AACGGTGCGATGATGCCAGCCGCAACTACCGCTCCCACCTATGA-------------------
54. Little_brown_bat Myotis lucifugus		AACGAGGCGATGATGCCAATCGCAATTACCGCTCCCACGTGTGA-------------------

Site # 125 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
55. Brandts_bat Myotis brandtii		AACGAGGCGATGATGCCAATCGCAATTACCGCTCCCACGTGTGA
56. Davids_myotis Myotis davidii		AACGAGGCGATGATGCCAATCGCAATTACCGTTCCCACGTGTGA
57. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		AACGGGGCGATGACGCCAATCGCAATTACCGCTCCCACGTGTGA
58. Large_flying_fox Pteropus vampyrus		AACGGAGCGATGATGCCAATCGCAATTACCGCTCTCACTTGTGA
59. Black_flying_fox Pteropus alecto		AACGGGGCGATGATGCAAATCGCAATTACCGCTCCCACGTGTGA
60. Egyptian_rousette Rousettus aegyptiacus		AACGGAGCGATGATGCCAATCGCAATTATCGCTCCCACTTGTGA
61. Big_brown_bat Eptesicus fuscus		AACGAGGCGATGATGCCAATCGCAATTACCGCTCCCACGTGTGA
62. Natal_long-fingered_bat Miniopterus natalensis		AACGAGGTGATGATGCCAATCGCAATTACCGCTCCCACGTGTGA
63. Wild_yak Bos mutus		AACGCTGTGACGATGCCAATCGCAATTTGCGCTCCCACTTGTGA
64. Cattle Bos taurus		AACGCTGTGACGATGCCAATCGCAATTTGCGCTCCCACTTGTGA
65. Zebu_cattle Bos indicus		AACGCTGTGACGATGCCAATCGCAATTTGCGCTCCCACTTGTGA
66. Water_buffalo Bubalus bubalis		AACGCTGTGACGATGCCAATCGCAATTTGCGCTCCCACTTGTGA
67. American_bison Bison bison bison		AACGCTGTGACGATGCCAATCGCAATTTGCGCTCCCACTTGTGA
68. European_shrew Sorex araneus		AACGGTGCGATGACGCCAATCGCAACTACCGTTCTCACGTATAA
69. African_savannah_elephant Loxodonta africana		AAAGAGGCGATGATGCCAATCGCAATTACCGCTCTCACTTGTGA
70. Goat Capra hircus		AACGCTGTGATGATGCCAATCGCAATTTCCGCTCCCACTTGTGA
71. Sheep Ovis aries		AACGCTGTGATGATGCCAATCGCAATTTCCGCTCCCACTTGTGA
72. Horse Equus caballus		AAAGGGGCGATGATGCCAATCGCAATTACCGCTCCCACGTGTGA
73. Przewalskis_horse Equus przewalskii		AAAGGGGCGATGATGCCAATCGCAATTACCGCTCCCACGTGTGA
74. Ass Equus asinus		AAAGGGGCGATGATGCCAATCGCAATTACCGCTCCCACGTGTGA
75. Chiru Pantholops hodgsonii		AACGCTATGATGATGCCAATCGCAATTTCCGCTCCCACTTGTGA
76. Alpaca Vicugna pacos		AACGGTGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
77. Bactrian_camel Camelus bactrianus		AACGGTGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
78. Wild_bacterian_camel Camelus ferus		AACGGTGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
79. Arabian_camel Camelus dromedarius		AACGGTGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
80. Minke_whale Balaenoptera acutorostrata scammoni		AACGGTGCAATGACGCCAATCGCAATTCCCGCTCCCACTTGTGA
81. Killer_whale Orcinus orca gene		AACGGCACAATGACGCCAATCGCAATTCCCGCTCCCACTTGTGA

Site # 125 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
82. Bottlenose_dolphin Tursiops truncatus		AACGGTACAATGACGCCAATCGCAATTCCCGCTCCCACTTGTGA
83. Beluga_whale Delphinapterus leucas		AACGGTACAATGACGCCAATCGCAATTCCCGCTCCCACTTGTGA
84. Yangtze_river_dolphin Lipotes vexillifer		AGCGGTACAATGACGCCAATTGCAATTCCCGCTCCCACTTGTGA
85. Northern_sea_otter Enhydra lutris kenyoni		AACGGGGCGACGATGCCAATCGCAATTACCGCTCCCACTTGTGA
86. Pacific_walrus Odobenus rosmarus divergens		AACGGGGCGATGATGCCAATCGCAATTACCGCTCCCACTTTTGA
87. Weddell_seal Leptonychotes weddellii		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
88. Hawaiian_monk_seal Neomonachus schauinslandi		AACGGGGTGATGATGCCAACCGCAATTACCGCTCCCACTTGTGA
89. Florida_manatee Trichechus manatus latirostris		AACGGGGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
90. Domestic_ferret Mustela putorius furo		AACGGGGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
91. Aardvark Orycteropus afer afer		AACGGGGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
92. Polar_bear Ursus maritimus		AACGGGGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
93. Pig Sus scrofa		AACGGTGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
94. Dog Canis lupus		AACGGGGCGATGACGCCAATCGCAATTACCGCTCCCACTTGTGA
95. Domestic_cat Felis catus		AACGGGGAGATGACTCCAATCGCCATTACCGCTCCCACTTGTGA
96. Cheetah Acinonyx jubatus		AACGGGGAGATGACTCCAATCGCCATTACCGCTCCCACTTGTGA
97. Leopard Panthera pardus		AACGGGGAGATGACTCCAATCGCCATTACCGCTCCCACTTGTGA
98. Amur_tiger Panthera tigris altaica		AACGGGGAGATGACTCCAATCGCCATTACCGCTCCCACTTGTGA
99. Giant_panda Ailuropoda melanoleuca		AACGGGGCGATGATGCCAATCGCAATTACCGCTCCCACTTGTGA
100. Nine-banded_armadillo Dasypus novemcinctus		AACGGGGAGAGGATGCCAGTCGCAATTACCGCTCCCACTTGTGA
101. Southern_white_rhinocerous Ceratotherium simum simu		AACGGGGTGATGATGCCAATCGCAATTACCGCTCCCACGTGTGA
102. Gray_short_tailed_opossum Monodelphis domestica		AGAGAAGTGATGAAGCTCACAGGACTTACCGTTCCAACTTGTGA
103. Tasmanian_devil Sarcophilus harrisii		AAAGAAGTGAGGAAGCTCACAGGACTTACCGTTCCAACTTGTGA
104. Tammar_wallaby Macropus eugenii		AGAGAAGTGAGGAAGCTCACAGGACTTACCGTTCCAACTTGTGA

Site # 125 ● with ○ w/o Gaps

The translated sequences

Species/Abbrv	Group Name	
1. Human Homo sapiens		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
2. Chimpanzee Pan troglodytes		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYHSHL*--------
3. Bonobo Pan paniscus		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYHSHL*--------
4. Gorilla Gorilla gorilla		MSTSRKLKSHGMRRSKSRSPHKGGKRGGSKRKYRKGNPKSRKRGDDASALVRFTQHQAATRTA
5. Gorilla Gorilla gorilla predicted mRNA (unaligned)		MSTSRKLKSHGMRRSKSRSPHKGGKRGGSKRKYRKGNPKSRKRGDDASALVRFTQHQAATRTA
6. Sumatran_orangutan Pongo abelii		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDASRNYRSHL*--------
7. Northern_WC_gibbon Nomascus leucogenys		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
8. Black_SN_monkey Rhinopithecus bieti		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
9. Golden_SN_monkey Rhinopithecus roxellana		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
10. Angolan_colobus Colobus angolensis palliatus		MSTSRKLKSRGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
11. Ugandan_red_colobus Piliocolobus tephrosceles		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSH**-------
12. Olive_baboon Papio anubis		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
13. Sooty_mangabey Cercocebus atys		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
14. Drill Mandrillus leucophaeus		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
15. Green_monkey Chlorocebus sabaeus		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
16. Southern_PT_macaque Macaca nemestrina		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
17. Rhesus_macaque Macaca mulatta		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
18. CE_macaque Macaca fascicularis		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRKGNLKSRKRGDDANRNYRSHL*--------
19. WH_capuchin Cebus capucinus		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRRGSLKSRKRGDDANRNYRSHL*--------
20. BC_squirrel_monkey Saimiri boliviensis boliviensis		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKYRRGSLKSRKRGDDANRNYRSHL*--------
21. NM_night_monkey Aotus nancymaae		MSTSRKLKSHGMRRSKSRSPHKGVKRGGSKRKHQKGSLKSRKRGNDANRNCRSHL*--------
22. Common_marmoset Callithrix jacchus		MSTSRKLKGHGMRRSKSRSPQKGVKRGGSKRKYRRGSLKSRKRGDDGNRNYRSHL*--------
23. Philippine_tarsier Tarsius syrichta		MSNSRKLKGHGMRRGKSRSPHKGVKKGGNKRKYRKSSMKSRKRSDDVNRNCRSHV*--------
24. Gray_mouse_lemur Microcebus murinus		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHV*--------
25. Coquerels_sifaka Propithecus coquereli		MSTSRRLKSHGMRRGKNRAPHKGVKRGGNKRKYRKGSLKSRKRGDDANRNYRSHL*--------
26. Northern_greater_galago Otolemur garnettii		MTTSRKFKSHGMRRGKNRSPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHL*--------
27. Sunda_flying_lemur Galeopterus variegatus		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRSYRSHM*--------

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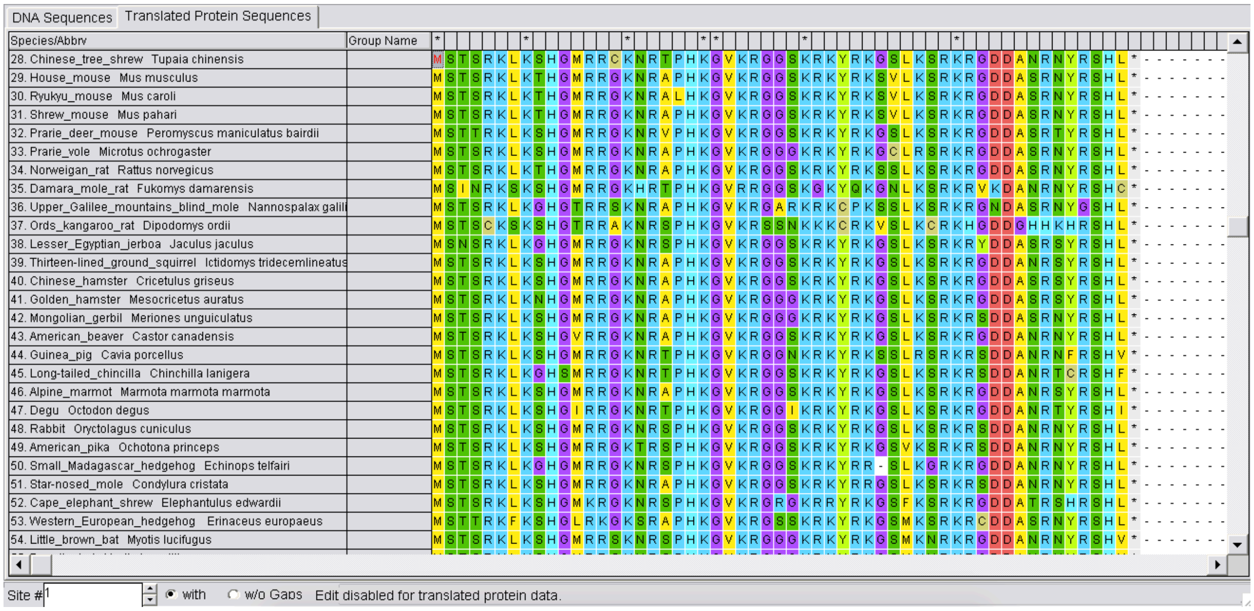

Species/Abbrv	Group Name	
28. Chinese_tree_shrew Tupaia chinensis		MSTSRKLKSHGMRRCKNRTPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHL*--------
29. House_mouse Mus musculus		MSTSRKLKTHGMRRGKNRAPHKGVKRGGSKRKYRKSVLKSRKRGDDASRNYRSHL*--------
30. Ryukyu_mouse Mus caroli		MSTSRKLKTHGMRRGKNRALHKGVKRGGSKRKYRKSVLKSRKRGDDASRNYRSHL*--------
31. Shrew_mouse Mus pahari		MSTSRKLKTHGMRRGKNRAPHKGVKRGGSKRKYRKSVLKSRKRGDDASRNYRSHL*--------
32. Prarie_deer_mouse Peromyscus maniculatus bairdii		MSTTRKLKSHGMRRGKNRVPHKGVKRGGSKRKYRKGSLKSRKRGDDASRTYRSHL*--------
33. Prarie_vole Microtus ochrogaster		MSTSRKLKSHGMRRGKNRAPHKGVKRGGGKRKYRKGCLRSRKRGDDASRNYRSHL*--------
34. Norweigan_rat Rattus norvegicus		MSTSRKLKTHGMRRGKNRAPHKGVKRGGSKRKYRKSSLKSRKRGDDASRNYRSHL*--------
35. Damara_mole_rat Fukomys damarensis		MSINRKSKSHGMRRGKHRTPHKGVRRGGSKGKYQKGNLKSRKRVKDANRNYRSHC*--------
36. Upper_Galilee_mountains_blind_mole Nannospalax galili		MSTSRKLKGHGTRRSKNRAPHKGVKRGARKRKCPKSSLKSRKRGNDASRNYGSHL*--------
37. Ords_kangaroo_rat Dipodomys ordii		MSTSCKSKSHGTRRAKNRSPHKGVKRSSNKKKCRKVSLKCRKHGDDGHHKHRSHL*--------
38. Lesser_Egyptian_jerboa Jaculus jaculus		MSNSRKLKGHGMRRGKNRSPHKGVKRGGSKRKYRKGSLKSRKRYDDASRSYRSHL*--------
39. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRSYRSHL*--------
40. Chinese_hamster Cricetulus griseus		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDASRSYRSHL*--------
41. Golden_hamster Mesocricetus auratus		MSTSRKLKNHGMRRGKNRAPHKGVKRGGGKRKYRKGSLKSRKRGDDASRSYRSHL*--------
42. Mongolian_gerbil Meriones unguiculatus		MSTSRKLKSHGMRRGKNRAPHKGVKRGGGKRKYRKGSLKSRKRSDDASRNYRSHL*--------
43. American_beaver Castor canadensis		MSTSRKLKSHGVRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHL*--------
44. Guinea_pig Cavia porcellus		MSTSRKLKSHGMRRGKNRTPHKGVKRGGNKRKYRKSSLRSRKRSDDANRNFRSHV*--------
45. Long-tailed_chincilla Chinchilla lanigera		MSTSRKLKGHSMRRGKNRTPHKGVKRGGSKRKYRKGSLKSRKRSDDANRTCRSHF*--------
46. Alpine_marmot Marmota marmota marmota		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRSYRSHL*--------
47. Degu Octodon degus		MSTSRKLKSHGIRRGKNRTPHKGVKRGGIKRKYRKGSLKSRKRGDDANRTYRSHI*--------
48. Rabbit Oryctolagus cuniculus		MSTSRKLKSHGMRRGKNRSPHKGVKRGGSKRKYRKGSLKSRKRSDDANRNYRSHL*--------
49. American_pika Ochotona princeps		MSTSRKLKSHGMRRGKTRSPHKGVKRGGSKRKYRKGSVKSRKRSDDANRNYRSHL*--------
50. Small_Madagascar_hedgehog Echinops telfairi		MSTSRKLKGHGMRRGKNRSPHKGVKRGGSKRKYRR-SLKGRKRGDDANRNYRSHL*--------
51. Star-nosed_mole Condylura cristata		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRRGSLKSRKRSDDANRNYRSHL*--------
52. Cape_elephant_shrew Elephantulus edwardii		MSTSRKLKSHGMKRGKNRSPHKGVKRGRGKRRYRKGSFKSRKRGDDATRSHRSHL*--------
53. Western_European_hedgehog Erinaceus europaeus		MSTTRKFKSHGLRKGKSRAPHKGVKRGSSKRKYRKGSMKSRKRCDDASRNYRSHL*--------
54. Little_brown_bat Myotis lucifugus		MSTSRKLKSHGMRRSKNRSPHKGVKRGGGKRKYRKGSMKNRKRGDDANRNYRSHV*--------

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Species/Abbr	Group Name	
55. Brandts_bat Myotis brandtii		MSTSRKLKSHGMRRSKNRSPHKGVKRGGGKRKYRKGSMKNRKRGDDANRNYRSHV*--------
56. Davids_myotis Myotis davidii		MSTSRKLKSHGMRRSKNRSPHKGVKRGGGKRKYRKGSLKNRKRGDDANRNYRSHV*--------
57. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		MSTSRKLKSHGIRRGKNRSPHKGVKRSGSKRKYRKGSLKSRKRGDDANRNYRSHV*--------
58. Large_flying_fox Pteropus vampyrus		MSTSRKLKSHGMRRGKNRSPHKGVKRSGTKRKYRKGSLKSRKRSDDANRNYRSHL*--------
59. Black_flying_fox Pteropus alecto		MSTNRKLKSHGIRRGKNRSPHKGVKRSVCKRKYRKGGLKGRKRGDDANRNYRSHV*--------
60. Egyptian_rousette Rousettus aegyptiacus		MSTSRKLKSHGMRRGKNRSPHKGVKRSGTKRKYRKGSLKSRKRSDDANRNYRSHL*--------
61. Big_brown_bat Eptesicus fuscus		MSTSRKLKSHGMRRSKNRSPHKGVKRGGSKRKYRKGGLKNRKRGDDANRNYRSHV*--------
62. Natal_long-fingered_bat Miniopterus natalensis		MSTSRKLKSHGMRRSKNRSPHKGVKRGGSKRKYRKGSLKNRKRGDDANRNYRSHV*--------
63. Wild_yak Bos mutus		MSTSRKLKSQGMRRGKNRTPHKGVKRSGSKRKYRESSLKSRKRCDDANRNLRSHL*--------
64. Cattle Bos taurus		MSTSRKLKSQGMRRGKNRTPHKGVKRSGSKRKYRKSSLKSRKRCDDANRNLRSHL*--------
65. Zebu_cattle Bos indicus		MSTSRKLKSQGMRRGKNRTPHKGVKRSGSKRKYRKSSLKSRKRCDDANRNLRSHL*--------
66. Water_buffalo Bubalus bubalis		MSTSRKLKSQGMRRGKNRTPHKGVKRGGSKRKYRKSSLKSRKRCDDANRNLRSHL*--------
67. American_bison Bison bison bison		MSTSRKLKSQGMRRGKNRTPHKGVKRSGSKRKYRKSSLKSRKRCDDANRNLRSHL*--------
68. European_shrew Sorex araneus		MSTSRKLKSHGMRKGKNRTPHKGVKRGSSKRKYRKASMKSRKRCDDANRNYRSHV*--------
69. African_savannah_elephant Loxodonta africana		MSTSRKLKSHGMRRGKNRSPHKGVKRGSSKRKYRKGSLKSRKRGDDANRNYRSHL*--------
70. Goat Capra hircus		MSTSRKLKSQGMRRGKNRTPHKGVKRGGSKRKYRKSSLKSRKRCDDANRNFRSHL*--------
71. Sheep Ovis aries		MSTSRKLKSQGTRRGKNRTPHKGVKRGCSKRKYRKSSLKSRKRCDDANRNFRSHL*--------
72. Horse Equus caballus		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHV*--------
73. Przewalskis_horse Equus przewalskii		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHV*--------
74. Ass Equus asinus		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHV*--------
75. Chiru Pantholops hodgsonii		MSTSRKLKSQGMRRGKNRTPHKGVKRGGSKRKYRKSSLKSRKRYDDANRNFRSHL*--------
76. Alpaca Vicugna pacos		MSTSRKFKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRCDDANRNYRSHL*--------
77. Bactrian_camel Camelus bactrianus		MSTSRKFKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRCDDANRNYRSHL*--------
78. Wild_bacterian_camel Camelus ferus		MSTSRKFKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRCDDANRNYRSHL*--------
79. Arabian_camel Camelus dromedarius		MSTSRKFKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRCDDANRNYRSHL*--------
80. Minke_whale Balaenoptera acutorostrata scammoni		MATSRKLKSHGMKKGKNRGPHKGVKRGGSKRKYQKGSLKSRKRCNDANRNSRSHL*--------
81. Killer_whale Orcinus orca		MSTSRKLKSHNMRKGKNQAPHKGVRRGGRKRKCQKGNLKTRKRHNDANRNSRSHL*--------

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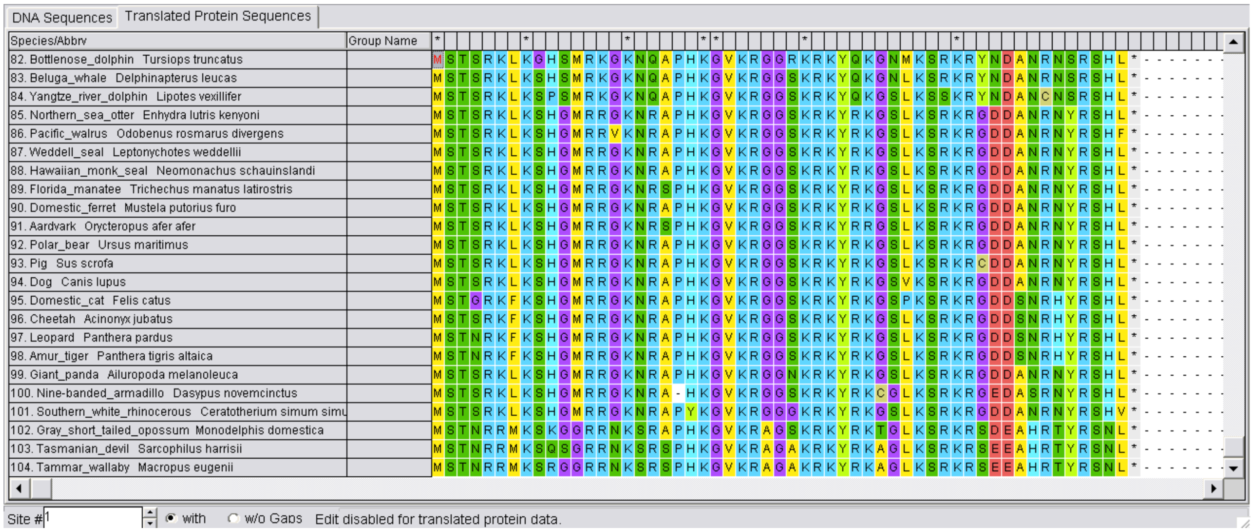
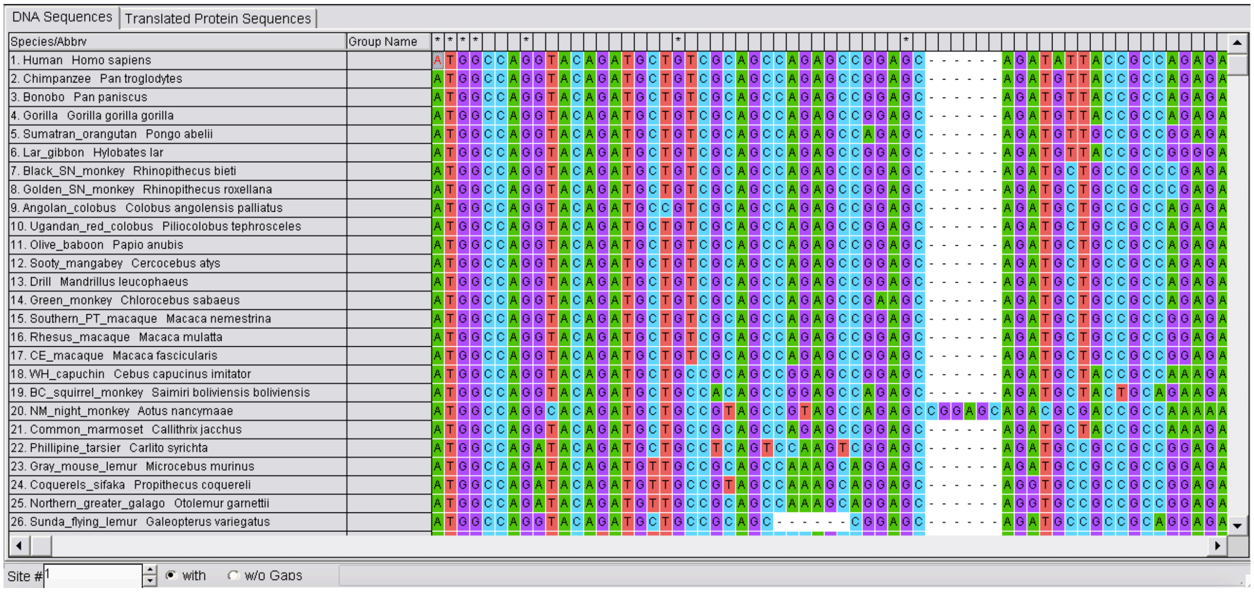


Species/Abbr	Group Name	
82. Bottlenose_dolphin Tursiops truncatus		MSTSRKLKGHSMRKGKNQAPHKGVKRGGRKRKYQKGNMKSRKRYNDANRNSRSHL*--------
83. Beluga_whale Delphinapterus leucas		MSTSRKLKSHSMRKGKNQAPHKGVKRGGSKRKYQKGNLKSRKRYNDANRNSRSHL*--------
84. Yangtze_river_dolphin Lipotes vexillifer		MSTSRKLKSPSMRKGKNQAPHKGVKRGGSKRKYQKGSLKSSKRYNDANCNSRSHL*--------
85. Northern_sea_otter Enhydra lutris kenyoni		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHL*--------
86. Pacific_walrus Odobenus rosmarus divergens		MSTSRKLKSHGMRRVKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHF*--------
87. Weddell_seal Leptonychotes weddellii		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHL*--------
88. Hawaiian_monk_seal Neomonachus schauinslandi		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHL*--------
89. Florida_manatee Trichechus manatus latirostris		MSTSRKLKSHGMRRGKNRSPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHL*--------
90. Domestic_ferret Mustela putorius furo		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHL*--------
91. Aardvark Orycteropus afer afer		MSTSRKLKSHGMRRGKNRSPHKGVKRGGSKRKYRRGSLKSRKRGDDANRNYRSHL*--------
92. Polar_bear Ursus maritimus		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDANRNYRSHL*--------
93. Pig Sus scrofa		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRCDDANRNYRSHL*--------
94. Dog Canis lupus		MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSVKSRKRGDDANRNYRSHL*--------
95. Domestic_cat Felis catus		MSTGRKFKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSPKSRKRGDDSNRHYRSHL*--------
96. Cheetah Acinonyx jubatus		MSTSRKFKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDSNRHYRSHL*--------
97. Leopard Panthera pardus		MSTNRKFKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDSNRHYRSHL*--------
98. Amur_tiger Panthera tigris altaica		MSTNRKFKSHGMRRGKNRAPHKGVKRGGSKRKYRKGSLKSRKRGDDSNRHYRSHL*--------
99. Giant_panda Ailuropoda melanoleuca		MSTSRKLKSHGMRRGKNRAPHKGVKRGGNKRKYRKGSLKSRKRGDDANRNYRSHL*--------
100. Nine-banded_armadillo Dasypus novemcinctus		MSTSRKLKSHGMRRGKNRA-HKGVKRGGSKRKYRKCGLKSRKRGEDASRNYRSHL*--------
101. Southern_white_rhinocerous Ceratotherium simum simu		MSTSRKLKSHGMRRGKNRAPYKGVKRGGGKRKYRKGSLKSRKRGDDANRNYRSHV*--------
102. Gray_short_tailed_opossum Monodelphis domestica		MSTNRRMKSKGGRRNKSRAPHKGVKRAGSKRKYRKTGLKSRKRSDEAHRTYRSNL*--------
103. Tasmanian_devil Sarcophilus harrisii		MSTNRRMKSQSGRRNKSRSPHKGVKRAGAKRKYRKAGLKSRKRSEEAHRTYRSNL*--------
104. Tammar_wallaby Macropus eugenii		MSTNRRMKSRGGRRNKSRSPHKGVKRAGAKRKYRKAGLKSRKRSEEAHRTYRSNL*--------

Site # 1 ● with ○ w/o Gaps Edit disabled for translated protein data.

Appendix Z) Alignment of mammalian *Prm1* coding exon sequences



Species/Abbrv	Group Name	**** * * *
1. Human Homo sapiens		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATATTACCGCCAGAGA
2. Chimpanzee Pan troglodytes		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGTTACCGCCAGAGA
3. Bonobo Pan paniscus		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGTTACCGCCAGAGA
4. Gorilla Gorilla gorilla gorilla		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGTTACCGCCAGAGA
5. Sumatran_orangutan Pongo abelii		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCAGAGC------AGATGTTGCCGCCGGAGA
6. Lar_gibbon Hylobates lar		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGTTACCGCCGGGGA
7. Black_SN_monkey Rhinopithecus bieti		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCCGAGA
8. Golden_SN_monkey Rhinopithecus roxellana		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCCGAGA
9. Angolan_colobus Colobus angolensis palliatus		ATGGCCAGGTACAGATGCCGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCAGAGA
10. Ugandan_red_colobus Piliocolobus tephrosceles		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCAGAGA
11. Olive_baboon Papio anubis		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCAGAGA
12. Sooty_mangabey Cercocebus atys		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCAGAGA
13. Drill Mandrillus leucophaeus		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCAGAGA
14. Green_monkey Chlorocebus sabaeus		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGAAGC------AGATGCTGCCGCCAGAGA
15. Southern_PT_macaque Macaca nemestrina		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCGGAGA
16. Rhesus_macaque Macaca mulatta		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCGGAGA
17. CE_macaque Macaca fascicularis		ATGGCCAGGTACAGATGCTGTCGCAGCCAGAGCCGGAGC------AGATGCTGCCGCCGGAGA
18. WH_capuchin Cebus capucinus imitator		ATGGCCAGGTACAGATGCTGCCGCAGCCGGAGCCGGAGC------AGATGCTACCGCCAAAGA
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		ATGGCCAGGTACAGATGCTGCCACAGCCGGAGCCAGAGC------AGATGCTACTGCAGAAGA
20. NM_night_monkey Aotus nancymaae		ATGGCCAGGCACAGATGCTGCCGTAGCCGTAGCCAGAGCCGGAGCAGACGCGACCGCCAAAAA
21. Common_marmoset Callithrix jacchus		ATGGCCAGGTACAGATGCTGCCGCAGCCAGAGCCGGAGC------AGATGCTACCGCCAAAGA
22. Phillipine_tarsier Carlito syrichta		ATGGCCAGATACAGATGCTGCCTCAGTCCAAGTCGGAGC------AGATGCCGCCGCCGGAGA
23. Gray_mouse_lemur Microcebus murinus		ATGGCCAGATACAGATGTTGCCGCAGCCAAAGCAGGAGC------AGATGCCGCCGCCGGAGA
24. Coquerels_sifaka Propithecus coquereli		ATGGCCAGATACAGATGTTGCCGTAGCCAAAGCAGGAGC------AGGTGCCGCCGCCGGAGA
25. Northern_greater_galago Otolemur garnettii		ATGGCCAGATACAGATGTTGCCGCAGCCAAAGCAGGAGC------AGGTGCCGCCGCCGGAGA
26. Sunda_flying_lemur Galeopterus variegatus		ATGGCCAGGTACAGATGCTGCCGCAGC------CGGAGC------AGATGCCGCCGCAGGAGA

Species/Abbrv	Group Name	**** * * *
27. Chinese_tree_shrew Tupaia chinensis		ATGGCCAGGTACATATGTTGCCGCAGCCCCAGCCGGAGC------AGATGCCGCCGCCGGAGA
28. House_mouse Mus musculus		ATGGCCAGATACCGATGCTGCCGCAGCAAAAGCAGGAGC------AGATGCCGCCGTCGCAGG
29. Ryukyu_mouse Mus_caroli		ATGGCCAGATACCGATGCTGCCGCAGCAAAAGCAGGAGC------AGATGCCGCCGTCGCAGG
30. Shrew_mouse Mus_pahari		ATGGCCAGGTACCGATGCTGCCGCAGCAAAAGCAGGAGC------AGATGCCGCCGTCGCAGG
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		ATGGCCAGATACCGATGCTGCCGCAGCAAAAGCAGGAGC------AGATGCCGCCGCCGCAGG
32. Norweigan_rat Rattus norvegicus		ATGGCCAGATACCGATGCTGCCGCAGCAAAAGCAGGAGC------AGATGCCGCCGCCGCAGG
33. Ords_kangaroo_rat Dipodomys ordii		ATGGCCAGATAC---TGCTGCCGCAGCCGCAGCCGGAGC------AGATGCCGC---CGGAGG
34. Prarie_vole Microtus ochrogaster		ATGGCCAGATACCGC---TGCCGCAGCAAAAGCAGGAGC------AGATCCCGCCGCAGCAGG
35. Mongolian_gerbil Meriones unguiculatus		ATGGCCAGATACCGATGCTGCCGCAGCAAAAGCAGGAGC------AGATGCCGCCGCCGCAGG
36. Golden_hamster Mesocricetus auratus		ATGGCCAGATACCGATGCTGCCGCAGCAAAAGCAGGAGC------AGATGCCGCCGCCGCAGG
37. Chinese_hamster Cricetulus griseus		ATGGCCAGATACCGATGCTGCCGCAGCAAAAGCAGGAGC------AGATGCCGCCGCCGCAGG
38. Damara_mole_rat Fukomys damarensis		ATGGCCAGACACAGATGCTGCCGCAGCCCAAGCCGGAGC------AGATGCCGCCGCCGCAGA
39. Lesser_Egyptian_jerboa Jaculus jaculus		ATGGCCAGATACAGATGCTGCCGCAGCCCAAGCAGGCGC------AGATGCCGCCGTCGCAGG
40. American_beaver Castor canadensis		ATGGGCAGATAC---TGCTGCCGTAGCACAAGCCGGAGC------AGATGTCGCCGCCGCCGC
41. Degu Octodon degus		ATGGCCAGATACAGATGCTGCCGCAGCCCAAGCCGGAGC------AGATGCCGCCGCCGTAGA
42. Domestic_guinea_pig Cavia porcellus		ATGGCCAGATACAGATGCTGCCGCAGCCCAAGCCGGAGC------AGGTGCCGCCGCCGCAGA
43. Long_tailed_chinchilla Chinchilla langiera		ATGGCCAGATACAGATGCTGCCGCAGCCCAAGCCGGAGC------AGATGCCGCCGCCGCAGA
44. Alpine_marmot Marmota marmota marmota		ATGGCACGATACACCTGCTGCCGCGCCCCATGCCGGAGC------AGATGCCGCCGCCAGAGA
45. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		ATGGCACGATACATATGCTGCCGCGCCCCCTGCCGCAGC------AGATGCCGCCGCCGCAGA
46. American_pika Ochotona princeps		ATGGTCAGATACAGATGCTGCCGCAGCCAGAGCCGGAGC------AGATGCCGCCGCCGGAGA
47. Rabbit Oryctolagus cuniculus		ATGGTCAGATACAGATGCTGCCGCAGCCAGAGCCGGAGC------AGATGCCGCCGCCGGAGA
48. Cattle Bos taurus		ATGGCCAGATACCGATGCTGCCTCACCCATAGCGGGAGC------AGATGCCGCCGCCGCCGC
49. American_bison Bison bison bison		ATGGCCAGATACCGATGCTGCCTCACCCATAGCGGGAGC------AGATGCCGCCGCCGCCGC
50. Water_buffalo Bubalus bubalis		ATGGCCAGATACCAATGCTGCCTCACCCATAGCCGGAGC------AGATGCCGCCGCCGCCGC
51. Minke_whale Balaenoptera acutorostrata		ATGGCCAGAAACAGTTGTTGCCGCAGCCCGAGCCGGAGC------AGACGCCGCCGCCCGAGA
52. Killer_whale Orcinus orca		ATGGCCAGAAACAGATGCCGC---AGCCCGAGCCAGAGC------AGATGCCGCCGCCCGAGG

Species/Abbrv	Group Name	
53. Bottlenose_dolphin Tursiops truncatus		ATGGCCAGAAACAGATGCCGC---AGCCCGAGCCAGAGC------AGATGCCGCCGCCCGAGG
54. Pig Sus scrofa		ATGGCCAGATACAGATGTTGCCGCAGCCATAGCCGGAGC------AGGTGCCGCCCCCGAAGA
55. Wild_bactrian_camel Camelus ferus		ATGGCCAGATACAGATGTTGCCGCAGCCATAGCCGGAGC------AGATGCCGCCCCCGGAGA
56. Domestic_cat Felis catus		ATGGCCAGATACAGATGCTGCCGCAGCCACAGCAGGAGC------AGGTGCCGTCGCCGCAGA
57. Domestic_ferret Mustela putorius furo		ATGGCCAGATACATATGCTGCCGTAGCCACAGCCGGAGC------AGATGCCGCCGCCGGAGA
58. Northern_sea_otter Enhydra lutris kenyoni		ATGGCCAGATACATATGCTGCCGTAGCCACAGCCGGAGC------AGATGCCGCCGCCGGAGA
59. Weddell_seal Leptonychotes weddellii		ATGGCCAGATACAGATGCAGCCGTAGCCATAGCCGGAGC------AGATGCCGCCGCCGGAGA
60. Giant_panda Ailuropoda melanoleuca		ATGGCCAGATACAGATGCTGTCGGAGCCAGAGCCGGAGC------AGGTGCCGCCGCCGGAGA
61. Dog Canis lupus familiaris		ATGGCCAGATACCGATGCTGCCGCAGCCAAAGCCGGAGC------AGATGCCGCCGCCGGAGA
62. Horse Equus caballus		ATGGCCAGATACAGATGCTGCCGCAGCCAGAGCCAGAGC------AGATGCCGTCGCCGCCGG
63. Ass Equus asinus		ATGGCCAGATACAGATGCTGCCGCAGCCAGAGCCAGAGC------AGATGCCGTCGCCGCCGG
64. Southern_white_rhinocerous Ceratotherium simum simur		ATGGCTAGATACAGATGCTGCCGCAGC------CAAAGC------AGGTGCCGCCGCCAGCGA
65. Little_brown_bat Myotis lucifugus		ATGGCCAGATACAGATGCTGCCGCAGC------CGGAGC------AGATGCCGCCGCCGGAGA
66. Star-nosed_mole Condylura cristata		ATGGCCAGATACAGATGCTGCCGGAGCCACAGCCGCAGC------AGGTGCCGCCGCCGCCGG
67. African_savannah_elephant Loxodonta africana		ATGGCCAGATACAGATGCTGCCGCAGCCGCAGCCGAAGC------AGATGCCGCAGTCGGAGA
68. Florida_manatee Trichechus manatus latirostris		ATGGCCAGATACAGTTGCTGCCGCAGCCGCAGCCGGAGC------AGATGCCGCCGCCGCCGG
69. Aardvark Orycteropus afer afer		ATGGCCAGGTACAGATGCTGTCGCAGCCGCAGCCGGAGC------AGATGCCGCCAACACCGG
70. Gray_short_tailed_opossum Monodelphis domestica		ATGGCAAGATATAGAAGACGC---AGCAGGAGCCGGAGTAGGAGCAGATATGGACGCCGGAGG
71. Platypus Ornithorhynchus anatinus		ATGGCAAGATTCAGGCGGAGCCGCAGC------CGCAGCCGCAGCCTCTACCGTCGCCGGCGG
72. Echidna Tachyglossus aculeatus		ATGGCAAGATTCAGGCCCAGCCGGAGC------CGCAGCCGCAGCCTGTACCGTCGCCGGCGG

Site # 1 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
1. Human Homo sapiens		CAAAGA------AGTCGC---AGACGAAGGAGGCGGAGCTGCCAGACACGGAGGAGAGCCATG
2. Chimpanzee Pan troglodytes		CAAAGA------AGTCGC---AGACGAAAGAGGCAGAGCTGCCAGACACAGAGGAGAGCCATG
3. Bonobo Pan paniscus		CGA---------AGTCGC---AGACGAAAGAGGCAGAGCTGCCAGACACAGAGGAGAGCCATG
4. Gorilla Gorilla gorilla gorilla		CAAACA------AGTCGC---AGACGAAGGAGGCGGAGCTGCCAGACACAGAGGAGAGCCATG
5. Sumatran_orangutan Pongo abelii		CAAAGA------TGTCAC---AGACGAAGGAGGCGTTGCTGCCAGACACGGAGGAGGGCCATG
6. Lar_gibbon Hylobates lar		CAAAGA------AGTCGC---AGACGAAGGAGGCGGAGCTGCCAGACACGCAGGAGAGCCATG
7. Black_SN_monkey Rhinopithecus bieti		CGAAGA------TGTCGC---AGACGAAGGAGGCGGAGCTGCCGGGCACGGAGGAGAGCCATG
8. Golden_SN_monkey Rhinopithecus roxellana		CGAAGA------TGTCGC---AGACGAAGGAGGCGGAGCTGCCGGGCACGGAGGAGAGCCATG
9. Angolan_colobus Colobus angolensis palliatus		CGAAGA------TGTCGC---AGACGAAGAAGGCAGAGATTCCGGGCACGGAAGAGAGCCATG
10. Ugandan_red_colobus Piliocolobus tephrosceles		CAAAGA------TGTCGC---AGACGAAGGAGGCAGAGATGCCGGGCACGGAGGAGAGCCATG
11. Olive_baboon Papio anubis		CGAAGA------TGTCGC---AGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATG
12. Sooty_mangabey Cercocebus atys		CGAAGA------TGTCGC---AGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATG
13. Drill Mandrillus leucophaeus		CGAAGA------TGTCGC---AGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATG
14. Green_monkey Chlorocebus sabaeus		CGAAGA------TGTCGC---AGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATG
15. Southern_PT_macaque Macaca nemestrina		CGAAGA------TGTCGC---AGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATG
16. Rhesus_macaque Macaca mulatta		CGAAGA------TGTCGC---AGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATG
17. CE_macaque Macaca fascicularis		CGAAGA------TGTCGC---AGACGAAGGAGGCGGAGATGCCGGGCACGGAGGAGAGCCATG
18. WH_capuchin Cebus capucinus imitator		CGAAGA------TGTCGC---AGACGAAGGAGGCGG---TGCCGGAGCCGGAGA---GCCAGG
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		CGAAGA------TGTGGC---ACACGAAGGAGGTGGTGCTGCCGGAGACAGAGA---GCCACG
20. NM_night_monkey Aotus nancymaae		CGAAGA------TGTCGC---ACACCAAGGAGGCGGAGTTGCCGGAGACGGACA---GCCAGG
21. Common_marmoset Callithrix jacchus		CGAAGA------GGTCGC---AGACGAAGGAGGCGGAGCTGCCGGAGACGGAGG---GCCAGC
22. Phillipine_tarsier Carlito syrichta		CGCAGG------TGTCGC---AGGCGGAGGAGGCCTTGCTGTCCCAGGCGCAGA---ACCAGG
23. Gray_mouse_lemur Microcebus murinus		CGAAGA------TGTCGC---AGACGGCGAAGGCGATGCTGTCGGAGAAGGAGGAGG------
24. Coquerels_sifaka Propithecus coquereli		CAAAGA------TGTCGC---AGACGGCGGAGGCGAAGCTGTCGGAGAAGGAGGAGG------
25. Northern_greater_galago Otolemur garnettii		CGAAGA------TGTCGC---AGACGAAGAAGGCGATGCTGTCGAAGACGGAGGAGG------
26. Sunda_flying_lemur Galeopterus variegatus		CGA---------AGTTGC---AGACGAAGGAGGCGA---TGTCGTAGACGAAGA---GCCAGG

Site # 64 ● with ○ w/o Gaps

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Species/Abbrv                                              Group Name
27. Chinese_tree_shrew  Tupaia chinensis                              CGAAGA------AGTCAC---AGACGGAGGAGGCGATGCTATCGCAGGCGGCGACGGGCAAGG
28. House_mouse  Mus musculus                                         CGAAGA------TGTCGC---AGACGGAGGAGGCGATGCTGCCGGCGGAGGAGGCGA------
29. Ryukyu_mouse  Mus_caroli                                          CGAAGA------TGTCGC---AGACGGAGGAGGCGATGCTGCCGGCGGAGGAGGCGA------
30. Shrew_mouse  Mus_pahari                                           CGAAGA------TGTCGC---AGACGGAGGAGGCGATGCTGCCGGCGGAGGAGGCAA------
31. Prarie_deer_mouse  Peromyscus maniculatus bairdii                  CGGAGA------TGTCGC---AGACGGAGGAGGCGATGCTGCCGGCGGAGGAGGCGA------
32. Norweigan_rat  Rattus norvegicus                                  CGAAGA------TGTCGC---AGACGGAGGAGGCGGTGCTGCAGGCGGAGGCGGCGAATCCTA
33. Ords_kangaroo_rat  Dipodomys ordii                                CGGAGA------TGCCGCAGACGCAGGAGGAGA---TGCTGCCGCAGACGCAGGAGA------
34. Prarie_vole  Microtus ochrogaster                                 CGGAGA------TGTCGC---AGACGGAGGAGGCGATGCTGCCGGAGGAGGAGGCGA------
35. Mongolian_gerbil  Meriones unguiculatus                           CGAAGA------TGTCGC------AGACGGAGGCGATGCTGCCGGAGGAGGAGGAGA------
36. Golden_hamster  Mesocricetus auratus                              CGGCGA------TGTCGCAGACGGAGGAGGCGA---TGCTGCCGGAGGAGGAGGCGA------
37. Chinese_hamster  Cricetulus griseus                               CGAAGA------TGTCGCAGACGGAGAAGGCGA---TGCTGCCGGAGGAGGAGGCGA------
38. Damara_mole_rat  Fukomys damarensis                               CCCAGA------TGCCAGAGACGGAGGAGGCCC---TCCCACCGC------AGAGGA------
39. Lesser_Egyptian_jerboa  Jaculus jaculus                           CGCAGA------TGCCGCAGACGGAGGCGG------TGCTGTCGGCGGAGGCGA---GCCAGG
40. American_beaver  Castor canadensis                                AGGCGGAGA---TGTCGCAGAGGAAGGAGACAG---TGCTGTCGGAGGCGGAGGCGGGCCAGG
41. Degu  Octodon degus                                               CGGAGA------TGCCATAGACGAAGGAGGCGG---TGCCATCGGAGACAGAGA---------
42. Domestic_guinea_pig  Cavia porcellus                              CGGAGA------TTCTATAGACGAAGGAGGCGG---TGCCATCGGAGACGGAGACAC---CTA
43. Long_tailed_chinchilla  Chinchilla langiera                       CGGAGA------TGCCATAGACGAAGGAGGCGG---TGCTATCGGAGACGGAGA---------
44. Alpine_marmot  Marmota marmota marmota                            CGAAGG------AGTCGCAGACGGAGGAGGCGT---TGCTGCCGGAGGCGGAGAGCC---TTA
45. Thirteen-lined_ground_squirrel  Ictidomys tridecemlineatus        CGGAGA------TGTCGCCGACGGAGGAGGCGT---TGCTGCCGCAGGCGGAGAGCC---TTA
46. American_pika  Ochotona princeps                                   CGAAGA------TGCCGACGCAGAAGGCGG------TGCTGCCGGAGGCGAAGAGTCAGG---
47. Rabbit  Oryctolagus cuniculus                                     CGGAGA------TGCCGCAGACGCAGGAGGCGG---TGCTGCCAGAGGCGAAGAGTCAGG---
48. Cattle  Bos taurus                                                CGAAGAAGA---TGTCGCAGACGAAGGAGGCGC---TTTGGTCGGAGGCGCAGGAGGAGAGCA
49. American_bison  Bison bison bison                                  CGAAGAAGA---TGTCGCAGACGAAGGAGGCGC---TTTTGTCGGAGGCGCAGGAGGAGA---
50. Water_buffalo  Bubalus bubalis                                    CGAAGAAGA---TGTGGCAGACGAAGGAGGCGC---TTTTGTCGGAGGCGCAGGAGGAGA---
51. Minke_whale  Balaenoptera acutorostrata                           CAAAGA------TGTCGCAGCCAGAGGAGGCGG---TGCTGCCGGAGGCGCAGGAGA------
52. Killer_whale  Orcinus orca                                        CGCAGA------TGTCGC---AGGAGGATACGG---TGCTGCCGGAGGCAGAGGAGAGCCGCA

Site #64    ● with    ○ w/o Gaps
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Species/Abbrv                                              Group Name
53. Bottlenose_dolphin  Tursiops truncatus                            CGCAGA------TGTCGC---AGGAGGAGACTG---TGCTGCCGGAGGCGGAGGAGAGCCGCA
54. Pig  Sus scrofa                                                   CGAAGA------TGTCGCAGACGAAGGAGGCGA---TGTTGTCCGAGGCGGAGGAGAGCAGCG
55. Wild_bactrian_camel  Camelus ferus                                CGAAGA------TGTCGCAGACGAAGGAGGCGA---TGTTGTCGGAGGCGGCGGAGGAGA---
56. Domestic_cat  Felis catus                                         CGCCGA------TGCCGCAGACGAAGGAGGCGA---TGTTGCAGGAGGCCGAGGAAGAGA---
57. Domestic_ferret  Mustela putorius furo                            CGCAGA------TGCCGCAGACGGAGGAGGCGG---TGCTGTCGGAGGCGGAGAAGGAGA---
58. Northern_sea_otter  Enhydra lutris kenyoni                        CGCAGA------TGCCGCAGACGGAGGAGGCGG---TGCTGTCGGAGGCGGAGAAGGAGA---
59. Weddell_seal  Leptonychotes weddellii                             CGGAGA------TGCCGCCGCCGAAGGAGACGG---TGCTGTCAGAGGCGGAGAAGGAGA---
60. Giant_panda  Ailuropoda melanoleuca                               CGCAGA------TGCCGCAGACGAAGGAGGCGA---TGTTGTCGGAGGCGGAGAAGGAGA---
61. Dog  Canis lupus familiaris                                       CGCAGA------TGCCGCAGACGAAGGAGGCGA---TGTTGTCGGAGGCGGAGAAGGAGA---
62. Horse  Equus caballus                                             AGACGAAGA---TGTCGCAGGCGAAGGAGGAGA---TCCGTTCGG---CAGAGGAGAGCCGCA
63. Ass  Equus asinus                                                AGACGAAGA---TGTCGCAGGCGAAGGAGGAGA---TGCGTTCGGCGGAGGAGAGGTAAAAAG
64. Southern_white_rhinocerous  Ceratotherium simum simur             CGAAGA------TGTCGCAGGCGAAGGAGGCGA---TGTGTCCGAAGGCGGAGA---------
65. Little_brown_bat  Myotis lucifugus                                AGGAGA------TGTTACAGACGAAGGAGGCGC---TGCTGTCGGAGGAGGAGGAGGAGAAGA
66. Star-nosed_mole  Condylura cristata                               AGAAGAAGA---TGTCGCAGGCGAAGGAGGCGA---TGCTGCCGGAGGCGGAGGAGGAGA---
67. African_savannah_elephant  Loxodonta africana                     CGACGCAGA---TCCCATAGACGAAGGAGGCGA---TGTGCTCGGAGGCGGAGGAGAACAAGA
68. Florida_manatee  Trichechus manatus latirostris                   ACACGACGCAGATGCCACAGACCAAGGAGGCGA---TGTGGTCGAAGGCGGACGAGAACGAGA
69. Aardvark  Orycteropus afer afer                                   AGACGACGCAGATGCCACAGACGGAGGAGGCGA---TGTGGCCAGAGGCGCAGGACAATGAGG
70. Gray_short_tailed_opossum  Monodelphis domestica                  AGACGC------AGCCGTAGTCGGAGGAGGAGA---AGC---AGGAGGAGAAGAAGAAGGAGA
71. Platypus  Ornithorhynchus anatinus                                AGGAGCCGCCGG---------------GGCGGCCGCCAAACCAGGTCCAGGAAGCTTAGC---
72. Echidna  Tachyglossus aculeatus                                   AGAAGCCGCCGGCAGAGAAGCCGCCGGGGAGGCCGCCAAACTGGGCCCAGGAAGATTACCCGC

