

## A survey of genes encoding H<sub>2</sub>O<sub>2</sub>-producing GMC oxidoreductases in 10 Polyporales genomes

Patricia Ferreira<sup>1</sup>

*Departamento de Bioquímica y Biología Molecular y Celular and BIFI, Universidad de Zaragoza, E-50009 Zaragoza, Spain*

Juan Carro<sup>1</sup>

Ana Serrano

Angel T. Martínez<sup>2</sup>

*Centro de Investigaciones Biológicas, CSIC, Ramiro de Maeztu 9, E-28040 Madrid, Spain*

**Abstract:** The genomes of three representative Polyporales (*Bjerkandera adusta*, *Phlebia brevispora* and a member of the *Ganoderma lucidum* complex) recently were sequenced to expand our knowledge on the diversity and distribution of genes involved in degradation of plant polymers in this Basidiomycota order, which includes most wood-rotting fungi. Oxidases, including members of the glucose-methanol-choline (GMC) oxidoreductase superfamily, play a central role in the above degradative process because they generate extracellular H<sub>2</sub>O<sub>2</sub> acting as the ultimate oxidizer in both white-rot and brown-rot decay. The survey was completed by analyzing the GMC genes in the available genomes of seven more species to cover the four Polyporales clades. First, an in silico search for sequences encoding members of the aryl-alcohol oxidase, glucose oxidase, methanol oxidase, pyranose oxidase, cellobiose dehydrogenase and pyranose dehydrogenase families was performed. The curated sequences were subjected to an analysis of their evolutionary relationships, followed by estimation of gene duplication/reduction history during fungal evolution. Second, the molecular structures of the near one hundred GMC oxidoreductases identified were modeled to gain insight into their structural variation and expected catalytic properties. In contrast to ligninolytic peroxidases, whose genes are present in all white-rot Polyporales genomes and absent from those of brown-rot species, the H<sub>2</sub>O<sub>2</sub>-generating oxidases are widely distributed in both fungal types. This indicates that the GMC oxidases provide H<sub>2</sub>O<sub>2</sub> for both ligninolytic peroxidase activity (in white-rot decay) and Fenton attack on cellulose (in brown-rot decay), after the transition between both decay patterns in Polyporales occurred.

**Key words:** brown-rot fungi, evolutionary relationships, GMC oxidoreductases, sequenced genome analysis, white-rot fungi

### INTRODUCTION

Although species from several Basidiomycota (and some Ascomycota) orders contribute to lignocellulose decay, the ability to degrade wood is a typical feature of the order Polyporales. This capability was an essential evolutionary trait acquired by ancestral basidiomycetes in the later Carboniferous period (Floudas et al. 2012), when the amount of carbon fixed by photosynthesis strongly increased due to colonization of land ecosystems by vascular plants. Nowadays fungal decay of wood represents a natural model for the sustainable use of plant resources in lignocellulose biorefineries (Martínez et al. 2009, Ragauskas et al. 2014).

The first basidiomycete genome to be sequenced was that of *Phanerochaete chrysosporium* (= *Phanerochaete chrysosporium*) (Martínez et al. 2004) due to the interest in this white-rot fungus of the order Polyporales as a model lignin-degrading organism (Kersten and Cullen 2007). Wood attack by white-rot fungi is based on their ability to degrade the recalcitrant polymer of lignin in a process that was defined as an enzymatic “combustion” (Kirk and Farrell 1987) and combines extracellular oxidases and peroxidases (Kersten and Cullen 2007, Ruiz-Dueñas and Martínez 2009). With a few exceptions corresponding to poor wood rotters (e.g. species of Jaapiales and Cantharellales), the presence of lignin peroxidase (LiP<sup>3</sup>, EC 1.11.1.14), manganese peroxidase (MnP, EC 1.11.1.13) or versatile peroxidase (VP, EC 1.11.1.16) genes is a constant characteristic of all typical white-rot fungi based on comparative genome analysis (Floudas et al. 2012, 2015; Ruiz-Dueñas et al. 2013). The diversity, distribution and evolutionary relationships of ligninolytic peroxidases in the order Polyporales has been studied (Ruiz-Dueñas et al. 2013).

Brown-rot fungi have developed an alternative strategy, based on Fenton chemistry, to overcome the lignin barrier (Baldrian and Valaskova 2008). H<sub>2</sub>O<sub>2</sub> reduction by ferrous iron yields hydroxyl free radical, which is able to access, oxidize and depolymerize wood cellulose with a more or less limited modification of lignin (Kirk 1975, Martínez et al. 2011, Yelle et al. 2011). In 2009 the genome of *Rhodonina placenta* (syn.: *Postia placenta*) was sequenced as the model brown-rot

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<sup>1</sup> These two authors contributed equally to this paper.

<sup>2</sup> Corresponding author. E-mail: atmartinez@cib.csic.es

fungus to increase our understanding of this type of wood decay (Martinez et al. 2009).

Several oxidases have been related to wood biodegradation as a source of extracellular H<sub>2</sub>O<sub>2</sub> (from O<sub>2</sub> reduction), including glucose oxidase (GOX, EC 1.1.3.4) (Kelley and Reddy 1986), methanol oxidase (MOX, EC 1.1.3.13, also known as ethanol/alcohol oxidase) (Nishida and Eriksson 1987, Daniel et al. 2007), aryl-alcohol oxidase (AAO, EC 1.1.3.7) (Guillén et al. 1990), pyranose 2-oxidase (P2O, EC 1.1.3.10) (Daniel et al. 1992) and glyoxal oxidase (GLX, EC 1.1.3.—) (Kersten and Kirk 1987). Although the involvement of some other intracellular oxidases has been suggested (Greene and Gould 1984, Kelley and Reddy 1986), wood decay is an extracellular process and secreted oxidases are more likely involved. Alternative mechanisms for H<sub>2</sub>O<sub>2</sub> generation have been suggested, including Mn(III)-mediated oxidation of glyoxylic/oxalic acids (Urzúa et al. 1998).

GLX belongs to the superfamily of copper-radical oxidases (Whittaker et al. 1996) whose distribution in Polyporales genomes has been reported (Kersten and Cullen 2014). In contrast all other oxidases mentioned above are flavooxidases from the GMC oxidoreductase superfamily whose first three members were GOX, MOX and choline dehydrogenase (Cavener 1992). Two additional GMC enzymes, which are inefficient reducing O<sub>2</sub> to H<sub>2</sub>O<sub>2</sub>, are cellobiose dehydrogenase (CDH, EC 1.1.99.18) and pyranose dehydrogenase (PDH, EC 1.1.99.29) (Zámocký et al. 2006, Krusá et al. 2008, Peterbauer and Volc 2010). All members of the GMC superfamily share similar structural features (Wierenga et al. 1986, Kiess et al. 1998). Recently several GMCs have been classified in the so-called subfamilies AA3\_1 (CDH), AA3\_2 (AAO/GOX), AA3\_3 (MOX) and AA3\_4 (P2O) of the CAZy database (Levasseur et al. 2013), but this nomenclature is not used here.

Three representative Polyporales—*Bjerkandera adusta*, *Ganoderma* sp. (*G. lucidum* complex) and *Phlebia brevispora*—were sequenced (Hibbett et al. 2013) and their different GMC gene families are analyzed here. *Bjerkandera adusta* is a strong lignin degrader, which produces AAO (Muheim et al. 1990) together with ligninolytic peroxidases (Kimura et al. 1991, Heinfling et al. 1998). Some species of *Ganoderma* cause extensive wood delignification (González et al. 1986; Martínez et al. 1995, 2011) and little is known about GMC production by these fungi (Peláez et al. 1995, Ralph et al. 1996). Finally, *P. brevispora* was investigated for wood biopulping due to selective lignin removal (Akhtar et al. 1993, Fonseca et al. 2014). Moreover, seven additional sequenced Polyporales genomes were screened and included in the present comparative analysis of GMC-encoding genes. The present study is part of a wider genomic project covering other gene families

(Ruiz-Dueñas et al. 2013, Hori et al. 2013, Mgbearhuie et al. 2013, Syed et al. 2013, Kovalchuk et al. 2013) as an example of genome-enabled mycology to gain insight into the biology and evolution of fungi (Hibbett et al. 2013).

## MATERIALS AND METHODS

*Genome sequencing.*—The genomic sequences of *B. adusta* (HHB-12826-SP), *P. brevispora* (HHB-7030-SS6) and *Ganoderma* sp. (10597-SS1) were obtained at the Joint Genome Institute (JGI), as part of the Saprotrophic Agaricomycotina Project coordinated by D.S. Hibbett (Clark University, USA). The genomes were produced as described by Binder et al. (2013), and the gene prediction is available at [http://genome.jgi.doe.gov/Bjead1\\_1](http://genome.jgi.doe.gov/Bjead1_1); <http://genome.jgi.doe.gov/Gansp1> and <http://genome.jgi.doe.gov/Phlbr1>, respectively.

*Genome screening for GMC gene families in Polyporales.*—The above genomes, plus those of *Dichomitus squalens*, *Fomitopsis pinicola*, *Gelatoporia subvermisporea* (syn.: *Ceriporiopsis subvermisporea*), *P. chrysosporium*, *R. placenta*, *Trametes versicolor* and *Wolfiporia cocos* (= *Wolfiporia extensa*) available at the JGI MycoCosm portal (<http://genome.jgi.doe.gov/programs/fungi>) (Grigoriev et al. 2012) were screened for genes of the AAO, MOX, GOX, CDH, P2O and PDH families in the GMC superfamily. Among the above genomes, those from the Antrodia clade (*F. pinicola*, *R. placenta*, *W. cocos*) correspond to wood decay by brown-rot species while the other species (*B. adusta*, *D. squalens*, *Ganoderma* sp., *G. subvermisporea*, *P. chrysosporium*, *P. brevispora* and *T. versicolor*) cause white-rot decay of wood.

The screening for each of the GMC families was performed by querying an entire set of filtered model proteins for each of the genomes with the following (GenBank) reference sequences: (i) AAO from *Pleurotus eryngii* (AAC72747); (ii) MOX from *Gloeophyllum trabeum*, *Pichia methanolica* and *Candida boidinii* (ABI14440, AF141329 and Q00922); (iii) GOXs from *Talaromyces flavus*, *Penicillium expansum*, *Penicillium amagasakiense*, *Aspergillus niger* and *Botryotinia fucheliana* (AAB09442, ABN79922, AAD01493, AAF59929 and CAD88590); (iv) CDHs from *P. chrysosporium*, *G. subvermisporea*, *Coniophora puteana*, *Pycnoporus cinnabarinus* (syn.: *Trametes cinnabarina*) and *T. versicolor* (CAA61359, ACF60617.1, BAD32781 AAC32197, AAC50004); (v) P2Os from *T. versicolor*, *Peniophora* sp., *P. chrysosporium*, *Lycophyllum shimeji* and *G. trabeum* (BAA11119, AAO13382, AAS93628, BAD12079 and ACJ54278); (vi) PDHs from *Leucogaricus meleagris* (syn.: *Agaricus meleagris*), *Agaricus xanthodermus* and *Agaricus bisporus* (AAW82997, AAW92123 and AAW92124).

*Sequence analysis.*—The genomic sequences with the highest similarities with the reference sequences for the different GMC families first were examined for the automatically annotated introns, searching for consensus 5'–3' and lariat sequences (Ballance 1986), as well as for the annotation of N- and C-termini. The presence/absence of secretion signal peptides predicted by the JGI automatic annotation pipeline was manually revised to detect possible mistakes (e.g. in neighbor introns) that could result in inaccurate

TABLE I. Inventory of 95 genes from six GMC families in the genomes of 10 Polyporales species (BJEAD, *B. adusta*; PHLBR, *P. brevispora*; PHACH, *P. chrysosporium*; DICSQ, *D. squalens*; GANSP, *Ganoderma* sp., TRAVE, *T. versicolor*; GELSU, *G. subvermispora*; FOMPI, *F. pinicola*; RHOPL, *R. placenta*; and WOLCO, *W. cocos*) from four clades, producing white-rot and brown-rot decay of wood

Clade	Phlebioid			Core polyporoid			Gelato-poria	Antrodia		
	BJEAD	PHLBR	PHACH	DICSQ	GANSP	TRAVE	GELSU	FOMPI	RHOPL	WOLCO
AAO	11	3	3	8	7	3	4	1	2	0
MOX	5	6	3	4	4	4	1	4	4	4
GOX	0	0	1	0	0	0	0	0	2	0
CDH	1	1	1	1	1	1	1	0	0	0
P2O	1	1	1	0	0	1	0	0	0	0
PDH	0	0	0	0	0	0	0	0	0	0
All GMCs	18	11	9	13	12	9	6	5	8	4
Ecology	White rot						Brown rot			

Four allelic variants (SUPPLEMENTARY TABLE I) are excluded from the inventory.

predictions, followed by inspection of the eventually revised sequences with the Signal P 4.0 server ([www.cbs.dtu.dk/services/SignalP-4.0](http://www.cbs.dtu.dk/services/SignalP-4.0)) (Petersen et al. 2011). Moreover, other servers as TargetP 1.1 (Emanuelsson et al. 2000), WoLF PSORT (Horton et al. 2007) and TMHMM 2.0 were used to confirm the secreted nature of proteins as well as to predict their putative subcellular locations. Predictions were confirmed by multiple alignment with MUSCLE (Edgar 2004) and by the comparison with reference sequences. Multiple alignments also were used for analysis of motifs conserved in GMC proteins (the ADP-binding domain and, at least, one of the two characteristic Prosite PS00623 and PS00624 sequences) (Cavener 1992). The sequences that lacked these GMC conserved motifs were discarded.

Finally, molecular models of 94 out of the 95 GMC sequences (references in SUPPLEMENTARY TABLE I) could be generated at the Swiss-Model server ([www.swissmodel.expasy.org](http://www.swissmodel.expasy.org)), which selected the most adequate templates (Bordoli et al. 2009). For AAO, MOX, GOX, CDH and P2O sequences, the crystallographic structures of *P. eryngii* AAO (PDB 3FIM), *Arthrobacter globiformis* choline oxidase (PDB 3LJP, note that no MOX crystal structure is available), *A. niger* GOX (PDB 1CF3), *P. chrysosporium* CDH (PDB 1KDG) and *Aspergillus oryzae* P2O (PDB 1TTO), respectively, were used as templates. Strictly conserved histidine and histidine/asparagine residues at the active site (Hernández-Ortega et al. 2012c, Wongnate et al. 2014) were searched for in all the models, and sequences lacking these residues were discarded.

**GMC evolutionary history.**—The evolutionary history of the (95) GMC sequences obtained was estimated with RaxML 7.7.1 (Stamatakis et al. 2008) from the multiple alignment obtained with MEGA 5 (Tamura et al. 2011) (alignment in SUPPLEMENTARY FIG. 1). For evolutionary tree construction, a maximal likelihood with clustering method was used, with the WAG model of amino acid substitutions, and the gaps treated as deletions (a 100-iteration bootstrap was performed). Identity degrees among all the above sequences were obtained after pairwise alignment with Clustal W2.

**Reconciliation analyses.**—The histories of gene duplication and losses for total GMCs (and the individual families) were inferred with Notung 2.6 (Durand et al. 2006). The gene tree was used as input and combined with a Polyporales phylogenetic tree (Binder et al. 2013) from TreeBASE ([www.treebase.org](http://www.treebase.org), tree ID Tr67497). The estimated numbers of gene duplications and deletions on each branch were used to hypothesize the number of sequences at the ancestral nodes. Two different threshold levels (30% and 90%) were used to assess the significance of the predictions obtained.

## RESULTS

**GMC gene families in three recently sequenced and other Polyporales genomes.**—A total of 41 GMC genes—21 AAO, 15 MOX, 3 CDH and 2 P2O genes (TABLE I)—were identified in the recently sequenced genomes of *B. adusta*, *Ganoderma* sp. and *P. brevispora*. Family classification was completed by inspection of the enzyme molecular models described below for characteristic flavin environment and catalytic residues (Gadda 2008, Hernández-Ortega et al. 2012a, Wongnate and Chaiyen 2013, Romero and Gadda 2014). The genome of *B. adusta* has the highest number of GMC genes (a total of 18), while similar numbers (11–12 genes) were found in the two other genomes (TABLE I). No GOX or PDH genes were found in any case and P2O genes also were absent from the *Ganoderma* sp. genome. AAO genes are the most abundant GMC genes in *B. adusta* and *Ganoderma* sp. (11 and 7, respectively) while MOX genes are the most abundant in *P. brevispora* (six genes). None of the 41 GMC genes identified in the three genomes had been cloned and deposited in databases (TABLE I).

Annotated genomes from seven more species of Polyporales were included for a wider comparison. The resulting 10 genomes include representatives of the Phlebioid (*B. adusta*, *P. brevispora*, *P. chrysosporium*),

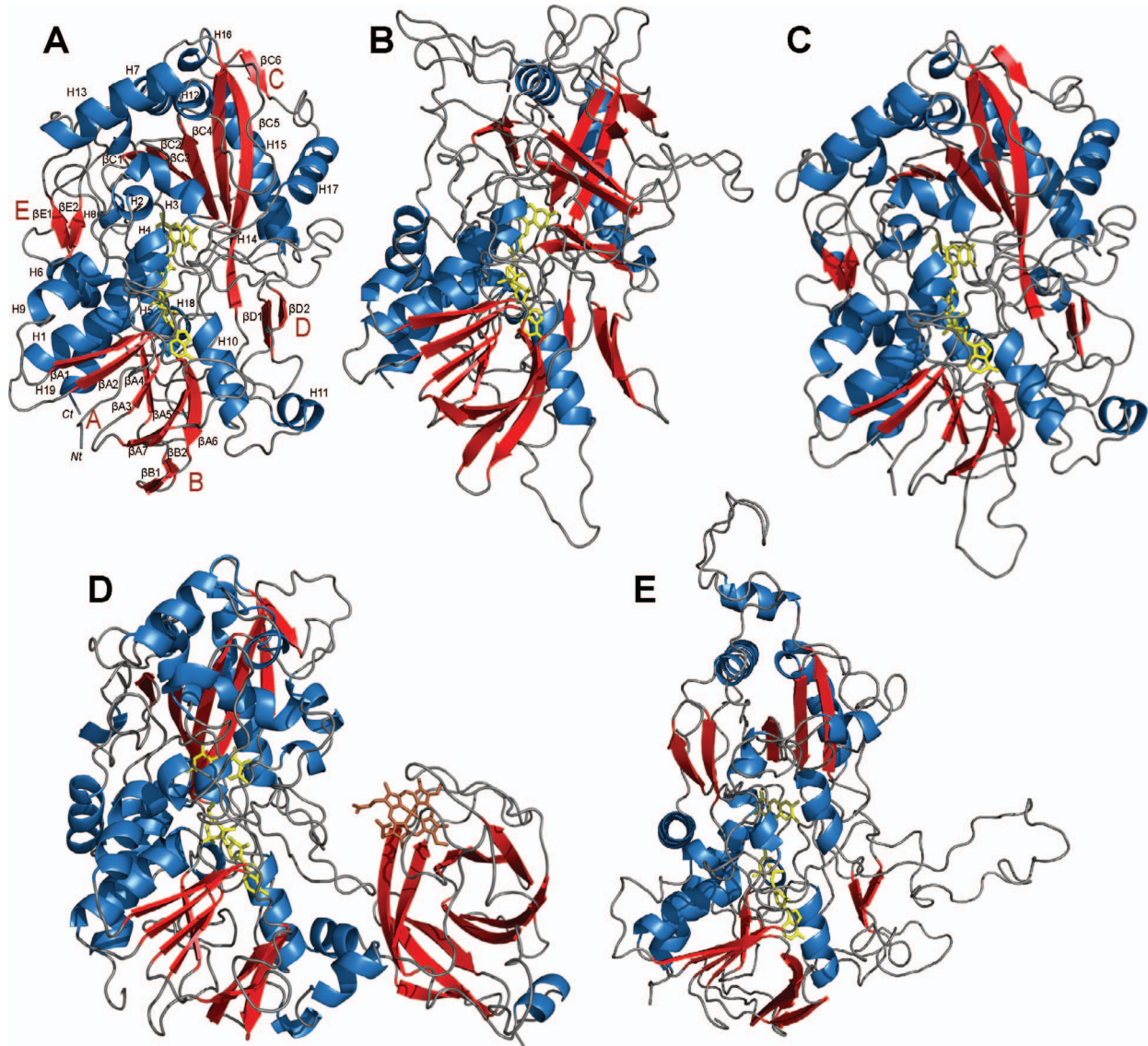


FIG. 1. Ribbon models for the molecular structures of representative members of the five GMC oxidoreductase families found in 10 Polyporales genomes (flavin and heme cofactors are shown as sticks). A. AAO of *B. adusta* (JGI protein ID 245059) indicating the position of four  $\beta$ -sheets, individual  $\beta$ -strands and 19  $\alpha$ -helices. B. MOX (monomer) of *F. pinicola* (JGI protein ID 156775). C. GOX (monomer) of *P. chrysosporium* (JGI protein ID 131961). D. CDH of *G. subvermispora* (JGI protein ID 84792) (flavin domain in the left and heme domain in the right). E. P2O (monomer) of *B. adusta* (JGI protein ID 34622). The molecular models were built with crystal structures of related proteins as templates.

core Polyporoid (*D. squalens*, *Ganoderma* sp., *T. versicolor*) Gelatoporia (*G. subvermispora*) and Antrodia (*F. pinicola*, *R. placenta*, *W. cocos*) clades (Binder et al. 2005). The number of genes of the different GMC families in each of the genomes is included herein (TABLE I), up to a total of 95 (JGI protein ID references are included [SUPPLEMENTARY TABLE I], as well as the existence of alleles and recognized signal peptides; and the complete sequences are provided in the alignment [SUPPLEMENTARY FIG. 1]). MOX genes are equally present in the white-rot and brown-rot genomes (average 4.0–4.4 genes/genome) while those of AAOs are nearly sixfold

more abundant in the genomes of white-rot (av. 5.7 genes/genome) than brown-rot (av. 1.0 gene/genome) species. Moreover, CDH genes were present in all the white-rot genomes (one copy per genome) but absent from the brown-rot genomes. Finally, P2O genes also were absent from the brown-rot genomes and no PDH genes were found in any of the genomes.

