

Replication of Genomes in Eukaryotes: Analyses of the Structure and Functions of the Replicative ϵ Polymerases from Yeasts, Plants and Animals

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Abstract

In all living organisms, genome replication is an indispensable activity in their life cycle. As compared to prokaryotes, genome replication in eukaryotes is much more complex. In eukaryotes, the genome replication is accomplished by a more specialized, multi-protein complex known as replisome. Therefore, for a complete understanding of the replication process in eukaryotes, the structure-function relationship of their replisome complex is important. The eukaryotic replisome complex is mainly composed of 3 replicative polymerases (pols), viz. α , ϵ and δ . The initiation of genome replication starts with the synthesis of primers by the α pol (a primase), which is followed by the synthesis of leading- and lagging-strands by the next two replicative pils, viz. ϵ and δ , respectively. Among them, the pol ϵ is an essential enzyme that links the DNA replication machinery to S-phase checkpoint-control in eukaryotes. The active sites of pol and proofreading (PR) domains of α and δ were analyzed from yeasts, animal and plant sources and reported by this author already [1, 2]. The third replicative enzyme, viz. the pol ϵ is analyzed and reported here. Interestingly, the yeast, animal and plant ϵ pils possess almost identical pol, PR and carboxyl terminal domains (CTD) with the same active site amino acids. Their catalytic cores use the same template-binding pair (-YG-), the catalytic amino acid (K), the nucleotide selection amino acid (Q) and similar catalytic metal-binding motifs in the pol domain as reported for the other replicative pils. However, they exhibit poor identities among themselves, e.g., the human pol ϵ showed only 46.69% and 43.19% identities to the plant (*Arabidopsis thaliana*) and yeast (*Saccharomyces cerevisiae*) pol ϵ sequences, respectively. Furthermore, these eukaryotic ϵ pils use the same active site amino acids in the PR exonuclease domain, and belong to the DEDD(Y)-superfamily of PR exonucleases. Moreover, similar to the other two replicative enzymes, the ϵ pils also use similar regulatory Zn²⁺-binding motifs (ZBMs) in their CTD. In addition, it harbours a unique ZBM in their pol domain. Interestingly, the two invariant motifs, viz -SLYPS- and -YGDTD- which are the characteristic motifs found in the other replicative α and δ pils and B-family of DNA pils, are not found in ϵ pils. Many specialized, conserved sequence motifs are also identified in the ϵ pils and discussed.

Keywords: Eukaryotic genome replication; DNA polymerase δ ; DNA polymerase ϵ ; DNA polymerase ϵ active sites; Proofreading exonuclease active sites; *Saccharomyces cerevisiae*; *Arabidopsis thaliana*; *Homo sapiens*

1. Introduction

In all living organisms, DNA pils play a central role in DNA replication to ensure faithful transmission of genetic information from one generation to another. Therefore, to accomplish this important task in their lifecycle, organisms have evolved and possess a high-fidelity genome replication machinery to preserve and maintain the blueprint of life. The replication machinery possesses several types of DNA pils and repair mechanisms to ensure the duplication of an exact copy of the original genome. To date, five different DNA pils have been characterized in *Escherichia coli*, eight in *S. cerevisiae*, and as many as 16 in humans [3]. However, only three of these DNA pils, viz. α , ϵ and δ are involved in the duplication of the nuclear genome in all eukaryotes [4]. Even though more than a dozen different DNA pils have also

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been reported to perform various replicative and repair functions in plant cells, yet the detailed properties of them are still very limited. Whereas the α pol (the primase) is involved in the synthesis of the DNA primers to initiate the DNA duplication process, the other two replicative pols, viz. δ and ϵ , use these DNA primers and replicate the whole genome and make an exact copy of the original genome. All three replicative pols belong to B-family pols which are not only involved in replication, but also in repair any error that may occur during the replication process [5]. The B-family DNA pols are reported to function in both prokaryotes and eukaryotes, e.g., pol II, pol B, pol α , pol ϵ , pol δ , pol ζ . They are bifunctional enzymes, i.e., in addition to polymerization, they also exhibit 3'→5' PR exonuclease (PR exo) repair function [6]. Even though the replicative pols have an efficient PR function, mutation(s) that rarely escape the replication and repair processes generate the most important new genetic variants in plants and animals. The structural and functional aspects of the replicative pols, viz. α and δ , from yeasts, higher fungi and animals have been extensively analyzed and reported by this author [1, 2]. In this article, the third replicative pol ϵ from yeasts, higher fungi, plants and animals is analyzed and reported.

The DNA replication process is highly conserved in all domains of life [7]. Though genome replication in eukaryotes is known to be incredibly more complex, but it is successfully accomplished by a highly sophisticated and coordinated series of molecular events. The replication process, apart from the essential roles played by the three replicative pols, also depends on the participation of other enzymes and regulatory proteins like, primases, cell-cycle kinases, replicative helicases, single-strand binding proteins (SSBs), additional repair enzymes, ligases, etc. Given the importance of accurate DNA replication, proper functioning of all these enzymes and the accessory proteins is critical to maintain the genome integrity.

The first step in genome replication in both prokaryotes and eukaryotes is the initiation. This is accomplished by a multi-structural enzyme and protein complex known as a primosome. The primosome essentially consists of an origin-of-replication initiator protein, a replicative helicase, a helicase loader, SSBs, a primase, a topoisomerase, etc. [8]. After successful initiation of replication, the replication process is taken over by a next multi-protein complex known as the replisome, which extends the replication process and completes it. In both prokaryotes and eukaryotes, the initiation step is performed by the enzyme, RNA primase, which synthesizes the required RNA primer (short segment of SS-RNA typically of 10-20 nucleotides) to initiate the replication process. However, for eukaryotic replications, in addition to the RNA primer, an additional primer, viz. a DNA primer is also required for further extension, which is provided by the enzyme, DNA pol α . The DNA pol α extends the RNA primers by synthesizing short stretches of DNA, which is used by the pol ϵ and pol δ for further extension of the DNA synthesis in a processive manner and complete the replication process. During replication, the leading-strand is synthesized by pol ϵ (pol2), and the lagging-strand is synthesized by pol δ (pol3). During replication the leading-strand is synthesized continuously, whereas the lagging-strand is synthesized discontinuously, in fragments of ~200 nucleotides long, known as the Okazaki fragments (OFs), named after the discoverer. All these OFs are connected together in the next step to form a complete complementary strand by a DNA ligase [9].

1.1. Eukaryotic ϵ DNA Polymerases

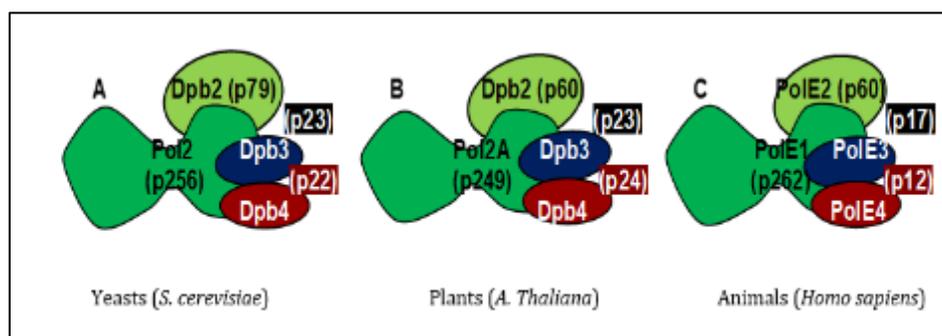
From the above discussions, it is clear that the bulk of the DNA synthesis in eukaryotes is performed by only two of the three replicative polymerases, viz. pols ϵ and δ . DNA pol ϵ (also known as Pol2 in yeasts and plants and PolE in humans) completes the leading- and lagging-strand syntheses, respectively. Pol ϵ was first isolated and characterized from yeast cells as early as 1970 as a nuclear polymerase [10]. It was initially considered to be a form of pol δ that was processive in the absence of proliferating cell nuclear antigen (PCNA) and replication factor C (RFC) [11] (The function of RFC is to load PCNA, the processivity factor of the eukaryotic DNA polymerases δ and ϵ , onto primed DNA templates). Later, it was found that pol ϵ is an independent replicative enzyme in all eukaryotes. Nowadays, its catalytic subunit is isolated and characterized and its gene is cloned and sequenced from several eukaryotes [11 and references therein]. This enzyme, along with the other two eukaryotic replicative (pols α and δ), are grouped under the B-family polymerases [12]. A great deal of information is available now on the structure and functions of the DNA pols ϵ from a large number of eukaryotes like yeasts, higher fungi, plants and animals. The plant enzyme from *A. thaliana* has been characterized in sufficient detail and used for further analysis and comparison.

1.1.1. Subunit structure

Interestingly, all the pol ϵ enzymes from eukaryotes are composed of 4 subunits exhibiting similar subunit structures. Figures 1A, B and C show the subunit structures of the ϵ pols from yeasts, plants and animals. For example, the yeast enzyme's 4 subunits are named as, Pol2, Dpb2, Dpb3 and Dpb4 (with the molecular masses of 256, 79, 23 and 22 kDa, respectively) and the plant enzyme also follows more or less the same nomenclature as the yeast enzyme as, Pol2A, Dpb2, Dpb3 and Dpb4 (with the molecular masses of 249, 60, 23 and 24 kDa, respectively), but the human enzyme subunits are named as, PolE1-PolE4 (with the molecular masses of 262, 60, 17 and 12 kDa, respectively). The 4 subunits

are assembled with a stoichiometry of 1:1:1:1. Thus, the DNA pol ϵ is a heterotetrameric enzyme, made up of the main catalytic subunit (Pol2/Pol2A/PolE1) which assumes a biloped structure, where the NTD and CTD lobes are connected by a linker region and the non-catalytic subunit (Dpb2/PolE2). The Dpb2/PolE2 subunit mediates the homodimerization of the enzyme to its active form and therefore, is essential for the enzyme activity and cell viability. Genetic and biochemical studies indicate that the putative zinc-finger regions in the catalytic subunit (Pol2/Pol2A/PolE1) are important for its interactions with the Dpb2/PolE2 essential subunit. The other two smaller subunits (Dpb3/PolE3 and Dpb4/PolE4) are found to be nonessential for the catalytic activity of the enzyme, but are found to play important regulatory roles [11]. For example, each of the smaller subunits, viz. PolE3 and PolE4 possess H2A/H2B type histone folds and form a tight PolE3-PolE4 dimer. The dimer interacts with the larger catalytic subunit of the enzyme. (For example, PolE3 interacts with subunits PolE1 and PolE4; and the PolE4 interacts with subunits PolE1 and PolE3 and with the subunit of chromatin remodelling complex, (CHRAC), a multi-protein assembly that regulate gene expression and chromatin structure. Though the non-catalytic subunits are highly conserved from yeasts to humans, they largely differ in their sizes in humans [11 and references therein].

Among the plant ϵ pols (Pol2), the pol ϵ from *A. thaliana* has been the most studied one. The pol ϵ complex in *A. thaliana* has been shown to play diverse regulatory roles. For example, it is implicated in DNA replication, DNA repair (nucleotide and base excision repairs), DNA recombination and also in epigenetic gene-silencing activities [11]. Unlike the yeast and human enzymes, the *Arabidopsis* enzyme possesses two isoenzymes, viz. Pol2A and Pol2B. The *Pol2A* gene is ~16 kb long (49 exons) and encodes a protein of 2,161 amino acids (pI/Mw: 6.19/2,48,897), whereas the ~13 kb long *Pol2B* gene with same number of exons (49 exons) encodes a protein of 2,138 amino acids which shows 78.5% identity to Pol2A [13]. Importantly, both the isozymes contain all the motifs that are necessary for a functional Pol2 catalytic subunit. However, the expression of *Pol2B* has been detected mostly under adverse environmental conditions and loss of function of *Pol2B* has resulted in no visible phenotype, suggesting that the Pol2A forms the main enzyme [13]. Furthermore, the knockout mutants of the (Pol2A) are found to be lethal, suggesting its importance [14, 12]. The non-enzymatic CTD plays a crucial role and it not only mediates the interaction of the main catalytic subunit with the other three smaller regulatory subunits, but also links the replication machinery to the S-phase checkpoint [15, 16]. However, its overall subunit composition and various domains of its catalytic subunit's structure are mostly understood from the data available from yeast and human enzymes.



Adapted from [11, 12].

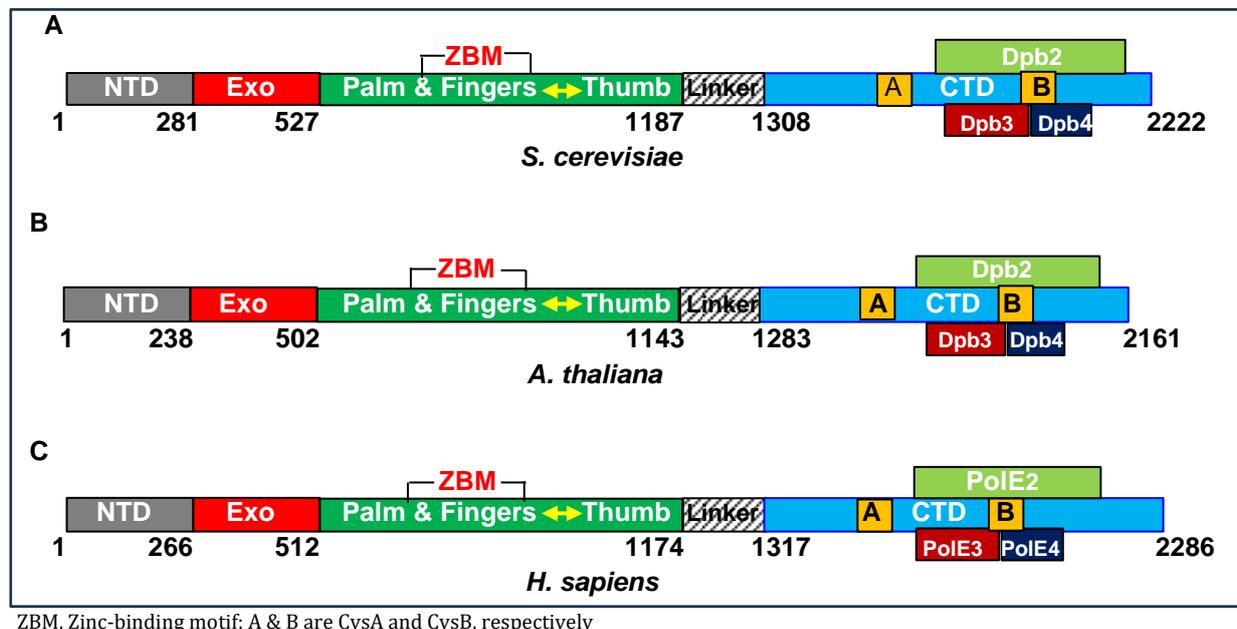
The pol ϵ subunit p17 has been identified as an integral subunit of the chromatin-remodelling factor, CHRAC (Chromatin Accessibility Complex). CHRAC is an ISWI (Imitation Switch), i.e., a chromatin remodelling nuclear-ATPase containing complex that regulates chromatin accessibility and nucleosome spacing. In CHRAC, the p17 forms a dimer with p12 subunit that can interact with histones as well as DNA [17].

Figures 1A, B and C. Subunit structures of the eukaryotic DNA pol ϵ (*S. cerevisiae*, *A. thaliana* and *Homo sapiens*) (the numbers in brackets indicate molecular masses of the subunits in kDa)

1.1.2. Domain organization of the pol ϵ catalytic subunit

The domain organization of the pol ϵ 's (pol2) catalytic subunit from the yeast, *S. cerevisiae*, has been extensively studied and characterized. It contains two pol modules, one in the N-terminal domain (NTD) and the other in the CTD. The NTD pol ϵ module possesses both the pol and PR exonuclease activities, whereas the CTD mediates the crucial interactions between the three smaller regulatory subunits with the catalytic subunit and also links the replication machinery to the S-phase checkpoint [11]. The pol ϵ exhibits the highest processivity as compared to the other two replicative pols, viz. pols α , and δ . This high processivity was found to be increased even further by the nonessential subunits, Dpb3 and Dpb4, through their interactions with the replication clamp, the PCNA. Furthermore, the genetic and biochemical studies indicate that the putative ZFMs in the main catalytic subunit of the enzyme are important for their interactions with the other subunits and for the catalytic efficiency of the enzyme [18].

The main catalytic subunit of the yeast pol ϵ holoenzyme is dissected into different functional domains as, NTD (31–281), PR exonuclease domain (282–527) and the palm (528–950), fingers (769–833), and thumb (951–1186) subdomains of the pol domain (that are organized into a toroid) [19], and a linker domain which connects the pol to the CTD. Figures 2A, 2B and 2C show the various domains and the interactions of the subunits with the CTD of the pols ϵ from different eukaryotic sources.



Figures 2A, B and C. Tentative domain organization the main catalytic subunit of the ϵ pols from eukaryotes (*S. cerevisiae*, *A. thaliana* and *Homo sapiens*) and their interacting accessory subunits

2. Materials and Methods

The protein sequence data of ϵ DNA pols from yeasts, higher fungi, plants and animals were obtained from PUBMED and SWISS-PROT databases. The advanced version of Clustal Omega was used for protein sequence analysis. Along with the conserved motifs identified by the bioinformatics analysis, and the data already available from biochemical, SDM, cryogenic-Electron Microscopy (cryo-EM) and X-ray crystallographic analyses on the ϵ pols are used to confirm the possible amino acids at the active sites of the pol, PR exonuclease domains and regulatory motifs.

3. Results and Discussion

3.1. MSA analysis of DNA polymerase ϵ from various plant sources

The DNA pol ϵ was analyzed from yeasts, higher fungi, plants and animal sources. The structural and functional aspects of this enzyme from yeasts and higher fungal sources were already reported by this author [8]. Fig. 3 shows the MSA of pol ϵ from various plant sources (only the required regions for the discussions are shown). The model plant, *A. thaliana*'s sequence is used as the standard and highlighted. All the major domains (NTD, PR Exo, Pol, Linker and CTD) are indicated with arrow marks. Large numbers of highly conserved small and large peptides are found from NTD to CTD. It is interesting to note that the highly conserved active site amino acids are usually embedded within these conserved peptides (highlighted). The NTD is conserved in all, but aligned with some gaps. It harbours 3 conserved -DxD- type metal-binding motifs and 3 polybasic peptides (highlighted) and some are implicated as nuclear localization signal (NLS). The NTD is followed by the PR exonuclease and pol domains. The proposed PR exonuclease active site amino acids are highly conserved in all the enzymes (highlighted) and it belongs to the DEDD-superfamily of exonucleases and uses an invariant Y as proton acceptor during catalysis. This is in complete agreement with the other DNA-dependent DNA pols (DdDps) from prokaryotes and eukaryotes [1, 6]. An invariant motif, -SYLPQGS- (highlighted in yellow) is found within the PR exo region in the plant ϵ pols as found in yeasts, higher fungi and animals [8]. This sequence is somewhat similar to the characteristic -SLYPS- motif found in the other two eukaryotic replicative DNA pols, α and δ . In both the cases, this motif is implicated in dNTP-binding. In the former, it is found within the proposed PR exo region, whereas in the latter two pols, it is located in the pol region itself. The PR exo domain is followed by the pol domain and

is also highly conserved in all. The proposed template-binding and catalytic pairs, and metal-binding sites are highlighted in yellow and green, respectively. The template-binding pair (-YG-), catalytic amino acid (K) and the nucleotide selection amino acid (Q) are in close agreement with other DdDps and DdRps [6]. Unlike other two eukaryotic replicative pols, the pol ε domain contains a ZBM (highlighted) within. The pol domain is followed by a linker region which connects the pol domain to the CTD. Interestingly, a second putative pol active site amino acids are identified in the CTD and highlighted in yellow. The CTD contains the two typical, highly conserved ZBMs and one of them (CysB) is known to bind the 4Fe-4S cluster (highlighted in orange). It is interesting to note that these 2 ZBMs are found invariably in all three replicative pols at their CTDs. In addition to the Cs which make these ZBMs, there are invariant Cs found throughout the sequence (data not shown) which may be involved in disulphide bond formation. The CTD also contains a -DxD- type metal-binding motif within the CysA. It is interesting to note that the NTD, pol and linker regions contain conserved polybasic peptides within them (highlighted) and are implicated as NLSs. (A NLS is a short amino acid sequence that tags proteins for transport into the nucleus of a cell. NLSs are made up of positively charged amino acids, such as Ks and Rs, that are exposed on the protein's surface, with a consensus sequence of -KK/RxK/R- e. g., -PKKKRKV- is the first discovered NLS from the SV40 large antigen. Interestingly, the deletion of an NLS usually disrupts the nuclear import process. In the same way, fusing a non-nuclear protein to an NLS often results in the protein being imported into the nucleus). A large number of invariant Ws are found throughout the sequence.