Site #64    ● with    ○ w/o Gaps
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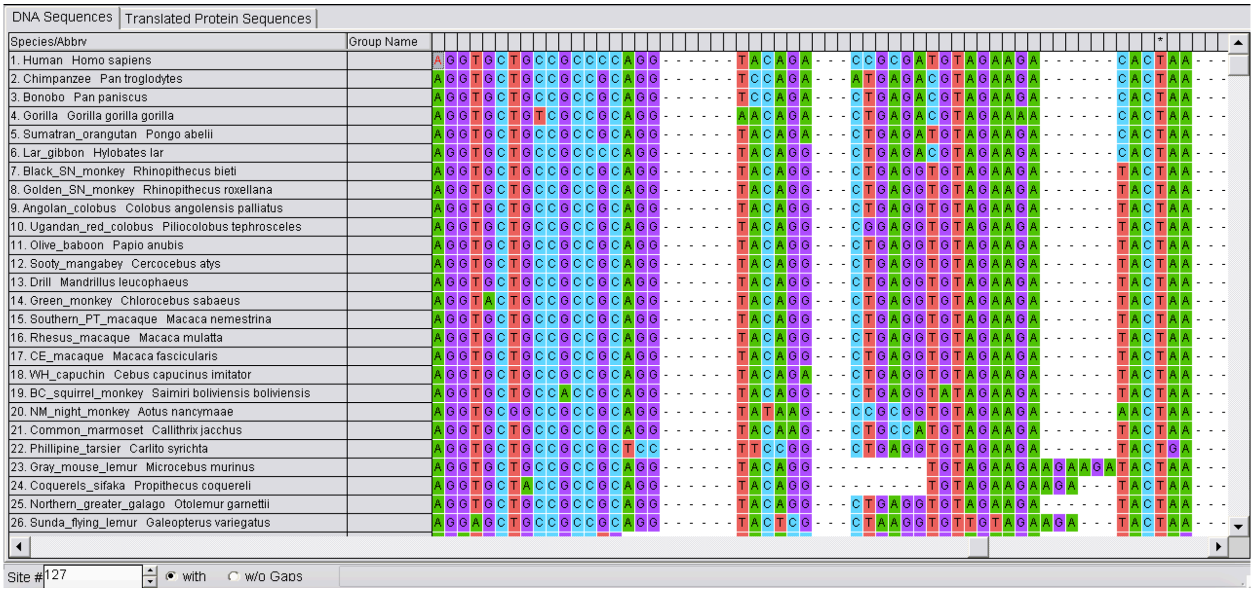
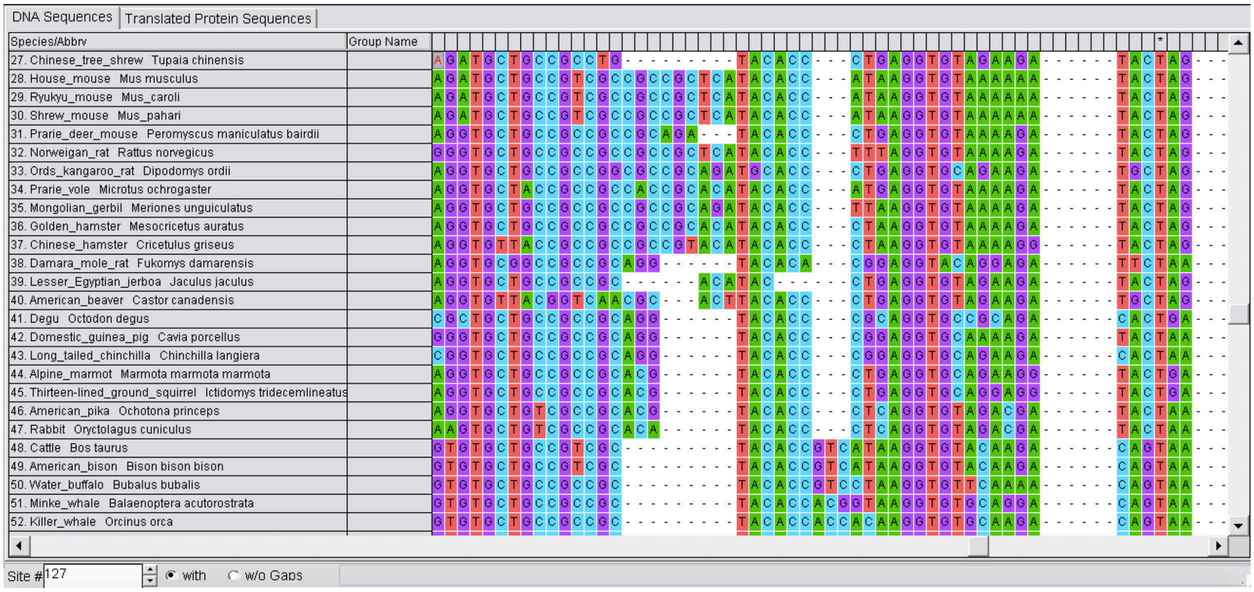


Species/Abbrv	Group Name	
1. Human Homo sapiens		AGGTGCTGCCGCCCCAGG------TACAGA---CCGCGATGTAGAAGA------CACTAA---
2. Chimpanzee Pan troglodytes		AGGTGCTGCCGCCGCAGG------TCCAGA---ATGAGACGTAGAAGA------CACTAA---
3. Bonobo Pan paniscus		AGGTGCTGCCGCCGCAGG------TCCAGA---CTGAGACGTAGAAGA------CACTAA---
4. Gorilla Gorilla gorilla gorilla		AGGTGCTGTCGCCGCAGG------AACAGA---CTGAGACGTAGAAAA------CACTAA---
5. Sumatran_orangutan Pongo abelii		AGGTGCTGCCGCCGCAGG------TACAGA---CTGAGATGTAGAAGA------CACTAA---
6. Lar_gibbon Hylobates lar		AGGTGCTGCCGCCCCAGG------TACAGG---CTGAGACGTAGAAGA------CACTAA---
7. Black_SN_monkey Rhinopithecus bieti		AGGTGCTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
8. Golden_SN_monkey Rhinopithecus roxellana		AGGTGCTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
9. Angolan_colobus Colobus angolensis palliatus		AGGTGCTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
10. Ugandan_red_colobus Piliocolobus tephrosceles		AGGTGCTGCCGCCGCAGG------TACAGG---CGGAGGTGTAGAAGA------TACTAA---
11. Olive_baboon Papio anubis		AGGTGCTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
12. Sooty_mangabey Cercocebus atys		AGGTGCTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
13. Drill Mandrillus leucophaeus		AGGTGCTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
14. Green_monkey Chlorocebus sabaeus		AGGTACTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
15. Southern_PT_macaque Macaca nemestrina		AGGTGCTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
16. Rhesus_macaque Macaca mulatta		AGGTGCTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
17. CE_macaque Macaca fascicularis		AGGTGCTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
18. WH_capuchin Cebus capucinus imitator		AGGTGCTGCCGCCGCAGG------TACAGA---CTGAGGTGTAGAAGA------TACTAA---
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		AGGTGCTGCCACCGCAGG------TACAGG---CTGAGGTATAGAAGA------TACTAA---
20. NM_night_monkey Aotus nancymaae		AGGTGCGGCCGCCGCAGG------TATAAG---CCGCGGTGTAGAAGA------AACTAA---
21. Common_marmoset Callithrix jacchus		AGGTGCTGCCGCCGCAGG------TACAAG---CTGCCATGTAGAAGA------TACTAA---
22. Phillipine_tarsier Carlito syrichta		AGGTGCTGCCGCCGCTCC------TTCCGG---CTGAGGTGTAGAAGA------TACTGA---
23. Gray_mouse_lemur Microcebus murinus		AGGTGCTGCCGCCGCAGG------TACAGG---------TGTAGAAGAAGAAGATACTAA---
24. Coquerels_sifaka Propithecus coquereli		AGGTGCTACCGCCGCAGG------TACAGG---------TGTAGAAGAAGA---TACTAA---
25. Northern_greater_galago Otolemur garnettii		AGGTGCTGCCGCCGCAGG------TACAGG---CTGAGGTGTAGAAGA------TACTAA---
26. Sunda_flying_lemur Galeopterus variegatus		AGGAGCTGCCGCCGCAGG------TACTCG---CTAAGGTGTTGTAGAAGA---TACTAA---



Species/Abbrv	Group Name	
27. Chinese_tree_shrew Tupaia chinensis		AGATGCTGCCGCCTG---------TACACC---CTGAGGTGTAGAAGA------TACTAG---
28. House_mouse Mus musculus		AGATGCTGCCGTCGCCGCCGCTCATACACC---ATAAGGTGTAAAAAA------TACTAG---
29. Ryukyu_mouse Mus_caroli		AGATGCTGCCGTCGCCGCCGCTCATACACC---ATAAGGTGTAAAAAA------TACTAG---
30. Shrew_mouse Mus_pahari		AGATGCTGCCGTCGCCGCCGCTCATACACC---ATAAGGTGTAAAAAA------TACTAG---
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		AGGTGCTGCCGCCGCCGCAGA---TACACC---CTGAGGTGTAAAAGA------TACTAG---
32. Norweigan_rat Rattus norvegicus		GGGTGCTGCCGCCGCCGCCGCTCATACACC---TTTAGGTGTAAAAGA------TACTAG---
33. Ords_kangaroo_rat Dipodomys ordii		AGGTGCTGCCGCCGGCGCCGCAGATGCACC---CTGAGGTGCAGAAGA------TGCTAG---
34. Prarie_vole Microtus ochrogaster		AGGTGCTACCGCCGCCACCGCACATACACC---ATGAGGTGTAAAAGA------TACTAG---
35. Mongolian_gerbil Meriones unguiculatus		AGGTGCTGCCGCCGCCGCCGCAGATACACC---TTAAGGTGTAAAAGA------TACTAG---
36. Golden_hamster Mesocricetus auratus		AGGTGCTGCCGCCGCCGCCGCACATACACC---CTAAGGTGTAAAAGA------TACTAG---
37. Chinese_hamster Cricetulus griseus		AGGTGTTACCGCCGCCGCCGTACATACACC---CTAAGGTGTAAAAGG------TACTAG---
38. Damara_mole_rat Fukomys damarensis		AGGTGCGGCCGCCGCAGG------TACACA---CGGAGGTACAGGAGA------TTCTAA---
39. Lesser_Egyptian_jerboa Jaculus jaculus		AGGTGCTGCCGCCGC------ACATAC------CTGAGGTGTAGAAGA------TACTAG---
40. American_beaver Castor canadensis		AGGTGTTACGGTCAACGC---ACTTACACC---CTGAGGTGTAGAAGA------TGCTAG---
41. Degu Octodon degus		CGCTGCTGCCGCCGCAGG------TACACC---CGCAGGTGCCGCAGA------CACTGA---
42. Domestic_guinea_pig Cavia porcellus		GGGTGCTGCCGCCGCAGG------TACACC---CGGAGGTGCAAAAGA------TACTAA---
43. Long_tailed_chinchilla Chinchilla langiera		CGGTGCTGCCGCCGCAGG------TACACC---CGGAGGTGCAGAAGA------CACTAA---
44. Alpine_marmot Marmota marmota marmota		AGGTGCTGCCGCCGCACG------TACACC---CTGAGGTGCAGAAGG------TACTGA---
45. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		AGGTGCTGCCGCCGCACG------TACACC---CTGAGGTGCAGGAGG------TACTGA---
46. American_pika Ochotona princeps		AGGTGCTGTCGCCGCACG------TACACC---CTCAGGTGTAGACGA------TACTAA---
47. Rabbit Oryctolagus cuniculus		AAGTGCTGTCGCCGCACA------TACACC---CTCAGGTGTAGACGA------TACTAA---
48. Cattle Bos taurus		GTGTGCTGCCGTCGC---------TACACCGTCATAAGGTGTACAAGA------CAGTAA---
49. American_bison Bison bison bison		GTGTGCTGCCGTCGC---------TACACCGTCATAAGGTGTACAAGA------CAGTAA---
50. Water_buffalo Bubalus bubalis		GTGTGCTGCCGCCGC---------TACACCGTCCTAAGGTGTTCAAAA------CAGTAA---
51. Minke_whale Balaenoptera acutorostrata		GTGTGCTGCCGCCGC---------TACACCACGGTAAGGTGTGCAGGA------CAGTAA---
52. Killer_whale Orcinus orca		GTGTGCTGCCGCCGC---------TACACCACCACAAGGTGTGCAAGA------CAGTAA---

Species/Abbrv	Group Name	
53. Bottlenose_dolphin Tursiops truncatus		GTGTGCTGCCGCCGC---------TACACCACCACAAGGTGTGCAAGA------CAGTAA---
54. Pig Sus scrofa		GTGTGCTGCCGCCGC---------TACACCGTTATAAGGTGTAGAAGA------TGCTAA---
55. Wild_bactrian_camel Camelus ferus		GTGTGCTGCCGCCGC---------TACACCATCATAAGGTGTAGAAGAAGG------TAA---
56. Domestic_cat Felis catus		GTGTGTTCCCGCCGC---------TACAGGGTGGGGAGGTGTAGGAGAAGA------TGA---
57. Domestic_ferret Mustela putorius furo		GTGTGCTGCCGTCGC---------TACACGGTGTTGAGATGTCAGAGAAGA------TGA---
58. Northern_sea_otter Enhydra lutris kenyoni		GTGTGCTGCCGTCGC---------TACACCGTGTTGAGATGTCGGAGAAGA------TGA---
59. Weddell_seal Leptonychotes weddellii		GCGTGTTACCGCCGC---------TACACCACGGTGAGGTGTAGGAGAAGA------TGA---
60. Giant_panda Ailuropoda melanoleuca		GTGTGCTGCCGCCGT---------TACACCATGGTGAGGTGCAGGAGAAGA------TGA---
61. Dog Canis lupus familiaris		GTGTGCTGCCGCCGC---------TACACCGTGGTGCGCTGTAGGAGAAGA------TGA---
62. Horse Equus caballus		GTGTGCTGCCGCCGC---------TACACTGTCCTGAGGTGTAGGAGAAGACGA---TAG---
63. Ass Equus asinus		GTGTGCTGCCGCCGC---------TACACTGTCCTGAGGTGTAGGAGAAGACGA---TAG---
64. Southern_white_rhinocerous Ceratotherium simum simur		GTGTGCTGCCGCCGC---------TACACTGTTGTGAGGTGTAGACGACGACGA---TAG---
65. Little_brown_bat Myotis lucifugus		GTGTGCTGCCGCCGC---------TACTCA------AGGTGTAGAAGAAGA------TAA---
66. Star-nosed_mole Condylura cristata		GTGTGCTGCCGCCGC---------TACACG---ATGAGGTGCAGGAGA------TACTAA---
67. African_savannah_elephant Loxodonta africana		AGAGGGTGCCGCCGCAGA------TACAGT---CTGAGG---CGTAGAAGA---TACTAA---
68. Florida_manatee Trichechus manatus latirostris		AGAGGGTGCCGCCGCAGA------TACGGT---CTGAGGCGTAGAAGA------TACTAA---
69. Aardvark Orycteropus afer afer		AGAAGGTCCTGCCGCAGA------TATGTG------AGGCGTCGAAGA------TACTAA---
70. Gray_short_tailed_opossum Monodelphis domestica		GGAAGGAGAGGCAGAGGTAAT---TAC------------TGTCGGAGGAGAAGA---TAA---
71. Platypus Ornithorhynchus anatinus		CGGAGCCGGAGAAGAGGGAGAAGCAGGAGGAGGAAAGGCAGACGCAGCAGGAGATCTTCTCGC
72. Echidna Tachyglossus aculeatus		CGGGGCCGGGGAAGAGGGAAAAGCAGGAGGAGGAGAGGTAGACGCAGCATGAGATCCTCTCGC

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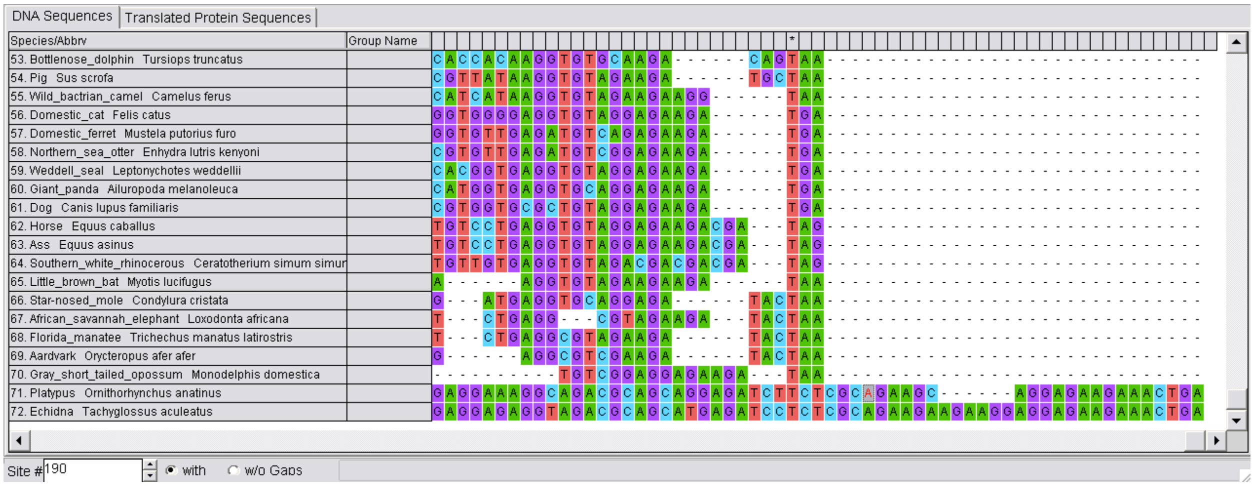

Species/Abbrv	Group Name	
53. Bottlenose_dolphin Tursiops truncatus		CACCACAAGGTGTGCAAGA------CAGTAA------------------------------
54. Pig Sus scrofa		CGTTATAAGGTGTAGAAGA------TGCTAA------------------------------
55. Wild_bactrian_camel Camelus ferus		CATCATAAGGTGTAGAAGAAGG------TAA------------------------------
56. Domestic_cat Felis catus		GGTGGGGAGGTGTAGGAGAAGA------TGA------------------------------
57. Domestic_ferret Mustela putorius furo		GGTGTTGAGATGTCAGAGAAGA------TGA------------------------------
58. Northern_sea_otter Enhydra lutris kenyoni		CGTGTTGAGATGTCGGAGAAGA------TGA------------------------------
59. Weddell_seal Leptonychotes weddellii		CACGGTGAGGTGTAGGAGAAGA------TGA------------------------------
60. Giant_panda Ailuropoda melanoleuca		CATGGTGAGGTGCAGGAGAAGA------TGA------------------------------
61. Dog Canis lupus familiaris		CGTGGTGCGCTGTAGGAGAAGA------TGA------------------------------
62. Horse Equus caballus		TGTCCTGAGGTGTAGGAGAAGACGA---TAG------------------------------
63. Ass Equus asinus		TGTCCTGAGGTGTAGGAGAAGACGA---TAG------------------------------
64. Southern_white_rhinocerous Ceratotherium simum simur		TGTTGTGAGGTGTAGACGACGACGA---TAG------------------------------
65. Little_brown_bat Myotis lucifugus		A------AGGTGTAGAAGAAGA------TAA------------------------------
66. Star-nosed_mole Condylura cristata		G---ATGAGGTGCAGGAGA------TACTAA------------------------------
67. African_savannah_elephant Loxodonta africana		T---CTGAGG---CGTAGAAGA---TACTAA------------------------------
68. Florida_manatee Trichechus manatus latirostris		T---CTGAGGCGTAGAAGA------TACTAA------------------------------
69. Aardvark Orycteropus afer afer		G------AGGCGTCGAAGA------TACTAA------------------------------
70. Gray_short_tailed_opossum Monodelphis domestica		----------TGTCGGAGGAGAAGA---TAA------------------------------
71. Platypus Ornithorhynchus anatinus		GAGGAAAGGCAGACGCAGCAGGAGATCTTCTCGCAGAAGC------AGGAGAAGAAACTGA
72. Echidna Tachyglossus aculeatus		GAGGAGAGGTAGACGCAGCATGAGATCCTCTCGCAGAAGAAGAAGGAGGAGAAGAAACTGA

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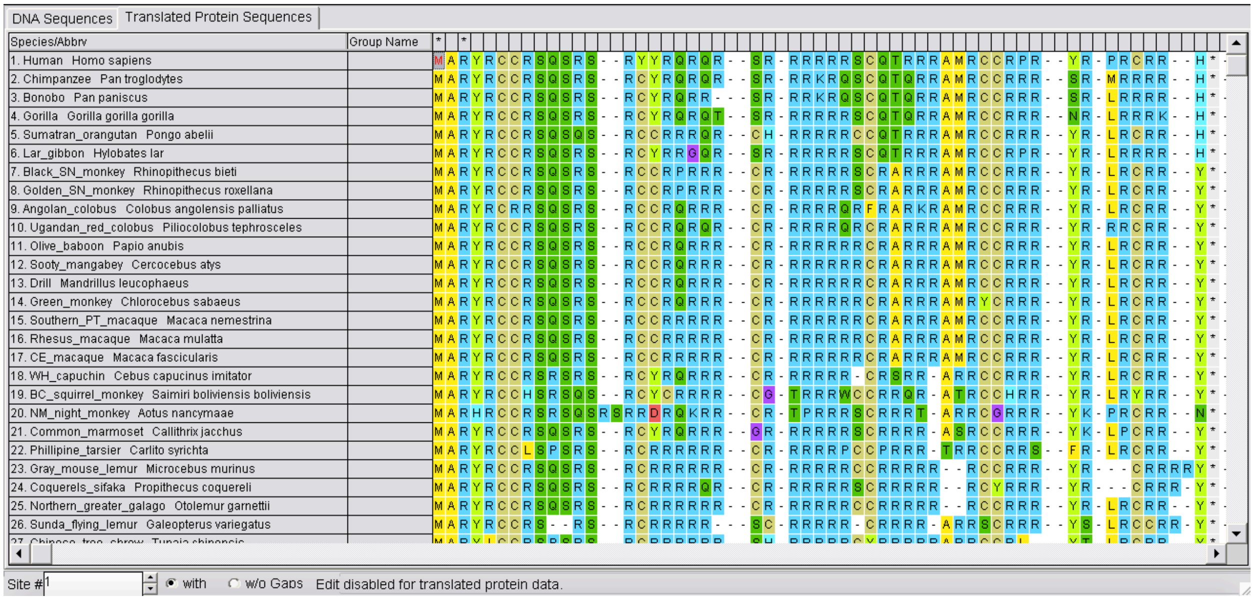

Species/Abbrv	Group Name	
1. Human Homo sapiens		MARYRCCRSQSRS--RYYRQRQR--SR-RRRRRSCQTRRRAMRCCRPR--YR-PRCRR--H*-
2. Chimpanzee Pan troglodytes		MARYRCCRSQSRS--RCYRQRQR--SR-RRKRQSCQTQRRAMRCCRRR--SR-MRRRR--H*-
3. Bonobo Pan paniscus		MARYRCCRSQSRS--RCYRQRR---SR-RRKRQSCQTQRRAMRCCRRR--SR-LRRRR--H*-
4. Gorilla Gorilla gorilla gorilla		MARYRCCRSQSRS--RCYRQRQT--SR-RRRRRSCQTQRRAMRCCRRR--NR-LRRRK--H*-
5. Sumatran_orangutan Pongo abelii		MARYRCCRSQSQS--RCCRRRQR--CH-RRRRRCCQTRRRAMRCCRRR--YR-LRCRR--H*-
6. Lar_gibbon Hylobates lar		MARYRCCRSQSRS--RCYRRGQR--SR-RRRRRSCQTRRRAMRCCRPR--YR-LRRRR--H*-
7. Black_SN_monkey Rhinopithecus bieti		MARYRCCRSQSRS--RCCRPRRR--CR-RRRRRSCRARRRAMRCCRRR--YR-LRCRR--Y*-
8. Golden_SN_monkey Rhinopithecus roxellana		MARYRCCRSQSRS--RCCRPRRR--CR-RRRRRSCRARRRAMRCCRRR--YR-LRCRR--Y*-
9. Angolan_colobus Colobus angolensis palliatus		MARYRCRRSQSRS--RCCRQRRR--CR-RRRRQRFRARKRAMRCCRRR--YR-LRCRR--Y*-
10. Ugandan_red_colobus Piliocolobus tephrosceles		MARYRCCRSQSRS--RCCRQRQR--CR-RRRRQRCRARRRAMRCCRRR--YR-RRCRR--Y*-
11. Olive_baboon Papio anubis		MARYRCCRSQSRS--RCCRQRRR--CR-RRRRRRCRARRRAMRCCRRR--YR-LRCRR--Y*-
12. Sooty_mangabey Cercocebus atys		MARYRCCRSQSRS--RCCRQRRR--CR-RRRRRRCRARRRAMRCCRRR--YR-LRCRR--Y*-
13. Drill Mandrillus leucophaeus		MARYRCCRSQSRS--RCCRQRRR--CR-RRRRRRCRARRRAMRCCRRR--YR-LRCRR--Y*-
14. Green_monkey Chlorocebus sabaeus		MARYRCCRSQSRS--RCCRQRRR--CR-RRRRRRCRARRRAMRYCRRR--YR-LRCRR--Y*-
15. Southern_PT_macaque Macaca nemestrina		MARYRCCRSQSRS--RCCRRRRR--CR-RRRRRRCRARRRAMRCCRRR--YR-LRCRR--Y*-
16. Rhesus_macaque Macaca mulatta		MARYRCCRSQSRS--RCCRRRRR--CR-RRRRRRCRARRRAMRCCRRR--YR-LRCRR--Y*-
17. CE_macaque Macaca fascicularis		MARYRCCRSQSRS--RCCRRRRR--CR-RRRRRRCRARRRAMRCCRRR--YR-LRCRR--Y*-
18. WH_capuchin Cebus capucinus imitator		MARYRCCRSRSRS--RCYRQRRR--CR-RRRRR-CRSRR-ARRCCRRR--YR-LRCRR--Y*-
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		MARYRCCHSRSQS--RCYCRRRR--CG-TRRRWCCRRQR-ATRCCHRR--YR-LRYRR--Y*-
20. NM_night_monkey Aotus nancymaae		MARHRCCRSRSQSRSRRDRQKRR--CR-TPRRRSCRRRT-ARRCGRRR--YK-PRCRR--N*-
21. Common_marmoset Callithrix jacchus		MARYRCCRSQSRS--RCYRQRRR--GR-RRRRRSCRRRR-ASRCCRRR--YK-LPCRR--Y*-
22. Phillipine_tarsier Carlito syrichta		MARYRCCLSPSRS--RCRRRRRR--CR-RRRRPCCPRRR-TRRCCRRS--FR-LRCRR--Y*-
23. Gray_mouse_lemur Microcebus murinus		MARYRCCRSQSRS--RCRRRRRR--CR-RRRRRCCRRRRR--RCCRRR--YR---CRRRRY*-
24. Coquerels_sifaka Propithecus coquereli		MARYRCCRSQSRS--RCRRRRQR--CR-RRRRRSCRRRRR--RCYRRR--YR---CRRR-Y*-
25. Northern_greater_galago Otolemur garnettii		MARYRCCRSQSRS--RCRRRRRR--CR-RRRRRCCRRRRR--RCCRRR--YR-LRCRR--Y*-
26. Sunda_flying_lemur Galeopterus variegatus		MARYRCCRS--RS--RCRRRRR---SC-RRRRR-CRRRR-ARRSCRRR--YS-LRCCRR-Y*-

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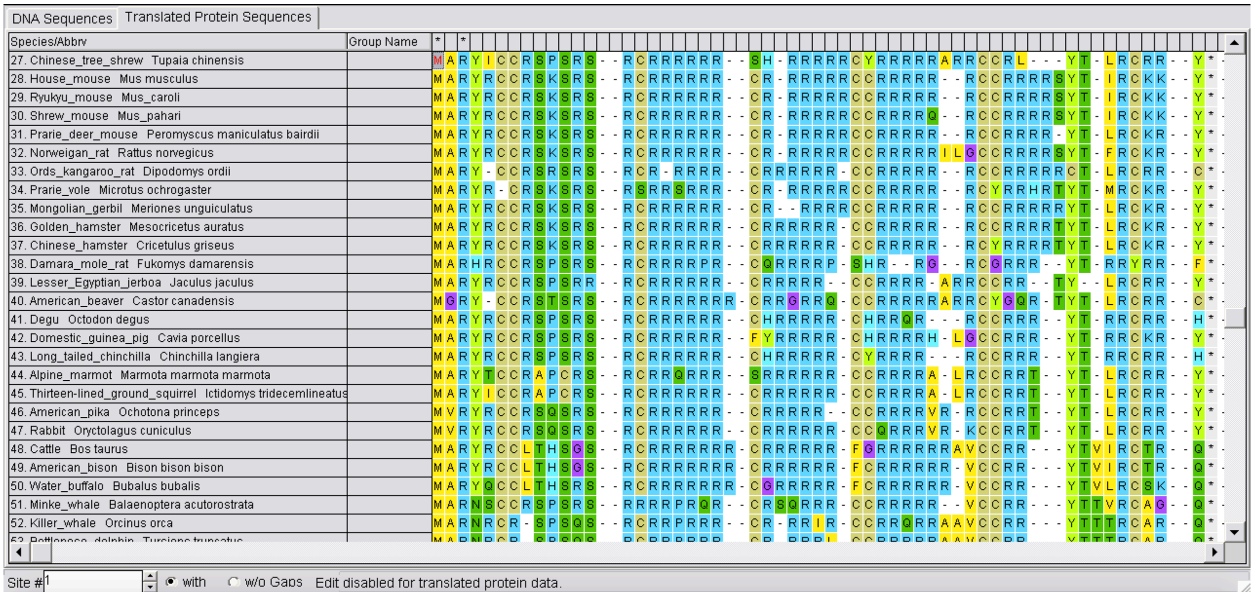

Species/Abbrv	Group Name	
27. Chinese_tree_shrew Tupaia chinensis		MARYICCRSPSRS--RCRRRRRR--SH-RRRRRCYRRRRRARRCCRL---YT-LRCRR--Y*-
28. House_mouse Mus musculus		MARYRCCRSKSRS--RCRRRRRR--CR-RRRRRCCRRRRR--RCCRRRRSYT-IRCKK--Y*-
29. Ryukyu_mouse Mus_caroli		MARYRCCRSKSRS--RCRRRRRR--CR-RRRRRCCRRRRR--RCCRRRRSYT-IRCKK--Y*-
30. Shrew_mouse Mus_pahari		MARYRCCRSKSRS--RCRRRRRR--CR-RRRRRCCRRRRQ--RCCRRRRSYT-IRCKK--Y*-
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		MARYRCCRSKSRS--RCRRRRRR--CR-RRRRRCCRRRRR--RCCRRRR-YT-LRCKR--Y*-
32. Norweigan_rat Rattus norvegicus		MARYRCCRSKSRS--RCRRRRRR--CR-RRRRRCCRRRRRILGCCRRRRSYT-FRCKR--Y*-
33. Ords_kangaroo_rat Dipodomys ordii		MARY-CCRSRSRS--RCR-RRRR--CRRRRRR-CCRRRRR--RCCRRRRRCT-LRCRR--C*-
34. Prarie_vole Microtus ochrogaster		MARYR-CRSKSRS--RSRRSRRR--CR-RRRRRCCRRRRR--RCYRRHRTYT-MRCKR--Y*-
35. Mongolian_gerbil Meriones unguiculatus		MARYRCCRSKSRS--RCRRRRRR--CR--RRRRCCRRRRR--RCCRRRRRYT-LRCKR--Y*-
36. Golden_hamster Mesocricetus auratus		MARYRCCRSKSRS--RCRRRRRR--CRRRRRR-CCRRRRR--RCCRRRRTYT-LRCKR--Y*-
37. Chinese_hamster Cricetulus griseus		MARYRCCRSKSRS--RCRRRRRR--CRRRRRR-CCRRRRR--RCYRRRRTYT-LRCKR--Y*-
38. Damara_mole_rat Fukomys damarensis		MARHRCCRSPSRS--RCRRRRPR--CQRRRRP-SHR--RG--RCGRRR--YT-RRYRR--F*-
39. Lesser_Egyptian_jerboa Jaculus jaculus		MARYRCCRSPSRR--RCRRRRRR--CRRRRR--CCRRRR-ARRCCRR--TY--LRCRR--Y*-
40. American_beaver Castor canadensis		MGRY-CCRSTSRS--RCRRRRRRR-CRRGRRQ-CCRRRRRARRCYGQR-TYT-LRCRR--C*-
41. Degu Octodon degus		MARYRCCRSPSRS--RCRRRRRR--CHRRRRR-CHRRQR---RCCRRR--YT-RRCRR--H*-
42. Domestic_guinea_pig Cavia porcellus		MARYRCCRSPSRS--RCRRRRRR--FYRRRRR-CHRRRRH-LGCCRRR--YT-RRCKR--Y*-
43. Long_tailed_chinchilla Chinchilla langiera		MARYRCCRSPSRS--RCRRRRRR--CHRRRRR-CYRRRR---RCCRRR--YT-RRCRR--H*-
44. Alpine_marmot Marmota marmota marmota		MARYTCCRAPCRS--RCRRQRRR--SRRRRRR-CCRRRRA-LRCCRRT--YT-LRCRR--Y*-
45. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		MARYICCRAPCRS--RCRRRRRR--CRRRRRR-CCRRRRA-LRCCRRT--YT-LRCRR--Y*-
46. American_pika Ochotona princeps		MVRYRCCRSQSRS--RCRRRRRR--CRRRRR--CCRRRRVR-RCCRRT--YT-LRCRR--Y*-
47. Rabbit Oryctolagus cuniculus		MVRYRCCRSQSRS--RCRRRRRR--CRRRRRR-CCQRRRVR-KCCRRT--YT-LRCRR--Y*-
48. Cattle Bos taurus		MARYRCCLTHSGS--RCRRRRRRR-CRRRRRR-FGRRRRRRAVCCRR---YTVIRCTR--Q*-
49. American_bison Bison bison bison		MARYRCCLTHSGS--RCRRRRRRR-CRRRRRR-FCRRRRRR-VCCRR---YTVIRCTR--Q*-
50. Water_buffalo Bubalus bubalis		MARYQCCLTHSRS--RCRRRRRRR-CGRRRRR-FCRRRRRR-VCCRR---YTVLRCSK--Q*-
51. Minke_whale Balaenoptera acutorostrata		MARNSCCRSPSRS--RRRRPRQR--CRSQRRR-CCRRRRR--VCCRR---YTTVRCAG--Q*-
52. Killer_whale Orcinus orca		MARNRCR-SPSQS--RCRRPRRR--CR-RRIR-CCRRQRRAAVCCRR---YTTTRCAR--Q*-

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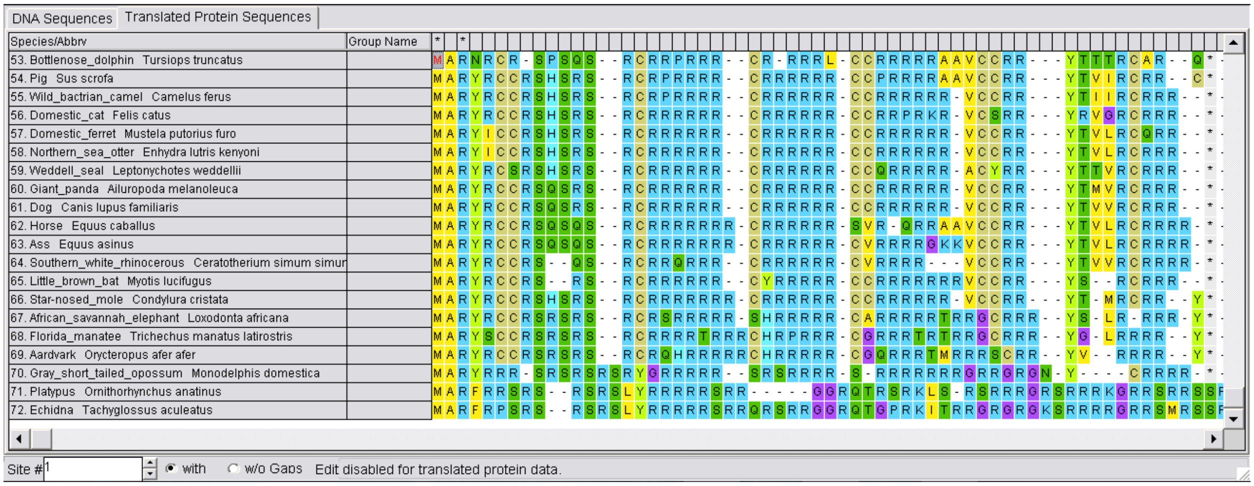

Species/Abbrv	Group Name	* *
53. Bottlenose_dolphin Tursiops truncatus		M A R N R C R - S P S Q S - - R C R R P R R R - - C R - R R R L - C C R R R R R A A V C C R R - - - Y T T T R C A R - - Q * -
54. Pig Sus scrofa		M A R Y R C C R S H S R S - - R C R P R R R R - - C R R R R R R - C C P R R R R A A V C C R R - - - Y T V I R C R R - - C * -
55. Wild_bactrian_camel Camelus ferus		M A R Y R C C R S H S R S - - R C R P R R R R - - C R R R R R R - C C R R R R R R - V C C R R - - - Y T I I R C R R R - - * -
56. Domestic_cat Felis catus		M A R Y R C C R S H S R S - - R C R R R R R R - - C R R R R R R - C C R R P R K R - V C S R R - - - Y R V G R C R R R - - * -
57. Domestic_ferret Mustela putorius furo		M A R Y I C C R S H S R S - - R C R R R R R R - - C R R R R R R - C C R R R R R R - V C C R R - - - Y T V L R C Q R R - - * -
58. Northern_sea_otter Enhydra lutris kenyoni		M A R Y I C C R S H S R S - - R C R R R R R R - - C R R R R R R - C C R R R R R R - V C C R R - - - Y T V L R C R R R - - * -
59. Weddell_seal Leptonychotes weddellii		M A R Y R C S R S H S R S - - R C R R R R R R - - C R R R R R R - C C Q R R R R R - A C Y R R - - - Y T T V R C R R R - - * -
60. Giant_panda Ailuropoda melanoleuca		M A R Y R C C R S Q S R S - - R C R R R R R R - - C R R R R R R - C C R R R R R R - V C C R R - - - Y T M V R C R R R - - * -
61. Dog Canis lupus familiaris		M A R Y R C C R S Q S R S - - R C R R R R R R - - C R R R R R R - C C R R R R R R - V C C R R - - - Y T V V R C R R R - - * -
62. Horse Equus caballus		M A R Y R C C R S Q S Q S - - R C R R R R R R R - C R R R R R R - S V R - Q R R A A V C C R R - - - Y T V L R C R R R R - * -
63. Ass Equus asinus		M A R Y R C C R S Q S Q S - - R C R R R R R R R - C R R R R R R - C V R R R R G K K V C C R R - - - Y T V L R C R R R R - * -
64. Southern_white_rhinocerous Ceratotherium simum simur		M A R Y R C C R S - - Q S - - R C R R Q R R R - - C R R R R R R - C V R R R R - - - V C C R R - - - Y T V V R C R R R R - * -
65. Little_brown_bat Myotis lucifugus		M A R Y R C C R S - - R S - - R C R R R R R R - - C Y R R R R R - C C R R R R R R R V C C R R - - - Y S - - R C R R R - - * -
66. Star-nosed_mole Condylura cristata		M A R Y R C C R S H S R S - - R C R R R R R R R - C R R R R R R - C C R R R R R R - V C C R R - - - Y T - M R C R R - - Y * -
67. African_savannah_elephant Loxodonta africana		M A R Y R C C R S R S R S - - R C R S R R R R R - S H R R R R R - C A R R R R R T R R G C R R R - - Y S - L R - R R R - Y * -
68. Florida_manatee Trichechus manatus latirostris		M A R Y S C C R S R S R S - - R C R R R R T R R R C H R P R R R - C G R R R T R T R R G C R R R - - Y G - L R R R R - - Y * -
69. Aardvark Orycteropus afer afer		M A R Y R C C R S R S R S - - R C R Q H R R R R R C H R R R R R - C G Q R R R T M R R R S C R R - - Y V - - R R R R - - Y * -
70. Gray_short_tailed_opossum Monodelphis domestica		M A R Y R R R - S R S R S R S R Y G R R R R R - - S R S R R R R - S - R R R R R R R G R R G R G N - Y - - - - C R R R R - * -
71. Platypus Ornithorhynchus anatinus		M A R F R R S R S - - R S R S L Y R R R R R S R R - - - - - G G R Q T R S R K L S - R S R R R G R S R R R K G R R S R R S S F
72. Echidna Tachyglossus aculeatus		M A R F R P S R S - - R S R S L Y R R R R R S R R Q R S R R G G R Q T G P R K I T R R G R G R G K S R R R R G R R S M R S S F

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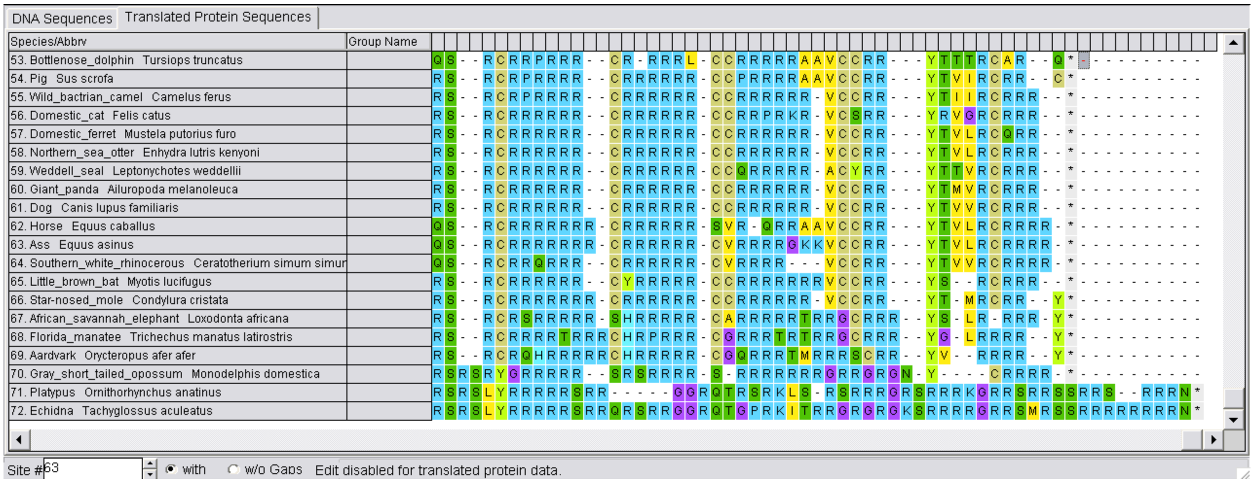

Species/Abbrv	Group Name	
53. Bottlenose_dolphin Tursiops truncatus		Q S - - R C R R P R R R - - C R - R R R L - C C R R R R R A A V C C R R - - - Y T T T R C A R - - Q * - - - - - - - - - -
54. Pig Sus scrofa		R S - - R C R P R R R R - - C R R R R R R - C C P R R R R A A V C C R R - - - Y T V I R C R R - - C * - - - - - - - - - -
55. Wild_bactrian_camel Camelus ferus		R S - - R C R P R R R R - - C R R R R R R - C C R R R R R R - V C C R R - - - Y T I I R C R R R - - * - - - - - - - - - -
56. Domestic_cat Felis catus		R S - - R C R R R R R R - - C R R R R R R - C C R R P R K R - V C S R R - - - Y R V G R C R R R - - * - - - - - - - - - -
57. Domestic_ferret Mustela putorius furo		R S - - R C R R R R R R - - C R R R R R R - C C R R R R R R - V C C R R - - - Y T V L R C Q R R - - * - - - - - - - - - -
58. Northern_sea_otter Enhydra lutris kenyoni		R S - - R C R R R R R R - - C R R R R R R - C C R R R R R R - V C C R R - - - Y T V L R C R R R - - * - - - - - - - - - -
59. Weddell_seal Leptonychotes weddellii		R S - - R C R R R R R R - - C R R R R R R - C C Q R R R R R - A C Y R R - - - Y T T V R C R R R - - * - - - - - - - - - -
60. Giant_panda Ailuropoda melanoleuca		R S - - R C R R R R R R - - C R R R R R R - C C R R R R R R - V C C R R - - - Y T M V R C R R R - - * - - - - - - - - - -
61. Dog Canis lupus familiaris		R S - - R C R R R R R R - - C R R R R R R - C C R R R R R R - V C C R R - - - Y T V V R C R R R - - * - - - - - - - - - -
62. Horse Equus caballus		Q S - - R C R R R R R R R - C R R R R R R - S V R - Q R R A A V C C R R - - - Y T V L R C R R R R - * - - - - - - - - - -
63. Ass Equus asinus		Q S - - R C R R R R R R R - C R R R R R R - C V R R R R G K K V C C R R - - - Y T V L R C R R R R - * - - - - - - - - - -
64. Southern_white_rhinocerous Ceratotherium simum simur		Q S - - R C R R Q R R R - - C R R R R R R - C V R R R R - - - V C C R R - - - Y T V V R C R R R R - * - - - - - - - - - -
65. Little_brown_bat Myotis lucifugus		R S - - R C R R R R R R - - C Y R R R R R - C C R R R R R R R V C C R R - - - Y S - - R C R R R - - * - - - - - - - - - -
66. Star-nosed_mole Condylura cristata		R S - - R C R R R R R R R - C R R R R R R - C C R R R R R R - V C C R R - - - Y T - M R C R R - - Y * - - - - - - - - - -
67. African_savannah_elephant Loxodonta africana		R S - - R C R S R R R R R - S H R R R R R - C A R R R R R T R R G C R R R - - Y S - L R - R R R - Y * - - - - - - - - - -
68. Florida_manatee Trichechus manatus latirostris		R S - - R C R R R R T R R R C H R P R R R - C G R R R T R T R R G C R R R - - Y G - L R R R R - - Y * - - - - - - - - - -
69. Aardvark Orycteropus afer afer		R S - - R C R Q H R R R R R C H R R R R R - C G Q R R R T M R R R S C R R - - Y V - - R R R R - - Y * - - - - - - - - - -
70. Gray_short_tailed_opossum Monodelphis domestica		R S R S R Y G R R R R R - - S R S R R R R - S - R R R R R R R G R R G R G N - Y - - - - C R R R R - * - - - - - - - - - -
71. Platypus Ornithorhynchus anatinus		R S R S L Y R R R R R S R R - - - - - G G R Q T R S R K L S - R S R R R G R S R R R K G R R S R R S S R R S - - R R R N *
72. Echidna Tachyglossus aculeatus		R S R S L Y R R R R R S R R Q R S R R G G R Q T G P R K I T R R G R G R G K S R R R R G R R S M R S S R R R R R R R R N *

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Appendix AA) Alignment of mammalian *Prm2* coding exon sequences

Species/Abbrv	Group Name	* * * * * * * * *
1. Human Homo sapiens		ATGGTCCGATACCGCGTGAGGAGCCTGAGCGAACGCTCGCACGAGGTGTACAGGCAGCAGTT
2. Chimpanzee Pan troglodytes		ATGGTCCGATACCGCGTGAGGAGCCCGAGCGAACCCTCGCACGAGGTGTACAGGCAGCAGTT
3. Bonobo Pan paniscus		ATGGTCCGATACCGCGTGAGGAGCCCGAGCGAACCCTCGCACGAGGTGTACAGGCAGCAGTT
4. Gorilla Gorilla gorilla gorilla		ATGGTCCGACGCCGCGTGAGGAGCCCGAGCGAACGCTCGCACGAGGTGTACAGGCAGCAGTT
5. Sumatran_orangutan Pongo abelii		ATGGTCCGATACTGTGTGAGGAGCCTGAGCGAACGCTCGCACGAGGTGTACGGGCAGCAGTT
6. Lar_gibbon Hylobates_lar		ATGGTCCGATACTGCGTGAGGAGCCTGAGCGAACGCTCGCACGAGGTGTACGGGCAGCAGTT
7. Black_SN_monkey Rhinopithecus bieti		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGT
8. Golden_SN_monkey Rhinopithecus roxellana		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCATGGGCAGCAGGT
9. Angolan_Colobus Colobus angolensis palliatus		ATGGTCCGATACCACATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACAGGCAGCAGGT
10. Ugandan_red_colobus Piliocolobus tephrosceles		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCAGGAGGTGCACGGGCAGCAGCT
11. Olive_baboon Papio anubis		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCAC---------GGGCAGCAGGT
12. Sooty_mangabey Cercocebus atys		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGT
13. Drill Mandrillus leucophaeus		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGT
14. Green_monkey Chlorocebus sabaeus		ATGGTCCGATACCGCACCAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGT
15. Southern_PT_macaque Macaca nemestrina		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGT
16. Rhesus_macaque Macaca mulatta		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGT
17. CE_macaque Macaca fascicularis		ATGGTCCGATACCGCATGAGGAGCCTGAGCGAACGCCCGCACGAGGTGCACGGGCAGCAGGT
18. WH_capuchin Cebus capucinus imitator		ATGGTCCGATGCCGCTTGAGGAGCCCGAGCGAACGCCCACACGAGGAGTACAGGCAGCTGGT
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		ATGGTCCGATACCGCTTGAGGAGCCCGAGCGAACGCCCACACGAGGAGTACAGGCAGCTGGT
20. NM_night_monkey Aotus nancymaae		ATGGTCCGATACCACGGGAGGAGCCCGAGCGAACGCCTCTACGAGGAGCACAGGCAGCTGGT
21. Common_marmoset Callithrix jacchus		ATGGTCCGATACCGCGTGAGGAGCCCGAGCGAACGCCCACACGAGGAGTACAGGCAGCTGGT
22. Coquerels_sifaka Propithecus coquereli		ATGGTCCGGTACCGCGAGAGGAGCCCCAGCGAACGCCCGCACCAGGGGTACAGGCAGCAAGG
23. Gray_mouse_lemur Microcebus murinus		ATGGTCCGGTACCGGGAGAGGAGCCCCAGCGAGCGCCCGCACCAGGGGTATAGGCAGCAAGG
24. Northern_greater_galago Otolemur garnettii		ATGGTCCGGTACCGTGTGAGGAGCCCCAGCGAACATGCGAACCAGGGGTTGAGGCAGGAAGG
25. Philippine_tarsier Carlito syrichta		ATGGTCCGCCACCGCGGGAGCAGCCCGAGCCAGCACCCGCCCCAGGGCTCCCAGGTGCAGGG
26. Sunda_flying_lemur Galeopterus variegatus		ATGGTCCGATACCGGGTGAGGAGCCCAAGTGAACATCCGAACCAGGGGTTCAGGCAGCAGAG

Species/Abbrv	Group Name	* * * * * * * * *
27. Chinese_tree_shrew Tupaia chinensis		ATGGTCCGGTACCGCGAGCGCAGCCCGAGTGAACACCCCCACCAGGGGCACATGCAGCAGGC
28. House_mouse Mus musculus		ATGGTTCGCTACCGAATGAGGAGCCCCAGTGAGGGTCCGCACCAGGGG--------------
29. Ryukyu_mouse Mus caroli		ATGGTTCGCTACCGAATGAGGAGCCCCAGTGAGGGTCCGCACCAGGGG--------------
30. Shrew_mouse Mus pahari		ATGGTTCGCTACCGAATGAGGAGCCCCAGTGAGGGACCCCACCAGGGG--------------
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		ATGGTTCGCTACCGAATGAGGAGCCCCAGTGAGCGTCCACACCAGGGG--------------
32. Norweigan_rat Rattus norvegicus		ATGGTTCGCTACCGAATGAGGAGCCCCAGTGAGGGTCAGCACCAGGGG--------------
33. Prarie_vole Microtus ochrogaster		ATGGTTCGTTACCGAATGAGGAGCCCCAGTGAGCATCCACACCAGGGG--------------
34. Mongolian_gerbil Meriones unguiculatus		ATGGTTCGTTACCTAATAAGGAGCCCCAGTGAGGGGCCTGGGCAAGAA--------------
35. Golden_hamster Mesocricetus auratus		ATGGTTCGTTACCGAATGAGGAGCCCCAGTGAGCGTCCGCACCAGGGG--------------
36. Lesser_Egyptian_jerboa Jaculus jaculus		ATGGTCCGCTACCGTGTGAGGAGCCCCAGCGAGCGTCCGGGGCAG-----------------
37. Upper_Galilee_mountains_blind_mole Nannospalax galili		ATGGTCCGATACCGCATAAGGAGCCCCAGTGAGCATCCGCACCAGGGG--------------
38. Naked_mole_rat Heterocephalus_glaber		ATGGTCCGCTGCCGCATGAGGAGCCCCAGTGAGCGCCCGCTCCAG-----------------
39. Damara_mole_rat Fukomys damarensis		ATGGTCCGCTGCTACACGAGGAGCCGCAGTGGGCGCCCGCTCCAG-----------------
40. Degu Octodon degus		ATGGTCCGCTGCCGAGCGAGGAGCCCCAGCGAGCACCGGCTCCAG-----------------
41. Long-tailed_chinchilla Chinchilla lanigera		ATGGTCCGCTGCCGAGTGAGGAGCCCCAGCCATCACCCTCACCAG-----------------
42. Alpine_marmot Marmota marmota marmota		ATGGTCCGATGCCGCGTGAGGAACCCCGGTGAGCGT---CTGCAGCAGGGGCCCAGGCAGGA
43. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		ATGGTCCGATGCCGCGTGAGGAACCCCGGTGACCGT---CTGCAGCAGGGGCCCAGGCAGGA
44. American_pika Ochotona princeps		ATGGTCCGGTATCGGGCGAGAAGCCAGAGCGAACACCCACACGAGAAA--------------
45. Rabbit Oryctolagus cuniculus		ATGGTCCGGTATCGAGCGAGGAGCCCGAGCGAACATCCACACGGGGAA--------------
46. Sheep Ovis aries musimon		ATGGTCCGATGCTGCGTGAAGAGTCCGACTGAAAGTCCACCC---------GGGCAGCAGGG
47. Goat Capra hircus		ATGGTCCGATGCTGCGTGAAGAGTCCGACTGAAAGTCCACCT---------GGGCAGCAGGG
48. Texas_white-tailed_deer Odocoileus virginianus texanus		ATGGTCCGATGCCGCGTGAAGAGTCCGACTGAAAGTCCAACC---------GGGCAGCAGGG
49. Cattle Bos taurus		ATGGTCCGATGCCACGTGAAGAGTCCAACTGAAAGTCCACCC---------GGGCAGCAGGG
50. American_bison Bison bison bison		ATGGTCCGATGCCACGTGAAGAGTCCGACTGAAAGTCCACCC---------GGGCAGCAGGG
51. Water_buffalo Bubalus bubalis		ATGGTCCGATGCCGTGTGAAGAGTCCGACTGAAAGTCGACCC---------AGGCAGCAGGG
52. Pig Sus scrofa		ATGGTCCGATGCCGCGTGCGGAGTCCGAGCGAAAGTCCG---------------CAGCAGGG
53. Domestc_cat Felis catus		ATGGTCCGATGCTGCAGGAGGAGTCCGAGCGGACACCCA------------CGGCAGGGGCA