*Structural modeling of GMC oxidoreductases from Polyporales genomes.*—Most of the predicted GMC sequences (94 of 95) were modeled with related crystal structures as templates. Five representative structures (FIG. 1)



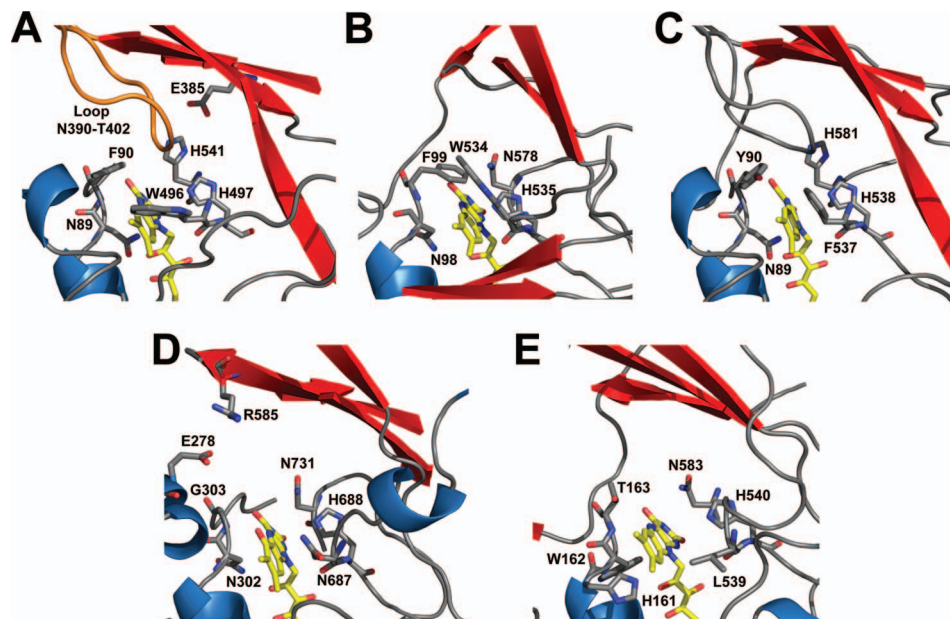


FIG. 2. Detail of active-site residues in the molecular models for the five Polyporales GMCs (FIG. 1). A. *B. adusta* AAO. B. *F. pinicola* MOX. C) *P. chrysosporium* GOX. D. *G. subvermispora* CDH. E. *B. adusta* P2O. Residue numbering corresponds to the putative mature proteins. FAD and the selected residues are shown as sticks. The N390-T402 loop of AAO is shown in A.

correspond to *B. adusta* AAO (A), *F. pinicola* MOX (B), *R. placenta* GOX (C), *G. subvermispora* CDH (D) and *B. adusta* P2O (E) mature proteins. All these GMCs show a common folding with the lower domain harboring the FAD cofactor. Specific features are present in AAO, which possesses a loop partially covering the entrance to the active site (FIG. 2A, left); and CDH, which has a heme domain connected by an unstructured linker (FIG. 1D). Of interest, AAOs and CDHs are known as monomeric proteins while GOXs, P2Os and MOXs form oligomers (Romero and Gadda 2014). One large  $\beta$ -sheet is present in both the FAD-binding (sheet A) and the substrate-binding (sheet C) domains, the former being accompanied by two small sheets (B, D) and the latter by only one (sheet E) (FIG. 1A). Similar numbers of  $\alpha$ -helices exist in the FAD-binding and the substrate-binding domains (9–10 in AAO), some of them (e.g. AAO helices 1, 4, 10) conserved in most GMCs. All the predicted models present the ADP-binding  $\beta\alpha\beta$  motif near their N-termini (SUPPLEMENTARY FIG. 2A) and the GMC signatures 1 and 2 (Prosite PS00623 and PS00624, respectively; SUPPLEMENTARY FIG. 2B, C), with the only exception of P2O that lacks signature 1.

The FAD flavin ring enters the GMC upper domain, where several residues form a substrate-binding site at the *re*-side of the isoalloxazine ring (FIG. 2). They include a histidine strictly conserved in the superfamily (SUPPLEMENTARY FIG. 1 multiple alignment), corresponding to *B. adusta* AAO His497

(FIG. 2A), *F. pinicola* MOX His535 (FIG. 2B), *P. chrysosporium* GOX His538 (FIG. 2C), *G. subvermispora* CDH His688 (FIG. 2D) and *B. adusta* P2O His540 (FIG. 2E). A second conserved histidine in AAO and GOX (His541 and His581 in FIG. 2A, C, respectively) is replaced by an asparagine in MOX, CDH and P2O proteins (Asn 578, Asn731, Asn583; FIG. 2B, D, E, respectively). An aromatic residue often precedes the fully conserved histidine, being a tryptophan in AAO (Trp496) and MOX (Trp534) and a phenylalanine in GOX (Phe537), while a leucine (Leu539) and an asparagine (Asn687) occupy this position in the P2Os and CDHs, respectively (FIG. 2). At the opposite (*si*) side of the isoalloxazine ring another aromatic residue, which points toward the active site, is conserved, being a phenylalanine in AAO (Phe90) and a tyrosine in MOX (Tyr99) and GOX (Tyr90) (FIG. 2A–C). An asparagine preceding the latter position is conserved in all the Polyporales GMCs (Asn89, Asn98, Asn89, Asn322 in FIG. 2 AAO, GOX, MOX, CDH, respectively) with the exception of P2Os. This asparagine residue, also conserved in other GMCs, is involved in flavin bent conformation (Kiess et al. 1998).

*Evolutionary history of GMC oxidoreductases in the Polyporales genomes.*—The evolutionary history of the 95 GMCs identified in the 10 Polyporales genomes (five allelic variants, SUPPLEMENTARY TABLE I, excluded) was inferred by comparing their predicted amino-acid sequences (mature proteins). It is worth

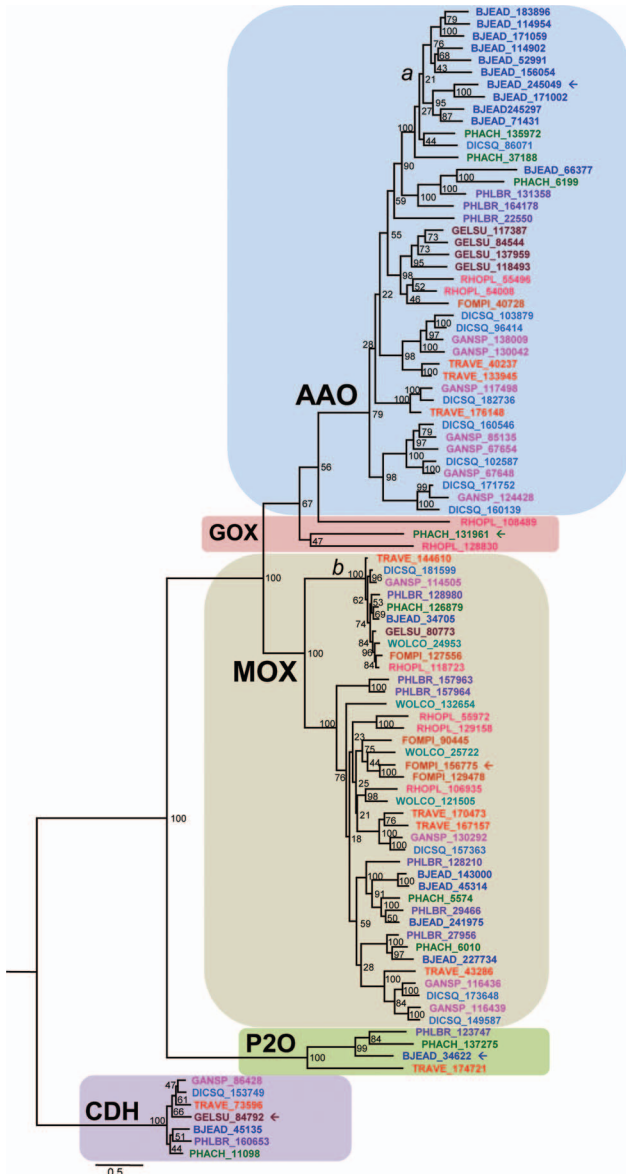


FIG. 3. Maximal likelihood evolutionary tree of the 95 GMC sequences (five allelic variants listed in SUPPLEMENTARY TABLE I excluded) from 10 Polyporales genomes (different color labels), prepared with RaxML (with gaps treated as deletions). The AAO, MOX, P2O and CDH groups (and the *a* and *b* subgroups mentioned in the text) are shown, together with a few GOX sequences related to AAOs. Numbers at nodes indicate bootstrap values. Those modeled sequences (FIGS. 1, 2) are indicated by arrows. Abbreviations of the fungal species are provided (TABLE I) as are complete amino-acid sequences (SUPPLEMENTARY FIG. 1).

noting that all the sequences from each of the GMC families cluster together in the maximal likelihood tree (FIG. 3). The two main groups correspond to the 39 MOXs and the 42 AAOs (100% and 79% bootstrap, respectively), with the only 3 GOXs distantly associated to the AAOs. Of interest, 10 of the 11

*B. adusta* AAOs are included in a 13-member subgroup (*a*, 100% bootstrap), suggesting recent duplication. In contrast MOXs include a subgroup (*b*, 100% bootstrap) of 10 sequences, each from one of the genomes. These 10 sequences share an insertion and a slightly longer C-terminus (SUPPLEMENTARY FIG. 1) involved in oligomerization and/or secretion of the enzymes through a unique secretory pathway (Danneel et al. 1994), suggesting a common origin of these genes. At the basal nodes the well supported (100% bootstrap) P2O (four sequences) and CDH (seven sequences) families appear unrelated between them and with the rest of the GMCs. The distant position of the latter families and the relatedness between AAOs, GOXs and MOXs agree with the pairwise identity values across and within gene families (SUPPLEMENTARY FIG. 3). In fact the average pairwise (interfamily) identity between P2O and CDH sequences is 8% and, among them and the rest of the families, range between 11% and 14%. These values are significantly lower than those between AAO and MOX (25% interfamily average), GOX and MOX (24% interfamily average) and AAO and GOX sequences (31% interfamily average). On the other hand the pairwise (intrafamily) identities within the CDH and P2O families are higher, 73% and 51%, respectively; whereas AAOs, GOXs and MOXs show values of 46%, 30% and 57%, respectively.

*GMC gene duplication and loss during diversification of Polyporales.*—The expansion or reduction in the number of GMC genes upon evolution of Polyporales was investigated by reconciliation of the evolutionary tree of the 95 GMC genes (FIG. 3) and the phylogenetic tree of the 10 species of Polyporales (from TreeBASE) using Notung. The results (using two different threshold levels) suggest that the ancestors of Polyporales had a high number of GMC genes, more than found in any of the extant species or the predicted intermediate ancestors (FIG. 4). Therefore during GMC evolution 14 contraction events and two expansions (from nodes *d* to node *g* and from node *e* to node *h*) were predicted. A similar tendency was observed for each of the individual GMC families (SUPPLEMENTARY FIG. 4A–E) with a total of 39 contractions and seven expansions. In this case expansions resulted in higher AAO (in node *g* and in *B. adusta*; SUPPLEMENTARY FIG. 4A), GOX (in *R. placenta*; SUPPLEMENTARY FIG. 4C) and P2O (in node *c*; SUPPLEMENTARY FIG. 4E) gene numbers (often after previous contractions) than predicted for the initial Polyporales ancestor. The stronger contraction of GMC gene numbers was evident in the Antrodia clade, resulting in only 4–5 genes in *W. cocos* and *F. pinicola*, and the largest expansion was observed

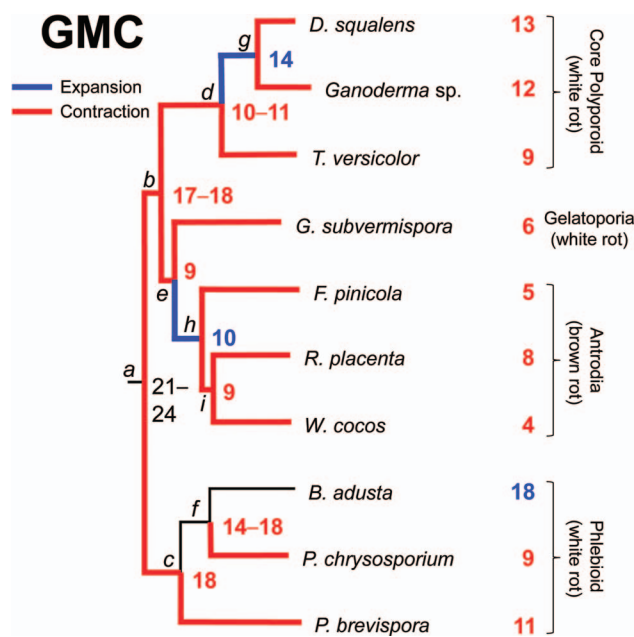


FIG. 4. Estimated range of GMC gene copies at the ancestral nodes (and extant species) of the represented phylogeny of Polyporales taken from Binder et al. (2013) after reconciliation with the gene evolutionary history (Fig. 3) using Notung (Durand et al. 2006). Branches and numbers after gene expansion and contraction are in black and gray, respectively (for reconciliation of the individual GMC families, see SUPPLEMENTARY FIG. 4).

in *B. adusta* (Phlebioid clade) with 18 GMC genes, including 11 AAOs (FIG. 4). Of interest, most of the remaining GMC genes in the Antrodia clade correspond to the MOX family (4/5 in *F. pinicola*, 4/8 in *R. placenta* and 4/4 in *W. cocos*).

#### DISCUSSION

The global reaction in initial wood decay by white-rot and brown-rot basidiomycetes is iron-catalyzed oxidation of lignin or polysaccharides, respectively, by  $H_2O_2$  generated by oxidases (from the GMC and/or the copper-protein radical superfamily). In white-rot decay this reaction is catalyzed by  $Fe^{3+}$  in the heme cofactor of ligninolytic peroxidases, while in brown-rot decay free  $Fe^{2+}$  reduces  $H_2O_2$  forming the highly reactive hydroxyl radical (Martínez et al. 2005; Kersten and Cullen 2007; Baldrian and Valaskova 2008, 2009). The information available on the presence and relevance of GMC families in Polyporales species is discussed below.

*Aryl-alcohol oxidase.*—AAO first was isolated from *Pleurotus* species (Agaricales) (Bourbonnais and Paice 1988; Guillén et al. 1990; Sannia et al. 1991, 1992) where it

generates  $H_2O_2$  by redox-cycling of anisaldehyde (Guillén and Evans 1994), an extracellular fungal metabolite (Gutiérrez et al. 1994). Subsequent studies focused on the *Pleurotus eryngii* enzyme, which was cloned and sequenced (Varela et al. 1999), heterologously expressed (Varela et al. 2001, Ruiz-Dueñas et al. 2006), crystallized (Fernández et al. 2009) and its reaction mechanisms investigated by a variety of techniques (Ferreira et al. 2005, 2006, 2009, 2010, 2015; Hernández-Ortega et al. 2011a, b, 2012b, c). Then a Polyporales AAO was isolated from *B. adusta* (Muheim et al. 1990). Although the above enzymes are known as secreted proteins (Hernández-Ortega et al. 2012a), recognized signal peptides are missing from four of the 42 sequences from the 10 Polyporales genomes, including one sequence from *B. adusta* and two from *D. squalens* and *P. chrysosporium*. The latter is in agreement with the description of an intracellular AAO in this fungus (Asada et al. 1995).

AAO activity has been detected in cultures of a few other Polyporales species (Peláez et al. 1995), although a Southern blot (using a *P. eryngii* probe) did not detect the corresponding gene in many of these (Varela et al. 2000), suggesting gene variability among different fungi. AAO activity in *B. adusta* (Romero et al. 2010), whose sequence corresponds to BJEAD\_171002 from the JGI genome, has been characterized largely showing higher activity on *p*-hydroxy and chlorinated benzyl alcohols than *Pleurotus* AAO (Romero et al. 2009). *p*-Hydroxybenzyl alcohols are the typical substrates of vanillyl alcohol oxidase, a flavoenzyme from a different superfamily (Leferink et al. 2008), but they are not efficiently oxidized by *Pleurotus* AAO, whose best substrates are *p*-methoxylated benzyl alcohols (Guillén et al. 1992, Ferreira et al. 2005). Therefore the best characterized Polyporales AAO shows catalytic properties intermediate between Agaricales AAO and vanillyl-alcohol oxidase. The higher activity of *B. adusta* AAO on chlorinated benzyl alcohols, which was noticed first by de Jong et al. (1994), is related to the ability of this species to synthesize 3-chloro-*p*-methoxybenzaldehyde (de Jong et al. 1992, de Jong and Field 1997). Redox cycling of this and related chlorinated compounds provides a continuous source of  $H_2O_2$  to *B. adusta* peroxidases (de Jong et al. 1994), similar to the *Pleurotus* anisaldehyde redox cycling. Chloroaromatics also could help wood colonization due to their antibiotic properties.

*Glucose oxidase.*—In contrast to AAO, which has been reported rarely in ascomycetes (Goetghebeur et al. 1992), GOX has been largely studied in *A. niger* (Frederick et al. 1990) and other ascomycetous fungi but rarely in basidiomycetes (Danneel et al. 1993). This is the protein with the largest sequence identity with

AAO, as shown in the gene tree, both sharing the general folding and active-site residues (Hecht et al. 1993, Wohlfahrt et al. 1999, Witt et al. 2000).

GOX is widely used in biosensors and other biotechnological applications (Bankar et al. 2009), but its involvement in lignocellulose degradation was discarded because the best known representatives are confirmed intracellular enzymes. However, two of the only three GOX sequences identified in the Polyporales genomes include a typical signal peptide, suggesting participation in the extracellular attack on lignocellulose.

*Pyranose 2-oxidase*.—P2O, which differs from GOX in glucose oxidation at the C2 (instead of the C1) position, is known as a secreted enzyme (Daniel et al. 1994) involved in lignocellulose degradation (Nyanhongo et al. 2007). This oxidoreductase first was investigated in *P. chrysosporium* (Artolozaga et al. 1997), and these studies suggested that P2O rather than GOX is secreted during wood decay (Volc et al. 1996). However, none of the four genes found in the Polyporales genomes have a recognized signal peptide, in agreement with the sequence obtained by Koker et al. (2004) for the cloned P2O gene from *P. chrysosporium*. Therefore if secreted this would be by an alternative mechanism, as suggested for MOX (see below).

P2O is produced by other Polyporales, including *Trametes multicolor* (= *Trametes ochracea*) (Leitner et al. 2001), and most recent P2O research focuses on this enzyme, whose reaction mechanisms have been elucidated in a variety of crystallographic, spectroscopic, directed mutagenesis, isotope labeling and kinetic studies (Hallberg et al. 2004; Sucharitakul et al. 2008; Prongjit et al. 2009, 2010; Pitsawong et al. 2010; Wongnate et al. 2011, 2014).

*Methanol oxidase*.—MOX is mostly known as a peroxysomal enzyme in methylotrophic ascomycetous yeasts, such as *Pichia pastoris* or *C. boidinii* (Ozimek et al. 2005). The first basidiomycete MOX was purified and characterized from *P. chrysosporium* (Nishida and Eriksson 1987) and it is also known from *Phlebiopsis gigantea* (Danneel et al. 1994). MOX was proposed as the main oxidase in brown-rot decay based on biochemical characterization and expression analyses in *Gloeophyllum trabeum* (Daniel et al. 2007). The corresponding gene is present in the genome of *R. placenta* (Martinez et al. 2009) and was overexpressed in wood-containing cultures of this brown-rot fungus and also in those of the white-rot *P. chrysosporium* (Vanden Wymelenberg et al. 2010).