CLUSTAL O (1.2.4) MSA of the ε DNA polymerases from various plant sources

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	-----MSGDMRRWRDKD- SRRSNTQKVVKTAEDELESKLGFG	36
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	-----MSGDMRRWRDKD- SRRSNTQKVVKTAEDELESKLGFG	36
sp F4HW04 DPOE1_ARATH	-----MSGDMRRWRDKD- TRWSKKPKVVNTAEDELESKLGFG	36 NLS
tr D7KI06 D7KI06_ARALL	-----MSGDMRRWRDKD- TRWSKKPKVVNTAEDELESKLGFG	36
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	-----MKADGRRWNRKDSGRS SKKQKLI RNAAEELDLKFGPD	37
tr A0A7J7C034 A0A7J7C034_TRIWF	-----MNGDSRRRDRRDLTRS SKKQKQI FSAEEEELESKLGID	37
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	-----MNGDARRRDLRDFGRS SKKQKLI RNSEELDLKFGPD	37
tr A0A2C9VYG0 A0A2C9VYG0_MANES	-----MNGDARRRDLRDFGRS SKKQKLI RNSEELDLKFGPD	37
tr A0A2N9F976 A0A2N9F976_FAGSY	-----MSGNGRKNWDRD- PRS FKKQKLI RTAEELLESKLGFD	36
tr A0A7N2KME6 A0A7N2KME6_QUELO	-----MNGEARRRDRD- PRS SKKQKLI RTAGEELESKFGFD	36
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	-----MAKGEGRGW- EKGRDRKRVSEQKLRFSKEDALEAKLGFD	37
tr A0A619QIG1 A0A619QIG1_ELAGV	-----MNSGGKWRER- S SRNPSKQKLR LNAAEVLERKLGFD	35
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	-----MNINGGRRRER- S SRNPSKQKLR LNAAEVLERKLGFD	35
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	-----MNINGGRRRER- S SRNPSKQKLR LNAAEVLERKLGFD	35
tr A0A816WFC8 A0A816WFC8_HORVV	MSGGDGRRRRP SAGGGGGGGGGGGGGGGGGGGSSAAKEQRLRLGAEELLEGLGFA	60
tr A0A452YAR6 A0A452YAR6_AEGTS	-----MSGGDGRRRRP SAGGGGGV-----GGVGGSWGRRSSAAKEQRLRLGAEELLEGLGFA	55
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	---MSGRRRPAATGGGG---GGGGGGGNW---RRSGSAKAKEQRLRLGAEELLESLGFA	52
tr A0A3L6E143 A0A3L6E143_MAIZE	---MSGRRRPAATGGGG---GGGGGGGNW---RRSGSAKAKEQRLRLGAEELLESLGFA	52
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	---MSGRRRPAAGGG---GGGGGNW---RRGSSAAKEQRLRLGAEELLESLGFA	46
tr A0A835B357 A0A835B357_9POAL	---MSGRRRPAAGGGGG---GGGGGGGNW---RRGSSAAKEQRLRLGAEELLESLGFA	51
tr A0A835EHQ0 A0A835EHQ0_9POAL	---MSGRRRPAAGGGGG---GGGGGGGNW---RRGSSAAKEQRLRLGAEELLESLGFA	51
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	---MSGRRRPAAGGGGG---GGGGGGGNW---RRGSSAAKEQRLRLGAEELLESLGFA	51
tr A0A368PL62 A0A368PL62_SETIT	---MSGRRRPAAGGGGGGGGGGGGGGGGNW---RRGSSAAKEQRLRLGAEELLESLGFA	55

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	LFSEGETRLGWLTLFASSSWEDDPDFGKTYSCVDLYFVTQDGFYFKTKYKFRPYFYAATKE	96
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	LFSEGETRLGWLTLFASSSWEDDPDFGKTYSCVDLYFVTQDGFYFKTKYKFRPYFYAATKE	96
sp F4HW04 DPOE1_ARATH	LFSEGETRLGWLTLFASSSWEDRDTGKTYSCVDLYFVTQDGFYFKTKYKFRPYFYAATKD	96
tr D7KI06 D7KI06_ARALL	LFSEGETRLGWLTLFASSSWEDRDTGKTYSCVDLYFVTQDGFYFKTKYKFRPYFYAATKD	96
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	LFSQDQKRLGWLTLFAPSSWEDDQTRVYHSCVDLYFVSDQDGFYFKSKYKFRPYFYAATKG	97
tr A0A7J7C034 A0A7J7C034_TRIWF	LFSEGDKRLGWLTLFASSSWEDDQFNKYSCIDLYFVTQDGFYFKSKCREPYFYAATKE	97
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	LFTGEDKRLGWLTLFASSSWEDDQFRKYSHSCVDLYFVSDQDGFYFKSKFKFRPYFYAATKD	97
tr A0A2C9VYG0 A0A2C9VYG0_MANES	LFTGEDKRLGWLTLFASSSWEDDQFRKYSHSCVDLYFVSDQDGFYFKSKFKFRPYFYAATKE	97
tr A0A2N9F976 A0A2N9F976_FAGSY	IFSEGEKRLGWLTLFAPSSWEDDQFRQYHSCVDLYFVTQDGFYFKAKHKFRPYFYAATKD	96
tr A0A7N2KME6 A0A7N2KME6_QUELO	LFSEGDKRLGWLTLFAPSSWEDDQFQHYHSCVDLYFVSDQDGFYFKSKYKFRPYFYAATKE	96
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	LFTSEGETRLGWLTLFASSSWEDDQFNKYSCVDLYFVTQDGFYFKCKYKFRPYFYAATKE	97
tr A0A619QIG1 A0A619QIG1_ELAGV	LFTSEGETRLGWLTLFAPSSWEDDQFNKYSCVDLYFVTQDGFYFKVKYFRPYFYAATKE	95
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	LFTSEGETRLGWLTLFAPSSWEDDQFNKYSCVDLYFVTQDGFYFKVKYFRPYFYAATKE	95
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	LFTSEGETRLGWLTLFAPSSWEDDQFNKYSCVDLYFVTQDGFYFKVKYFRPYFYAATKE	95
tr A0A816WFC8 A0A816WFC8_HORVV	PYTDGERRLGWLTLFAPSSWEDDQFNKYSCVDLYFVSDQDGFYFKVKYFRPYFYAATKE	120
tr A0A452YAR6 A0A452YAR6_AEGTS	PYTDGERRLGWLTLFAPSSWEDDQFNKYSCVDLYFVSDQDGFYFKVKYFRPYFYAATKE	60
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	PYTDGERRLGWLTLFAPSSWEDDQFNKYSCVDLYFVSDQDGFYFKVKYFRPYFYAATKE	115
tr A0A3L6E143 A0A3L6E143_MAIZE	PYTDGERRLGWLTLFAPSSWEDDQFNKYSCVDLYFVSDQDGFYFKAKYKFRPYFYAATKD	112
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	PYTDGERRLGWLTLFAPSSWEDDQFNKYSCVDLYFVSDQDGFYFKVKYFRPYFYAATKD	112
tr A0A835B357 A0A835B357_9POAL	PYTDGERRLGWLTLFAPSSWEDDQFNKYSCVDLYFVSDQDGFYFKVKYFRPYFYAATKD	106
tr A0A835EHQ0 A0A835EHQ0_9POAL	PYTDGERRLGWLTLFAPSSWEDDQFNKYSCVDLYFVSDQDGFYFKVKYFRPYFYAATKD	111
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	PYTDGERRLGWLTLFAPSSWEDDQFNKYSCVDLYFVSDQDGFYFKVKYFRPYFYAATKD	111
tr A0A368PL62 A0A368PL62_SETIT	PYTDGERRLGWLTLFAPSSWEDDQFNKYSCIDLYFVSDQDGFYFKVKYFRPYFYAATKD	115

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	KMELEVEAYLRRRYERQVA	DIEI	VEKE	DLD	LKNHLSGL	RRKYLK	VS	FDIV	QQLMEV	KR	154			
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	KMELEVEAYLRRRYERQVA	DIEI	VEKE	DLD	LKNHLSGL	RRKYLK	VS	FDIV	QQLMEV	KR	154			
sp F4HW04 DPOE1_ARATH	KMELEVEAYLRRRYERQVA	DIEI	VEKE	DLD	LKNHLSGL	QKKYLKIS	FDIV	QQLMEV	KR	154	NLS			
tr D7K106 D7K106_ARALL	KMELEVEAYLRRRYERQVA	DIEI	VEKE	DLD	LKNHLSGL	QKKYLKIS	FDIV	QQLMEV	KR	154				
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	KMEADVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	RKL	YKLS	FDIV	QQLM	DKR	155			
tr A0A7J7C034 A0A7J7C034_TRIWF	KMEMDVAEYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	RKL	YKLS	FDIV	QQLM	DKR	155			
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	KMEMDVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	RKL	YKLS	FDIV	QQLM	DKR	155			
tr A0A2C9VYGO A0A2C9VYGO_MANES	KMEMDVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	RKL	YKLS	FDIV	QQLM	DKR	155			
tr A0A2N9F976 A0A2N9F976_FAGSY	KMEVDVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	N	SPLGSK	AYG	QLT	PPEN	QLP	156		
tr A0A7N2KME6 A0A7N2KME6_QUELO	KTEVDVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	H	KPYL	KLS	FDIV	QQLM	NVKS	154		
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	NMERDVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	Q	KY	LKLS	Q	F	DIV	QQLM	MRVKS	155
tr A0A6I9QIG1 A0A6I9QIG1_ELAVG	KMELEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	H	KAY	LKLS	FDIV	QQLM	HVKN	153		
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	KMGLEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	H	KAY	LKLS	FDIV	QQLM	HVKN	153		
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	KMGLEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	H	KAY	LKLS	FDIV	QQLM	HVKN	153		
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	KTELEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	R	KY	LKLS	Q	F	DIV	QQLM	MRVRS	178
tr A0A452YAR6 A0A452YAR6_AEGTS	KTELEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	R	KY	LKLS	Q	F	DIV	QQLM	MRVRS	178
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	KTELEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	R	KY	LKLS	Q	F	DIV	QQLM	MRVRS	113
tr A0A3L6EI43 A0A3L6EI43_MAIZE	KMELEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	R	KY	LKLS	Q	F	DIV	QQLM	MRVRS	170
tr A0A1D6H820 A0A1D6H820_MAIZE	KMELEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	R	KY	LKLS	Q	F	DIV	QQLM	MRVRS	170
tr A0A835B357 A0A835B357_9POAL	KMELEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	R	KY	LKLS	Q	F	DIV	QQLM	MRVRS	164
tr A0A835EHQ0 A0A835EHQ0_9POAL	KMELEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	R	KY	LKLS	Q	F	DIV	QQLM	MRVRS	169
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	KMELEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	R	KY	LKLS	Q	F	DIV	QQLM	MRVRS	169
tr A0A368PL62 A0A368PL62_SETIT	KMELEVEAYLRRRYEQVA	DIEI	VEKE	DLD	LKNHLSGL	R	KY	LKLS	Q	F	DIV	QQLM	MRVRS	173
	: : : : *	***	*	:	***	*	:	***	*	:	***	*	:	

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	EQRLDQCLDLSL	DLREYDVPYHVRFAI	DKD	VR	SGQWYNVSI	SST	DVT	LEKRT	DL	LQR	AEV	241		
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	EQRLDQCLDLSL	DLREYDVPYHVRFAI	DKD	VR	SGQWYNVSI	SST	DVT	LEKRT	DL	LQR	AEV	241		
sp F4HW04 DPOE1_ARATH	EQRPDQCLDLSI	DLREYDVPYHVRFAI	DND	VR	SGQWYNVSI	SST	DVT	LEKRT	DL	LQR	AEV	241		
tr D7K106 D7K106_ARALL	EQRPDQCLDLSI	DLREYDVPYHVRFAI	DND	VR	SGQWYNVSI	SST	DVT	LEKRT	DL	LQR	AEV	241		
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	EQRLDQFLDLSI	DLREYDVPYHVRFAI	DND	VR	CGQWYDVSV	SS	TG	VML	LEKRT	DL	LQR	AEV	257	
tr A0A7J7C034 A0A7J7C034_TRIWF	EQRPDQFLDCV	DLREYDVPYHVRFAI	DND	VR	CGQWYDVSV	SS	TG	VML	LEKRT	DL	LQR	AEV	242	
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	EQRPDQLDLCV	DLREYDVPYHVRFAI	DND	VR	CGQWYDVTV	SN	R	GV	T	LEKRT	DL	LQR	AEV	243
tr A0A2C9VYGO A0A2C9VYGO_MANES	EQRPDQLDLCV	DLREYDVPYHVRFAI	DND	VR	CGQWYDVTV	SN	R	GV	T	LEKRT	DL	LQR	AEV	242
tr A0A2N9F976 A0A2N9F976_FAGSY	NKGPQDFLDCV	DLREYDVPYHVRFAI	DND	VR	CGQWYDVSV	SS	TG	VML	LEKRT	DL	LQR	AEV	261	
tr A0A7N2KME6 A0A7N2KME6_QUELO	EQRPDQFLDCV	DLREYDVPYHVRFAI	DND	VR	CGQWYDVSV	SS	TG	VML	LEKRT	DL	LQR	AEV	241	
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	KERPQDFLDCV	DLREYDVPYHVRFAI	DND	VR	CGQWYDVSI	SG	N	VLL	LEKRT	DL	LQR	AEV	242	
tr A0A6I9QIG1 A0A6I9QIG1_ELAVG	KERPQDYIDCI	DLREYDVPYHVRFAI	DND	VR	CGQWYDVNV	SS	G	IL	LEKRT	DL	LQR	AEV	240	
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	KERPQDYIDCI	DLREYDVPYHVRFAI	DND	VR	CGQWYDIN	V	SS	G	IL	LEKRT	DL	LQR	AEV	240
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	KERPQDYIDCI	DLREYDVPYHVRFAI	DND	VR	CGQWYDIN	V	SS	G	IL	LEKRT	DL	LQR	AEV	240
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	VERPQDYINCI	DLREYDVPYHVRFAI	DND	VR	SGQWYNV	SV	SS	D	VLL	LEKRT	DL	LQR	AEV	265
tr A0A452YAR6 A0A452YAR6_AEGTS	VERPQDYINCI	DLREYDVPYHVRFAI	DND	VR	SGQWYNV	SV	SS	D	VLL	LEKRT	DL	LQR	AEV	205
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	VERPQDYINCI	DLREYDVPYHVRFAI	DND	VR	SGQWYNV	SV	SS	D	VLL	LEKRT	DL	LQR	AEV	260
tr A0A3L6EI43 A0A3L6EI43_MAIZE	VERPQDYINYI	DLREYDVPYHVRFAI	DND	VR	SGQWYNV	SV	SS	D	VLL	LEKRT	DL	LQR	AEV	257
tr A0A1D6H820 A0A1D6H820_MAIZE	VERPQDYINYI	DLREYDVPYHVRFAI	DND	VR	SGQWYNV	SV	SS	D	VLL	LEKRT	DL	LQR	AEV	257
tr A0A835B357 A0A835B357_9POAL	VERPQDYINYI	DLREYDVPYHVRFAI	DND	VR	CGQWYNV	SV	SS	D	VLL	LEKRT	DL	LQR	AEV	251
tr A0A835EHQ0 A0A835EHQ0_9POAL	VERPQDYINYI	DLREYDVPYHVRFAI	DND	VR	CGQWYNV	SV	SS	D	VLL	LEKRT	DL	LQR	AEV	256
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	VERPQDYINYI	DLREYDVPYHVRFAI	DND	VR	CGQWYNV	SV	SS	D	VLL	LEKRT	DL	LQR	AEV	256
tr A0A368PL62 A0A368PL62_SETIT	VERPQDYINYI	DLREYDVPYHVRFAI	DKD	VR	CGQWYNV	SV	SS	D	VLL	LEKRT	DL	LQR	AEV	260
	: * * : :	*****	*	:	***	*	:	***	*	:	***	*	:	

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	RVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	298	
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	RVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	298	
sp F4HW04 DPOE1_ARATH	RVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	298	
tr D7K106 D7K106_ARALL	RVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	301	
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	HI	CAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	314
tr A0A7J7C034 A0A7J7C034_TRIWF	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	299	
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	RVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	300	
tr A0A2C9VYGO A0A2C9VYGO_MANES	RVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	299	
tr A0A2N9F976 A0A2N9F976_FAGSY	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	318	
tr A0A7N2KME6 A0A7N2KME6_QUELO	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	298	
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	299	
tr A0A6I9QIG1 A0A6I9QIG1_ELAVG	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	297	
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	297	
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	297	
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	322	
tr A0A452YAR6 A0A452YAR6_AEGTS	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	262	
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N	R	E	---	CV	G	E	D	I	E	D	L	E	Y	T	P	K	317	
tr A0A3L6EI43 A0A3L6EI43_MAIZE	HVCAF	DIE	TKL	LKF	PD	AEYD	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	295	
tr A0A1D6H820 A0A1D6H820_MAIZE	HVCAF	DIE	TKL	LKF	PD	AEYD	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	295	
tr A0A835B357 A0A835B357_9POAL	HVCAF	DIE	TKL	LKF	PD	AEYD	Q	MMIS	Y	M	V	D	G	G	F	L	I	N</																		

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD MFSSANKDGVLDK-----	1219
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD MFSSANKDGVLDK-----	1219
sp F4HW04 DPOE1_ARATH	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD MFSSANKDGVLDLDT-----	1167 NLS
tr D7KI06 D7KI06_ARALL	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD MFSSANKDGGLET-----	1184
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	EDKFRQRKLD DIFSLCNKDAVLRNTTDDGT	1189
tr A0A7J7C034 A0A7J7C034_TRIWF	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	EDKFRQRKLD DIFSSSHRNDLLEKANN-SI	1173
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	EDKFRQRKLD DIFSLNSNGDESSRRTSD--S	1173
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	EDKFRQRKLD DIFSLNSNGDESSRRTSD--S	1172
tr A0A2N9F976 A0A2N9F976_FAGSY	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	EDKFRQRKLD DIFSLNKKDLDLTKNSDAAG	1158
tr A0A7N2KME6 A0A7N2KME6_QUELO	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	EDKFRQRKLD DIFSSLNDRDEFLLKNSDAAG	1173
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD DMFGPI NGGTMQNHAS-VD	1173
tr A0A6I9QIG1 A0A6I9QIG1_ELAGV	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	EDKFRQRKLD DIFSTVNKDETIMQ-----	1166
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	SI PAAMQKV ANPVPRLV HPDWL HKKVREK	EDKFRQRKLD DIFNTVNKDETMQ-----	1165
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	SI PAAMQKV ANPVPRLV HPDWL HKKVREK	EDKFRQRKLD DIFNTVNKDETMQ-----	1165
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD DMFSPLNKDMGM-H-----	1189
tr A0A452YAR6 A0A452YAR6_AEGTS	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD DMFSPLNKDMGM-H-----	1129
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD DMFSPLNKDMGM-H-----	1184
tr A0A3L6EI43 A0A3L6EI43_MAIZE	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD DIFSPLAKEEGL-H-----	1162
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD DIFSPLAKEEGL-H-----	1162
tr A0A835B357 A0A835B357_9POAL	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD DIFSPLAKDERI-Q-----	1175
tr A0A835EHQ0 A0A835EHQ0_9POAL	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD DIFSPLAKDERI-Q-----	1180
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD DIFSPLAKEDEGM-Q-----	1180
tr A0A368PL62 A0A368PL62_SETIT	TI PAAMQKV ANPVPRLV HPDWL HKKVREK	DDKFRQRKLD DIFSPLAKEDEGM-R-----	1184