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Species/Abbrv                                         Group Name  ***** **              *  *
54. Domestic_ferret  Mustela putorius furo                        ATGGTCCGCTGCCATGCACTGAACCCGAGTGAGCGTTCGCAGCAGGGGCAGGGCCAGGGGCAG
55. Northern_sea_otter  Enhydra lutris kenyoni                    ATGGTCCGCCACCGGGCACTGAACCCGAGTGCGCGTCCGCAGCAGGGGCAGGGCCAGGGGCAG
56. Weddell_seal  Leptonychotes weddellii                          ATGGTCCGCTGCCGCGGGAGGAGTCCGAGCGAGCGTCCACAGCAGGGGCAGGGCCATGGGCAG
57. Dog  Canis lupus familiaris                                   ATGGTCCGATGCCGCGGGAGGAGTCCCAGCGAACATCCA---------------CAGCATGGG
58. Przewalskiis_horse  Equus przewalskii                         ATGGTCCGATACCGTGTGCGGAGTCCCAGCGAACGGCCC---------------CAGTCGGGG
59. Horse  Equus caballus                                         ATGGTCCGATACCGTGTGCGGAGTCCCAGCGAACGGCCC---------------CAGTCGGGG
60. Ass  Equus asinus                                             ATGGTCCGATACCGCGTGCGGAGTCCCAGCGAACGGCCC---------------CAGTCGGGG
61. Southern_white_rhinocerous  Ceratotherium simum simur         ATGGTCCGCCACCGCGTGAGGAGTCCCAGCGAGCGGCCC---------------CAGCAGGGG
62. Little_brown_bat  Myotis lucifugus                            ATGGTCCGACACAACGCGAGGAGTCTGAGCCAACGCCCA------------------------
63. Brandts_bat  Myotis brandtii                                  ATGGTCCGACACAACGCGAGGAGTCTGAGCCAACGCCCA------------------------
64. Big_brown_bat  Eptesicus fuscus                               ATGGTCCGACACAACGCCAGGAGTCTGAGCGAACGCCCA------------------------
65. Egyptian rousette  Rousettus aegyptiacus                      ATGGTCCGACACCGCACGAGGAGTCCGAGTGAAACTCCA------------------------
66. Large_flying_fox  Pteropus vampyrus                           ATGGTCCGACACCGCACGAAGAGTCCAAGTGAAACTCCA------------------------
67. Small_Madagscar_hedgehog  Echinops telfairi                   ATGGTCCGATACCGCGTGAGGAGCCCCAGCGAGCATCCGCAGGAGGGCTGCAGGCAGCAGGGC
68. African_savannah_elephant  Loxodonta africana                 ATGGTCCGATACCGCGTGAGGAGCCCAAGCGAGCGTCGGTATCAGGTGTACAGGCAGCAGGGC
69. Florida_manatee  Trichechus manatus latirostris               ATGGTCCGATACCGCGTGAGGAGCCCGAGCGAGCGTCCGCATCTGGTGTACAGGCAGCAGGGC
70. Aardvark  Orycteropus afer afer                               ATGGTCCGCTACCGCACGAGGAGCCCGAGCGAGCATCTGCGCCAGGGGTACAGGCTGCAGAAC
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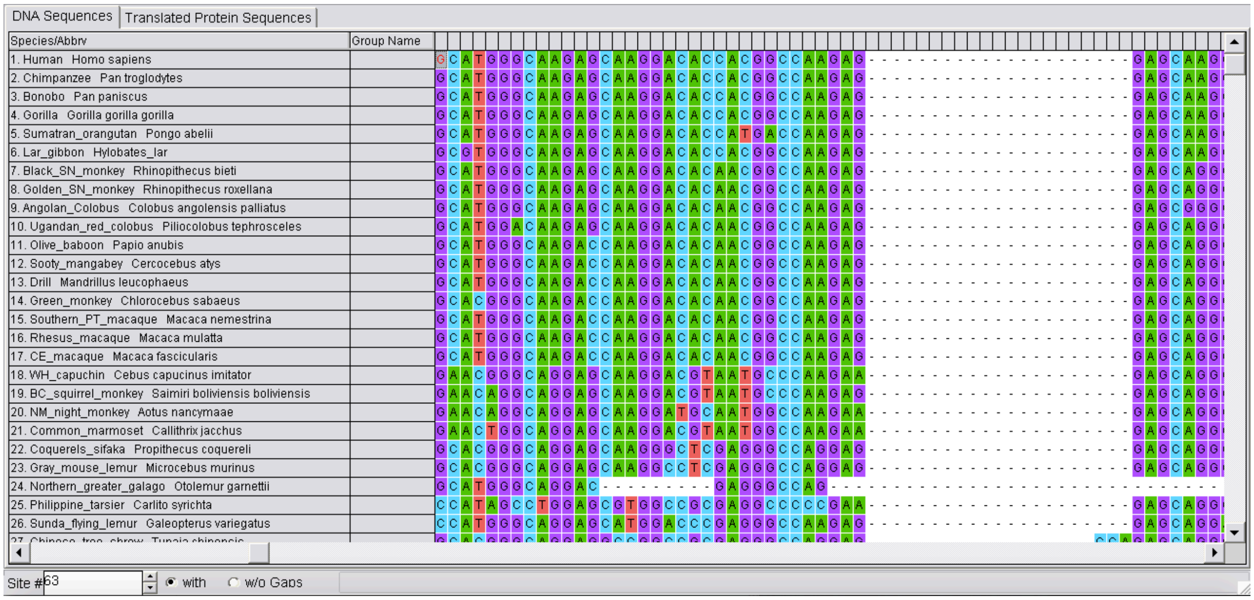