The MOX gene of *G. trabeum* and other basidiomycetes does not include a recognized signal peptide. However, the extracellular location of MOX has

been demonstrated and operation of an alternative secretion mechanism was proposed (Daniel et al. 2007). The rationale for MOX involvement in brown-rot decay is that demethoxylation, resulting in methanol release, was reported first by Kirk (1975) and confirmed by 2D-NMR analyses (Martínez et al. 2011) as the main lignin modification in brown-rot decay.

*Pyranose and cellobiose dehydrogenases*.—PDH and CDH use electron acceptors different from O<sub>2</sub> and therefore do not contribute to H<sub>2</sub>O<sub>2</sub> supply. However, they oxidize plant carbohydrates and participate in electron transfer to other lignocellulose-degrading oxidoreductases.

PDH catalyzes the same oxidations of P2O but uses quinones as electron acceptors, being an enzyme of interest in biotechnology (Peterbauer and Volc 2010). The first PDH was isolated from *Agaricus bisporus* (Volc et al. 1997) and also found in related species (Kujawa et al. 2007, Kittl et al. 2008) including *L. meleagris* where it was thoroughly investigated (Tan et al. 2013; Krondorfer et al. 2014a, b). Screening for PDH revealed its exclusive presence in the above and other litter-degrading Agaricales (Volc et al. 2001), an observation that is consistent with its absence from all the (wood-rotting) Polyporales genomes analyzed.

CDH includes both flavin and heme domains, the former being able to oxidize cellobiose to cellobiolactone by transferring the electrons to Fe<sup>3+</sup> via the heme domain (Henriksson et al. 2000, Zámocký et al. 2006). CDH first was described in *P. chrysosporium* (whose conidial state was referred as *Sporotrichum pulverulentum* in some of these studies) (Ayers et al. 1978, Bao et al. 1993). The ancestral fusion between the two CDH domains and the subsequent evolution in different fungi has been discussed (Zámocký et al. 2004). One CDH gene was present in the genomes of the seven white-rot Polyporales analyzed and absent from the three brown-rot Polyporales genomes, in agreement with Hori et al. (2013), in which CDH was found only in white-rot genomes. However, this GMC seems to be present in other brown-rot fungi, as revealed by its early description in *C. puteana* (order Boletales) (Schmidhalter and Canevascini 1993) and its detection in the genomes of brown-rot fungi from other Agaricomycotina orders (Floudas et al. 2012).

Its ability to generate hydroxyl radical by simultaneous Fe<sup>3+</sup> and O<sub>2</sub> reduction has been suggested (Kremer and Wood 1992), but O<sub>2</sub> reduction by CDH is inefficient and only takes place in the absence of Fe<sup>3+</sup>. However, recent studies showed that CDH increases the cellulolysis yield and contributes to the action of lytic polysaccharide monooxygenase (Langston et al. 2011).

CDH from *P. chrysosporium* experiences proteolytic cleavage in cultures releasing the flavin domain (Wood



and Wood 1992), which was described as a different enzyme, cellobiose-quinone oxidoreductase (Westermarck and Eriksson 1974). However, the physiological significance of such cleavage and the role of cellobiose-quinone oxidoreductase under natural conditions is unknown (Raices et al. 2002).

*GMC oxidoreductases in Polyporales: final evolutionary/ecological remarks.*—The total number of GMC genes cloned to date from species of the order Polyporales is fewer than 10: from *P. chrysosporium*, *P. cinnabarinus*, *Pycnoporus sanguineus* (syn.: *Trametes sanguinea*), *T. ochracea* and *T. versicolor* (Leitner et al. 1998, Raices et al. 1995, Dumonceaux et al. 1998, Moukha et al. 1999, Vecerek et al. 2004, de Koker et al. 2004, Sulej et al. 2013). However, the present survey of GMC genes from a broader sampling including 10 Polyporales genomes (from different clades and survival strategies) reveals nearly 100 GMC genes representing five of the six best-known families (no PDH genes present).

The GMC superfamily is thought to have evolved from an old common ancestor, which very likely exhibited broad substrate specificity and poor kinetic parameters and gave rise to more specialized and efficient enzymes as evolution proceeded (Cavener 1992). The present study suggests that this diversification took place at a more ancestral stage of fungal evolution, with predominant gene loss among members of the Polyporales. This resulted in two main GMC types (groups) corresponding to AAO and MOX, with an average of  $\sim 4$  gene copies per genome, and three small groups corresponding to P2O, CDH and GOX (neighbor to the AAO group) with 0–1 copies per genome, in agreement with Zámocký et al. (2004) and Kittl et al. (2008).

While ligninolytic peroxidases (from the LiP, MnP and VP families) were absent from the brown-rot fungal genomes but present in all the white-rot fungal genomes (Ruiz-Dueñas et al. 2013), H<sub>2</sub>O<sub>2</sub>-producing GMCs were present in genomes of both white-rot and brown-rot species. Floudas et al. (2012) showed that the first wood-rotting fungus appeared by incorporation of secreted high redox-potential (ligninolytic) peroxidase genes in the genome of an ancestral basidiomycete. This was most likely accompanied by the evolution of several extracellular H<sub>2</sub>O<sub>2</sub>-producing oxidases, some of them with different evolutionary origin. These included copper-radical oxidases and several families of GMCs derived from related enzymes involved in intracellular metabolism.

White-rot decay was likely the ancestral survival strategy in wood-decay basidiomycetes (Floudas et al. 2012, Ruiz-Dueñas et al. 2013) and brown-rot evolved several times among Polyporales and other Agaricomycotina orders. The white-rot to brown-rot transition in

Polyporales included loss of the ligninolytic peroxidase genes, which are not required because lignin remained polymeric in brown-rotted wood. However, extracellular H<sub>2</sub>O<sub>2</sub>, used as peroxidase-activating substrate in white-rot decay, also plays an important role in brown-rot decay as the precursor of the hydroxyl radical formed by Fenton reaction. Therefore it seems that the same H<sub>2</sub>O<sub>2</sub>-generating oxidase types present in white-rot fungi remained in the derived brown-rot species. During evolution some differences in the frequency of the individual GMC families appeared. In this way MOX genes are the most abundant GMC genes in the brown-rot Polyporales while AAO genes are the most abundant in the white-rot species (up to 11 copies in *B. adusta*). Finally, the number of CDH genes predicted in the ancestor of Polyporales diminished, but all the white-rot species maintain one CDH gene, which contributes to polysaccharide degradation by these fungi. However, CDH genes disappeared in brown-rot fungi, where Fenton chemistry is the main mechanism for polysaccharide attack.

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**TABLE SI.** JGI ([www.jgi.doe.gov](http://www.jgi.doe.gov)) references (protein ID #) for the 95 GMC genes (plus 5 alleles) identified in the genomes of ten wood-rotting Polyporales (for species abbreviations see **TABLE I**; the existence of alleles and recognized signal peptides is indicated, see notes below)

----- *White-rot* ----- *Brown-rot* -----

	<b>BJEAD</b>	<b>PHLBR</b>	<b>PHACH</b>	<b>DICSQ</b>	<b>GANSP</b>	<b>TRAVE</b>	<b>GELSU</b>	<b>FOMPI</b>	<b>RHOPL</b>	<b>WOLCO</b>
<b>AAO</b>	<u>52991</u> #	<u>22550</u>	6199	<u>96414</u>	<u>67648</u>	<u>40237</u>	<u>84544</u>	<u>40728</u>	<u>44654</u> *	
	<u>66377</u>	<u>131358</u>	37188	<u>102587</u>	<u>67654</u>	<u>176148</u>	<u>117387</u>		<u>54008</u>	
	<u>71431</u>	<u>164178</u>	<u>135972</u>	<u>103879</u>	<u>85135</u>	<u>133945</u>	<u>118493</u>		<u>55496</u>	
	<u>114902</u>			86071	<u>117498</u>		<u>137959</u>		<u>58266</u> *	
	114954			<u>160139</u>	<u>124428</u>					
	<u>156054</u>			<u>160546</u>	<u>130042</u>					
	<u>171002</u>			<u>171752</u>	<u>138009</u>					
	<u>171059</u>			<u>182736</u>						
	<u>183896</u>									
	<u>245049</u>									
<u>245297</u>										
<b>MOX</b>	34705	27956	5574	149587	114505	144610	80773	90445	55972	24953
	45314	29466	6010	157363	116436	167157		127556	56055*	25722
	143000	128210	126879	173648	116439	170473		129478	106935	121505
	227734	128980		181599	130292	43286		156775	118723	132654
	241975	157963							126217*	
	157964							129158		
								129841*		
<b>GOX</b>			131961						<u>108849</u>	
									<u>128830</u>	
<b>CDH</b>	<u>45135</u>	<u>160653</u>	<u>11098</u>	<u>153749</u>	<u>86428</u>	<u>73596</u>	<u>84792</u>			
<b>P2O</b>	34622	123747	137275			174721				

\* RHOPL\_129841, RHOPL\_126217 and RHOPL\_56055 are allelic variants of MOX RHOPL\_118723, RHOPL\_129158 and RHOPL\_55972, respectively; while RHOPL\_44654 and RHOPL\_58266 were considered as variants of AAO RHOPL\_55496. # The protein models including a recognized signal peptide are underlined.



1 FIG. S1. Alignment of the complete 95 GMC sequences. Numbers correspond to amino  
2 acidic sequences in mature proteins (signal peptides numbered using negative values).  
3 The variable conservation of residues equivalent to AAO/GOX/MOX/P2O/CDH  
4 N89/N89/N98/S128/N302 (highlighted in blue), F90/Y90/F99/F131/G303 (in red),  
5 W496/F537/W534/L539/N687 and H497/H538/H535/H540/H688 (in yellow), and  
6 H541/H581/N578/N583/N731 (in green), located near the flavin ring (see FIG. 2), is  
7 indicated. The insertions and C-termini of MOX sequences belonging to subcluster *b*  
8 (see FIG. 3) is highlighted in purple.

9  
10 FIG. S2. Sequence logo of the ADP-binding motif (A), with consensus sequence [DP]-x-  
11 [VIL]-[VI]-x-G-x-G-x(2)-[GA]-x(3)-A-X-[RKT]-L-x(7)-[VT]-x(2)-[LIV]-E-x-G, and  
12 GMC signatures 1 (B) and 2 (C), with consensus sequences [GA]-[RKNC]-x-[LIVW]-  
13 G(2)-[GST](2)-x-[LIVM]-[NH]-x(3)-[FYWA]-x(2)-[PAG]-x(5)-[DNESHQA] and  
14 [GS]-[PSTA]-x(2)-[ST]-[PS]-x-[LIVM](2)-x(2)-S-G-[LIVM]-G respectively, in 95  
15 GMC sequences (TABLE SI) from 10 Polyporales genomes. The overall height of each  
16 stack represents the sequence conservation at that position, and the height of each letter  
17 reflects the relative frequency of the corresponding amino acid. Residues in A, B and C  
18 correspond to positions 2-33, 73-100 and 264-283, respectively in *B. adusta* AAO (JGI  
19 protein ID 245059), and equivalent positions in the other GMCs.

20  
21 FIG. S3. Pairwise identity matrix among the 95 GMC sequences included in Fig. S1.  
22 Numbers indicate percentage of identities and colors range from green (most similar) to  
23 red (lest similar).

24

25 FIG. S4. Estimated range of individual AAO (A), MOX (B), GOX (C), CDH (D) and  
26 P2O (E) gene copies, and total GMC from sum of family gene numbers (F), at the  
27 ancestral nodes (and extant species) of the represented phylogeny of Polyporales taken  
28 from Binder et al. (2013) after reconciliation with the gene phylogeny (FIG. 2) using  
29 Notung (Durand et al. 2006). Branches and numbers after gene expansion and  
30 contraction are in blue and red color, respectively. See Fig. 4 for gene reconciliation in  
31 the whole GMC superfamily.

TRAVE_174721	0	-----	0
PHLBR_123747	0	-----	0
PHACH_137275	0	-----	0
BJEAD_34622	0	-----	0
GELSU_84792	-20	-MFGRFLLALLPLVGSVLSQSGSSYTDPDNGFVFNIGITDPVYGVTVYGVVFPPEPSSSGTYPDEFIGEIVAPLTAEWIGVSVFSGGAMLDCLLLVAVPNEDSIVASTRYATDYVQPTIYDGP-V	98
TRAVE_73596	-21	MKFKSLLLSELLPLVGSVYSQVAAPYVDSGNGFVFDGVTDPVHSVTVYGVIVLPQAST----STEFIGEIVAPNEAQWIGLALGGAMIGNLLVAVPDGNKIVSSPRYATGYTLPAAYAGP-T	94
DICSQ_153749	-21	MKSKRLLSLLPFVGTAFQAQVAAPYTDGNGFVFDGITDPTVYGVTVYGVIVLPQANT----STEFIGEIVAPIAAKWVGVAFFGGAMIGDLLVAVPNNGNDIVASTRWATDYIQPTIYDGP-T	94
GANSP_86428	-21	MKLRKRLSLLPVGSAQAQVAAPYTDGNGFVFDGITDPAVYGVYQYGVIVLPQADS----STEFIGEIVAPIAAKWIGVAFGGAMIGDLLVAVPNNGNDIVASTRYATAYQPTIYDGP-T	94
PHLBR_160653	-20	-MLRRSLLTLLPFIGTALSQASATFVDPVNGYQFTGLTDPVHDVTVYGFVFPPLPTSGSDSTEFIGEIVAPIDSQWIGLALGGAMIQDLLVAVPNNGDQIVFSTRWATDYIQPVAYTGDAT	99
BJEAD_45135	-20	-MLRRSLFALLPLVGTAFSQAQVAAPYTDGNGFVFDGITDPAVYGVYQYGVIVLPQADS----STEFIGEIVAPIAAKWIGVAFGGAMIGNLLVAVPNNGNDIVFSTRFSTSYALPPPYTGDV	99
PHACH_11098	-20	-MLGRSLLALLPFVGLAFSQAQVAAPYTDGNGFVFDGITDPAVYGVYQYGVIVLPQADS----STEFIGEIVAPIAASKWIGIALGGAMNNDLLVAVANGNQIVSSTRWATGYVQPTIYTGAT	99
GANSP_114505	0	-----	0
DICSQ_181599	0	-----	0
TRAVE_144610	0	-----	0
PHLBR_128980	0	-----	0
BJEAD_34705	0	-----	0
PHACH_126879	0	-----	0
FOMPI_127556	0	-----	0
GELSU_80773	0	-----	0
RHOPL_118723	0	-----	0
WOLCO_24953	0	-----	0
TRAVE_43286	0	-----	0
DICSQ_149587	0	-----	0
GANSP_116439	0	-----	0
DICSQ_173648	0	-----	0
GANSP_116436	0	-----	0
PHLBR_157963	0	-----	0
PHLBR_157964	0	-----	0
PHLBR_128210	0	-----	0
BJEAD_143000	0	-----	0
BJEAD_45314	0	-----	0
PHACH_5574	0	-----	0
BJEAD_241975	0	-----	0
PHLBR_29466	0	-----	0
RHOPL_129158	0	-----	0
RHOPL_55972	0	-----	0
BJEAD_227734	0	-----	0
PHLBR_27956	0	-----	0
PHACH_6010	0	-----	0
DICSQ_157363	0	-----	0
GANSP_130292	0	-----	0
TRAVE_167157	0	-----	0
TRAVE_170473	0	-----	0
RHOPL_106935	0	-----	0
WOLCO_121505	0	-----	0
WOLCO_132654	0	-----	0
FOMPI_90445	0	-----	0
WOLCO_25722	0	-----	0
FOMPI_129478	0	-----	0
FOMPI_156775	0	-----	0
DICSQ_160139	0	-----	0
GANSP_124428	0	-----	0
DICSQ_171752	0	-----	0
GANSP_67648	0	-----	0
DICSQ_102587	0	-----	0
GANSP_67654	0	-----	0
GANSP_85135	0	-----	0
DICSQ_160546	0	-----	0
PHLBR_22550	0	-----	0
TRAVE_176148	0	-----	0
GANSP_117498	0	-----	0
DICSQ_182736	0	-----	0
TRAVE_40237	0	-----	0
TRAVE_133945	0	-----	0
GANSP_130042	0	-----	0
GANSP_138009	0	-----	0
DICSQ_103879	0	-----	0
DICSQ_96414	0	-----	0
FOMPI_40728	0	-----	0
RHOPL_55496	0	-----	0
GELSU_118493	0	-----	0
RHOPL_54008	0	-----	0
GELSU_137959	0	-----	0
GELSU_117387	0	-----	0
GELSU_84544	0	-----	0
PHACH_37188	0	-----	0
PHACH_135972	0	-----	0
DICSQ_86071	0	-----	0
BJEAD_156054	0	-----	0
BJEAD_171059	0	-----	0
BJEAD_114954	0	-----	0
BJEAD_183896	0	-----	0
BJEAD_114902	0	-----	0
BJEAD_52991	0	-----	0
BJEAD_245297	0	-----	0
BJEAD_71431	0	-----	0
BJEAD_171002	0	-----	0
BJEAD_245049	0	-----	0
BJEAD_66377	0	-----	0
PHACH_6199	0	-----	0
PHLBR_131358	0	-----	0
PHLBR_164178	0	-----	0
RHOPL_108489	0	-----	0
PHACH_131961	0	-----	0
RHOPL_128830	0	-----	0