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	-NHSVAQDDMDI EIEFCENK-PGVKGPKP--IARSYEVNKEQFGRQOE-----	1265
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	-NHSVAQDDMDI EIEFCENK-PGVKGPKP--IARSYEVNKEQFGRQOE-----	1265
sp F4HW04 DPOE1_ARATH	-DLFVTKDNVE DIEFCENK--PSVKGPKP--IARSYEVNKKQSECEQOE-----	1213
tr D7KI06 D7KI06_ARALL	-DHPVTKNVVE DIEFCENK--PSVKGPKP--IARSYEVNKKQSEREQOE-----	1230
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	SNH-LADRNVQ DLEDFLNQS--SSVNGPRP--IVRSYEVSNKGSVVKKTG---KVDSEAO	1241
tr A0A7J7C034 A0A7J7C034_TRIWF	INPVTNGEHEV DMEDFGSKTR-SPVNGPRP--VVNSYEFNKNKRPVQITIG---QVESLQ	1227
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	ADHIMNKENVE DLEDFGNKS--SSKNGPRP--IVRLYEMNKGKCLQNTAG---RMDSSQ	1226
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	ADHIMNKENVE DLEDFGNKS--SSKNGPRP--IVRLYEMNKGKCLQNTAG---RMDSSQ	1225
tr A0A2N9F976 A0A2N9F976_FAGSY	TDGVMNEEIVE DLEDFGNK--SSVNGPRP--IVRCYEVNRRQHSVKTNG---QVGHLLR	1212
tr A0A7N2KME6 A0A7N2KME6_QUELO	ANGVMNEEIVK DLEDFGNKSR-KSVTGRPP--IVRCYEVNRRQHSVKTND---QVGLQ	1227
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	SNHELHEMIEI DMEFLIMNKEHSSVTGPRP--TVRSYAANKENLLANASSPCSKLDRQ	1231
tr A0A6I9QIG1 A0A6I9QIG1_ELAVG	-----DEMNVG DMEFLIAKQDV-S-KGPRP--VVHSYEVNKENYSSKQSCPEAGLLSH	1217
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	-----DGTNVG DMEFLVTRKRV-SEVGLRP--VAHSYEVNKENYSSKQSCPEAGVLLNHG	1217
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	-----DGTNVG DMEFLVTRKRV-SEVGLRP--VAHSYEVNKENYSSKQSCPEAGVLLNHG	1217
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	-----NLNGTG DIEDLLTSD---KGLRKTASHGFNMGKGNHFNGLPSAEASLGHCNK	1239
tr A0A452YAR6 A0A452YAR6_AEGTS	-----NLNGTG DIEDLLTSD---KGLRKTASHGFNMGKGNHFNGLPSAEASLGHCNK	1179
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	-----NLNGTG DIEDLLTSD---KGLRKTASHGFNMGKGNHFNGLPSAEASLGHCNK	1234
tr A0A3L6EI43 A0A3L6EI43_MAIZE	-----NLNRTG DMEFLIISN---KDLRKN-PSHGLDIDKENNPNVASVGS-G-LNISKK	1210
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	-----NLNRTG DMEFLIISN---KDLRKN-PSHGLDIDKENNPNVASVGS-G-LNISKK	1210
tr A0A835B357 A0A835B357_9POAL	-----NLNGTG DMEFLLVSN---KDLRKN-SSHGLDIDKENNPNVASVGS-G-SNNSKN	1223
tr A0A835EHQ0 A0A835EHQ0_9POAL	-----NLNGTG DMEFLLVSN---KDLRKN-SSHGLDIDKENNPNVASVGS-G-SNNSKN	1228
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	-----NLNGAG DMEFLLVSN---KDLRKN-SSHGLDIDKENNPNVASVGS-G-SNNSKN	1228
tr A0A368PL62 A0A368PL62_SETIT	-----SLNGTG DMEFLLVSN---KDLRKN-SSHGLDIDKENNPNVASVGS-G-SNNSKN	1232

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	---S-----KDPKDDDISFENIDKNVDYQGWLVEKRRKWKVIVEKRRRRLGDRSL	1315
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	---S-----KDPKDDDISFENIDKNVDYQGWLVEKRRKWKVIVEKRRRRLGDRSL	1315
sp F4HW04 DPOE1_ARATH	---S-----WDTEF-HDISFQNIKDSVNYQGWLVEKRRKWKVTLKRRRRLGDLRSL	1262 NLS
tr D7KI06 D7KI06_ARALL	---S-----WDPEF-HDISFQNIKDSVNYQGWLVEKRRKWKVTLKRRRRLGDLRSL	1279
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	QSSHTAEIHEFSSQLNTPSEDI DRNVYDQGWLVVKKRKKWETLAKRKKQLGSLGTS	1301
tr A0A7J7C034 A0A7J7C034_TRIWF	QTDGK-----NDLFTDNI DNKNDYQGWLEKRRKWKDTLAKRKRRLGSLRTP	1275
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	QINN-----RESIELLQNASSTESIDRNVDYQGWLEKRRKWKDVLDRKRKRRLGSLRNS	1282
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	QINN-----RESIELLQNASSTESIDRNVDYQGWLEKRRKWKDVLDRKRKRRLGSLRNS	1281
tr A0A2N9F976 A0A2N9F976_FAGSY	QDDHSENVLQELPPLQNSLSENI DRNVYDQGWLEKRRKWKDTLEKRRKRRLGSLRTP	1272
tr A0A7N2KME6 A0A7N2KME6_QUELO	QTDHRL-----PALSENI DNKNDYQGWLEKRRKWKDTLEKRRKRRLGSLRTP	1276
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	QEDGAHGKHPQLLSPMENLISTSDS IDRNVDYQGWLEKRRKWKDTREKRRRRLGAMGDS	1291
tr A0A6I9QIG1 A0A6I9QIG1_ELAVG	QQNA--TLCRPLLSNQNGTCESEVDRNI DYQAWLEKRRKWKDTREKRRRRLGITKMS	1275
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	QQNA--TLCRPLLSFNQNDICSEIVDRNVYQAWLEKRRKWKDTREKRRRRLGITKMS	1275
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	QQNA--TLCRPLLSFNQNDICSEIVDRNVYQAWLEKRRKWKDTREKRRRRLGITKMS	1275
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	QQKSVIRSNP-----LRDSDADVRDSTDYQGWLEKRRKWKVREKRRRRLGAAASS	1295
tr A0A452YAR6 A0A452YAR6_AEGTS	QQKSVIRSNP-----LRDSDADVRDSTDYQGWLEKRRKWKVREKRRRRLGAAASS	1235
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	QQKSVIRSNP-----LRDSDADVRDSTDYQGWLEKRRKWKVREKRRRRLGAAASS	1290
tr A0A3L6EI43 A0A3L6EI43_MAIZE	QQNCMTGLNVPCSTQIQNAASYETVDKGTDYQGWLEKRRKWKVREKRRRRLGAAATF	1270
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	QQNCMTGLNVPCSTQIQNAASYETVDKGTDYQGWLEKRRKWKVREKRRRRLGAAATF	1270
tr A0A835B357 A0A835B357_9POAL	QRNSKTGLNAPLSSQMPNVADEITDRSSDYQGWLEKRRKWKVREKRRRRLGAAATF	1288
tr A0A835EHQ0 A0A835EHQ0_9POAL	QRNSKTGLNAPLSSQMPNVADEITDRSSDYQGWLEKRRKWKVREKRRRRLGAAATF	1288
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	QQNSVTGLNVPLSSQIQNAVADEITDRSTDYQGWLEKRRKWKVREKRRRRLGAAATF	1288
tr A0A368PL62 A0A368PL62_SETIT	QQNSITGLNVPLSSQIQNAVADEITDRSTDYQGWLEKRRKWKVREKRRRRLGAAATF	1292

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	KQIESH-----EIKKVVTVRRGVGS	FFRRPEEALTSSSHQWI-----	1352
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	KQIESH-----EIKKVVTVRRGVGS	FFRRPEEALTSSSHQWI-----	1352
sp F4HW04 DPOE1_ARATH	NQVDTH-----EINQKVGQGRGGVGS	YFRRPEEALTSSSHQWI-----	1299
tr D7KI06 D7KI06_ARALL	NQSDAH-----EINQKVGQGRGGVGS	YFRRPEEALTSSSHQWVCT-----	1318
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	RGSDGAFEHLSGLGTEKE	YFTRPEVVLTRCHWQ-----	1343
tr A0A7J7C034 A0A7J7C034_TRIWF	HRADGASEVMEGMISKRG---DQAKTGVGS	YFRRHEVALTRCHWQ-----	1317
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	NRANGASEPLGSLINNK---AQHRTGVGS	YFATHEISLTRCHWQ-----	1324
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	NRANGASEPLGSLINNK---AQHRTGVGS	YFATHEISLTRCHWQ-----	1323
tr A0A2N9F976 A0A2N9F976_FAGSY	HRNGVSDLLGGVTNGKD---TQGRSGVGS	YFRRQEVALLTRCHWQ-----	1314
tr A0A7N2KME6 A0A7N2KME6_QUELO	RRGKGVLEVLGDVTHNKD---TQGRSGVGS	YFRRHEVALTRCHWQ-----	1318
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	SQFVAMAGNHESMTSNKH---NIAKNGAVS	YFRRQELLVHNNHWQ-----	1333
tr A0A6I9QIG1 A0A6I9QIG1_ELAVG	QQSAGAALKPASMFPYRRG---QDRSGVSS	FFRRQELALVQSHWQ-----	1317
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	QQSAGAALKPASMFPYRHH---QDRSGVSS	FFRRQELALVQSHWQ-----	1317
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	QQSAGAALKPASMFPYRHH---QDRSGVSS	FFRRQELALVQSHWQ-----	1317
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	EGSPNN-----LFSARNGSQLHGNGRNRST	FFQKQELSLFRSHWQ-----	1335
tr A0A452YAR6 A0A452YAR6_AEGTS	EGSPNN-----LFSARNVSQLHGNSRNRST	FFQKQELSLFRSHWQ-----	1275
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	EGSPNN-----LFSARNDSQLHGNGRNRST	FFQKQELSLFRSHWQ-----	1330
tr A0A3L6EI43 A0A3L6EI43_MAIZE	HVS-LL-----LPGWVLPPLLTLLTLCRSF	YFRRQELALVQSHWQ-----	1295
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	DDP-NA-----LLSARHANQLPNSRNRST	FFQKQELALFRSHWQACV---FCYLLCSVA	1321
tr A0A835B357 A0A835B357_9POAL	DGPTNA-----LLSSRNANQLPNSRNRST	FFQKQELALFRSHWQ-----	1323
tr A0A835EHQ0 A0A835EHQ0_9POAL	DGPTNA-----LLSSRNANQLPNSRNRST	FFQKQELALFRSHWQ-----	1328
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	DGPTNA-----LLSSRNVSQLPNSRNRST	FFQKQELALFRSHWQ-----	1328
tr A0A368PL62 A0A368PL62_SETIT	DGPTNA-----LLSSRNVSQLPNSRNRST	FFQKQELALFRSHWQ-----	1332

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	LHKVMQKVFALLLTDLRR	LGATIIYADFSKVIIDT	GKFDLSAAKAY	CSLLTAVGNSDIF	1866
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	LHKVMQKVFALLLTDLRR	LGATIIYADFSKVIIDT	GKFDLSAAKAY	CSLLTAVGNSDIF	1866
sp F4HW04 DPOE1_ARATH	LHKVMQKVFALLLTDLRR	LGATIIYADFSKVIIDT	VKFDLSAAKAY	CSLLSTVGNSDIF	1847
tr D7KI06 D7KI06_ARALL	LHKVMQKVFALLLTDLRR	LGATIIYADFSKVIIDT	VKFDLSAAKAY	CSLLSTVGNRVS	1865
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	LHKVMQKVFALLLAEELRR	LGATIIYADFSKVIIDT	GKFNLSAAQAY	CNSLVKTLQSRMF	1907
tr A0A7J7C034 A0A7J7C034_TRIWF	LHKVMQKVFALLLAEELRR	LGATIIYADFSKVIIDT	GKSDIAAAKAY	CDSLVKALQTRFL	1866
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKLSLSAAKAY	CDSLLKTLQSRFL	1874
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKLSLSAAKAY	CDSLLKTLQSRFL	1873
tr A0A2N9F976 A0A2N9F976_FAGSY	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKFDLSAAKAY	CDSLLKTLQNRDLF	1864
tr A0A7N2KME6 A0A7N2KME6_QUELO	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKFDLSAAKAY	CDSLLKTLQKRDLF	1867
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKFDLSAAKAY	CDSLLKALQARDLL	1874
tr A0A6I9QIG1 A0A6I9QIG1_ELAGV	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKIDLSAAKAY	CDSLLKTLQTRDLF	1864
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKIDLSAAKAY	CDSLLKTLQTRDLF	1864
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKIDLSAAKAY	CDSLLKTLQTRDLF	1867
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKVDLPSAAKAY	CDSLLKTLQTRDLF	1879
tr A0A452YAR6 A0A452YAR6_AEGTS	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKVDLPSAAKAY	CDSLLKTLQTRDLF	1819
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKVDLPSAAKAY	CDSLLKTLQTRDLF	1874
tr A0A3L6EI43 A0A3L6EI43_MAIZE	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKVDLSAAKAY	CDSLLKTLQTRDLF	1870
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKVDLSAAKAY	CDSLLKTLQTRDLF	1887
tr A0A835B357 A0A835B357_9POAL	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKVDLSAAQAY	CNSLLKTLQTRDLF	1865
tr A0A835EHQ0 A0A835EHQ0_9POAL	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKVDLSAAQAY	CNSLLKTLQTRDLF	1872
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKVDLSAAHAY	CNSLLKTLQTRDLF	1872
tr A0A368PL62 A0A368PL62_SETIT	LHKVMQKVFALLLAEFRK	LGATIIYADFSKVIIDT	GKVDLSAAHAY	CNSLLKTLQTRDLF	1876

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	-----VMKRNLLKYINVKEFAAEAEFLDPGPFILPNV	CSNC	DAYR	2066
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	-----ILFLKLCFAVMKRNLLKYINVKEFAAEAEFLDPGPFILPNV	CSNC	DAYR	2080
sp F4HW04 DPOE1_ARATH	-----VMKRSLLYKVKCEAAAEFLDPGPFILPNV	CSNC	DAYR	2046
tr D7KI06 D7KI06_ARALL	SNLSIGNLVLETMTNRMKRSLLKYIKVKECAAEAEFLDPGPFILPNV	CSNC	DAYR	2126
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	-----VMRNLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2145
tr A0A7J7C034 A0A7J7C034_TRIWF	-----VMRNLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2091
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	-----VMRNLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2111
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	-----VMRNLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2110
tr A0A2N9F976 A0A2N9F976_FAGSY	-----VMRNLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2054
tr A0A7N2KME6 A0A7N2KME6_QUELO	-----VMRNLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2094
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2103
tr A0A6I9QIG1 A0A6I9QIG1_ELAGV	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2097
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2097
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2100
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2108
tr A0A452YAR6 A0A452YAR6_AEGTS	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2048
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2103
tr A0A3L6EI43 A0A3L6EI43_MAIZE	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2094
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2111
tr A0A835B357 A0A835B357_9POAL	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2093
tr A0A835EHQ0 A0A835EHQ0_9POAL	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2098
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2098
tr A0A368PL62 A0A368PL62_SETIT	-----RMRNLLKLVVRFVREFAAEAEFLDPGPFILPNV	CSNC	DAYR	2102

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	LDIGRDPALLTEKEWCC	DSQC	KIYDREQ	MENSLQMVQRERMYHMQD	IFCF	NOVK	2126
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	LDIGRDPALLTEKEWCC	DSQC	KIYDREQ	MENSLQMVQRERMYHMQD	IFCF	NOVK	2140
sp F4HW04 DPOE1_ARATH	LDICRDPALLTEKEWCS	ADTQC	GKIYDREQ	MENSLQMVQRERMYHMQD	IVIR	NOVK	2106
tr D7KI06 D7KI06_ARALL	LDICRDPALLTEKEWCS	ADTQC	KIYDREQ	MENSLQMVQRERMYHMQD	IFCF	NOVK	2186
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	LDICRDPALLTEKEWCS	ADTQC	KIYDREQ	MENSLQMVQRERMYHMQD	IFCF	NOVK	2204
tr A0A7J7C034 A0A7J7C034_TRIWF	LDICRDSALL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2150
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	LDICRDPALLTEKEWCS	ADTQC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2170
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	LDICRDPALLTEKEWCS	ADTQC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2169
tr A0A2N9F976 A0A2N9F976_FAGSY	LDICRDSVLL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2113
tr A0A7N2KME6 A0A7N2KME6_QUELO	LDICRDSVLL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2153
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	LDLSRDSALL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2162
tr A0A6I9QIG1 A0A6I9QIG1_ELAGV	LDICRDSALS-DNEWR	CSVPC	QSYNREQ	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2156
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	LDICRDSALS-DNEWR	CSVPC	QSYNREQ	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2156
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	LDICRDSALS-DNEWR	CSVPC	QSYNREQ	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2159
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	LDICRDSVLL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2167
tr A0A452YAR6 A0A452YAR6_AEGTS	LDICRDSVLL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2107
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	LDICRDSVLL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2162
tr A0A3L6EI43 A0A3L6EI43_MAIZE	LDICRDSALS-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2153
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	LDICRDSALS-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2170
tr A0A835B357 A0A835B357_9POAL	LDICRDSVLL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2152
tr A0A835EHQ0 A0A835EHQ0_9POAL	LDICRDSVLL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2157
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	LDICRDSVLL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2157
tr A0A368PL62 A0A368PL62_SETIT	LDICRDSVLL-AQEWRC	AVPCC	QPYDREVM	MENSLQIVRQRERLYHLQD	IVCF	NOVK	2161

tr A0A8D9D0I3 A0A8D9D0I3_BRACM	AAHLTEQC	SGSFRCKESGSEFLKRM	EFLDIAKQKFKLLEECTSWILDPTG	SWQNTNT	2186
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	AAHLTEQC	SGSFRCKESGSEFLKRM	EFLDIAKQKFKLLEECTSWILDPTG	SWQNTNT	2200
sp F4HW04 DPOE1_ARATH	AAHLTEQC	SGSFRCKESGSEFLKRM	EFLDIAKQKFKLLEECTSWILDPTG	SWQNTNT	2161
tr D7KI06 D7KI06_ARALL	AAHLTEQC	SGSFRCKESGSEFLKRM	EFLDIAKQKFKLLEECTSWILDPTG	SWQNTNT	2241
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	AAHLTEQC	SGSFRCKESGSEFLKRM	EFLDIAKQKFKLLEECTSWILDPTG	SWQNTNT	2257
tr A0A7J7C034 A0A7J7C034_TRIWF	AAHLTEQC	SGSFRCKEDVSEFRKMQV	FLNVAIHQKFKLLREECTSWILEV	Q-----	2203
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	AAHLTEQC	SGSFRCKEDVSEFRKMQV	FLNVAIHQKFKLLREECTSWILEV	Q-----	2223
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	AAHLTEQC	SGSFRCKEDVSEFRKMQV	FLNVAIHQKFKLLREECTSWILEV	Q-----	2222
tr A0A2N9F976 A0A2N9F976_FAGSY	AAHLTEQC	SGSFRCKEDVSEFRKMQV	FLNVAIHQKFKLLREECTSWILEV	Q-----	2166
tr A0A7N2KME6 A0A7N2KME6_QUELO	AAHLTEQC	SGSFRCKEDVSEFRKMQV	FLNVAIHQKFKLLREECTSWILEV	Q-----	2206
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	ADHLAEC	CGSFGCEESSADFLRMMQV	FLKVALGQKFLLLRDCVSWILEV	Q-----	2215
tr A0A6I9QIG1 A0A6I9QIG1_ELAGV	ADHLAEC	CGSFRCKEDVSEFRKMQV	FLNVAIHQKFKLLREECTSWILEV	Q-----	2209
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	AAHLTEQC	SGSFRCKEDVSEFRKMQV	FLNVAIHQKFKLLREECTSWILEV	Q-----	2209
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	AAHLTEQC	SGSFRCKEDVSEFRKMQV	FLNVAIHQKFKLLREECTSWILEV	Q-----	2212
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	AAHVSEC	CGSFRCKEEAPQFLGKMRV	FLNVAIVSQKFLLDQCVRWILEV	Q-----	2218
tr A0A452YAR6 A0A452YAR6_AEGTS	AAHVSEC	CGSFRCKEEAPQFLGKMRV	FLNVAIVSQKFLLDQCVRWILEV	Q-----	2160
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	AAHVSEC	CGSFRCKEEAPQFLGKMRV	FLNVAIVSQKFLLDQCVRWILEV	Q-----	2215
tr A0A3L6EI43 A0A3L6EI43_MAIZE	AAHLSEC	CGSFRCKEESPFLSKMRV	FLKVAIVSQKFLLDQCVRWILEV	Q-----	2206
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	AAHLSEC	CGSFRCKEESPFLSKMRV	FLKVAIVSQKFLLDQCVRWILEV	Q-----	2223
tr A0A835B357 A0A835B357_9POAL	AAHLSEC	CGSFRCKEESPFLSKMRV	FLKVAIVSQKFLLDQCVRWILEV	Q-----	2205
tr A0A835EHQ0 A0A835EHQ0_9POAL	AAHLSEC	CGSFRCKEESPFLSKMRV	FLKVAIVSQKFLLDQCVRWILEV	Q-----	2210
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	AAHLSDC	CGSFRCKEESPFLSKMRV	FLNVAIVSQKFLLDQCVRWILEV	Q-----	2210
tr A0A368PL62 A0A368PL62_SETIT	AAHLSDC	CGSFRCKEESPFLSKMRV	FLNVAIVSQKFLLDQCVRWILEV	Q-----	2214