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Species/Abbrv                                         Group Name
1. Human  Homo sapiens                                            GCATGGGCAAGAGCAAGGACACCACGGCCAAGAG---------------------GAGCAAG
2. Chimpanzee  Pan troglodytes                                    GCATGGGCAAGAGCAAGGACACCACGGCCAAGAG---------------------GAGCAAG
3. Bonobo  Pan paniscus                                           GCATGGGCAAGAGCAAGGACACCACGGCCAAGAG---------------------GAGCAAG
4. Gorilla  Gorilla gorilla gorilla                               GCATGGGCAAGAGCAAGGACACCACGGCCAAGAG---------------------GAGCAAG
5. Sumatran_orangutan  Pongo abelii                               GCATGGGCAAGAGCAAGGACACCATGACCAAGAG---------------------GAGCAAG
6. Lar_gibbon  Hylobates_lar                                      GCGTGGGCAAGAGCAAGGACACCACGGCCAAGAG---------------------GAGCAAG
7. Black_SN_monkey  Rhinopithecus bieti                           GCATGGGCAAGAGCAAGGACACAACGGCCAAGAG---------------------GAGCAGG
8. Golden_SN_monkey  Rhinopithecus roxellana                      GCATGGGCAAGAGCAAGGACACAACGGCCAAGAG---------------------GAGCAGG
9. Angolan_Colobus  Colobus angolensis palliatus                  GCATGGGCAAGAGCAAGGACACAACGGCCAAGAG---------------------GAGCGGG
10. Ugandan_red_colobus  Piliocolobus tephrosceles                GCATGGACAAGAGCAAGGACACAACGGCCAAGAG---------------------GAGCAGG
11. Olive_baboon  Papio anubis                                    GCATGGGCAAGACCAAGGACACAACGGCCAAGAG---------------------GAGCAGG
12. Sooty_mangabey  Cercocebus atys                               GCATGGGCAAGACCAAGGACACAACGGCCAAGAG---------------------GAGCAGG
13. Drill  Mandrillus leucophaeus                                 GCATGGGCAAGACCAAGGACACAACGGCCAAGAG---------------------GAGCAGG
14. Green_monkey  Chlorocebus sabaeus                             GCACGGGCAAGACCAAGGACACAACGGCCAAGAG---------------------GAGCAGG
15. Southern_PT_macaque  Macaca nemestrina                        GCATGGGCAAGACCAAGGACACAACGGCCAAGAG---------------------GAGCAGG
16. Rhesus_macaque  Macaca mulatta                                GCATGGGCAAGACCAAGGACACAACGGCCAAGAG---------------------GAGCAGG
17. CE_macaque  Macaca fascicularis                               GCATGGGCAAGACCAAGGACACAACGGCCAAGAG---------------------GAGCAGG
18. WH_capuchin  Cebus capucinus imitator                         GAACGGGCAGGAGCAAGGACGTAATGCCCAAGAA---------------------GAGCAGG
19. BC_squirrel_monkey  Saimiri boliviensis boliviensis           GAACAGGCAGGAGCAAGGACGTAATGCCCAAGAG---------------------GAGCAGG
20. NM_night_monkey  Aotus nancymaae                              GAACAGGCAGGAGCAAGGATGCAATGGCCAAGAA---------------------GAGCAGG
21. Common_marmoset  Callithrix jacchus                            GAACTGGCAGGAGCAAGGACGTAATGGCCAAGAA---------------------GAGCAGG
22. Coquerels_sifaka  Propithecus coquereli                       GCACGGGCAGGAGCAAGGGCTCGAGGGCCAGGAG---------------------GAGCAGG
23. Gray_mouse_lemur  Microcebus murinus                          GCACGGGCAGGAGCAAGGCCTCGAGGGCCAGGAG---------------------GAGCAGG
24. Northern_greater_galago  Otolemur garnettii                   GCATGGGCAGGAC---------GAGGGCCAG-------------------------------
25. Philippine_tarsier  Carlito syrichta                          CCATAGCCTGGAGCGTGGCCGCGAGGCCCCCGAA---------------------GAGCAGG
26. Sunda_flying_lemur  Galeopterus variegatus                    CCATGGGCAGGAGCATGGACCCGAGGGCCAAGAG---------------------GAGCAGG
27. Chinese_tree_shrew  Tupaia chinensis                          GCACGGGCAGGAGGCCGGCCGCGAGGGCCAGGAG------------------CCAGAGCAGG
```
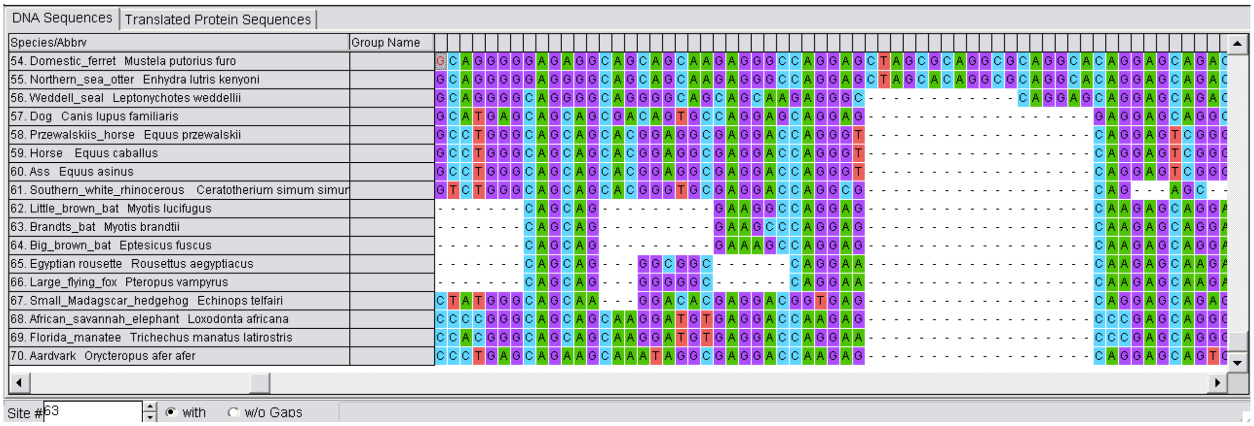

Site # 63 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
27. Chinese_tree_shrew Tupaia chinensis		GCACGGGCAGGAGGCCGGCCGCGAGGGCCAGGAG------------------CCAGAGCAGG
28. House_mouse Mus musculus		-CCTGGACAAGACCATGAACGCGAGGAGCAGGGG------------------CAGGGGCAAG
29. Ryukyu_mouse Mus caroli		-CCTGGGCAAGACCATGAACGCGAGGAGCAGGGG------------------CAGGGGCAAG
30. Shrew_mouse Mus pahari		-CCTGGGCAAGACCATGAACGTGAGGAGCAGGGG------------------CAGGGGCAAG
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		-CCTGGGCAAGAACATGGACGAGAAGAGGAA---------------------CAGGGGCAAG
32. Norweigan_rat Rattus norvegicus		-CCTGGGCAAGACCATGAGCGCGAGGAGCAGGGG------------------CAGGGGCAAG
33. Prarie_vole Microtus ochrogaster		-CCTGGGCGAGACGATGGACCCGACGAGCAGGGG------------------CAGGGGCAAG
34. Mongolian_gerbil Meriones unguiculatus		-CATGGA------------CGCGAGGAGCAGAGG------------------CAAGGG----
35. Golden_hamster Mesocricetus auratus		-CCTGGGCAAGAACATGGACGTGAAGAGCAAGGG------------------CAGGGGCAAG
36. Lesser_Egyptian_jerboa Jaculus jaculus		----------GACCGTGGGTCTGAGGGC------------------------CAGGAGCAGG
37. Upper_Galilee_mountains_blind_mole Nannospalax galili		-CCTGGGCAGGAATATGGACGTGAGGAGCAGGGA------------------GAGGAGCAGG
38. Naked_mole_rat Heterocephalus_glaber		-GCGAACAGCCCGGAGTCTGGTGAGGGCCAGGAG------------------CAGGAGCGGG
39. Damara_mole_rat Fukomys damarensis		-GTGCACAGCCTGAAGTCTGGCGAGGGCCAAGAG------------------CAGGAGCAGA
40. Degu Octodon degus		-GCACACAGCCAGGAGTCTGGTGAGGGCCAGGAG------------------CAGGGGCAGG
41. Long-tailed_chinchilla Chinchilla lanigera		-------------GAGTCTGGTGAGGGCCAGCAG------------------CAGGAGCAGG
42. Alpine_marmot Marmota marmota marmota		CCCGGGATGTGAGCACCAGGACCAGGAGCAGGAC------------------CGGGAGCAGG
43. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		CGCGGGATGTGAGGACCCGGAGCGGGAGCAGGAG------------------CAGGGGCAGG
44. American_pika Ochotona princeps		-CATGAGCGGCAGCATGAACATGACGACCAGGAC------------------CCGGATCAGG
45. Rabbit Oryctolagus cuniculus		-CATGGGCCGGAGCACGAAGGCGAGGGCCAGGAG------------------CCGGACCAGG
46. Sheep Ovis aries musimon		CTCCGGGCAGCAGGGCGAGACGGAGAGCCCAGAT------------------CAGACGCGGG
47. Goat Capra hircus		CTCCGGGCAGCAGGGCGAGACAGAGAGCCCGGAT------------------CAGACGCGGG
48. Texas_white-tailed_deer Odocoileus virginianus texanus		CTCCGGGCAGCAGGGCGAGACGGAGCGCCCGGAA------------------GAGACGCAGG
49. Cattle Bos taurus		CTCCGGGCAGCAGGGCGAGACGGAGCACCCGGAT------------------CAGGCACGGG
50. American_bison Bison bison bison		CTCCGGGCAGCAGGGCGAGACGGAGCACCCGGAT------------------CAGGCACGGG
51. Water_buffalo Bubalus bubalis		CTCCGGGCAGCAGGGCGAGACAGAGCACCCGGAT------------------CAGGCGCGGG
52. Pig Sus scrofa		CTCTGGGCAGCAGCGCGAAAACGAGCGCCAGGAC------------------CAGGACCAGG
53. Domestc_cat Felis catus		GGAGCACGGCCAGCACGAGTGCCAGGACAAGGAG------------------CGGGAGCAGG

Site # 63 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
54. Domestic_ferret Mustela putorius furo		GCAGGGGGAGAGGCAGCAGCAAGAGGGCCAGGAGCTAGCGCAGGCGCAGGCACAGGAGCAGA
55. Northern_sea_otter Enhydra lutris kenyoni		GCAGGGGGAGGGGCAGCAGCAAGAGGGCCAGGAGCTAGCACAGGCGCAGGCACAGGAGCAGA
56. Weddell_seal Leptonychotes weddellii		GCAGGGGCAGGGGCAGGGGCAGCAGCAAGAGGGC------------CAGGAGCAGGAGCAGA
57. Dog Canis lupus familiaris		GCATGAGCAGCAGCGACAGTGCCAGGAGCAGGAG------------------GAGGAGCAGG
58. Przewalskiis_horse Equus przewalskii		GCCTGGGCAGCAGCACGGAGGCGAGGACCAGGGT------------------CAGGAGTCGG
59. Horse Equus caballus		GCCTGGGCAGCAGCACGGAGGCGAGGACCAGGGT------------------CAGGAGTCGG
60. Ass Equus asinus		GCCTGGGCAGCAGCACGGAGGCGAGGACCAGGGT------------------CAGGAGTCGG
61. Southern_white_rhinocerous Ceratotherium simum simur		GTCTGGGCAGCAGCACGGGTGCGAGGACCAGGCG------------------CAG---AGC-
62. Little_brown_bat Myotis lucifugus		-------CAGCAG---------GAAGGCCAGGAG------------------CAAGAGCAGG
63. Brandts_bat Myotis brandtii		-------CAGCAG---------GAAGCCCAGGAG------------------CAAGAGCAGG
64. Big_brown_bat Eptesicus fuscus		-------CAGCAG---------GAAAGCCAGGAG------------------CAAGAGCAGG
65. Egyptian rousette Rousettus aegyptiacus		-------CAGCAG---GGCGGC------CAGGAA------------------CAAGAGCAAG
66. Large_flying_fox Pteropus vampyrus		-------CAGCAG---GGGGGC------CAGGAA------------------CAAGAGCAAG
67. Small_Madagscar_hedgehog Echinops telfairi		CTATGGGCAGCAA---GGACACGAGGACGGTGAG------------------CAGGAGCAGA
68. African_savannah_elephant Loxodonta africana		CCCCGGGCAGCAGCAAGGATGTGAGGACCAAGAG------------------CCCGAGCAGG
69. Florida_manatee Trichechus manatus latirostris		CCACGGGCAGCAGCAAGGATGTGAGGACCAGGAA------------------CCCGAGCAGG
70. Aardvark Orycteropus afer afer		CCCTGAGCAGAAGCAAATAGGCGAGGACCAAGAG------------------CAGGAGCAGT

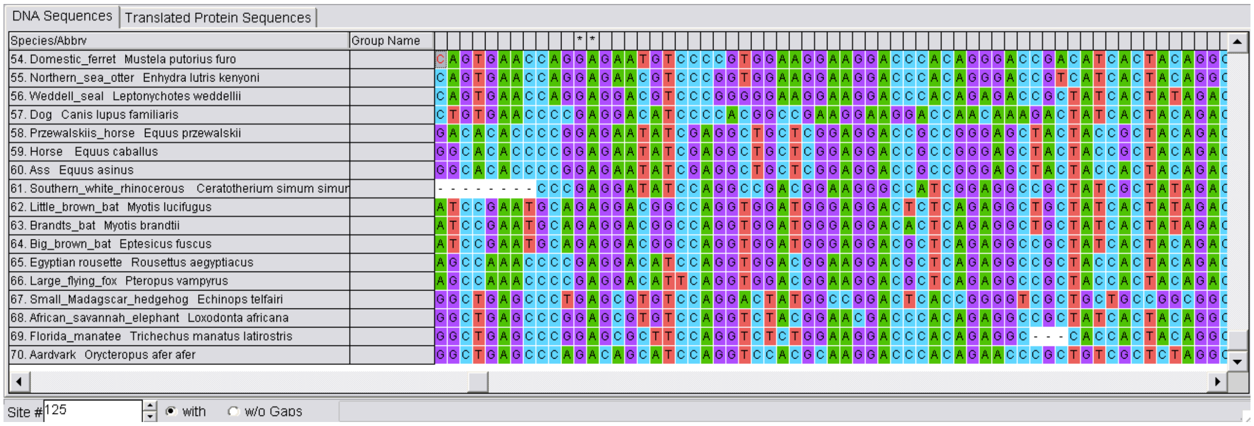
Site # 63 ● with ○ w/o Gaps

Species/Abbrv	Group Name
1. Human Homo sapiens	
2. Chimpanzee Pan troglodytes	
3. Bonobo Pan paniscus	
4. Gorilla Gorilla gorilla gorilla	
5. Sumatran_orangutan Pongo abelii	
6. Lar_gibbon Hylobates_lar	
7. Black_SN_monkey Rhinopithecus bieti	
8. Golden_SN_monkey Rhinopithecus roxellana	
9. Angolan_Colobus Colobus angolensis palliatus	
10. Ugandan_red_colobus Piliocolobus tephrosceles	
11. Olive_baboon Papio anubis	
12. Sooty_mangabey Cercocebus atys	
13. Drill Mandrillus leucophaeus	
14. Green_monkey Chlorocebus sabaeus	
15. Southern_PT_macaque Macaca nemestrina	
16. Rhesus_macaque Macaca mulatta	
17. CE_macaque Macaca fascicularis	
18. WH_capuchin Cebus capucinus imitator	
19. BC_squirrel_monkey Saimiri boliviensis boliviensis	
20. NM_night_monkey Aotus nancymaae	
21. Common_marmoset Callithrix jacchus	
22. Coquerels_sifaka Propithecus coquereli	
23. Gray_mouse_lemur Microcebus murinus	
24. Northern_greater_galago Otolemur garnettii	
25. Philippine_tarsier Carlito syrichta	
26. Sunda_flying_lemur Galeopterus variegatus	

Site # 125 ● with ○ w/o Gaps

Species/Abbrv	Group Name
27. Chinese_tree_shrew Tupaia chinensis	
28. House_mouse Mus musculus	
29. Ryukyu_mouse Mus caroli	
30. Shrew_mouse Mus pahari	
31. Prarie_deer_mouse Peromyscus maniculatus bairdii	
32. Norweigan_rat Rattus norvegicus	
33. Prarie_vole Microtus ochrogaster	
34. Mongolian_gerbil Meriones unguiculatus	
35. Golden_hamster Mesocricetus auratus	
36. Lesser_Egyptian_jerboa Jaculus jaculus	
37. Upper_Galilee_mountains_blind_mole Nannospalax galili	
38. Naked_mole_rat Heterocephalus_glaber	
39. Damara_mole_rat Fukomys damarensis	
40. Degu Octodon degus	
41. Long-tailed_chinchilla Chinchilla lanigera	
42. Alpine_marmot Marmota marmota marmota	
43. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus	
44. American_pika Ochotona princeps	
45. Rabbit Oryctolagus cuniculus	
46. Sheep Ovis aries musimon	
47. Goat Capra hircus	
48. Texas_white-tailed_deer Odocoileus virginianus texanus	
49. Cattle Bos taurus	
50. American_bison Bison bison bison	
51. Water_buffalo Bubalus bubalis	
52. Pig Sus scrofa	
53. Domestc_cat Felis catus	

Site # 125 ● with ○ w/o Gaps

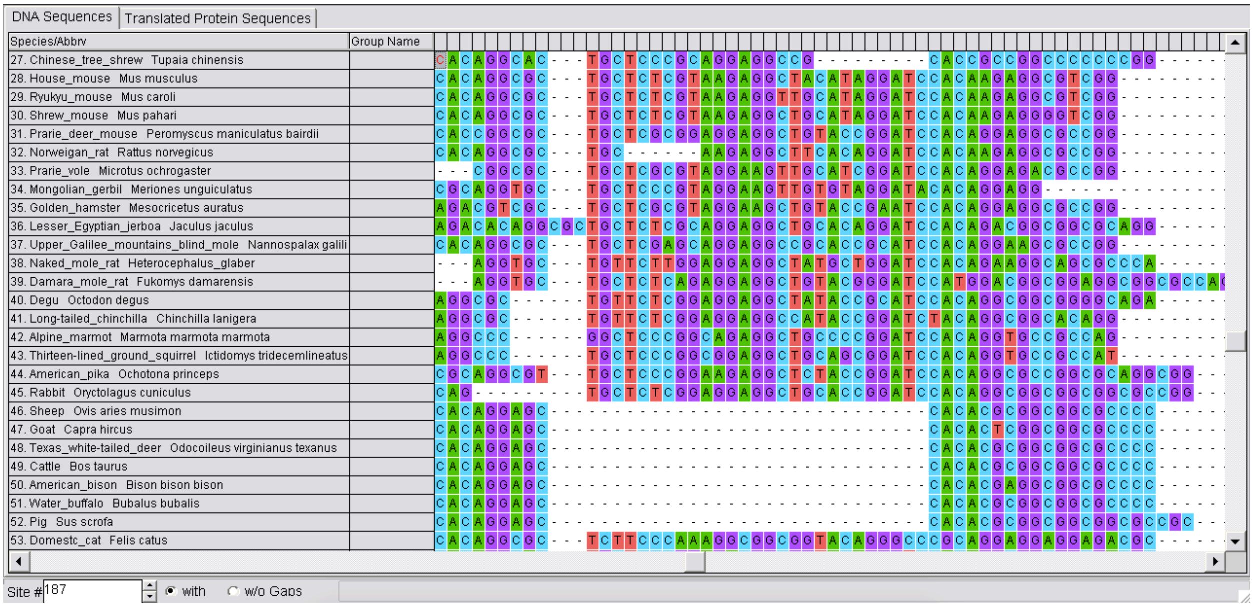


Species/Abbrv	Group Name	* *
54. Domestic_ferret Mustela putorius furo		CAGTGAACCAGGAGAATGTCCCCGTGGAAGGAAGGACCCACAGGGACCGACATCACTACAGGC
55. Northern_sea_otter Enhydra lutris kenyoni		CAGTGAACCAGGAGAACGTCCCGGTGGAAGGAAGGACCCACAGGGACCGTCATCACTACAGGC
56. Weddell_seal Leptonychotes weddellii		CAGTGAACCAGGAGGACGTCCCGGGGGAAGGAAGGACCCACAGAGACCGCTATCACTATAGAC
57. Dog Canis lupus familiaris		CTGTGAACCCCGAGGACATCCCCACGGCCGAAGGAAGGACCAACAAAGACTATCACTACAGAC
58. Przewalskiis_horse Equus przewalskii		GACACACCCCGGAGAATATCGAGGCTGCTCGGAGGACCGCCGGGAGCTACTACCGCTACAGAC
59. Horse Equus caballus		GGCACACCCCGGAGAATATCGAGGCTGCTCGGAGGACCGCCGGGAGCTACTACCGCTACAGAC
60. Ass Equus asinus		GGCACACCCCGGAGAATATCGAGGCTGCTCGGAGGACCGCCGGGAGCTACTACCACTACAGAC
61. Southern_white_rhinocerous Ceratotherium simum simur		--------CCCGAGGATATCCAGGCCGACGGAAGGGCCATCGGAGGCCGCTATCGCTATAGAC
62. Little_brown_bat Myotis lucifugus		ATCCGAATGCAGAGGACGGCCAGGTGGATGGGAGGACTCTCAGAGGCTGCTATCACTATAGAC
63. Brandts_bat Myotis brandtii		ATCCGAATGCAGAGGACGGCCAGGTGGATGGGAGGACACTCAGAGGCTGCTATCACTATAGAC
64. Big_brown_bat Eptesicus fuscus		ATCCGAATGCAGAGGACGGCCAGGTGGATGGGAGGACGCTCAGAGGCCGCTATCACTACAGAC
65. Egyptian rousette Rousettus aegyptiacus		AGCCAAACCCCGAGGACATCCAGGTGGACGGAAGGACGCTCAGAGGCCGCTACCACTACAGAC
66. Large_flying_fox Pteropus vampyrus		AGCCAAACCCCGAGGACATTCAGGTGGACGGAAGGACGCTCAGAGGCCGCTACCACTACAGAC
67. Small_Madagscar_hedgehog Echinops telfairi		GGCTGAGCCCTGAGCGTGTCCAGGACTATGGCCGGACTCACCGGGGTCGCTGCTGCCGGCGGC
68. African_savannah_elephant Loxodonta africana		GGCTGAGCCCGGAGCGTGTCCAGGTCTACGGAACGACCCACAGAGGCCGCTATCACTACAGGC
69. Florida_manatee Trichechus manatus latirostris		GGCTGAGCCCGGAGCGCTTCCAGGTCTCTGGAAGGACCCACAGAGGC---CACCACTACAGGC
70. Aardvark Orycteropus afer afer		GGCTGAGCCCAGACAGCATCCAGGTCCACGCAAGGACCCACAGAACCCGCTGTCGCTCTAGGC

Site # 125 ● with ○ w/o Gaps

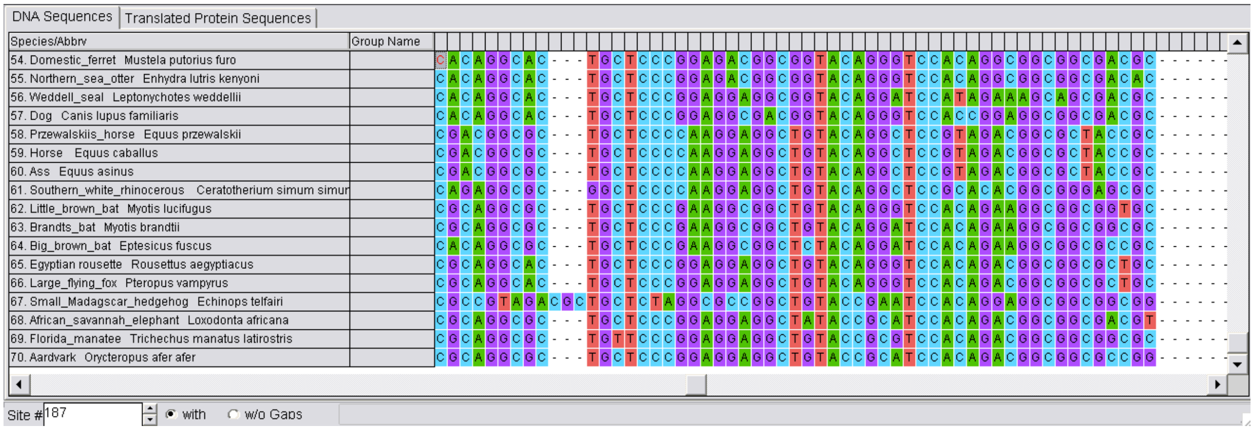
Species/Abbrv	Group Name	
1. Human Homo sapiens		CGCAGACAC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGGCGGCAGCATCGC-----
2. Chimpanzee Pan troglodytes		CGCAGACAC---TGCTCTCGAAGGAGGCTGCGTCGGATCCACAGACAGCAGCATCGC-----
3. Bonobo Pan paniscus		CGCAGACAC---TGCTCTCGAAGGAGGCTGCGCCGGATCCACAGACAGCAGCATCGC-----
4. Gorilla Gorilla gorilla gorilla		CGCAGACAC---TGCTCTCAAAGGAGGCTGCGCCGGATCCACAGACAGCAGCATCGC-----
5. Sumatran_orangutan Pongo abelii		CGCAGGCAC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACAGCAGCATCGC-----
6. Lar_gibbon Hylobates_lar		CGCAGGCAC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACAGCAGCATCGC-----
7. Black_SN_monkey Rhinopithecus bieti		CGCAGGCGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACGGCGGCATCGC-----
8. Golden_SN_monkey Rhinopithecus roxellana		CGCAGGCGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACGGCGGCATCGC-----
9. Angolan_Colobus Colobus angolensis palliatus		AGCAGGAGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACGGCGGCATCGC-----
10. Ugandan_red_colobus Piliocolobus tephrosceles		AGCAGGCGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACGGCGGCATCGC-----
11. Olive_baboon Papio anubis		CGCAGGCGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACGGCGGCATCGC-----
12. Sooty_mangabey Cercocebus atys		CGCAGGCGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACAGCGGCATCGC-----
13. Drill Mandrillus leucophaeus		CGCAGGCGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACGGCGGCATCGC-----
14. Green_monkey Chlorocebus sabaeus		CGCAGGCGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACGGCAGCATCGC-----
15. Southern_PT_macaque Macaca nemestrina		CGCAGGCGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACGGCGGCATCGC-----
16. Rhesus_macaque Macaca mulatta		CGCAGGCGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACGGCGGCATCGC-----
17. CE_macaque Macaca fascicularis		CGCAGGCGC---TGCTCTCGAAGGAGGCTGCACCGGATCCACAGACGGCGGCATCGC-----
18. WH_capuchin Cebus capucinus imitator		CGCAGGCGC---TGCTCTCGCAGACGGCTGTACCGGATTCACAGAAGACGGCGTCGC-----
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		CGCAGGCGC---TGCTCTCGCAGGAGGCTGTACCGGATCCACAGAAGACGGCGTCGC-----
20. NM_night_monkey Aotus nancymaae		CGCAGGAGC---TGCTCTCGCAGGAGGTTGAACCGGATCCACAGTAGACGGCGTCCC-----
21. Common_marmoset Callithrix jacchus		CGCAGGCGC---TGCTCTCGCAGGAGGCGGTACCGGATTCACAGAAGACGGAGTCGC-----
22. Coquerels_sifaka Propithecus coquereli		---AGGCGC---TGCTCTCGGAGGAGGCTGTGCCGGATCCACAGGCGGCGGCGACGC-----
23. Gray_mouse_lemur Microcebus murinus		AGGCGGCGC---TGCTCTCGGAGGAGGCTGTGCCGGATCCACAGGCGGCGGCGGCGC-----
24. Northern_greater_galago Otolemur garnettii		CACAGGCAC---TGCTCTCGGAGGAGACTGTACCGGATCCACAGACGGCGGCGCCGC-----
25. Philippine_tarsier Carlito syrichta		CAACGGCGC---TGCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN--
26. Sunda_flying_lemur Galeopterus variegatus		CGCAGGCGC---TGCTCTCCGAGGAGGCTAAGCCGGATGCACAGACGGCGGCGTCGG-----

Site # 187 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
27. Chinese_tree_shrew Tupaia chinensis		CACAGGCAC---TGCTCCCGCAGGAGGCCG---------CACCGCCGGCCCCCCCGG------
28. House_mouse Mus musculus		CACAGGCGC---TGCTCTCGTAAGAGGCTACATAGGATCCACAAGAGGCGTCGG--------
29. Ryukyu_mouse Mus caroli		CACAGGCGC---TGCTCTCGTAAGAGGTTGCATAGGATCCACAAGAGGCGTCGG--------
30. Shrew_mouse Mus pahari		CACAGGCGC---TGCTCTCGTAAGAGGCTGCATAGGATCCACAAGAGGGGTCGG--------
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		CACCGGCGC---TGCTCGCGGAGGAGGCTGTACCGGATCCACAGGAGGCGCCGG--------
32. Norweigan_rat Rattus norvegicus		CACAGGCGC---TGC------AAGAGGCTTCACAGGATCCACAAGAGGCGCCGG--------
33. Prarie_vole Microtus ochrogaster		---CGGCGC---TGCTCGCGTAGGAAGTTGCATCGGATCCACAGGAGACGCCGG--------
34. Mongolian_gerbil Meriones unguiculatus		CGCAGGTGC---TGCTCCCGTAGGAAGTTGTGTAGGATACACAGGAGG--------------
35. Golden_hamster Mesocricetus auratus		AGACGTCGC---TGCTCGCGTAGGAAGCTGTACCGAATCCACAGGAGGCGCCGG--------
36. Lesser_Egyptian_jerboa Jaculus jaculus		AGACACAGGCGCTGCTCTCGCAGGAGGCTGCACAGGATCCACAGACGGCGGCGCAGG-----
37. Upper_Galilee_mountains_blind_mole Nannospalax galili		CACAGGCGC---TGCTCGAGCAGGAGGCCGCACCGCATCCACAGGAAGCGCCGG--------
38. Naked_mole_rat Heterocephalus_glaber		---AGGTGC---TGTTCTTGGAGGAGGCTATGCTGGATCCACAGAAGGCAGCGCCCA-----
39. Damara_mole_rat Fukomys damarensis		---AGGTGC---TGCTCTCAGAGGAGGCTGTACGGGATCCATGGACGGCGGAGGCGGCGCCA
40. Degu Octodon degus		AGGCGC------TGTTCTCGGAGGAGGCTATACCGCATCCACAGGCGGCGGGGCAGA-----
41. Long-tailed_chinchilla Chinchilla lanigera		AGGCGC------TGTTCTCGGAGGAGGCCATACCGGATCTACAGGCGGCACAGG--------
42. Alpine_marmot Marmota marmota marmota		AGGCCC------GGCTCCCGGCAGAGGCTGCCCCGGATCCACAGGTGCCGCCAG--------
43. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		AGGCCC------TGCTCCCGGCGGAGGCTGCAGCGGATCCACAGGTGCCGCCAT--------
44. American_pika Ochotona princeps		CGCAGGCGT---TGCTCCCGGAAGAGGCTCTACCGGATCCACAGGCGCCGGCGCAGGCGG---
45. Rabbit Oryctolagus cuniculus		CAG---------TGCTCTCGGAGGAGGCTGCACCGGATCCACAGGCGGCGGCGGCGCCGG---
46. Sheep Ovis aries musimon		CACAGGAGC------------------------------CACACGCGGCGGCGCCCC-----
47. Goat Capra hircus		CACAGGAGC------------------------------CACACTCGGCGGCGCCCC-----
48. Texas_white-tailed_deer Odocoileus virginianus texanus		CACAGGAGC------------------------------CACACGCGGCGGCGCCCC-----
49. Cattle Bos taurus		CACAGGAGC------------------------------CACACGCGGCGGCGCCCC-----
50. American_bison Bison bison bison		CACAGGAGC------------------------------CACACGAGGCGGCGCCCC-----
51. Water_buffalo Bubalus bubalis		CACAGGAGC------------------------------CACACGCGGCGGCGCCCC-----
52. Pig Sus scrofa		CACAGGAGC------------------------------CACACGCGGCGGCGGCGCCGC---
53. Domestc_cat Felis catus		CACAGGCGC---TCTTCCCAAAGGCGGCGGTACAGGGCCCGCAGGAGGAGGAGACGC-----

Site # 187 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
54. Domestic_ferret Mustela putorius furo		CACAGGCAC---TGCTCCCGGAGACGGCGGTACAGGGTCCACAGGCGGCGGCGACGC-----
55. Northern_sea_otter Enhydra lutris kenyoni		CACAGGCAC---TGCTCCCGGAGACGGCGGTACAGGGTCCACAGGCGGCGGCGACAC-----
56. Weddell_seal Leptonychotes weddellii		CACAGGCAC---TGCTCCCGGAGGAGGCGGTACAGGATCCATAGAAAGCAGCGACGC-----
57. Dog Canis lupus familiaris		CACAGGCAC---TGCTCCCGGAGGCGACGGTACAGGGTCCACCGGAGGCGGCGACGC-----
58. Przewalskiis_horse Equus przewalskii		CGACGGCGC---TGCTCCCCAAGGAGGCTGTACAGGCTCCGTAGACGGCGCTACCGC-----
59. Horse Equus caballus		CGACGGCGC---TGCTCCCCAAGGAGGCTGTACAGGCTCCGTAGACGGCGCTACCGC-----
60. Ass Equus asinus		CGACGGCGC---TGCTCCCCAAGGAGGCTGTACAGGCTCCGTAGACGGCGCTACCGC-----
61. Southern_white_rhinocerous Ceratotherium simum simur		CAGAGGCGC---GGCTCCCCAAGGAGGCTGTACAGGCTCCGCACACGGCGGGAGCGC-----
62. Little_brown_bat Myotis lucifugus		CGCAGGCGC---TGCTCCCGAAGGCGGCTGTACAGGGTCCACAGAAGGCGGCGGTGC-----
63. Brandts_bat Myotis brandtii		CGCAGGCGC---TGCTCCCGAAGGCGGCTGTACAGGATCCACAGAAGGCGGCGGCGC-----
64. Big_brown_bat Eptesicus fuscus		CACAGGCGC---TGCTCCCGAAGGCGGCTCTACAGGATCCACAGAAGGCGGCGCCGC-----
65. Egyptian rousette Rousettus aegyptiacus		CGCAGGCAC---TGCTCCCGGAGGAGGCTGTACAGGGTCCACAGACGGCGGCGCTGC-----
66. Large_flying_fox Pteropus vampyrus		CGCAGGCAC---TGCTCCCGGAGGAGGCTGTACAGGGTCCACAGACGGCGGCGCTGC-----
67. Small_Madagscar_hedgehog Echinops telfairi		CGCCGTAGACGCTGCTCTAGGCGCCGGCTGTACCGAATCCACAGGAGGCGGCGGCGG-----
68. African_savannah_elephant Loxodonta africana		CGCAGGCGC---TGCTCCCGGAGGAGGCTATACCGCATCCACAGACGGCGGCGACGT-----
69. Florida_manatee Trichechus manatus latirostris		CGCAGGCGC---TGTTCCCGGAGGAGGCTGTACCGCGTCCACAGACGGCGGCGGCGC-----
70. Aardvark Orycteropus afer afer		CGCAGGCGC---TGCTCCCGGAGGAGGCTGTACCGCATCCACAGACGGCGGCGCCGG-----

Site # 187 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
1. Human Homo sapiens		-TCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
2. Chimpanzee Pan troglodytes		-TCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
3. Bonobo Pan paniscus		-TCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
4. Gorilla Gorilla gorilla gorilla		-TCCTGCAGAAGGCGCAAAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
5. Sumatran_orangutan Pongo abelii		-TCCTGCAAAAGGCGCAGAAGA---------CACTCCTGTAGGCACCGGAGGAAGCATCGCA
6. Lar_gibbon Hylobates_lar		-TCCTGCGGAAGGCGCCGAAGA---------CGCTCCTGCAGGCAGCGGAGGAGGCATCGCA
7. Black_SN_monkey Rhinopithecus bieti		-TCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
8. Golden_SN_monkey Rhinopithecus roxellana		-TCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
9. Angolan_Colobus Colobus angolensis palliatus		-TCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCAACGGAGGAGGCATCGCA
10. Ugandan_red_colobus Piliocolobus tephrosceles		-TCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCAACGGAGGAGGCATCGCA
11. Olive_baboon Papio anubis		-TCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
12. Sooty_mangabey Cercocebus atys		-TCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
13. Drill Mandrillus leucophaeus		-TCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
14. Green_monkey Chlorocebus sabaeus		-TCGTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
15. Southern_PT_macaque Macaca nemestrina		-TCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
16. Rhesus_macaque Macaca mulatta		-TCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
17. CE_macaque Macaca fascicularis		-TCCTGCAGAAGGCGCAGAAGA---------CGCTCCTGCAGGCACCGGAGGAGGCATCGCA
18. WH_capuchin Cebus capucinus imitator		-TCCTGCAGAAGGCGCAGAAGA---------CGTTGCTGCCGATACCGGAGGCGGTATCGCA
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		-TCCTGCAGAAGGCGCAGAAGG---------CGCTGCTGCCGATACCGGAGGCGGCACCGCA
20. NM_night_monkey Aotus nancymaae		-TCCTGCGGAAGGCGCAGAAAA---------CGCTGCTGCCGATCCCGGAGGAGGCCTCGCA
21. Common_marmoset Callithrix jacchus		-TCCTGCAGAAGGCGCAGAAGA---------CGCAGCTGCCGATACCGGAGAAGGCCTCGCA
22. Coquerels_sifaka Propithecus coquereli		-TCCTGCCGAAGGCGCAGAAGA---------CGCTGCTGCAGG------CGGAGGCATCGCA
23. Gray_mouse_lemur Microcebus murinus		-TCCTGCCGAAGGCGCAGGAGA---------CGCTGCTGCAGG------CGGAGGCACCGCA
24. Northern_greater_galago Otolemur garnettii		-TCCTGCCGGAGACGCAGACACAGACACACACGCTGCTGCAGACACAGGAGGAGG------A
25. Philippine_tarsier Carlito syrichta		-NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
26. Sunda_flying_lemur Galeopterus variegatus		-TCCTGCAGGAGACGCAGGAGA---------CGCAGCTGCAGG---AGGAGGCGT---CGCA

Site # 249 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
27. Chinese_tree_shrew Tupaia chinensis		-------CGGCGGCGGCGGCGC---------TCCAGCCGGAGGCACAGGAGGCGGCACCGCA
28. House_mouse Mus musculus		-TCATGCAGAAGGCGGAGGAGA---------CACTCCTGCCGCCACAGGAGGCGGCATCGCA
29. Ryukyu_mouse Mus caroli		-TCATGCAGAAGGCGGAGGAGA---------CACTCCTGCCGCTACAGGAGGCGGCATCGCA
30. Shrew_mouse Mus pahari		-TCATGCAGAAGGCGGAGGAGA---------CACTCCTGCGGCCAAAGGAGGCGGCATCGCA
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		-TCATGCCGGAGGCGAAGGAGA---------CGCTCCTGCCGCCACAGAAGGCGGCATCGCA
32. Norweigan_rat Rattus norvegicus		-TCATGCAGAAGGCGGAGGAGA---------CACTCCTGCCGCCACAGGAGGCGGCATCGCA
33. Prarie_vole Microtus ochrogaster		-TCATGCAGGAGGCGGAGACGT------------TCCTGCCGCCACAGGAGGCGGCATCGTA
34. Mongolian_gerbil Meriones unguiculatus		-TCGTGCAGGAGGCGGAGACGC------------TGCTGCCGCCACAGGAGGCGC------A
35. Golden_hamster Mesocricetus auratus		-TCATGCAGGAGGCGGAGGAGA---------CACTCCTGCCGTCACAGGAGACGGCATCGCA
36. Lesser_Egyptian_jerboa Jaculus jaculus		-TCCTGCAGGCGGCGCAGGAGACGC---------TCCTGCCGACACAGGAGGCGGCATCGCA
37. Upper_Galilee_mountains_blind_mole Nannospalax galili		-TCCTGCAGGAGGCCGAGGAGA---------CGCTCCTGCTGCCACAGGAAGCGGCAGCACA
38. Naked_mole_rat Heterocephalus_glaber		-TCCTGTCGAAGGCGCAGGAGA---------TGCACCTGTAGGAGGAGATGTCGCCAA----
39. Damara_mole_rat Fukomys damarensis		GTCCTGCGGAAGGCGCAGGAGA---------TGCACCTGTAGGAGGCCACGTCGCCGA----
40. Degu Octodon degus		-TCCTGCCGGAGGCGCAGGAGACGC---------AGCTGCAGGAGGCGACGT----------
41. Long-tailed_chinchilla Chinchilla lanigera		-TCCTGCCGAAGGCGCAGGAGACGC---------AGCTGCAGGAGACGCAGC---TGCAGGA
42. Alpine_marmot Marmota marmota marmota		-TCCTGCCAGAGGCACCGCAGGCGC------TGCAGGTGCAGATACAGGCGGCGGTGCTGCC
43. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		-TCCTGCCAGAGGCACCGCAGGCGC------TGCAGGTGCAGGTACAGGCGGCGGTGCTGCC
44. American_pika Ochotona princeps		-ATCTGCCGAAGGCGCAGGAGA---------CGTGTTTGCCGGCACCGGAGGCGCCACCATA
45. Rabbit Oryctolagus cuniculus		-GTGTGCAGGAGGCGCCGGAGA---------CGCGTTTGCCGGCACAGGAGGAGGCACCGCA
46. Sheep Ovis aries musimon		----TGCCGAAGGCGCCGGAGA---------AGGGCCTGCAGGCACAGGAGGCGC---CGCA
47. Goat Capra hircus		----TGCCGAAGGCGCCGGAGA---------AGGGCCTGCAGGCACAGGAGGCGC---CGCA
48. Texas_white-tailed_deer Odocoileus virginianus texanus		----TGCAGGAGGCGCCGGAGA---------CGGGCCTGCAGGCACAGGAGGCGC---CGTA
49. Cattle Bos taurus		----TACCGGAGGCGCCGGAGA---------AGGGCCTGCAGGCACAGGAGGCGC---CGCA
50. American_bison Bison bison bison		----TACCGGAGGCGCCGGAGA---------AGGGCCTGCAGGCACAGGAGGCGC---CGCA
51. Water_buffalo Bubalus bubalis		----TGCCGGAGGCGCCGGAGA---------AGGGCCTGCAGGCTCAGGAGGCGC---CTCA
52. Pig Sus scrofa		-TCCTGCCGGAGGCGCAGGAGA---------CGCGCCTGCCGGCACAGGCGGCAC---CGCA
53. Domestc_cat Felis catus		-TCCTGCCAGAGGAGAAGGCGCCAGAGA---GGTGCCTGCAGGTCCAGGACCGGAGGTGTGG

Site # 249 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
54. Domestic_ferret Mustela putorius furo		-TCCTGCTGCAGGAGGTGCCAGAGA------TGGGCTTGCAGGCGCAGGAGGCAC---CGCAG
55. Northern_sea_otter Enhydra lutris kenyoni		-TCCTGCTGCAGGAGGTGCCAGAGA------TGGGCTTGTAGGCGCAGGAGGCAC---CACAG
56. Weddell_seal Leptonychotes weddellii		-TCCTGCCGGAGGAGGCGGCACCGAAGA---TGCACCTGCAGGCACGGAAGGCAC---CACAG
57. Dog Canis lupus familiaris		-TCCTGCCGGAGGCGCCGCAGA---------CGGGCCTGCAGGCACAGGAGACAT---CACCG
58. Przewalskiis_horse Equus przewalskii		-TCCTCCAGGAGACGCCGGAGA---------CGCCCCTGCAGGCGCCGGAGGCAT---CGCAG
59. Horse Equus caballus		-TCCTCCAGGAGACGCCGGAGA---------CGCCCCTGCAGGCGCCGGAGGCAT---CGCAG
60. Ass Equus asinus		-TCCTCCAGGAGACGCAGGAGA---------CGCCCCTGCAGGCGCCGGAGGCAT---CGCAG
61. Southern_white_rhinocerous Ceratotherium simum simur		-TCGTGTGGAAGGCGCCAGAGA---------CGCGCGTGCAGGCACAGGAGGCGC---CGCAG
62. Little_brown_bat Myotis lucifugus		-TCATGCCGGAGACGCCGGAGA---------CGCTGCTGCAGGCGCAGGAGGCGC---CGCAG
63. Brandts_bat Myotis brandtii		-TCATGCCGGAGACGCCGGAGA---------CGCTGCTGCAGGCGCAGGAGGCGC---CGCAG
64. Big_brown_bat Eptesicus fuscus		-TCATGCCGGAGACGCCGGAGA---------CGTGCCTGCAGGCACAGGAGGCAC---CGCAG
65. Egyptian rousette Rousettus aegyptiacus		-TCCTGCCGAAGACGCCGCAGA---------CGCGCCTGCAGGCACAGAAGGCAC---CGCAG
66. Large_flying_fox Pteropus vampyrus		-TCCTGCCGAAGACGCCGCAGA---------CGCGCCTGCAGGCATAGGAGACAC---CGCAG
67. Small_Madagscar_hedgehog Echinops telfairi		-TCCTGTCGTCGGCGCCGCAGA---------CGCTGCTGCCGGCGACGCAGGCAT---CGTAG
68. African_savannah_elephant Loxodonta africana		-TCCTGCCGCAGTCGCCGGAGA---------CGGTGCTGCAGGCGCAGG---CAT---CGCAG
69. Florida_manatee Trichechus manatus latirostris		-TCCTGCCGCAGGCGCCGGAGA---------CGGTGCTGCAGGCGCGGG---CAT---CGCAG
70. Aardvark Orycteropus afer afer		-TCCTGCGGCAGACGCCGCCGC---------CGCTGTTGCAGGCGTAGG---CAT---CGCAG

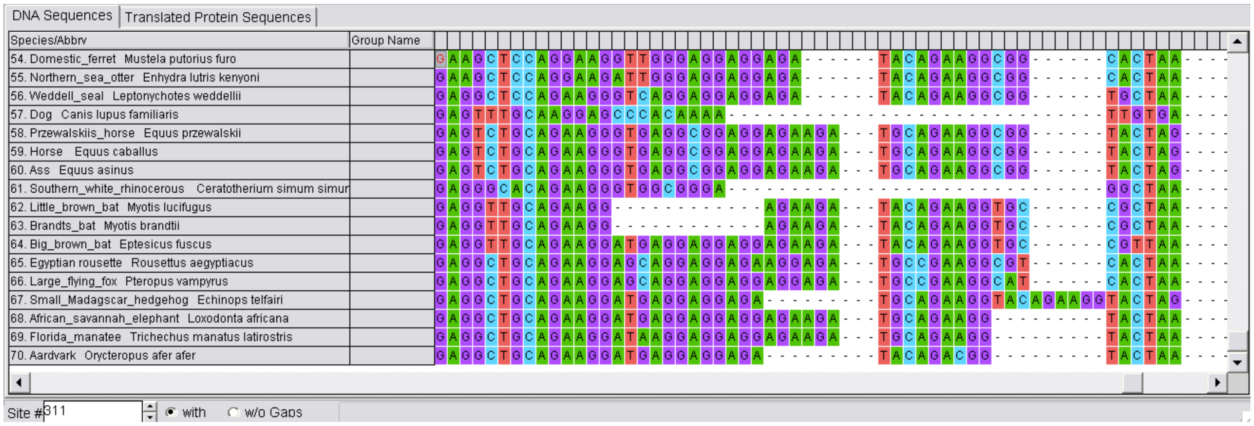
Site #249 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
1. Human Homo sapiens		GAGGCTGCAGA---ACCAGGAAGAGAACA------------TGCAGAAGG------CACTAA
2. Chimpanzee Pan troglodytes		GAGGCTGCAGA---ACCAGGAGGAGAACA------------TGCAGAAAG------CACTAA
3. Bonobo Pan paniscus		GAGGCTGCAGA---ACCAGGAGGAGAACA------------TGCAGAAAG------CACTAA
4. Gorilla Gorilla gorilla gorilla		AAGGCTGCAGA---ACCAGGAGGAGAACA------------TGCAGAAGG------CACTAA
5. Sumatran_orangutan Pongo abelii		GAGGCTGCAGA---ACCAGGAGGAGAACA------------TGCAGAAGG------CACTAA
6. Lar_gibbon Hylobates_lar		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------CACTAA
7. Black_SN_monkey Rhinopithecus bieti		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------TACTAA
8. Golden_SN_monkey Rhinopithecus roxellana		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------TACTAA
9. Angolan_Colobus Colobus angolensis palliatus		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------TACTAA
10. Ugandan_red_colobus Piliocolobus tephrosceles		GAGGTTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------TACTAA
11. Olive_baboon Papio anubis		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------CACTAA
12. Sooty_mangabey Cercocebus atys		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------CACTAA
13. Drill Mandrillus leucophaeus		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------CACTAA
14. Green_monkey Chlorocebus sabaeus		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------TACTAA
15. Southern_PT_macaque Macaca nemestrina		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------CACTAA
16. Rhesus_macaque Macaca mulatta		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------CACTAA
17. CE_macaque Macaca fascicularis		GAGGCTGCAGA---ACCAGGAGGAGAAGA------------TGCAGAAGG------CACTAA
18. WH_capuchin Cebus capucinus imitator		GAGGTAGCAGA---TCCAGGAGGAGGAGAAGA---------TGCAGAAGG------TACTAA
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		GAGTCTGCAAA---TCCAGGAGGAGGAGAAGA---------TGCAGAAGG------TACTAA
20. NM_night_monkey Aotus nancymaae		GAGGCTGCAGA---TCCAGGAGGAGGAGAAGA---------TGCAGAAGG------AACTAA
21. Common_marmoset Callithrix jacchus		GAGGCTGCAGA---TCCAGGAGGAGGAGAAGA---------TGCAGAAGG------TACTAA
22. Coquerels_sifaka Propithecus coquereli		GAGGCTGCAGA------AGGAGGAGGAGAAGA---------TGCAGAAGGCGCTACTACTAA
23. Gray_mouse_lemur Microcebus murinus		GAGGCTGCAGA------AGGAGGAGGAGAAGA---------TGCAGAAGGCGCTACTACTGA
24. Northern_greater_galago Otolemur garnettii		GAGGCTGCAGA------AGGAGGAGGAGAAGA---------TGCAGAAGACGC---TACTAA
25. Philippine_tarsier Carlito syrichta		CTTGCAGA------CAGAGGAGACGG---------------TGCAGAAGGCCT------TAA
26. Sunda_flying_lemur Galeopterus variegatus		GAGTCTGCAGAAGAAGA------------------------------TACAGAAGGTACTAA
27. Chinese_tree_shrew Tupaia chinensis		

Site #311 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
27. Chinese_tree_shrew Tupaia chinensis		GAGGCTGCAGAAGAACCAGGAGGAGG---------------------GGATACAGAAGGTAC
28. House_mouse Mus musculus		GAGGCTGCAGAAGATCCCGAAGGAGGAGGAGA---TGCAGGTGCAGGAAATGTAGGAGGCAC
29. Ryukyu_mouse Mus caroli		GAGGCTGCAGAAGATCCCGAAGGAGGAGGAGA---TGCAGGTGCAGGAAATGTAGGAGGCAC
30. Shrew_mouse Mus pahari		GAGGCTGCAGAAGATCCCGAAGGAGGAGGAGA---TGCAGGTGCAGGAAATGTAGGAGGCAC
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		GAGGCTGCAGAAGATCCCGAAGGAGGAGGAGA---TGCAGGTGCAGGAGGTGTAGGAGG---
32. Norweigan_rat Rattus norvegicus		GAGGCTGCAGAAGATCCCGAAGGAGGAGGAGC---TGCAGGTGCAGGAAATGCAGGTGGCAC
33. Prarie_vole Microtus ochrogaster		GAGGCAGCAGAAGATCCCGAAGGAGGAGGAGA---TGTAGGTGCAGGAAGTGTAGGAGGCGC
34. Mongolian_gerbil Meriones unguiculatus		AAGGCTGC---------AGAAGGAGGAGGAGA---TGCAGGTGCAGAAGGTGCAGGAAG---
35. Golden_hamster Mesocricetus auratus		GAGGCTGCAGAAGATCACGCAGGAGGAGGAGA---TGCAGGTGCAGGAGGTGTAGGAGGCAC
36. Lesser_Egyptian_jerboa Jaculus jaculus		GAGGCTGCAGAAGGTACAGGAGGAGA---------TGCAGGTGCCGAAGACGCAGGCGGCAC