TRAVE_174721	1	-----MSTSSS-----DPFFNFTKSSFRSAA-----AQKASATSLPPLPG-----PDKKVPGM	43
PHLBR_123747	1	-----MV-----FYSVHDHG	10
PHACH_137275	1	-----MF-----LDITPFRA	10
BJEAD_34622	1	-----M-----RLHSACQQ	9
GELSU_84792	99	LTTLPSSVNSTHWKYVYRCQNCITWQG---GGISLGGTGVLAWAYSNVGVDDPSDPESDFLEHTDFGFFGENFGQAE--NANYNRYVNGNPGTPTSTPPTTSPGPTTTPASPTAS	212
TRAVE_73596	95	ITQLPSSSVNSTHWKFVYRCQNCITAWNG---GSIDPSGTGVFAWAFSNVAVDDPSDPNSFFAEHTDFGFFGINFPDAQ--SSNYQNYLAGNAGTPPTSPVSPG---SSTTTTGTAT	205
DICSQ_153749	95	LTTLPSSVNSTHWKYVYRCQNCITWQGG---GGIDPTGTGVFAWAYSSVGVDDPSDPESDFQEHDFGFFGINFPDAQ--NSNYQNYLQGNPGTPTSTTTTTT---STSTTTGTAT	206
GANSP_86428	95	LTTLPSSVNSTHWKYVYRCQNCITWEGG---GGINPTGTGVFAWAYSNIGVDDPSDPNSTFQEHDFGFFGINFPDAQ--NANYQNYLQGNPGTPTSTTTTTT---TSTSTAPTPT	205
PHLBR_160653	100	VTTISS--SINSTYWRWVFRCEGCTSWTG---GGIDVDESGVLAWAFSNIAVDDPSDPESDFQEHDFGFFGIDYSTAHVSSSTYSYSGYLNGQGSSSPPTTSSAPPSQ--TSSAPPGTPT	213
BJEAD_45135	100	LTTLPSSVNSTHWKWFVRCQCTQMSGASSGGIDATSGVLAWAFMSAAVDTPADPNSTFKEHDFGFFGIDYSTH--NANYQNYLQGNAGTTPGPGSGGCTPT---TTATSTGTPTV	214
PHACH_11098	100	LTTLPETTINSTHWKWFVRCQCTEWNG---GGIDVTSQGVLAWAFSNVAVDDPSDPSTFSEHTDFGFFGIDYSTAH--SANYQNYLNGDSGNPTTSTKPTST---SSSVTTGTPTV	211
GANSP_114505	1	-----MGH	3
DICSQ_181599	1	-----MGH	3
TRAVE_144610	1	-----MGH	3
PHLBR_128980	1	-----MGQ	3
BJEAD_34705	1	-----MGH	3
PHACH_126879	1	-----MGH	3
FOMPI_127556	1	-----MH	2
GELSU_80773	1	-----MVH	3
RHOPL_118723	1	-----MH	2
WOLCO_24953	1	-----MH	2
TRAVE_43286	1	-----MASPSLH	7
DICSQ_149587	1	-----MTTPQL	6
GANSP_116439	1	-----MAAQL	6
DICSQ_173648	1	-----MTTPQL	6
GANSP_116436	1	-----MDSPRV	6
PHLBR_157963	1	-----MSAPPLI	7
PHLBR_157964	1	-----MPAQLI	7
PHLBR_128210	0	-----M	0
BJEAD_143000	1	-----MASAS	5
BJEAD_45314	1	-----MTSSP	5
PHACH_5574	1	-----MSS	3
BJEAD_241975	1	-----MSTTN	5
PHLBR_29466	1	-----MASA	4
RHOPL_129158	1	-----MSE	3
RHOPL_55972	0	-----	0
BJEAD_227734	1	-----MASPQ	5
PHLBR_27956	1	-----MSHTPS	6
PHACH_6010	1	-----MASPS	5
DICSQ_157363	1	-----MS	2
GANSP_130292	1	-----MS	2
TRAVE_167157	1	-----MAD	3
TRAVE_170473	1	-----MT	2
RHOPL_106935	1	-----MAGA	4
WOLCO_121505	1	-----MS	2
WOLCO_132654	1	-----MANSTNP	7
FOMPI_90445	1	-----MPS	3
WOLCO_25722	1	-----MSCSS	5
FOMPI_129478	1	-----MAISL	5
FOMPI_156775	1	-----MTTS	4
DICSQ_160139	-38	-----MITPSFLQAALLFL--AVAAPQAA-----YATLYQSA-----DAAAAKTS	-3
GANSP_124428	-18	-----MD-----HDAAAQLA	-3
DICSQ_171752	-35	-----MFHSHVRAALL---LSALSSSS---LGALLQSA-----DDAADQLT	-3
GANSP_67648	-30	-----MLATRLRAL--FAYCAAQ-----ALSAIV-----ESPTSEL	-3
DICSQ_102587	-30	-----MFSSPLLCL--YVFCITH-----VLGAIF-----ESPTPEIL	-3
GANSP_67654	-35	-----MLGFGGILRKRPFLLI--LALTTA-----HAVGVV-----FDGPTDIL	-3
GANSP_85135	-30	-----MRGTVLTF--AFSIVAS-----ALGALV-----ERPTQEVL	-3
DICSQ_160546	-29	-----MLHKTGLVL--AFSVAS-----VLAALH-----QGPTAEVL	-3
PHLBR_22550	-31	-----MGHLTALSVLFLSLI-----VASRAAIY-----ESPTQLPS	-2
TRAVE_176148	-31	-----MLSRPLPLGLLCLL-----GQSSALL-----TDHTLVAH	-2
GANSP_117498	-31	-----MLLRHSSLIGLLCFL-----QQGSALL-----ADPSQVAK	-2
DICSQ_182736	-31	-----MSIRSFILALLCFL-----ENGLAALL-----TDHTRLTK	-2
TRAVE_40237	-40	-----MGFKCSLTGLLTLATIFAVQVL-----POARAALY-----TDPALPA	-3
TRAVE_133945	-39	-----MGSKRSPTNLLTTL--TLFAAVL-----PHARAALF-----TDPALPQ	-3
GANSP_130042	-38	-----MFSPNLATTLV--PLALGLVAFP-----TSTRAALF-----TNYADLPT	-3
GANSP_138009	-31	-----MGGLA--TVALLLAAGL-----DPANLAF-----TNPADVLT	-3
DICSQ_103879	-32	-----MRKNLA--IPAFALAANL-----ELTSALF-----TNPADVLT	-3
DICSQ_96414	-32	-----MHRNFL--VLSAVAANL-----GLASAALF-----TDPADILA	-3
FOMPI_40728	-32	-----MRSFLALTALIAPTLW-----RLTEAALY-----TDPALLPQ	-2
RHOPL_55496	-32	-----MLVSLFLSTIAASRW-----SLARGALY-----TDPALPQ	-2
GELSU_118493	-31	-----MRLFLDC--LLAISWA-----PTTICMLH-----TNPSQLEK	-2
RHOPL_54008	0	-----	0
GELSU_137959	-29	-----MFWLTLCGIVLSI-----QCIHSTVL-----TDPQLHK	-2
GELSU_117387	-29	-----MLLPSLISALLIL-----QSAQAEFL-----TDPQLTK	-2
GELSU_84544	-35	-----MVHCHTLRVLAAAGALLVL-----PTVHAALY-----TDPAKLPK	-2
PHACH_37188	1	-----	5
PHACH_135972	-34	-----MALALRP--VFASLITLTA-----TLANAALY-----TDSQLPD	-2
DICSQ_86071	1	-----M	1
BJEAD_156054	-32	-----MAVLR--TICVGLALSTS-----LVQGTFF-----TEFSQLPS	-2
BJEAD_171059	-29	-----MSMSR--LLSLVLLA-----TAVRGAVY-----TDSQLPT	-2
BJEAD_114954	0	-----	0
BJEAD_183896	-29	-----MQMIW--AILWLLAA-----QAALAALY-----TDVNQLPG	-2
BJEAD_114902	-29	-----MGL--RT-ALTFALFS-----SVARGALF-----TDVKQLPS	-2
BJEAD_52991	-31	-----MSVLW--KC-TVLTLLG-----LAHAATPH-----TVPNKORA	-2
BJEAD_245297	-29	-----MRLASPL-VA-----LAGA-----GLASAAYV-----TDIKQLPT	-2
BJEAD_71431	-36	-----MGFARSL-VQ--KIIILAGVVARL-----VSVRAALY-----TDSQLPT	-2
BJEAD_171002	-39	-----MDSSKFR-SKRFAALFASILLNSG-----LTNAVYFF-----TDSQLPA	-2
BJEAD_245049	-38	-----MSPSSRF-SKRF-GVLLAAILANS-----GVANAGLF-----TDSQLPS	-2
BJEAD_66377	-31	-----MRSHALVGAGLLSSL-----GTVALGRI-----LTSPEQIQ	-2
PHACH_6199	1	-----MTDRRI	13
PHLBR_131358	-32	-----MA-PWTYFLVAALGL-SSI-----TPASASIL-----TSPTQIK	-2
PHLBR_164178	-37	-----MSSFR-CLSQFVLLSLLLSL-----LPVSTLY-----QSPSLIT	-2
RHOPL_108489	-48	-----MRAVSLF--L-AA-VPLASV-----AGYSTGRHPDAYHDFHERELLRRNIYDGSIA	-2
PHACH_131961	1	-----MPF	11
RHOPL_128830	-39	-----MDAPTVF--L--VFILAVFTL-----RAQTCPLFPNPPSE-----SDIESFLR	-2



TRAVE 174721 44 DIKVDVIVGSGPTICTYRBDIV--EAGYKVMFMDI--EIDS-----GLKIGAHK---KNTVEYQKNIDKFVNVVIGQMSVSVFVN 119  
PHLBR 123747 11 DMETDVFVLAGSPICANVYKCKV--DAGLRVLMVFEV--GAARHS---SFTSDSMTSKFVPHDASHLRKVEFRPHGVLLGYHK---KNEIEYQKIDDRF---GASSTVSIPTS 111  
PHACH 137275 11 DEHTDVFVLAGSPICATFVKLCV--DANLRVCMVBI---CAA--D---SFTSKPMKGD---PNAPRSVQFPGQVPIGYHK---KNEIEYQKIDDRFVNVVIGKASSTVSIPTS 108  
BJEAD 34622 10 DEHTDVFVLAGSPICATFVKCFV--DAGLHVVMARI---GAA--D---SFTVSRPAKGAT---SPGKPEYSVTFAPGEVIVGYHK---KNEIEYQKIDDRFVNVVIGKASSTVSVPS 111  
GELSU 84792 213 ATPFDYVIVGAGCGGIIADRLS--QNNKKVLLER---GPPSTGTTGGTYVADWAGTN---LTKFDI--GLFESMFDPPDV---YWCSDVT 294  
TRAVE 73596 206 ATPFDYVIVGAGCGGIIADRLS--EAGKVVLLER---GPPSTAETGGTYDAPWAKSAN---LTKFDV--GLFETLFTDTPNF---WCKDIN 287  
DICSQ 153749 207 ATPFDYVIVGAGCGGIIADRLS--EAGKVVLLER---GPPSTAETGGTYDAPWQSAN---LTKFDV--GLFESLFTDNDW---WCKDIT 288  
GANSF 86428 206 ATPFDYVIVGAGCGGIIADRLS--EAGKVVLLER---GPPSTAETGGTYDAPWQSAN---LTKFDV--GLFESMFTDSNAP---WCKDIN 287  
PHLBR 160653 214 AVADYVIVGAGCGGIIADRLS--EAGKVVLLER---GPPSTAETGGNYVAPWAAGSN---LTKFDI--GLFESMFTDPPDV---WCKDIT 297  
BJEAD 45135 215 ATPFDYVIVGAGCGGIIADRLS--EAGKVVLLER---GPPSTQETGGTYVSPWVKAAGSD---LTKFDI--GQFESMFTDTPNY---WCKDVT 298  
PHACH 11098 212 ATPFDYVIVGAGCGGIIADRLS--EAGKVVLLER---GPPSTQETGGTYVAPWATSSG---LTKFDI--GLFESLFTDSNPF---WCKDIT 293  
GANSF 114505 4 PEEVDYVIVGCGGPGAGVAGRIAYADTLKVMILEG---GANNRD---DPWVYR--GIYVRNQDQGVNDKATFYTDQSSSHRGRRSI-- 86  
DICSQ 181599 4 PEEVDYVIVGCGGPGAGVAGRIAYADTLKVMILEG---GANNRD---DPWVYR--GIYVRNQDQGVNDKATFYTDQSSSHRGRRAI-- 86  
TRAVE 144610 4 PEEVDYVIVGCGGPGAGVAGRIAYADTLKVMILEG---GANNRD---DPWVYR--GIYVRNQDQGVNDKATFYEDSMQSSSHRGRRSI-- 86  
PHLBR 128980 4 PEEVDYVIVGCGGPGAGVAGRIAYADTLKVMILEG---GANNRD---DPWVYR--GIYVRNQDQGVNDKATFYTDQSSSHRGRRSI-- 86  
BJEAD 34705 4 PEEVDYVIVGCGGPGAGVAGRIAYADTLKVMILEG---GANNRD---DPWVYR--GIYVRNQDQGVNDKATFYTDQSSSHRGRRSI-- 86  
PHACH 126879 4 PEEVDYVIVGCGGPGAGVAGRIAYADTLKVMILEGTSGHCG---GANNRD---DPWVYR--GIYVRNQDQGVNDKATFYTDQSSSHRGRRSI-- 91  
FOMPI 127556 3 PEEVDYVIVGCGGPGAGVAGRIAYADTLKVMILEG---GANNRD---DPWVYR--GIYVRNQDQGVNDKATFYTDQSSSHRGRRSI-- 85  
GELSU 80773 4 PEEVDYVIVGCGGPGAGVAGRIAYADTLKVMILEG---GANNRD---DPWVYR--GIYVRNQDQGVNDKATFYTDQSSSHRGRRSI-- 86  
RHOPF 118723 3 PEEVDYVIVGCGGPGAGVAGRIAYADTLKVMILEG---GANNRD---DPWVYR--GIYVRNQDQGVNDKATFYTDQSSSHRGRRSI-- 85  
WOLCO 24953 3 PEEVDYVIVGCGGPGAGVAGRIAYADTLKVMILEG---GSNRRD---DPWVYR--GIYVRNQDQGVNDKATFYTDQSSSHRGRRSI-- 85  
TRAVE 43286 8 EEEEDHILAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTLN---DPAHVQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 87  
DICSQ 149587 7 FDEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHIQD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 85  
GANSF 116439 7 FDEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHIQD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 85  
DICSQ 173648 7 FDEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHIQD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 85  
GANSF 116436 7 LDEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTKD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 86  
PHLBR 157963 8 ESEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTKD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 86  
PHLBR 157964 8 EAEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTKD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 86  
PHLBR 128210 2 PSEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTLN---DPAHVQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 87  
BJEAD 143000 6 VQESDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHIQD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 85  
BJEAD 45314 6 PEEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHIQD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 85  
PHACH 5574 4 STEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTKD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 83  
BJEAD 241975 6 NAEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTKD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 85  
PHLBR 29466 5 NAEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTKD---DLAHLQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 84  
RHOPF 129158 4 SLEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPPVRE---DPAHVQ--BARFLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 83  
RHOPF 55972 0 -----GCTSGCVIAGRIADANSLKTLVVEA---GPPVRD---DMAHIV--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 89  
BJEAD 227734 6 RDEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHVQE---NDSFVQ--BARCLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 85  
PHLBR 27956 7 LAEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHVRE---DDAFVQ--BARCLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 86  
PHACH 6010 6 LDEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHVKE---DDNFVQ--BARCLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 85  
DICSQ 157363 3 HNTFDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTRD---DPAHVQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 82  
GANSF 130292 3 QHTFDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTRD---DPAHVQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 82  
TRAVE 167157 4 SATYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTRD---DPAHVQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 82  
PHLBR 170473 3 QATYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTRG---DPAHVQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 82  
RHOPF 106935 5 ELEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTHE---DLAHLQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 84  
WOLCO 121505 8 NMIVDYLIVAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTYE---DLAHLQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 82  
WOLCO 132654 8 VSDYDYLIVAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTYE---DLAHLQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 87  
FOMPI 90445 4 KDEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTYE---DPAHVQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 83  
WOLCO 25722 6 GREYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTLN---DPAHVQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 85  
FOMPI 129478 6 PIEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTLN---DPAHVQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 85  
FOMPI 156775 5 PVEYDILFAGGCTAGTIVAGRIADANSLKTLVVEA---GPHTLN---DPAHVQ--BARYLSHLTPGSKT---AKHVVARBESEHNGRSLI-- 84  
DICSQ 160139 -2 RTKYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSDYN---NNTNRI--BWLAP--ALTSQST---DWNVTTPQVGNDRSIAI-- 75  
GANSF 124428 -2 STPYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSDYN---DNTIQI--BWLAT--VLSHSQF---DWNVTTPQVGNDRSIAI-- 75  
DICSQ 171752 -2 STYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSDYN---NNTNRI--BWLAP--ALTSQST---DWNVTTPQVGNDRSIAI-- 75  
GANSF 67648 -2 TKNYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSDFM---NLNISA--GRSS--ALTSRFR---DWNVTTPQVGNDRSIAI-- 75  
DICSQ 102587 -2 NSKYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSDFM---NNTNLA--GLAT--SLSRSKF---DWNVTTPQVGNDRSIAI-- 75  
GANSF 67654 -2 NSIYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSDFN---NLNITI--BGRAS--SLIRSFT---DWNVTTPQVGNDRSIAI-- 75  
GANSF 85135 -2 DGTYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSDFE---NLNISI--BGRAS--SLIRSFT---DWNVTTPQVGNDRSIAI-- 75  
DICSQ 160546 -2 NKDYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSDFE---NLNISI--BGRAS--SLIRSFT---DWNVTTPQVGNDRSIAI-- 75  
PHLBR 22550 -1 -TKYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSNEG---LDLYIV--EFFTV--FTRSNNPQ---DWNVTTPQVGNDRSIAI-- 76  
TRAVE 176148 -1 -KAYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSNNAAG---PN---VDEIQI--BYFVS---QIDATF---DWNVTTPQVGNDRSIAI-- 77  
PHLBR 117498 -1 -KAYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSNTDGG---INDIQV--BYFVV---DIPPSF---DWNVTTPQVGNDRSIAI-- 77  
DICSQ 182736 -1 -KSYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GSSNIDG---LDIQV--BYFVV---DIPPSF---DWNVTTPQVGNDRSIAI-- 77  
TRAVE 40237 -2 HKEYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDAG---ELSLI--EFLAA--QIQENKPF---DWNVTTPQVGNDRSIAI-- 76  
TRAVE 133945 -2 YKAYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDAG---EPDLEI--ELLAS--QIQENKPF---DWNVTTPQVGNDRSIAI-- 76  
GANSF 130042 -2 SKQYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VFAIQV--BLLAT--GLQENTLY---DWNVTTPQVGNDRSIAI-- 76  
GANSF 138009 -2 NQRYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 76  
DICSQ 103879 -2 NKQYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 76  
DICSQ 96414 -2 DKQYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 76  
FOMPI 40728 -1 -LRYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 76  
RHOPF 55496 -1 -TRDYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
GELSU 118493 -1 -TEYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
RHOPF 54008 1 -----AGTAGLVNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 68  
GELSU 137959 -1 -TEYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
GELSU 117387 -1 -SEYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
GELSU 84544 -1 -SEYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
PHACH 37188 5 -TSDYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 82  
PHACH 135972 -1 -NTYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
DICSQ 86071 1 -DVEDYVIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 79  
BJEAD 156054 -1 -STYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
BJEAD 171059 -1 -TTDYVIVVGGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
BJEAD 114954 1 -----AGAGNVNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 68  
BJEAD 183896 -1 -RSEDYVIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
BJEAD 114902 -1 -STDYVIVVGGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
BJEAD 52991 -1 -DVEDYVIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
BJEAD 245297 -1 -TTRDYVIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
BJEAD 71431 -1 -DTEYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
BJEAD 171002 -1 -TVDYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
BJEAD 245049 -1 -ATYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 77  
BJEAD 66377 -1 -ATYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 76  
PHACH 6199 14 -PDYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 76  
PHLBR 131358 -1 -STDYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 90  
PHLBR 164178 -1 -TEYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 76  
RHOPF 108489 -1 -SSDYVIVVGGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 78  
PHACH 131961 11 -VQDYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 88  
RHOPF 128830 -1 -VDYDYLIVGAGGAGGVLNARIS--EDSTKVVLLER---GPNDEG---VLPTEV--BYLGY--TLQENTLY---DWNVTTPQVGNDRSIAI-- 76