//End of the plant pol ε sequences		
tr A0A8D9D0I3 A0A8D9D0I3_BRACM	GRHHS	2191
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	GRHHS	2205
sp F4HW04 DPOE1_ARATH	-----	2161
tr D7KI06 D7KI06_ARALL	-----	2241
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	-----	2257
tr A0A7J7C034 A0A7J7C034_TRIWF	-----	2203
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	-----	2223
tr A0A2C9VYG0 A0A2C9VYG0_MANES	-----	2222
tr A0A2N9F976 A0A2N9F976_FAGSY	-----	2166
tr A0A7N2KME6 A0A7N2KME6_QUELO	-----	2206
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	-----	2215
tr A0A6I9QIG1 A0A6I9QIG1_ELAGV	-----	2209
tr A0A8B8JBU2 A0A8B8JBU2_PHODC	-----	2209
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	-----	2212
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	-----	2218
tr A0A452YAR6 A0A452YAR6_AEGTS	-----	2160
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	-----	2215
tr A0A3L6EI43 A0A3L6EI43_MAIZE	-----	2206
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	-----	2223
tr A0A835B357 A0A835B357_9POAL	-----	2205
tr A0A835EHQ0 A0A835EHQ0_9POAL	-----	2210
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	-----	2210
tr A0A368PL62 A0A368PL62_SETIT	-----	2214

NLS, Nuclear Localization Signal

A0A8D9D0I3_BRACM, <i>Brassica campestris</i>	A0A3P5YCF9_BRACM, <i>Brassica campestris</i>
F4HW04 DPOE1_ARATH, <i>Arabidopsis thaliana</i>	D7KI06_ARALL, <i>Arabidopsis lyrata</i> subsp. <i>lyrata</i>
A0A9Q0FIP5_9ROSI, <i>Turnerasubulata</i>	A0A7J7C034_TRIWF, <i>Tripterygium wilfordii</i>
A0A2C9VYJ6_MANES, <i>Manihot esculenta</i>	A0A2C9VYG0_MANES, <i>Manihot esculenta</i>
A0A2N9F976_FAGSY, <i>Fagus sylvatica</i>	A0A7N2KME6_QUELO, <i>Quercus lobata</i>
A0A7I8KHB8_SPIIN, <i>Spirodela intermedia</i>	A0A6I9QIG1_ELAGV, <i>Elaeisguineensis</i> var. <i>tenera</i>
A0A8B8JBC2_PHODC, <i>Phoenix dactylifera</i>	A0A8B8JBU2_PHODC, <i>Phoenix dactylifera</i>
A0A8I6WFC8_HORVV, <i>Hordeum vulgare</i>	A0A452YAR6_AEGTS, <i>Aegilops tauschii</i> subsp. <i>stragulata</i>
A0A3B5XXC3_WHEAT, <i>Triticum aestivum</i>	A0A3L6EI43_MAIZE, <i>Zea mays</i>
A0A1D6H8Z0_MAIZE, <i>Zea mays</i>	A0A835B357_9POAL, <i>Digitaria exilis</i>
A0A835EHQ0_9POAL, <i>Digitaria exilis</i>	A0A2S3GPC0_9POAL, <i>Panicum hallii</i>
A0A368PL62_SETIT, <i>Setariaitalica</i>	

Figure 3 MSA of the catalytic subunit of the DNA pol ε (Pol2A) from various plant sources

Figure 4 shows the MSA of the DNA pol ε from various animal sources (only the required regions for the discussions are shown here). The human sequence is used as the standard and highlighted. The PR exo and pol regions in the human sequence are highlighted in red and green, respectively, and the PR active site amino acids are highlighted in light blue and the pol active site amino acids are highlighted in yellow. The typical, completely conserved –DEDD- superfamily of PR exonuclease active site amino acids are found with an invariant Y as proton acceptor in the NTD and is in close agreement with the other RdRps/DdDps [8]. The proposed template-binding pair (-YG-), catalytic amino acid (K) and the dNTP selection amino acid (Q) are found in the pol domain and are in close agreement as reported in other DdDps and DdRps [8,16] and also with the plant enzymes (Fig.3). Unlike other two eukaryotic replicative pols, the pol ε harbours a unique ZBM within the pol domain, similar to the pol ε from the plant sources (highlighted). A dNTP selecting –SYLPVGS- motif is found within the first PR exo region as found in plant enzymes, –SYLPQGS-. However, a second PR exonuclease active site and a putative pol catalytic core are also identified in the CTD (highlighted). Similar to the –SYLPXXS- at the NTD, a –SYLEPGS- motif (highlighted in yellow) is found within the second PR exo region in the CTD. A large NTD deletion analysis has implicated a possible second pol region in the CTD, e.g., a large N-terminal deletion (Δ176-1134 amino acids) of the yeast *pol ε* gene (which deletes both the pol and PR exo domains), but retains the C-terminal region intact, showed that the yeast was viable, but grew slowly, suggesting a possible second pol active site in the CTD as discussed elsewhere [20]. The CTD contains the two regular ZBMs and one of them (CysB) binds the 4Fe-4S cluster (highlighted in orange) as found in all the three eukaryotic replicative pols. The putative NLSs are highlighted. Many conserved Ws are observed in the CTD, suggesting their possible involvement in interactions with the other subunits.

CLUSTAL O (1.2.4) MSA of ε DNA pols from various animal sources

		NTD ←	→ PR Exo		
tr A0A6Q2WNN8 A0A6Q2WNN8 ESOLU	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	291
tr A0A673YLH4 A0A673YLH4 SALTR	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A4W5MAK2 A0A4W5MAK2 9TELE	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A6F6MI98 A0A6F6MI98 CARAU	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	296
tr A0A498LK69 A0A498LK69 LABRO	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	295
tr A0A3Q2YTI5 A0A3Q2YTI5 HIPCM	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	296
tr M4A042 M4A042 XIPMA	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A6P8SZE0 A0A6P8SZE0 GYMCA	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	295
tr A0A3Q2PG22 A0A3Q2PG22 FUNHE	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A6A4SMP2 A0A6A4SMP2 SCOMX	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A673CZR7 A0A673CZR7 9TELE	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A671YAK3 A0A671YAK3 SPAUA	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A6F7J2Q5 A0A6F7J2Q5 9TELE	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A7N8YN60 A0A7N8YN60 9TELE	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	305
tr A0A3P8N896 A0A3P8N896 ASTCA	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	296
tr A0A3B4GLI9 A0A3B4GLI9 9CICH	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	296
tr A0A6A5F6M3 A0A6A5F6M3 FERFL	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A3Q1FLK4 A0A3Q1FLK4 9TELE	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A4W6G9K4 A0A4W6G9K4 LATCA	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A3B4YTJ5 A0A3B4YTJ5 SERLL	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A665X3K2 A0A665X3K2 ECHNA	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A7J7RQ84 A0A7J7RQ84 RHIFE	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	269
tr A0A6P6D0R3 A0A6P6D0R3 PTEVA	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	288
tr A0A7J8H4F1 A0A7J8H4F1 ROUAE	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	302
tr A0A5F4D2S5 A0A5F4D2S5 CANLF	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	331
sp Q07864 DP0E1 HUMAN	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	296
tr A0A2I3S482 A0A2I3S482 PANTR	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	296
tr A0A2K6CI58 A0A2K6CI58 MACNE	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	296
tr A0A834DIT3 A0A834DIT3 9CHIR	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	296
tr F62911 F62911 HORSE	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	296
tr A0A5G2RB90 A0A5G2RB90 FIG	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A670JF16 A0A670JF16 PODMU	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	294
tr A0A852LC41 A0A852LC41 UROIN	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	312
tr F62FB6 F62FB6 ORNAN	-----	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	171
tr A0A6P5LNS3 A0A6P5LNS3 PHACI	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	297
tr A0A4X2K1K8 A0A4X2K1K8 VOMUR	KIHVAHWYNVRYRGSAYPPEIITLRSDLVER	PDPVVLAF	DIE	TTKLLPKFFDAETDQIMMI	281
		*****	..*	*****	

tr A0A6Q2WNN8 A0A6Q2WNN8 ESOLU	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	411
tr A0A673YLH4 A0A673YLH4 SALTR	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A4W5MAK2 A0A4W5MAK2 9TELE	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A6F6MI98 A0A6F6MI98 CARAU	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	416
tr A0A498LK69 A0A498LK69 LABRO	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	415
tr A0A3Q2YTI5 A0A3Q2YTI5 HIPCM	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	416
tr M4A042 M4A042 XIPMA	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A6P8SZE0 A0A6P8SZE0 GYMCA	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	415
tr A0A3Q2PG22 A0A3Q2PG22 FUNHE	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A6A4SMP2 A0A6A4SMP2 SCOMX	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A673CZR7 A0A673CZR7 9TELE	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A671YAK3 A0A671YAK3 SPAUA	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A6F7J2Q5 A0A6F7J2Q5 9TELE	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A7N8YN60 A0A7N8YN60 9TELE	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	425
tr A0A3P8N896 A0A3P8N896 ASTCA	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	416
tr A0A3B4GLI9 A0A3B4GLI9 9CICH	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	416
tr A0A6A5F6M3 A0A6A5F6M3 FERFL	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A3Q1FLK4 A0A3Q1FLK4 9TELE	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A4W6G9K4 A0A4W6G9K4 LATCA	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A3B4YTJ5 A0A3B4YTJ5 SERLL	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A665X3K2 A0A665X3K2 ECHNA	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A7J7RQ84 A0A7J7RQ84 RHIFE	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	389
tr A0A6P6D0R3 A0A6P6D0R3 PTEVA	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	408
tr A0A7J8H4F1 A0A7J8H4F1 ROUAE	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	422
tr A0A5F4D2S5 A0A5F4D2S5 CANLF	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	451
sp Q07864 DP0E1 HUMAN	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	414
tr A0A2I3S482 A0A2I3S482 PANTR	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	416
tr A0A2K6CI58 A0A2K6CI58 MACNE	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	416
tr A0A834DIT3 A0A834DIT3 9CHIR	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	416
tr F62911 F62911 HORSE	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	416
tr A0A5G2RB90 A0A5G2RB90 FIG	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	389
tr A0A670JF16 A0A670JF16 PODMU	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	414
tr A0A852LC41 A0A852LC41 UROIN	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	432
tr F62FB6 F62FB6 ORNAN	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	291
tr A0A6P5LNS3 A0A6P5LNS3 PHACI	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	417
tr A0A4X2K1K8 A0A4X2K1K8 VOMUR	EIEFVTYNGDF	FDNPFVFE	TRAAHHGLNMYE	IGFQKDNQGEYKA	SQAI	HMD	FRVWVKRDSY	401
	*****	..*	*****	*****	..*	*****	*****	

tr A0A6Q2WNN8 A0A6Q2WNN8 ESOLU	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	470
tr A0A673YLH4 A0A673YLH4 SALTR	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A4W5MAK2 A0A4W5MAK2 9TELE	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A6F6MI98 A0A6F6MI98 CARAU	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	475
tr A0A498LK69 A0A498LK69 LABRO	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	474
tr A0A3Q2YTI5 A0A3Q2YTI5 HIPCM	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	475
tr M4A042 M4A042 XIPMA	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A6P8SZE0 A0A6P8SZE0 GYMCA	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	474
tr A0A3Q2PG22 A0A3Q2PG22 FUNHE	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A6A4SMP2 A0A6A4SMP2 SCOMX	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A673CZR7 A0A673CZR7 9TELE	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A671YAK3 A0A671YAK3 SPAUA	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A6F7J2Q5 A0A6F7J2Q5 9TELE	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A7N8YN60 A0A7N8YN60 9TELE	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	484
tr A0A3P8N896 A0A3P8N896 ASTCA	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	475
tr A0A3B4GLI9 A0A3B4GLI9 9CICH	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	475
tr A0A6A5F6M3 A0A6A5F6M3 FERFL	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A3Q1FLK4 A0A3Q1FLK4 9TELE	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A4W6G9K4 A0A4W6G9K4 LATCA	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A3B4YTJ5 A0A3B4YTJ5 SERLL	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A665X3K2 A0A665X3K2 ECHNA	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A7J7RQ84 A0A7J7RQ84 RHIFE	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	448
tr A0A6P6D0R3 A0A6P6D0R3 PTEVA	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	467
tr A0A7J8H4F1 A0A7J8H4F1 ROUAE	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	481
tr A0A5F4D2S5 A0A5F4D2S5 CANLF	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	510
sp Q07864 DP0E1 HUMAN	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	475
tr A0A2I3S482 A0A2I3S482 PANTR	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	475
tr A0A2K6CI58 A0A2K6CI58 MACNE	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	475
tr A0A834DIT3 A0A834DIT3 9CHIR	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	475
tr F62911 F62911 HORSE	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	475
tr A0A5G2RB90 A0A5G2RB90 FIG	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	448
tr A0A670JF16 A0A670JF16 PODMU	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	473
tr A0A852LC41 A0A852LC41 UROIN	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	492
tr F62FB6 F62FB6 ORNAN	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	360
tr A0A6P5LNS3 A0A6P5LNS3 PHACI	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	476
tr A0A4X2K1K8 A0A4X2K1K8 VOMUR	LVFGS	HNLKAAAKAKLGYDPVELDPEEMCRMATEE	FPQ-TLATY	SVS	DAVATYLYLMKYVH	460
	*****	*****	*****	*****	*****	

		Pol-ZBM			
tr	IA0A6Q2WNN8 IA0A6Q2WNN8_ESOLU	ARHEKRLGDCRRAYKK HHTRLERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	770
tr	IA0A673YLH4 IA0A673YLH4_SALTR	ARHEKRLGDCRRAYKK RQTKLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A4W5MAK2 IA0A4W5MAK2_9TELE	ARHEKRLGDCRRAYKK RQTKLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A6P6MI98 IA0A6P6MI98_CARAU	ARHEKRLGDCRRAYKK HHTRLERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	775
tr	IA0A498LK69 IA0A498LK69_LABRO	ARHEKRLGDCRRAYKK HHTRLERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	751
tr	IA0A3Q2YT15 IA0A3Q2YT15_HIPCM	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	775
tr	IM4A042 IM4A042_XIFMA	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A6P8SZE0 IA0A6P8SZE0_GYMAC	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	774
tr	IA0A3Q2PG22 IA0A3Q2PG22_FUNHE	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A6A4SMP2 IA0A6A4SMP2_SCOMX	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	754
tr	IA0A673CZR7 IA0A673CZR7_9TELE	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A671YAK3 IA0A671YAK3_SPAAU	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A6P7J2Q5 IA0A6P7J2Q5_9TELE	AKHEKRLADYCKKAYKK HITKVEERL	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A7N8YN60 IA0A7N8YN60_9TELE	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	784
tr	IA0A3P8N896 IA0A3P8N896_ASTCA	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	775
tr	IA0A3B4GLI9 IA0A3B4GLI9_9CICH	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	775
tr	IA0A6A5F6M3 IA0A6A5F6M3_PERFL	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A3Q1FLK4 IA0A3Q1FLK4_9TELE	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A4W6G9K4 IA0A4W6G9K4_LATCA	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A3B4YTJ5 IA0A3B4YTJ5_SERLL	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A665X3K2 IA0A665X3K2_ECHNA	AKHEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A7J7RQ84 IA0A7J7RQ84_RHIFE	AKYEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	748
tr	IA0A6P6DOR3 IA0A6P6DOR3_PTEVA	AKYEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	767
tr	IA0A7J8H4F1 IA0A7J8H4F1_ROUAE	AKYEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	781
tr	IA0A5F4D2S5 IA0A5F4D2S5_CANLF	AKYEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	810
sp	IQ07864 DPOE1_HUMAN	AKYEKRLADYCKKAYKK HITKVEERL	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	773
tr	IA0A2I3S482 IA0A2I3S482_PANTR	AKYEKRLADYCKKAYKK HITKVEERL	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	775
tr	IA0A2K6CI58 IA0A2K6CI58_MACNE	AKYEKRLADYCKKAYKK HITKVEERL	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	775
tr	IA0A834DIT3 IA0A834DIT3_9CHIR	AKYEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	775
tr	F62911 F62911_HORSE	AKYEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	775
tr	IA0A5G2RB90 IA0A5G2RB90_PIG	AKYEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	748
tr	IA0A670JP16 IA0A670JP16_PODMU	AKYEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	773
tr	IA0A852LC41 IA0A852LC41_UROIN	AKYEKRLADYCKKAYKK HVTLEERV	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	792
tr	F62FB6 F62FB6_ORNAN	AKYEKRLADYCKKAYKK HITKVEERL	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	650
tr	IA0A6P5LNS3 IA0A6P5LNS3_PHACI	AKYEKRLADYCKKAYKK HITKVEERL	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	776
tr	IA0A4X2K1K8 IA0A4X2K1K8_VOMUR	AKYEKRLADYCKKAYKK HITKVEERL	TTI	DRENSFYVDTVRAFDRDRRYEFGGLHKVV	760
		*:***:*.***:***:*	:*::**	*****	

tr	IA0A6Q2WNN8 IA0A6Q2WNN8_ESOLU	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	830
tr	IA0A673YLH4 IA0A673YLH4_SALTR	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A4W5MAK2 IA0A4W5MAK2_9TELE	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A6P6MI98 IA0A6P6MI98_CARAU	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	835
tr	IA0A498LK69 IA0A498LK69_LABRO	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	811
tr	IA0A3Q2YT15 IA0A3Q2YT15_HIPCM	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	835
tr	IM4A042 IM4A042_XIFMA	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A6P8SZE0 IA0A6P8SZE0_GYMAC	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A3Q2PG22 IA0A3Q2PG22_FUNHE	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A6A4SMP2 IA0A6A4SMP2_SCOMX	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	814
tr	IA0A673CZR7 IA0A673CZR7_9TELE	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A671YAK3 IA0A671YAK3_SPAAU	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A6P7J2Q5 IA0A6P7J2Q5_9TELE	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A7N8YN60 IA0A7N8YN60_9TELE	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	844
tr	IA0A3P8N896 IA0A3P8N896_ASTCA	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	835
tr	IA0A3B4GLI9 IA0A3B4GLI9_9CICH	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	835
tr	IA0A6A5F6M3 IA0A6A5F6M3_PERFL	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A3Q1FLK4 IA0A3Q1FLK4_9TELE	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A4W6G9K4 IA0A4W6G9K4_LATCA	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A3B4YTJ5 IA0A3B4YTJ5_SERLL	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A665X3K2 IA0A665X3K2_ECHNA	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A7J7RQ84 IA0A7J7RQ84_RHIFE	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	808
tr	IA0A6P6DOR3 IA0A6P6DOR3_PTEVA	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	827
tr	IA0A7J8H4F1 IA0A7J8H4F1_ROUAE	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	841
tr	IA0A5F4D2S5 IA0A5F4D2S5_CANLF	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	870
sp	IQ07864 DPOE1_HUMAN	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	835
tr	IA0A2I3S482 IA0A2I3S482_PANTR	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	835
tr	IA0A2K6CI58 IA0A2K6CI58_MACNE	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	835
tr	IA0A834DIT3 IA0A834DIT3_9CHIR	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	835
tr	F62911 F62911_HORSE	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	835
tr	IA0A5G2RB90 IA0A5G2RB90_PIG	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	808
tr	IA0A670JP16 IA0A670JP16_PODMU	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	833
tr	IA0A852LC41 IA0A852LC41_UROIN	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	852
tr	F62FB6 F62FB6_ORNAN	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	710
tr	IA0A6P5LNS3 IA0A6P5LNS3_PHACI	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	836
tr	IA0A4X2K1K8 IA0A4X2K1K8_VOMUR	KKKLSAQAQSGDAALVKRC NMELIYDSL	LAH	KLNSF	YVMMRKGARWYSMEMAGIV	820
		*:***:*.***:***:*	:*::**	*****		