37. Upper_Galilee_mountains_blind_mole Nannospalax galili		GAGGTTGCAGAAGATCCCGAAGGAGGAGA------TGCAGGTGCAGGAGGTGTAGGAGACAC
38. Naked_mole_rat Heterocephalus_glaber		--GGTTGCAGAAGA---AGGAGGAGAAGA------TGCAGG------------------AGG
39. Damara_mole_rat Fukomys damarensis		--GGCTGCAGAAGA---CGGAGGACAAGT------TATAGG------------------AGG
40. Degu Octodon degus		-----CGCCGAGCCTGCAGAAGG---AGGAGGAGG---AGA---------TGC---AGGAGG
41. Long-tailed_chinchilla Chinchilla lanigera		GGCGACGCCGAGCCTGCAGAAGA---CGCAGGAGG---AGA------AGATGC---GGGAGG
42. Alpine_marmot Marmota marmota marmota		GCTGCTACCGAGTCTGCAGAAGAATCAGGAGGAAGAGGAGGTGCCGGAGGCAG---TAG---
43. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		GCTGCTACCGAGTCTGCAGAAGAGTCAGGAGGAAGAGGAGGTGCAGGAGGCGG---TAG---
44. American_pika Ochotona princeps		GA---------GTTTGCAGACAATCCGGGAGGAGGAGAAGATGCAGGAGGCACCAATGA---
45. Rabbit Oryctolagus cuniculus		GAGCTGGC------AAACGAACGAGGAGGAGG---AGAAGATGCAGGAGGCGCCACTAA---
46. Sheep Ovis aries musimon		GAGGCTGCCGAAGGATGAAGAGGAGGAGGAGGAGATGCGGAAGG------CAGCTCTAA---
47. Goat Capra hircus		GAGGCTGCCGAAGGATGAAGAGGAGGAGGAGGAGATGCGGAAGG------CAGCTCTAA---
48. Texas_white-tailed_deer Odocoileus virginianus texanus		GAGGCTGCCGAAGGATGAAGAGAAGGAGGAGGAGATGCGGAAGG------CAGCTCTAA---
49. Cattle Bos taurus		GAGGCTGCCGAAGGATGAGGAGGAGGAGGAGGAGATGCAGAAGG------CAGCTCTAA---
50. American_bison Bison bison bison		GAGGCTGCCGAAGGATGAGGAGGAGGAGGAGA---TGCGGAAGG------CAGCTCTAA---
51. Water_buffalo Bubalus bubalis		GAGGCTGCCAAAGGATGAGGAGGAGGAGGAGGAGATGCGGAAGG------CAGCTCTAA---
52. Pig Sus scrofa		GAGGCTGCAGACGGATCAGGAGGAGGAGAAGA---TGCAGAAGGAGG------CTCTAA---
53. Domestc_cat Felis catus		CCAGCCACAGAAGGGTCAGGACAAGGAGG------TGCCAGAGGCGA------CACTAA---

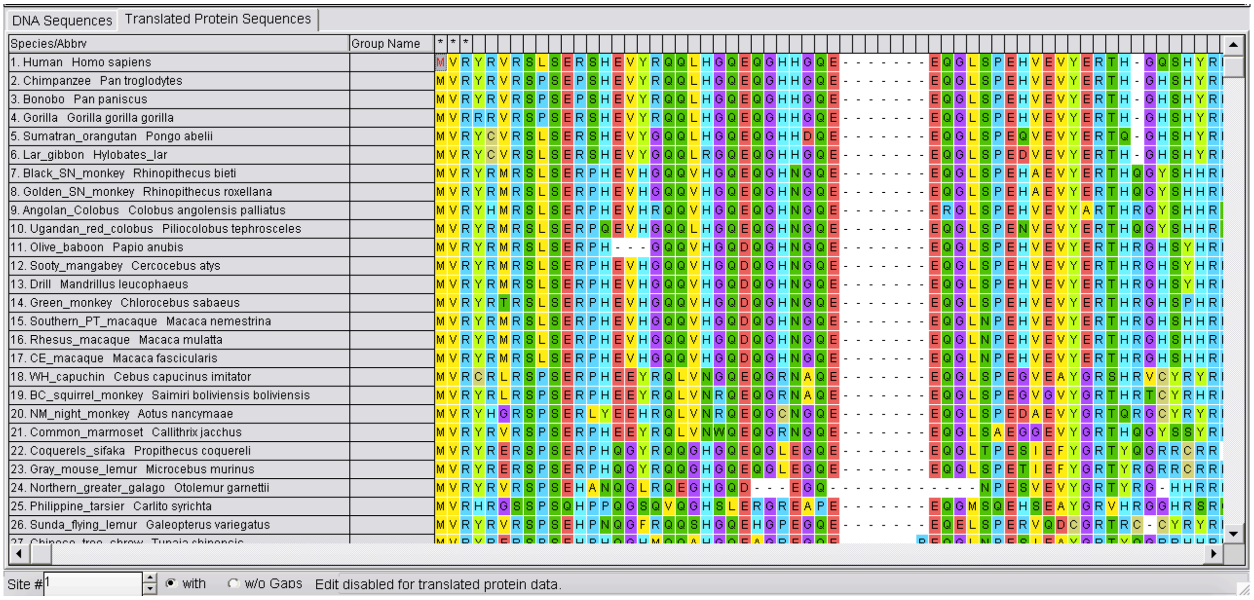
Site #311 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
54. Domestic_ferret Mustela putorius furo		GAAGCTCCAGGAAGGTTGGGAGGAGGAGA------TACAGAAGGCGG------CACTAA---
55. Northern_sea_otter Enhydra lutris kenyoni		GAAGCTCCAGGAAGATTGGGAGGAGGAGA------TACAGAAGGCGG------CACTAA---
56. Weddell_seal Leptonychotes weddellii		GAGGCTCCAGAAGGGTCAGGAGGAGGAGA------TACAGAAGGCGG------TGCTAA---
57. Dog Canis lupus familiaris		GAGTTTGCAAGGAGCCCACAAAA------------------------------TTGTGA---
58. Przewalskiis_horse Equus przewalskii		GAGTCTGCAGAAGGGTGAGGCGGAGGAGAAGA---TGCAGAAGGCGG------TACTAG---
59. Horse Equus caballus		GAGTCTGCAGAAGGGTGAGGCGGAGGAGAAGA---TGCAGAAGGCGG------TACTAG---
60. Ass Equus asinus		GAGTCTGCAGAAGGGTGAGGCGGAGGAGAAGA---TGCAGAAGGCGG------TACTAG---
61. Southern_white_rhinocerous Ceratotherium simum simur		GAGGGCACAGAAGGGTGGCGGGA------------------------------GGCTAA---
62. Little_brown_bat Myotis lucifugus		GAGGTTGCAGAAGG------------AGAAGA---TACAGAAGGTGC------CGCTAA---
63. Brandts_bat Myotis brandtii		GAGGTTGCAGAAGG------------AGAAGA---TACAGAAGGTGC------CGCTAA---
64. Big_brown_bat Eptesicus fuscus		GAGGTTGCAGAAGGATGAGGAGGAGGAGAAGA---TACAGAAGGTGC------CGTTAA---
65. Egyptian rousette Rousettus aegyptiacus		GAGGCTGCAGAAGGAGCAGGAGGAGAAGGAGA---TGCCGAAGGCGT------CACTAA---
66. Large_flying_fox Pteropus vampyrus		GAGGCTGCAGAAGGAGCAGGAGGAGGAGGAGA---TGCCGAAGGCAT------CACTAA---
67. Small_Madagscar_hedgehog Echinops telfairi		GAGGCTGCAGAAGGATGAGGAGGAGA---------TGCAGAAGGTACAGAAGGTACTAG---
68. African_savannah_elephant Loxodonta africana		GAGGCTGCAGAAGGATGAGGAGGAGGAGAAGA---TGCAGAAGG---------TACTAA---
69. Florida_manatee Trichechus manatus latirostris		GAGGCTGCAGAAGGATAAGGAGGAGGAGAAGA---TGCAGAAGG---------TACTAA---
70. Aardvark Orycteropus afer afer		GAGGCTGCAGAAGGATGAGGAGGAGA---------TACAGACGG---------TACTAA---

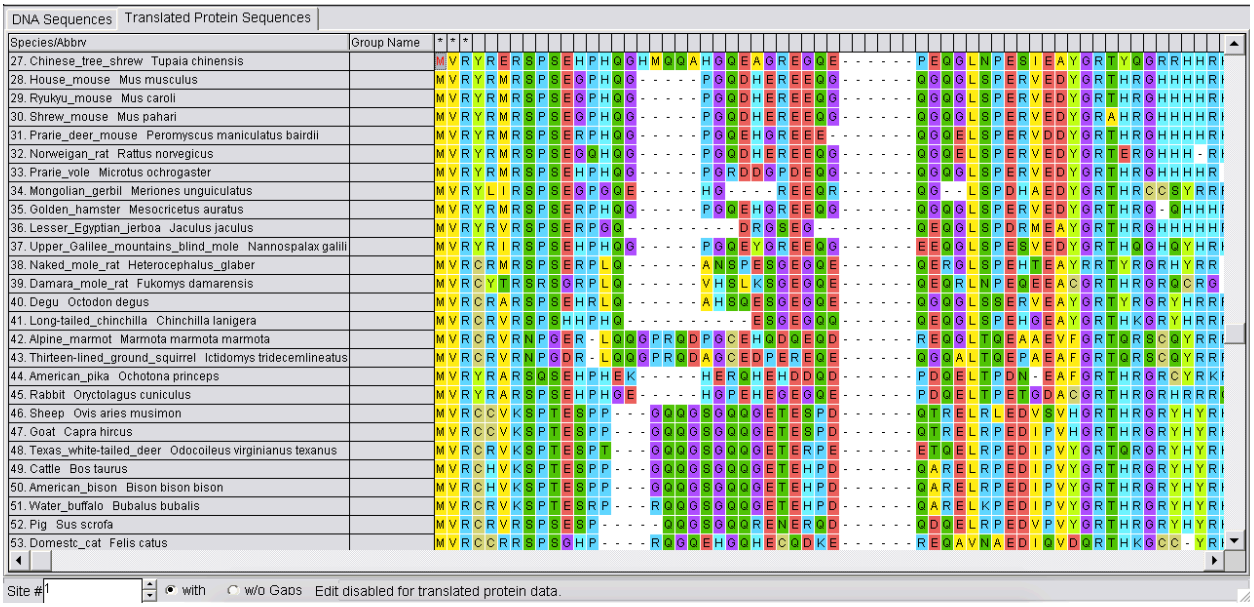
Site #311 ● with ○ w/o Gaps

The translated sequences



Species/Abbrv	Group Name	* * *
1. Human Homo sapiens		MVRYRVRSLSERSHEVYRQQLHGQEQGHHGQE-------EQGLSPEHVEVYERTH-GQSHYR
2. Chimpanzee Pan troglodytes		MVRYRVRSPSEPSHEVYRQQLHGQEQGHHGQE-------EQGLSPEHVEVYERTH-GHSHYR
3. Bonobo Pan paniscus		MVRYRVRSPSEPSHEVYRQQLHGQEQGHHGQE-------EQGLSPEHVEVYERTH-GHSHYR
4. Gorilla Gorilla gorilla gorilla		MVRRRVRSPSERSHEVYRQQLHGQEQGHHGQE-------EQGLSPEHVEVYERTH-GHSHYR
5. Sumatran_orangutan Pongo abelii		MVRYCVRSLSERSHEVYGQQLHGQEQGHHDQE-------EQGLSPEQVEVYERTQ-GHSHYR
6. Lar_gibbon Hylobates_lar		MVRYCVRSLSERSHEVYGQQLRGQEQGHHGQE-------EQGLSPEDVEVYERTH-GHSHYR
7. Black_SN_monkey Rhinopithecus bieti		MVRYRMRSLSERPHEVHGQQVHGQEQGHNGQE-------EQGLSPEHAEVYERTHQGYSHHR
8. Golden_SN_monkey Rhinopithecus roxellana		MVRYRMRSLSERPHEVHGQQVHGQEQGHNGQE-------EQGLSPEHAEVYERTHQGYSHHR
9. Angolan_Colobus Colobus angolensis palliatus		MVRYHMRSLSERPHEVHRQQVHGQEQGHNGQE-------ERGLSPEHVEVYARTHRGYSHHR
10. Ugandan_red_colobus Piliocolobus tephrosceles		MVRYRMRSLSERPQEVHGQQLHGQEQGHNGQE-------EQGLSPENVEVYERTHQGYSHHR
11. Olive_baboon Papio anubis		MVRYRMRSLSERPH---GQQVHGQDQGHNGQE-------EQGLSPEHVEVYERTHRGHSYHR
12. Sooty_mangabey Cercocebus atys		MVRYRMRSLSERPHEVHGQQVHGQDQGHNGQE-------EQGLSPEHVEVYERTHRGHSYHR
13. Drill Mandrillus leucophaeus		MVRYRMRSLSERPHEVHGQQVHGQDQGHNGQE-------EQGLSPEHVEVYERTHRGHSYHR
14. Green_monkey Chlorocebus sabaeus		MVRYRTRSLSERPHEVHGQQVHGQDQGHNGQE-------EQGLSPEHVEVYERTHRGHSPHR
15. Southern_PT_macaque Macaca nemestrina		MVRYRMRSLSERPHEVHGQQVHGQDQGHNGQE-------EQGLNPEHVEVYERTHRGHSHHR
16. Rhesus_macaque Macaca mulatta		MVRYRMRSLSERPHEVHGQQVHGQDQGHNGQE-------EQGLNPEHVEVYERTHRGHSHHR
17. CE_macaque Macaca fascicularis		MVRYRMRSLSERPHEVHGQQVHGQDQGHNGQE-------EQGLNPEHVEVYERTHRGHSHHR
18. WH_capuchin Cebus capucinus imitator		MVRCRLRSPSERPHEEYRQLVNGQEQGRNAQE-------EQGLSPEGVEAYGRSHRVCYRYR
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		MVRYRLRSPSERPHEEYRQLVNRQEQGRNAQE-------EQGLSPEGVGVYGRTHRTCYRHR
20. NM_night_monkey Aotus nancymaae		MVRYHGRSPSERLYEEHRQLVNRQEQGCNGQE-------EQGLSPEDAEVYGRTQRGCYRYR
21. Common_marmoset Callithrix jacchus		MVRYRVRSPSERPHEEYRQLVNWQEQGRNGQE-------EQGLSAEGGEVYGRTHQGYSSYR
22. Coquerels_sifaka Propithecus coquereli		MVRYRERSPSERPHQGYRQQGHGQEQGLEGQE-------EQGLTPESIEFYGRTYQGRRCRR
23. Gray_mouse_lemur Microcebus murinus		MVRYRERSPSERPHQGYRQQGHGQEQGLEGQE-------EQGLSPETIEFYGRTYRGRRCRR
24. Northern_greater_galago Otolemur garnettii		MVRYRVRSPSEHANQGLRQEGHGQD---EGQ------------NPESVEVYGRTYRG-HHRR
25. Philippine_tarsier Carlito syrichta		MVRHRGSSPSQHPPQGSQVQGHSLERGREAPE-------EQGMSQEHSEAYGRVHRGGHRSR
26. Sunda_flying_lemur Galeopterus variegatus		MVRYRVRSPSEHPNQGFRQQSHGQEHGPEGQE-------EQELSPERVQDCGRTRC-CYRYR

Site # 1 ● with ○ w/o Gaps Edit disabled for translated protein data.



Species/Abbrv	Group Name	* * *
27. Chinese_tree_shrew Tupaia chinensis		MVRYRERSPSEHPHQGHMQQAHGQEAGREGQE------PEQGLNPESIEAYGRTYQGRRHHR
28. House_mouse Mus musculus		MVRYRMRSPSEGPHQG-----PGQDHEREEQG------QGQGLSPERVEDYGRTHRGHHHHR
29. Ryukyu_mouse Mus caroli		MVRYRMRSPSEGPHQG-----PGQDHEREEQG------QGQGLSPERVEDYGRTHRGHHHHR
30. Shrew_mouse Mus pahari		MVRYRMRSPSEGPHQG-----PGQDHEREEQG------QGQGLSPERVEDYGRAHRGHHHHR
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		MVRYRMRSPSERPHQG-----PGQEHGREEE-------QGQELSPERVDDYGRTHRGHHHHR
32. Norweigan_rat Rattus norvegicus		MVRYRMRSPSEGQHQG-----PGQDHEREEQG------QGQELSPERVEDYGRTERGHHH-R
33. Prarie_vole Microtus ochrogaster		MVRYRMRSPSEHPHQG-----PGRDDGPDEQG------QGQGLSPERVEDYGRTHRGHHHHR
34. Mongolian_gerbil Meriones unguiculatus		MVRYLIRSPSEGPGQE-----HG----REEQR------QG--LSPDHAEDYGRTHRCCSYRR
35. Golden_hamster Mesocricetus auratus		MVRYRMRSPSERPHQG-----PGQEHGREEQG------QGQGLSPERVEDYGRTHRG-QHHH
36. Lesser_Egyptian_jerboa Jaculus jaculus		MVRYRVRSPSERPGQ---------DRGSEG--------QEQGLSPDRMEAYGRTHRGHHHHH
37. Upper_Galilee_mountains_blind_mole Nannospalax galili		MVRYRIRSPSEHPHQG-----PGQEYGREEQG------EEQGLSPESVEDYGRTHQGHQYHR
38. Naked_mole_rat Heterocephalus_glaber		MVRCRMRSPSERPLQ------ANSPESGEGQE------QERGLSPEHTEAYRRTYRGRHYRR
39. Damara_mole_rat Fukomys damarensis		MVRCYTRSRSGRPLQ------VHSLKSGEGQE------QEQRLNPEQEEACGRTHRGRQCRG
40. Degu Octodon degus		MVRCRARSPSEHRLQ------AHSQESGEGQE------QGQGLSSERVEAYGRTYRGRYHRR
41. Long-tailed_chinchilla Chinchilla lanigera		MVRCRVRSPSHHPHQ----------ESGEGQQ------QEQGLSPEHGEAYGRTHKGRYHRR
42. Alpine_marmot Marmota marmota marmota		MVRCRVRNPGER-LQQGPRQDPGCEHQDQEQD------REQGLTQEAAEVFGRTQRSCQYRR
43. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		MVRCRVRNPGDR-LQQGPRQDAGCEDPEREQE------QGQALTQEPAEAFGRTQRSCQYRR
44. American_pika Ochotona princeps		MVRYRARSQSEHPHEK-----HERQHEHDDQD------PDQELTPDN-EAFGRTHRGRCYRK
45. Rabbit Oryctolagus cuniculus		MVRYRARSPSEHPHGE-----HGPEHEGEGQE------PDQELTPETGDACGRTHRGRHRRR
46. Sheep Ovis aries musimon		MVRCCVKSPTESPP---GQQGSGQQGETESPD------QTRELRLEDVSVHGRTHRGRYHYR
47. Goat Capra hircus		MVRCCVKSPTESPP---GQQGSGQQGETESPD------QTRELRPEDIPVHGRTHRGRYHYR
48. Texas_white-tailed_deer Odocoileus virginianus texanus		MVRCRVKSPTESPT---GQQGSGQQGETERPE------ETQELRPEDIPVYGRTQRGRYHYR
49. Cattle Bos taurus		MVRCHVKSPTESPP---GQQGSGQQGETEHPD------QARELRPEDIPVYGRTHRGRYHYR
50. American_bison Bison bison bison		MVRCHVKSPTESPP---GQQGSGQQGETEHPD------QARELRPEDIPVYGRTHRGRYHYR
51. Water_buffalo Bubalus bubalis		MVRCRVKSPTESRP---RQQGSGQQGETEHPD------QARELKPEDIPVYGRTHRGRYHYR
52. Pig Sus scrofa		MVRCRVRSPSESP-----QQGSGQQRENERQD------QDQELRPEDVPVYGRTHRGRYHYR
53. Domestc_cat Felis catus		MVRCCRRSPSGHP----RQGQEHGQHECQDKE------REQAVNAEDIQVDQRTHKGCC-YR

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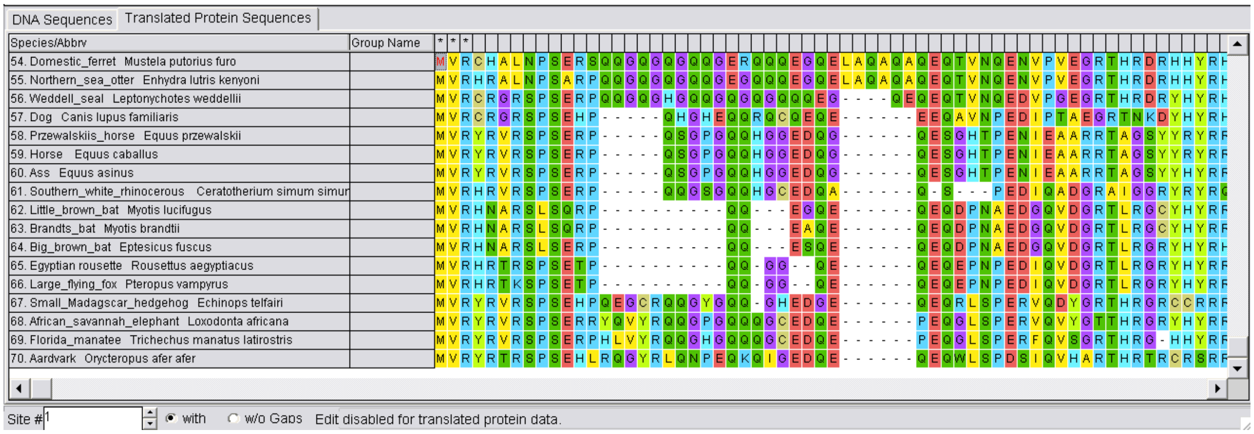

DNA Sequences | Translated Protein Sequences

Species/Abbrv	Group Name	* * *
54. Domestic_ferret Mustela putorius furo		MVRCHALNPSERSQQGQGQGQQGERQQQEGQELAQAQAQEQTVNQENVPVEGRTHRDRHHYRH
55. Northern_sea_otter Enhydra lutris kenyoni		MVRHRALNPSARPQQGQGQGQQGEGQQQEGQELAQAQAQEQTVNQENVPVEGRTHRDRHHYRH
56. Weddell_seal Leptonychotes weddellii		MVRCRGRSPSERPQQGQGHGQQGQGQGQQQEG----QEQEQTVNQEDVPGEGRTHRDRYHYRH
57. Dog Canis lupus familiaris		MVRCRGRSPSEHP-----QHGHEQQRQCQEQE------EEQAVNPEDIPTAEGRTNKDYHYRH
58. Przewalskiis_horse Equus przewalskii		MVRYRVRSPSERP-----QSGPGQQHGGEDQG------QESGHTPENIEAARRTAGSYYRYRR
59. Horse Equus caballus		MVRYRVRSPSERP-----QSGPGQQHGGEDQG------QESGHTPENIEAARRTAGSYYRYRR
60. Ass Equus asinus		MVRYRVRSPSERP-----QSGPGQQHGGEDQG------QESGHTPENIEAARRTAGSYYHYRR
61. Southern_white_rhinocerous Ceratotherium simum simur		MVRHRVRSPSERP-----QQGSGQQHGCEDQA------Q-S---PEDIQADGRAIGGRYRYRG
62. Little_brown_bat Myotis lucifugus		MVRHNARSLSQRP----------QQ---EGQE------QEQDPNAEDGQVDGRTLRGCYHYRR
63. Brandts_bat Myotis brandtii		MVRHNARSLSQRP----------QQ---EAQE------QEQDPNAEDGQVDGRTLRGCYHYRR
64. Big_brown_bat Eptesicus fuscus		MVRHNARSLSERP----------QQ---ESQE------QEQDPNAEDGQVDGRTLRGRYHYRH
65. Egyptian rousette Rousettus aegyptiacus		MVRHRTRSPSETP----------QQ-GG--QE------QEQEPNPEDIQVDGRTLRGRYHYRR
66. Large_flying_fox Pteropus vampyrus		MVRHRTKSPSETP----------QQ-GG--QE------QEQEPNPEDIQVDGRTLRGRYHYRR
67. Small_Madagscar_hedgehog Echinops telfairi		MVRYRVRSPSEHPQEGCRQQGYGQQ-GHEDGE------QEQRLSPERVQDYGRTHRGRCCRRR
68. African_savannah_elephant Loxodonta africana		MVRYRVRSPSERRYQVYRQQGPGQQQGCEDQE------PEQGLSPERVQVYGTTHRGRYHYRR
69. Florida_manatee Trichechus manatus latirostris		MVRYRVRSPSERPHLVYRQQGHGQQQGCEDQE------PEQGLSPERFQVSGRTHRG-HHYRR
70. Aardvark Orycteropus afer afer		MVRYRTRSPSEHLRQGYRLQNPEQKQIGEDQE------QEQWLSPDSIQVHARTHRTRCRSRR

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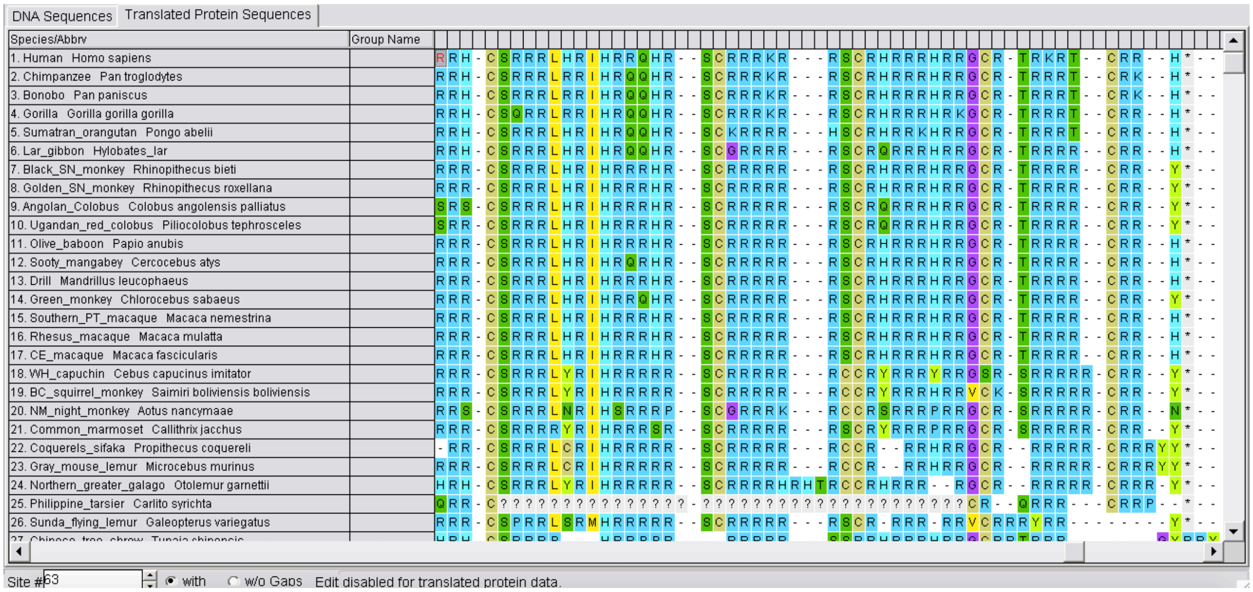

DNA Sequences | Translated Protein Sequences

Species/Abbrv	Group Name	
1. Human Homo sapiens		RRH-CSRRRLHRIHRRQHR--SCRRRKR---RSCRHRRRHRRGCR-TRKRT--CRR--H*--
2. Chimpanzee Pan troglodytes		RRH-CSRRRLRRIHRQQHR--SCRRRKR---RSCRHRRRHRRGCR-TRRRT--CRK--H*--
3. Bonobo Pan paniscus		RRH-CSRRRLRRIHRQQHR--SCRRRKR---RSCRHRRRHRRGCR-TRRRT--CRK--H*--
4. Gorilla Gorilla gorilla gorilla		RRH-CSQRRLRRIHRQQHR--SCRRRKR---RSCRHRRRHRKGCR-TRRRT--CRR--H*--
5. Sumatran_orangutan Pongo abelii		RRH-CSRRRLHRIHRQQHR--SCKRRRR---HSCRHRRKHRRGCR-TRRRT--CRR--H*--
6. Lar_gibbon Hylobates_lar		RRH-CSRRRLHRIHRQQHR--SCGRRRR---RSCRQRRRHRRGCR-TRRRR--CRR--H*--
7. Black_SN_monkey Rhinopithecus bieti		RRR-CSRRRLHRIHRRRHR--SCRRRRR---RSCRHRRRHRRGCR-TRRRR--CRR--Y*--
8. Golden_SN_monkey Rhinopithecus roxellana		RRR-CSRRRLHRIHRRRHR--SCRRRRR---RSCRHRRRHRRGCR-TRRRR--CRR--Y*--
9. Angolan_Colobus Colobus angolensis palliatus		SRS-CSRRRLHRIHRRRHR--SCRRRRR---RSCRQRRRHRRGCR-TRRRR--CRR--Y*--
10. Ugandan_red_colobus Piliocolobus tephrosceles		SRR-CSRRRLHRIHRRRHR--SCRRRRR---RSCRQRRRHRRGCR-TRRRR--CRR--Y*--
11. Olive_baboon Papio anubis		RRR-CSRRRLHRIHRRRHR--SCRRRRR---RSCRHRRRHRRGCR-TRRRR--CRR--H*--
12. Sooty_mangabey Cercocebus atys		RRR-CSRRRLHRIHRQRHR--SCRRRRR---RSCRHRRRHRRGCR-TRRRR--CRR--H*--
13. Drill Mandrillus leucophaeus		RRR-CSRRRLHRIHRRRHR--SCRRRRR---RSCRHRRRHRRGCR-TRRRR--CRR--H*--
14. Green_monkey Chlorocebus sabaeus		RRR-CSRRRLHRIHRRQHR--SCRRRRR---RSCRHRRRHRRGCR-TRRRR--CRR--Y*--
15. Southern_PT_macaque Macaca nemestrina		RRR-CSRRRLHRIHRRRHR--SCRRRRR---RSCRHRRRHRRGCR-TRRRR--CRR--H*--
16. Rhesus_macaque Macaca mulatta		RRR-CSRRRLHRIHRRRHR--SCRRRRR---RSCRHRRRHRRGCR-TRRRR--CRR--H*--
17. CE_macaque Macaca fascicularis		RRR-CSRRRLHRIHRRRHR--SCRRRRR---RSCRHRRRHRRGCR-TRRRR--CRR--H*--
18. WH_capuchin Cebus capucinus imitator		RRR-CSRRRLYRIHRRRRR--SCRRRRR---RCCRYRRRYRRGSR-SRRRRR-CRR--Y*--
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		RRR-CSRRRLYRIHRRRRR--SCRRRRR---RCCRYRRRHRRVCK-SRRRRR-CRR--Y*--
20. NM_night_monkey Aotus nancymaae		RRS-CSRRRLNRIHSRRRP--SCGRRRK---RCCRSRRRPRRGCR-SRRRRR-CRR--N*--
21. Common_marmoset Callithrix jacchus		RRR-CSRRRRYRIHRRRSR--SCRRRRR---RSCRYRRRPRRGCR-SRRRRR-CRR--Y*--
22. Coquerels_sifaka Propithecus coquereli		-RR-CSRRRLCRIHRRRRR--SCRRRRR---RCCR--RRHRRGCR--RRRRR-CRRRYY*--
23. Gray_mouse_lemur Microcebus murinus		RRR-CSRRRLCRIHRRRRR--SCRRRRR---RCCR--RRHRRGCR--RRRRR-CRRRYY*--
24. Northern_greater_galago Otolemur garnettii		HRH-CSRRRLYRIHRRRRR--SCRRRRHRHTRCCRHRRR--RGCR--RRRRR-CRRR-Y*--
25. Philippine_tarsier Carlito syrichta		QRR-C???????????????-?????????????????????CR--QRRR---CRRP--*--
26. Sunda_flying_lemur Galeopterus variegatus		RRR-CSPRRLSRMHRRRRR--SCRRRRR---RSCR-RRR-RRVCRRRYRR--------Y*--

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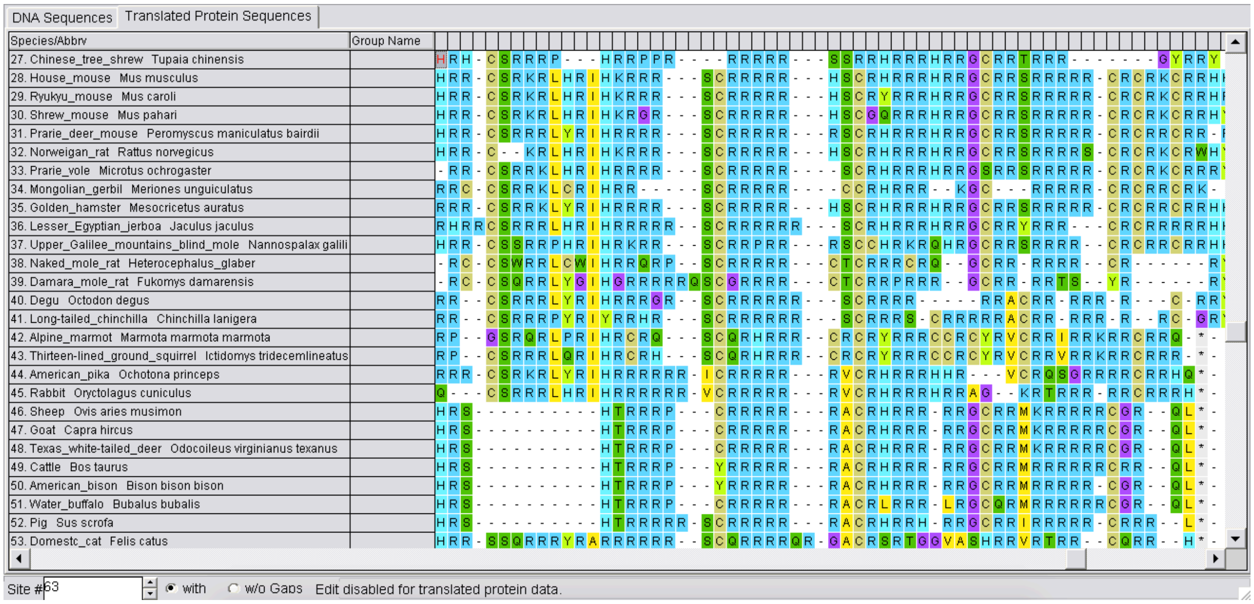

Species/Abbrv	Group Name	
27. Chinese_tree_shrew Tupaia chinensis		HRH-CSRRRP---HRRPPR----RRRRR---SSRRHRRRHRRGCRRTRRR-------GYRRY
28. House_mouse Mus musculus		HRR-CSRKRLHRIHKRRR---SCRRRRR---HSCRHRRRHRRGCRRSRRRRR-CRCRKCRRH
29. Ryukyu_mouse Mus caroli		HRR-CSRKRLHRIHKRRR---SCRRRRR---HSCRYRRRHRRGCRRSRRRRR-CRCRKCRRH
30. Shrew_mouse Mus pahari		HRR-CSRKRLHRIHKRGR---SCRRRRR---HSCGQRRRHRRGCRRSRRRRR-CRCRKCRRH
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		HRR-CSRRRLYRIHRRRR---SCRRRRR---RSCRHRRRHRRGCRRSRRRRR-CRCRRCRR-
32. Norweigan_rat Rattus norvegicus		HRR-C--KRLHRIHKRRR---SCRRRRR---HSCRHRRRHRRGCRRSRRRRS-CRCRKCRWH
33. Prarie_vole Microtus ochrogaster		-RR-CSRRKLHRIHRRRR---SCRRRRR----SCRHRRRHRRGSRRSRRRRR-CRCRKCRRR
34. Mongolian_gerbil Meriones unguiculatus		RRC-CSRRKLCRIHRR-----SCRRRRR----CCRHRRR--KGC---RRRRR-CRCRRCRK-
35. Golden_hamster Mesocricetus auratus		RRR-CSRRKLYRIHRRRR---SCRRRRR---HSCRHRRRHRRGCRRSRRRRR-CRCRRCRRH
36. Lesser_Egyptian_jerboa Jaculus jaculus		RHRRCSRRRLHRIHRRRRR--SCRRRRRR---SCRHRRRHRRGCRRYRRR---CRCRRRRRH
37. Upper_Galilee_mountains_blind_mole Nannospalax galili		HRR-CSSRRPHRIHRKRR---SCRRPRR---RSCCHRKRQHRGCRRSRRRR--CRCRRCRRH
38. Naked_mole_rat Heterocephalus_glaber		-RC-CSWRRLCWIHRRQRP--SCRRRRR---CTCRRRCRQ--GCRR-RRRR--CR------R
39. Damara_mole_rat Fukomys damarensis		-RC-CSQRRLYGIHGRRRRRQSCGRRRR---CTCRRPRRR--GCRR-RRTS--YR------R
40. Degu Octodon degus		RR--CSRRRLYRIHRRRGR--SCRRRRRR---SCRRRR-----RRACRR-RRR-R---C-RR
41. Long-tailed_chinchilla Chinchilla lanigera		RR--CSRRRPYRIYRRHR---SCRRRRRR---SCRRRS-CRRRRRACRR-RRR-R--RC-GR
42. Alpine_marmot Marmota marmota marmota		RP--GSRQRLPRIHRCRQ---SCQRHRRR--CRCRYRRRCCRCYRVCRRIRRKRRCRRQ-*-
43. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		RP--CSRRRLQRIHRCRH---SCQRHRRR--CRCRYRRRCCRCYRVCRRVRRKRRCRRR-*-
44. American_pika Ochotona princeps		RRR-CSRKRLYRIHRRRRRR-ICRRRRR---RVCRHRRRHHR---VCRQSGRRRRCRRHQ*-
45. Rabbit Oryctolagus cuniculus		Q---CSRRRLHRIHRRRRRR-VCRRRRR---RVCRHRRRHRRAG--KRTRRR-RRCRRRH*-
46. Sheep Ovis aries musimon		HRS----------HTRRRP---CRRRRR---RACRHRRR-RRGCRRMKRRRRRCGR--QL*-
47. Goat Capra hircus		HRS----------HTRRRP---CRRRRR---RACRHRRR-RRGCRRMKRRRRRCGR--QL*-
48. Texas_white-tailed_deer Odocoileus virginianus texanus		HRS----------HTRRRP---CRRRRR---RACRHRRR-RRGCRRMKRRRRRCGR--QL*-
49. Cattle Bos taurus		HRS----------HTRRRP---YRRRRR---RACRHRRR-RRGCRRMRRRRRRCRR--QL*-
50. American_bison Bison bison bison		HRS----------HTRRRP---YRRRRR---RACRHRRR-RRGCRRMRRRRR-CGR--QL*-
51. Water_buffalo Bubalus bubalis		HRS----------HTRRRP---CRRRRR---RACRLRRR-LRGCQRMRRRRRRCGR--QL*-
52. Pig Sus scrofa		HRS----------HTRRRRR-SCRRRRR---RACRHRRH-RRGCRRIRRRRR-CRRR--L*-
53. Domestc_cat Felis catus		HRR-SSQRRRYRARRRRRR--SCQRRRRQR-GACRSRTGGVASHRRVRTRR--CQRR--H*-

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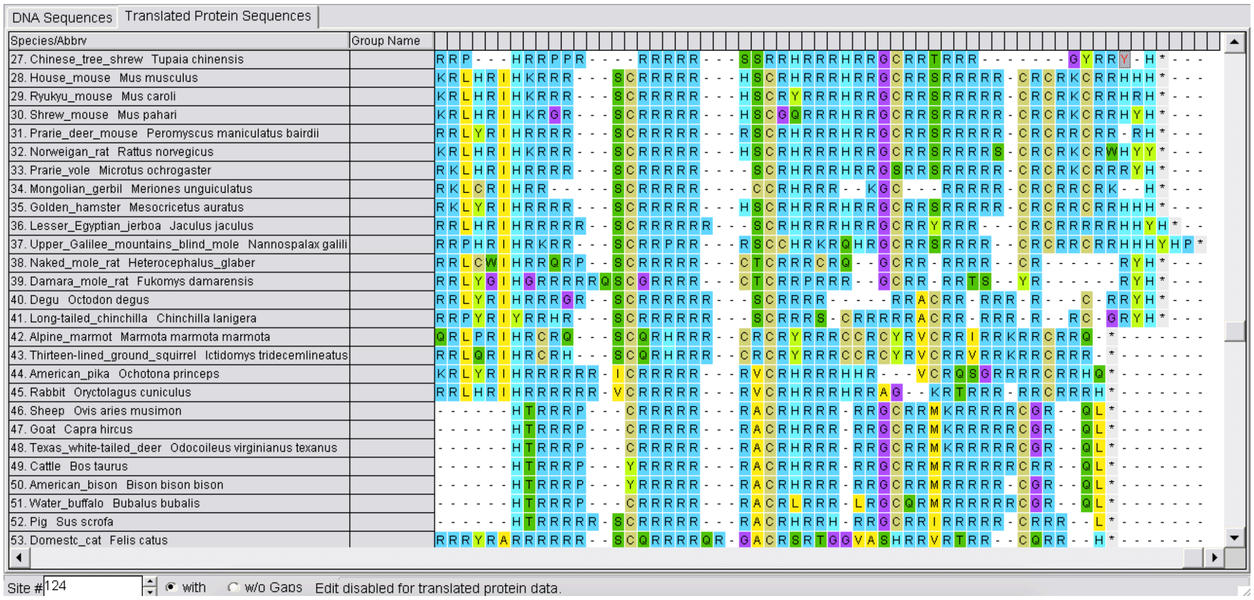

Species/Abbrv	Group Name	
27. Chinese_tree_shrew Tupaia chinensis		RRP---HRRPPR----RRRRR---SSRRHRRRHRRGCRRTRRR-------GYRRY-H*---
28. House_mouse Mus musculus		KRLHRIHKRRR---SCRRRRR---HSCRHRRRHRRGCRRSRRRRR-CRCRKCRRHHH*---
29. Ryukyu_mouse Mus caroli		KRLHRIHKRRR---SCRRRRR---HSCRYRRRHRRGCRRSRRRRR-CRCRKCRRHRH*---
30. Shrew_mouse Mus pahari		KRLHRIHKRGR---SCRRRRR---HSCGQRRRHRRGCRRSRRRRR-CRCRKCRRHYH*---
31. Prarie_deer_mouse Peromyscus maniculatus bairdii		RRLYRIHRRRR---SCRRRRR---RSCRHRRRHRRGCRRSRRRRR-CRCRRCRR-RH*---
32. Norweigan_rat Rattus norvegicus		KRLHRIHKRRR---SCRRRRR---HSCRHRRRHRRGCRRSRRRRS-CRCRKCRWHYY*---
33. Prarie_vole Microtus ochrogaster		RKLHRIHRRRR---SCRRRRR----SCRHRRRHRRGSRRSRRRRR-CRCRKCRRRYH*---
34. Mongolian_gerbil Meriones unguiculatus		RKLCRIHRR-----SCRRRRR----CCRHRRR--KGC---RRRRR-CRCRRCRK--H*---
35. Golden_hamster Mesocricetus auratus		RKLYRIHRRRR---SCRRRRR---HSCRHRRRHRRGCRRSRRRRR-CRCRRCRRHHH*---
36. Lesser_Egyptian_jerboa Jaculus jaculus		RRLHRIHRRRRR--SCRRRRRR---SCRHRRRHRRGCRRYRRR---CRCRRRRRHHYH*--
37. Upper_Galilee_mountains_blind_mole Nannospalax galili		RRPHRIHRKRR---SCRRPRR---RSCCHRKRQHRGCRRSRRRR--CRCRRCRRHHHYHP*
38. Naked_mole_rat Heterocephalus_glaber		RRLCWIHRRQRP--SCRRRRR---CTCRRRCRQ--GCRR-RRRR--CR------RYH*---
39. Damara_mole_rat Fukomys damarensis		RRLYGIHGRRRRRQSCGRRRR---CTCRRPRRR--GCRR-RRTS--YR------RYH*---
40. Degu Octodon degus		RRLYRIHRRRGR--SCRRRRRR---SCRRRR-----RRACRR-RRR-R---C-RRYH*---
41. Long-tailed_chinchilla Chinchilla lanigera		RRPYRIYRRHR---SCRRRRRR---SCRRRS-CRRRRRACRR-RRR-R--RC-GRYH*---
42. Alpine_marmot Marmota marmota marmota		QRLPRIHRCRQ---SCQRHRRR--CRCRYRRRCCRCYRVCRRIRRKRRCRRQ-*-------
43. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		RRLQRIHRCRH---SCQRHRRR--CRCRYRRRCCRCYRVCRRVRRKRRCRRR-*-------
44. American_pika Ochotona princeps		KRLYRIHRRRRRR-ICRRRRR---RVCRHRRRHHR---VCRQSGRRRRCRRHQ*-------
45. Rabbit Oryctolagus cuniculus		RRLHRIHRRRRRR-VCRRRRR---RVCRHRRRHRRAG--KRTRRR-RRCRRRH*-------
46. Sheep Ovis aries musimon		------HTRRRP---CRRRRR---RACRHRRR-RRGCRRMKRRRRRCGR--QL*-------
47. Goat Capra hircus		------HTRRRP---CRRRRR---RACRHRRR-RRGCRRMKRRRRRCGR--QL*-------
48. Texas_white-tailed_deer Odocoileus virginianus texanus		------HTRRRP---CRRRRR---RACRHRRR-RRGCRRMKRRRRRCGR--QL*-------
49. Cattle Bos taurus		------HTRRRP---YRRRRR---RACRHRRR-RRGCRRMRRRRRRCRR--QL*-------
50. American_bison Bison bison bison		------HTRRRP---YRRRRR---RACRHRRR-RRGCRRMRRRRR-CGR--QL*-------
51. Water_buffalo Bubalus bubalis		------HTRRRP---CRRRRR---RACRLRRR-LRGCQRMRRRRRRCGR--QL*-------
52. Pig Sus scrofa		------HTRRRRR-SCRRRRR---RACRHRRH-RRGCRRIRRRRR-CRRR--L*-------
53. Domestc_cat Felis catus		RRRYRARRRRRR--SCQRRRRQR-GACRSRTGGVASHRRVRTRR--CQRR--H*-------

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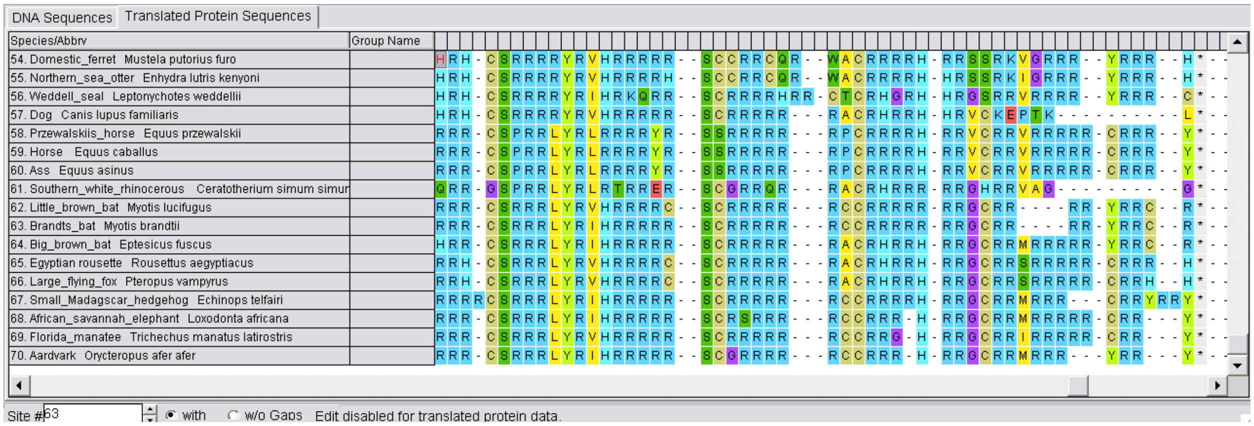
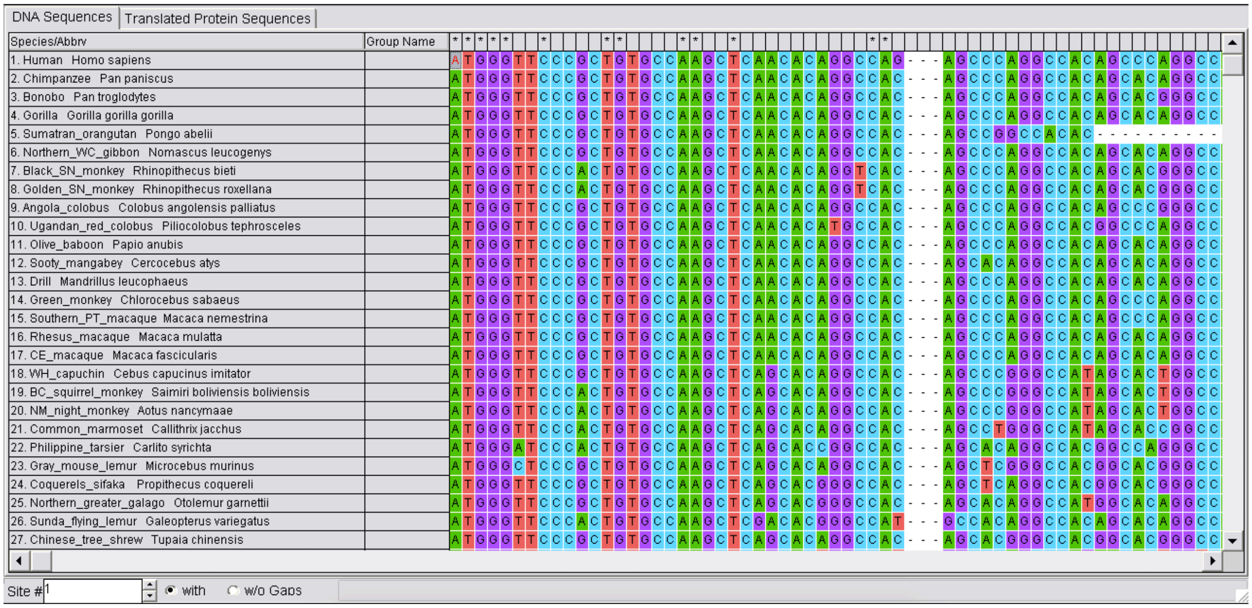


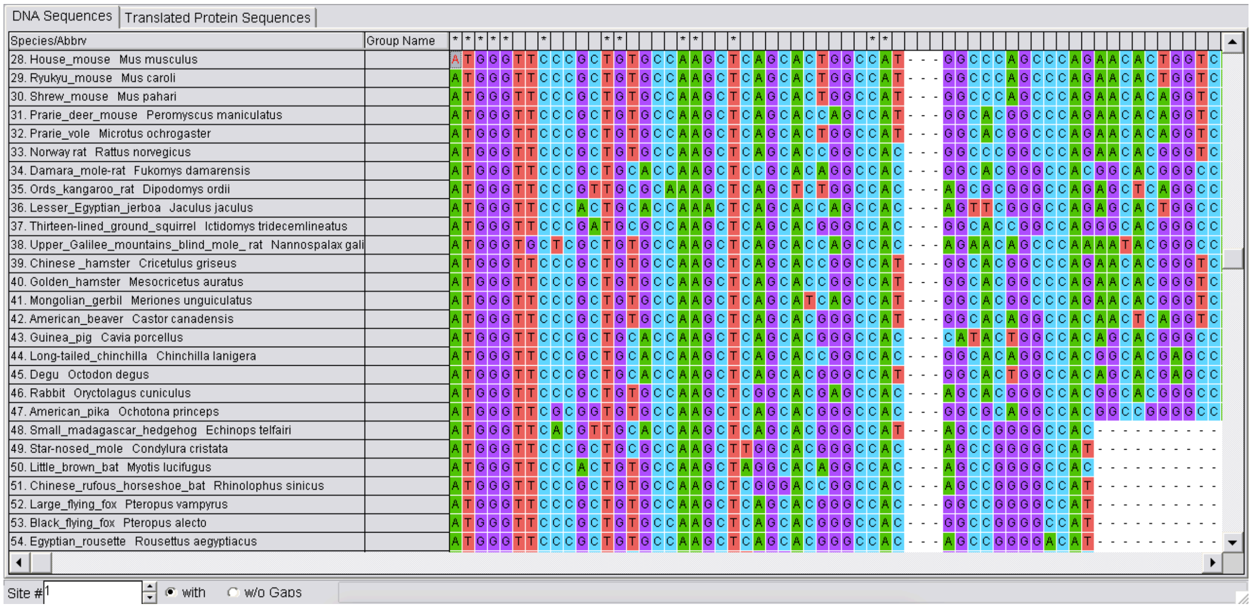
Species/Abbrv	Group Name	
54. Domestic_ferret Mustela putorius furo		H R H - C S R R R R Y R V H R R R R R - - S C C R R C Q R - - W A C R R R R H - R R S S R K V G R R R - - Y R R R - - H * - -
55. Northern_sea_otter Enhydra lutris kenyoni		H R H - C S R R R R Y R V H R R R R H - - S C C R R C Q R - - W A C R R R R H - H R S S R K I G R R R - - Y R R R - - H * - -
56. Weddell_seal Leptonychotes weddellii		H R H - C S R R R R Y R I H R K Q R R - - S C R R R R H R R - C T C R H G R H - H R G S R R V R R R R - - Y R R R - - C * - -
57. Dog Canis lupus familiaris		H R H - C S R R R R Y R V H R R R R R - - S C R R R R R - - - R A C R H R R H - H R V C K E P T K - - - - - - - - - - L * - -
58. Przewalskiis_horse Equus przewalskii		R R R - C S P R R L Y R L R R R R Y R - - S S R R R R R - - - R P C R R R R H - R R V C R R V R R R R R - C R R R - - Y * - -
59. Horse Equus caballus		R R R - C S P R R L Y R L R R R R Y R - - S S R R R R R - - - R P C R R R R H - R R V C R R V R R R R R - C R R R - - Y * - -
60. Ass Equus asinus		R R R - C S P R R L Y R L R R R R Y R - - S S R R R R R - - - R P C R R R R H - R R V C R R V R R R R R - C R R R - - Y * - -
61. Southern_white_rhinocerous Ceratotherium simum simur		Q R R - G S P R R L Y R L R T R R E R - - S C G R R Q R - - - R A C R H R R R - R R G H R R V A G - - - - - - - - - - G * - -
62. Little_brown_bat Myotis lucifugus		R R R - C S R R R L Y R V H R R R R C - - S C R R R R R - - - R C C R R R R R - R R G C R R - - - - R R - Y R R C - - R * - -
63. Brandts_bat Myotis brandtii		R R R - C S R R R L Y R I H R R R R R - - S C R R R R R - - - R C C R R R R R - R R G C R R - - - - R R - Y R R C - - R * - -
64. Big_brown_bat Eptesicus fuscus		H R R - C S R R R L Y R I H R R R R R - - S C R R R R R - - - R A C R H R R H - R R G C R R M R R R R R - Y R R C - - R * - -
65. Egyptian rousette Rousettus aegyptiacus		R R H - C S R R R L Y R V H R R R R C - - S C R R R R R - - - R A C R H R R H - R R G C R R S R R R R R - C R R R - - H * - -
66. Large_flying_fox Pteropus vampyrus		R R H - C S R R R L Y R V H R R R R C - - S C R R R R R - - - R A C R H R R H - R R G C R R S R R R R R - C R R H - - H * - -
67. Small_Madagscar_hedgehog Echinops telfairi		R R R R C S R R R L Y R I H R R R R R - - S C R R R R R - - - R C C R R R R H - R R G C R R M R R R - - - C R R Y R R Y * - -
68. African_savannah_elephant Loxodonta africana		R R R - C S R R R L Y R I H R R R R R - - S C R S R R R - - - R C C R R R - H - R R G C R R M R R R R R - C R R - - - Y * - -
69. Florida_manatee Trichechus manatus latirostris		R R R - C S R R R L Y R V H R R R R R - - S C R R R R R - - - R C C R R G - H - R R G C R R I R R R R R - C R R - - - Y * - -
70. Aardvark Orycteropus afer afer		R R R - C S R R R L Y R I H R R R R R - - S C G R R R R - - - R C C R R R - H - R R G C R R M R R R - - - Y R R - - - Y * - -

Site # 63 ● with ○ w/o Gaps Edit disabled for translated protein data.

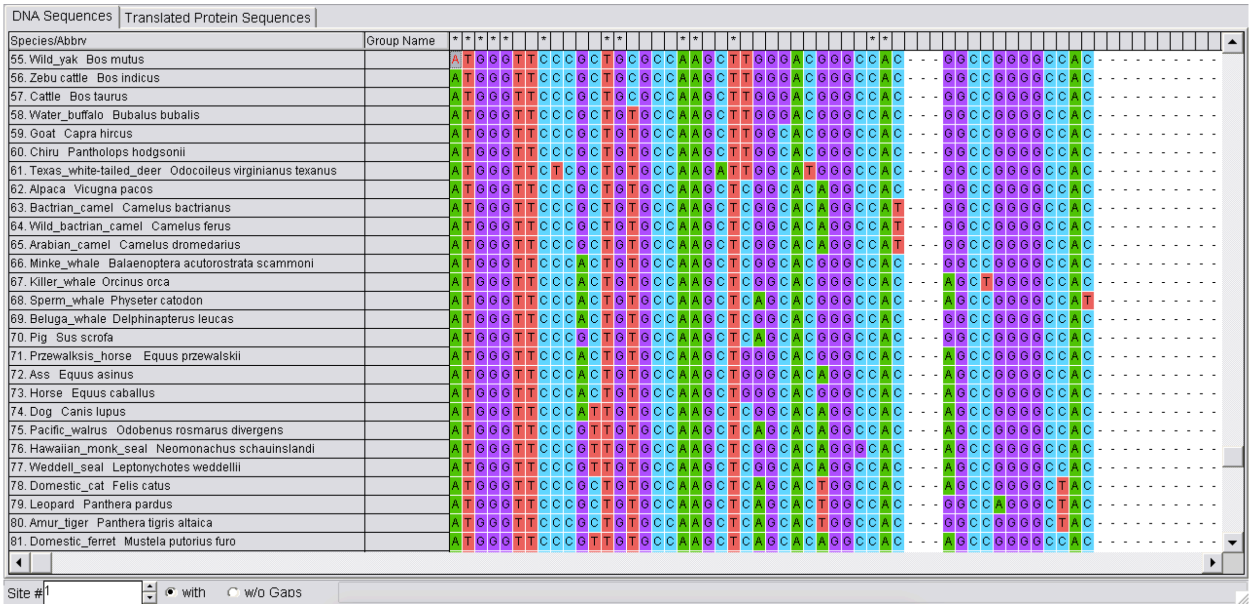
Appendix BB) Alignment of mammalian *Prm3* coding exon sequences



Species/Abbrv	Group Name	***** * ** ** * **
1. Human Homo sapiens		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAG---AGCCCAGGCCACAGCCCAGGCC
2. Chimpanzee Pan paniscus		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCACAGGCC
3. Bonobo Pan troglodytes		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCACGGGCC
4. Gorilla Gorilla gorilla gorilla		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCACAGGCC
5. Sumatran_orangutan Pongo abelii		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCGGCCACAC----------
6. Northern_WC_gibbon Nomascus leucogenys		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCACAGGCC
7. Black_SN_monkey Rhinopithecus bieti		ATGGGTTCCCACTGTGCCAAGCTCAACACAGGTCAC---AGCCCAGGCCACAGCACGGGCC
8. Golden_SN_monkey Rhinopithecus roxellana		ATGGGTTCCCACTGTGCCAAGCTCAACACAGGTCAC---AGCCCAGGCCACAGCACGGGCC
9. Angola_colobus Colobus angolensis palliatus		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCCCGGGCC
10. Ugandan_red_colobus Piliocolobus tephrosceles		ATGGGTTCCCGCTGTGCCAAGCTCAACACATGCCAC---AGCCCAGGCCACGGCCCAGGCC
11. Olive_baboon Papio anubis		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCACAGGCC
12. Sooty_mangabey Cercocebus atys		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCACAGGCCACAGCACAGGCC
13. Drill Mandrillus leucophaeus		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCACAGGCC
14. Green_monkey Chlorocebus sabaeus		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCCCAGGCC
15. Southern_PT_macaque Macaca nemestrina		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCCCAGGCC
16. Rhesus_macaque Macaca mulatta		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCACAGGCC
17. CE_macaque Macaca fascicularis		ATGGGTTCCCGCTGTGCCAAGCTCAACACAGGCCAC---AGCCCAGGCCACAGCACAGGCC
18. WH_capuchin Cebus capucinus imitator		ATGGGTTCCCGCTGTGCCAAGCTCAGCACAGGCCAC---AGCCCGGGCCATAGCACTGGCC
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		ATGGGTTCCCACTGTGCCAAGCTCAGCACAGGCCAC---AGCCCGGGCCATAGCACTGGCC
20. NM_night_monkey Aotus nancymaae		ATGGGTTCCCACTGTGCCAAGCTCAGCACAGGCCAC---AGCCCGGGCCATAGCACTGGCC
21. Common_marmoset Callithrix jacchus		ATGGGTTCCCACTGTGCCAAGCTCAGCACAGGCCAC---AGCCTGGGCCATAGCACCGGCC
22. Philippine_tarsier Carlito syrichta		ATGGGATCCCACTGTGCCAAGCTCAGCACCGGCCAC---AGCACAGGCCACGGCCAGGGCC
23. Gray_mouse_lemur Microcebus murinus		ATGGGCTCCCGCTGTGCCAAGCTCAGCACAGGCCAC---AGCTCGGGCCACGGCACGGGCC
24. Coquerels_sifaka Propithecus coquereli		ATGGGTTCCCGCTGTGCCAAGCTCAGCACGGGCCAC---AGCTCAGGCCACGGCACGGGCC
25. Northern_greater_galago Otolemur garnettii		ATGGGTTCCCGCTGTGCCAAGCTCAGCACGGGCCAC---AGCACAGGCCATGGCACAGGCC
26. Sunda_flying_lemur Galeopterus variegatus		ATGGGTTCCCACTGTGCCAAGCTCGACACGGGCCAT---GCCACAGGCCACAGCACAGGCC
27. Chinese_tree_shrew Tupaia chinensis		ATGGGTTCCCGCTGTGCCAAGCTCAGCACAGGCCAC---AGCACGGGCCACGGCACGGGCC



Species/Abbrv	Group Name	***** * ** ** * **
28. House_mouse Mus musculus		ATGGGTTCCCGCTGTGCCAAGCTCAGCACTGGCCAT---GGCCCAGCCCAGAACACTGGTC
29. Ryukyu_mouse Mus caroli		ATGGGTTCCCGCTGTGCCAAGCTCAGCACTGGCCAT---GGCCCAGCCCAGAACACTGGTC
30. Shrew_mouse Mus pahari		ATGGGTTCCCGCTGTGCCAAGCTCAGCACTGGCCAT---GGCCCAGCCCAGAACACAGGTC
31. Prarie_deer_mouse Peromyscus maniculatus		ATGGGTTCCCGCTGTGCCAAGCTCAGCACCAGCCAT---GGCACGGCCCAGAACACAGGTC
32. Prarie_vole Microtus ochrogaster		ATGGGTTCCCGCTGTGCCAAGCTCAGCACTGGCCAT---GGCACGGCCCAGAACACAGGTC
33. Norway rat Rattus norvegicus		ATGGGTTCCCGCTGTGCCAAGCTCAGCACCGGCCAC---GGCCCGGCCCAGAACACGGGTC
34. Damara_mole-rat Fukomys damarensis		ATGGGTTCCCGCTGCACCAAGCTCCGCACAGGCCAC---GGCACGGGCCACGGCACGGGCC
35. Ords_kangaroo_rat Dipodomys ordii		ATGGGTTCCCGTTGCGCAAAGCTCAGCTCTGGCCAC---AGCGCGGGCCAGAGCTCAGGCC
36. Lesser_Egyptian_jerboa Jaculus jaculus		ATGGGTTCCCACTGCACCAAACTCAGCACCAGCCAC---AGTTCGGGCCAGAGCACTGGCC
37. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		ATGGGTTCCCGATGCGCCAAGCTCAGCACGGGCCAC---GGCACCGGCCAGGGCACGGGCC
38. Upper_Galilee_mountains_blind_mole_ rat Nannospalax gali		ATGGGTGCTCGCTGTGCCAAGCTCAGCACCAGCCAC---AGAACAGCCCAAAATACGGGCC
39. Chinese _hamster Cricetulus griseus		ATGGGTTCCCGCTGTGCCAAGCTCAGCACCGGCCAT---GGCACGGCCCAGAACACGGGTC
40. Golden_hamster Mesocricetus auratus		ATGGGTTCCCGCTGTGCCAAGCTCAGCACCGGCCAT---GGCACGGCCCAGAACACGGGTC
41. Mongolian_gerbil Meriones unguiculatus		ATGGGTTCCCGCTGTGCCAAGCTCAGCATCAGCCAT---GGCACGGCCCAGAACACGGGTC
42. American_beaver Castor canadensis		ATGGGTTCCCGCTGTGCCAAGCTCAGCACGGGCCAT---GGCACAGGCCACAACTCAGGTC
43. Guinea_pig Cavia porcellus		ATGGGTTCCCGCTGCACCAAGCTCAGCACGGGCCAC---CATACTGGCCACAGCACGGGCC
44. Long-tailed_chinchilla Chinchilla lanigera		ATGGGTTCCCGCTGCACCAAGCTCAGCACCGGCCAC---GGCACAGGCCACGGCACGAGCC
45. Degu Octodon degus		ATGGGTTCCCGCTGCACCAAGCTCAGCACGGGCCAT---GGCACTGGCCACAGCACGAGCC
46. Rabbit Oryctolagus cuniculus		ATGGGTTCCCGCTGTGCCAAGCTCGGCACGAGCCAC---AGCACGGGCCACGGCACGGGCC
47. American_pika Ochotona princeps		ATGGGTTCGCGGTGTGCCAAGCTCAGCACGGGCCAC---GGCGCAGGCCACGGCCGGGGCC
48. Small_madagascar_hedgehog Echinops telfairi		ATGGGTTCACGTTGCACCAAGCTCAGCACGGGCCAT---AGCCGGGGCCAC----------
49. Star-nosed_mole Condylura cristata		ATGGGTTCCCGCTGCGCCAAGCTTGGCACGGGCCAC---AGCCGGGGCCAT----------
50. Little_brown_bat Myotis lucifugus		ATGGGTTCCCACTGTGCCAAGCTAGGCACAGGCCAC---AGCCGGGGCCAC----------
51. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		ATGGGTTCCCGCTGTGCCAAGCTCGGGACCGGCCAC---AGCCGGGGCCAT----------
52. Large_flying_fox Pteropus vampyrus		ATGGGTTCCCGCTGTGCCAAGCTCAGCACGGGCCAC---GGCCGGGGCCAT----------
53. Black_flying_fox Pteropus alecto		ATGGGTTCCCGCTGTGCCAAGCTCAGCACGGGCCAC---GGCCGGGGCCAT----------
54. Egyptian_rousette Rousettus aegyptiacus		ATGGGTTCCCGCTGTGCCAAGCTCAGCACGGGCCAC---AGCCGGGGACAT----------



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Species/Abbrv                                        *****  *    **    **  *          **
55. Wild_yak  Bos mutus                              ATGGGTTCCCGCTGCGCCAAGCTTGGGACGGGCCAC---GGCCGGGGCCAC----------
56. Zebu cattle  Bos indicus                         ATGGGTTCCCGCTGCGCCAAGCTTGGGACGGGCCAC---GGCCGGGGCCAC----------
57. Cattle  Bos taurus                               ATGGGTTCCCGCTGCGCCAAGCTTGGGACGGGCCAC---GGCCGGGGCCAC----------
58. Water_buffalo  Bubalus bubalis                   ATGGGTTCCCGCTGTGCCAAGCTTGGGACGGGCCAC---GGCCGGGGCCAC----------
59. Goat  Capra hircus                               ATGGGTTCCCGCTGTGCCAAGCTTGGCACGGGCCAC---GGCCGGGGCCAC----------
60. Chiru  Pantholops hodgsonii                      ATGGGTTCCCGCTGTGCCAAGCTTGGCACGGGCCAC---GGCCGGGGCCAC----------
61. Texas_white-tailed_deer  Odocoileus virginianus texanus  ATGGGTTCTCGCTGTGCCAAGATTGGCATGGGCCAC---GGCCGGGGCCAC----------
62. Alpaca  Vicugna pacos                            ATGGGTTCCCGCTGTGCCAAGCTCGGCACAGGCCAC---GGCCGGGGCCAC----------
63. Bactrian_camel  Camelus bactrianus               ATGGGTTCCCGCTGTGCCAAGCTCGGCACAGGCCAT---GGCCGGGGCCAC----------
64. Wild_bactrian_camel  Camelus ferus               ATGGGTTCCCGCTGTGCCAAGCTCGGCACAGGCCAT---GGCCGGGGCCAC----------
65. Arabian_camel  Camelus dromedarius               ATGGGTTCCCGCTGTGCCAAGCTCGGCACAGGCCAT---GGCCGGGGCCAC----------
66. Minke_whale  Balaenoptera acutorostrata scammoni ATGGGTTCCCACTGTGCCAAGCTCGGCACGGGCCAC---GGCCGGGGCCAC----------
67. Killer_whale  Orcinus orca                       ATGGGTTCCCACTGTGCCAAGCTCGGCACGGGCCAC---AGCTGGGGCCAC----------
68. Sperm_whale  Physeter catodon                    ATGGGTTCCCACTGTGCCAAGCTCAGCACGGGCCAC---AGCCGGGGCCAT----------
69. Beluga_whale  Delphinapterus leucas              ATGGGTTCCCACTGTGCCAAGCTCGGCACGGGCCAC---GGCCGGGGCCAC----------
70. Pig  Sus scrofa                                  ATGGGTTCCCGCTGTGCCAAGCTCAGCACGGGCCAC---GGCCGGGGCCAC----------
71. Przewalksis_horse  Equus przewalskii             ATGGGTTCCCACTGTGCCAAGCTGGGCACGGGCCAC---AGCCGGGGCCAC----------
72. Ass  Equus asinus                                ATGGGTTCCCACTGTGCCAAGCTGGGCACAGGCCAC---AGCCGGGGCCAC----------
73. Horse  Equus caballus                            ATGGGTTCCCACTGTGCCAAGCTGGGCACGGGCCAC---AGCCGGGGCCAC----------
74. Dog  Canis lupus                                 ATGGGTTCCCATTGTGCCAAGCTCGGCACAGGCCAC---AGCCGGGGCCAC----------
75. Pacific_walrus  Odobenus rosmarus divergens      ATGGGTTCCCGTTGTGCCAAGCTCAGCACAGGCCAC---AGCCGGGGCCAC----------
76. Hawaiian_monk_seal  Neomonachus schauinslandi    ATGGGTTCCCGTTGTGCCAAGCTCGGCACAGGGCAC---AGCCGGGGCCAC----------