TRAVE\_174721 120 TLVIDTSLPTSQWAS----SFFVRNGSNPEQDPLRNLGGQAVTRVVGGMSTH-----WTCATPRFREQ-----R-----BLLVDD-----T-----DADDA 193  
PHLBR\_123747 112 NVNIPTVDDPSQATLVSFSTPFLFMGRNPAQNPFENLGAEAVTRVVGGMSTH-----WTCATPRLNPHI-----ER-----EVLDDP-----A-----TNEK 190  
PHACH\_137275 109 NNHIATLDDPSVVSNS---LDKPFVSLGKNPAQNPFVNLGAEAVTRVVGGMSTH-----WTCATPEFPAHDFNAPHRER-----EKLSTDA-----A-----EDAR 191  
BJEAD\_34622 112 NENVATLDDPLSFQNT---KSKPFVSLGKNPAQNPFVNLGAEAVTRVVGGMSTH-----WTCATPELNPYI-----ER-----EVLDDPS-----A-----KNQD 187  
GELSU\_84792 295 FYAECILGGGNSV---GALVWYPPDTEFSTAR-----GWPSSWSNHQEYTNAMT---QRLPSTDHP----- 350  
TRAVE\_73596 288 FFACILGGGNSV---GALVWYPNRDFSTAS-----GWPSSWGNHOFIDTLK---QRLPSTDHP----- 343  
DICSQ\_153749 289 FFACILGGGNSV---GALVWYPPADSEFSTEN-----GWPSSWANHOEYTSLQ---QRLPSTDHP----- 344  
GANSF\_86428 288 VFAECILGGGNSV---GALVWYPPDSEFRTAN-----GWPSSWGNHABYTSLK---QRLPSTDHP----- 343  
PHLBR\_160653 298 VFAECILGGGNSV---GALVWYPNRDFSTGV-----GWPSSWNTABEYTNQLI---ARLPSDAP----- 353  
BJEAD\_45135 299 ---GALVWYPNRDFSPSI-----GWPSSWSNHQETPLNKI---QRIPSTHA----- 354  
PHACH\_11098 294 VFAECILGGGNSV---GALVWYPPNDGPFSSV-----GWPSSWTHABYTSLS---SRLPSTDHP----- 349  
GANSF\_114505 86 VFCANILGGGSS---NFMYTRASASDWDFFK---M-EGW---TARDLPELMLKRL---NYQKPVNN----- 141  
DICSQ\_181599 86 ---NFMYTRASASDWDFFK---M-EGW---TANDLPELMLKRL---NYQKPVNN----- 141  
TRAVE\_144610 86 VFCANILGGGSS---NFMYTRASASDWDFFK---T-EGW---TAEDLPELMLKRL---NYQKPTNN----- 141  
PHLBR\_128980 86 ---NFMYTRASASDWDFFK---T-EGW---TAKDLPELMLKRL---NYQKPVNN----- 141  
BJEAD\_34705 86 VFCANILGGGSS---NFMYTRASASDWDFFK---T-EGW---TCKDLPELMLKRL---NYQKPCNN----- 141  
PHACH\_126879 91 ---NFMYTRASASDWDFFK---T-EGW---TCKDLPELMLKRL---NYQKPCNN----- 146  
FOMPI\_127556 85 VFCANILGGGSS---NFMYTRASASDWDFFK---T-EGW---TAQDLPELMLKRL---RYQKPVNN----- 140  
GELSU\_80773 86 VFCANILGGGSS---NFMYTRASASDWDFFK---T-EGW---TCKDLPELMLKRL---NYQKPVNN----- 141  
RHOPL\_118723 85 VFCANILGGGSS---NFMYTRASASDWDFFK---T-EGW---TAKDLPELMLKRL---NYQKPVNN----- 140  
WOLCO\_24953 85 ---NFMYTRASASDWDFFK---T-EGW---TAKDLPELMLKRL---NYQKPVNN----- 140  
TRAVE\_43286 87 VQCCQCVGGSSV---NFMYTRAPASDWDWVYNN---PGW---AFKDLPELMLKRI---TYQVSGVEH----- 148  
DICSQ\_149587 86 VQCCQCVGGSSV---NFMYTRAPASDWDWVLYDN---PGW---SWADLPELMLKAB---TYQVAPGR-D----- 145  
GANSF\_116439 86 VQCCQCVGGSSV---NFMYTRAPASDWDWVSHEN---PGW---SWADLPELMLKAB---TYQVAPGR-D----- 145  
DICSQ\_173648 86 VQCCQCVGGSSV---NFMYTRAPASDWDWVHLYNN---PGW---SFHELLSFLIKAB---TYQVAPGR-D----- 145  
GANSF\_116436 86 VQCCQCVGGSSV---NFMYTRAPASDWDWVHVDN---PGW---GFDDLPELMLKAB---TYQVAPGR-D----- 145  
PHLBR\_157963 87 VMAESCILGGSSV---NFMYTRASASDWDWQTHAN---PGW---GFKDLPELMLKRI---TYQVAPGR-D----- 146  
PHLBR\_157964 87 VLAESCILGGSSV---NFMYTRASASDWDWQTYAN---PGW---GFKDLPELMLKRI---TYQVAPGR-D----- 148  
PHLBR\_128210 81 VFCANILGGGSS---NFMYTRASASDWDWMEKF---DN-SGW---GSKDLPELMLKRL---TYQVAPGR-D----- 139  
BJEAD\_143000 85 VFTBHCVGGSSV---NFMYTRASASDWDWERYGN---KGW---GSKDLPELMLKRL---TYEAPGR-D----- 145  
BJEAD\_45314 85 VFTBHCVGGSSV---NFMYTRASASDWDWETVYDN---KGW---GSKDLPELMLKRL---TYEAPGR-D----- 145  
PHACH\_5574 83 VFCANILGGGSS---NFMYTRASASDWDWQKYEN---PGW---GAKDLPELMLKRI---TYEAPGR-D----- 143  
BJEAD\_241975 85 VFTBHCVGGSSV---NFMYTRASASDWDWENTFFKN---PGW---GSKDLPELMLKRI---TYEAPGR-D----- 145  
PHLBR\_29466 84 VFTBHCVGGSSV---NFMYTRASASDWDWMEKFFNN---PGW---GSDVIVEMIKRI---TYQVAPGR-D----- 144  
RHOPL\_129158 83 VFAECILGGGNSV---NFMYTRASASDWDWELKLYSN---PGW---GSADLPELMLKRI---TNQALPK----- 142  
RHOPL\_55972 69 VSHAQCLGGASS---NFMYTRASASDWDWTRVYKN---PGW---ASADLPELMLKRI---TYQVAPGR-D----- 128  
BJEAD\_227734 85 VTCANILGGGSS---NFMYTRASASDWDWAEHKN---PGW---GAKDLPELMLKRI---TYQVAPGR-D----- 145  
PHLBR\_27956 86 VTCANILGGGSSV---NFMYTRASASDWDWENLYGN---PGW---GSKDLPELMLKRI---TYQVAPGR-E----- 146  
PHACH\_6010 85 VTCANILGGGSSV---NFMYTRASASDWDWQVHKN---PGW---GARDLPELMLKRI---TYQVAPGR-D----- 145  
DICSQ\_157363 82 VFCANILGGGSS---NFMYTRASASDWDWVTYGN---PGW---SSTLPELMLKRI---TYEAPGR-D----- 141  
GANSF\_130292 82 VFCANILGGGSS---NFMYTRASASDWDWVHGN---PGW---SSKDLPELMLKRI---TYEAPGR-D----- 141  
TRAVE\_167157 83 VFCANILGGGSSV---NFMYTRASASDWDWVTYGN---KGW---SAADLPELMLKRI---TYQVAPGR-D----- 142  
TRAVE\_170473 82 VFCANILGGGSSV---NFMYTRASASDWDWENLYGN---PGW---GSADLPELMLKRI---TYEAPGR-D----- 141  
RHOPL\_106935 84 VESHCILGGGSSV---NFMYTRASASDWDWVNYGN---PGW---GSEDLPELMLKRI---K----- 136  
WOLCO\_121505 82 VFCANILGGGSSV---NFMYTRASASDWDWESYDN---PGW---GSRDLPELMLKRI---TYQVAPGR-D----- 141  
WOLCO\_132654 87 VFCANILGGGSSV---NFMYTRASASDWDWEMKMGW---PGW---GCTSLPELMLKRI---TYQVAPGR-D----- 146  
FOMPI\_90445 83 VFCANILGGGSSV---NFMYTRASASDWDWETIYGN---AGW---SSEDLPELMLKRI---TYQVAPGR-D----- 142  
WOLCO\_25722 85 VFCANILGGGSSV---NFMYTRASASDWDWESLHGN---PGW---GSKDLPELMLKRI---TYQVAPGR-D----- 144  
FOMPI\_129478 85 VFCANILGGGSSV---NFMYTRASASDWDWEMKLYSN---KGW---GSRDLPELMLKRI---TYQVAPGR-D----- 144  
FOMPI\_156775 84 VLSQCLGGSSV---NFMYTRASASDWDWETVWGN---EGW---SSRELPELMLKRI---TYQVAPGR-D----- 143  
DICSQ\_160139 76 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---SGW---NWNMNFYFLKRI---DFTNSPQVVS-----AST 139  
GANSF\_124428 76 YARCKVLGGSSV---NFMYTRASASDWDWVSAVD---DCW---SWSILPELMLKRI---K----- 126  
DICSQ\_171752 76 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---NWSNLSYAKLRI---AFONSQVNVN-----ATS 139  
GANSF\_67648 76 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---KGW---SNTLPELMLKRI---KMTAPDGHN-----TTG 139  
DICSQ\_102587 76 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---EGW---SNTLPELMLKRI---NMTTPTDGHN-----TTG 139  
GANSF\_67654 76 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---EGW---SNTLPELMLKRI---RMTAPDGHN-----PSG 139  
GANSF\_85135 76 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---RMTAPDGHN-----TTG 139  
DICSQ\_160546 76 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---RMTAPDGHN-----TTG 139  
PHLBR\_22550 77 YLRKMLGGSSV---NFMYTRASASDWDWVAVTGD---PGW---SMDALPELMLKRI---HWMPDGHN-----TTG 140  
TRAVE\_176148 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---TLTTPADGHN-----TVG 141  
GANSF\_117498 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---TLTTPADGHN-----TTG 141  
DICSQ\_182736 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---TLTTPADGHN-----TTG 141  
TRAVE\_40237 77 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---HLVPPADGHN-----TTG 139  
TRAVE\_133945 77 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---HLVPPADGHN-----TTG 140  
GANSF\_130042 77 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---QFVPPADGHN-----TSN 140  
GANSF\_138009 77 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---HLVPPADGHN-----TTG 140  
DICSQ\_103879 77 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---HLVPPADGHN-----TTG 140  
DICSQ\_96414 77 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---HLVPPADGHN-----TTG 140  
FOMPI\_40728 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---HLVPPADGHN-----TTG 140  
RHOPL\_55496 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---HLVPPADGHN-----TTG 140  
GELSU\_118493 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
RHOPL\_54008 69 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 132  
GELSU\_137959 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---QLVPPADGHN-----TTG 140  
GELSU\_117387 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
GELSU\_84544 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
PHACH\_37188 83 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 146  
PHACH\_135972 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
DICSQ\_86071 80 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
BJEAD\_156054 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
BJEAD\_171059 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 139  
BJEAD\_114954 69 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 133  
BJEAD\_183896 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 169  
BJEAD\_114902 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 138  
BJEAD\_52991 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 139  
BJEAD\_245297 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
BJEAD\_71431 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
BJEAD\_171002 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
BJEAD\_245049 78 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
BJEAD\_66377 77 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 140  
PHACH\_6199 91 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 154  
PHLBR\_131358 77 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 139  
PHLBR\_164178 77 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 139  
RHOPL\_108489 79 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 139  
PHACH\_131961 89 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 156  
RHOPL\_128830 77 YARCKVLGGSSV---NFMYTRASASDWDWVAVTGD---DCW---SNTLPELMLKRI---SLVAPPDGHN-----TTG 149

TRAVE 174721 194 EWDRLYTKAESYFKTGTDFQKESIRHNLVNLKLAEBEY--KQORDFQOIPLAATR-RSPTFVW--SSANTVFDLQNRPTDAPNERFNLFPVACERVVRNT-- 290
PHLBR 123747 191 IWDLYTAEBEELIGTSTQFNKSRQTLVLEALGE--TNRARFVPLPLACHRLDDPGYVW--HATDRILEELF--TDLKSKRFTLMTNHCIRKUSVMP-- 284
PHACH 132725 192 ICKDLYAQAKELIGTSTQFNKSRQTLVLEALGE--TNRARFVPLPLACHRLDDPGYVW--HATDRILEELF--TDPVKGRFTLITNHRCKRFLVFK-- 290
BUEAD 34622 188 LWAALYKARALIGTSTQFNKSRQTLVLEALGE--TNRARFVPLPLACHRLDDPGYVW--HATDRILEELF--TDPVKGRFTLITNHRCKRFLVFK-- 283
GELSU 84792 351 ---STDGQ---RYLEQSAQVAM-QLLNSQQYS--QATINDNPKSKDH--VYGS--AFDFLNGRRGGPVATYF-QTAKARBNFYKYDYVLSSVVRNG-- 434
TRAVE 73596 344 ---STDGQ---RYLEQSAQVAM-QLLNSQQYS--QATINDNPKSKDH--VYGS--AFDFLNGRRGGPVATYF-QTAKARBNFYKYDYVLSSVVRNG-- 428
DICSQ 153749 345 ---STDGQ---RYLEESANVVV-QLLNSQQYS--NITINDNPKSKDH--VYGS--AFDFLNGRRGGPVATYF-QTAKARBNFYKYDYVLSSVVRNG-- 428
GANSF 86428 344 ---STDGQ---RYLEESAAIVA-QLLNSQQYS--NITINDNPKSKDH--VYGS--AFDFLNGRRGGPVATYF-QTAKARBNFYKYDYVLSSVVRNG-- 429
PHLBR 160653 354 ---STDGQ---RYLEESATLVG-QLLNSQQYS--QATINDNPKSKDH--VYGS--AFDFLNGRRGGPVATYF-QTAKARBNFYKYDYVLSSVVRNG-- 437
BUEAD 45135 355 ---STDGQ---RYLEQSAQVAM-QLLNSQQYS--QATINDNPKSKDH--VYGS--AFDFLNGRRGGPVATYF-QTAKARBNFYKYDYVLSSVVRNG-- 438
PHACH 11098 350 ---STDGQ---RYLEQSAQVAM-QLLNSQQYS--QATINDNPKSKDH--VYGS--AFDFLNGRRGGPVATYF-QTAKARBNFYKYDYVLSSVVRNG-- 433
GANSF 114505 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 236
DICSQ 181599 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 236
TRAVE 144610 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 236
PHLBR 128980 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 232
BUEAD 34705 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 236
PHACH 126879 146 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 243
FOMPI 127556 140 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 235
GELSU 80773 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 236
RHOPJ 118723 140 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 235
WOLCO 24953 140 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 235
TRAVE 43286 148 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 236
DICSQ 149587 145 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 235
GANSF 116439 145 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 243
DICSQ 173648 145 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 243
GANSF 116436 145 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 243
PHLBR 157963 146 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 244
PHLBR 157964 146 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 245
PHLBR 128210 139 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 230
BUEAD 143000 145 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 239
BUEAD 45314 145 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 239
PHACH 5574 143 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 238
BUEAD 241975 145 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 240
PHLBR 29466 144 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 245
RHOPJ 129158 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 238
RHOPJ 55972 128 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 223
BUEAD 227734 145 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 241
PHLBR 27956 146 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 239
PHACH 6010 145 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 238
DICSQ 157363 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 237
GANSF 130292 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 236
TRAVE 167157 142 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 238
TRAVE 170473 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 242
RHOPJ 106935 136 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 239
WOLCO 121505 141 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 241
WOLCO 132654 146 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 242
FOMPI 90445 142 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 237
WOLCO 25722 144 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 239
FOMPI 129478 144 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 233
FOMPI 156775 143 ---DTHGVDGELTAINSGQIQPVAQ-DFPRAAHAI---GVYSDIIDIQLKT--AHGAEIW---AKYINRHTQRRSDAATAVHVSVMVDQNSNVLRCNARVSRVLFDA-- 238
DICSQ 160139 140 KFPVSLNHTTQBLGAGLPEVTLATDN-IGLQAQQLSA--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 238
GANSF 124428 137 ---AAVHGKNGEAGAGLPGVSLADTDQ-LGNAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 235
DICSQ 171752 140 KFPVSLNHTTQBLGAGLPEVTLATDN-IGLQAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 238
GANSF 67648 140 QFIPALSHRGTREVDISVPLSLADTDQ-LGNAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 238
DICSQ 102587 140 QFNPALENDQVVDISVPLSLADTDQ-LGNAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 238
GANSF 67654 140 QFNPALENDQVVDISVPLSLADTDQ-LGNAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 237
GANSF 85135 140 QFNPALENDQVVDISVPLSLADTDQ-LGNAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 237
DICSQ 160546 140 QFNPALENDQVVDISVPLSLADTDQ-LGNAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 237
PHLBR 22550 141 QFNPALENDQVVDISVPLSLADTDQ-LGNAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 239
TRAVE 176148 142 QFNPALENDQVVDISVPLSLADTDQ-LGNAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 240
GANSF 117498 142 QFNPALENDQVVDISVPLSLADTDQ-LGNAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 240
DICSQ 182736 142 QFNPALENDQVVDISVPLSLADTDQ-LGNAQQLS--EPAYNDQVNSGDM--IGFSWT--PF--SIQ-NGARSSATGVL-QPALRSDNDVUNVNAQVTKLVQTTTS-- 240
TRAVE 40237 140 ELLPNLHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 238
TRAVE 133945 141 ELLPNLHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--K 238
GANSF 130042 141 ELLPNLHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--K 239
GANSF 138009 141 ELLPNLHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--K 241
DICSQ 103879 141 QIDQIHTGRBLNLTANNPYPIDS-HVINTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 241
DICSQ 96414 141 QIDQIHTGRBLNLTANNPYPIDS-HVINTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 241
FOMPI 40728 141 EIDVSLHGHKGNVNLASATPIDG-RITHTHDLQ--LFPYNDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 241
RHOPJ 55496 141 KVDSSVHGNGHNLISLEFPVNDIQD-RIGMNTLTPP--VDFVNDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 241
GELSU 118493 141 ELLPNLHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 240
RHOPJ 54008 133 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 240
GELSU 137959 141 ELLPNLHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 242
GELSU 117387 141 ELLPNLHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 240
GELSU 84544 141 ELLPNLHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 241
PHACH 37188 147 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 244
PHACH 435972 141 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 238
DICSQ 86071 143 LVPNADHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 241
BUEAD 156054 141 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 237
BUEAD 171059 140 LVPNADHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 236
BUEAD 114954 134 LVPNADHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 230
BUEAD 183896 140 LVPNADHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 236
BUEAD 114902 139 LVPNADHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 235
BUEAD 52991 140 NFDSSRPHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 237
BUEAD 245297 141 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 238
BUEAD 71431 141 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 238
BUEAD 171002 141 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 238
BUEAD 245049 141 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 237
BUEAD 66377 141 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 242
PHACH 6199 155 FVPSVHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 251
PHLBR 131358 140 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 237
PHLBR 164178 140 QVDPVLRHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 238
RHOPJ 108489 146 EYNSRPHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 243
PHACH 131961 157 YAMKPDLEHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 254
RHOPJ 128830 150 KILPKVDHGTSGBLNLSLPEAPLPSDS-RVIQTTQLS--EPFNEDMSSGNP--LIGWV--QS--TIG-HGVRSSAATFLAETLTKLRSNDVIGRTRILQTER--D 247