tr	IA0A6Q2WNN8 IA0A6Q2WNN8_ESOLU	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	890
tr	IA0A673YLH4 IA0A673YLH4_SALTR	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A4W5MAK2 IA0A4W5MAK2_9TELE	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A6P6MI98 IA0A6P6MI98_CARAU	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	895
tr	IA0A498LK69 IA0A498LK69_LABRO	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	871
tr	IA0A3Q2YT15 IA0A3Q2YT15_HIPCM	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	895
tr	IM4A042 IM4A042_XIFMA	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A6P8SZE0 IA0A6P8SZE0_GYMAC	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	894
tr	IA0A3Q2PG22 IA0A3Q2PG22_FUNHE	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A6A4SMP2 IA0A6A4SMP2_SCOMX	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	874
tr	IA0A673CZR7 IA0A673CZR7_9TELE	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A671YAK3 IA0A671YAK3_SPAAU	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A6P7J2Q5 IA0A6P7J2Q5_9TELE	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A7N8YN60 IA0A7N8YN60_9TELE	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	904
tr	IA0A3P8N896 IA0A3P8N896_ASTCA	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	895
tr	IA0A3B4GLI9 IA0A3B4GLI9_9CICH	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	895
tr	IA0A6A5F6M3 IA0A6A5F6M3_PERFL	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A3Q1FLK4 IA0A3Q1FLK4_9TELE	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A4W6G9K4 IA0A4W6G9K4_LATCA	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A3B4YTJ5 IA0A3B4YTJ5_SERLL	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A665X3K2 IA0A665X3K2_ECHNA	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNTFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A7J7RQ84 IA0A7J7RQ84_RHIFE	CFTGASIIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	IKTSCMKPKVT SYPGA	868
tr	IA0A6P6DOR3 IA0A6P6DOR3_PTEVA	CFTGASIIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	IKTSSVKKPKVT SYPGA	887
tr	IA0A7J8H4F1 IA0A7J8H4F1_ROUAE	CFTGASIIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	IKTSSVKKPKVT SYPGA	901
tr	IA0A5F4D2S5 IA0A5F4D2S5_CANLF	CFTGASIIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	IKTSSVKKPKVT SYPGA	930
sp	IQ07864 DPOE1_HUMAN	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	895
tr	IA0A2I3S482 IA0A2I3S482_PANTR	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	895
tr	IA0A2K6CI58 IA0A2K6CI58_MACNE	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	895
tr	IA0A834DIT3 IA0A834DIT3_9CHIR	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	895
tr	F62911 F62911_HORSE	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	895
tr	IA0A5G2RB90 IA0A5G2RB90_PIG	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	868
tr	IA0A670JP16 IA0A670JP16_PODMU	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	893
tr	IA0A852LC41 IA0A852LC41_UROIN	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	912
tr	F62FB6 F62FB6_ORNAN	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	770
tr	IA0A6P5LNS3 IA0A6P5LNS3_PHACI	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	896
tr	IA0A4X2K1K8 IA0A4X2K1K8_VOMUR	CYTGANIITQARELVEIQGRPLEL	DD	GIWCVLPNSFFPENFV	VKTSNEKKPKVT SYPGA	880
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		ZBM-CTD-Pol →			
tr A0A6Q2WNN8 A0A6Q2WNN8_ESOLU	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1724
tr A0A673YLH4 A0A673YLH4_SALTR	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1731
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1729
tr A0A6P6MI98 A0A6P6MI98_CARAU	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1727
tr A0A498LK69 A0A498LK69_LABRO	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1723
tr A0A3Q2YTI5 A0A3Q2YTI5_HIFCM	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1728
tr M4A042 M4A042_XIPMA	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1728
tr A0A6P8SZE0 A0A6P8SZE0_GYMAC	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1727
tr A0A3Q2PG22 A0A3Q2PG22_FUNHE	GSDLFLARHLRKK	NNHLLWLSPTV	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1729
tr A0A6A4SMP2 A0A6A4SMP2_SCOMX	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1706
tr A0A673CZR7 A0A673CZR7_9TELE	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1729
tr A0A671YAK3 A0A671YAK3_SPAAU	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1723
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1727
tr A0A7N8YN60 A0A7N8YN60_9TELE	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1736
tr A0A3P8N896 A0A3P8N896_ASTCA	GSDLFLARHLRKK	NNHLLWLSPTS	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1727
tr A0A3B4GLI9 A0A3B4GLI9_9CICH	GSDLFLARHLRKK	NNHLLWLSPTS	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1728
tr A0A6A5F6M3 A0A6A5F6M3_PERFL	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1727
tr A0A3Q1FLK4 A0A3Q1FLK4_9TELE	GSDLFLARHLRKK	NNHLLWLSPTS	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1728
tr A0A4W6G9K4 A0A4W6G9K4_LATCA	GSDLFLARHLRKK	NNHLLWLSPTA	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1725
tr A0A3B4YTJ5 A0A3B4YTJ5_SERLL	GSDLFLARHLRKK	NNHLLWLSPTS	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1728
tr A0A665X3K2 A0A665X3K2_ECHNA	GSDLFLARHLRKK	NNHLLWLSPTS	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1728
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	GSDLFLARHLRKK	NNHLLWLSPTS	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1700
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	GSDLFLARHLRKK	NNHLLWLSPTS	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1719
tr A0A7J8H4F1 A0A7J8H4F1_ROUAE	GSDLFLARHLRKK	NNHLLWLSPTS	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1733
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	GSDLFLARHLRKK	NNHLLWLSPTS	RPDLGGKEADD	SRLVMEADDRGSMENAQQ	1762
sp Q07864 DPOE1_HUMAN	GSDLFFARHLRKH	NNHLLWLSPTA	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1727
tr A0A2I3S482 A0A2I3S482_PANTR	GSDLFFARHLRKH	NNHLLWLSPTA	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1727
tr A0A2K6C158 A0A2K6C158_MACNE	GSDLFFARHLRKH	NNHLLWLSPTA	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1704
tr A0A834DIT3 A0A834DIT3_9CHIR	GSDLFFARHLRKH	NNHLLWLSPTS	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1726
tr F6Z911 F6Z911_HORSE	GSDLFFARHLRKH	NNHLLWLSPTS	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1727
tr A0A5G2RB90 A0A5G2RB90_PIG	GSDLFFARHLRKH	NNHLLWLSPTS	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1700
tr A0A670JP16 A0A670JP16_PODMU	GSDLFFARHLRKH	NNHLLWLSPTS	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1723
tr A0A852LC41 A0A852LC41_UROIN	GSDLFFARHLRKH	NNHLLWLSPTS	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1744
tr F6ZPB6 F6ZPB6_ORNAN	GSDLFFARHLRKH	NNHLLWLSPTS	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1602
tr A0A6P5LNS3 A0A6P5LNS3_PHACI	GSDLFFARHLRKH	NNHLLWLSPTS	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1728
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	GSDLFFARHLRKH	NNHLLWLSPTS	RPDLGGKEADD	NCLVMEFDDQATVEINSSG	1712
	*:***::**	:****:***	*****	.*:***::**	***:***

		ZBM-CTD-Pol			
tr A0A6Q2WNN8 A0A6Q2WNN8_ESOLU	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1844
tr A0A673YLH4 A0A673YLH4_SALTR	CSNDFSRLLKSMVVGWVRE	ITRYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1850
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	CSNDFSRLLKSMVVGWVRE	ITRYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1848
tr A0A6P6MI98 A0A6P6MI98_CARAU	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1846
tr A0A498LK69 A0A498LK69_LABRO	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1822
tr A0A3Q2YTI5 A0A3Q2YTI5_HIFCM	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1847
tr M4A042 M4A042_XIPMA	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1847
tr A0A6P8SZE0 A0A6P8SZE0_GYMAC	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1846
tr A0A3Q2PG22 A0A3Q2PG22_FUNHE	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1848
tr A0A6A4SMP2 A0A6A4SMP2_SCOMX	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1825
tr A0A673CZR7 A0A673CZR7_9TELE	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1848
tr A0A671YAK3 A0A671YAK3_SPAAU	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1843
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1846
tr A0A7N8YN60 A0A7N8YN60_9TELE	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1855
tr A0A3P8N896 A0A3P8N896_ASTCA	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1847
tr A0A3B4GLI9 A0A3B4GLI9_9CICH	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1847
tr A0A6A5F6M3 A0A6A5F6M3_PERFL	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1847
tr A0A3Q1FLK4 A0A3Q1FLK4_9TELE	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1844
tr A0A4W6G9K4 A0A4W6G9K4_LATCA	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1847
tr A0A3B4YTJ5 A0A3B4YTJ5_SERLL	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1847
tr A0A665X3K2 A0A665X3K2_ECHNA	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1847
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1819
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1838
tr A0A7J8H4F1 A0A7J8H4F1_ROUAE	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1852
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1881
sp Q07864 DPOE1_HUMAN	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1846
tr A0A2I3S482 A0A2I3S482_PANTR	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1846
tr A0A2K6C158 A0A2K6C158_MACNE	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1823
tr A0A834DIT3 A0A834DIT3_9CHIR	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1845
tr F6Z911 F6Z911_HORSE	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1846
tr A0A5G2RB90 A0A5G2RB90_PIG	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1819
tr A0A670JP16 A0A670JP16_PODMU	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1842
tr A0A852LC41 A0A852LC41_UROIN	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1863
tr F6ZPB6 F6ZPB6_ORNAN	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1721
tr A0A6P5LNS3 A0A6P5LNS3_PHACI	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1847
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	CSNDFSRLLKSMVVGWVRE	ITQYHNVAADNVQMHFYRWLRSPS	SLLYDPALHRT	LHNSMMK	1831
	*:***::**	:****:***	*****	.*:***::**	***:***

		ZBM-CTD-Pol			
tr A0A6Q2WNN8 A0A6Q2WNN8_ESOLU	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1904
tr A0A673YLH4 A0A673YLH4_SALTR	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1910
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1908
tr A0A6P6MI98 A0A6P6MI98_CARAU	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1906
tr A0A498LK69 A0A498LK69_LABRO	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1882
tr A0A3Q2YTI5 A0A3Q2YTI5_HIFCM	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1907
tr M4A042 M4A042_XIPMA	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1905
tr A0A6P8SZE0 A0A6P8SZE0_GYMAC	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1906
tr A0A3Q2PG22 A0A3Q2PG22_FUNHE	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1902
tr A0A6A4SMP2 A0A6A4SMP2_SCOMX	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1908
tr A0A673CZR7 A0A673CZR7_9TELE	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1885
tr A0A671YAK3 A0A671YAK3_SPAAU	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1903
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1906
tr A0A7N8YN60 A0A7N8YN60_9TELE	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1915
tr A0A3P8N896 A0A3P8N896_ASTCA	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1907
tr A0A3B4GLI9 A0A3B4GLI9_9CICH	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1907
tr A0A6A5F6M3 A0A6A5F6M3_PERFL	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1907
tr A0A3Q1FLK4 A0A3Q1FLK4_9TELE	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1904
tr A0A4W6G9K4 A0A4W6G9K4_LATCA	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1907
tr A0A3B4YTJ5 A0A3B4YTJ5_SERLL	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1907
tr A0A665X3K2 A0A665X3K2_ECHNA	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1907
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1879
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1898
tr A0A7J8H4F1 A0A7J8H4F1_ROUAE	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1912
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1941
sp Q07864 DPOE1_HUMAN	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1906
tr A0A2I3S482 A0A2I3S482_PANTR	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1906
tr A0A2K6C158 A0A2K6C158_MACNE	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1883
tr A0A834DIT3 A0A834DIT3_9CHIR	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1905
tr F6Z911 F6Z911_HORSE	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1906
tr A0A5G2RB90 A0A5G2RB90_PIG	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1879
tr A0A670JP16 A0A670JP16_PODMU	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1902
tr A0A852LC41 A0A852LC41_UROIN	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1923
tr F6ZPB6 F6ZPB6_ORNAN	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1781
tr A0A6P5LNS3 A0A6P5LNS3_PHACI	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1907
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	KVFLQLVAE	FPKRLG	STVVYGNFNRI	ILCTKKRRIDDAIGVEYITNSIHSKEIFHSLTIS	1891
	*:***::**	:****:***	*****	.*:***::**	***:***

tr A0A6Q2WNN8 A0A6Q2WNN8_ESOLU	FSRWCWFLMWM	PSNHGGVVKKLPSSVLYGHTAQK---KK---GTGDEEGSEDEDEA---DG	1957
tr A0A673YLH4 A0A673YLH4_SALTR	FSRWCWFLMWM	LANYGGVVKKLPSSVLYGHPVSSSAKY---EDGEEEGSEDEDEEA---DE	1965
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	FSRWCWFLMWM	LANYGGVVKKLPSSVLYGHPVSSS---DGEDEEGSEDEDEEA---D-	1958
tr A0A6F6MI98 A0A6F6MI98_CARAU	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGEGANEKKKKKVV---EDGSEDEE---DDEEN	1963
tr A0A498LK69 A0A498LK69_LABRO	FSRWCWFLMWM	PANCCGVVKKLPSSVLYGEGHANEKKKKKNDGEE---EDGSEDEE---EDEVN	1939
tr A0A3Q2YT15 A0A3Q2YT15_HIPCM	FSCQWFLMWM	PANNGGVVKKLPSSVLYGEGAVVQVOT---DDEEEDDEAN	1952
tr M4A042 M4A042_XIPMA	FSRWCWFLMWM	PSNYGGVVKKLPSSVLYGEGAGAKQKKRQGEDEEGSEDEDE---DD	1951
tr A0A6P8SZE0 A0A6P8SZE0_GYMAC	FSRWCWFLMWM	PSNFGVVKKLPSSVLYGEGDAGAKQKKRSGEGDEEGSEDEE---DF	1962
tr A0A3Q2PG22 A0A3Q2PG22_FUNHE	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGEGKKR---QGEDEEGSE---DEAD	1959
tr A0A6A4SMP2 A0A6A4SMP2_SCOMX	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGEGGKRRKRRRGGDEGSEDEE---DEAN	1941
tr A0A673CZR7 A0A673CZR7_9TELE	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGERKK---TQQQGEADGSEDEDEEDAR	1964
tr A0A671YAK3 A0A671YAK3_SPAAU	FSRWCWFLMWM	PANCCGVVKKLPSSVLYGEGAKRKKRQEEDEEGSEDEDEE---A	1953
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGEGAKRKKRQEEDEEGSEDEDEE---N	1962
tr A0A7N8YN60 A0A7N8YN60_9TELE	FSRWCWFLMWM	PSNYGGVVKKLPSSVLYGEGAKQKKRQEGEGHEGSDDEDE---DEAD	1973
tr A0A3P8N896 A0A3P8N896_ASTCA	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGEGKTR---QEEGDEEGSE---DEDEEN	1958
tr A0A3B4GLI9 A0A3B4GLI9_9CICH	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGEGKTR---QEEGDEEGSE---DEDEEN	1958
tr A0A6A5F6M3 A0A6A5F6M3_PERFL	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGEGAQKKRSGEGDEEGSDDEDE---DEAV	1965
tr A0A3Q1FLK4 A0A3Q1FLK4_9TELE	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGEGDAGAKQKKRQGEDEEGSEDEE---EED	1960
tr A0A4W6G9K4 A0A4W6G9K4_LATCA	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGEGAGAKRKKR---GDEGSEDEE---EDEEAG	1963
tr A0A3B4YTJ5 A0A3B4YTJ5_SERLL	FSRWCWFLMWM	PANYGGVVKKLPSSVLYGEGTKKKRQGGDEEGSEDEDE---DEAD	1965
tr A0A665X3K2 A0A665X3K2_ECHNA	FSRWCWFLMWM	PANHGGVVKKLPSSVLYGEGERAKKKRQGGDDQDGEDEDEDEDEAD	1967
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	FSRWCWFLMWM	PSNYGGIKGVSSGTHCGQDSPKKGGSTQDDE---DDEDD---DEEN	1928
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	FSRWCWFLMWM	PSNYGGIKGVSSGTHCGQDSPEKGEQDDE---DDEDD---DEEN	1947
tr A0A7J8H4F1 A0A7J8H4F1_ROUAE	FSRWCWFLMWM	PSNYGGIKGVSSVHCQDQDQNEKGEQDDE---GD---G---DEEN	1959
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	FSRWCWFLMWM	PSNYGGIKGVSSVHYGQDQDSKGRVVEE---EEDDEE---EE---	1992
sp Q07864 DPOE1_HUMAN	FSRWCWFLMWM	PSNYGGIKGVSSRTHCGQDSQKAGGAEDQ---ENEDD---EEDR---	1959
tr A0A2I3S482 A0A2I3S482_PANTR	FSRWCWFLMWM	PSNYGGIKGVSSRTHCGQDSQKAGGAEDQ---ENEDD---EEDR---	1959
tr A0A2K6C158 A0A2K6C158_MACNE	FSRWCWFLMWM	PSNYGGIKGVSSRTHCGQDSQKAGGAEDQ---ENEDD---EEDR---	1936
tr A0A834DIT3 A0A834DIT3_9CHIR	FSCWFLMWM	PSNFGGKGVSSRTHCGQDSQKAGGAEDQ---EEDDEE---EEDP	1960
tr F62911 F62911_HORSE	FSCWFLMWM	PCNYGGIKGVSSVTHCGQDSQKAGGAEDQ---EEDDEE---EEDP	1959
tr A0A5G2RB90 A0A5G2RB90_PIG	FSCWFLMWM	PSNYGGIKGVSSRTHCGQDSQKAGGAEDQ---EEDDEE---EEDP	1950
tr A0A852LC41 A0A852LC41_UROIN	FSCWFLMWM	PANYGGIKGVSSRTHCGQDSQKAGGAEDQ---EEDDEE---EEDP	1974
tr F62FB6 F62FB6_ORNAN	FSCWFLMWM	PSNYGGIKGVSSRTHCGQDSQKAGGAEDQ---EEDDEE---EEDP	1834
tr A0A6P5LNS3 A0A6P5LNS3_PHACI	FSCWFLMWM	PANYGGIKGVSSRTHCGQDSQKAGGAEDQ---EEDDEE---EEDP	1961
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	FSCWFLMWM	PANYGGIKGVSSRTHCGQDSQKAGGAEDQ---EEDDEE---EEDP	1940
:*:*:*:* * .*:			

CTD-Pol

tr A0A6Q2WNN8 A0A6Q2WNN8_ESOLU	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2186
tr A0A673YLH4 A0A673YLH4_SALTR	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2193
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2186
tr A0A6F6MI98 A0A6F6MI98_CARAU	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2192
tr A0A498LK69 A0A498LK69_LABRO	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2168
tr A0A3Q2YT15 A0A3Q2YT15_HIPCM	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2181
tr M4A042 M4A042_XIPMA	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2180
tr A0A6P8SZE0 A0A6P8SZE0_GYMAC	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2191
tr A0A3Q2PG22 A0A3Q2PG22_FUNHE	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2016
tr A0A6A4SMP2 A0A6A4SMP2_SCOMX	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2170
tr A0A673CZR7 A0A673CZR7_9TELE	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2193
tr A0A671YAK3 A0A671YAK3_SPAAU	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2182
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2191
tr A0A7N8YN60 A0A7N8YN60_9TELE	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2202
tr A0A3P8N896 A0A3P8N896_ASTCA	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2190
tr A0A3B4GLI9 A0A3B4GLI9_9CICH	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2015
tr A0A6A5F6M3 A0A6A5F6M3_PERFL	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2194
tr A0A3Q1FLK4 A0A3Q1FLK4_9TELE	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2010
tr A0A4W6G9K4 A0A4W6G9K4_LATCA	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2195
tr A0A3B4YTJ5 A0A3B4YTJ5_SERLL	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2194
tr A0A665X3K2 A0A665X3K2_ECHNA	LVDVGFSEDAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2196
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2157
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2184
tr A0A7J8H4F1 A0A7J8H4F1_ROUAE	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2174
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2184
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tr A0A2I3S482 A0A2I3S482_PANTR	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2188
tr A0A2K6C158 A0A2K6C158_MACNE	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2165
tr A0A834DIT3 A0A834DIT3_9CHIR	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2189
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tr A0A5G2RB90 A0A5G2RB90_PIG	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2159
tr A0A670JP16 A0A670JP16_PODMU	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2179
tr A0A852LC41 A0A852LC41_UROIN	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2202
tr F62FB6 F62FB6_ORNAN	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2061
tr A0A6P5LNS3 A0A6P5LNS3_PHACI	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2190
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	LVDVGFSEEAQFRDPCNSYILPEVICHQCNFCRDLILCK---	DPSVAQDGSVLPQWFC3	2169