77. Weddell_seal  Leptonychotes weddellii            ATGGGTTCCCGTTGTGCCAAGCTCGGCACAGGCCAC---AGCCGGGGCCAC----------
78. Domestic_cat  Felis catus                        ATGGGTTCCCGCTGTGCCAAGCTCAGCACTGGCCAC---AGCCGGGGCTAC----------
79. Leopard  Panthera pardus                         ATGGGTTCCCGCTGTGCCAAGCTCAGCACTGGCCAC---GGCCAGGGCTAC----------
80. Amur_tiger  Panthera tigris altaica              ATGGGTTCCCGCTGTGCCAAGCTCAGCACTGGCCAC---GGCCGGGGCTAC----------
81. Domestic_ferret  Mustela putorius furo           ATGGGTTCCCGTTGTGCCAAGCTCAGCACAGGCCAC---AGCCGGGGCCAC----------
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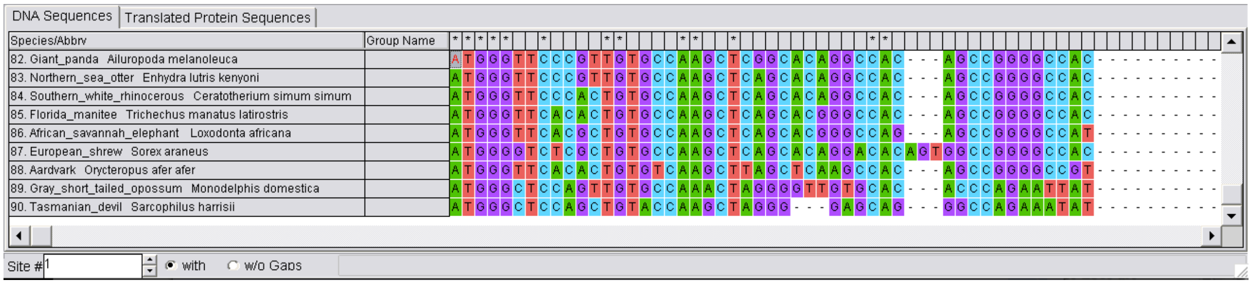

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Species/Abbrv                                        *****  *    **    **  *          **
82. Giant_panda  Ailuropoda melanoleuca              ATGGGTTCCCGTTGTGCCAAGCTCGGCACAGGCCAC---AGCCGGGGCCAC----------
83. Northern_sea_otter  Enhydra lutris kenyoni       ATGGGTTCCCGTTGTGCCAAGCTCAGCACAGGCCAC---AGCCGGGGCCAC----------
84. Southern_white_rhinocerous  Ceratotherium simum simum  ATGGGTTCCCACTGTGCCAAGCTCAGCACAGGCCAC---AGCCGGGGCCAC----------
85. Florida_manitee  Trichechus manatus latirostris  ATGGGTTCACACTGTGCCAAGCTCAGCACGGGCCAC---AGCCGGGGCCAC----------
86. African_savannah_elephant  Loxodonta africana   ATGGGTTCACGCTGTGCCAAGCTCAGCACGGGCCAG---AGCCGGGGCCAT----------
87. European_shrew  Sorex araneus                     ATGGGGTCTCGCTGTGCCAAGCTCAGCACAGGACACAGTGGCCGGGGCCAC----------
88. Aardvark  Orycteropus afer afer                  ATGGGTTCACACTGTGTCAAGCTTAGCTCAAGCCAC---AGCCGGGGCCGT----------
89. Gray_short_tailed_opossum  Monodelphis domestica ATGGGCTCCAGTTGTGCCAAACTAGGGGTTGTGCAC---ACCCAGAATTAT----------
90. Tasmanian_devil  Sarcophilus harrisii             ATGGGCTCCAGCTGTACCAAGCTAGGG---GAGCAG---GGCCAGAAATAT----------
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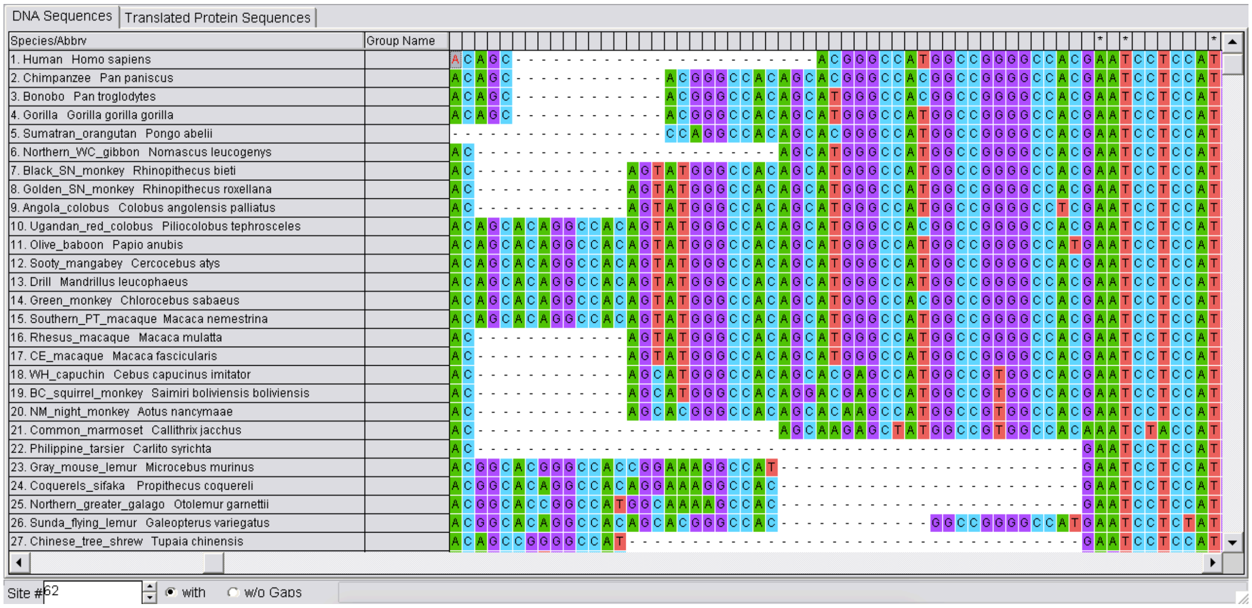
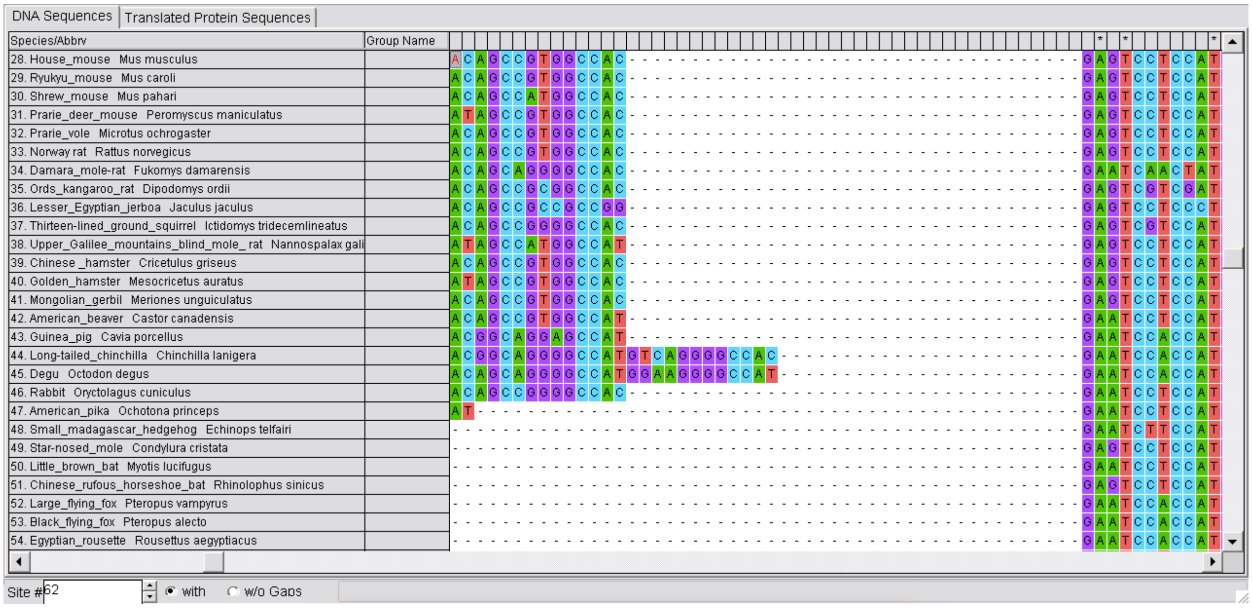


Species/Abbrv	Group Name	
1. Human Homo sapiens		ACAGC------------------------ACGGGCCATGGCCGGGGCCACGAATCCTCCAT
2. Chimpanzee Pan paniscus		ACAGC------------ACGGGCCACAGCACGGGCCACGGCCGGGGCCACGAATCCTCCAT
3. Bonobo Pan troglodytes		ACAGC------------ACGGGCCACAGCATGGGCCACGGCCGGGGCCACGAATCCTCCAT
4. Gorilla Gorilla gorilla gorilla		ACAGC------------ACGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCAT
5. Sumatran_orangutan Pongo abelii		-----------------CCAGGCCACAGCACGGGCCATGGCCGGGGCCACGAATCCTCCAT
6. Northern_WC_gibbon Nomascus leucogenys		AC------------------------AGCATGGGCCATGGCCGGGGCCACGAATCCTCCAT
7. Black_SN_monkey Rhinopithecus bieti		AC------------AGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCAT
8. Golden_SN_monkey Rhinopithecus roxellana		AC------------AGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCAT
9. Angola_colobus Colobus angolensis palliatus		AC------------AGTATGGGCCACAGCATGGGCCATGGCCGGGGCCTCGAATCCTCCAT
10. Ugandan_red_colobus Piliocolobus tephrosceles		ACAGCACAGGCCACAGTATGGGCCACAGCATGGGCCACGGCCGGGGCCACGAATCCTCCAT
11. Olive_baboon Papio anubis		ACAGCACAGGCCACAGTATGGGCCACAGCATGGGCCATGGCCGGGGCCATGAATCCTCCAT
12. Sooty_mangabey Cercocebus atys		ACAGCACAGGCCACAGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCAT
13. Drill Mandrillus leucophaeus		ACAGCACAGGCCACAGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCAT
14. Green_monkey Chlorocebus sabaeus		ACAGCACAGGCCACAGTATGGGCCACAGCATGGGCCACGGCCGGGGCCACGAATCCTCCAT
15. Southern_PT_macaque Macaca nemestrina		ACAGCACAGGCCACAGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCAT
16. Rhesus_macaque Macaca mulatta		AC------------AGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCAT
17. CE_macaque Macaca fascicularis		AC------------AGTATGGGCCACAGCATGGGCCATGGCCGGGGCCACGAATCCTCCAT
18. WH_capuchin Cebus capucinus imitator		AC------------AGCATGGGCCACAGCACGAGCCATGGCCGTGGCCACGAATCCTCCAT
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		AC------------AGCATGGGCCACAGGACGAGCCATGGCCGTGGCCACGAATCCTCCAT
20. NM_night_monkey Aotus nancymaae		AC------------AGCACGGGCCACAGCACAAGCCATGGCCGTGGCCACGAATCCTCCAT
21. Common_marmoset Callithrix jacchus		AC------------------------AGCAAGAGCTATGGCCGTGGCCACAAATCTACCAT
22. Philippine_tarsier Carlito syrichta		AC--GAATCCTCCAT
23. Gray_mouse_lemur Microcebus murinus		ACGGCACGGGCCACCGGAAAGGCCAT------------------------GAATCCTCCAT
24. Coquerels_sifaka Propithecus coquereli		ACGGCACAGGCCACAGGAAAGGCCAC------------------------GAATCCTCCAT
25. Northern_greater_galago Otolemur garnettii		ACGGCACCGGCCATGGCAAAAGCCAC------------------------GAATCCTCCAT
26. Sunda_flying_lemur Galeopterus variegatus		ACGGCACAGGCCACAGCACGGGCCAC------------GGCCGGGGCCATGAATCCTCTAT
27. Chinese_tree_shrew Tupaia chinensis		ACAGCCGGGGCCAT------------------------------------GAATCCTCCAT

Site # 62 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
28. House_mouse Mus musculus		ACAGCCGTGGCCAC------------------------------------GAGTCCTCCAT
29. Ryukyu_mouse Mus caroli		ACAGCCGTGGCCAC------------------------------------GAGTCCTCCAT
30. Shrew_mouse Mus pahari		ACAGCCATGGCCAC------------------------------------GAGTCCTCCAT
31. Prarie_deer_mouse Peromyscus maniculatus		ATAGCCGTGGCCAC------------------------------------GAGTCCTCCAT
32. Prarie_vole Microtus ochrogaster		ACAGCCGTGGCCAC------------------------------------GAGTCCTCCAT
33. Norway rat Rattus norvegicus		ACAGCCGTGGCCAC------------------------------------GAGTCCTCCAT
34. Damara_mole-rat Fukomys damarensis		ACAGCAGGGGCCAC------------------------------------GAATCAACTAT
35. Ords_kangaroo_rat Dipodomys ordii		ACAGCCGCGGCCAC------------------------------------GAGTCGTCGAT
36. Lesser_Egyptian_jerboa Jaculus jaculus		ACAGCCGCCGCCGG------------------------------------GAGTCCTCCCT
37. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		ACAGCCGGGGCCAC------------------------------------GAGTCGTCCAT
38. Upper_Galilee_mountains_blind_mole_ rat Nannospalax gali		ATAGCCATGGCCAT------------------------------------GAGTCCTCCAT
39. Chinese _hamster Cricetulus griseus		ACAGCCGTGGCCAC------------------------------------GAGTCCTCCAT
40. Golden_hamster Mesocricetus auratus		ATAGCCGTGGCCAC------------------------------------GAGTCCTCCAT
41. Mongolian_gerbil Meriones unguiculatus		ACAGCCGTGGCCAC------------------------------------GAGTCCTCCAT
42. American_beaver Castor canadensis		ACAGCCGTGGCCAT------------------------------------GAATCCTCCAT
43. Guinea_pig Cavia porcellus		ACGGCAGGAGCCAT------------------------------------GAATCCACCAT
44. Long-tailed_chinchilla Chinchilla lanigera		ACGGCAGGGGCCATGTCAGGGGCCAC------------------------GAATCCACCAT
45. Degu Octodon degus		ACAGCAGGGGCCATGGAAGGGGCCAT------------------------GAATCCACCAT
46. Rabbit Oryctolagus cuniculus		ACAGCCGGGGCCAC------------------------------------GAATCCTCCAT
47. American_pika Ochotona princeps		AT--GAATCCTCCAT
48. Small_madagascar_hedgehog Echinops telfairi		--GAATCTTCCAT
49. Star-nosed_mole Condylura cristata		--GAGTCCTCCAT
50. Little_brown_bat Myotis lucifugus		--GAATCCTCCAT
51. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		--GAGTCCTCCAT
52. Large_flying_fox Pteropus vampyrus		--GAATCCACCAT
53. Black_flying_fox Pteropus alecto		--GAATCCACCAT
54. Egyptian_rousette Rousettus aegyptiacus		--GAATCCACCAT

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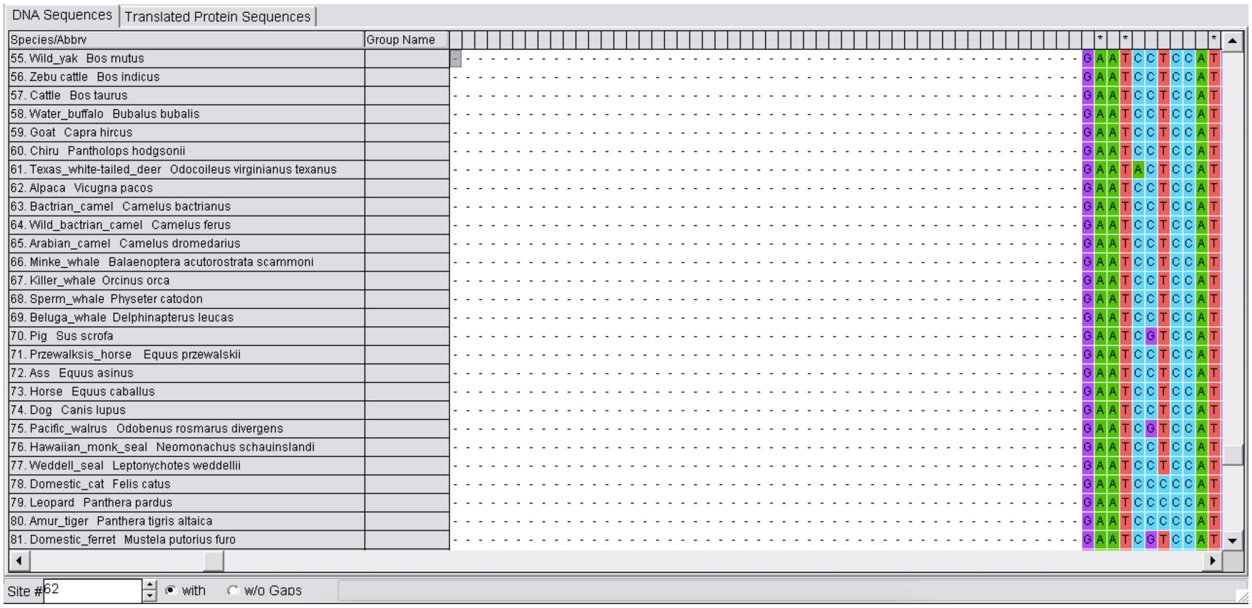
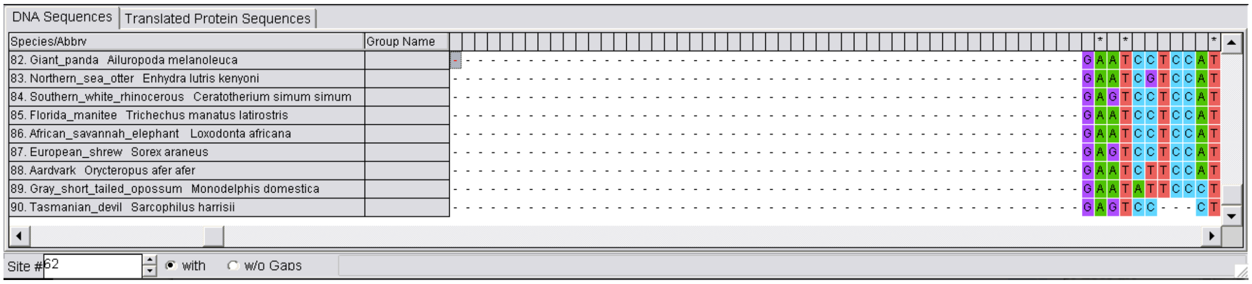


Species/Abbrv	Group Name	
55. Wild_yak Bos mutus		--GAATCCTCCAT
56. Zebu cattle Bos indicus		--GAATCCTCCAT
57. Cattle Bos taurus		--GAATCCTCCAT
58. Water_buffalo Bubalus bubalis		--GAATCCTCCAT
59. Goat Capra hircus		--GAATCCTCCAT
60. Chiru Pantholops hodgsonii		--GAATCCTCCAT
61. Texas_white-tailed_deer Odocoileus virginianus texanus		--GAATACTCCAT
62. Alpaca Vicugna pacos		--GAATCCTCCAT
63. Bactrian_camel Camelus bactrianus		--GAATCCTCCAT
64. Wild_bactrian_camel Camelus ferus		--GAATCCTCCAT
65. Arabian_camel Camelus dromedarius		--GAATCCTCCAT
66. Minke_whale Balaenoptera acutorostrata scammoni		--GAATCCTCCAT
67. Killer_whale Orcinus orca		--GAATCCTCCAT
68. Sperm_whale Physeter catodon		--GAATCCTCCAT
69. Beluga_whale Delphinapterus leucas		--GAATCCTCCAT
70. Pig Sus scrofa		--GAATCGTCCAT
71. Przewalksis_horse Equus przewalskii		--GAATCCTCCAT
72. Ass Equus asinus		--GAATCCTCCAT
73. Horse Equus caballus		--GAATCCTCCAT
74. Dog Canis lupus		--GAATCCTCCAT
75. Pacific_walrus Odobenus rosmarus divergens		--GAATCGTCCAT
76. Hawaiian_monk_seal Neomonachus schauinslandi		--GAATCCTCCAT
77. Weddell_seal Leptonychotes weddellii		--GAATCCTCCAT
78. Domestic_cat Felis catus		--GAATCCCCCAT
79. Leopard Panthera pardus		--GAATCCCCCAT
80. Amur_tiger Panthera tigris altaica		--GAATCCCCCAT
81. Domestic_ferret Mustela putorius furo		--GAATCGTCCAT

Site #62 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
82. Giant_panda Ailuropoda melanoleuca		--GAATCCTCCAT
83. Northern_sea_otter Enhydra lutris kenyoni		--GAATCGTCCAT
84. Southern_white_rhinocerous Ceratotherium simum simum		--GAGTCCTCCAT
85. Florida_manitee Trichechus manatus latirostris		--GAATCCTCCAT
86. African_savannah_elephant Loxodonta africana		--GAATCCTCCAT
87. European_shrew Sorex araneus		--GAGTCCTCCAT
88. Aardvark Orycteropus afer afer		--GAATCTTCCAT
89. Gray_short_tailed_opossum Monodelphis domestica		--GAATATTCCCT
90. Tasmanian_devil Sarcophilus harrisii		--GAGTCC---CT

Site #62 ● with ○ w/o Gaps

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Species/Abbrv                                    Group Name  *** *      *    **  * *     **  **       * ** **             
1. Human   Homo sapiens                                      GAAAAAGCTCATGGCCTGTGTGAGTCAGGATAACTTCTCCTTGTCATCAGCGGGCGAGGAA
2. Chimpanzee   Pan paniscus                                 GAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGCGGGCGAGGAA
3. Bonobo   Pan troglodytes                                  GAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGCGGGCGAGGAA
4. Gorilla   Gorilla gorilla gorilla                         GAAAAAGCTCGTGGCCTGTGTGAGTAAGGATAACTTCTCCTTGTCATCAGCGGGCGAGGAA
5. Sumatran_orangutan   Pongo abelii                         GAAGAAGCTCGTGGCCTGTGTGAGCCAGGATAACTTCTCCTTGTCATCAGAGGGCGAGGAA
6. Northern_WC_gibbon   Nomascus leucogenys                  GAAGAAGCTCATGGCCTGTGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGCGAGGAA
7. Black_SN_monkey   Rhinopithecus bieti                     GAAGAAGCTTGTGGCCTGCTTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGTGAGGAA
8. Golden_SN_monkey   Rhinopithecus roxellana                GAAGAAGCTTGTGGCCTGCTTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGTGAGGAA
9. Angola_colobus   Colobus angolensis palliatus             GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGTGAGGAA
10. Ugandan_red_colobus   Piliocolobus tephrosceles          GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGTGAGGAA
11. Olive_baboon   Papio anubis                              GAAGAAGCTCGTGGCCTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAGGGTGAGGAG
12. Sooty_mangabey   Cercocebus atys                         GAAGAAGCTCGTGGCCTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAGGGTGAGGAA
13. Drill   Mandrillus leucophaeus                           GAAGAAGCTCGTGGCCTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAGGGTGAGGAG
14. Green_monkey   Chlorocebus sabaeus                       GAAGAAGCTCGTGGCCTGTGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGGTGAGGAA
15. Southern_PT_macaque  Macaca nemestrina                  GAAGAAGCTCGTGGCCTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAGGGTGAGGAA
16. Rhesus_macaque   Macaca mulatta                          GAAGAAGCTCGTGGCCTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAAGGTGAGGAA
17. CE_macaque   Macaca fascicularis                         GAAGAAGCTCGTGGCCTGCGTCAGTCAAGATAACTTCTCCTTGTCATCAGAGGGTGAGGAA
18. WH_capuchin   Cebus capucinus imitator                   GAAGAAGCTCGTGGTCTGCGTGAGTCAGGATAACTTCTCCCTGTCATCAGAGGGCGAGGAA
19. BC_squirrel_monkey   Saimiri boliviensis boliviensis     GAAGAAGCTCGTGGCTTGCGTGAGTCAGGATAACTTCTCCCTGTCATCAGAGGGCGAGGAA
20. NM_night_monkey   Aotus nancymaae                        GAAGAAGTTCGTGGCCTGCGTGAGTCAGGACAAC---TCCCTGTCATCAGAGAGCGAGGAA
21. Common_marmoset   Callithrix jacchus                     GAAGAAGCTCATGACCTGCATGAGTCAGGATAACTTCTGTCTGTCATCAGAGGGCGAAGAA
22. Philippine_tarsier   Carlito syrichta                    GAAGAAGCTTATGGGCTGCGTGAGCCGAGATGACTTCTCCTTGTCGTCGGAG---gAGGAA
23. Gray_mouse_lemur   Microcebus murinus                    GAAGAAGCTCGTGGCCTGTGTGAGTCAGGATAACTTCTCCCTGTCGTCGGAGGGCGAGGAA
24. Coquerels_sifaka   Propithecus coquereli                 GAAGAAGCTTGTGGCCTGTGTAAGTCAGGATAACTTCTCCCTGTCATCAGAGGGTGAGGAA
25. Northern_greater_galago   Otolemur garnettii             GAAGAAGCTTGTGGCCTGTGTGAGTCAGGATAACTTCTCCCTGTCGTCAGAGGGCGAGGAA
26. Sunda_flying_lemur   Galeopterus variegatus              GAAGAAGCTTATGGCCTGTGTGAGTCAGGACAACTTCTCCCTGTCATCAGAGGGTGAGGAG
27. Chinese_tree_shrew   Tupaia chinensis                    GAAGAAATTTGTGGCCTGCGTGAGTCAGGACAACTTCTCCTTGTCTTCCAAGGGCGAGGAA
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Site # 123 ● with ○ w/o Gaps

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Species/Abbrv                                                 Group Name  *** *      *    **  * *     **  **       * ** **             
28. House_mouse   Mus musculus                                            GAAGAAGCTCGTGGCCTGTGTGAGTCAAGACAACTTTTCCCTGTCATCAGAGGGCGAGGAA
29. Ryukyu_mouse   Mus caroli                                             GAAGAAGCTCGTGGCCTGTGTGAGTCAAGACAACTTTTCCCTGTCATCAGAGGGCGAGGAA
30. Shrew_mouse   Mus pahari                                              GAAGAAGCTCGTGGCCTGTGTGAGTCAAGACAACTTTTCCCTGTCATCAGAGGGCGAGGAA
31. Prarie_deer_mouse   Peromyscus maniculatus                            GAAGAAGCTCGTGGCCTGCGTGAGTCAAGACAACTTCTCCCTGTCATCAGAGGGTGAGGAG
32. Prarie_vole   Microtus ochrogaster                                    GAAGAAGCTCATGGCCTGTGTGAGTCAAGACAACTTCTCCCTGTCATCAGAGGGCGAGGAA
33. Norway rat   Rattus norvegicus                                        GAAGAAACTCGTGGCCTGTGTGAGTCAAGACAACTTCTCCCTGTCATCAGAGGGTGAGGAA
34. Damara_mole-rat   Fukomys damarensis                                  GAAGAAGCTGCTGGCCTGTGTGAGTCAGGATAACTTCTGCCTGTCATCAGAGGAGGAGGAG
35. Ords_kangaroo_rat   Dipodomys ordii                                   GAAGAAGCTCGTGGCCTGTGTGAGTCAGGACAACTTCTCTCTGTCGTCGGAGGGTGAGGAG
36. Lesser_Egyptian_jerboa   Jaculus jaculus                              GAAAAAGCTCGTGGCCTGTGTGAGTCAGGACAACTTCTCCCTGTCATCAGAGAGTGAGGAG
37. Thirteen-lined_ground_squirrel   Ictidomys tridecemlineatus           GAAGAAGCTGGTGGCCTGCGTGAGCCAGGATAACTTCTCCCTGTCGTCAGAGGGGGAGGGG
38. Upper_Galilee_mountains_blind_mole_ rat   Nannospalax gali            GAAGAAACTTGTGGCCTGTGTGAGTCAGGACAACTTCTCCCTGTCATCAGAGGGTGAGGAG
39. Chinese _hamster   Cricetulus griseus                                 GAAGAAGCTCGTGGCCTGTGTGAGTCAAGACAACTTCTCCCTGTCATCAGAGGGTGAGGAA
40. Golden_hamster   Mesocricetus auratus                                 GAAGAAGCTCGTGGCCTGTGTGAGTCAAGACAACTTCTCCCTGTCATCAGAGGGTGAGGAG
41. Mongolian_gerbil   Meriones unguiculatus                              GAAGAAGCTCGTGGCCTGTGTGAGTCAAGACAACTTCTCCCTGTCATCTGAGGGTGAAGAG
42. American_beaver   Castor canadensis                                   GAAGAAGCTTGTGGCCTGTGTGAGTCAAGATAACTTCTCTCTGTCGTCGGAGGGTGAGGAC
43. Guinea_pig   Cavia porcellus                                          GAAGAAGCTCCTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGAGGAGGAG
44. Long-tailed_chinchilla   Chinchilla lanigera                          GAAGAAGCTCCTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGAGGAAGAG
45. Degu   Octodon degus                                                  GAAGAAGCTCCTGGCCTGTGTGAGTCAGGATAACTTCTCCTTGTCATCAGAGGAAGAAGAG
46. Rabbit   Oryctolagus cuniculus                                        GAAGAAACTCGTGGCTTGCGTGAGTCAAGATAACTTCTCCCTGTCTTCTGAGGGTGAGGAA
47. American_pika   Ochotona princeps                                     GAAGAAGCTCGTGGCCTGCGTGAGTCAAGATAACTTCTCCCTGTCCTCGGAGGGTGAAGAA
48. Small_madagascar_hedgehog   Echinops telfairi                         GAAGAAGCTCGTGGCCTGTGTGAGTCAGGACAACTTCTCTCTGTCATCAGAGGGTGAGGAG
49. Star-nosed_mole   Condylura cristata                                  GAAGAAGCTGGTGGCCTGCGTGAGTCAGGATAACATCTCCCTGTCATCGGAGGGCGAGGAG
50. Little_brown_bat   Myotis lucifugus                                   GAAGAAGCTCGTGGCCTGCGTGAGTCAAGATAACTTCTCCTTGTCCTCAGAGGGTGAGGAA
51. Chinese_rufous_horseshoe_bat   Rhinolophus sinicus                    GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCAGAGGGCGAGGAA
52. Large_flying_fox   Pteropus vampyrus                                  GAAGAAACTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCAGAGGGAGAGGAA
53. Black_flying_fox   Pteropus alecto                                    GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCAGAGGGAGAGGAA
54. Egyptian_rousette   Rousettus aegyptiacus                             GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCAGAAGGAGAGGAA
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Site # 123 ● with ○ w/o Gaps

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Species/Abbrv                                               Group Name  *** *      *    **  * *     **  **       * ** **
55. Wild_yak  Bos mutus                                                 GAAGAAGCTCGTGGCCTGCGTGAGCCAGGATAACTTCTCCTTGTCGTCGGAGGGCGAGGAG
56. Zebu cattle  Bos indicus                                            GAAGAAGCTCGTGGCCTGCGTGAGCCAGGATAACTTCTCCTTGTCGTCGGAGGGCGAGGAG
57. Cattle  Bos taurus                                                  GAAGAAGCTCGTGGCCTGCGTGAGCCAGGATAACTTCTCCTTGTCGTCGGAGGGCGAGGAG
58. Water_buffalo  Bubalus bubalis                                      GAAGAAGCTCGTGGCCTGCGTGAGCCAGGATAACTTCTCCTTGTCGTCGGAGGGCGAGGAG
59. Goat  Capra hircus                                                  GAAGAAGCTCGTGGCCTGCGTGAGCCAGGATAACTTCTCCTTGTCGTCGGAGGGCGAGGAG
60. Chiru  Pantholops hodgsonii                                         GAAGAAGCTCGTGGCCTGTGTGAGCCAGGATAACTTCTCCTTGTCATCGGAGGGCGAGGAG
61. Texas_white-tailed_deer  Odocoileus virginianus texanus             GAAGAAGCTCGTGGCCTGCGTGAGCCAGGATAACTTCTCCTTGTCGTCGGAGGGCGAGGAG
62. Alpaca  Vicugna pacos                                               GAAGAAGCTTGTGGCCTGCGTGAGTCAGGACAACTTCTCCTTGTCGTCGGAGAGTGAGGAA
63. Bactrian_camel  Camelus bactrianus                                  GAAGAAGCTTGTGGCCTGCGTGAGTCAGGACAACTTCTCCTTGTCGTCGGAGAGTGAGGAA
64. Wild_bactrian_camel  Camelus ferus                                  GAAGAAGCTTGTGGCCTGCGTGAGTCAGGACAACTTCTCCTTGTCGTCGGAGAGTGAGGAA
65. Arabian_camel  Camelus dromedarius                                  GAAGAAGCTTGTGGCCTGCGTGAGTCAGGACAACTTCTCCTTGTCGTCGGAGAGTGAGGAA
66. Minke_whale  Balaenoptera acutorostrata scammoni                    GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCGGAGGGTGAGGAG
67. Killer_whale  Orcinus orca                                          GAAGAAGTTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCGGCGGGTGAGGAG
68. Sperm_whale  Physeter catodon                                       GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTC---TTGTCTTCGGAGGGGGAGGAG
69. Beluga_whale  Delphinapterus leucas                                 GAAGAAGCTCGTGGCCTGCATGAGTCAGGATAACGTCTCATTGTCGTCGGAGGGTGAGGAG
70. Pig  Sus scrofa                                                     GAAGAAGCTGGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCGGAGGGCGAGGAA
71. Przewalksis_horse  Equus przewalskii                                GAAGAAGCTGGTGGCCTGCGTGAGTCAAGATAACTTCTCCCTGTCATCGGAGGGCGAGGAA
72. Ass  Equus asinus                                                   GAAGAAGCTGGTAGCCTGCGTGAGTCAGGATAACTTCTCCCTGTCATCGGAGGGCGAGGAA
73. Horse  Equus caballus                                               GAAGAAGCTGGTGGCCTGCGTGAGTCAAGATAACTTCTCCCTGTCATCGGAGGGCGAGGAA
74. Dog  Canis lupus                                                    GAAGAAGCTCATGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCAGAAGGCGAGGAA
75. Pacific_walrus  Odobenus rosmarus divergens                         GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCCGAGGCTGAGGAA
76. Hawaiian_monk_seal  Neomonachus schauinslandi                       GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTATCATCCGAGGGTGAGGAA
77. Weddell_seal  Leptonychotes weddellii                               GAAGAAGCTCGTGGCCTGCATGAGTCAGGATAACTTCTCCTTATCGTCCGAGGGTGAGGAA
78. Domestic_cat  Felis catus                                           GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCCGAGGGGAAGGGA
79. Leopard  Panthera pardus                                            GAAGAAGCTCATGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCCGAGGGGGAGGGA
80. Amur_tiger  Panthera tigris altaica                                 GAAGAAGCTCATGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCCGAGGGGGAGGGA
81. Domestic_ferret  Mustela putorius furo                              GAAGAAACTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCATCTGAGGGTGAGGAA
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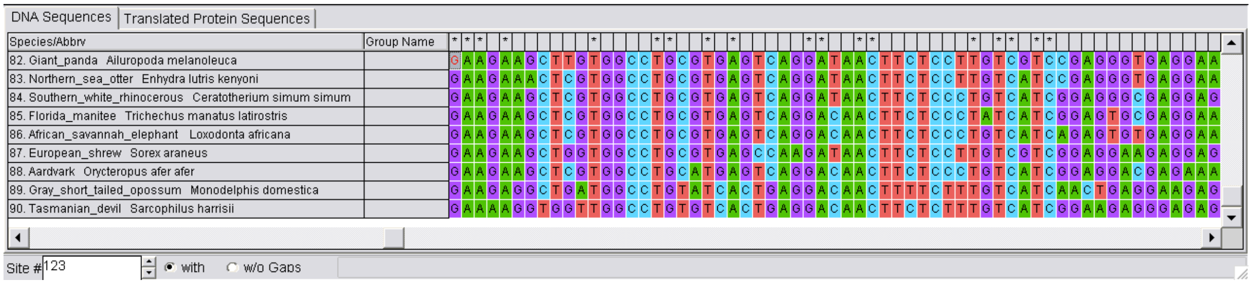

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Species/Abbrv                                               Group Name  *** *      *    **  * *     **  **       * ** **
82. Giant_panda  Ailuropoda melanoleuca                                 GAAGAAGCTTGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCGTCCGAGGGTGAGGAA
83. Northern_sea_otter  Enhydra lutris kenyoni                          GAAGAAACTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCTTGTCATCCGAGGGTGAGGAA
84. Southern_white_rhinocerous  Ceratotherium simum simum               GAAGAAGCTCGTGGCCTGCGTGAGTCAGGATAACTTCTCCCTGTCATCGGAGGGCGAGGAG
85. Florida_manitee  Trichechus manatus latirostris                     GAAGAAGCTCGTGGCCTGCGTGAGTCAGGACAACTTCTCCCTATCATCGGAGTGCGAGGAA
86. African_savannah_elephant  Loxodonta africana                       GAAGAAGCTCGTGGCCTGCGTGAGTCAGGACAACTTCTCCCTGTCATCAGAGTGTGAGGAA
87. European_shrew  Sorex araneus                                       GAAGAAGCTGGTGGCCTGCGTGAGCCAAGATAACTTCTCCTTGTCGTCGGAGGAAGAGGAG
88. Aardvark  Orycteropus afer afer                                     GAAGAAGCTCGTGGCCTGCATGAGTCAGGACAACTTCTCCCTGTCATCGGAGGACGAGAAA
89. Gray_short_tailed_opossum  Monodelphis domestica                    GAAGAGGCTGATGGCCTGTATCACTGAGGACAACTTTTCTTTGTCATCAACTGAGGAAGAG
90. Tasmanian_devil  Sarcophilus harrisii                               GAAAAGGTGGTTGGCCTGTGTCACTGAGGACAACTTCTCTTTGTCATCGGAAGAGGGAGAG
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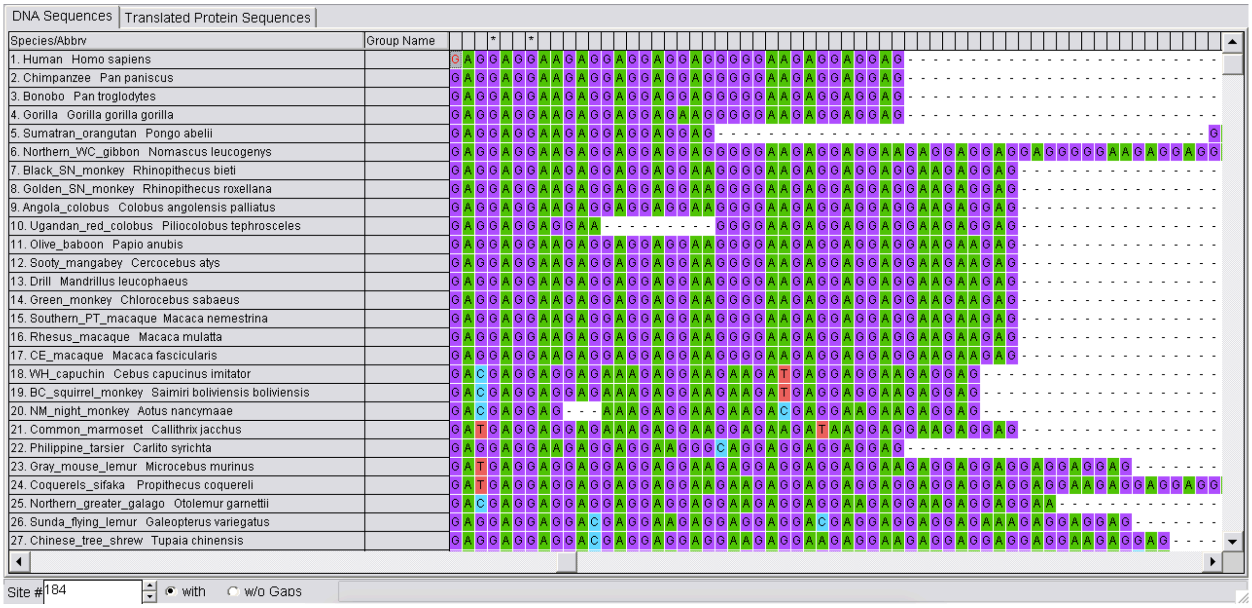
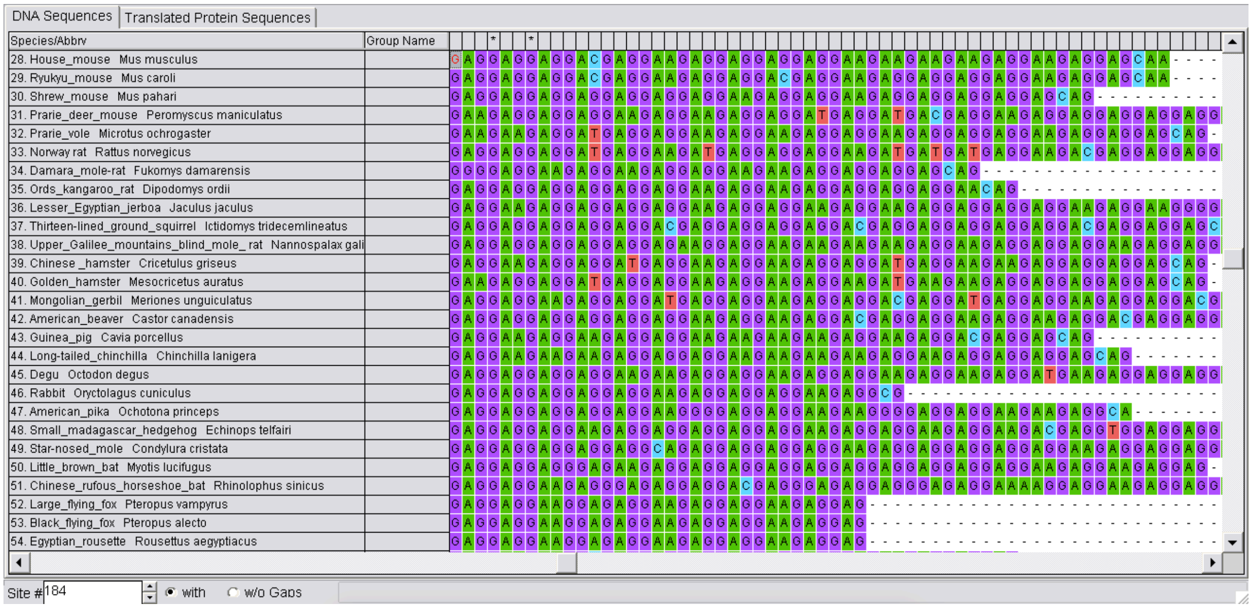


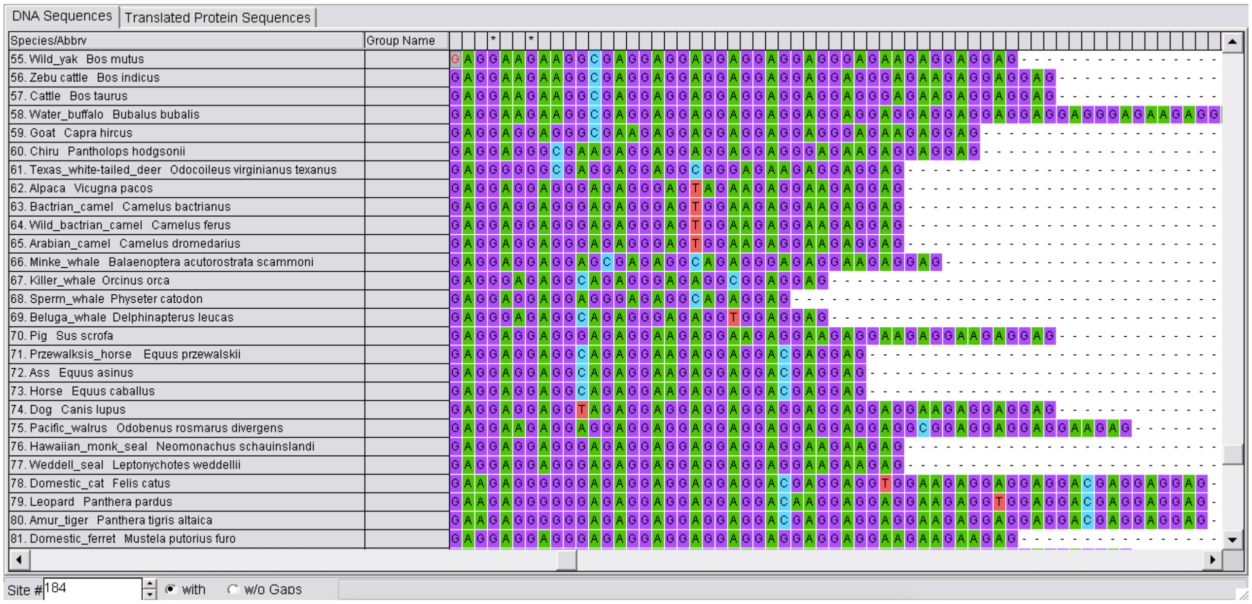
Species/Abbrv	Group Name	
1. Human Homo sapiens		GAGGAGGAAGAGGAGGAGGAGGGGGAAGAGGAGGAG-------------------------
2. Chimpanzee Pan paniscus		GAGGAGGAAGAGGAGGAGGAGGGGGAAGAGGAGGAG-------------------------
3. Bonobo Pan troglodytes		GAGGAGGAAGAGGAGGAGGAGGGGGAAGAGGAGGAG-------------------------
4. Gorilla Gorilla gorilla gorilla		GAGGAGGAAGAGGAGGAGAAGGGGGAAGAGGAGGAG-------------------------
5. Sumatran_orangutan Pongo abelii		GAGGAGGAAGAGGAGGAGGAG---------------------------------------G
6. Northern_WC_gibbon Nomascus leucogenys		GAGGAGGAAGAGGAGGAGGAGGGGGAAGAGGAGGAAGAGGAGGAGGAGGGGGAAGAGGAGG
7. Black_SN_monkey Rhinopithecus bieti		GAGGAGGAAGAGGAGGAGGAAGGGGAAGAGGAGGAGGAAGAGGAG----------------
8. Golden_SN_monkey Rhinopithecus roxellana		GAGGAGGAAGAGGAGGAGGAAGGGGAAGAGGAGGAGGAAGAGGAG----------------
9. Angola_colobus Colobus angolensis palliatus		GAGGAGGAAGAGGAGGAGGAAGGGGAAGAGGAGGAGGAAGAGGAG----------------
10. Ugandan_red_colobus Piliocolobus tephrosceles		GAGGAGGAGGAA---------GGGGAAGAGGAGGAGGAAGAGGAG----------------
11. Olive_baboon Papio anubis		GAGGAGGAAGAGGAGGAGGAAGGGGAAGAGGAGGAGGAAGAAGAG----------------
12. Sooty_mangabey Cercocebus atys		GAGGAGGAAGAGGAGGAGGAAGGGGAAGAGGAGGAGGAAGAAGAG----------------
13. Drill Mandrillus leucophaeus		GAGGAGGAAGAGGAGGAGGAAGGGGAAGAGGAGGAGGAAGAAGAG----------------
14. Green_monkey Chlorocebus sabaeus		GAGGAGGAAGAGGAGGAGGAAGGGGAAGAGGAGGAGGAAGAAGAG----------------
15. Southern_PT_macaque Macaca nemestrina		GAGGAGGAAGAGGAGGAGGAAGGGGAAGAGGAGGAGGAAGAAGAG----------------
16. Rhesus_macaque Macaca mulatta		GAGGAGGAAGAGGAGGAGGAAGGGGAAGAGGAGGAGGAAGAAGAG----------------
17. CE_macaque Macaca fascicularis		GAGGAGGAAGAGGAGGAGGAAGGGGAAGAGGAGGAGGAAGAAGAG----------------
18. WH_capuchin Cebus capucinus imitator		GACGAGGAGGAGAAAGAGGAAGAAGATGAGGAGGAAGAGGAG-------------------
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		GACGAGGAGGAGAAAGAGGAAGAAGATGAGGAGGAAGAGGAG-------------------
20. NM_night_monkey Aotus nancymaae		GACGAGGAG---AAAGAGGAAGAAGACGAGGAAGAAGAGGAG-------------------
21. Common_marmoset Callithrix jacchus		GATGAGGAGGAGAAAGAGGAAGGAGAAGATAAGGAGGAAGAGGAG----------------
22. Philippine_tarsier Carlito syrichta		GAGGAGGAAGAGGAGGAAGGGCAGGAGGAGGAGGAG-------------------------
23. Gray_mouse_lemur Microcebus murinus		GATGAGGAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAGGAGGAG-------
24. Coquerels_sifaka Propithecus coquereli		GATGAGGAGGAGGAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAGGAGGAGG
25. Northern_greater_galago Otolemur garnettii		GACGAGGAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGAGGAGGAA-------------
26. Sunda_flying_lemur Galeopterus variegatus		GAGGAGGAGGACGAGGAAGAGGAGGAGGACGAGGAGGAGGAGAAAGAGGAGGAG-------
27. Chinese_tree_shrew Tupaia chinensis		GAGGAGGAGGACGAGGAGGAGGAAGAGGAAGAGGAAGAGGAGGAGGAGGAAGAGGAG----

Site # 184 ● with ○ w/o Gaps

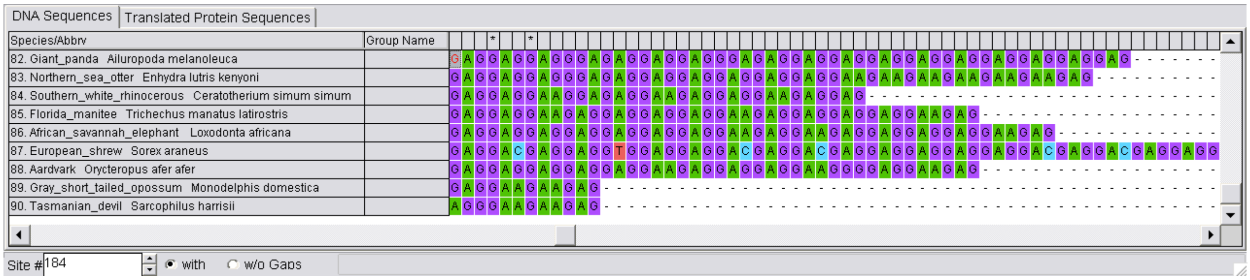


Species/Abbrv	Group Name	
28. House_mouse Mus musculus		GAGGAGGAGGACGAGGAAGAGGAGGAGGAGGAAGAAGAAGAAGAGGAAGAGGAGCAA----
29. Ryukyu_mouse Mus caroli		GAGGAGGAGGACGAGGAAGAGGAGGACGAGGAAGAGGAGGAGGAGGAAGAGGAGCAA----
30. Shrew_mouse Mus pahari		GAGGAGGAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAGGAGGAGGAGCAG----------
31. Prarie_deer_mouse Peromyscus maniculatus		GAAGAGGAGGAGGAAGAGGAAGAGGAGGATGAGGATGACGAGGAAGAGGAGGAGGAGGAGG
32. Prarie_vole Microtus ochrogaster		GAAGAAGAGGATGAGGAGGAAGAGGAAGAGGAGGAAGAGGAGGAGGAAGAGGAGGAGCAG-
33. Norway rat Rattus norvegicus		GAGGAGGAGGATGAGGAAGATGAGGAGGAGGAAGATGATGATGAGGAAGACGAGGAGGAGG
34. Damara_mole-rat Fukomys damarensis		GGGGAGGAAGAGGAAGAGGAGGAAGAAGAGGAGGAGGAGCAG-------------------
35. Ords_kangaroo_rat Dipodomys ordii		GAGGAGGAGGAGGAGGAGGAAGAGGAAGAGGAGGAGGAGGAACAG----------------
36. Lesser_Egyptian_jerboa Jaculus jaculus		GAGGAAGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGAGGAGGAGGAGGAAGAGGAAGGGG
37. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		GAGGAGGAGGAGGAGGACGAGGAGGAGGAGGACGAGGAGGAGGAGGAGGACGAGGAGGAGC
38. Upper_Galilee_mountains_blind_mole_ rat Nannospalax gali		GAGGAGGAGGAGGAGGAGAAGGAGGAAGAAGAAGAAGAGGAAGAGGAGGAGGAAGAGGAGG
39. Chinese _hamster Cricetulus griseus		GAGGAAGAGGAGGATGAGGAAGAGGAAGAGGAGGATGAGGAAGAAGAGGAGGAGGAGCAG-
40. Golden_hamster Mesocricetus auratus		GAAGAGGAGGATGAGGAGGAAGAGGAAGAGGAAGATGAAGAAGAGGAGGAGGAGGAGCAG-
41. Mongolian_gerbil Meriones unguiculatus		GAGGAGGAAGAGGAGGATGAGGAGGAAGAGGAGGACGAGGATGAGGAGGAAGAGGAGGACG
42. American_beaver Castor canadensis		GAGGAGGAGGAGGAGGAGGAAGAGGAAGAGGACGAGGAGGAAGAGGAAGAGGACGAGGAGG
43. Guinea_pig Cavia porcellus		GAGGAAGAGGAAGAGGAGGAAGAAGAAGAAGAGGAAGAGGACGAGGAGCAG----------
44. Long-tailed_chinchilla Chinchilla lanigera		GAGGAAGAAGAAGAGGAGGAGGAAGAAGAAGAAGAGGAAGAGGAGGAGGAGCAG-------
45. Degu Octodon degus		GAGGAGGAGGAGGAAGAAGAGGAGGAAGAGGAGGAAGAGGAAGAGGATGAAGAGGAGGAGG
46. Rabbit Oryctolagus cuniculus		GAGGAGGAGGAGGAGGAAGAGGAGGAGGAAGAGGCG-------------------------
47. American_pika Ochotona princeps		GAGGAGGAGGAGGAGGAAGGGGAGGAGGAAGAAGGGGAGGAGGAAGAAGAGGCA-------
48. Small_madagascar_hedgehog Echinops telfairi		GAGGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGACGAGGTGGAGGAGG
49. Star-nosed_mole Condylura cristata		GAGGAGGAGGAGGAGGCAGAGGAGGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGGAGGAGG
50. Little_brown_bat Myotis lucifugus		GAGGAGGAGGGAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGAGGAAGAGGAG-
51. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		GAGGAGGAAGAGGGAGAGGAGGACGAGGGAGAGGAGGGAGAGGAAAAGGAGGAAGAGGAGG
52. Large_flying_fox Pteropus vampyrus		GAGGAGGAAGGAGAGGAAGAGGAGGAAGAGGAG----------------------------
53. Black_flying_fox Pteropus alecto		GAGGAGGAAGGAGAGGAAGAGGAGGAAGAGGAG----------------------------
54. Egyptian_rousette Rousettus aegyptiacus		GAGGAGGAAGGAGAGGAAGAGGAGGAAGAGGAG----------------------------

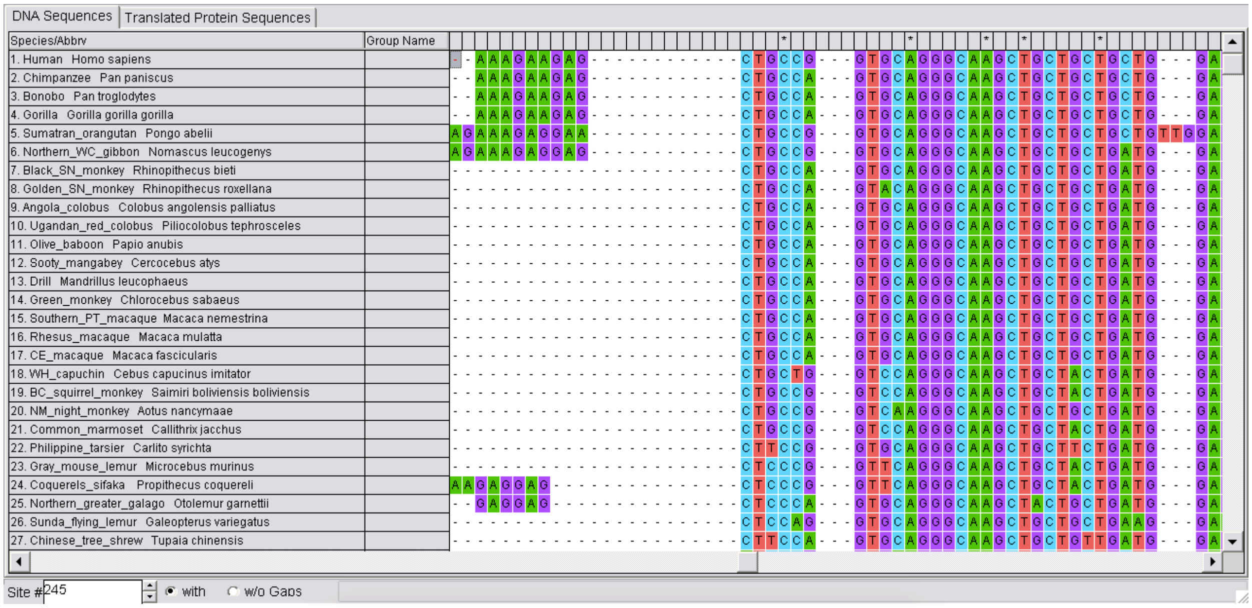
Site # 184 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
55. Wild_yak Bos mutus		GAGGAAGAAGGCGAGGAGGAGGAGGAGGAGGGAGAAGAGGAGGAG
56. Zebu cattle Bos indicus		GAGGAAGAAGGCGAGGAGGAGGAGGAGGAGGAGGGAGAAGAGGAGGAG
57. Cattle Bos taurus		GAGGAAGAAGGCGAGGAGGAGGAGGAGGAGGAGGGAGAAGAGGAGGAG
58. Water_buffalo Bubalus bubalis		GAGGAAGAAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGGAGAAGAGG
59. Goat Capra hircus		GAGGAGGAGGGCGAAGAGGAGGAGGAGGAGGGAGAAGAGGAG
60. Chiru Pantholops hodgsonii		GAGGAGGGCGAAGAGGAGGAGGAGGAGGGAGAAGAGGAGGAG
61. Texas_white-tailed_deer Odocoileus virginianus texanus		GAGGGGGGCGAGGAGGAGGCGGGAGAAGAGGAGGAG
62. Alpaca Vicugna pacos		GAGGAGGAGGGAGAGGGAGTAGAAGAGGAAGAGGAG
63. Bactrian_camel Camelus bactrianus		GAGGAGGAGGGAGAGGGAGTGGAAGAGGAAGAGGAG
64. Wild_bactrian_camel Camelus ferus		GAGGAGGAGGGAGAGGGAGTGGAAGAGGAAGAGGAG
65. Arabian_camel Camelus dromedarius		GAGGAGGAGGGAGAGGGAGTGGAAGAGGAAGAGGAG
66. Minke_whale Balaenoptera acutorostrata scammoni		GAGGAGGAGGAGCGAGAGGCAGAGGGAGAGGAAGAGGAG
67. Killer_whale Orcinus orca		GAGGGAGAGGCAGAGGGAGAGGCGGAGGAG
68. Sperm_whale Physeter catodon		GAGGAGGAGGAGGGAGAGGCAGAGGAG
69. Beluga_whale Delphinapterus leucas		GAGGGAGAGGCAGAGGGAGAGGTGGAGGAG
70. Pig Sus scrofa		GAGGAGGAGGGAGAGGAAGAGGAAGAGGAAGAGGAAGAGGAAGAGGAG
71. Przewalksis_horse Equus przewalskii		GAGGAGGAGGCAGAGGAAGAGGAGGACGAGGAG
72. Ass Equus asinus		GAGGAGGAGGCAGAGGAAGAGGAGGACGAGGAG
73. Horse Equus caballus		GAGGAGGAGGCAGAGGAAGAGGAGGACGAGGAG
74. Dog Canis lupus		GAGGAGGAGGTAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAGGAGGAG
75. Pacific_walrus Odobenus rosmarus divergens		GAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCGGAGGAGGAGGAAGAG
76. Hawaiian_monk_seal Neomonachus schauinslandi		GAGGAGGAGGGAGAGGAGGAGGAGGAGGAAGAAGAG
77. Weddell_seal Leptonychotes weddellii		GAGGAGGAGGGAGAGGAGGAGGAGGAGGAAGAAGAG
78. Domestic_cat Felis catus		GAAGAGGGGGGAGAGGAGGAGGAGGACGAGGAGGTGGAAGAGGAGGAGGACGAGGAGGAG
79. Leopard Panthera pardus		GAAGAGGGGGGAGAGGAGGAGGAGGACAAGGAGGAGGAAGAGGTGGAGGACGAGGAGGAG
80. Amur_tiger Panthera tigris altaica		GAAGAGGGGGGAGAGGAGGAGGAGGACGAGGAGGAGGAAGAGGAGGAGGACGAGGAGGAG
81. Domestic_ferret Mustela putorius furo		GAGGAGGAGGGAGAGGAGGAGGAGGAGGAGGAGGAAGAAGAAGAG

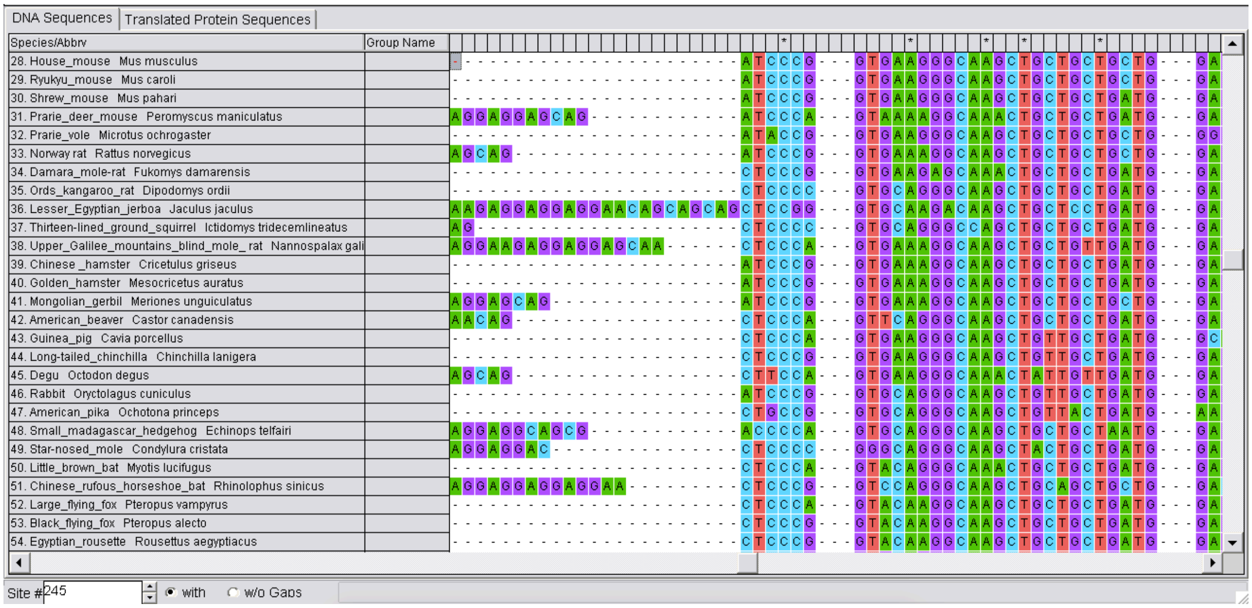


Species/Abbrv	Group Name	
82. Giant_panda Ailuropoda melanoleuca		GAGGAGGAGGGAGAGGAGGAGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
83. Northern_sea_otter Enhydra lutris kenyoni		GAGGAGGAGGGAGAGGAGGAGGAGGAGGAGGAAGAAGAAGAAGAAGAAGAG
84. Southern_white_rhinocerous Ceratotherium simum simum		GAGGAGGAAGGAGAGGAAGAGGAGGAAGAGGAG