TRAVE\_174721 291 ----SNSEFSLHIHDLISG-----DRFEIKADVFLVLT-----CAVHNAQTLVNSGFQOL-----GRPDPANPPRLPSLISYITHEQSLVFCQVMSTELIDSVKSDMI 381
PHLBR\_123747 285 RLKGP-----GGEQDYQYAYVIAC-----GAVGTAQVLANSPREPELID-----GENEDDKTIIETPLTINLSEYIETQEMTCQVVLNDAIAKVFTE 368
PHACH\_137275 291 YRPGEEENEDYALVEDLLPHMQNPGNPASVKKIYARYSVVAC-----GAVAHAVYVANSHTPPDDVVIPPPGGEKGSQGGGERDATTPTPLMLMLSKYITHEQMTFCQVVLNDSLEMEVVRNP 406
BUEAD\_34622 284 FNPQQPNEGYAEVESLLPRTEGRRSST-FAIRAKIYVIAC-----GAVGSAVLANSNVNPETKGFPPYD-----PNRDMTEDIDTRLMPNLERMYTQEMTCFQVVLNGLINSVDD 393
GELSU\_84792 435 ----SQILGVTNTMTA-IGPN-----GFIPILNPNGRVLLSA-----GSFGTPRILFQSGIGPTDMQIQVQNAQAA--ANLPPQSEWNLPL-VCGMVSNDNSINLVFTHPS--IDAYDNW 534
TRAVE\_73596 428 ----STILGVRTNDMT-LGPD-----GIVPLNPNGRVLLSA-----GSFGTPRILFQSGIGPTDMQIQVQNAQAA--ANLPPQSEWNLPL-VCGMVSNDNSINLVFTHPS--IDAYDNW 527
DICSQ\_153749 429 ----ATTIGVRTNDTS-LGPN-----GIVPLNPNGRVLLSA-----GSFGTPRILFQSGIGPTDMQIQVQNAQAA--ANLPPQSEWNLPL-VCGMVSNDNSINLVFTHPS--IDAYDNW 528
GANSF\_86428 430 ----STIGVRTNDTS-LGPN-----GIILPLNPNGRVLLSA-----GSFGTPRILFQSGIGPTDMQIQVQNAQAA--ANLPPQSEWNLPL-VCGMVSNDNSINLVFTHPS--IDAYDNW 527
PHLBR\_160653 438 ----SQITGVQNTNDTS-LGPN-----GVVPLTPNGRVLISA-----GSFGTPRILFQSGIGPTDMQIQVQNAQAA--ANLPPQSEWNLPL-VCGMVSNDNSINLVFTHPS--INSDYDNW 537
BUEAD\_45135 439 ----SQITGVQNTNDTS-LGPN-----GIILPLTPNGRVLISA-----GSFGTPRILFQSGIGPTDMQIQVQNAQAA--ANLPPQSEWNLPL-VCGMVSNDNSINLVFTHPS--IDAYDNW 538
PHACH\_11098 434 ----SQILGVTNDPT-LGPN-----GFIPVTPKGRVLLSA-----GAFGSPRILFQSGIGPTDMQIQVQSNPTAA--AALPPQSQWNLPL-VCGMVSNDNSINLVFTHPS--IDAYENW 533
GANSF\_114505 236 ----NNKAVGVAVVPSRNRANNADV-----LETIVKARKMVLSS-----GTLGTPOLLERSGVGNAELNKLNLPVV-----SFLGCVGEYQDHYTTLSLYRWSN-ETQITDDF 332
DICSQ\_181599 236 ----NNKAVGVAVVPSRNRANNQV-----VETIVKARKMVLSS-----GTLGTPOLLERSGVGNAELNKLNLPVV-----SFLGCVGEYQDHYTTLSLYRWSN-ETSITDDF 332
TRAVE\_144610 236 ----NNKAVGVAVVPSRNRTHGGQV-----QETIVKARKMVLSS-----GTLGTPOLLERSGVGNAELNKLNLPVV-----SFLGCVGEYQDHYTTLSLYRWSN-ETQITDDF 332
PHLBR\_128980 232 ----NNKAVGVAVVPAKRANHNEI-----QETIVKARKMVLSS-----GTLGTPOLLERSGVGNGDLRQLGKVV-----SFLGCVGEYQDHYTTLSLYRWSN-ETVITDDF 328
BUEAD\_34705 236 ----NNKAVGVAVVPSRNRANAGEV-----QETIVKARKMVLSS-----GTLGTPOLLERSGVGNGDLRQLGKVV-----SFLGCVGEYQDHYTTLSLYRWSN-ETMIDDDF 332
PHACH\_126879 243 ----NNKAVGVAVVPSRNRTHGGKL-----HETIVKARKMVLSS-----GTLGTPOLLERSGVGNGDLRQLGKVV-----SFLGCVGEYQDHYTTLSLYRWSN-ETSITDDF 339
FOMPI\_127556 235 ----NNKAVGVAVVPSRNRASGGKV-----QETIVKARKMVLSS-----GTLGTPOLLERSGVGNAELRDLGKVV-----SFLGCVGEYQDHYTTLSLYRWSN-ETETDDF 331
GELSU\_80773 236 ----NNKAVGVAVVPSRNRHGGKV-----VETIVKARKMVLSS-----GTLGTPOLLERSGVGNGEMNQLGKVV-----SFLGCVGEYQDHYTTLSLYRWSN-DTITDDF 332
RHOPL\_118723 235 ----NNKAVGVAVVPSRNRTHSGKV-----HETIVKARKMVLSS-----GTLGTPOLLERSGVGNAELRDLGKVV-----SFLGCVGEYQDHYTTLSLYRWSN-DTQITDDF 331
WOLCO\_24953 235 ----NNKAVGVAVVPSRNRTHGGKV-----QETIVKARKMVLSS-----GTLGTPOLLERSGVGNAELRDLGKVV-----SFLGCVGEYQDHYTTLSLYRWSN-ETETDDF 331
TRAVE\_43286 246 ----GRAVGEVYVPRNPRINADADD-----VLHIAKARKMVLSSA-----GTFGSPALLERSGIGAPGIDKAVGKVPIL-----VDLPGVGENYDQHVLFFPYFAAE-DSELDIGI 341
DICSQ\_149587 243 ----GRATGVEYVFRNAQVFPDDVD-----TIRVAQSKQLVLSA-----GAFGSAALLERSGIGKDKVBERNGEQK-----VNLPGVGENYDQHVLFFPYFAAE-DSELDIGI 330
GANSF\_116439 235 ----GRAAGVEYVFRNAQVLPDASD-----APRTARARKMVLSSA-----GAFGSAALLERSGIGKDKVBERNGEQK-----VNLPGVGENYDQHVLFFPYFAAE-DAEIDIGI 338
DICSQ\_173648 243 ----GKATGVEYVFLHNLISDDAT-----TPRIVRARKMVLSSA-----GTFGSPALLERSGIGSKDIDRNSKQV-----VDLPGVGENYDQHVLFFPYFAAE-DADLDIGI 338
GANSF\_116436 243 ----GKATGVEYVFLNSQVLPDAD-----MPRIARARKMVLSSA-----GAFGSPALLERSGIGAKDIDARNDKQV-----VDLPGVGENYDQHVLFFPYFAAE-DADLDIGI 338
PHLBR\_157963 244 ----NRAGVEYVQWNSVQLSDVDC-----EVHTVARKMVLSS-----GAFGTPALLERSGIGKAVLEKINLPK-----VDLPGVGENYDQHVLFFPYFAAE-DTKLDDAI 339
PHLBR\_157964 245 ----DRAGVEYVQRWNGHLPEADS-----DVHTVARKMVLSS-----GTFGSPALLERSGIGAKSLEKLEKLPVK-----VNLPGVGENYDQHVLFFPYFAAE-DTQFDPAI 340
PHLBR\_128210 230 ----KRAVGEVYVPRNPRNMTTGS-----EVTVFRARKMVLSSA-----GSLGSPVLLERSGIGAKSVBEKGVKPI-----VDLPGVGENYDQHVLFFPYFAAE-EQSLDDEI 325
BUEAD\_143000 233 ----NRAGVEYVPRNPRVYNATTS-----KVTARARKMVLSS-----GSLGSPVLLERSGIGAKSVEKAQVVK-----VDLPGVGENYDQHVLFFPYFAAE-ETSSIDAI 335
BUEAD\_45314 239 ----TRAVGEYVPRNPRVYNATG-----KVTARARKMVLSS-----GSLGSPVLLERSGIGAKSVEKAQVVK-----VDLPGVGENYDQHVLFFPYFAAE-ETSSIDAI 334
PHACH\_5574 238 ----KRAVGEYVQNKVFPVPEAK-----DILLVAKRMLVLSA-----GTFGSPVLLERSGIGAKVBEKAQVQPL-----VDLPGVGENYDQHVLFFPYFAAE-DSELDIGI 333
BUEAD\_241975 240 ----KRAVGEYVQNPFRNPNATK-----DVLVIARARKMVLSSA-----GTFGSPVLLERSGIGAKVBEKAQVQPL-----VDLPGVGENYDQHVLFFPYFAAE-DAEIDIGI 335
PHLBR\_29466 245 ----GRAVGEYVPRNPRVYNATK-----DVLIAKARKMVLSSA-----GTFGTPVLLERSGIGAKHIEKYGKQI-----VDLPGVGENYDQHVLFFPYFAAE-ESDLDIAI 340
RHOPL\_129158 238 ----TRATGVEYVFNARYNPDDEK-----TPRIARARKMVLSSA-----GTFGTPSVLLERSGIGAKRIRKALGKVT-----SFLGCVGENYDQHVLFFPYFAAE-NADLDIGI 333
PHLBR\_155972 223 ----GRAVGEYVPLAKSRFHPQETQ-----TPRIARARKMVLSSA-----GTFGSPVLLERSGIGAEARLEKLDVDM-----VDLPGVGENYDQHVLFFPYFAAE-EDLDLGI 318
BUEAD\_227734 241 ----TRATGVEYVFNPNIPQNASME-----GRTVTRARKMVLSSA-----GTFGSPVLLERSGIGKRDVBEAAGVVK-----VDLPGVGENYDQHVLFFPYFAAE-DSFDLGI 336
PHLBR\_27956 239 ----KRAVGEYVPRNPRVQPNASPE-----AKVVRARKMVLSSA-----GTFGSPVLLERSGIGKDVBEKAQVVK-----VDLPGVGENYDQHVLFFPYFAAE-DSFDLGI 334
PHACH\_6010 238 ----KRAVGEYVANPIQFPEASKD-----LVRTVARKMVLSSA-----GTFGSPVLLERSGIGAKVBEKAQVQPL-----VDLPGVGENYDQHVLFFPYFAAE-DSFDLGI 334
DICSQ\_157363 237 ----QOATGVEYVSNPNKRYSDEAQQ-----GVLSAIRARKMVLSSA-----GTFGSPVLLERSGIGKSVBEKAQVQI-----VDLPGVGENYDQHVLFFPYFAAE-EKLDLGI 332
GANSF\_130292 236 ----GRATGVEYVPRNKRFPHASL-----EVSISARARKMVLSSA-----GAFGSAALLERSGIGAKTVTKVGKQI-----VDLPGVGENYDQHVLFFPYFAAE-GTDLDIGI 331
TRAVE\_167157 238 ----GRAVGEYVPIPTNRFPDAPK-----EVLTAARARKMVLSSA-----GAFGSAALLERSGIGSGEATDKVGKQV-----VDLPGVGENYDQHVLFFPYFAAE-TVNLDDAI 333
PHACH\_170473 242 ----KRAVGEYVPIPTNRFPDAPK-----EVLTAARARKMVLSSA-----GAFGSAALLERSGIGSGEATDKVGKQV-----VDLPGVGENYDQHVLFFPYFAAE-DVHLDIGI 337
RHOPL\_106935 239 ----SRAGVEYVPRNPNKLNDDTTQ-----MVRTARARKMVLSSA-----GAFGPGALGDRQREAPAGANDRVSC-----RPSRYHVLVLPYPMAD-EAELDGI 324
WOLCO\_121505 241 ----NKRAGVEYVPIPNISVNGLELLP-----QVHTAHARKMVLSSA-----GAFGSAALLERSGIGAKSLEKLEKLDVK-----VDLPGVGENYDQHVLFFPYFAAE-NDLNLDGI 337
WOLCO\_132654 242 ----TRAVGEYVDPKNSVFDVQ-----QYVVARARKMVLSSA-----GTFGSPVLLERSGIGAESLQGLGQI-----VDLPGVGENYDQHVLFFPYFAAE-SVPLDGI 337
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WOLCO\_25722 233 ----ERAVGEYVLPNTRFRPEAAS-----GERIVRARKMVLSSA-----GAFGSAALLERSGIGTSSLVPLGTL-----VDLPGVGENYDQHVLFFPYFAAE-EAELDGI 335
FOMPI\_129478 239 ----GRATGVEYVPLNPLRTPTEEQ-----TPRIARARKMVLSSA-----GAFGSAALLERSGIGQRRARQALGIDV-----SFLGCVGENYDQHVLFFPYFAAE-SAELDGI 328
FOMPI\_156775 238 ----GRATGVEYVPLNPRFRNEEQ-----TIRARARKMVLSSA-----GAFGSAALLERSGIGERNRQALGIDV-----VDLPGVGENYDQHVLFFPYFAAE-RAELDGI 333
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TRAVE\_176148 241 SATPTFLGVELAQTA-----TG-----PRVQVTKARKMVLSSA-----GSLGTPHLLERSGIGDAATHALGKPK-----VNLPAVGTNMDQHVLFFPYFAAE-NDLNLDGI 329
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GELSU\_137959 241 DRLPNFNTVEAQSP-----TG-----KRMNTPARKMVLSSA-----GSVGTPOLLERSGIGNATLERSVVKPI-----VNLSDVGENYDQHVLFFPYFAAE-NDSLESA 331
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PHACH\_37188 245 SGQPSFRSSTLKS-----KA-----KRSTATARKMVLSSA-----GAVNTPOLLERSGIGDRQAASVGTVP-----VNLSDVGENYDQHVLFFPYFAAE-NMLDL 335
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BUEAD\_171059 237 HGLPTFKVBEFAPS-----DA-----HRSVVTARKMVLSSA-----GALGSPOLLERSGIGDHDHAAALGKPK-----VNLSDVGENYDQHVLFFPYFAAE-NMFDYDL 327
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BUEAD\_183896 237 KGLPTFKVBEFAPS-----DS-----PRYVTSKKEKILISA-----GAVNTPOLLERSGIGDREELIANGKPK-----VNLSDVGENYDQHVLFFPYFAAE-ADVFD 327
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BUEAD\_52991 238 HGTPEFTVBEFAASQ-----NG-----PRQNTVARKMVLSSA-----GAVNTPOLLERSGIGDREELIANGKPK-----VNLSDVGENYDQHVLFFPYFAAE-TNFDV 328
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BUEAD\_71431 239 RNPSPFKVBEFAASA-----SG-----RHRTVTKKILISA-----GTIGTAOLLERSGIGDREELIANGKPK-----VNLSDVGENYDQHVLFFPYFAAE-TEGDDT 329
BUEAD\_171002 239 NGLPSFMKBEFARDA-----LS-----ARSVVTKKILISA-----GSVGTPOLLERSGIGDREELIANGKPK-----VNLSDVGENYDQHVLFFPYFAAE-NMFDYDL 329
BUEAD\_245049 238 GTPSPFMKBEFARSA-----TS-----KHTVTKKILISA-----GSMGTPOLLERSGIGDREELIANGKPK-----VNLSDVGENYDQHVLFFPYFAAE-NMFDYDL 328
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PHACH\_131961 255 GDLRRVAVBEYLKGG-----I-----QLRIDNVKRDVILAA-----GTLGTPOLLERSGIGNATLERSVVKPI-----VNLSDVGENYDQHVLFFPYFAAE-R 338
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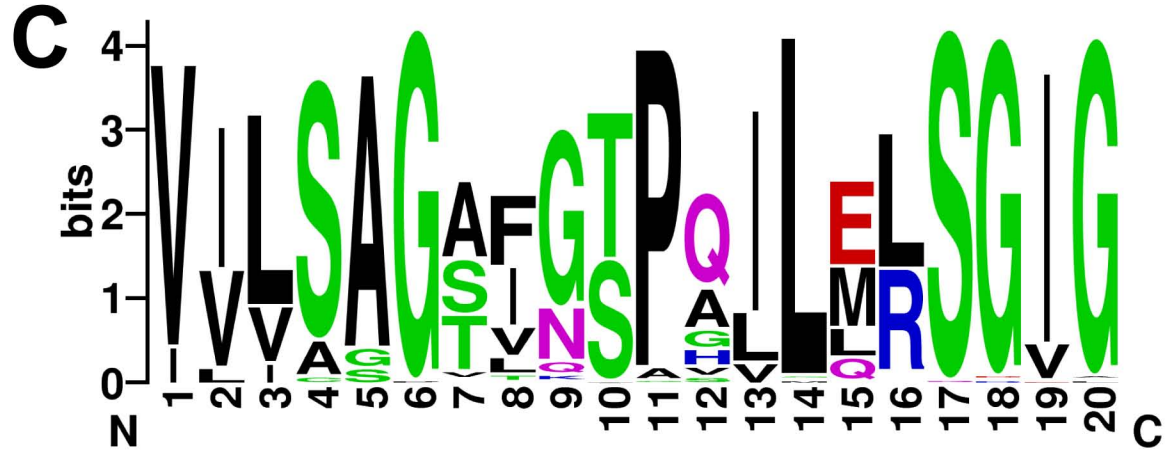
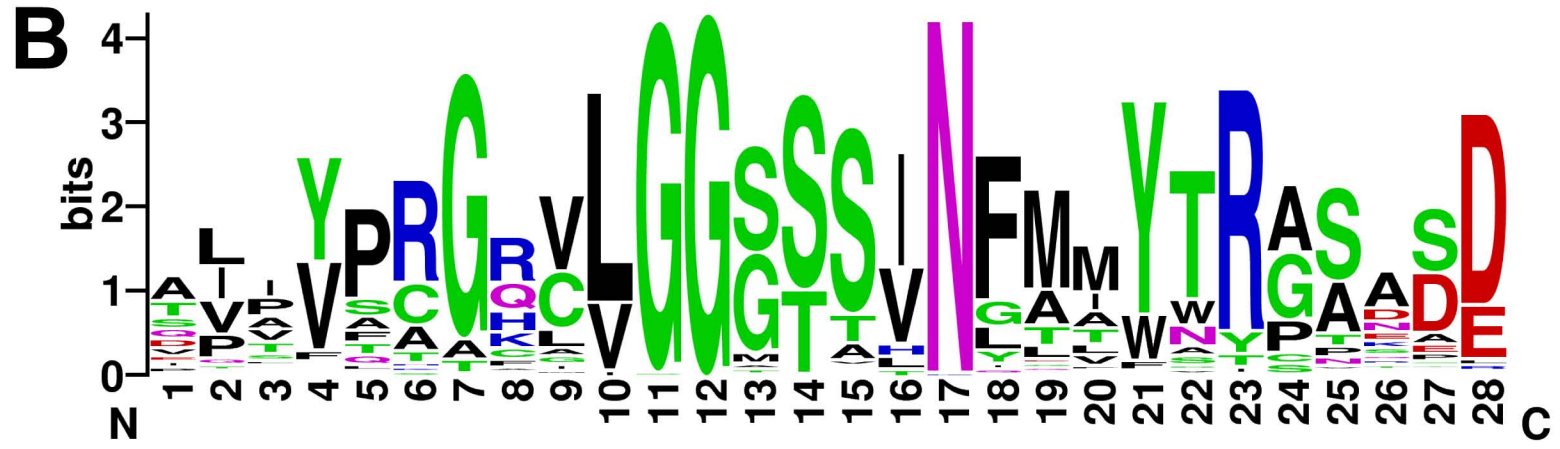
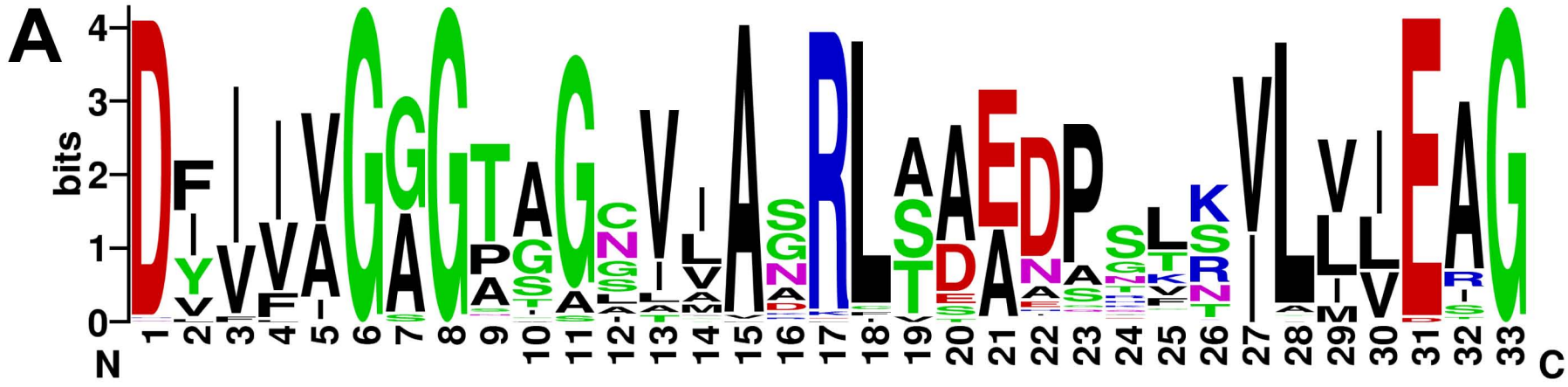
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PHACH\_137275 407 -----PWPGLDWKEK-----VARHVEAFPNDPI-I--PDRDPEP-----QVITKF 445  
BJEAD\_34622 394 -----LENKPAWREG-----VEKHKADNPDPPI-I--PDRDPEP-----QVITPF 432  
GELSU\_84792 535 ADVWTDPR-----PADAQVYLAS-QSOFVAGASP--KLNFWRAYGSDGI-----QRSAGQ-TVRGAAVS- 591  
TRAVE\_73596 528 ADVWSNFR-----PADAQVYLS-RSGLVLAGASP--KLNFWRAYGSDGI-----TRYAQQ-TVRGAAVS- 584  
DICSQ\_153749 529 ADVWSDFR-----PADAQVYLS-RSOFVAGASP--KLNFWRAYGSDGI-----TRYAQQ-TVRGAAVS- 585  
GANSF\_86428 528 ADVWSDFR-----PADAQVYLD-RSOFVAGASP--KLNFWRAYGSDGI-----TRYAQQ-TVRGAAVS- 584  
PHLBR\_160653 538 ADVWTDPR-----SADAQVYLS-RSGLVLAGASP--KLNFWRAYGSDGI-----TYAQQ-TVRGAAVS- 593  
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WOLCO\_121505 338 VINDPAI-----EKWSTQVLD-GTGLMAHNAEAGKLRPSRELAIG--BEN--ERWSEFYANBPKSILW 403  
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DICSQ\_102587 330 HNAT-----LASBQLQVNEAN-GTGLMGL-PPTNQVFWRADPS--F--KLNATDPSA--G-PTSHEFLIF 390  
GANSF\_67654 329 HNAT-----LAAEAFSLQVNET-GTGLPLS-LGATQVGLRIPAEATFF-RQLGVDDPSA--G-RTSAHFELP 391  
GANSF\_85135 327 HNAT-----FAAQALQVQV-GTGLPLV-GTGSQVGLRIPVQIGIF-QSFGISDPSA--G-PTSHEFLIF 389  
DICSQ\_160546 329 HNAT-----LAAEALQVQV-GTGLPLS-LGATQVGLRIPAEATFF-RQLGVDDPSA--G-RTSAHFELP 391  
PHLBR\_22550 316 HNAT-----FRNELLQVNET-HGGRVLD-AYSTWTGFSRMPNASIF-E--THPDPA--G-PTSHEFLIF 376  
TRAVE\_176148 332 HNAT-----LNNQLLQVDSK-QQVANNPQGNQVGFRLPNSSVL-K--QVGDPA--G-PTSHEFLIF 393  
GANSF\_117498 330 HNAT-----LNNQLLQVDSK-QQVANNPQGNQVGFRLPNSSVL-K--QVGDPA--G-PTSHEFLIF 393  
DICSQ\_182736 332 HNAT-----IFNAAVQVNET-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 393  
TRAVE\_40237 332 HNAT-----IFNAAVQVNET-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 393  
TRAVE\_133945 333 HNAT-----FAGALVQVNET-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 393  
GANSF\_130042 335 HNAT-----LNDLLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 395  
GANSF\_138009 335 HNAT-----LNDLLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 395  
DICSQ\_103879 335 HNAT-----LNFELLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 395  
DICSQ\_96414 335 HNAT-----LNFELLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 395  
FOMPI\_40728 333 HNAT-----LATELQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 394  
RHOPL\_55496 332 HNAT-----LAAEALQVNET-GTGLPLV-GTGSQVGLRIPVQIGIF-QSFGISDPSA--G-PTSHEFLIF 390  
GELSU\_118493 332 HNAT-----VATELQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 386  
RHOPL\_54008 324 HNAT-----LATELQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 384  
GELSU\_137959 332 HNAT-----LTLLELQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 389  
GELSU\_117387 332 HNAT-----LLEKDLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 389  
GELSU\_84544 333 HNAT-----LVADDLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 390  
PHACH\_37188 336 HNAT-----VYDANMAQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 396  
PHACH\_135972 330 HNAT-----VYDANMAQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 390  
DICSQ\_86071 335 HNAT-----LLEAALQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 395  
BJEAD\_156054 329 HNAT-----LFDIGLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 389  
BJEAD\_171059 328 HNAT-----RFNAPLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 388  
BJEAD\_114954 322 HNAT-----VFNQVLAQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 382  
BJEAD\_183896 328 HNAT-----LFDLMAQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 388  
BJEAD\_114902 327 HNAT-----VFNADLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 388  
BJEAD\_52991 329 HNAT-----VFNADLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 388  
BJEAD\_245297 330 HNAT-----LMDANLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 390  
BJEAD\_71431 330 HNAT-----VFNADLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 388  
BJEAD\_171002 330 HNAT-----VFNADLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 390  
BJEAD\_245049 329 HNAT-----VFNADLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 389  
BJEAD\_66377 335 HNAT-----VFNADLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 395  
PHACH\_6199 343 HNAT-----VFNADLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 403  
PHLBR\_131358 329 HNAT-----VFNADLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 389  
PHLBR\_164178 325 HNAT-----VFNADLQVNETS-KQVANNPQGNQVGFRLPNSSVL-S--QVGDPA--G-PTSHEFLIF 385  
RHOPL\_108489 335 YGNVSNLNDVPTTTPFLSFINSAIVNFSALIAPEYTAQIADAVDSASITLV---PQVSEV-VGQ-----YKAIYNTLTAQKLLS-----SIGDMELL 424  
PHACH\_131961 339 -----DETTDVLADPLMLVLRALASEYCNISQAQDGHWSKQQAHAQNTVLANITLPSLKSGLKQYA-IQRKLLNDKHQSQAETVQLYNSIKVLS-----VSPSRLLQF 439  
RHOPL\_128830 302 -----QKELYFANRTGLLAATDNTVTLLIPLQSVVDEEFASLLALFDHEAQKPLS---QLKQYQP-IQRSWLETGDPYVYELI-----QW 379