CysA

tr A0A6Q2WNN8 A0A6Q2WNN8_ESOLU	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2246
tr A0A673YLH4 A0A673YLH4_SALTR	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2253
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2246
tr A0A6F6MI98 A0A6F6MI98_CARAU	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2252
tr A0A498LK69 A0A498LK69_LABRO	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2199
tr A0A3Q2YT15 A0A3Q2YT15_HIPCM	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2241
tr M4A042 M4A042_XIPMA	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2240
tr A0A6P8SZE0 A0A6P8SZE0_GYMAC	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2254
tr A0A3Q2PG22 A0A3Q2PG22_FUNHE	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2016
tr A0A6A4SMP2 A0A6A4SMP2_SCOMX	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2201
tr A0A673CZR7 A0A673CZR7_9TELE	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2242
tr A0A671YAK3 A0A671YAK3_SPAAU	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2251
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2242
tr A0A7N8YN60 A0A7N8YN60_9TELE	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2262
tr A0A3P8N896 A0A3P8N896_ASTCA	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2036
tr A0A3B4GLI9 A0A3B4GLI9_9CICH	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2015
tr A0A6A5F6M3 A0A6A5F6M3_PERFL	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2010
tr A0A3Q1FLK4 A0A3Q1FLK4_9TELE	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2255
tr A0A4W6G9K4 A0A4W6G9K4_LATCA	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2254
tr A0A3B4YTJ5 A0A3B4YTJ5_SERLL	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2256
tr A0A665X3K2 A0A665X3K2_ECHNA	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2257
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2248
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2244
tr A0A7J8H4F1 A0A7J8H4F1_ROUAE	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2248
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2234
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tr A0A2I3S482 A0A2I3S482_PANTR	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2248
tr A0A2K6C158 A0A2K6C158_MACNE	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2245
tr A0A834DIT3 A0A834DIT3_9CHIR	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2229
tr F62911 F62911_HORSE	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2248
tr A0A5G2RB90 A0A5G2RB90_PIG	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2248
tr A0A670JP16 A0A670JP16_PODMU	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2239
tr A0A852LC41 A0A852LC41_UROIN	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2252
tr F62FB6 F62FB6_ORNAN	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2251
tr A0A6P5LNS3 A0A6P5LNS3_PHACI	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2120
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	NCDQAYETESIEMALVEALQKLLMSYTLQDLVCPKRGVKEANMPLCSAGDFELTFPT	2229

CysA

4Fe-4S

//End of ε pol sequences from animal sources			
tr A0A6Q2WWN8 A0A6Q2WWN8_ESOLU	AAHYNMNFLEETIDWLLVMSPQISQAARH-		2288
tr A0A673YLH4 A0A673YLH4_SALTR	AAHYNMNFLEETIDWLLVMSPQINQSR---		2293
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	AAHYNMNFLEETIDWLLVMSPQISQSR---		2286
tr A0A6P6MI98 A0A6P6MI98_CARAU	AAHYNMNFLEETIDWVLSMNA-----		2286
tr A0A498LK69 A0A498LK69_LABRO	AAHYNMNFLEETIDWVLSMNA-----		2232
tr A0A3Q2YTI5 A0A3Q2YTI5_HIPCM	ASHYNMSFLKETIDWLMVMSFPQISQSAS--		2282
tr M4A042 M4A042_XIPMA	ASHYNMRFLEETIDWLLVMSFPQISQSRH--		2281
tr A0A6P8SZE0 A0A6P8SZE0_GYMAC	ASHYSMSYLGETIDWLLVMSPQISQSAL--		2292
tr A0A3Q2PG22 A0A3Q2PG22_FUNHE	-----		2016
tr A0A6A4SMP2 A0A6A4SMP2_SCOMX	ASHYNMSFLEETIDWLLVMSPHVGQSIH--		2236
tr A0A673CZR7 A0A673CZR7_9TELE	ASHYNMSFLEETIEWLRGMSFPQINQSTHKI		2296
tr A0A671YAK3 A0A671YAK3_SPAAU	ASHYSMSFLEETIDWLVVMSPHINQ SAR--		2283
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	ASHYNMTFLEETIDWLLMSFPQISQSAR--		2292
tr A0A7N8YN60 A0A7N8YN60_9TELE	ASHYNMRFLEETIDWLLVMSPQISQSAH--		2303
tr A0A3P8N896 A0A3P8N896_ASTCA	-----		2036
tr A0A3B4GLI9 A0A3B4GLI9_9CICH	-----		2015
tr A0A6A5F6M3 A0A6A5F6M3_PERFL	ASHYKMSFLDETLDWLLVMSPQISQNAH--		2295
tr A0A3Q1FLK4 A0A3Q1FLK4_9TELE	-----		2010
tr A0A4W6G9K4 A0A4W6G9K4_LATCA	ASHYSMSFLEETIDWLLVMSPQISQSAR--		2296
tr A0A3B4YTJ5 A0A3B4YTJ5_SERLL	ASHYNMSFLEETIDWLLAMSPQISQSAH--		2295
tr A0A665X3K2 A0A665X3K2_ECHNA	ASHYNMSFLEETIDLLAMSPQISQTAH--		2297
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	AQHYGMSYLMETLEWLLKPNPQLGH-----		2255
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	AQHCMSYLMETLEWLLQKNPQLGH-----		2282
tr A0A7J8H4F1 A0A7J8H4F1_ROUAE	AQHCMSYLMETLEWLLQKNPQLGH-----		2286
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	AQHYGMSYLTETLEWLLQKNPQLGH-----		2319
sp Q07864 DPOE1_HUMAN	AQHYGMSYLTETLEWLLQKNPQLGH-----		2286
tr A0A2I3S482 A0A2I3S482_PANTR	AQHYGMSYLTETLEWLLQKNPQLGR-----		2286
tr A0A2K6CI58 A0A2K6CI58_MACNE	AQHYGMSYLTETLEWLLQKNPQRGR-----		2263
tr A0A834DIT3 A0A834DIT3_9CHIR	AQHYGMSYLMETLEWLLQKNPQLSH-----		2287
tr F6Z911 F6Z911_HORSE	AQHYGMSYLMESLEWLLQKNPQLGH-----		2286
tr A0A5G2RB90 A0A5G2RB90_PIG	AQHYGMSYLTETLEWLLQKNPQLGH-----		2257
tr A0A670JP16 A0A670JP16_PODMU	ARHYNMDYLLLENIKWLLQMNPLQLL-----		2277
tr A0A852LC41 A0A852LC41_UROIN	ARHYSMALLETIEWLLSTNPLQLRP-----		2300
tr F6ZFB6 F6ZFB6_ORNAN	AQHYAMSYLETIEWLLQMNPLRPR-----		2159
tr A0A6P5LNS3 A0A6P5LNS3_PHACI	ARHYGMTYLTETIEWLLQMNPLQLAN-----		2288
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	ARHYGMTYLTETIEWLLQMNPLQLAN-----		2267

A0A6Q2WWN8_ESOLU, <i>Esox lucius</i>	A0A673YLH4_SALTR, <i>Salmo trutta</i>
A0A4W5MAK2_9TELE, <i>Hucho hucho</i>	A0A6P6MI98_CARAU, <i>Carassius auratus</i>
A0A498LK69_LABRO, <i>Labeo rohita</i>	A0A3Q2YTI5_HIPCM, <i>Hippocampus comes</i>
M4A042_XIPMA, <i>Xiphophorus maculatus</i>	A0A6P8SZE0_GYMAC, <i>Gymnodraco acuticeps</i>
A0A3Q2PG22_FUNHE, <i>Fundulus heteroclitus</i>	A0A6A4SMP2_SCOMX, <i>Scophthalmus maximus</i>
A0A673CZR7_9TELE, <i>Sphaeramia orbicularis</i>	A0A671YAK3_SPAAU, <i>Sparus aurata</i>
A0A6P7J2Q5_9TELE, <i>Parambassis ranga</i>	A0A7N8YN60_9TELE, <i>Mastacembelus armatus</i>
A0A3P8N896_ASTCA, <i>Astatotilapia calliptera</i>	A0A3B4GLI9_9CICH, <i>Pundamilia nyererei</i>
A0A6A5F6M3_PERFL, <i>Perca fluviatilis</i>	A0A3Q1FLK4_9TELE, <i>Acanthochromis polyacanthus</i>
A0A4W6G9K4_LATCA, <i>Lates calcarifer</i>	A0A3B4YTJ5_SERLL, <i>Seriola lalandi dorsalis</i>
A0A665X3K2_ECHNA, <i>Echeneis naucrates</i>	A0A7J7RQ84_RHIFE, <i>Rhinolophus ferrumequinum</i>
A0A6P6D0R3_PTEVA, <i>Pteropus vampyrus</i>	A0A7J8H4F1_ROUAE, <i>Rousettus aegyptiacus</i>
A0A5F4D2S5_CANLF, <i>Canis lupus familiaris</i>	Q07864 DPOE1_HUMAN, <i>Homo sapiens</i>
A0A2I3S482_PANTR, <i>Pan troglodytes</i>	A0A2K6CI58_MACNE, <i>Macaca nemestrina</i>
A0A834DIT3_9CHIR, <i>Phyllostomus discolor</i>	F6Z911_HORSE, <i>Equus caballus</i>
A0A5G2RB90_PIG, <i>Sus scrofa</i>	A0A670JP16_PODMU, <i>Podarcis muralis</i>
A0A852LC41_UROIN, <i>Urocolius indicus</i>	F6ZFB6_ORNAN, <i>Ornithorhynchus anatinus</i>
A0A6P5LNS3_PHACI, <i>Phascolarctos cinereus</i>	A0A4X2K1K8_VOMUR, <i>Vombatus ursinus</i>

Figure 4 MSA of ε DNA polymerases from various animal sources

3.2. 'Mix and Match' MSA analysis of the DNA pols ε from yeasts, higher fungi, plants and animals

Figure 5 shows the 'Mix and Match' MSA of the ε pols from all the four eukaryotic sources, viz. yeasts, higher fungi, plants and animals (only the required regions for the discussions are shown). *S. cerevisiae*, *Aspergillus niger*, *A. thaliana* and human sequences are used as the standards and highlighted. All the major domains (NTD, PR Exo, Pol, Linker and CTD) are indicated tentatively with arrow marks. The NTDs show many gaps in the alignment, but with a small number of conserved peptides. Strikingly, a highly conserved dodecapeptide is found in this region. The NTD is followed by a highly conserved PR exo domain. The proposed PR exonuclease active site amino acids are completely conserved in all (highlighted) and it belongs to the DEDD-superfamily with an invariant Y as a proton acceptor. The presence of a typical -DEDD-superfamily exonuclease active site in all ε pols is in close agreement with the other DdDps [8]. An invariant, characteristic motif -SYLPQ/VGS- (highlighted in yellow) is found within the PR exo domain in the ε pols of all eukaryotes. This sequence is somewhat similar to the characteristic -SLYPS- motif reported in the other two replicative pols, α and δ [2] and, in general, in all the B-family pols. In all these pols, viz. ε, δ and α, this motif is implicated in dNTP-binding.

The PR exo domain is followed by the pol domain and is also highly conserved in all. Interestingly, the template-binding pair (-YG-), catalytic amino acid (K) and dNTP selection amino acid (Q) are completely conserved in all (highlighted in yellow) and are in close agreement with other DdDps and DdRps [6, 21]. The ε pol's active site amino acids are found within highly conserved large peptides. The pol domain also contains the completely conserved-DxD- type catalytic Mg²⁺ site and is in close agreement with other DNA pols. A unique ZBM that is conserved within the pol domain in all ε pols (highlighted) is suggested to play a role in linking redox status of cells to replication. The pol domain is followed by a linker region which connects the pol to the CTD. The linker region contains a highly conserved NLS-like motif in all pols ε (highlighted). The linker region is not conserved much. The CTD possesses two invariant ZBMs and one of them binds to the 4Fe-4S cluster (highlighted in orange) and a -DxD- type metal-binding motif is found within the first ZBM. The second pol and PR exo active sites do not align in all. Interestingly, the catalytic amino acid K, pairs with -C- as -KC- in plant and animal enzymes, but with -V- as -KV- in yeasts and higher fungal enzymes.

CLUSTAL O (1.2.4) 'Mix and Match' MSA of all the four eukaryotic ε DNA pols (from yeasts, higher fungi, plants and animals)

tr A0A3P5YCF9 A0A3P5YCF9_BRACM	ILAGK-----REQRQDCLDSLIDLREYDVPYHVR	FAVDKDVRSGQWY	218
sp P4HW04 DPOE1_ARATH	ILAGK-----REQRQDCLDSIVDLREYDVPYHVR	FAIDNDVRSGQWY	218
tr D7KI06 D7KI06_ARALL	ILAGK-----REQRQDCLDSIVDLREYDVPYHVR	FAIDNDVRSGQWY	218
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	IYGVK-----RVERPQDYINCIIDLREYDVPYHVR	FAIDNDVRSGQWY	242
tr A0A452YAR6 A0A452YAR6_AEGTS	IYGVK-----RVERPQDYINCIIDLREYDVPYHVR	FAIDNDVRSGQWY	182
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	IYGVK-----RVERPQDYINCIIDLREYDVPYHVR	FAIDNDVRSGQWY	237
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	IHGVK-----RVERPQDYINYIIDLREYDVPYHVR	FAIDNDVRSGQWY	234
tr A0A835B357 A0A835B357_9POAL	IHGVK-----RVERPQDYINYIIDLREYDVPYHVR	FAIDNDVRSGQWY	228
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	IHGVK-----RVERPQDYINYIIDLREYDVPYHVR	FAIDNDVRSGQWY	233
tr A0A368PL62 A0A368PL62_SETIT	IHGVK-----RVERPQDYINYIIDLREYDVPYHVR	FAIDNDVRSGQWY	237
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	IFTGK-----SKERPQDFIDCVLREYDVPYHVR	FAIDNDVRSGQWY	219
tr A0A6I9QIG1 A0A6I9QIG1_ELAGV	IYNGK-----SKERPQDYIDCVLREYDVPYHVR	FAIDNDVRSGQWY	217
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	MYNGK-----SKERPQDYIDCVLREYDVPYHVR	FAIDNDVRSGQWY	217
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	ILSGKR--QVFDHMHMELHETHYFLEQRQDFLDSIIDLREYDVPYHVR	FAIDNDVRSGQWY	234
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	LLTGKS-----REQRQDCLDSIVDLREYDVPYHVR	FAIDNDVRSGQWY	220
tr A0A7J7C034 A0A7J7C034_TRIWF	ILTGK-----REQRQDCLDSIVDLREYDVPYHVR	FAIDNDVRSGQWY	219
tr A0A2N9F976 A0A2N9F976_FAGSY	FDISV-----ENKGPQDFIDCVLREYDVPYHVR	FAIDNDVRSGQWY	238
tr A0A7N2KME6 A0A7N2KME6_QUELO	I IAGK-----REQRQDCLDSIVDLREYDVPYHVR	FAIDNDVRSGQWY	218
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	MLSSALAGGSV--SAA--DEDGMSKTSQDMDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	245
tr A0A8C7Q9V4 A0A8C7Q9V4_ONCMY	MLSSALAGGSV--SAA--DEDGLSKTSQDMDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	203
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	MLSSALSGGTV--ASA--DEDSISKISIDQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	245
tr A0A6P8SZE0 A0A6P8SZE0_GYMAC	MLSSALSGGNV--NTA--EEDGPKRSISDQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	243
tr A0A8J0QX44 A0A8J0QX44_XENTR	MLSSALTGNM--GA--EEEGPSKKISDQMNIVDMREYDVPYHVR	LSIDLKIHVAHWY	242
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	MLSSALMGGSV--TT--DEEGSKKIADQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	229
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	MLSSVLQGGSV--VI--DEEASAKKVTQDLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	279
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	MLSSVLQGGSV--IL--DEEASAKKADQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	217
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	MLSSVLQGGGA--II--DEEETSKKIADQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	236
tr A0A2K6C1S8 A0A2K6C1S8_MACNE	LLSSVLQGGV--IT--DEEETSKKIADQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	244
tr F6QAQ1 F6QAQ1_MACMU	LLSSVLQGGV--IT--DEEETSKKIADQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	246
tr G3RQP2 G3RQP2_GORGO	LLSSVLQGGV--IT--DEEETSKKIADQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	223
sp Q07864 DPOE1_HUMAN	LLSSVLQGGV--IT--DEEETSKKIADQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	244
tr A0A2I3S482 A0A2I3S482_PANTR	LLSSVLQGGV--IT--DEEETSKKIADQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	244
tr F6Z911 F6Z911_HORSE	MLSSVLQGGSV--II--DEEETSKKMDQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	244
tr A0A5G2RB90 A0A5G2RB90_PIG	MLSSVLQGGSV--VM--DEEETSKKIADQLDNIVDMREYDVPYHVR	LSIDLKIHVAHWY	217
tr A0A420PL83 A0A420PL83_FUSOX	---NGDFDLFDDSRD--DDRNMTALSDFIIVDIREYDVPYHVR	VMIDLDIRAGKQWY	222
tr A0A1V6PGE7 A0A1V6PGE7_PENDC	MSSATASFDLFDDEII--NEQRPN--GNLQASDFIIVDIREYDVPYHVR	VCIDKDIRIGKQWY	257
tr A0A0G4NU82 A0A0G4NU82_PENCA	MTSATAGIDLFDDEII--NEQRPN--GNLQASDFIIVDIREYDVPYHVR	VCIDKDIRIGKQWY	257
tr A0A1V6TET5 A0A1V6TET5_9EURO	MTSATAGIDLFDDEII--NEQRPN--GNLQASDFIIVDIREYDVPYHVR	VCIDKDIRIGKQWY	257
tr A0A167WJ50 A0A167WJ50_PENCH	MTSATAGIDLFDDEII--NEQRPN--GNLQASDFIIVDIREYDVPYHVR	VCIDKDIRIGKQWY	257
tr A0A3A2Z9P9 A0A3A2Z9P9_9EURO	ISSANAGFDLFDDELI--NESRPN--NSMNASDFIIVDIREYDVPYHVR	VAIDKDIRIGKQWY	257
tr A0A401L0U3 A0A401L0U3_ASPAW	ISSANAGFDLFDDELI--NESRPN--ATMNASDFIIVDIREYDVPYHVR	VAIDKDIRIGKQWY	257
tr A0A317VH96 A0A317VH96_ASPCC	ISSANAGFDLFDDELI--NESRPN--ATMNASDFIIVDIREYDVPYHVR	VAIDKDIRIGKQWY	253
tr A0A117E1M7 A0A117E1M7_ASPNG	ISSANAGFDLFDDELI--NESRPN--ATMNASDFIIVDIREYDVPYHVR	VAIDKDIRIGKQWY	257
tr A0A1D8PTD0 A0A1D8PTD0_CANAL	KEI-----ETIMDPSVYIIDIREYDVPYHVR	VSIDRNRVGVKQWY	263
tr C5M3R9 C5M3R9_CANTT	KDV-----DSSSDPSTYIIDIREYDVPYHVR	VSIDKQLRVGVKQWY	258
sp Q6FNY7 DPOE_CANGA	SNISNGNGLSSNVNR--FASSVQDKDAKQYIEDIREYDVPYHVR	VSIDKDIRVGVKQWY	265
sp P21951 DPOE_YEAST	AAN-----GSEKVDAKHLIEDIREYDVPYHVR	VSIDKDIRVGVKQWY	205
tr A0A7H9HLU1 A0A7H9HLU1_9SACH	QGA-----GNSFRDAKSLIEVREYDVPYHVR	VSIDKNIRVGVKQWY	255
sp Q6CUS7 DPOE_KLULA	GSD-----YSTRDVKTLEIEDIREYDVPYHVR	VSIDKNIRVGVKQWY	182
sp Q752B8 DPOE_ASHGO	NDT-----TNRDRAKMLIIDIREYDVPYHVR	VCIDKDIRVGVKQWY	179