85. Florida_manitee Trichechus manatus latirostris		GAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAG
86. African_savannah_elephant Loxodonta africana		GAGGAGGAGGAGGAGGAGGAGGAAGAGGAAGAGGAGGAGGAGGAAGAG
87. European_shrew Sorex araneus		GAGGACGAGGAGGTGGAGGAGGACGAGGACGAGGAGGAGGAGGAGGACGAGGACGAGGAGG
88. Aardvark Orycteropus afer afer		GAGGAGGAGGAGGAGGAAGAGGAGGAGGAAGGGGAGGAAGAG
89. Gray_short_tailed_opossum Monodelphis domestica		GAGGAAGAAGAG
90. Tasmanian_devil Sarcophilus harrisii		AGGGAAGAAGAG



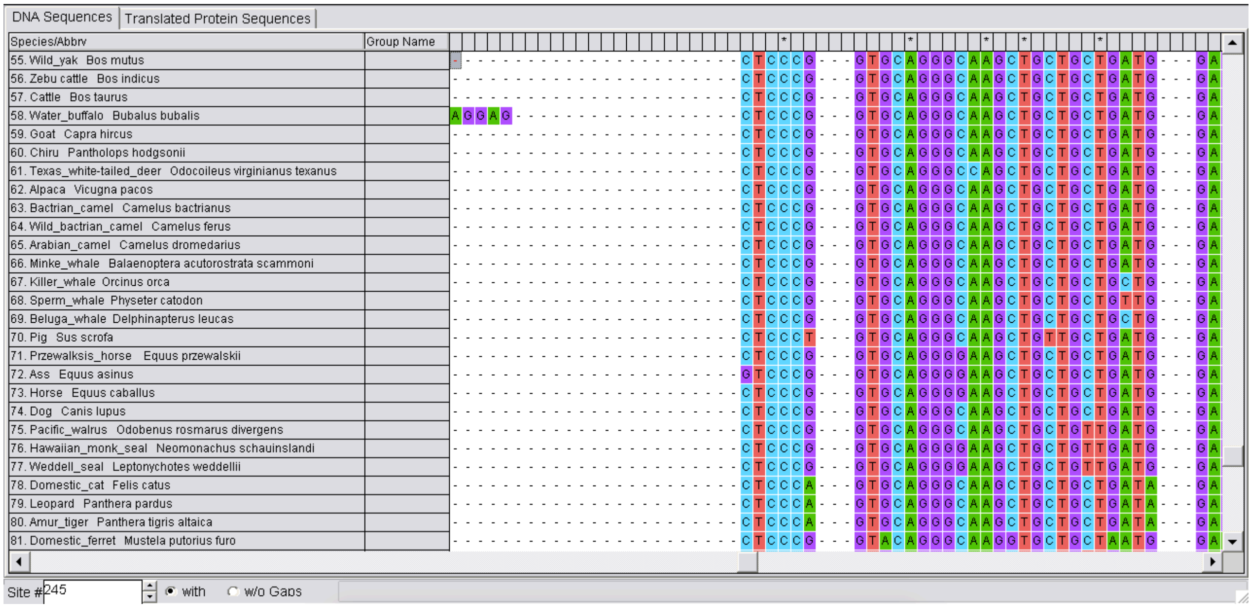
Species/Abbrv	Group Name	
1. Human Homo sapiens		--AAAGAAGAG------------CTGCCG---GTGCAGGGCAAGCTGCTGCTGCTG---GA
2. Chimpanzee Pan paniscus		--AAAGAAGAG------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGCTG---GA
3. Bonobo Pan troglodytes		--AAAGAAGAG------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGCTG---GA
4. Gorilla Gorilla gorilla gorilla		--AAAGAAGAG------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGCTG---GA
5. Sumatran_orangutan Pongo abelii		AGAAAGAGGAA------------CTGCCG---GTGCAGGGCAAGCTGCTGCTGCTGTTGGA
6. Northern_WC_gibbon Nomascus leucogenys		AGAAAGAGGAG------------CTGCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
7. Black_SN_monkey Rhinopithecus bieti		-----------------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGATG---GA
8. Golden_SN_monkey Rhinopithecus roxellana		-----------------------CTGCCA---GTACAGGGCAAGCTGCTGCTGATG---GA
9. Angola_colobus Colobus angolensis palliatus		-----------------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGATG---GA
10. Ugandan_red_colobus Piliocolobus tephrosceles		-----------------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGATG---GA
11. Olive_baboon Papio anubis		-----------------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGATG---GA
12. Sooty_mangabey Cercocebus atys		-----------------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGATG---GA
13. Drill Mandrillus leucophaeus		-----------------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGATG---GA
14. Green_monkey Chlorocebus sabaeus		-----------------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGATG---GA
15. Southern_PT_macaque Macaca nemestrina		-----------------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGATG---GA
16. Rhesus_macaque Macaca mulatta		-----------------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGATG---GA
17. CE_macaque Macaca fascicularis		-----------------------CTGCCA---GTGCAGGGCAAGCTGCTGCTGATG---GA
18. WH_capuchin Cebus capucinus imitator		-----------------------CTGCTG---GTCCAGGGCAAGCTGCTACTGATG---GA
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		-----------------------CTGCCG---GTCCAGGGCAAGCTGCTACTGATG---GA
20. NM_night_monkey Aotus nancymaae		-----------------------CTGCCG---GTCAAGGGCAAGCTGCTGCTGATG---GA
21. Common_marmoset Callithrix jacchus		-----------------------CTGCCG---GTCCAGGGCAAGCTGCTACTGATG---GA
22. Philippine_tarsier Carlito syrichta		-----------------------CTTCCG---GTGCAGGGCAAGCTGCTTCTGATG---GA
23. Gray_mouse_lemur Microcebus murinus		-----------------------CTCCCG---GTTCAGGGCAAGCTGCTACTGATG---GA
24. Coquerels_sifaka Propithecus coquereli		AAGAGGAG---------------CTCCCG---GTTCAGGGCAAGCTGCTACTGATG---GA
25. Northern_greater_galago Otolemur garnettii		--GAGGAG---------------CTCCCA---GTGCAGGGCAAGCTACTGCTGATG---GA
26. Sunda_flying_lemur Galeopterus variegatus		-----------------------CTCCAG---GTGCAGGGCAAGCTGCTGCTGAAG---GA
27. Chinese_tree_shrew Tupaia chinensis		-----------------------CTTCCA---GTGCAGGGCAAGCTGCTGTTGATG---GA

Site # 245 ● with ○ w/o Gaps



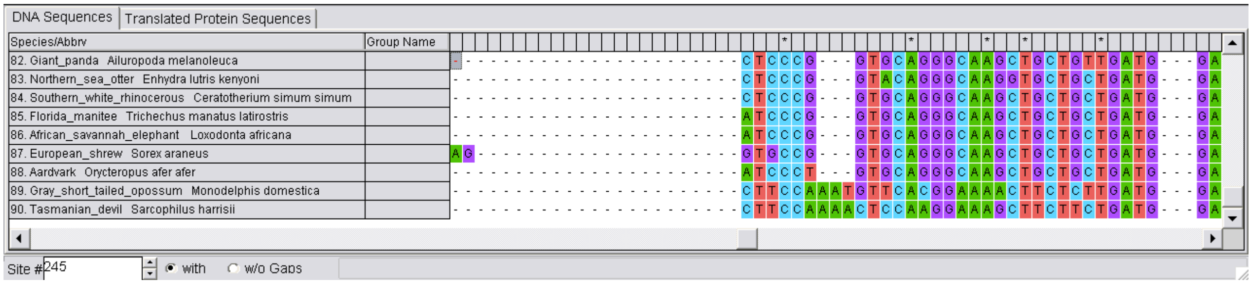
Species/Abbrv	Group Name	
28. House_mouse Mus musculus		-----------------------ATCCCG---GTGAAGGGCAAGCTGCTGCTGCTG---GA
29. Ryukyu_mouse Mus caroli		-----------------------ATCCCG---GTGAAGGGCAAGCTGCTGCTGCTG---GA
30. Shrew_mouse Mus pahari		-----------------------ATCCCG---GTGAAGGGCAAGCTGCTGCTGATG---GA
31. Prarie_deer_mouse Peromyscus maniculatus		AGGAGGAGCAG------------ATCCCA---GTAAAAGGCAAACTGCTGCTGATG---GA
32. Prarie_vole Microtus ochrogaster		-----------------------ATACCG---GTGAAGGGCAAGCTGCTGCTGCTG---GG
33. Norway rat Rattus norvegicus		AGCAG------------------ATCCCG---GTGAAAGGCAAGCTGCTGCTGCTG---GA
34. Damara_mole-rat Fukomys damarensis		-----------------------CTCCCG---GTGAAGAGCAAACTGCTGCTGATG---GA
35. Ords_kangaroo_rat Dipodomys ordii		-----------------------CTCCCC---GTGCAGGGCAAGCTGCTGCTGATG---GA
36. Lesser_Egyptian_jerboa Jaculus jaculus		AAGAGGAGGAGGAACAGCAGCAGCTCCGG---GTGCAAGACAAGCTGCTCCTGATG---GA
37. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		AG---------------------CTCCCC---GTGCAGGGCCAGCTGCTGCTGATG---GA
38. Upper_Galilee_mountains_blind_mole_rat Nannospalax gali		AGGAAGAGGAGGAGCAA------CTCCCA---GTGAAAGGCAAGCTGCTGTTGATG---GA
39. Chinese _hamster Cricetulus griseus		-----------------------ATCCCG---GTGAAAGGCAAGCTGCTGCTGATG---GA
40. Golden_hamster Mesocricetus auratus		-----------------------ATCCCG---GTGAAAGGCAAGCTGCTGCTGATG---GA
41. Mongolian_gerbil Meriones unguiculatus		AGGAGCAG---------------ATCCCG---GTGAAAGGCAAGCTGCTGCTGCTG---GA
42. American_beaver Castor canadensis		AACAG------------------CTCCCA---GTTCAGGGCAAGCTGCTGCTGATG---GA
43. Guinea_pig Cavia porcellus		-----------------------CTCCCA---GTGAAGGGCAAGCTGTTGCTGATG---GC
44. Long-tailed_chinchilla Chinchilla lanigera		-----------------------CTCCCG---GTGAAGGGCAAGCTGTTGCTGATG---GA
45. Degu Octodon degus		AGCAG------------------CTTCCA---GTGAAGGGCAAACTATTGTTGATG---GA
46. Rabbit Oryctolagus cuniculus		-----------------------ATCCCG---GTGCAGGGCAAGCTGTTGCTGATG---GA
47. American_pika Ochotona princeps		-----------------------CTGCCG---GTGCAGGGCAAGCTGTTACTGATG---AA
48. Small_madagascar_hedgehog Echinops telfairi		AGGAGGCAGCG------------ACCCCA---GTGCAGGGCAAGCTGCTGCTAATG---GA
49. Star-nosed_mole Condylura cristata		AGGAGGAC---------------CTCCCC---GGGCAGGGCAAGCTACTGCTGATG---GA
50. Little_brown_bat Myotis lucifugus		-----------------------CTCCCA---GTACAGGGCAAACTGCTGCTGATG---GA
51. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		AGGAGGAGGAGGAA---------CTCCCG---GTCCAGGGCAAGCTGCAGCTGCTG---GA
52. Large_flying_fox Pteropus vampyrus		-----------------------CTCCCA---GTACAAGGCAAGCTGCTGCTGATG---GA
53. Black_flying_fox Pteropus alecto		-----------------------CTCCCG---GTACAAGGCAAGCTGCTGCTGATG---GA
54. Egyptian_rousette Rousettus aegyptiacus		-----------------------CTCCCG---GTACAAGGCAAGCTGCTGCTGATG---GA

Site # 245 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
55. Wild_yak Bos mutus		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
56. Zebu cattle Bos indicus		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
57. Cattle Bos taurus		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
58. Water_buffalo Bubalus bubalis		AGGAG------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
59. Goat Capra hircus		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
60. Chiru Pantholops hodgsonii		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
61. Texas_white-tailed_deer Odocoileus virginianus texanus		-----------------------CTCCCG---GTGCAGGGCCAGCTGCTGCTGATG---GA
62. Alpaca Vicugna pacos		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
63. Bactrian_camel Camelus bactrianus		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
64. Wild_bactrian_camel Camelus ferus		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
65. Arabian_camel Camelus dromedarius		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
66. Minke_whale Balaenoptera acutorostrata scammoni		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
67. Killer_whale Orcinus orca		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGCTG---GA
68. Sperm_whale Physeter catodon		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGTTG---GA
69. Beluga_whale Delphinapterus leucas		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGCTG---GA
70. Pig Sus scrofa		-----------------------CTCCCT---GTGCAGGGCAAGCTGTTGCTGATG---GA
71. Przewalksis_horse Equus przewalskii		-----------------------CTCCCG---GTGCAGGGGAAGCTGCTGCTGATG---GA
72. Ass Equus asinus		-----------------------GTCCCG---GTGCAGGGGAAGCTGCTGCTGATG---GA
73. Horse Equus caballus		-----------------------CTCCCG---GTGCAGGGGAAGCTGCTGCTGATG---GA
74. Dog Canis lupus		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
75. Pacific_walrus Odobenus rosmarus divergens		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGTTGATG---GA
76. Hawaiian_monk_seal Neomonachus schauinslandi		-----------------------CTCCCG---GTGCAGGGGAAGCTGCTGTTGATG---GA
77. Weddell_seal Leptonychotes weddellii		-----------------------CTCCCG---GTGCAGGGGAAGCTGCTGTTGATG---GA
78. Domestic_cat Felis catus		-----------------------CTCCCA---GTGCAGGGCAAGCTGCTGCTGATA---GA
79. Leopard Panthera pardus		-----------------------CTCCCA---GTGCAGGGCAAGCTGCTGCTGATA---GA
80. Amur_tiger Panthera tigris altaica		-----------------------CTCCCA---GTGCAGGGCAAGCTGCTGCTGATA---GA
81. Domestic_ferret Mustela putorius furo		-----------------------CTCCCG---GTACAGGGCAAGGTGCTGCTAATG---GA

Site #245 ● with ○ w/o Gaps

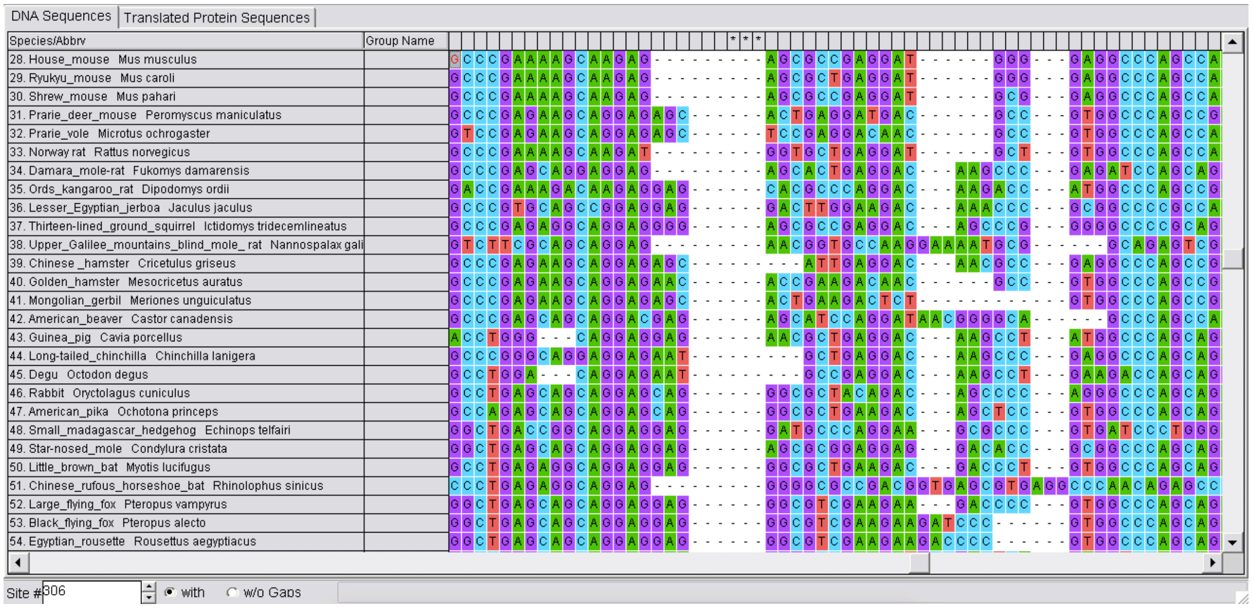


Species/Abbrv	Group Name	
82. Giant_panda Ailuropoda melanoleuca		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGTTGATG---GA
83. Northern_sea_otter Enhydra lutris kenyoni		-----------------------CTCCCG---GTACAGGGCAAGGTGCTGCTGATG---GA
84. Southern_white_rhinocerous Ceratotherium simum simum		-----------------------CTCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
85. Florida_manitee Trichechus manatus latirostris		-----------------------ATCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
86. African_savannah_elephant Loxodonta africana		-----------------------ATCCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
87. European_shrew Sorex araneus		AG---------------------GTGCCG---GTGCAGGGCAAGCTGCTGCTGATG---GA
88. Aardvark Orycteropus afer afer		-----------------------ATCCCT---GTGCAGGGCAAGCTGCTGCTGATG---GA
89. Gray_short_tailed_opossum Monodelphis domestica		-----------------------CTTCCAAATGTTCACGGAAAACTTCTCTTGATG---GA
90. Tasmanian_devil Sarcophilus harrisii		-----------------------CTTCCAAAACTCCAAGGAAAGCTTCTTCTGATG---GA

Site #245 ● with ○ w/o Gaps

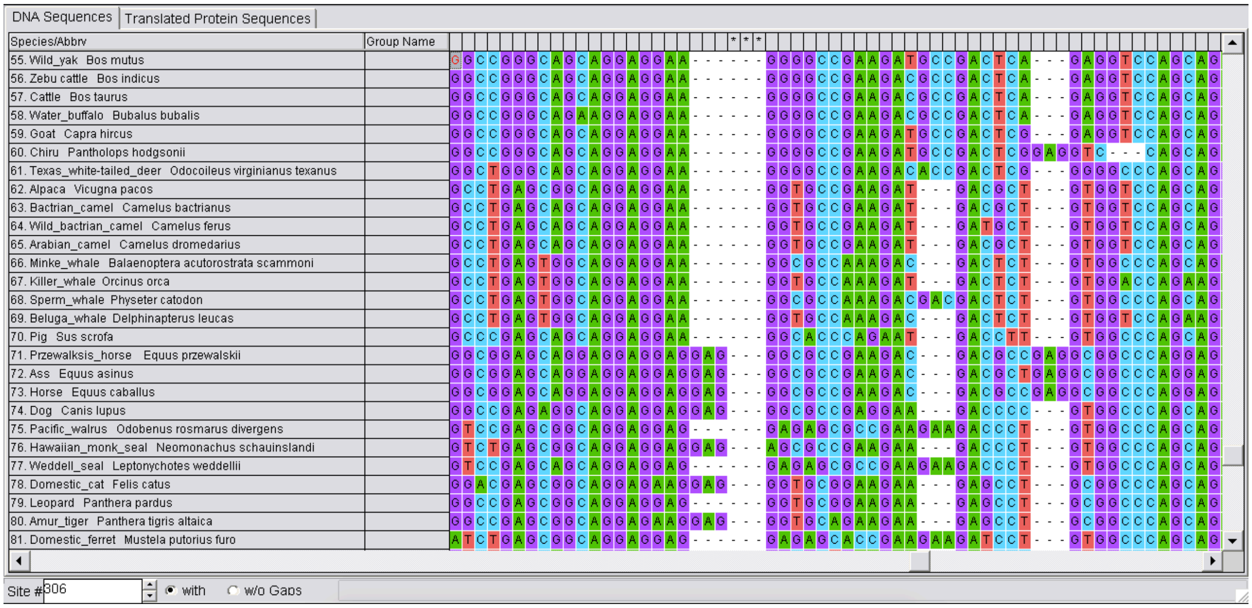
Species/Abbrv	Group Name	* * *
1. Human Homo sapiens		GCCTGAGCGGCAGGAGGAG------GGCCACAAGGAC---AACGCC---GAGGCCCAGCAG
2. Chimpanzee Pan paniscus		GCCTGAGCGGCAGGAGGAG------GGCCAGAAGGAC---AACGCC---GAGGCCCAGCAG
3. Bonobo Pan troglodytes		GCCTGAGCGGCAGGAGGAG------GGCCAGAAGGAC---AACGCC---GAGGCCCAGCAG
4. Gorilla Gorilla gorilla gorilla		GCCTGAGCGGCAGGAGGAG------GGCCAGAAGGAC---AACGCC---GAGGCCCAGCAG
5. Sumatran_orangutan Pongo abelii		GCCTGAGCGGCAGGAGGAG------GGCCAGAAGGAC---AACGCT---GAGGCCCAGCAG
6. Northern_WC_gibbon Nomascus leucogenys		GCGTGAGCGGCAGGAGGAG------GGCCAG---GAC---AATGCC---GAGGCCCAGCAG
7. Black_SN_monkey Rhinopithecus bieti		GCCTGAGCGGCAGGAGGAG------GCCCAGGAGGAC---AACGCC---GAGGCCCAGCAG
8. Golden_SN_monkey Rhinopithecus roxellana		GCCTGAGCGGCAGGAGGAG------GCCCAGGAGGAC---AACGCT---GAGGCCCAGCAG
9. Angola_colobus Colobus angolensis palliatus		GCCTGAGAGGCAGGAGGAG------GCCCAGGAGGAC---AATGCC---GAGGCCCAGCAG
10. Ugandan_red_colobus Piliocolobus tephrosceles		GCCTGAGCGGCAGGAGGAG------GCCCAGGAGGAC---AACGCC---GAGGCCCAGCAG
11. Olive_baboon Papio anubis		GCCTGAGCGGCAGGAGGAG------GGCCAGGAGGAC---AACGCC---GAGGCCCAGAAG
12. Sooty_mangabey Cercocebus atys		GCCTGAGCGGCAGGAGGAG------GGCCAGGAGGAC---AACGCC---GAGGCCCAGAAG
13. Drill Mandrillus leucophaeus		GCCTGAGCGGCAGGAGGAG------GGCCAGGAGGAC---AACGCC---GAGGCCCAGAAG
14. Green_monkey Chlorocebus sabaeus		GCCTGAGCGGCACGAGGAG------GACCAGGAGGAC---AACGCC---GAGGCCCAGCAG
15. Southern_PT_macaque Macaca nemestrina		GCCTGAGCGGCAGGAGGAG------GGCCAGGAGGAC---AACGCT---GAGGCCCAGAAG
16. Rhesus_macaque Macaca mulatta		GCCTGAGCGGCAGGAGGAG------GGCCAGGAGGAC---AACGCT---GAGGCCCAGAAG
17. CE_macaque Macaca fascicularis		GCCTGAGCGGCAGGAGGAG------GGCCAGGAGGAC---AACGCT---GAGGCCCAGAAG
18. WH_capuchin Cebus capucinus imitator		GTCGGAGCGGCAGGAAGAGGAT---------GAGGAC---AGTGCC---AAGGCCAAGCAG
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		GCCGGAGCGGCAGGAAGAG------------gAGGAC---AGTGCC---AAGGCCAAGCAG
20. NM_night_monkey Aotus nancymaae		GCCGGAGCGGCAGAAAGAGGAT---------GAGGAC---AGTGCC---AAAGCCAAGCAG
21. Common_marmoset Callithrix jacchus		GCCGGAGCAGCAGGAAGGG------ATGAGG---------ACAGTG---CCAAGGACAAGC
22. Philippine_tarsier Carlito syrichta		GCCCGAGTGGAAGGAGGAG------AGCACAGTGGAC---AACCCC---ATGACCCAGCAG
23. Gray_mouse_lemur Microcebus murinus		GTCGGAGCAGCAGGAGGCG------GCGGCCGAGGAC---AGCCCC---GTGGCCCAGCAG
24. Coquerels_sifaka Propithecus coquereli		GCCTGAGCAGCAGGAGGAG------ACGGCCGAAGAC---AGCCCC---GTGGCCCAGCAG
25. Northern_greater_galago Otolemur garnettii		GTCTGAGCAACAGGAAGAG------GAGGCCGAAGAT---AGCCCC---GCAGCCCAGCAG
26. Sunda_flying_lemur Galeopterus variegatus		ACCCGAGCTGCAGGAGGAC------AGCACTAGAGAC---AATCCT---GTGACCCAGCAG
27. Chinese_tree_shrew Tupaia chinensis		GGCCGAGCGGCAGGAGGAG------AGCGCCGAGGAC---AGCCCC---ATGGCCGAGCAG

Site # 306 ● with ○ w/o Gaps



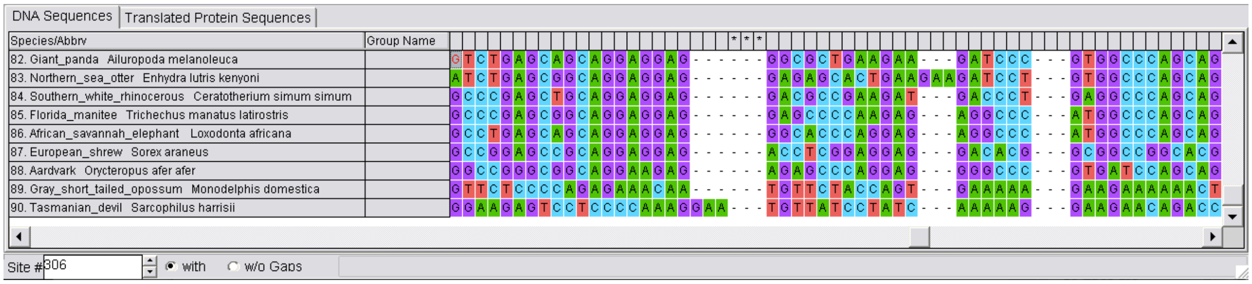
Species/Abbrv	Group Name	* * *
28. House_mouse Mus musculus		GCCCGAAAAGCAAGAG---------AGCGCCGAGGAT------GGG---GAGGCCCAGCCA
29. Ryukyu_mouse Mus caroli		GCCCGAAAAGCAAGAG---------AGCGCTGAGGAT------GGG---GAGGCCCAGCCA
30. Shrew_mouse Mus pahari		GCCCGAAAAGCAAGAG---------AGCGCCGAGGAT------GCG---GAGGCCCAGCCA
31. Prarie_deer_mouse Peromyscus maniculatus		GCCCGAGAAGCAGGAGAGC------ACTGAGGATGAC------GCC---GTGGCCCAGCCG
32. Prarie_vole Microtus ochrogaster		GTCCGAGAAGCAGGAGAGC------TCCGAGGACAAC------GCC---GTGGCCCAGCCA
33. Norway rat Rattus norvegicus		GCCCGAAAAGCAAGAT---------GGTGCTGAGGAT------GCT---GTGGCCCAGCCA
34. Damara_mole-rat Fukomys damarensis		GCCCGAGCAGGAGGAG---------AGCACTGAGGAC---AAGCCC---GAGATCCAGCAG
35. Ords_kangaroo_rat Dipodomys ordii		GACCGAAAGACAAGAGGAG------CACGCCCAGGAC---AAGACC---ATGGCCCAGCCG
36. Lesser_Egyptian_jerboa Jaculus jaculus		GCCCGTGCAGCCGGAGGAG------GACTTGGAAGAC---AAACCC---GCGGCCCCGCCA
37. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		GCCCGAGAGGCAGGAGGGG------AGCGCCGAGGAC---AGCCCG---GGGGCCCCGCAG
38. Upper_Galilee_mountains_blind_mole_rat Nannospalax gali		GTCTTCGCAGCAGGAG---------AACGGTGCCAAGGAAAATGCG------GCAGAGTCG
39. Chinese _hamster Cricetulus griseus		GCCCGAGAAGCAGGAGAGC---------ATTGAGGAC---AACGCC---GAGGCCCAGCCG
40. Golden_hamster Mesocricetus auratus		GCCCGAGAAGCAGGAGAAC------ACCGAAGACAAC------GCC---GTGGCCCAGCCG
41. Mongolian_gerbil Meriones unguiculatus		GCCCGAGAAGCAGGAGAGC------ACTGAAGACTCT------------GTGGCCCAGCCG
42. American_beaver Castor canadensis		GCCCGAGCAGCAGGACGAG------AGCATCCAGGATAACGGGGCA------GCCCAGCCA
43. Guinea_pig Cavia porcellus		ACCTGGG---CAGGAGGAG------AACGCTGAGGAC---AAGCCT---ATGGCCCAGCAG
44. Long-tailed_chinchilla Chinchilla lanigera		GCCCGGGCAGGAGGAGAAT---------GCTGAGGAC---AAGCCC---GAGGCCCAGCAG
45. Degu Octodon degus		GCCTGGA---CAGGAGAAT---------GCCGAGGAC---AAGCCT---GAAGACCAGCAG
46. Rabbit Oryctolagus cuniculus		GCCTGAGCAGCAGGAGCAG------GGCGCTACAGAC---AGCCCC---AGGGCCCAGCAG
47. American_pika Ochotona princeps		GCCAGAGCAGCAGGAGCAG------GGCGCTGAAGAC---AGCTCC---GTGGCCCAGCAG
48. Small_madagascar_hedgehog Echinops telfairi		GGCTGACCGGCAGGAGGAG------GATGCCCAGGAA---GCGCCC---GTGATCCCTGGG
49. Star-nosed_mole Condylura cristata		GGCTGAGCAGCAGGAGGAG------AGCGCGGAGGAG---GACACC---GCGGCCCAGCAG
50. Little_brown_bat Myotis lucifugus		GCCTGAGAGGCAGGAGGAG------GGCGCTGAAGAC---GACCCT---GTGGCCCAGCAG
51. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		CCCTGAGAGGCAGGAG---------GGGGCGCCGACGGTGAGCGTGAGGCCCAACAGAGCC
52. Large_flying_fox Pteropus vampyrus		GGCTGAGCAGCAGGAGGAG------GGCGTCGAAGAA---GACCCC---GTGGCCCAGCAG
53. Black_flying_fox Pteropus alecto		GGCTGAGCAGCAGGAGGAG------GGCGTCGAAGAAGATCCC------GTGGCCCAGCAG
54. Egyptian_rousette Rousettus aegyptiacus		GGCTGAGCAGCAGGAGGAG------GGCGTCGAAGAAGACCCC------GTGGCCCAGCAG

Site # 306 ● with ○ w/o Gaps



Species/Abbrv	Group Name	***
55. Wild_yak Bos mutus		GGCCGGGCAGCAGGAGGAA------GGGGCCGAAGATGCCGACTCA---GAGGTCCAGCAG
56. Zebu cattle Bos indicus		GGCCGGGCAGCAGGAGGAA------GGGGCCGAAGACGCCGACTCA---GAGGTCCAGCAG
57. Cattle Bos taurus		GGCCGGGCAGCAGGAGGAA------GGGGCCGAAGACGCCGACTCA---GAGGTCCAGCAG
58. Water_buffalo Bubalus bubalis		GGCCGGGCAGAAGGAGGAA------GGGGCCGAAGACGCCGACTCA---GAGGTCCAGCAG
59. Goat Capra hircus		GGCCGGGCAGCAGGAGGAA------GGGGCCGAAGATGCCGACTCG---GAGGTCCAGCAG
60. Chiru Pantholops hodgsonii		GGCCGGGCAGCAGGAGGAA------GGGGCCGAAGATGCCGACTCGGAGGTC---CAGCAG
61. Texas_white-tailed_deer Odocoileus virginianus texanus		GGCTGGGCAGCAGGAGGAA------GGGGCCGAAGACACCGACTCG---GGGGCCCAGCAG
62. Alpaca Vicugna pacos		GCCTGAGCGGCAGGAGGAA------GGTGCCGAAGAT---GACGCT---GTGGTCCAGCAG
63. Bactrian_camel Camelus bactrianus		GCCTGAGCAGCAGGAGGAA------GGTGCCGAAGAT---GACGCT---GTGGTCCAGCAG
64. Wild_bactrian_camel Camelus ferus		GCCTGAGCAGCAGGAGGAA------GGTGCCGAAGAT---GATGCT---GTGGTCCAGCAG
65. Arabian_camel Camelus dromedarius		GCCTGAGCAGCAGGAGGAA------GGTGCCGAAGAT---GACGCT---GTGGTCCAGCAG
66. Minke_whale Balaenoptera acutorostrata scammoni		GCCTGAGTGGCAGGAGGAA------GGCGCCAAAGAC---GACTCT---GTGGCCCAGCAG
67. Killer_whale Orcinus orca		GCCTGAGTGGCAGGAGGAA------GGTGCCAAAGAT---GACTCT---GTGGACCAGAAG
68. Sperm_whale Physeter catodon		GCCTGAGTGGCAGGAGGAA------GGCGCCAAAGACGACGACTCT---GTGGCCCAGCAG
69. Beluga_whale Delphinapterus leucas		GCCTGAGTGGCAGGAGGAA------GGTGCCAAAGAC---GACTCT---GTGGTCCAGAAG
70. Pig Sus scrofa		GCCCGAGCAGCAGGAGGAA------GGCACCCAGAAT---GACCTT---GTGGCCCAGCAG
71. Przewalksis_horse Equus przewalskii		GGCGGAGCAGGAGGAGGAGGAG---GGCGCCGAAGAC---GACGCCGAGGCGGCCCAGGAG
72. Ass Equus asinus		GGCGGAGCAGGAGGAGGAGGAG---GGCGCCGAAGAC---GACGCTGAGGCGGCCCAGGAG
73. Horse Equus caballus		GGCGGAGCAGGAGGAGGAGGAG---GGCGCCGAAGAC---GACGCCGAGGCGGCCCAGGAG
74. Dog Canis lupus		GGCCGAGAGGCAGGAGGAGGAG---GGCGCCGAGGAA---GACCCC---GTGGCCCAGCAG
75. Pacific_walrus Odobenus rosmarus divergens		GTCCGAGCGGCAGGAGGAG------GAGAGCGCCGAAGAAGACCCT---GTGGCCCAGCAG
76. Hawaiian_monk_seal Neomonachus schauinslandi		GTCTGAGCGGCAGGAGGAGGAG---AGCGCCGAAGAA---GACCCT---GTGGCCCAGCAG
77. Weddell_seal Leptonychotes weddellii		GTCCGAGCAGCAGGAGGAG------GAGAGCGCCGAAGAAGACCCT---GTGGCCCAGCAG
78. Domestic_cat Felis catus		GGACGAGCGGCAGGAGAAGGAG---GGTGCGGAAGAA---GAGCCT---GCGGCCCAGCAG
79. Leopard Panthera pardus		GGCCGAGCGGCAGGAGGAG------GGTGCGGAAGAA---GAGCCT---GCGGCCCAGCAG
80. Amur_tiger Panthera tigris altaica		GGCCGAGCGGCAGGAGAAGGAG---GGTGCAGAAGAA---GAGCCT---GCGGCCCAGCAG
81. Domestic_ferret Mustela putorius furo		ATCTGAGCGGCAGGAGGAG------GAGAGCACCGAAGAAGATCCT---GTGGCCCAGCAG

Site #306 ● with ○ w/o Gaps



Species/Abbrv	Group Name	***
82. Giant_panda Ailuropoda melanoleuca		GTCTGAGCAGCAGGAGGAG------GGCGCTGAAGAA---GATCCC---GTGGCCCAGCAG
83. Northern_sea_otter Enhydra lutris kenyoni		ATCTGAGCGGCAGGAGGAG------GAGAGCACTGAAGAAGATCCT---GTGGCCCAGCAG
84. Southern_white_rhinocerous Ceratotherium simum simum		GCCCGAGCTGCAGGAGGAG------GACGCCGAAGAT---GACCCT---GAGGCCCAGCAG
85. Florida_manitee Trichechus manatus latirostris		GCCCGAGCGGCAGGAGGAG------GAGCCCCAAGAG---AGGCCC---ATGGCCCAGCAG
86. African_savannah_elephant Loxodonta africana		GCCTGAGCAGCAGGAGGAG------GGCACCCAGGAG---AGGCCC---ATGGCCCAGCAG
87. European_shrew Sorex araneus		GCCGGAGCCGCAGGAGGAG------ACCTCGGAGGAG---GACACG---GCGGCCGGCACG
88. Aardvark Orycteropus afer afer		GGCCGGGCGGCAGGAAGAG------AGAGCCCAGGAG---GGGCCC---GTGATCCAGCAG
89. Gray_short_tailed_opossum Monodelphis domestica		GTTCTCCCCAGAGAAACAA------TGTTCTACCAGT---GAAAAA---GAAGAAAAAACT
90. Tasmanian_devil Sarcophilus harrisii		GGAAGAGTCCTCCCCAAAGGAA---TGTTATCCTATC---AAAAAG---GAAGAACAGACC

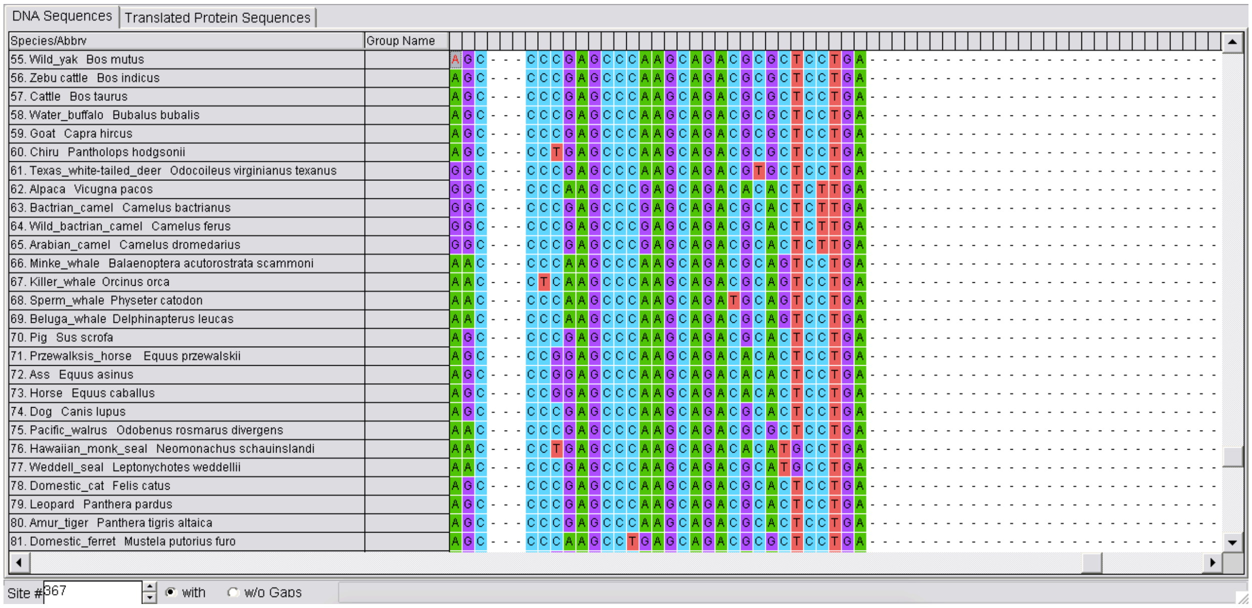
Site #306 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
1. Human Homo sapiens		AGC---CCCGAGCCCAAGCGGACACCCTCCTGA----------------------------
2. Chimpanzee Pan paniscus		AGC---CCCGAGCCCAAGCAGACACCCTCCTGA----------------------------
3. Bonobo Pan troglodytes		AGC---CCCGAGCCCAAGCAGACACCCTCCTGA----------------------------
4. Gorilla Gorilla gorilla gorilla		AGC---CCCGAGCCCAAGCAGACACCCTCCTGA----------------------------
5. Sumatran_orangutan Pongo abelii		AGC---CCCGAGCCCAAGCAGACACACTCCTGA----------------------------
6. Northern_WC_gibbon Nomascus leucogenys		AAC---CCCGAGCCCAAGCAGACACACTCCTGA----------------------------
7. Black_SN_monkey Rhinopithecus bieti		AGC---CCTGAGTCCAAGGAGACACACTCCTGA----------------------------
8. Golden_SN_monkey Rhinopithecus roxellana		AGC---CCCGAGTCCAAGGAGACACACTCCTGA----------------------------
9. Angola_colobus Colobus angolensis palliatus		AGC---CCCGAGTCCAAGGAGACACACTCCTGA----------------------------
10. Ugandan_red_colobus Piliocolobus tephrosceles		AGC---CCCGAGTCCAAGGAGACACACTCCTGA----------------------------
11. Olive_baboon Papio anubis		AGC---CCCGAGTCCAAGCAGATACACTCCTGA----------------------------
12. Sooty_mangabey Cercocebus atys		AGC---CCCGAGCCCAAGCAGACACACTCCTGA----------------------------
13. Drill Mandrillus leucophaeus		AGC---CCCGAGTCCAAGCAGACACACTCCTGA----------------------------
14. Green_monkey Chlorocebus sabaeus		AGC---CCCGAGTCCAAGCAGACACACTCCTGA----------------------------
15. Southern_PT_macaque Macaca nemestrina		AGC---CCCGAGTCCAAGCAGACACACTCCTGA----------------------------
16. Rhesus_macaque Macaca mulatta		AGC---CCCGAGTCCAAGCAGACACACTCCTGA----------------------------
17. CE_macaque Macaca fascicularis		AGC---CCCGAGTCCAAGCAGACACACTCCTGA----------------------------
18. WH_capuchin Cebus capucinus imitator		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
20. NM_night_monkey Aotus nancymaae		AGC---CCCGAGCCCAAGCAGACGCACTCCTGCCCATGA----------------------
21. Common_marmoset Callithrix jacchus		AGA---ACCCCGAGCCCAAGCAGATGCACTCCTGACCCATGA-------------------
22. Philippine_tarsier Carlito syrichta		GGT---CCCAAGCCCACGCAGACGTGCTCCGGACAGCCTGGGGAGTGGTGCCCGCTGACGT
23. Gray_mouse_lemur Microcebus murinus		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
24. Coquerels_sifaka Propithecus coquereli		AGC---TCTGAGCCCAAGCAGACGCACTCCTGA----------------------------
25. Northern_greater_galago Otolemur garnettii		AGC---CCCGAACCCAAGAAGACACACTCCTGA----------------------------
26. Sunda_flying_lemur Galeopterus variegatus		AGC---CCCGAGAGCAAGCAGACACACTCCTGA----------------------------
27. Chinese_tree_shrew Tupaia chinensis		AGT---CCTGAGCCCAAGCAGGTGCACTCCTGA----------------------------

Site # 367 ● with ○ w/o Gaps

Species/Abbrv	Group Name	
28. House_mouse Mus musculus		AGC---CCCGAGCCCAAGCAGACACACTCCTGA----------------------------
29. Ryukyu_mouse Mus caroli		AGC---CCCGAGCCCAAGCAGACACACTCCTGA----------------------------
30. Shrew_mouse Mus pahari		AGT---CCTGAGCCCAAGCAGACACACTCCTGA----------------------------
31. Prarie_deer_mouse Peromyscus maniculatus		AGC---CCTGAGCCCAAGCAGACACACTCCTGA----------------------------
32. Prarie_vole Microtus ochrogaster		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
33. Norway rat Rattus norvegicus		AGC---CCGGAGCCCAAGCAGAAGCACTCCTGA----------------------------
34. Damara_mole-rat Fukomys damarensis		GGC---CCTGAGCCCCAGCAGACGCACTCCTGA----------------------------
35. Ords_kangaroo_rat Dipodomys ordii		AGC---CCCGAGCCCAAACAGACGCACTCCTGA----------------------------
36. Lesser_Egyptian_jerboa Jaculus jaculus		AGC---TCCGAGCCCGAGGAGACGCGCTCCTGA----------------------------
37. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		AGC---CCCGAGGCCAAGCAGACGCACGCCTAA----------------------------
38. Upper_Galilee_mountains_blind_mole_ rat Nannospalax gali		AGC---CCTGATCCTGATCCACCATGA----------------------------------
39. Chinese _hamster Cricetulus griseus		AGC---CCCGAGCCCAAGCAGACACACTCCTGA----------------------------
40. Golden_hamster Mesocricetus auratus		AGC---CCCGAGCCCAAGCAGACACACTCCTGA----------------------------
41. Mongolian_gerbil Meriones unguiculatus		AGC---CCTGAGCCCAAGCAGACGCACTCCTGA----------------------------
42. American_beaver Castor canadensis		AAC---CCTGAGCCCAAGCAGACGCACTCCTAA----------------------------
43. Guinea_pig Cavia porcellus		AAC---CCTGAACCCAAGCAGACGCACTCCTGA----------------------------
44. Long-tailed_chinchilla Chinchilla lanigera		AGC---CCTGAGCCCAAGCAGACGCACTCCTGA----------------------------
45. Degu Octodon degus		GGC---CCTGAGTCCGAGCAGACGCACTCCTGA----------------------------
46. Rabbit Oryctolagus cuniculus		AGC---CCCACGTCCAAGCAGACGCGCTCCTGA----------------------------
47. American_pika Ochotona princeps		AGC---CCCAAGACCAAGCAGACACACTCCTGA----------------------------
48. Small_madagascar_hedgehog Echinops telfairi		AGC---CCTGAGCCCAAGCTGGCTCACTCCTGA----------------------------
49. Star-nosed_mole Condylura cristata		AGC---CCCGAGCCCAAGCAGCCCAAGCAGACGCGTTCCTGA-------------------
50. Little_brown_bat Myotis lucifugus		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
51. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		CTGAGCCCACACACTCCTGA---
52. Large_flying_fox Pteropus vampyrus		AGC---CCTGAGCCCAAGCAGATGCACTCCTGA----------------------------
53. Black_flying_fox Pteropus alecto		AGC---CCTGAGCCCAAGCAGATGCACTCCTGA----------------------------
54. Egyptian_rousette Rousettus aegyptiacus		AGC---CCTGAGCCCAAGCCGATGCACTCCTGA----------------------------

Site # 367 ● with ○ w/o Gaps



Species/Abbrv	Group Name	
55. Wild_yak Bos mutus		AGC---CCCGAGCCCAAGCAGACGCGCTCCTGA----------------------------
56. Zebu cattle Bos indicus		AGC---CCCGAGCCCAAGCAGACGCGCTCCTGA----------------------------
57. Cattle Bos taurus		AGC---CCCGAGCCCAAGCAGACGCGCTCCTGA----------------------------
58. Water_buffalo Bubalus bubalis		AGC---CCCGAGCCCAAGCAGACGCGCTCCTGA----------------------------
59. Goat Capra hircus		AGC---CCCGAGCCCAAGCAGACGCGCTCCTGA----------------------------
60. Chiru Pantholops hodgsonii		AGC---CCTGAGCCCAAGCAGACGCGCTCCTGA----------------------------
61. Texas_white-tailed_deer Odocoileus virginianus texanus		GGC---CCCGAGCCCAAGCAGACGTGCTCCTGA----------------------------
62. Alpaca Vicugna pacos		GGC---CCCAAGCCCGAGCAGACACACTCTTGA----------------------------
63. Bactrian_camel Camelus bactrianus		GGC---CCCGAGCCCGAGCAGACGCACTCTTGA----------------------------
64. Wild_bactrian_camel Camelus ferus		GGC---CCCGAGCCCGAGCAGACGCACTCTTGA----------------------------
65. Arabian_camel Camelus dromedarius		GGC---CCCGAGCCCGAGCAGACGCACTCTTGA----------------------------
66. Minke_whale Balaenoptera acutorostrata scammoni		AAC---CCCAAGCCCAAGCAGACGCAGTCCTGA----------------------------
67. Killer_whale Orcinus orca		AAC---CTCAAGCCCAAGCAGACGCAGTCCTGA----------------------------
68. Sperm_whale Physeter catodon		AAC---CCCAAGCCCAAGCAGATGCAGTCCTGA----------------------------
69. Beluga_whale Delphinapterus leucas		AAC---CCCAAGCCCAAGCAGACGCAGTCCTGA----------------------------
70. Pig Sus scrofa		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
71. Przewalksis_horse Equus przewalskii		AGC---CCGGAGCCCAAGCAGACACACTCCTGA----------------------------
72. Ass Equus asinus		AGC---CCGGAGCCCAAGCAGACACACTCCTGA----------------------------
73. Horse Equus caballus		AGC---CCGGAGCCCAAGCAGACACACTCCTGA----------------------------
74. Dog Canis lupus		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
75. Pacific_walrus Odobenus rosmarus divergens		AAC---CCCGAGCCCAAGCAGACGCGCTCCTGA----------------------------
76. Hawaiian_monk_seal Neomonachus schauinslandi		AAC---CCTGAGCCCAAGCAGACACATGCCTGA----------------------------
77. Weddell_seal Leptonychotes weddellii		AAC---CCCGAGCCCAAGCAGACGCATGCCTGA----------------------------
78. Domestic_cat Felis catus		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
79. Leopard Panthera pardus		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
80. Amur_tiger Panthera tigris altaica		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
81. Domestic_ferret Mustela putorius furo		AGC---CCCAAGCCTGAGCAGACGCGCTCCTGA----------------------------

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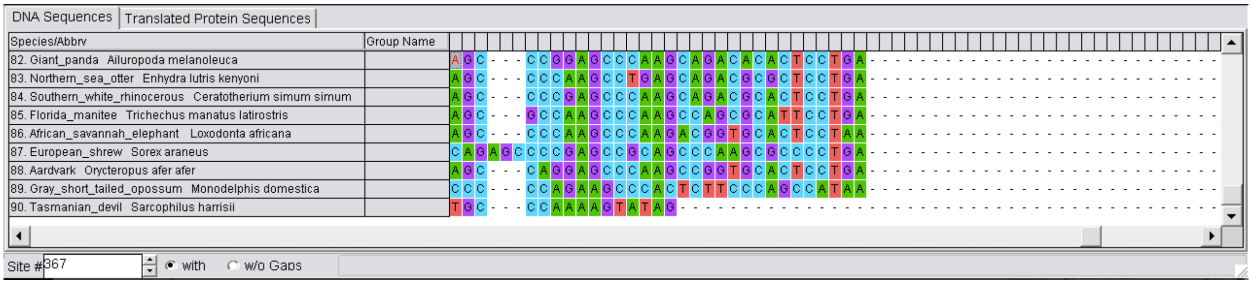

Species/Abbrv	Group Name	
82. Giant_panda Ailuropoda melanoleuca		AGC---CCGGAGCCCAAGCAGACACACTCCTGA----------------------------
83. Northern_sea_otter Enhydra lutris kenyoni		AGC---CCCAAGCCTGAGCAGACGCGCTCCTGA----------------------------
84. Southern_white_rhinocerous Ceratotherium simum simum		AGC---CCCGAGCCCAAGCAGACGCACTCCTGA----------------------------
85. Florida_manitee Trichechus manatus latirostris		AGC---GCCAAGCCCAAGCCAGCGCATTCCTGA----------------------------
86. African_savannah_elephant Loxodonta africana		AGC---CCCAAGCCCAAGACGGTGCACTCCTAA----------------------------
87. European_shrew Sorex araneus		CAGAGCCCCGAGCCGCAGCCCAAGCGCCCCTGA----------------------------
88. Aardvark Orycteropus afer afer		AGC---CAGGAGCCCAAGCCGGTGCACTCCTGA----------------------------
89. Gray_short_tailed_opossum Monodelphis domestica		CCC---CCAGAAGCCCACTCTTCCCAGCCATAA----------------------------
90. Tasmanian_devil Sarcophilus harrisii		TGC---CCAAAAGTATAG---

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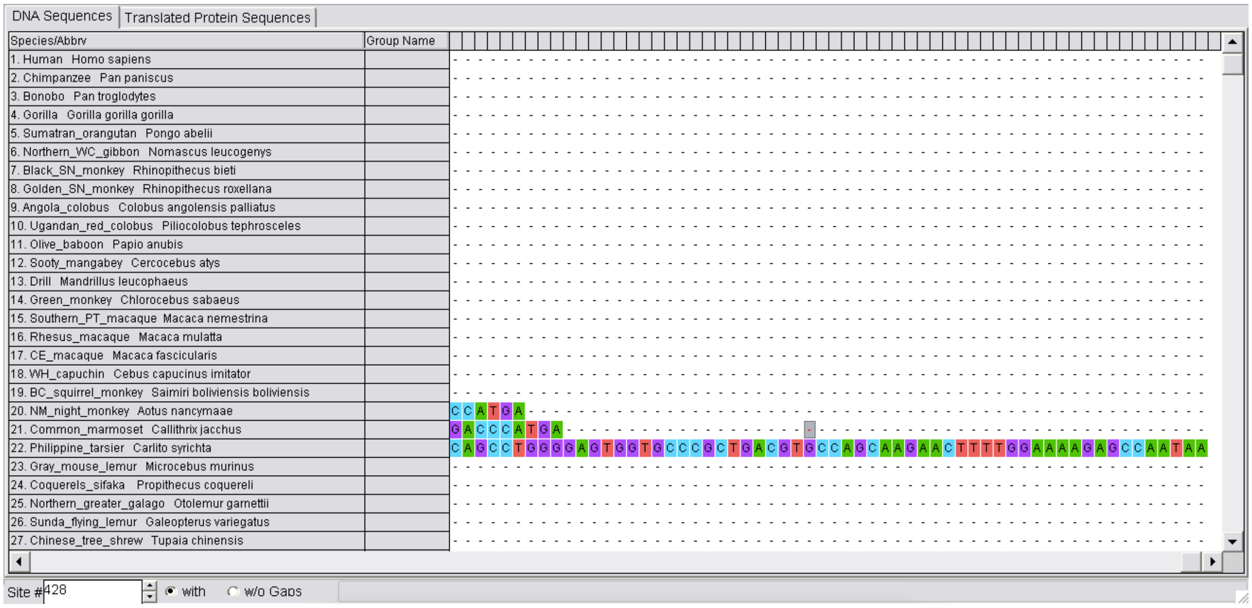
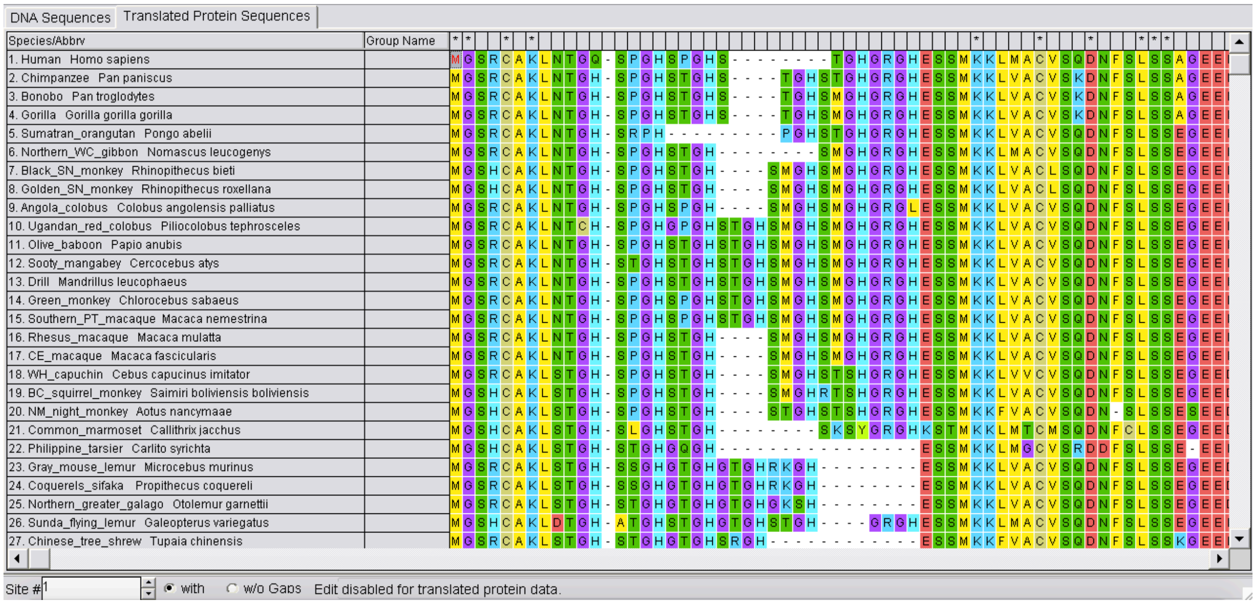


Species/Abbrv	Group Name	
1. Human Homo sapiens		--
2. Chimpanzee Pan paniscus		--
3. Bonobo Pan troglodytes		--
4. Gorilla Gorilla gorilla gorilla		--
5. Sumatran_orangutan Pongo abelii		--
6. Northern_WC_gibbon Nomascus leucogenys		--
7. Black_SN_monkey Rhinopithecus bieti		--
8. Golden_SN_monkey Rhinopithecus roxellana		--
9. Angola_colobus Colobus angolensis palliatus		--
10. Ugandan_red_colobus Piliocolobus tephrosceles		--
11. Olive_baboon Papio anubis		--
12. Sooty_mangabey Cercocebus atys		--
13. Drill Mandrillus leucophaeus		--
14. Green_monkey Chlorocebus sabaeus		--
15. Southern_PT_macaque Macaca nemestrina		--
16. Rhesus_macaque Macaca mulatta		--
17. CE_macaque Macaca fascicularis		--
18. WH_capuchin Cebus capucinus imitator		--
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		--
20. NM_night_monkey Aotus nancymaae		CCATGA--
21. Common_marmoset Callithrix jacchus		GACCCATGA---
22. Philippine_tarsier Carlito syrichta		CAGCCTGGGGAGTGGTGCCCGCTGACGTGCCAGCAAGAACTTTTGGAAAAGAGCCAATAA
23. Gray_mouse_lemur Microcebus murinus		--
24. Coquerels_sifaka Propithecus coquereli		--
25. Northern_greater_galago Otolemur garnettii		--
26. Sunda_flying_lemur Galeopterus variegatus		--
27. Chinese_tree_shrew Tupaia chinensis		--

Site # 428 ● with ○ w/o Gaps

The translated sequence



Species/Abbrv	Group Name	* * * * * * * * * *
1. Human Homo sapiens		MGSRCAKLNTGQ-SPGHSPGHS--------TGHGRGHESSMKKLMACVSQDNFSLSSAGEE
2. Chimpanzee Pan paniscus		MGSRCAKLNTGH-SPGHSTGHS----TGHSTGHGRGHESSMKKLVACVSKDNFSLSSAGEE
3. Bonobo Pan troglodytes		MGSRCAKLNTGH-SPGHSTGHS----TGHSMGHGRGHESSMKKLVACVSKDNFSLSSAGEE
4. Gorilla Gorilla gorilla gorilla		MGSRCAKLNTGH-SPGHSTGHS----TGHSMGHGRGHESSMKKLVACVSKDNFSLSSAGEE
5. Sumatran_orangutan Pongo abelii		MGSRCAKLNTGH-SRPH---------PGHSTGHGRGHESSMKKLVACVSQDNFSLSSEGEE
6. Northern_WC_gibbon Nomascus leucogenys		MGSRCAKLNTGH-SPGHSTGH--------SMGHGRGHESSMKKLMACVSQDNFSLSSEGEE
7. Black_SN_monkey Rhinopithecus bieti		MGSHCAKLNTGH-SPGHSTGH----SMGHSMGHGRGHESSMKKLVACLSQDNFSLSSEGEE
8. Golden_SN_monkey Rhinopithecus roxellana		MGSHCAKLNTGH-SPGHSTGH----SMGHSMGHGRGHESSMKKLVACLSQDNFSLSSEGEE
9. Angola_colobus Colobus angolensis palliatus		MGSRCAKLNTGH-SPGHSPGH----SMGHSMGHGRGLESSMKKLVACVSQDNFSLSSEGEE
10. Ugandan_red_colobus Piliocolobus tephrosceles		MGSRCAKLNTCH-SPGHGPGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEE
11. Olive_baboon Papio anubis		MGSRCAKLNTGH-SPGHSTGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEE
12. Sooty_mangabey Cercocebus atys		MGSRCAKLNTGH-STGHSTGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEE
13. Drill Mandrillus leucophaeus		MGSRCAKLNTGH-SPGHSTGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEE
14. Green_monkey Chlorocebus sabaeus		MGSRCAKLNTGH-SPGHSPGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEE
15. Southern_PT_macaque Macaca nemestrina		MGSRCAKLNTGH-SPGHSPGHSTGHSMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEE
16. Rhesus_macaque Macaca mulatta		MGSRCAKLNTGH-SPGHSTGH----SMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEE
17. CE_macaque Macaca fascicularis		MGSRCAKLNTGH-SPGHSTGH----SMGHSMGHGRGHESSMKKLVACVSQDNFSLSSEGEE
18. WH_capuchin Cebus capucinus imitator		MGSRCAKLSTGH-SPGHSTGH----SMGHSTSHGRGHESSMKKLVVCVSQDNFSLSSEGEE
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		MGSHCAKLSTGH-SPGHSTGH----SMGHRTSHGRGHESSMKKLVACVSQDNFSLSSEGEE
20. NM_night_monkey Aotus nancymaae		MGSHCAKLSTGH-SPGHSTGH----STGHSTSHGRGHESSMKKFVACVSQDN-SLSSESEE
21. Common_marmoset Callithrix jacchus		MGSHCAKLSTGH-SLGHSTGH--------SKSYGRGHKSTMKKLMTCMSQDNFCLSSEGEE
22. Philippine_tarsier Carlito syrichta		MGSHCAKLSTGH-STGHGQGH----------------ESSMKKLMGCVSRDDFSLSSE-EE
23. Gray_mouse_lemur Microcebus murinus		MGSRCAKLSTGH-SSGHGTGHGTGHRKGH--------ESSMKKLVACVSQDNFSLSSEGEE
24. Coquerels_sifaka Propithecus coquereli		MGSRCAKLSTGH-SSGHGTGHGTGHRKGH--------ESSMKKLVACVSQDNFSLSSEGEE
25. Northern_greater_galago Otolemur garnettii		MGSRCAKLSTGH-STGHGTGHGTGHGKSH--------ESSMKKLVACVSQDNFSLSSEGEE
26. Sunda_flying_lemur Galeopterus variegatus		MGSHCAKLDTGH-ATGHSTGHGTGHSTGH----GRGHESSMKKLMACVSQDNFSLSSEGEE
27. Chinese_tree_shrew Tupaia chinensis		MGSRCAKLSTGH-STGHGTGHSRGH------------ESSMKKFVACVSQDNFSLSSKGEE

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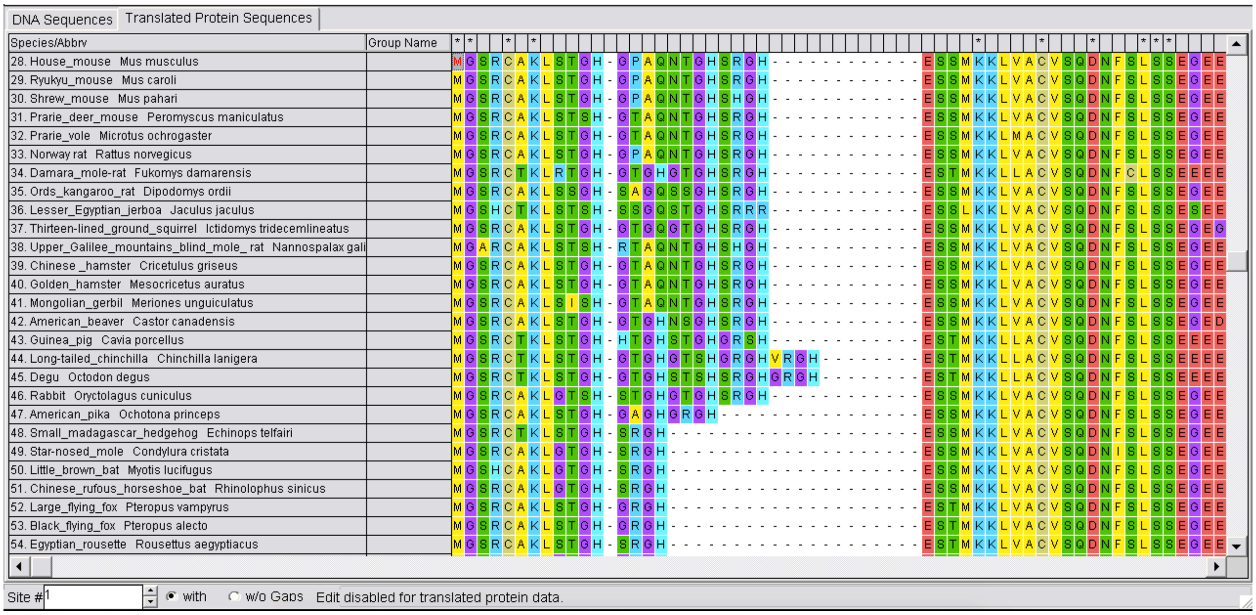

Species/Abbrv	Group Name	* * * * * * * * * *
28. House_mouse Mus musculus		MGSRCAKLSTGH-GPAQNTGHSRGH------------ESSMKKLVACVSQDNFSLSSEGEE
29. Ryukyu_mouse Mus caroli		MGSRCAKLSTGH-GPAQNTGHSRGH------------ESSMKKLVACVSQDNFSLSSEGEE
30. Shrew_mouse Mus pahari		MGSRCAKLSTGH-GPAQNTGHSHGH------------ESSMKKLVACVSQDNFSLSSEGEE
31. Prarie_deer_mouse Peromyscus maniculatus		MGSRCAKLSTSH-GTAQNTGHSRGH------------ESSMKKLVACVSQDNFSLSSEGEE
32. Prarie_vole Microtus ochrogaster		MGSRCAKLSTGH-GTAQNTGHSRGH------------ESSMKKLMACVSQDNFSLSSEGEE
33. Norway rat Rattus norvegicus		MGSRCAKLSTGH-GPAQNTGHSRGH------------ESSMKKLVACVSQDNFSLSSEGEE
34. Damara_mole-rat Fukomys damarensis		MGSRCTKLRTGH-GTGHGTGHSRGH------------ESTMKKLLACVSQDNFCLSSEEEE
35. Ords_kangaroo_rat Dipodomys ordii		MGSRCAKLSSGH-SAGQSSGHSRGH------------ESSMKKLVACVSQDNFSLSSEGEE
36. Lesser_Egyptian_jerboa Jaculus jaculus		MGSHCTKLSTSH-SSGQSTGHSRRR------------ESSLKKLVACVSQDNFSLSSESEE
37. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		MGSRCAKLSTGH-GTGQGTGHSRGH------------ESSMKKLVACVSQDNFSLSSEGEG
38. Upper_Galilee_mountains_blind_mole_rat Nannospalax gali		MGARCAKLSTSH-RTAQNTGHSHGH------------ESSMKKLVACVSQDNFSLSSEGEE
39. Chinese_hamster Cricetulus griseus		MGSRCAKLSTGH-GTAQNTGHSRGH------------ESSMKKLVACVSQDNFSLSSEGEE
40. Golden_hamster Mesocricetus auratus		MGSRCAKLSTGH-GTAQNTGHSRGH------------ESSMKKLVACVSQDNFSLSSEGEE
41. Mongolian_gerbil Meriones unguiculatus		MGSRCAKLSISH-GTAQNTGHSRGH------------ESSMKKLVACVSQDNFSLSSEGEE
42. American_beaver Castor canadensis		MGSRCAKLSTGH-GTGHNSGHSRGH------------ESSMKKLVACVSQDNFSLSSEGED
43. Guinea_pig Cavia porcellus		MGSRCTKLSTGH-HTGHSTGHGRSH------------ESTMKKLLACVSQDNFSLSSEEEE
44. Long-tailed_chinchilla Chinchilla lanigera		MGSRCTKLSTGH-GTGHGTSHGRGHVRGH--------ESTMKKLLACVSQDNFSLSSEEEE
45. Degu Octodon degus		MGSRCTKLSTGH-GTGHSTSHSRGHGRGH--------ESTMKKLLACVSQDNFSLSSEEEE
46. Rabbit Oryctolagus cuniculus		MGSRCAKLGTSH-STGHGTGHSRGH------------ESSMKKLVACVSQDNFSLSSEGEE
47. American_pika Ochotona princeps		MGSRCAKLSTGH-GAGHGRGH----------------ESSMKKLVACVSQDNFSLSSEGEE
48. Small_madagascar_hedgehog Echinops telfairi		MGSRCTKLSTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
49. Star-nosed_mole Condylura cristata		MGSRCAKLGTGH-SRGH--------------------ESSMKKLVACVSQDNISLSSEGEE
50. Little_brown_bat Myotis lucifugus		MGSHCAKLGTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
51. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		MGSRCAKLGTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
52. Large_flying_fox Pteropus vampyrus		MGSRCAKLSTGH-GRGH--------------------ESTMKKLVACVSQDNFSLSSEGEE
53. Black_flying_fox Pteropus alecto		MGSRCAKLSTGH-GRGH--------------------ESTMKKLVACVSQDNFSLSSEGEE
54. Egyptian_rousette Rousettus aegyptiacus		MGSRCAKLSTGH-SRGH--------------------ESTMKKLVACVSQDNFSLSSEGEE

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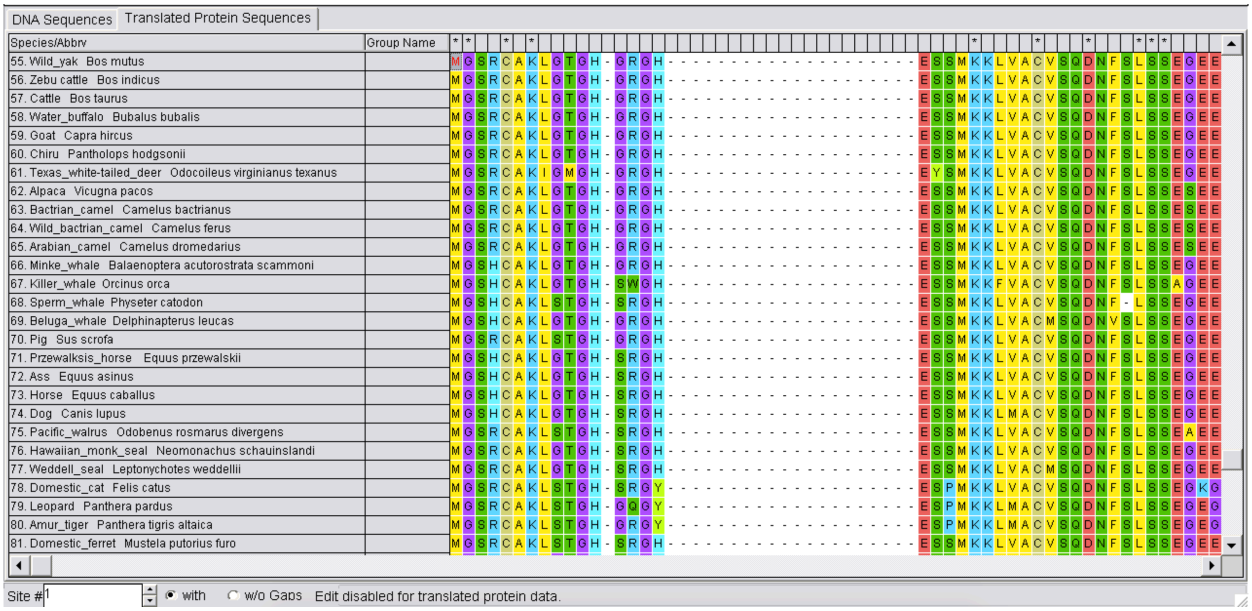

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Species/Abbrv                                               Group Name  **  * *                                  *    *   *   ***
55. Wild_yak  Bos mutus                                                 MGSRCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
56. Zebu cattle  Bos indicus                                            MGSRCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
57. Cattle  Bos taurus                                                  MGSRCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
58. Water_buffalo  Bubalus bubalis                                      MGSRCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
59. Goat  Capra hircus                                                  MGSRCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
60. Chiru  Pantholops hodgsonii                                         MGSRCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
61. Texas_white-tailed_deer  Odocoileus virginianus texanus             MGSRCAKIGMGH-GRGH--------------------EYSMKKLVACVSQDNFSLSSEGEE
62. Alpaca  Vicugna pacos                                               MGSRCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSESEE
63. Bactrian_camel  Camelus bactrianus                                  MGSRCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSESEE
64. Wild_bactrian_camel  Camelus ferus                                  MGSRCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSESEE
65. Arabian_camel  Camelus dromedarius                                  MGSRCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSESEE
66. Minke_whale  Balaenoptera acutorostrata scammoni                     MGSHCAKLGTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
67. Killer_whale  Orcinus orca                                          MGSHCAKLGTGH-SWGH--------------------ESSMKKFVACVSQDNFSLSSAGEE
68. Sperm_whale  Physeter catodon                                       MGSHCAKLSTGH-SRGH--------------------ESSMKKLVACVSQDNF-LSSEGEE
69. Beluga_whale  Delphinapterus leucas                                 MGSHCAKLGTGH-GRGH--------------------ESSMKKLVACMSQDNVSLSSEGEE
70. Pig  Sus scrofa                                                     MGSRCAKLSTGH-GRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
71. Przewalksis_horse  Equus przewalskii                                MGSHCAKLGTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
72. Ass  Equus asinus                                                   MGSHCAKLGTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
73. Horse  Equus caballus                                                MGSHCAKLGTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
74. Dog  Canis lupus                                                    MGSHCAKLGTGH-SRGH--------------------ESSMKKLMACVSQDNFSLSSEGEE
75. Pacific_walrus  Odobenus rosmarus divergens                         MGSRCAKLSTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEAEE
76. Hawaiian_monk_seal  Neomonachus schauinslandi                       MGSRCAKLGTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
77. Weddell_seal  Leptonychotes weddellii                                MGSRCAKLGTGH-SRGH--------------------ESSMKKLVACMSQDNFSLSSEGEE
78. Domestic_cat  Felis catus                                            MGSRCAKLSTGH-SRGY--------------------ESPMKKLVACVSQDNFSLSSEGKG
79. Leopard  Panthera pardus                                            MGSRCAKLSTGH-GQGY--------------------ESPMKKLMACVSQDNFSLSSEGEG
80. Amur_tiger  Panthera tigris altaica                                 MGSRCAKLSTGH-GRGY--------------------ESPMKKLMACVSQDNFSLSSEGEG
81. Domestic_ferret  Mustela putorius furo                              MGSRCAKLSTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
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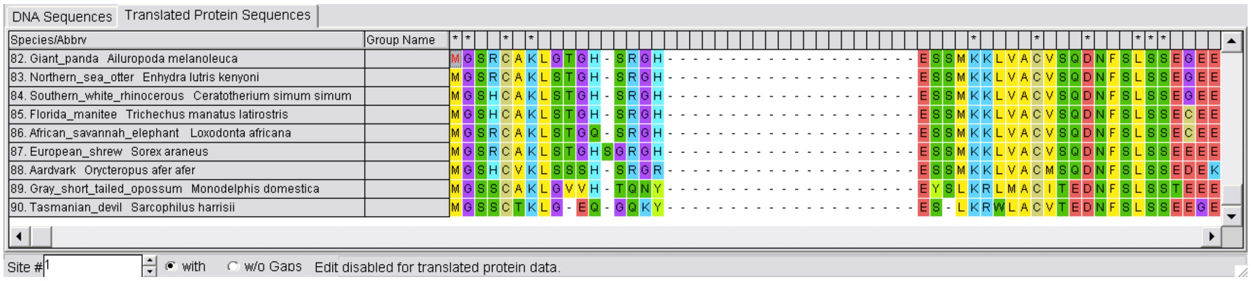

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Species/Abbrv                                               Group Name  **  * *                                  *    *   *   ***
82. Giant_panda  Ailuropoda melanoleuca                                 MGSRCAKLGTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
83. Northern_sea_otter  Enhydra lutris kenyoni                          MGSRCAKLSTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
84. Southern_white_rhinocerous  Ceratotherium simum simum               MGSHCAKLSTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSEGEE
85. Florida_manitee  Trichechus manatus latirostris                     MGSHCAKLSTGH-SRGH--------------------ESSMKKLVACVSQDNFSLSSECEE
86. African_savannah_elephant  Loxodonta africana                       MGSRCAKLSTGQ-SRGH--------------------ESSMKKLVACVSQDNFSLSSECEE
87. European_shrew  Sorex araneus                                      MGSRCAKLSTGHSGRGH--------------------ESSMKKLVACVSQDNFSLSSEEEE
88. Aardvark  Orycteropus afer afer                                     MGSHCVKLSSSH-SRGR--------------------ESSMKKLVACMSQDNFSLSSEDEK
89. Gray_short_tailed_opossum  Monodelphis domestica                    MGSSCAKLGVVH-TQNY--------------------EYSLKRLMACITEDNFSLSSTEEE
90. Tasmanian_devil  Sarcophilus harrisii                               MGSSCTKLG-EQ-GQKY--------------------ES-LKRWLACVTEDNFSLSSEEGE
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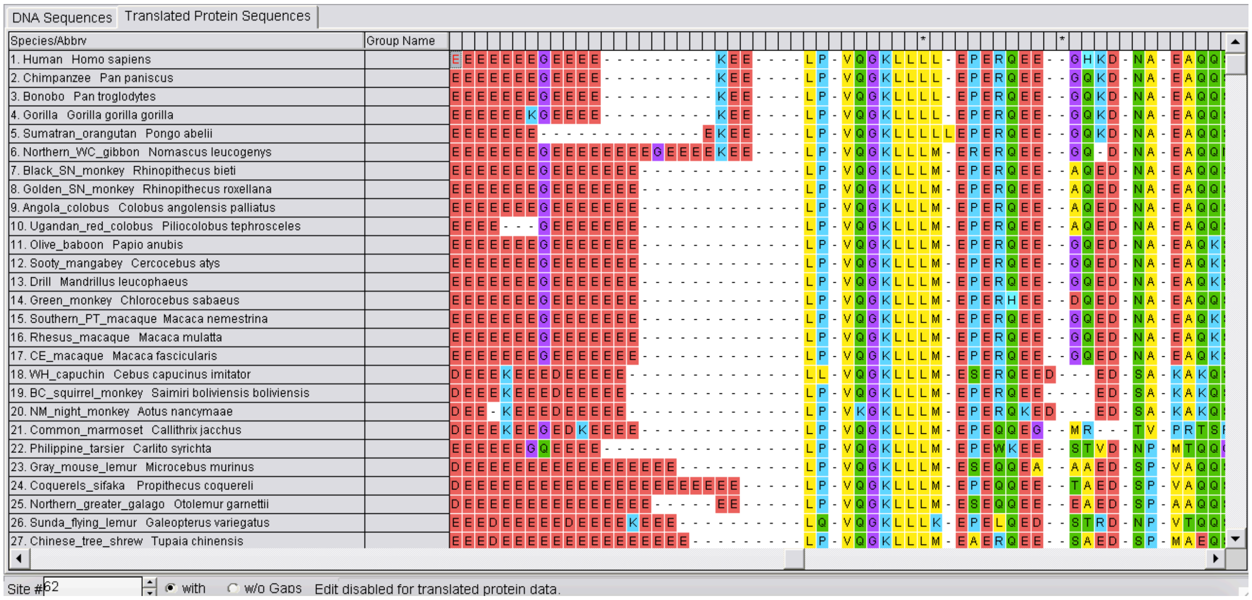

Species/Abbrv	Group Name	
1. Human Homo sapiens		E E E E E E E G E E E E - - - - - - - - - K E E - - - - L P - V Q G K L L L L - E P E R Q E E - - G H K D - N A - E A Q Q
2. Chimpanzee Pan paniscus		E E E E E E E G E E E E - - - - - - - - - K E E - - - - L P - V Q G K L L L L - E P E R Q E E - - G Q K D - N A - E A Q Q
3. Bonobo Pan troglodytes		E E E E E E E G E E E E - - - - - - - - - K E E - - - - L P - V Q G K L L L L - E P E R Q E E - - G Q K D - N A - E A Q Q
4. Gorilla Gorilla gorilla gorilla		E E E E E E K G E E E E - - - - - - - - - K E E - - - - L P - V Q G K L L L L - E P E R Q E E - - G Q K D - N A - E A Q Q
5. Sumatran_orangutan Pongo abelii		E E E E E E E - - - - - - - - - - - - - E K E E - - - - L P - V Q G K L L L L L E P E R Q E E - - G Q K D - N A - E A Q Q
6. Northern_WC_gibbon Nomascus leucogenys		E E E E E E E G E E E E E E E E G E E E E K E E - - - - L P - V Q G K L L L M - E R E R Q E E - - G Q - D - N A - E A Q Q
7. Black_SN_monkey Rhinopithecus bieti		E E E E E E E G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - A Q E D - N A - E A Q Q
8. Golden_SN_monkey Rhinopithecus roxellana		E E E E E E E G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - A Q E D - N A - E A Q Q
9. Angola_colobus Colobus angolensis palliatus		E E E E E E E G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - A Q E D - N A - E A Q Q
10. Ugandan_red_colobus Piliocolobus tephrosceles		E E E E - - - G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - A Q E D - N A - E A Q Q
11. Olive_baboon Papio anubis		E E E E E E E G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - G Q E D - N A - E A Q K
12. Sooty_mangabey Cercocebus atys		E E E E E E E G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - G Q E D - N A - E A Q K
13. Drill Mandrillus leucophaeus		E E E E E E E G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - G Q E D - N A - E A Q K
14. Green_monkey Chlorocebus sabaeus		E E E E E E E G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R H E E - - D Q E D - N A - E A Q Q
15. Southern_PT_macaque Macaca nemestrina		E E E E E E E G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - G Q E D - N A - E A Q K
16. Rhesus_macaque Macaca mulatta		E E E E E E E G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - G Q E D - N A - E A Q K
17. CE_macaque Macaca fascicularis		E E E E E E E G E E E E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - G Q E D - N A - E A Q K
18. WH_capuchin Cebus capucinus imitator		D E E E K E E E D E E E E E - - - - - - - - - - - - - - L L - V Q G K L L L M - E S E R Q E E D - - - E D - S A - K A K Q
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		D E E E K E E E D E E E E E - - - - - - - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - - - E D - S A - K A K Q
20. NM_night_monkey Aotus nancymaae		D E E - K E E E D E E E E E - - - - - - - - - - - - - - L P - V K G K L L L M - E P E R Q K E D - - - E D - S A - K A K Q
21. Common_marmoset Callithrix jacchus		D E E E K E E G E D K E E E E - - - - - - - - - - - - - L P - V Q G K L L L M - E P E Q Q E G - - M R - - - T V - P R T S
22. Philippine_tarsier Carlito syrichta		E E E E E E G Q E E E E - - - - - - - - - - - - - - - - L P - V Q G K L L L M - E P E W K E E - - S T V D - N P - M T Q Q
23. Gray_mouse_lemur Microcebus murinus		D E E E E E E E E E E E E E E E E E - - - - - - - - - - L P - V Q G K L L L M - E S E Q Q E A - - A A E D - S P - V A Q Q
24. Coquerels_sifaka Propithecus coquereli		D E E E E E E E E E E E E E E E E E E E E E E - - - - - L P - V Q G K L L L M - E P E Q Q E E - - T A E D - S P - V A Q Q
25. Northern_greater_galago Otolemur garnettii		D E E E E E E E E E E E E E E E - - - - - E E - - - - - L P - V Q G K L L L M - E S E Q Q E E - - E A E D - S P - A A Q Q
26. Sunda_flying_lemur Galeopterus variegatus		E E E D E E E E E D E E E E K E E E - - - - - - - - - - L Q - V Q G K L L L K - E P E L Q E D - - S T R D - N P - V T Q Q
27. Chinese_tree_shrew Tupaia chinensis		E E E D E E E E E E E E E E E E E E E - - - - - - - - - L P - V Q G K L L L M - E A E R Q E E - - S A E D - S P - M A E Q

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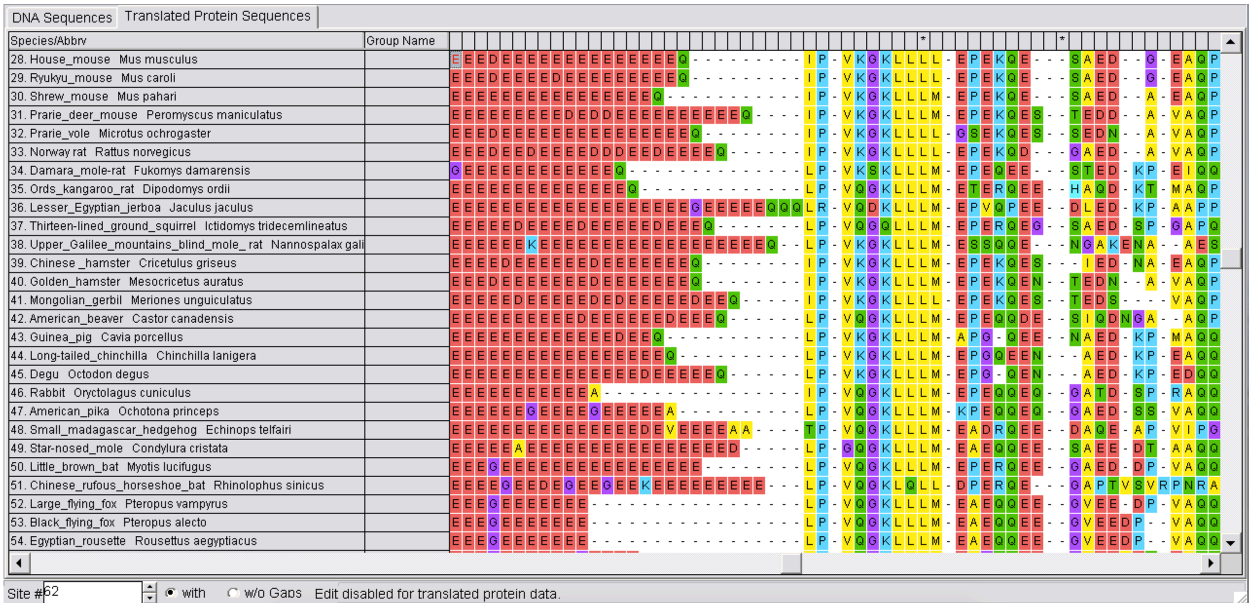

Species/Abbrv	Group Name	
28. House_mouse Mus musculus		E E E D E E E E E E E E E E E E E E Q - - - - - - - - - I P - V K G K L L L L - E P E K Q E - - - S A E D - - G - E A Q P
29. Ryukyu_mouse Mus caroli		E E E D E E E E D E E E E E E E E E Q - - - - - - - - - I P - V K G K L L L L - E P E K Q E - - - S A E D - - G - E A Q P
30. Shrew_mouse Mus pahari		E E E E E E E E E E E E E E E E Q - - - - - - - - - - - I P - V K G K L L L M - E P E K Q E - - - S A E D - - A - E A Q P
31. Prarie_deer_mouse Peromyscus maniculatus		E E E E E E E E E D E D D E E E E E E E E E E Q - - - - I P - V K G K L L L M - E P E K Q E S - - T E D D - - A - V A Q P
32. Prarie_vole Microtus ochrogaster		E E E D E E E E E E E E E E E E E E E Q - - - - - - - - I P - V K G K L L L L - G S E K Q E S - - S E D N - - A - V A Q P
33. Norway rat Rattus norvegicus		E E E D E E D E E E E D D D E E D E E E E Q - - - - - - I P - V K G K L L L L - E P E K Q D - - - G A E D - - A - V A Q P
34. Damara_mole-rat Fukomys damarensis		G E E E E E E E E E E E E Q - - - - - - - - - - - - - - L P - V K S K L L L M - E P E Q E E - - - S T E D - K P - E I Q Q
35. Ords_kangaroo_rat Dipodomys ordii		E E E E E E E E E E E E E E Q - - - - - - - - - - - - - L P - V Q G K L L L M - E T E R Q E E - - H A Q D - K T - M A Q P
36. Lesser_Egyptian_jerboa Jaculus jaculus		E E E E E E E E E E E E E E E E E E E G E E E E E Q Q Q L R - V Q D K L L L M - E P V Q P E E - - D L E D - K P - A A P P
37. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		E E E E E D E E E E D E E E E E D E E E Q - - - - - - - L P - V Q G Q L L L M - E P E R Q E G - - S A E D - S P - G A P Q
38. Upper_Galilee_mountains_blind_mole_ rat Nannospalax gali		E E E E E E K E E E E E E E E E E E E E E E E E E Q - - L P - V K G K L L L M - E S S Q Q E - - - N G A K E N A - - A E S
39. Chinese _hamster Cricetulus griseus		E E E E D E E E E E E D E E E E E E E Q - - - - - - - - I P - V K G K L L L M - E P E K Q E S - - - I E D - N A - E A Q P
40. Golden_hamster Mesocricetus auratus		E E E D E E E E E E E D E E E E E E E Q - - - - - - - - I P - V K G K L L L M - E P E K Q E N - - T E D N - - A - V A Q P
41. Mongolian_gerbil Meriones unguiculatus		E E E E E D E E E E E D E D E E E E E D E E Q - - - - - I P - V K G K L L L L - E P E K Q E S - - T E D S - - - - V A Q P
42. American_beaver Castor canadensis		E E E E E E E E E E D E E E E E E D E E E Q - - - - - - L P - V Q G K L L L M - E P E Q Q D E - - S I Q D N G A - - A Q P
43. Guinea_pig Cavia porcellus		E E E E E E E E E E E E E D E E Q - - - - - - - - - - - L P - V K G K L L L M - A P G - Q E E - - N A E D - K P - M A Q Q
44. Long-tailed_chinchilla Chinchilla lanigera		E E E E E E E E E E E E E E E E E Q - - - - - - - - - - L P - V K G K L L L M - E P G Q E E N - - - A E D - K P - E A Q Q
45. Degu Octodon degus		E E E E E E E E E E E E E E E D E E E E E Q - - - - - - L P - V K G K L L L M - E P G - Q E N - - - A E D - K P - E D Q Q
46. Rabbit Oryctolagus cuniculus		E E E E E E E E E E E A - - - - - - - - - - - - - - - - I P - V Q G K L L L M - E P E Q Q E Q - - G A T D - S P - R A Q Q
47. American_pika Ochotona princeps		E E E E E E G E E E E G E E E E E A - - - - - - - - - - L P - V Q G K L L L M - K P E Q Q E Q - - G A E D - S S - V A Q Q
48. Small_madagascar_hedgehog Echinops telfairi		E E E E E E E E E E E E E E E D E V E E E E A A - - - - T P - V Q G K L L L M - E A D R Q E E - - D A Q E - A P - V I P G
49. Star-nosed_mole Condylura cristata		E E E E E A E E E E E E E E E E E E E E E E D - - - - - L P - G Q G K L L L M - E A E Q Q E E - - S A E E - D T - A A Q Q
50. Little_brown_bat Myotis lucifugus		E E E G E E E E E E E E E E E E E E E E - - - - - - - - L P - V Q G K L L L M - E P E R Q E E - - G A E D - D P - V A Q Q
51. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		E E E E G E E D E G E E G E E K E E E E E E E E E - - - L P - V Q G K L Q L L - D P E R Q E - - - G A P T V S V R P N R A
52. Large_flying_fox Pteropus vampyrus		E E E G E E E E E E E - - - - - - - - - - - - - - - - - L P - V Q G K L L L M - E A E Q Q E E - - G V E E - D P - V A Q Q
53. Black_flying_fox Pteropus alecto		E E E G E E E E E E E - - - - - - - - - - - - - - - - - L P - V Q G K L L L M - E A E Q Q E E - - G V E E D P - - V A Q Q
54. Egyptian_rousette Rousettus aegyptiacus		E E E G E E E E E E E - - - - - - - - - - - - - - - - - L P - V Q G K L L L M - E A E Q Q E E - - G V E E D P - - V A Q Q

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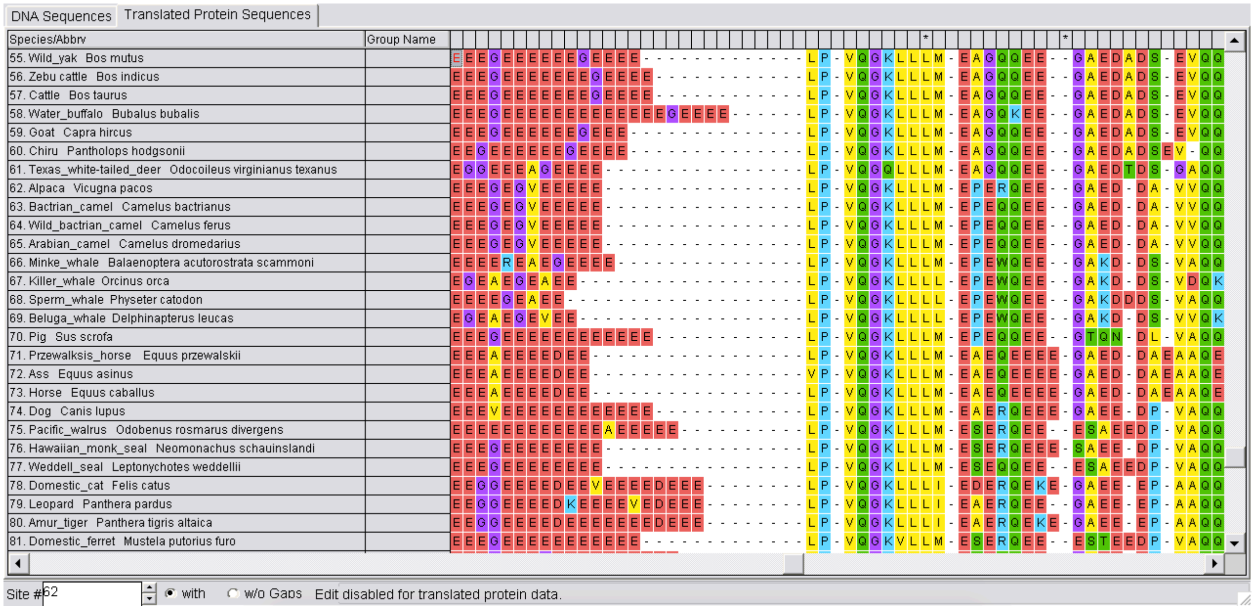

Species/Abbrv	Group Name	
55. Wild_yak Bos mutus		EEEGEEEEEEGEEEE-------------LP-VQGKLLLM-EAGQQEE--GAEDADS-EVQQ
56. Zebu cattle Bos indicus		EEEGEEEEEEEGEEEE------------LP-VQGKLLLM-EAGQQEE--GAEDADS-EVQQ
57. Cattle Bos taurus		EEEGEEEEEEEGEEEE------------LP-VQGKLLLM-EAGQQEE--GAEDADS-EVQQ
58. Water_buffalo Bubalus bubalis		EEEGEEEEEEEEEEEEEGEEEE------LP-VQGKLLLM-EAGQKEE--GAEDADS-EVQQ
59. Goat Capra hircus		EEEGEEEEEEGEEE--------------LP-VQGKLLLM-EAGQQEE--GAEDADS-EVQQ
60. Chiru Pantholops hodgsonii		EEGEEEEEEGEEEE--------------LP-VQGKLLLM-EAGQQEE--GAEDADSEV-QQ
61. Texas_white-tailed_deer Odocoileus virginianus texanus		EGGEEEAGEEEE----------------LP-VQGQLLLM-EAGQQEE--GAEDTDS-GAQQ
62. Alpaca Vicugna pacos		EEEGEGVEEEEE----------------LP-VQGKLLLM-EPERQEE--GAED-DA-VVQQ
63. Bactrian_camel Camelus bactrianus		EEEGEGVEEEEE----------------LP-VQGKLLLM-EPEQQEE--GAED-DA-VVQQ
64. Wild_bactrian_camel Camelus ferus		EEEGEGVEEEEE----------------LP-VQGKLLLM-EPEQQEE--GAED-DA-VVQQ
65. Arabian_camel Camelus dromedarius		EEEGEGVEEEEE----------------LP-VQGKLLLM-EPEQQEE--GAED-DA-VVQQ
66. Minke_whale Balaenoptera acutorostrata scammoni		EEEEREAEGEEEE---------------LP-VQGKLLLM-EPEWQEE--GAKD-DS-VAQQ
67. Killer_whale Orcinus orca		EGEAEGEAEE------------------LP-VQGKLLLL-EPEWQEE--GAKD-DS-VDQK
68. Sperm_whale Physeter catodon		EEEEGEAEE-------------------LP-VQGKLLLL-EPEWQEE--GAKDDDS-VAQQ
69. Beluga_whale Delphinapterus leucas		EGEAEGEVEE------------------LP-VQGKLLLL-EPEWQEE--GAKD-DS-VVQK
70. Pig Sus scrofa		EEEGEEEEEEEEEEEE------------LP-VQGKLLLM-EPEQQEE--GTQN-DL-VAQQ
71. Przewalksis_horse Equus przewalskii		EEEAEEEEDEE-----------------LP-VQGKLLLM-EAEQEEEE-GAED-DAEAAQE
72. Ass Equus asinus		EEEAEEEEDEE-----------------VP-VQGKLLLM-EAEQEEEE-GAED-DAEAAQE
73. Horse Equus caballus		EEEAEEEEDEE-----------------LP-VQGKLLLM-EAEQEEEE-GAED-DAEAAQE
74. Dog Canis lupus		EEEVEEEEEEEEEEEE------------LP-VQGKLLLM-EAERQEEE-GAEE-DP-VAQQ
75. Pacific_walrus Odobenus rosmarus divergens		EEEEEEEEEEEEAEEEEE----------LP-VQGKLLLM-ESERQEE--ESAEEDP-VAQQ
76. Hawaiian_monk_seal Neomonachus schauinslandi		EEEGEEEEEEEE----------------LP-VQGKLLLM-ESERQEEE-SAEE-DP-VAQQ
77. Weddell_seal Leptonychotes weddellii		EEEGEEEEEEEE----------------LP-VQGKLLLM-ESEQQEE--ESAEEDP-VAQQ
78. Domestic_cat Felis catus		EEGGEEEEDEEVEEEEDEEE--------LP-VQGKLLLI-EDERQEKE-GAEE-EP-AAQQ
79. Leopard Panthera pardus		EEGGEEEEDKEEEEVEDEEE--------LP-VQGKLLLI-EAERQEE--GAEE-EP-AAQQ
80. Amur_tiger Panthera tigris altaica		EEGGEEEEDEEEEEEEDEEE--------LP-VQGKLLLI-EAERQEKE-GAEE-EP-AAQQ
81. Domestic_ferret Mustela putorius furo		EEEGEEEEEEEEEEE-------------LP-VQGKVLLM-ESERQEE--ESTEEDP-VAQQ

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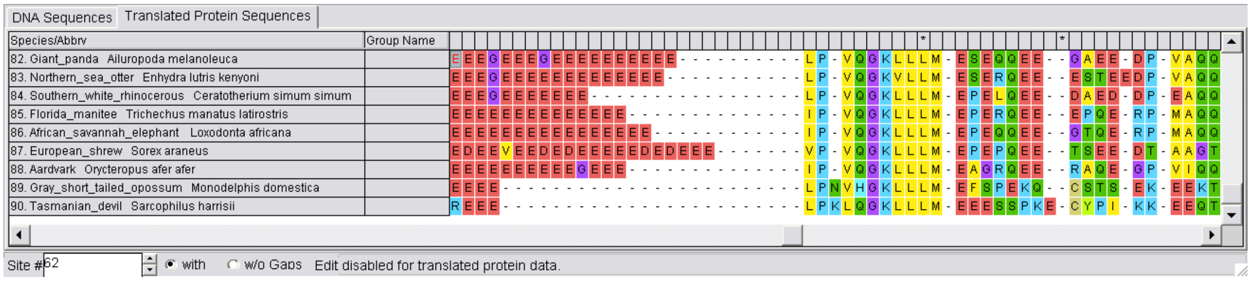

Species/Abbrv	Group Name	
82. Giant_panda Ailuropoda melanoleuca		EEEGEEEGEEEEEEEEEE----------LP-VQGKLLLM-ESEQQEE--GAEE-DP-VAQQ
83. Northern_sea_otter Enhydra lutris kenyoni		EEEGEEEEEEEEEEEEE-----------LP-VQGKVLLM-ESERQEE--ESTEEDP-VAQQ
84. Southern_white_rhinocerous Ceratotherium simum simum		EEEGEEEEEEE-----------------LP-VQGKLLLM-EPELQEE--DAED-DP-EAQQ
85. Florida_manitee Trichechus manatus latirostris		EEEEEEEEEEEEEE--------------IP-VQGKLLLM-EPERQEE--EPQE-RP-MAQQ
86. African_savannah_elephant Loxodonta africana		EEEEEEEEEEEEEEEE------------IP-VQGKLLLM-EPEQQEE--GTQE-RP-MAQQ
87. European_shrew Sorex araneus		EDEEVEEDEDEEEEEDEDEEE-------VP-VQGKLLLM-EPEPQEE--TSEE-DT-AAGT
88. Aardvark Orycteropus afer afer		EEEEEEEEEEGEEE--------------IP-VQGKLLLM-EAGRQEE--RAQE-GP-VIQQ
89. Gray_short_tailed_opossum Monodelphis domestica		EEEE------------------------LPNVHGKLLLM-EFSPEKQ--CSTS-EK-EEKT
90. Tasmanian_devil Sarcophilus harrisii		REEE------------------------LPKLQGKLLLM-EEESSPKE-CYPI-KK-EEQT

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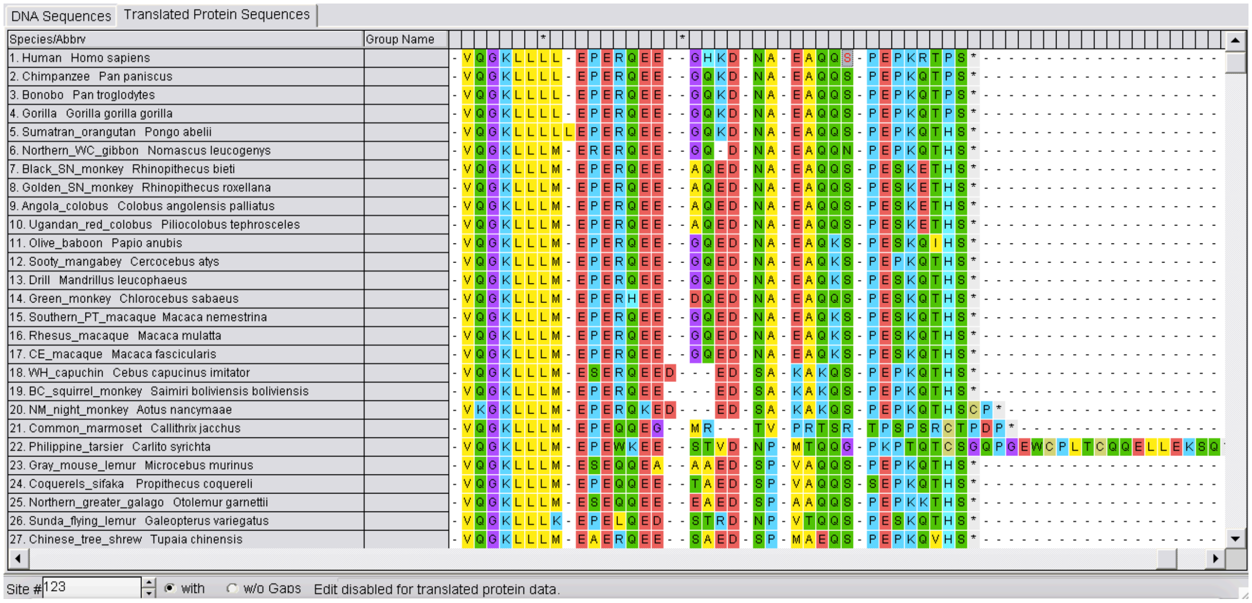

Species/Abbrv	Group Name	
1. Human Homo sapiens		-VQGKLLLL-EPERQEE--GHKD-NA-EAQQS-PEPKRTPS*
2. Chimpanzee Pan paniscus		-VQGKLLLL-EPERQEE--GQKD-NA-EAQQS-PEPKQTPS*
3. Bonobo Pan troglodytes		-VQGKLLLL-EPERQEE--GQKD-NA-EAQQS-PEPKQTPS*
4. Gorilla Gorilla gorilla gorilla		-VQGKLLLL-EPERQEE--GQKD-NA-EAQQS-PEPKQTPS*
5. Sumatran_orangutan Pongo abelii		-VQGKLLLLLEPERQEE--GQKD-NA-EAQQS-PEPKQTHS*
6. Northern_WC_gibbon Nomascus leucogenys		-VQGKLLLM-ERERQEE--GQ-D-NA-EAQQN-PEPKQTHS*
7. Black_SN_monkey Rhinopithecus bieti		-VQGKLLLM-EPERQEE--AQED-NA-EAQQS-PESKETHS*
8. Golden_SN_monkey Rhinopithecus roxellana		-VQGKLLLM-EPERQEE--AQED-NA-EAQQS-PESKETHS*
9. Angola_colobus Colobus angolensis palliatus		-VQGKLLLM-EPERQEE--AQED-NA-EAQQS-PESKETHS*
10. Ugandan_red_colobus Piliocolobus tephrosceles		-VQGKLLLM-EPERQEE--AQED-NA-EAQQS-PESKETHS*
11. Olive_baboon Papio anubis		-VQGKLLLM-EPERQEE--GQED-NA-EAQKS-PESKQIHS*
12. Sooty_mangabey Cercocebus atys		-VQGKLLLM-EPERQEE--GQED-NA-EAQKS-PEPKQTHS*
13. Drill Mandrillus leucophaeus		-VQGKLLLM-EPERQEE--GQED-NA-EAQKS-PESKQTHS*
14. Green_monkey Chlorocebus sabaeus		-VQGKLLLM-EPERHEE--DQED-NA-EAQQS-PESKQTHS*
15. Southern_PT_macaque Macaca nemestrina		-VQGKLLLM-EPERQEE--GQED-NA-EAQKS-PESKQTHS*
16. Rhesus_macaque Macaca mulatta		-VQGKLLLM-EPERQEE--GQED-NA-EAQKS-PESKQTHS*
17. CE_macaque Macaca fascicularis		-VQGKLLLM-EPERQEE--GQED-NA-EAQKS-PESKQTHS*
18. WH_capuchin Cebus capucinus imitator		-VQGKLLLM-ESERQEED---ED-SA-KAKQS-PEPKQTHS*
19. BC_squirrel_monkey Saimiri boliviensis boliviensis		-VQGKLLLM-EPERQEE----ED-SA-KAKQS-PEPKQTHS*
20. NM_night_monkey Aotus nancymaae		-VKGKLLLM-EPERQKED---ED-SA-KAKQS-PEPKQTHSCP*
21. Common_marmoset Callithrix jacchus		-VQGKLLLM-EPEQQEG--MR---TV-PRTSR-TPSPSRCTPDP*
22. Philippine_tarsier Carlito syrichta		-VQGKLLLM-EPEWKEE--STVD-NP-MTQQG-PKPTQTCSGQPGEWCPLTCQQELLEKSQ
23. Gray_mouse_lemur Microcebus murinus		-VQGKLLLM-ESEQQEA--AAED-SP-VAQQS-PEPKQTHS*
24. Coquerels_sifaka Propithecus coquereli		-VQGKLLLM-EPEQQEE--TAED-SP-VAQQS-SEPKQTHS*
25. Northern_greater_galago Otolemur garnettii		-VQGKLLLM-ESEQQEE--EAED-SP-AAQQS-PEPKKTHS*
26. Sunda_flying_lemur Galeopterus variegatus		-VQGKLLLK-EPELQED--STRD-NP-VTQQS-PESKQTHS*
27. Chinese_tree_shrew Tupaia chinensis		-VQGKLLLM-EAERQEE--SAED-SP-MAEQS-PEPKQVHS*

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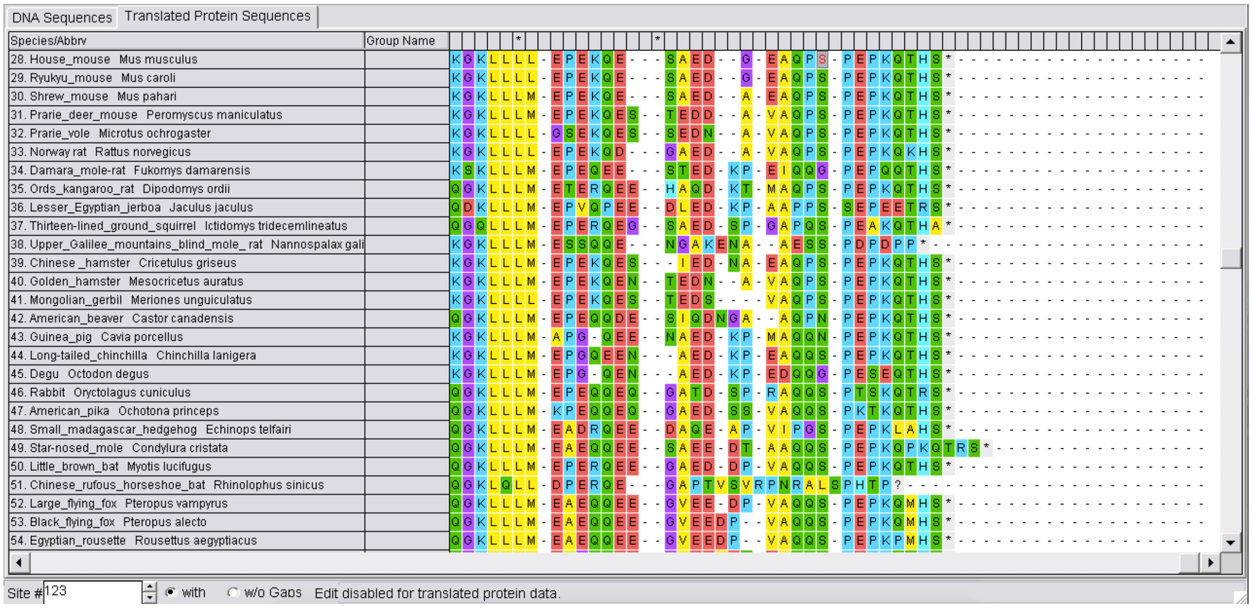

Species/Abbrv	Group Name	
28. House_mouse Mus musculus		KGKLLLL-EPEKQE---SAED--G-EAQPS-PEPKQTHS*
29. Ryukyu_mouse Mus caroli		KGKLLLL-EPEKQE---SAED--G-EAQPS-PEPKQTHS*
30. Shrew_mouse Mus pahari		KGKLLLM-EPEKQE---SAED--A-EAQPS-PEPKQTHS*
31. Prarie_deer_mouse Peromyscus maniculatus		KGKLLLM-EPEKQES--TEDD--A-VAQPS-PEPKQTHS*
32. Prarie_vole Microtus ochrogaster		KGKLLLL-GSEKQES--SEDN--A-VAQPS-PEPKQTHS*
33. Norway rat Rattus norvegicus		KGKLLLL-EPEKQD---GAED--A-VAQPS-PEPKQKHS*
34. Damara_mole-rat Fukomys damarensis		KSKLLLM-EPEQEE---STED-KP-EIQQG-PEPQQTHS*
35. Ords_kangaroo_rat Dipodomys ordii		QGKLLLM-ETERQEE--HAQD-KT-MAQPS-PEPKQTHS*
36. Lesser_Egyptian_jerboa Jaculus jaculus		QDKLLLM-EPVQPEE--DLED-KP-AAPPS-SEPEETRS*
37. Thirteen-lined_ground_squirrel Ictidomys tridecemlineatus		QGQLLLM-EPERQEG--SAED-SP-GAPQS-PEAKQTHA*
38. Upper_Galilee_mountains_blind_mole_rat Nannospalax gali		KGKLLLM-ESSQQE---NGAKENA--AESS-PDPDPP*
39. Chinese _hamster Cricetulus griseus		KGKLLLM-EPEKQES---IED-NA-EAQPS-PEPKQTHS*
40. Golden_hamster Mesocricetus auratus		KGKLLLM-EPEKQEN--TEDN--A-VAQPS-PEPKQTHS*
41. Mongolian_gerbil Meriones unguiculatus		KGKLLLL-EPEKQES--TEDS----VAQPS-PEPKQTHS*
42. American_beaver Castor canadensis		QGKLLLM-EPEQQDE--SIQDNGA--AQPN-PEPKQTHS*
43. Guinea_pig Cavia porcellus		KGKLLLM-APG-QEE--NAED-KP-MAQQN-PEPKQTHS*
44. Long-tailed_chinchilla Chinchilla lanigera		KGKLLLM-EPGQEEN---AED-KP-EAQQS-PEPKQTHS*
45. Degu Octodon degus		KGKLLLM-EPG-QEN---AED-KP-EDQQG-PESEQTHS*
46. Rabbit Oryctolagus cuniculus		QGKLLLM-EPEQQEQ--GATD-SP-RAQQS-PTSKQTRS*
47. American_pika Ochotona princeps		QGKLLLM-KPEQQEQ--GAED-SS-VAQQS-PKTKQTHS*
48. Small_madagascar_hedgehog Echinops telfairi		QGKLLLM-EADRQEE--DAQE-AP-VIPGS-PEPKLAHS*
49. Star-nosed_mole Condylura cristata		QGKLLLM-EAEQQEE--SAEE-DT-AAQQS-PEPKQPKQTRS*
50. Little_brown_bat Myotis lucifugus		QGKLLLM-EPERQEE--GAED-DP-VAQQS-PEPKQTHS*
51. Chinese_rufous_horseshoe_bat Rhinolophus sinicus		QGKLQLL-DPERQE---GAPTVSVRPNRALSPHTP?
52. Large_flying_fox Pteropus vampyrus		QGKLLLM-EAEQQEE--GVEE-DP-VAQQS-PEPKQMHS*
53. Black_flying_fox Pteropus alecto		QGKLLLM-EAEQQEE--GVEEDP--VAQQS-PEPKQMHS*
54. Egyptian_rousette Rousettus aegyptiacus		QGKLLLM-EAEQQEE--GVEEDP--VAQQS-PEPKPMHS*

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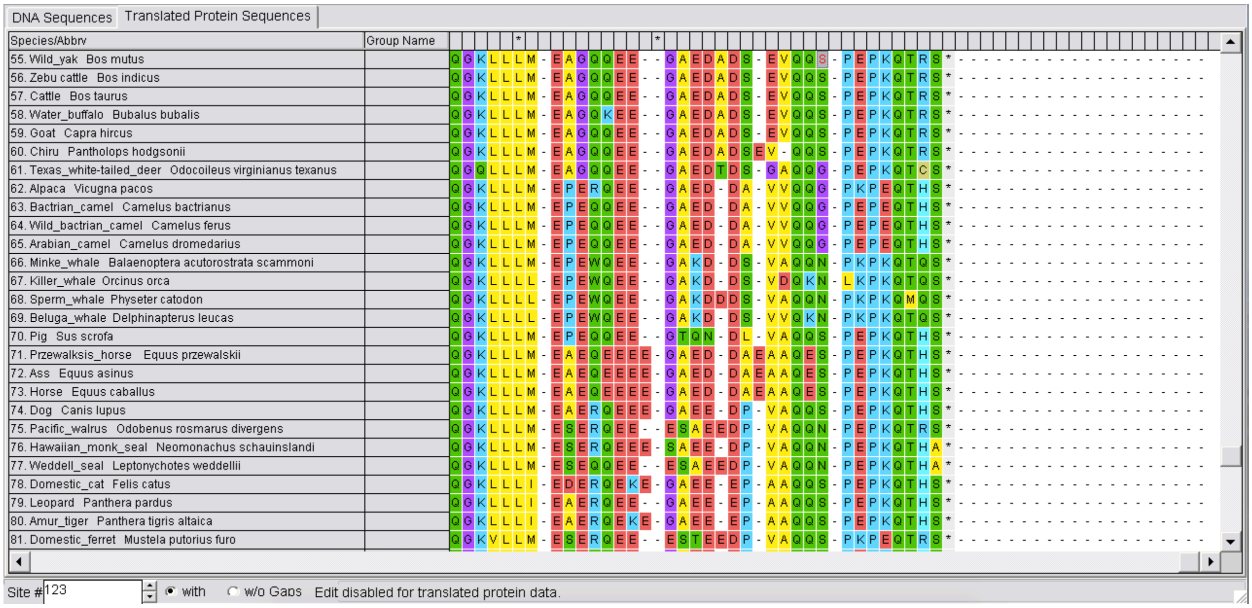

Species/Abbrv	Group Name	
55. Wild_yak Bos mutus		QGKLLLM-EAGQQEE--GAEDADS-EVQQS-PEPKQTRS*--------------------
56. Zebu cattle Bos indicus		QGKLLLM-EAGQQEE--GAEDADS-EVQQS-PEPKQTRS*--------------------
57. Cattle Bos taurus		QGKLLLM-EAGQQEE--GAEDADS-EVQQS-PEPKQTRS*--------------------
58. Water_buffalo Bubalus bubalis		QGKLLLM-EAGQKEE--GAEDADS-EVQQS-PEPKQTRS*--------------------
59. Goat Capra hircus		QGKLLLM-EAGQQEE--GAEDADS-EVQQS-PEPKQTRS*--------------------
60. Chiru Pantholops hodgsonii		QGKLLLM-EAGQQEE--GAEDADSEV-QQS-PEPKQTRS*--------------------
61. Texas_white-tailed_deer Odocoileus virginianus texanus		QGQLLLM-EAGQQEE--GAEDTDS-GAQQG-PEPKQTCS*--------------------
62. Alpaca Vicugna pacos		QGKLLLM-EPERQEE--GAED-DA-VVQQG-PKPEQTHS*--------------------
63. Bactrian_camel Camelus bactrianus		QGKLLLM-EPEQQEE--GAED-DA-VVQQG-PEPEQTHS*--------------------
64. Wild_bactrian_camel Camelus ferus		QGKLLLM-EPEQQEE--GAED-DA-VVQQG-PEPEQTHS*--------------------
65. Arabian_camel Camelus dromedarius		QGKLLLM-EPEQQEE--GAED-DA-VVQQG-PEPEQTHS*--------------------
66. Minke_whale Balaenoptera acutorostrata scammoni		QGKLLLM-EPEWQEE--GAKD-DS-VAQQN-PKPKQTQS*--------------------
67. Killer_whale Orcinus orca		QGKLLLL-EPEWQEE--GAKD-DS-VDQKN-LKPKQTQS*--------------------
68. Sperm_whale Physeter catodon		QGKLLLL-EPEWQEE--GAKDDDS-VAQQN-PKPKQMQS*--------------------
69. Beluga_whale Delphinapterus leucas		QGKLLLL-EPEWQEE--GAKD-DS-VVQKN-PKPKQTQS*--------------------
70. Pig Sus scrofa		QGKLLLM-EPEQQEE--GTQN-DL-VAQQS-PEPKQTHS*--------------------
71. Przewalksis_horse Equus przewalskii		QGKLLLM-EAEQEEEE-GAED-DAEAAQES-PEPKQTHS*--------------------
72. Ass Equus asinus		QGKLLLM-EAEQEEEE-GAED-DAEAAQES-PEPKQTHS*--------------------
73. Horse Equus caballus		QGKLLLM-EAEQEEEE-GAED-DAEAAQES-PEPKQTHS*--------------------
74. Dog Canis lupus		QGKLLLM-EAERQEEE-GAEE-DP-VAQQS-PEPKQTHS*--------------------
75. Pacific_walrus Odobenus rosmarus divergens		QGKLLLM-ESERQEE--ESAEEDP-VAQQN-PEPKQTRS*--------------------
76. Hawaiian_monk_seal Neomonachus schauinslandi		QGKLLLM-ESERQEEE-SAEE-DP-VAQQN-PEPKQTHA*--------------------
77. Weddell_seal Leptonychotes weddellii		QGKLLLM-ESEQQEE--ESAEEDP-VAQQN-PEPKQTHA*--------------------
78. Domestic_cat Felis catus		QGKLLLI-EDERQEKE-GAEE-EP-AAQQS-PEPKQTHS*--------------------
79. Leopard Panthera pardus		QGKLLLI-EAERQEE--GAEE-EP-AAQQS-PEPKQTHS*--------------------
80. Amur_tiger Panthera tigris altaica		QGKLLLI-EAERQEKE-GAEE-EP-AAQQS-PEPKQTHS*--------------------
81. Domestic_ferret Mustela putorius furo		QGKVLLM-ESERQEE--ESTEEDP-VAQQS-PKPEQTRS*--------------------

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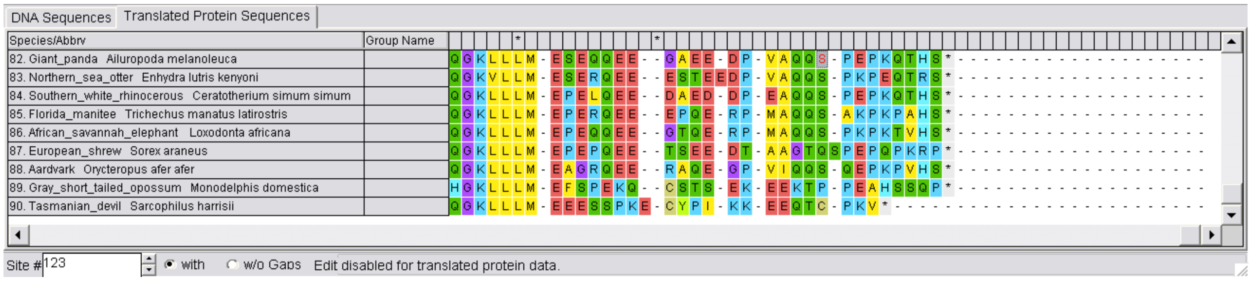

Species/Abbrv	Group Name	
82. Giant_panda Ailuropoda melanoleuca		QGKLLLM-ESEQQEE--GAEE-DP-VAQQS-PEPKQTHS*--------------------
83. Northern_sea_otter Enhydra lutris kenyoni		QGKVLLM-ESERQEE--ESTEEDP-VAQQS-PKPEQTRS*--------------------
84. Southern_white_rhinocerous Ceratotherium simum simum		QGKLLLM-EPELQEE--DAED-DP-EAQQS-PEPKQTHS*--------------------
85. Florida_manitee Trichechus manatus latirostris		QGKLLLM-EPERQEE--EPQE-RP-MAQQS-AKPKPAHS*--------------------
86. African_savannah_elephant Loxodonta africana		QGKLLLM-EPEQQEE--GTQE-RP-MAQQS-PKPKTVHS*--------------------
87. European_shrew Sorex araneus		QGKLLLM-EPEPQEE--TSEE-DT-AAGTQSPEPQPKRP*--------------------
88. Aardvark Orycteropus afer afer		QGKLLLM-EAGRQEE--RAQE-GP-VIQQS-QEPKPVHS*--------------------
89. Gray_short_tailed_opossum Monodelphis domestica		HGKLLLM-EFSPEKQ--CSTS-EK-EEKTP-PEAHSSQP*--------------------
90. Tasmanian_devil Sarcophilus harrisii		QGKLLLM-EEESSPKE-CYPI-KK-EEQTC-PKV*------------------------

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