TRAVE\_174721 440 QP-----SHPWHT-----QIHRDAFSYCAIA-----QSIDSRLVIVRFFGRTPEKKNLWFSKIDITDYNMQPOTFFDRFPAGRTSIEADMMTDMCVMSAKIIGGLPGS 536  
PHLBR\_123747 407 SA-----DHPWHT-----QIHRDAFSYCAIA-----ENIDPRLVIVRFFGRTPEKKNLWFSKIDITDYNMQPOTFFDRFPAGRTSIEADMMTDMCVMSAKIIGGLPGS 502  
PHACH\_137275 446 TE-----EHPVHW-----QIHRDAFSYCAIA-----ENIDTRVIVRFFGRTPEKKNLWFSKIDITDYNMQPOTFFDRFPAGRTSIEADMMTDMCVMSAKIIGGLPGS 541  
BJEAD\_34622 433 TK-----SHPWHT-----QIHRDAFSYCAIA-----ENIDTRVIVRFFGRTPEKKNLWFSKIDITDYNMQPOTFFDRFPAGRTSIEADMMTDMCVMSAKIIGGLPGS 528  
GELSU\_84792 592 -----N--TTLEYNASQIFITVYLSGQISRCRIGIDAA--LNAVALBDPWLTD--PVDKTVLLQAL--EDVISTLPSVPLTMTITP-- 666  
TRAVE\_73596 585 -----N--TSVAYNASQIFITVYLSGQISRCRIGIDAA--LNAKALVNPWLTD--SVDKTVLLQAL--EDVISTLPSVPLTMTITP-- 659  
DICSQ\_153749 586 -----N--TSLLEYNASQIFITVYLSGQISRCRIGIDAA--LNAQATNPWLTD--TBDKTVLLQAL--HDVADNKSIFNLTITP-- 660  
GANSP\_86428 585 -----N--SLEYNASQIFITVYLSGQISRCRIGIDAA--LNAKALSNPWLTD--PDKTVLLQAL--HDVSNMDSISNLTITP-- 659  
PHLBR\_160653 594 -----N--TSVENNTQIFITVYLSGQISRCRIGIDAA--LRASLPQNPWLTD--PDKTVLLQAL--NDVATNKSIFNLTITP-- 668  
BJEAD\_45135 595 -----N--SLEYNASQIFITVYLSGQISRCRIGIDAA--LRASLPQNPWLTD--PDKTVLLQAL--NDVAAASVNDVSGLTMTITP-- 670  
PHACH\_11098 591 -----N--SLEYNASQIFITVYLSGQISRCRIGIDAA--LRGTVLTPWLTD--PDKTVLLQAL--HDVVSNIIGSIPGLTMTITP-- 665  
GANSP\_114505 400 GSTVGGGA-YADHALLP--PGKYIMFQYL--EYPASRCKIHKVSA--NEYVEPFFSGFMNN--KADFPPIRWSY--KTRREARRMDAFCRGLTSHHPHF 489  
DICSQ\_181599 400 GSTVAGA-YADHALLP--PGKYIMFQYL--EYPASRCKIHKVSA--NEYVEPFFSGFMNN--KADFPPIRWSY--KTRREARRMDAFCRGLTSHHPHF 489  
TRAVE\_144610 400 GSTVAGA-YADHALLP--PGKYIMFQYL--EYPASRCKIHKVSA--NEYVEPFFSGFMNN--KADFPPIRWSY--KTRREARRMDAFCRGLTSHHPHF 489  
PHLBR\_128980 396 GSTVAGA-YADHALLP--PGKYIMFQYL--EYPASRCKIHKVSA--NEYVEPFFSGFMNN--KADFPPIRWSY--KTRREARRMDAFCRGLTSHHPHF 485  
BJEAD\_34705 400 GSTVAGA-YADHALLP--PGKYIMFQYL--EYPASRCKIHKVSA--NEYVEPFFSGFMNN--KADFPPIRWSY--KTRREARRMDAFCRGLTSHHPHF 489  
PHACH\_126879 407 GSTVAGA-YADHALLP--PGKYIMFQYL--EYPASRCKIHKVSA--NEYVEPFFSGFMNN--KADFPPIRWSY--KTRREARRMDAFCRGLTSHHPHF 496  
FOMPI\_127556 399 GSTVGGGA-YADHALLP--PGKYIMFQYL--EYPASRCKIHKVSA--NEYVEPFFSGFMNN--KADFPPIRWSY--KTRREARRMDAFCRGLTSHHPHF 488  
GELSU\_80773 400 GSTVAGA-YADHALLP--PGKYIMFQYL--EYPASRCKIHKVSA--NEYVEPFFSGFMNN--KADFPPIRWSY--KTRREARRMDAFCRGLTSHHPHF 489  
RHOPJ\_118723 399 GSTVGGGA-YADHALLP--PGKYIMFQYL--EYPASRCKIHKVSA--NEYVEPFFSGFMNN--KADFPPIRWSY--KTRREARRMDAFCRGLTSHHPHF 488  
WOLCO\_24953 399 ASIVGGGA-YADHALLP--PGKYIMFQYL--EYPASRCKIHKVSA--NEYVEPFFSGFMNN--KADFPPIRWSY--KTRREARRMDAFCRGLTSHHPHF 488  
TRAVE\_43286 408 IGEALAMV-VGDSQPSB--DNVLCFCCTGGFS--MVEBSGIESWHITSGEDHAPVDFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 494  
DICSQ\_149587 399 IGMISQY-VGTAPPPP--DHKCYCTFAYL--TYEAGTSGWHITSAHVDVAPVDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 489  
GANSP\_116439 407 GILISQY-VGTAPPPP--DHKCYCTFAYL--TYEAGTSGWHITSAHVDVAPVDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 497  
DICSQ\_173648 405 AQOISQY-VGLSPPAA--NHKAFCTGVYS--THDVTGTSWHITSAHVDVAPVDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 495  
GANSP\_116436 405 TGEISTY-VGVRPPAA--NHKAFCTGVYS--THDVTGTSWHITSAHVDVAPVDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 494  
PHLBR\_157963 406 LGQGSML-VGVPFLLP--PQNFYFLGYFN--LYPLARGSWHITSAHVDVAPVDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 496  
PHLBR\_157964 407 IGLGAML-VGDPVAVP--SOKYFLGYFN--LYPLARGSWHITSAHVDVAPVDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 496  
PHLBR\_128210 395 MGVISML-VGDLINAP--DKKVFSSYYL--AYPSARGFWHITSS--DDFTVLEHFTGYLKH--ADDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 488  
BJEAD\_143000 402 HTALNLV-VGDPAG-V--QSKFYSMGFTT--CHEPGRGWHIRDRGQDSVQVEBFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 491  
BJEAD\_45314 401 HTALNLV-VGDPAG-V--QSKFYSMGFTT--CHEPGRGWHIRDRGQDSVQVEBFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 491  
PHACH\_5574 400 FGLSML-VGDPSPAC--PRKVFSLGYV--EHPSTLGFVHIRDRGQDSVQVEBFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 490  
BJEAD\_241975 402 IGPVSMV-VGDPSTTS--NRKYFVSGYV--EHPSTLGFVHIRDRGQDSVQVEBFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 492  
PHLBR\_29466 407 FGPVSMV-VGDPSTTS--NRKYFVSGYV--EHPSTLGFVHIRDRGQDSVQVEBFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 497  
RHOPJ\_129158 400 IACSAF-VGNPMVGS--PRRYLAIYAT--WYSAVCYLHTDANOVDAPLDFPDTITNG--KBDTAMRHWY--KRGREIGRRMMSYRCEVYADHPHF 490  
RHOPJ\_55972 385 IACSAF-VGNPMVGS--PRRYLAIYAT--WYSAVCYLHTDANOVDAPLDFPDTITNG--KBDTAMRHWY--KRGREIGRRMMSYRCEVYADHPHF 475  
BJEAD\_227734 403 MCLPSMF-VGDPFVSV--PRKVFYMGYV--AYPSARGFWHITSS--DDFTVLEHFTGYLKH--ADDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 493  
PHLBR\_27956 401 MCLPSMF-VGDPFVSV--PRKVFYMGYV--AYPSARGFWHITSS--DDFTVLEHFTGYLKH--ADDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 491  
PHACH\_6010 386 FCLPSMF-VGDPFVSV--PRKVFYMGYV--AYPSARGFWHITSS--DDFTVLEHFTGYLKH--ADDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 475  
DICSQ\_157363 399 FGLLALY-VGDLISRV--VDKAYSVGMWY--QHPASIRLHITSDRNVAPLDFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 489  
GANSP\_130292 398 FGLVALY-VGDRSQV--VNSYAVGMWY--QHPASIRLHITSDRNVAPLDFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 488  
TRAVE\_167157 400 IATLSVL-VGDRPASAT--KQKWSVGMWY--EHPSTLGFVHITSAHVDVAPLDFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 492  
TRAVE\_170473 404 MGTMSMF-VGDRSQV--VNSYAVGMWY--QHPASIRLHITSDRNVAPLDFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 494  
RHOPJ\_106935 376 LGILAQY-VGDPSTV--ARKYCCADYFL--DYBASTYWHITST--DVPADDFDPKFLSC--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 465  
WOLCO\_121504 403 LGILAMV-VGDRSTV--ARKYCCADYFL--DYBASTYWHITST--DVPADDFDPKFLSC--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 464  
WOLCO\_132654 404 LGPFAFQ-AG-YAPNE--PNKCCNMFFI--EYPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 493  
FOMPI\_90445 399 FGSIAFQ-AG-YAPNE--PNKCCNMFFI--EYPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 493  
WOLCO\_25722 402 FGSIALY-VGDPSTV--PRKYYSIGYV--EHPSTLGFVHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 492  
FOMPI\_129478 395 LGAVSLF-VGDRSIV--AKKYYSIGYV--EHPSTLGFVHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 485  
FOMPI\_156775 400 LGAVSMV-VGDRSIV--AKKYYSIGYV--EHPSTLGFVHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 490  
DICSQ\_160139 391 SDLYIAFAG--GSRP--DCHFLILISNL--YTPSARGFWHITST--NADFYDILNPLGSDKGGEDITHMTRAL--KAGREFL--SAPAKMSWIVGEFGS 479  
GANSP\_124428 380 SDLYIAFAG--GSRP--DCHFLILISNL--YTPSARGFWHITST--NADFYDILNPLGSDKGGEDITHMTRAL--KAGREFL--SAPAKMSWIVGEFGS 469  
DICSQ\_171752 391 SDLYIAFAG--GSRP--DCHFLILISNL--YTPSARGFWHITST--NADFYDILNPLGSDKGGEDITHMTRAL--KAGREFL--SAPAKMSWIVGEFGS 479  
GANSP\_67648 391 SDNFASKRV--ALPA--BGRFLFVTNV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 477  
DICSQ\_102587 391 SDNFASKRV--ALPA--BGRFLFVTNV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 477  
GANSP\_67654 392 TNAFISTE--ALPA--EGHFFSIVSV--MSPARGNLSLNS--DEFDAPLINPLGSD--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 478  
GANSP\_85135 390 TNAFVSKVL--ALPA--EGHFFSIVSV--MSPARGNLSLNS--DEFDAPLINPLGSD--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 476  
DICSQ\_160546 392 TNAFVSKVT--ALPA--EGHFFSIVSV--MSPARGNLSLNS--DEFDAPLINPLGSD--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 478  
PHLBR\_22550 377 ENGAL--ALPA--EGHFFSIVSV--MSPARGNLSLNS--DEFDAPLINPLGSD--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 459  
TRAVE\_176148 394 GNSFLSF-TQ--PVDP--TCNRMSCVAL--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 480  
GANSP\_117498 394 GNSFLSF-TQ--PVDP--TCNRMSCVAL--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 480  
DICSQ\_182736 394 GNSFLSF-TQ--PVDP--TCNRMSCVAL--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 480  
TRAVE\_40237 393 VGPFMSS--SGTFFPA--AGFFNLLTAL--VTPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 480  
TRAVE\_133945 394 APGFVSS--GGTTPAPT--TGFFNFFTAL--VTPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 481  
GANSP\_130042 396 SPGFVST-IA--TTPA--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 482  
GANSP\_138009 396 RPFGTST-VGTPVPE--TGFFMISAVV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 484  
DICSQ\_103879 396 DDGVA--GATPAP--TGFFMISAVV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 480  
DICSQ\_96414 396 RFAFASV-IPGTATPE--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 485  
FOMPI\_40728 395 ENGAFIS-VQ--SLPA--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 481  
RHOPJ\_55496 391 ANAMVSM-QQ--PRPA--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 477  
GELSU\_118493 387 FDGFASL-VQ--AVPE--TCQYFLGAAV--SPPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 473  
RHOPJ\_54008 385 ADGYASF-VA--PLPE--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 471  
GELSU\_137959 390 ADGFGSF-TQ--PIPE--TGFFMISAVV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 476  
GELSU\_117387 390 VDGFVSF-TE--ATPD--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 476  
GELSU\_84544 391 VDGFVSF-VE--ATPD--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 477  
PHACH\_37188 397 ADGWSAS-EN--SIPS--TGHYFLINTIV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 483  
PHACH\_135972 391 LDGYAPA--ALPA--EGHFFSIVSV--MSPARGNLSLNS--DEFDAPLINPLGSD--PDDIALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 475  
DICSQ\_86071 396 ADGYGAV-SV--POPE--TGHYFLINTIV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 482  
BJEAD\_156054 390 ANGYTTT-VD--POPA--TGHYFLINTIV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 476  
BJEAD\_171059 389 ADGFASNEVA--QAPP--TGHYFLINTIV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 476  
BJEAD\_114954 383 QDGLALSDVA--TTPP--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 476  
BJEAD\_183896 389 GDRFAADTAV--SRPE--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 470  
BJEAD\_114902 389 ADGFGQT-VL--SEPA--NGSFLINTIV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 475  
BJEAD\_52991 389 ADGFAQT-VL--TOPA--BGRFLFVTNV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 475  
BJEAD\_245297 391 TNGFAPD-VA--TTPA--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 477  
BJEAD\_71431 389 NGFAPD-VA--SIFE--TGHYFLINTIV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 474  
BJEAD\_171002 391 SNQWTE-VQ--IPPA--TGHYFLINTIV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 477  
BJEAD\_245049 390 SNGFVQ-VQ--LVPE--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 476  
BJEAD\_66377 396 VSGFAPFGPI--PPPS--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 483  
PHACH\_6199 404 CNVAFYFGGA--PPPA--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 491  
PHLBR\_131358 390 NNGFAPFGT--APPT--TCNFMVIVSV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 477  
PHLBR\_164178 386 VDSFAPFGVA--AQPV--EGYFILLVAV--VSPSARGFWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 473  
RHOPJ\_108489 425 -----LIG--AGQY--EKPVISIQAL--QHPASIRLHITSDRNVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 505  
PHACH\_131961 440 AGRQPMPYAP--PAEP--GKRYTSLFCAI--THDVTGTSWHITSAHVDVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 487  
RHOPJ\_128830 380 SE-----GFY--DPOQ--NESYIVLGGN--MHPASIRLHITSDRNVAPLDFVSGVSS--KEDVALMRHWY--KRGREIGRRMMSYRCEVYADHPHF 500