		← NTD →	PR Exo →	
tr A0A3P5YCF9 A0A3P5YCF9_BRACM	NVSISSST-D-VLEKRTDILQR	A E V R V C A F	D I E T T K L P L K F P D A E Y D Q I M M I S Y M I D G G Q	276
sp F4HW04 DPOE1_ARATH	NVSISSST-D-VLEKRTDILQR	A E V R V C A F	D I E T T K L P L K F P D A E Y D Q I M M I S Y M I D G G Q	276
tr D7KI06 D7KI06_ARALL	NVSISSST-D-VLEKRTDILQR	A E V R V C A F	D I E T T K L P L K F P D A E Y D Q I M M I S Y M I D G G Q	276
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	NVSVSGSD-VLLQRREDDLQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D S V M M I S Y M I D G G Q	300
tr A0A452YAR6 A0A452YAR6_AEGTS	NVSVSGSD-VLLQRREDDLQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D S V M M I S Y M I D G G Q	240
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	NVSVSGSD-VLLQRREDDLQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D S V M M I S Y M I D G G Q	295
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	NVSVSGSD-VLLQRREDDLQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D S V M M I S Y M I D G G Q	279
tr A0A835B357 A0A835B357_9POAL	NVSVSGSD-VLLQRREDDLQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D S V M M I S Y M I D G G Q	286
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	NVSVSGSD-VLLQRREDDLQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D S V M M I S Y M I D G G Q	291
tr A0A368PL62 A0A368PL62_SETIT	NVSVSGSD-VLLQRREDDLQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D S V M M I S Y M I D G G Q	295
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	DVSISSGIN-VLLQKRNDDLQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D Q V M M I S Y M I D G G Q	277
tr A0A6I9QIG1 A0A6I9QIG1_ELAGV	DVNVSSAG-ILLQRREDDLQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D Q I M M I S Y M I D G G Q	275
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	DINVSSSG-ILLQKRTDILQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D Q I M M I S Y M I D G G Q	275
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	DVSVSSTG-VLMKRRDILQR	A E V H I C A F	D I E T T K L P L K F P D A E Y D Q V M M I S Y M I D G G Q	292
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	DVTVSNRG-VLEKRTDILQR	A E V R V C A F	D I E T T K L P L K F P D A E Y D I L M M I S Y M I D G G Q	278
tr A0A7J7C034 A0A7J7C034_TRIFW	DVSVSSNG-VVLEKRTDILQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D L M M I S Y M I D G G Q	277
tr A0A2N9F976 A0A2N9F976_FAGSY	DVSVSSTG-LMLKRTDILQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D L M M I S Y M I D G G Q	296
tr A0A7N2KME6 A0A7N2KME6_QUELO	DVSVSSTG-LMLKRTDILQR	A E V H V C A F	D I E T T K L P L K F P D A E Y D L M M I S Y M I D G G Q	276
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	305
tr A0A8C7Q9V4 A0A8C7Q9V4_ONCMY	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	303
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	265
tr A0A6P8SZE0 A0A6P8SZE0_GYMAC	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E S D Q I M M I S Y M I D G G Q	302
tr A0A8J0QX44 A0A8J0QX44_XENTR	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	303
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	389
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	299
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	277
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	296
tr A0A2K6C158 A0A2K6C158_MACNE	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	304
tr F6QAQ1 F6QAQ1_MACMU	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	306
tr G3RQP2 G3RQP2_GORGO	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	283
sp Q07864 DPOE1_HUMAN	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	304
tr A0A2I3S482 A0A2I3S482_PANTR	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	304
tr F6Z911 F6Z911_HORSE	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	304
tr A0A5G2RB90 A0A5G2RB90_PIG	NVRYRGSAYPPEIILRSDLVER	P D P V V L A F	D I E T T K L P L K F P D A E T D Q I M M I S Y M I D G G Q	277
tr A0A420PL83 A0A420PL83_FUSOX	FVEAKHGV-TKIPYNEERSLP	A E P V V M A F	D I E T T K L P L K F P D A A T D Q I M I M S Y M I D G G Q	280
tr A0A1V6PGE7 A0A1V6PGE7_PENDC	NVQAKHGV-ISLTCLEERLQR	A D P V V L A F	D I E T T K L P L K F P D A I D Q I M M I S Y M I D G G Q	315
tr A0A0G4NU82 A0A0G4NU82_PENCA	NVEADHGV--ISLTCLEERLQR	R A D P V V L A F	D I E T T K L P L K F P D A T M D Q I M M I S Y M I D G G Q	315
tr A0A1V6TET5 A0A1V6TET5_9EURO	NVEADHGV-ISLTCLEERLQR	A D P V V L A F	D I E T T K L P L K F P D A A M D Q I M M I S Y M I D G G Q	315
tr A0A167WJ50 A0A167WJ50_PENCH	NVEADHGV-ISLTCLEERLQR	A D P V V L A F	D I E T T K L P L K F P D A A T D Q I M M I S Y M I D G G Q	315
tr A0A3A2Z9P9 A0A3A2Z9P9_9EURO	TVEAKHGL-ISLTCLEERLQR	A D P V V L A F	D I E T T K L P L K F P D S V I D Q I M I S Y M I D G G Q	315
tr A0A401L0U3 A0A401L0U3_ASPAW	TVEAKHGV-ISLTCLEERLQR	A D P V V L A F	D I E T T K L P L K F P D S V I D Q I M M I S Y M I D G G Q	315
tr A0A317VH96 A0A317VH96_ASEPC	TVEAKHGV-ISLTCLEERLQR	A D P V V L A F	D I E T T K L P L K F P D S V I D Q I M M I S Y M I D G G Q	311
tr A0A117E1M7 A0A117E1M7_ASPNG	TVEAKHGV-ISLTCLEERLQR	A D P V V L A F	D I E T T K L P L K F P D S V I D Q I M M I S Y M I D G G Q	315
tr A0A1D8PTD0 A0A1D8PTD0_CANAL	DVYAKHSK-VDFVDEKKEIAF	A D P V V L A F	D I E T T K A P L K F P D A I D Q I M M I S Y M I D G G Q	321
tr C5M3R9 C5M3R9_CANTT	DVYAKHSK-IEIVDEKKEIAF	A D P V V L A F	D I E T T K A P L K F P D A K V D Q I M M I S Y M I D G G Q	319
sp Q6FNY7 DPOE_CANGA	KVTH-----EGFVWPKKIVAF	A D P V V L A F	D I E T T K A P L K F P E A S V D Q V M M I S Y M I D G G Q	316
sp P21951 DPOE_YEAST	KVTQ-----QGFIEDTRKIAF	A D P V V M A F	D I E T T K P P L K F P D S A V D Q I M M I S Y M I D G G Q	259
tr A0A7H9HLU1 A0A7H9HLU1_9SACH	KVAS-----DGLHEITEKVAF	A D P V V L A F	D I E T T K A P L K F P D S A V D Q I M M I S Y M I D G G Q	309
tr Q6CUS7 DPOE_KLULA	AVSA-----QGLVELEEKVTF	A D P V V L A F	D I E T T K A P L K F P D S A I D Q I M M I S Y M I D G G Q	236
tr Q752B8 DPOE_ASHGO	RVTS-----GGLVEYTDKIVAF	A D P V V L A F	D I E T T K A P L K F P D S A I D Q I M M I S Y M I D G G Q	233
:	:	:	*** : * **** : *	:

tr A0A3P5YCF9 A0A3P5YCF9_BRACM	YNGDFD	N P F F E R R A S H H G I K M N E E L G F R C D N Q G E C R A K F V C H L D C F A W V K R D S Y L P Q G	393
sp F4HW04 DPOE1_ARATH	YNGDFD	N P F F E R R A S H H G I K M N E E L G F R C D N Q G E C R A K F A C H L D C F A W V K R D S Y L P Q G	393
tr D7KI06 D7KI06_ARALL	YNGDFD	N P F F E R R A S H H G I K M N E E L G F R C D N Q G E C R A K F V C H L D C F A W V K R D S Y L P Q G	396
tr A0A8I6WFC8 A0A8I6WFC8_HORVV	YNGDFD	N P F F E R R A S H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	417
tr A0A452YAR6 A0A452YAR6_AEGTS	YNGDFD	N P F F E R R A S H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	357
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	YNGDFD	N P F F E R R A S H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	412
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	YNGDFD	N P F F E R R A S H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	390
tr A0A835B357 A0A835B357_9POAL	YNGDFD	N P F F E R R A S H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	403
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	YNGDFD	N P F F E R R A S H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	408
tr A0A368PL62 A0A368PL62_SETIT	YNGDFD	N P F F E R R A S H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	412
tr A0A7I8KHB8 A0A7I8KHB8_SPIIN	YNGDFD	N P F F E R R A S H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	394
tr A0A6I9QIG1 A0A6I9QIG1_ELAGV	YNGDFD	N P F F E R R A S H H G I K L S E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	392
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	YNGDFD	N P F F E R R A S A A H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	392
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	YNGDFD	N P F F E R R A S A A H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	399
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	YNGDFD	N P F F E R R A S A A H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	405
tr A0A7J7C034 A0A7J7C034_TRIFW	YNGDFD	N P F F E R R A S A A H H G I L S N E L G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	413
tr A0A2N9F976 A0A2N9F976_FAGSY	YNGDFD	N P F F E R R A S A A H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	393
tr A0A7N2KME6 A0A7N2KME6_QUELO	YNGDFD	N P F F E R R A S A A H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	421
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	YNGDFD	N P F F E R R A S A A H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	393
tr A0A8C7Q9V4 A0A8C7Q9V4_ONCMY	YNGDFD	N P F F E R R A S A A H H G I K M N E E I G F Q C D S N Q G E C R A K F S C H L D C F A W V K R D S Y L P Q G	421
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	YNGDFD	N P F F E R R A S L H G L S M R E I G F Q K D - S Q G E Y K S S Q C I H M D C L R W V K R D S Y L P Q G	379
tr A0A6P8SZE0 A0A6P8SZE0_GYMAC	YNGDFD	N P F F E R R A S L H G L D M Y E I G F Q K D - N Q G E Y K S S Q C I H M D C L R W V K R D S Y L P Q G	418
tr A0A8J0QX44 A0A8J0QX44_XENTR	YNGDFD	N P F F E R R A S V H G M S M L Q E I G F Q K D - N Q G E Y K S S P P C I H M D C L R W V K R D S Y L P Q G	419
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	YNGDFD	N P F F E R R A A A V H G L S M Q Q E I G F Q K D - S Q G E Y K S S Q C I H M D C L R W V K R D S Y L P Q G	405
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	YNGDFD	N P F F E R R A A A V H G L S M Y Q E I G F Q K D - S Q G E Y K A S Q C I H M D C L R W V K R D S Y L P Q G	455
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	YNGDFD	N P F F E R R A A A H G L S M Q Q E I G F Q K D - S Q G E Y K A P Q C I H M D C L R W V K R D S Y L P Q G	393
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	YNGDFD	N P F F E R R A A A H G L S M Y Q E I G F Q K D - S Q G E Y K A P Q C I H M D C L R W V K R D S Y L P Q G	412
tr A0A2K6C158 A0A2K6C158_MACNE	YNGDFD	N P F F E R R A A A V H G L S M Q Q E I G F Q K D - S Q G E Y K A P Q C I H M D C L R W V K R D S Y L P Q G	420
tr F6QAQ1 F6QAQ1_MACMU	YNGDFD	N P F F E R R A A A V H G L S M Q Q E I G F Q K D - S Q G E Y K A P Q C I H M D C L R W V K R D S Y L P Q G	422
tr G3RQP2 G3RQP2_GORGO	YNGDFD	N P F F E R R A A A V H G L S M Q Q E I G F Q K D - S Q G E Y K A P Q C I H M D C L R W V K R D S Y L P Q G	399
sp Q07864 DPOE1_HUMAN	YNGDFD	N P F F E R R A A A V H G L S M Q Q E I G F Q K D - S Q G E Y K A P Q C I H M D C L R W V K R D S Y L P Q G	420
tr A0A2I3S482 A0A2I3S482_PANTR	YNGDFD	N P F F E R R A A A V H G L S M Q Q E I G F Q K D - S Q G E Y K A P Q C I H M D C L R W V K R D S Y L P Q G	420
tr F6Z911 F6Z911_HORSE	YNGDFD	N P F F E R R A A A V H G L S M Y Q E I G F Q K D - N Q G E Y K A P Q C I H M D C L R W V K R D S Y L P Q G	420
tr A0A5G2RB90 A0A5G2RB90_PIG	YNGDFD	N P F F E R R A A A V H G L S M Q Q E I G F Q K D - S Q G E Y K S S Q C I H M D C L R W V K R D S Y L P Q G	393
tr A0A420PL83 A0A420PL83_FUSOX	YNGDFD	N P F F E R R A S I N G I D M Y E I G W K K D - N E D Y Q K N Y S V H M D C F A W V N R D S Y L P Q G	396
tr A0A1V6PGE7 A0A1V6PGE7_PENDC	YNGDFD	N P F F E R R A S T R A S V Q G I D M Y E I G F R K N - S E D I Y Q S D Y C V H M D C F A W V N R D S Y L P Q G	431
tr A0A0G4NU82 A0A0G4NU82_PENCA	YNGDFD	N P F F E R R A S I L G L D M Y E I G F R K N - S E D I Y Q A D N C V H M D C F A W V N R D S Y L P Q G	431
tr A0A1V6TET5 A0A1V6TET5_9EURO	YNGDFD	N P F F E R R A S I L G L D M Y E I G F R K N - S E D I Y Q A D N C V H M D C F A W V N R D S Y L P Q G	431
tr A0A167WJ50 A0A167WJ50_PENCH	YNGDFD	N P F F E R R A S I L G L D M Y E I G F R K N - S E D I Y Q A D N C V H M D C F A W V N R D S Y L P Q G	431
tr A0A3A2Z9P9 A0A3A2Z9P9_9EURO	YNGDFD	N P F F E R R A S V L G I D M Y E I G F R K N - S E D I Y Q S D H C V H M D C F A W V N R D S Y L P Q G	431
tr A0A401L0U3 A0A401L0U3_ASPAW	YNGDFD	N P F F E R R A S V L G I D M Y E I G F R K N - S E D I Y Q S D H C V H M D C F A W V N R D S Y L P Q G	431
tr A0A317VH96 A0A317VH96_ASEPC	YNGDFD	N P F F E R R A S V L G I D M Y E I G F R K N - S E D I Y Q S D H C V H M D C F A W V N R D S Y L P Q G	427
tr A0A117E1M7 A0A117E1M7_ASPNG	YNGDFD	N P F F E R R A S V L G I D M Y E I G F R K N - S E D I Y Q S D H C V H M D C F A W V N R D S Y L P Q G	431
tr A0A1D8PTD0 A0A1D8PTD0_CANAL	FNGDFD	N P F F E N T R F H D M D M F E E I G F A K D - N E G E Y K S K Y C V H M D C F R W V K R D S Y L P Q G	437
tr C5M3R9 C5M3R9_CANTT	FNGDFD	N P F F E R R A R F H D M D M F D E I G F A K D - N E D E Y K S K Y C V H M D C F R W V K R D S Y L P Q G	432
sp Q6FNY7 DPOE_CANGA	FNGDFD	N P F F E R R A S V R G L M D M F E E I G F A P D - S E G E Y K S S Y C V H M D C F R W V K R D S Y L P Q G	435
sp P21951 DPOE_YEAST	FNGDFD	N P F F I H N R S K I H G L D M F D E I G F A P D - A E G E Y K S S Y C S H M D C F R W V K R D S Y L P Q G	375
tr A0A7H9HLU1 A0A7H9HLU1_9SACH	FNGDFD	N P F F I D N R S K I H G L D M F E E I G F L P D - S E G E Y K S S Y C S H M D C F R W V K R D S Y L P Q G	425
tr Q6CUS7 DPOE_KLULA	FNGDFD	N P F F E N R A K F H L N M F D E I G F A P D - S E G E Y K S S Y C T H M D C F R W V K R D S Y L P Q G	352
tr Q752B8 DPOE_ASHGO	FNGDFD	N P F F E R A R S K I R G L S M F D E I G F A P D - S E G E Y K S S Y C A H M D C Y R W V K R D S Y L P Q G	349
:	:	*** : * **** : *	:

tr AOA3P5YCF9 AOA3P5YCF9 BRACM	S HGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	453
sp E4HW04 DPOE1 ARATH	S HGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	453
tr D7KI06 D7KI06 ARALL	S HGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	456
tr AOA8I6WFC8 AOA8I6WFC8 HORVV	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	417
tr AOA452YAR6 AOA452YAR6 AEGTS	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	477
tr AOA3B5XXC3 AOA3B5XXC3 WHEAT	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	472
tr AOA1D6H820 AOA1D6H820 MAIZE	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	450
tr AOA835B357 AOA835B357 9POAL	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	463
tr AOA2S3GPC0 AOA2S3GPC0 9POAL	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	468
tr AOA368PL62 AOA368PL62 SETTIT	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	472
tr AOA7I8KHB8 AOA7I8KHB8 SPIIN	S HGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	454
tr AOA6I9QIG1 AOA6I9QIG1 ELAGV	S HGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	452
tr AOA8B8JBC2 AOA8B8JBC2 PHODC	S HGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	459
tr AOA9Q0FIP5 AOA9Q0FIP5 9ROSI	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	452
tr AOA2C9VYJ6 AOA2C9VYJ6 MANES	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	455
tr AOA7J7C034 AOA7J7C034 TRIWF	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	454
tr AOA2N9F976 AOA2N9F976 FAGSY	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	473
tr AOA7N2KME6 AOA7N2KME6 QUELO	S DGLKAVTKAKLGYDPLEVNPE	DMVRFAMEKQPOTMASVSVS	DAVATYYLYMTYVHVPFIFS	453
tr AOA4W5MAK2 AOA4W5MAK2 9TELE	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	481
tr AOA8C7Q9V4 AOA8C7Q9V4 ONCMY	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	439
tr AOA6P7J2Q5 AOA6P7J2Q5 9TELE	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	481
tr AOA6P8SZE0 AOA6P8SZE0 GYMAC	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	479
tr AOA8J0QX44 AOA8J0QX44 XENTR	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	478
tr AOA4X2K1K8 AOA4X2K1K8 VOMUR	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	465
tr AOA5F4D2S5 AOA5F4D2S5 CANLF	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	478
tr AOA7J7RQ84 AOA7J7RQ84 RHIFE	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	515
tr AOA6P6D0R3 AOA6P6D0R3 PTEVA	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	453
tr AOA2K6CI58 AOA2K6CI58 MACNE	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	472
tr F6QAQ1 F6QAQ1 MACMU	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	480
tr G3RQP2 G3RQP2 GORGO	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	482
sp Q07864 DPOE1 HUMAN	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	459
tr AOA2I3S482 AOA2I3S482 PANTR	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	480
tr F6Z911 F6Z911 HORSE	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	480
tr AOA5G2RB90 AOA5G2RB90 PIG	S HNLKAAAKAKLGYDPELDPE	EMCRMATEEQPOTLATYVSVS	DAVATYYLYMTYVHVPFIFS	453
tr AOA420PL83 AOA420PL83 FUSOX	S RGLKAVTVAKLGYDPELDPE	LMTYASERPOTLAEYSVSVS	DAVATYYLYMTYVHVPFIFS	456
tr AOA1V6PGE7 AOA1V6PGE7 PENDC	S RGLKAVTVAKLGYDPELDPE	LMTYASERPOTLAEYSVSVS	DAVATYYLYMTYVHVPFIFS	491
tr AOA0G4NU82 AOA0G4NU82 PENCA	S RGLKAVTVAKLGYDPELDPE	LMTYASERPOTLAEYSVSVS	DAVATYYLYMTYVHVPFIFS	491
tr AOA1V6TET5 AOA1V6TET5 9EURO	S RGLKAVTVAKLGYDPELDPE	LMTYASERPOTLAEYSVSVS	DAVATYYLYMTYVHVPFIFS	491
tr AOA167WJ50 AOA167WJ50 PENCH	S RGLKAVTVAKLGYDPELDPE	LMTYASERPOTLAEYSVSVS	DAVATYYLYMTYVHVPFIFS	491
tr AOA3A2Z9P9 AOA3A2Z9P9 9EURO	S RGLKAVTVAKLGYDPELDPE	LMTYASERPOTLAEYSVSVS	DAVATYYLYMTYVHVPFIFS	491
tr AOA401L0U3 AOA401L0U3 ASPAW	S RGLKAVTVAKLGYDPELDPE	LMTYASERPOTLAEYSVSVS	DAVATYYLYMTYVHVPFIFS	491
tr AOA317VH96 AOA317VH96 ASPCC	S RGLKAVTVAKLGYDPELDPE	LMTYASERPOTLAEYSVSVS	DAVATYYLYMTYVHVPFIFS	487
tr AOA117E1M7 AOA117E1M7 ASPNG	S RGLKAVTVAKLGYDPELDPE	LMTYASERPOTLAEYSVSVS	DAVATYYLYMTYVHVPFIFS	491
tr AOA1D8PTD0 AOA1D8PTD0 CANAL	S DGLKAVTTAKLGYDPELDPE	LMTYAYEKPPQLLSEYSVSVS	DAVATYYLYMTYVHVPFIFS	497
tr C5M3R9 C5M3R9 CANTT	S DGLKAVTTAKLGYDPELDPE	LMTYAYEKPPQLLSEYSVSVS	DAVATYYLYMTYVHVPFIFS	492
tr Q6FNY7 DPOE CANGA	S DGLKAVTTAKLGYDPELDPE	LMTYAYEKPPQLLSEYSVSVS	DAVATYYLYMTYVHVPFIFS	495
sp P21951 DPOE YEAST	S DGLKAVTQSKLGYDPELDPE	LMTYAYEKKPQHLSEYSVSVS	DAVATYYLYMTYVHVPFIFS	435
tr AOA7H9HLU1 AOA7H9HLU1 9SACH	S DGLKAVTQSKLGYDPELDPE	LMTYAYEKKPQHLSEYSVSVS	DAVATYYLYMTYVHVPFIFS	485
tr Q6CUS7 DPOE KLULA	S DGLKAVTQSKLGYDPELDPE	LMTYAYEKKPQHLSEYSVSVS	DAVATYYLYMTYVHVPFIFS	412
tr Q752B8 DPOE ASHGO	S DGLKAVTQSKLGYDPELDPE	LMTYAYEKKPQHLSEYSVSVS	DAVATYYLYMTYVHVPFIFS	409