TRAVE\_174721 537 L-----P-----QFMPEGLVLLGGTHRIGFDEQ---EDKCCNNTDSRVFQFKNLFLGGCGNITAYGA 592  
PHLBR\_123747 503 E-----P-----QFMTPLGLALAGTTRVGRK-----ETVADTYCKVWFNDVYVGGNGVITGFAA 553  
PHACH\_137275 542 E-----P-----QFMTPLGLALAGTTRCGLDQ-----KTVGNTHCKVHFNFNLYVGGNGVITGFAA 595  
BUEAD\_34622 529 E-----P-----QFMTPLGLPLLAGTTRAGLDQK-----TIVADTYCKVWFNSVYVGGNGVITGFAA 582  
GELSU\_84792 667 -----DSGMTLEQYVDLY- DPSTMCSN WWSGAKIGTSSD-----TAVVDENAKVNTNNTNLFIDASTIPSLPTG 730  
TRAVE\_73596 660 -----DNMTMLEQYVAAY- DPATMCSN WWSGAKIGTSSS-----TAVVDENAKVNTNNTNLFIDASTIPSLPTG 723  
DICSQ\_153749 661 -----DPTMTLEQYVDAY- DPSTMCSN WWSGAKIGTSSA-----NAVVDENAKVNTNNTNLFIDASTIPALPTG 724  
GANSF\_86428 660 -----DATMTLEQYVDAY- DPGTMCNS WWSGAKIGTSSS-----TAVVDENAKVNTNNTNLFIDASTIPSLPMG 723  
PHLBR\_160653 669 -----DYTQTIQYVDAY- DPGTMCNS WWSGAKIGTSSS-----NSVVDENAKVNTNNTNLFIDASTIPSLPTG 732  
BUEAD\_45135 671 -----DRMTMLEQYVDAY- DPATMNSN WWSGAKIGTSSD-----TAVVDENAKVNTNNTNLFIDASTIPSLPTG 734  
PHACH\_11098 666 -----DVTQTIQYVDAY- DPATMNSN WWSSTTIGSSPQ-----SAVVDENAKVNTNNTNLFIDASTIPSLPTG 729  
GANSF\_114505 490 HFDSPAARDIDIKTARELLPNLTVGIHMGTWHTSEPFYDASKVHDDIKYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 603  
DICSQ\_181599 490 HFDSSAACRDIIDIKTARELLPNLTVGIHMGTWHTSEPFYDASKVHDDIKYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 603  
TRAVE\_144610 490 HPASPAACRDIIDIKTARELLPNLTVGIHMGTWHTSEPFYDASKVHDDIKYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 603  
PHLBR\_128980 486 HPASPAACRDIIDIKTARELLPNLTVGIHMGTWHTSEPFYDASKVHDDIKYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 599  
BUEAD\_34705 490 HPASPAACRDIIDIKTARELLPNLTVGIHMGTWHTSEPFYDASKVHDDIKYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 603  
PHACH\_126879 497 HPASPAACRDIIDIKTARELLPNLTVGIHMGTWHTSEPFYDASKVHDDIKYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 610  
FOMPI\_127556 489 HPNSPAACRDIIDIKTARELLPNLTVGIHMGTWHTSEPFYDASKVHDDIKYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 602  
GELSU\_80773 490 HPASPAACRDIIDIKTARELLPNLTVGIHMGTWHTSEPFYDASKVHDDIKYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 603  
RHOPL\_118723 489 HPNSPAACRDIIDIKTARELLPNLTVGIHMGTWHTSEPFYDASKVHDDIKYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 602  
WOLCO\_24953 489 HPNSPAACRDIIDIKTARELLPNLTVGIHMGTWHTSEPFYDASKVHDDIKYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 602  
TRAVE\_43286 499 PDGSAAHGPEA-----LTGMPVVDHAPDLVYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 587  
DICSQ\_149587 490 AASAAAVPKA-----P--VRVPSIDAVDLYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 577  
GANSF\_116439 498 APGSAAVIQG-----PQASAVGTDVFDVYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 587  
DICSQ\_173648 496 PQDSEAAVSP-----DHNTFVAIDAPDIVYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 583  
GANSF\_116436 495 PAGESAAVSP-----EHSFVSDIADPDIYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 582  
PHLBR\_157963 497 PDGSKASATQE-----GTFFAVDHDVYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 583  
PHLBR\_157964 497 PFGSKAGLIAE-----GVPTTIDYPRVEYTKEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 583  
PHLBR\_128210 485 PEGSAAAGLD-----VRPVAVDADLLYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 571  
BUEAD\_143000 492 SEKSDAACAKA-----SGPVINAPDIRYSEEDDKVLEVLKAVNNTNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 578  
BUEAD\_45314 491 S--EQAACKAA-----SGPVPLEAPDIYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 575  
PHACH\_5574 491 APASARTG-E-----SAPVFPDAPDIYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 554  
BUEAD\_241975 493 AAGSALCKGE-----IQPAAVDADPDIYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 579  
PHLBR\_29466 498 PAGESAALCKGE-----ISPAADFADPDIYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 584  
RHOPL\_129158 491 PEGSAAAVRPS-----AEPTLDTPKIVYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 577  
RHOPL\_55972 476 ASDSPAAVQVE-----QQPKLSDPVVYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 562  
BUEAD\_227734 494 DSSPARCTGDVDAKG-----EQVTVPPVPSAPRLYSAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 589  
PHLBR\_27956 492 NETSEALCRQD-----LKSVDIADPRLTYTQEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 578  
PHACH\_6010 476 AEDSPARCREG-----TAPVFPDAPDIYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 556  
DICSQ\_157363 490 SETSVAAPRLH-----DSVPFNATPRLVYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 576  
GANSF\_130292 489 SEKSQATPRLY-----DGPVPIIAPKQFYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 575  
TRAVE\_167157 493 HPTSKVAAGAR-----DGPVPIIAPKQFYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 579  
TRAVE\_170473 495 APSSKAATGPR-----SGPVPVTPADPDIYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 581  
RHOPL\_106935 466 SEESTAACLRLQ-----RAPAAAGDPPIVYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 552  
WOLCO\_121505 495 PEGSAAACRAD-----RPVVEINDPDIYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 581  
WOLCO\_132654 494 SEGSQAFCNME-----ASPVDLSEFNIEYTPEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 580  
FOMPI\_90445 490 FOMPSAACSAD-----AVFPVMDAALQYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 576  
WOLCO\_25722 493 PEGSKAKCHDN-----VRPVPVSAPEIYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 579  
FOMPI\_129478 486 PAGESAACKED-----AKPVDHAPDIYTAEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 572  
FOMPI\_156775 491 PAGESAQCASAS-----AGPTATQEDDQADDDWIADHVEITNLSLGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 577  
DICSQ\_160139 480 A-----SA--QTSABIESFIRONALVNNVSGTVMGKANT--IAKGSALNPDITVKGVTGRLVVDASAFEPFIPAA 547  
GANSF\_124428 470 A-----NA--TSDAADAYIRKKNALVNNVSGTVMGKSGD--SSKGAALNPDITVKGVTGRLVVDASAFEPFIPAA 539  
DICSQ\_171752 480 A-----NA--TSDAADAYIRKKNALVNNVSGTVMGKSGD--SSKGAALNPDITVKGVTGRLVVDASAFEPFIPAA 547  
GANSF\_67648 478 A-----NA--TTDEELNAYIRDNADIVD PVGTVMGKGGP--GALNADITVKGVTGRLVVDASAFEPFIPAA 540  
DICSQ\_102587 478 A-----NA--TTDEELNAYIRDNADIVD PVGTVMGKGGP--GALNADITVKGVTGRLVVDASAFEPFIPAA 540  
GANSF\_67654 479 A-----NA--TTDEELEYIRDNADIVD PVGTVMGKGGP--APLTPDKVKTGRLVVDASAFEPFIPAA 541  
GANSF\_85135 477 A-----NA--TTSDALDAYIRNTSDRID PVGTVMGKNDAD--RADSHDKVKTGRLVVDASAFEPFIPAA 539  
DICSQ\_160546 479 A-----NA--TTTDELEVIRKNSDIDV PVGTVMGQGTN--APLTPDKVKTGRLVVDASAFEPFIPAA 541  
PHLBR\_22550 460 A-----N--ATTDAQEAFARANAAPDG VVGTAAASAADA--GFPVDDPDRVKTGRLVVDASAFEPFIPAA 524  
TRAVE\_176148 481 A-----Q--TTTDDIRAYIRNMLAIFR PMGTARSTAEHD--AAVVDPRDRVKTGRLVVDASAFEPFIPAA 542  
PHLBR\_117498 481 T-----N--TTTDDIRAYIRNMLAIFR PMGTARSTAEHD--AAVVDPRDRVKTGRLVVDASAFEPFIPAA 542  
DICSQ\_182736 481 V-----N--TTTDDIRAYIRNMLAIFR PMGTARSTAEHD--AAVVDPRDRVKTGRLVVDASAFEPFIPAA 542  
TRAVE\_40237 481 A-----EVDIHDDADVADWARTQASRIF PVGTARSTAEHD--A--HGVVNDPDRVKTGRLVVDASAFEPFIPAA 548  
TRAVE\_133945 482 A-----DVIDIDDSDVDAWARQASRIF PVGTARSTAEHD--AGAVVNDPDRVKTGRLVVDASAFEPFIPAA 548  
GANSF\_130042 483 A-----DVIDLGSSEVDADWARSQRTIRIHPGTARSTAEHD--KNSVNDPDRVKTGRLVVDASAFEPFIPAA 549  
GANSF\_138009 485 A-----DVIDLSSNDADWARSQASRIFHPGTARSTAEHD--EDSVDDPDRVKTGRLVVDASAFEPFIPAA 541  
DICSQ\_103879 481 A-----NVDLDDLDESVDADWARSQASRIFHPGTARSTAEHD--TGSVDDPDRVKTGRLVVDASAFEPFIPAA 547  
DICSQ\_96414 486 A-----DVIDLNDADWARSQASRIFHPGTARSTAEHD--VEEGVDDPDRVKTGRLVVDASAFEPFIPAA 554  
FOMPI\_40728 482 A-----Q--ASTDAELAAVARNYSTAN PVGTARSTAEHD--SEGLVDDPDRVKTGRLVVDASAFEPFIPAA 546  
RHOPL\_55496 478 A-----A--AQTYEELAAVARNYSTAN PVGTARSTAEHD--D--LEAVVDDPDRVKTGRLVVDASAFEPFIPAA 543  
GELSU\_118493 474 T-----P--ASSDAELAAVARNYSTAN PVGTARSTAEHD--QEVVDDPDRVKTGRLVVDASAFEPFIPAA 538  
RHOPL\_54008 472 S-----A--AQTYEELAAVARNYSTAN PVGTARSTAEHD--NEEVVDDPDRVKTGRLVVDASAFEPFIPAA 536  
GELSU\_137959 477 A-----T--ATADNFEDVARNYSTAN PVGTARSTAEHD--KTGVVNSMLOVKNTPGRLVVDASAFEPFIPAA 541  
GELSU\_117387 477 S-----EA--TASDAELAAVARNYSTAN PVGTARSTAEHD--SDVVDPDRVKTGRLVVDASAFEPFIPAA 542  
GELSU\_84544 478 A-----G--AKTDAELAAVARNYSTAN PVGTARSTAEHD--A--SGVVDPDRVKTGRLVVDASAFEPFIPAA 543  
PHACH\_37188 484 G-----TA--ESDAELAAVARNYSTAN PVGTARSTAEHD--AVGVDDPDRVKTGRLVVDASAFEPFIPAA 548  
PHACH\_135972 476 G-----EA--ESDDELAAVARNYSTAN PVGTARSTAEHD--SVGVDDPDRVKTGRLVVDASAFEPFIPAA 540  
DICSQ\_86071 483 G-----DA--ETDEELAAVARNYSTAN PVGTARSTAEHD--SVGVDDPDRVKTGRLVVDASAFEPFIPAA 547  
BUEAD\_156054 477 G-----AA--QTDALDELAAVARNYSTAN PVGTARSTAEHD--TWGVDDPDRVKTGRLVVDASAFEPFIPAA 541  
BUEAD\_171059 477 G-----SA--QTDALDELAAVARNYSTAN PVGTARSTAEHD--TWGVDDPDRVKTGRLVVDASAFEPFIPAA 541  
BUEAD\_114954 471 G-----SA--NTTDEELAAVARNYSTAN PVGTARSTAEHD--KWGVDDPDRVKTGRLVVDASAFEPFIPAA 535  
BUEAD\_183896 477 G-----AA--ETDEELAAVARNYSTAN PVGTARSTAEHD--PWGVDDPDRVKTGRLVVDASAFEPFIPAA 541  
BUEAD\_114902 476 S-----SA--SSDDELAAVARNYSTAN PVGTARSTAEHD--KSGVDDPDRVKTGRLVVDASAFEPFIPAA 540  
BUEAD\_52991 476 G-----LS--NTTDDDELAAVARNYSTAN PVGTARSTAEHD--TWGVDDPDRVKTGRLVVDASAFEPFIPAA 540  
BUEAD\_245297 478 G-----AA--NTTDEELAAVARNYSTAN PVGTARSTAEHD--NFGVDDPDRVKTGRLVVDASAFEPFIPAA 542  
BUEAD\_71431 475 G-----MA--ETDEELAAVARNYSTAN PVGTARSTAEHD--DWGVDDPDRVKTGRLVVDASAFEPFIPAA 539  
BUEAD\_171002 478 G-----DT--DDEADLAAVARNYSTAN PVGTARSTAEHD--TDGVDDPDRVKTGRLVVDASAFEPFIPAA 543  
BUEAD\_245049 477 G-----DA--STEDELAAVARNYSTAN PVGTARSTAEHD--DYGVDDPDRVKTGRLVVDASAFEPFIPAA 541  
BUEAD\_66377 484 R-----DNDDDAEARQAAYITKTAWPNN PAGSARSTAEHD--GCAVDDPDRVKTGRLVVDASAFEPFIPAA 554  
PHACH\_6199 492 A-----ELDSDAPRVERFVRENVAIIN PCGTCAKMPREQ-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 555  
PHLBR\_131358 478 A-----HA--TTTDLQAVFAENAVIIN PSCCKMSSANS-----NDGVDDPDRVKTGRLVVDASAFEPFIPAA 542  
PHLBR\_164178 474 A-----NA--TTDAGLAFANFNANNVNV CVMGAYSPANA-----SAVVDNDPDRVKTGRLVVDASAFEPFIPAA 538  
RHOPL\_108489 506 G-----GSSVQSEQNETWQNSYFEY PSCCKMPPQSQ-----GAVVDNDPDRVKTGRLVVDASAFEPFIPAA 570  
PHACH\_131961 488 P-----ETLARGEAGAEYVKAHCGPVF PVGTARSTAEHD-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 593  
RHOPL\_128830 501 P-----PLTNLTNGDLESYVNSAAGGD LIGTAPAMPRA-----GVVDDKRLNIVYGTQNKRCVDLSTCPDNLGT 565

TRAVE_174721	593	PTLTAMSLAIKSCYVKNFNTPSPFTDQAO*	624
PHLBR_123747	554	PTLTSICYALICGSKITEKLNGLN*	579
PHACH_137275	596	PTLTSICYALIRASNDIAKFRHRG	621
BJEAD_34622	583	PTLTSICFATRAADSDIAKIKCHK*	608
GELSU_84792	731	PHGTVMASABQAVANLALSGP*	755
TRAVE_73596	724	PHQVLMASABQAVSRLLALAGP*	748
DICSQ_153749	725	PHGQLMSABQAAKHLALAGP*	749
GANSP_86428	724	PHGMLMSABQAVAKHLALSGP*	748
PHLBR_160653	733	PHGLLMSABQAVARVVALAGP*	757
BJEAD_45135	735	PHGLLMSVABQAVARITALAGP*	759
PHACH_11098	730	PHQTLMSABQAAKHLALAGP	753
GANSP_114505	604	NTYSSALLVGBKGADLAEEDLKLKLRPHAPVPHAPVPGKPATQLVR*	652
DICSQ_181599	604	NTYSSALLVGBKGADLAEEDLKLKLRPHAPVPHAPVPTGKPSQARR*	653
TRAVE_144610	604	NTYSSALLVGBKGADLAEEDLKLKLRPHAPVPHAPVPTGKPAAPLFR*	652
PHLBR_128980	600	NTYSSALLVGBKGADLAEEDLKLKLRPHAPVPHAPVPTGKPSQARR*	648
BJEAD_34705	604	NTYSSALLVGBKGADLAEEDLKLKLRPHAPVPHAPVPTGKPAAPLFR*	654
PHACH_126879	611	NTYSSALLVGBKGADLAEEDLKLKLRPHAPVPHAPVPTGKPSQARR*	659
FOMPI_127556	603	NTYSSALLVGBKGADLAEEDLKLKLRPHAPVPHAPVPTGKPSQARR*	650
GELSU_80773	604	NTYSSALLVGBKGADLAEEDLKLKLRPHAPVPHAPVPTGKPSQARR*	652
RHOPL_118723	603	NTYSSALLVGBKGADLAEEDLKLKLRPHAPVPHAPVPTGKPSQARR*	651
WOLCO_24953	603	NTYSSALLVGBKGADLAEEDLKLKLRPHAPVPHAPVPTGKPSQARR*	651
TRAVE_43286	588	NTYSTALTIGERAAVITAEELITGV*	614
DICSQ_149587	578	NTYSTALTIGERAAVITAEELITGV*	604
GANSP_116439	588	NTYSTALTIGERAAVITAEELITGV*	614
DICSQ_173648	584	NTYSTAVMIGERAAVITAEEDLAEV*	610
GANSP_116436	583	NTYSTAVMIGERAAVITAEEDLAEV*	609
PHLBR_157963	584	NTYSTALVIGERAAVITAEELITGV*	610
PHLBR_157964	584	NTYSTALVIGERAAVITAEELITGV*	610
PHLBR_128210	572	NTYSTTLAERAAVITAEEDLITGV*	597
BJEAD_143000	579	NTYSTALLAERAAVITAEELITGV*	605
BJEAD_45314	576	NTYSTALLAERAAVITAEELITGV*	602
PHACH_5574	555	NTYSTTLAERAAVITAEELITGV*	581
BJEAD_241975	580	NTYSTTLAERAAVITAEEDLITGV*	606
PHLBR_29466	585	NTYSTTLAERAAVITAEEDLITGV*	611
RHOPL_129158	578	NTYSTALTIGERAAVITAEELITGV*	603
RHOPL_55972	563	NTYSSAVLIGERAAVITAEELITGV*	588
BJEAD_227734	590	NTYSTALVIGERAAVITAEELITGV*	618
PHLBR_27956	579	NTYSTSLVIGERAAVITAEELITGV*	605
PHACH_6010	557	NTYSTALLVIGERAAVITAEELITGV*	582
DICSQ_157363	577	NTYSTALLVIGERAAVITAEELITGV*	612
GANSP_130292	576	NTYSTALVIGERAAVITAEELITGV*	618
TRAVE_167157	580	NTYSTAVLIGERAAVITAEELITGV*	617
TRAVE_170473	582	NTYSTAVLIGERAAVITAEELITGV*	610
RHOPL_106935	553	NTYSTAVLIGERAAVITAEELITGV*	579
WOLCO_121505	582	NTYSTALVIGERAAVITAEELITGV*	608
WOLCO_132654	581	NTYSTAVLIGERAAVITAEELITGV*	604
FOMPI_90445	577	NTYSTALVIGERAAVITAEELITGV*	605
WOLCO_25722	580	NTYSTALVIGERAAVITAEELITGV*	617
FOMPI_129478	573	NTYSSAVLIGERAAVITAEELITGV*	597
FOMPI_156775	578	NTYSTAVLIGERAAVITAEELITGV*	602
DICSQ_160139	548	NTYPTVYLAERAAVITAEELITGV*	569
GANSP_124428	540	NTYPTVYLAERAAVITAEELITGV*	558
DICSQ_171752	548	NTYPTVYLAERAAVITAEELITGV*	605
GANSP_67648	541	NTYPTVYLAERAAVITAEELITGV*	572
DICSQ_102587	541	NTYPTVYLAERAAVITAEELITGV*	577
GANSP_67654	542	NTYPTVYLAERAAVITAEELITGV*	565
GANSP_85135	540	NTYPTVYLAERAAVITAEELITGV*	561
DICSQ_160546	542	NTYPTVYLAERAAVITAEELITGV*	563
PHLBR_22550	525	NTYPTVYLAERAAVITAEELITGV*	547
TRAVE_176148	543	NTYPTVYLAERAAVITAEELITGV*	573
GANSP_117498	546	NTYPTVYLAERAAVITAEELITGV*	571
DICSQ_182736	546	NTYPTVYLAERAAVITAEELITGV*	573
TRAVE_40237	549	NTYPTVYLAERAAVITAEELITGV*	574
TRAVE_133945	549	NTYPTVYLAERAAVITAEELITGV*	574
GANSP_130042	550	NTYPTVYLAERAAVITAEELITGV*	574
GANSP_138009	542	NTYPTVYLAERAAVITAEELITGV*	564
DICSQ_103879	548	NTYPTVYLAERAAVITAEELITGV*	571
DICSQ_96414	555	NTYPTVYLAERAAVITAEELITGV*	579
FOMPI_40728	547	NTYPTVYLAERAAVITAEELITGV*	568
RHOPL_55496	544	NTYPTVYLAERAAVITAEELITGV*	567
GELSU_118493	539	NTYPTVYLAERAAVITAEELITGV*	560
RHOPL_54008	537	NTYPTVYLAERAAVITAEELITGV*	562
GELSU_137959	542	NTYPTVYLAERAAVITAEELITGV*	563
GELSU_117387	543	NTYPTVYLAERAAVITAEELITGV*	564
GELSU_84544	544	NTYPTVYLAERAAVITAEELITGV*	566
PHACH_37188	549	NTYPTVYLAERAAVITAEELITGV*	566
PHACH_135972	541	NTYPTVYLAERAAVITAEELITGV*	564
DICSQ_86071	548	NTYPTVYLAERAAVITAEELITGV*	570
BJEAD_156054	542	NTYPTVYLAERAAVITAEELITGV*	564
BJEAD_171059	542	NTYPTVYLAERAAVITAEELITGV*	564
BJEAD_114954	536	NTYPTVYLAERAAVITAEELITGV*	564
BJEAD_183896	542	NTYPTVYLAERAAVITAEELITGV*	570
BJEAD_114902	541	NTYPTVYLAERAAVITAEELITGV*	564
BJEAD_52991	541	NTYPTVYLAERAAVITAEELITGV*	566
BJEAD_245297	543	NTYPTVYLAERAAVITAEELITGV*	569
BJEAD_71431	540	NTYPTVYLAERAAVITAEELITGV*	563
BJEAD_171002	544	NTYPTVYLAERAAVITAEELITGV*	567
BJEAD_245049	542	NTYPTVYLAERAAVITAEELITGV*	566
BJEAD_66377	555	NTYPTVYLAERAAVITAEELITGV*	595
PHACH_6199	556	NTYPTVYLAERAAVITAEELITGV*	592
PHLBR_131358	543	NTYPTVYLAERAAVITAEELITGV*	566
PHLBR_164178	539	NTYPTVYLAERAAVITAEELITGV*	564
RHOPL_108489	571	NTYPTVYLAERAAVITAEELITGV*	648
PHACH_131961	594	NTYPTVYLAERAAVITAEELITGV*	669
RHOPL_128830	566	NTYPTVYLAERAAVITAEELITGV*	587





MOX

AAO

GOX

CDH

P2O

Table with columns for MOX, AAO, GOX, CDH, and P2O, listing various reactor models and their corresponding values.

MOX

AAO

GOX

CDH

P2O