tr AOA3P5YCF9 AOA3P5YCF9 BRACM	LAT IIPMV	EVLVRKSGSGLCEMLLMVVE	PR exo ←	→ Pol	NVVC PNKNQADPEKF-YQS	503
sp E4HW04 DPOE1 ARATH	LAT IIPMV	EVLVRKSGSGLCEMLLMVVE	PR exo ←	→ Pol	NVVC PNKNQADPEKF-YQN	503
tr D7KI06 D7KI06 ARALL	LAT IIPMV	EVLVRKSGSGLCEMLLMVQVSTYLPQAQAYKV			NVVC PNKNQADPEKF-YQN	515
tr AOA8I6WFC8 AOA8I6WFC8 HORVV	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AFKA			SVICPNKHQADLEKF-YNN	527
tr AOA452YAR6 AOA452YAR6 AEGTS	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AFQA			NIICPNKHQADLEKF-YNN	467
tr AOA3B5XXC3 AOA3B5XXC3 WHEAT	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AFQA			NIICPNKHQADLEKF-YNN	522
tr AOA1D6H820 AOA1D6H820 MAIZE	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AFKA			SVICPNKHQADLEKF-YNN	500
tr AOA835B357 AOA835B357 9POAL	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AFKA			NVICPNKHQADLEKF-YNN	513
tr AOA2S3GPC0 AOA2S3GPC0 9POAL	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AFKA			NVICPNKHQADLEKF-YNN	518
tr AOA368PL62 AOA368PL62 SETTIT	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AFKA			NVICPNKHQADLEKF-YNN	522
tr AOA7I8KHB8 AOA7I8KHB8 SPIIN	LAT IIPMP	EVLVRKSGSGLCEMLLMVQ-----AYKA			NVICPNKHQADPEKF-YNN	504
tr AOA6I9QIG1 AOA6I9QIG1 ELAGV	LAT IIPMT	EVLVRKSGSGLCEMLLMVQ-----AYKA			NIICPNKHQDDPEKF-YNN	502
tr AOA8B8JBC2 AOA8B8JBC2 PHODC	LAT IIPMT	EVLVRKSGSGLCEMLLMVQ-----AYKA			NIICPNKHQDDPEKF-YNN	502
tr AOA9Q0FIP5 AOA9Q0FIP5 9ROSI	LST IIPMS	EVLVRKSGSGLCEMLLMVQ-----AYKA			NVICPNKHQSDPEKF-HRN	519
tr AOA2C9VYJ6 AOA2C9VYJ6 MANES	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----SYKA			NVICPNKHQSDPEKF-YKN	505
tr AOA7J7C034 AOA7J7C034 TRIWF	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AYKA			NVICPNKHQSDPEKF-YKN	504
tr AOA2N9F976 AOA2N9F976 FAGSY	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AYEA			NVICPNKHQSDPEKF-YTN	523
tr AOA7N2KME6 AOA7N2KME6 QUELO	LAT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AYQA			NVICPNKHQSDPEKF-YNS	503
tr AOA4W5MAK2 AOA4W5MAK2 9TELE	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AYHA			NIVFPNKQEQVFNKLTDDG	532
tr AOA8C7Q9V4 AOA8C7Q9V4 ONCMY	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AYHA			NIVFPNKQEQVFNKLTDDG	490
tr AOA6P7J2Q5 AOA6P7J2Q5 9TELE	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIIFPNKQEQVFNKLTDDG	532
tr AOA6P8SZE0 AOA6P8SZE0 GYMAC	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIVFPNKQEQVFNKLTDDG	530
tr AOA8J0QX44 AOA8J0QX44 XENTR	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AYHA			NIIFPNKQEQVFNKLTDDG	529
tr AOA4X2K1K8 AOA4X2K1K8 VOMUR	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIVFPNKQEQVFNKLTDDG	516
tr AOA5F4D2S5 AOA5F4D2S5 CANLF	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIIFPNKQEQVFNKLTDDG	566
tr AOA7J7RQ84 AOA7J7RQ84 RHIFE	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIIFPNKQEQVFNKLTDDG	504
tr AOA6P6D0R3 AOA6P6D0R3 PTEVA	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIVFPNKQEQVFNKLTDDG	523
tr AOA2K6CI58 AOA2K6CI58 MACNE	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIIFPNKQEQVFNKLTDDG	531
tr F6QAQ1 F6QAQ1 MACMU	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIIFPNKQEQVFNKLTDDG	533
tr G3RQP2 G3RQP2 GORGO	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIIFPNKQEQVFNKLTDDG	510
sp Q07864 DPOE1 HUMAN	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIIFPNKQEQVFNKLTDDG	531
tr AOA2I3S482 AOA2I3S482 PANTR	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIIFPNKQEQVFNKLTDDG	531
tr F6Z911 F6Z911 HORSE	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIIFPNKQEQVFNKLTDDG	531
tr AOA5G2RB90 AOA5G2RB90 PIG	LCT IIPME	EVLVRKSGSGLCEMLLMVQ-----AFHA			NIIFPNKQEQVFNKLTDDG	504
tr AOA420PL83 AOA420PL83 FUSOX	LCT IIPMS	EVLVRKSGSGLCEMLLMVQ-----AYQR			EIVLPNKYITPEKFAF-WDC	506
tr AOA1V6PGE7 AOA1V6PGE7 PENDC	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYQH			EIILPNKHKDPEEAF-YDG	541
tr AOA0G4NU82 AOA0G4NU82 PENCA	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYQH			EIVLPNKHKNPPEAF-YEG	541
tr AOA1V6TET5 AOA1V6TET5 9EURO	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYQH			EIVLPNKHKNPPEAF-YEG	541
tr AOA167WJ50 AOA167WJ50 PENCH	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYQG			EIILPNKHKDPEEAF-YEG	541
tr AOA3A2Z9P9 AOA3A2Z9P9 9EURO	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYQG			NIVLPNKHKDPEEAF-YEG	541
tr AOA401L0U3 AOA401L0U3 ASPAW	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYQG			NIVLPNKHKDPEEAF-YEG	537
tr AOA317VH96 AOA317VH96 ASPCC	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYQG			NIVLPNKHKDPEEAF-YEG	541
tr AOA117E1M7 AOA117E1M7 ASPNG	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYEG			NILLPNKHSDFIERF-YEG	547
tr AOA1D8PTD0 AOA1D8PTD0 CANAL	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYEG			NILLPNKHSDFIERF-YDG	542
tr C5M3R9 C5M3R9 CANTT	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYQG			NILLPNKHTDPIERF-YDG	545
tr Q6FNY7 DPOE CANGA	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYQH			NILLPNKHTDPIERF-YDG	485
tr AOA7H9HLU1 AOA7H9HLU1 9SACH	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYNG			NILLPNKHTDPIERF-YDG	535
tr Q6CUS7 DPOE KLULA	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYQN			SVLLPNKHTDPIERF-YDG	462
tr Q752B8 DPOE ASHGO	LCT IIPLN	DET LRKGTGTLCEMLLMVQ-----AYDH			GILLPNKHTDPIERF-YDG	459

tr AOA3P5YCF9 AOA3P5YCF9 BRACM	EKLKRDCEPIREEGPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTNEI	678
sp F4HW04 DPOE1 ARATH	EKLKRDCEPIREEGPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDEI	678
tr D7KI06 D7KI06 ARALL	EKLKRDCEPIREEGPLIYHLDAVAAAMPNIILTNRLQVHLIS	PSPSIVTDEI	678
tr AOA816WFC8 AOA816WFC8 HORVV	VSLRDHPTRRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDV	678
tr AOA452YAR6 AOA452YAR6 AEGTS	VSLRDHPTRRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDV	678
tr AOA3B5XXC3 AOA3B5XXC3 WHEAT	VSLRDHPTRRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDV	678
tr AOA1D6H8Z0 AOA1D6H8Z0 MAIZE	VSLRDHPTRRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDV	678
tr AOA835B357 AOA835B357 9POAL	VSLRDHPTRRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDV	678
tr AOA2S3GPC0 AOA2S3GPC0 9POAL	VSLRDHPTRRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDV	678
tr AOA368PL62 AOA368PL62 SETIT	VSLRDHPTRRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDV	678
tr AOA718KHB8 AOA718KHB8 SPIIN	QSLRDHPTRRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVSDV	678
tr AOA619QIG1 AOA619QIG1 ELAGV	IFLRDHPTRRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVSDV	678
tr AOA8B8JBC2 AOA8B8JBC2 PHODC	ILLRDRPTRECEPLIYHLDAVAAAMPNIILTNRL----	QPLSIVSDV	678
tr AOA90QFIP5 AOA90QFIP5 9ROSI	LSLRDDPVRRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDEI	678
tr AOA2C9VYJ6 AOA2C9VYJ6 MANES	VRLRDEPITRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDEI	678
tr AOA7J7C034 AOA7J7C034 TRIWF	VRLQDEPITRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDDV	678
tr AOA2N9F976 AOA2N9F976 FAGSY	-----	KPFSIVTDEI	678
tr AOA7N2KME6 AOA7N2KME6 QUELO	VRLQDEPITRECEPLIYHLDAVAAAMPNIILTNRL----	QPPSIVTDEI	678
tr AOA4W5MAK2 AOA4W5MAK2 9TELE	ISLKEVFNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr AOA8C7Q9V4 AOA8C7Q9V4 ONCMY	LSLKEVFNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr AOA6P7J2Q5 AOA6P7J2Q5 9TELE	ISLKEVFNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr AOA6P8SZE0 AOA6P8SZE0 GYMCA	ISLKEVFNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAVVDEAT	678
tr AOA8J0QX44 AOA8J0QX44 XENTR	NSLKEVFNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr AOA4X2K1K8 AOA4X2K1K8 VOMUR	TSLKDVFNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAVVDEAT	678
tr AOA5F4D2S5 AOA5F4D2S5 CANLF	TSLKDVFNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAVVDEAT	678
tr AOA7J7RQ84 AOA7J7RQ84 RHIFE	TSLKDVFNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr AOA6P6D0R3 AOA6P6D0R3 PTEVA	TSLRDVPNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr AOA2K6C158 AOA2K6C158 MACNE	ASLKDVSPRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr F6QAQ1 F6QAQ1 MACMU	ASLKDVSPRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr G3RQP2 G3RQP2 GORGO	ASLKDVSPRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
sp Q07864 DPOE1 HUMAN	ASLKDVSPRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr AOA213S482 AOA213S482 PANTR	ASLKDVSPRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr F6Z911 F6Z911 HORSE	TSLKDVFNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr AOA5G2RB90 AOA5G2RB90 PIG	TSLKDVFNRIECPILYHLDAVAAAMPNIILTNRL----	QPSAMVDEAT	678
tr AOA420PL83 AOA420PL83 FUSOX	NKLTETPNRNEKPLIYHLDAVAAAMPNIIMTNRL----	QPSMIQESD	678
tr AOA1V6PGE7 AOA1V6PGE7 PENDC	LDLKNPVRNEVFFIYHLDAVAAAMPNIIMTNRL----	QPDSLIIKESD	678
tr AOA0G4NU82 AOA0G4NU82 PENCA	LDLKNPVRNEVFFIYHLDAVAAAMPNIIMTNRL----	QPDSLIIKESD	678
tr AOA1V6TET5 AOA1V6TET5 9EURO	LDLKNPVRNEVFFIYHLDAVAAAMPNIIMTNRL----	QPDSLIIKESD	678
tr AOA167WJ50 AOA167WJ50 PENCH	LDLKNPVRNEVFFIYHLDAVAAAMPNIIMTNRL----	QPDSLIIKESD	678
tr AOA3A2Z9P9 AOA3A2Z9P9 9EURO	ADMRDRPVRNEVFFIYHLDAVAAAMPNIIMTNRL----	QPDSMIQESN	678
tr AOA401L0U3 AOA401L0U3 ASPAW	IDLKERPHRDEVPFIYHLDAVAAAMPNIIMTNRL----	QPDSMIQESN	678
tr AOA317VH96 AOA317VH96 ASPEC	IDLKERPHRDEVPFIYHLDAVAAAMPNIIMTNRL----	QPDSMIQESN	678
tr AOA117EIM7 AOA117EIM7 ASPNG	IDLKERPHRDEVPFIYHLDAVAAAMPNIIMTNRL----	QPDSMIQESN	678
tr AOA1D8PTD0 AOA1D8PTD0 CANAL	LELKNPFRQEKPLIYHLDAVAAAMPNIIMTNRL----	QPDSMKSEDD	678
tr C5M3R9 C5M3R9 CANTT	LNKLNTPITREKPLIYHLDAVAAAMPNIIMTNRL----	QPDSMKTEDE	678
tr Q6FNY7 DPOE CANGA	LELKENNRHEKPLIYHLDAVAAAMPNIIMTNRL----	QPDSIKTEKDC	678
sp P21951 DPOE YEAST	LELKENNRHEKPLIYHLDAVAAAMPNIIMTNRL----	QPDSIKTEKDC	678
tr AOA7H9HLU1 AOA7H9HLU1 9SACH	LDLKTNNKRCLEPLIYHLDAVAAAMPNIIMTNRL----	QPDSMKTERD	678
tr Q6CUS7 DPOE KLULA	TDLKNKRNLEPLIYHLDAVAAAMPNIIMTNRL----	QPDSMKDEKDC	678
tr Q752B8 DPOE ASHGO	QELKMNKRKLEPLIYHLDAVAAAMPNIIMTNRL----	QPDSMKTERD	678

tr AOA3P5YCF9 AOA3P5YCF9 BRACM	LRKLEWVWRGTYMMAKSDYHLKQIESEFVDAGANIQ--	SSKSFLLDPKVEQOSKLL	736
sp F4HW04 DPOE1 ARATH	LRKLEWVWRGTYMMAKSDYHLKQIESEFVDAGANIQ--	SSKSFLLDPKVDQOSKLL	736
tr D7KI06 D7KI06 ARALL	LRKLEWVWRGTYMMAKSDYHLKQIESEFVDAGANIQ--	SSKSFLLDPKLDQOSKLL	736
tr AOA816WFC8 AOA816WFC8 HORVV	CLRTLLEWVRGTYTAKKSDYHHRKQIESEMIQAG-GVT--	SSKFFLLDPKPEHLLKLL	736
tr AOA452YAR6 AOA452YAR6 AEGTS	CLRTLLEWVRGTYTAKKSDYHHRKQIESEMIQAG-GVT--	SSKFFLLDPKPEHLLKLL	736
tr AOA3B5XXC3 AOA3B5XXC3 WHEAT	CLRTLLEWVRGTYTAKKSDYHHRKQIESEMIQAG-GVT--	SSKFFLLDPKPEHLLKLL	736
tr AOA1D6H8Z0 AOA1D6H8Z0 MAIZE	CLRTLLEWVRGTYMMAKSDYHHRKQIESELIQSG-GIA--	SSKFFLLDPKPEHLLKLL	736
tr AOA835B357 AOA835B357 9POAL	CLRKLEWVWRGTYMMAKSDYHHRKQIESELIQSG-GIA--	SSKFFLLDPKPEHLLKLL	736
tr AOA2S3GPC0 AOA2S3GPC0 9POAL	CLRKLEWVWRGTYMMAKSDYHHRKQIESELIQSG-GIA--	SSKFFLLDPKPEHLLKLL	736
tr AOA368PL62 AOA368PL62 SETIT	CLRKLEWVWRGTYTAKKSDYHHRKQIESELIQSG-GIA--	SSKFFLLDPKPEHLLKLL	736
tr AOA718KHB8 AOA718KHB8 SPIIN	CLRKLEWVWRGTYTAKKSDYHHRKQIESELVENG-EDR--	LSKAFLLDPKPEHLLKLL	736
tr AOA619QIG1 AOA619QIG1 ELAGV	CLRKLEWVWRGTYMMAKSDYHHRKQIESELVENG-EGQ--	AIKFFLLDPKPEHLLKLL	736
tr AOA8B8JBC2 AOA8B8JBC2 PHODC	CLRKLEWVWRGTYMMAKSDYHHRKQIESELVENG-EGQ--	TIKFFLLDPKPEHLLKLL	736
tr AOA90QFIP5 AOA90QFIP5 9ROSI	CLRKLEWVWRGTYMMAKSDYHHRKQIESEFVDGA-DGQ--	LSKFFLLDPKPEHLLKLL	736
tr AOA2C9VYJ6 AOA2C9VYJ6 MANES	CLRKLEWVWRGTYMMAKSDYHHRKQIESEFVDGA-DGQ--	LSKFFLLDPKPEHLLKLL	736
tr AOA7J7C034 AOA7J7C034 TRIWF	CLRKLEWVWRGTYMMAKSDYHHRKQIESEFVGG-NGQ--	LSKFFLLDPKPEHLLKLL	736
tr AOA2N9F976 AOA2N9F976 FAGSY	CLRKLEWVWRGTYMMAKSDYHHRKQIESEFVDGA-GGK--	LPSFFLLDPKPEHLLKLL	736
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tr AOA8C7Q9V4 AOA8C7Q9V4 ONCMY	CRKMSWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
tr AOA6P7J2Q5 AOA6P7J2Q5 9TELE	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
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tr AOA5F4D2S5 AOA5F4D2S5 CANLF	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
tr AOA7J7RQ84 AOA7J7RQ84 RHIFE	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
tr AOA6P6D0R3 AOA6P6D0R3 PTEVA	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
tr AOA2K6C158 AOA2K6C158 MACNE	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
tr F6QAQ1 F6QAQ1 MACMU	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
tr G3RQP2 G3RQP2 GORGO	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
sp Q07864 DPOE1 HUMAN	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
tr AOA213S482 AOA213S482 PANTR	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
tr F6Z911 F6Z911 HORSE	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
tr AOA5G2RB90 AOA5G2RB90 PIG	CRKMAWQWRGTYMMAKSDYHHRKQIESEKFPPLFPNG--	RPRAFHLLNLEEQAQKHE	736
tr AOA420PL83 AOA420PL83 FUSOX	DRRLPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr AOA1V6PGE7 AOA1V6PGE7 PENDC	DRRMPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr AOA0G4NU82 AOA0G4NU82 PENCA	DRRMPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr AOA1V6TET5 AOA1V6TET5 9EURO	DRRMPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr AOA167WJ50 AOA167WJ50 PENCH	DRRMPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr AOA3A2Z9P9 AOA3A2Z9P9 9EURO	DRRMPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr AOA401L0U3 AOA401L0U3 ASPAW	DRRMPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr AOA317VH96 AOA317VH96 ASPEC	DRRMPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr AOA117EIM7 AOA117EIM7 ASPNG	DRRMPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr AOA1D8PTD0 AOA1D8PTD0 CANAL	DRRLPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr C5M3R9 C5M3R9 CANTT	DRRLPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr Q6FNY7 DPOE CANGA	DRRLPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
sp P21951 DPOE YEAST	DRRLPWAWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr AOA7H9HLU1 AOA7H9HLU1 9SACH	DRRLKWSWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr Q6CUS7 DPOE KLULA	DRRLKWSWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736
tr Q752B8 DPOE ASHGO	DRRLKWSWRGEFLLPAKRDYNNIRATANERFPGRYKNS--	PMRFTFQELSADEQANLVK	736

tr AOA3P5YCF9 AOA3P5YCF9_BRACM	KNVDYQGWLEVKRRKWKGVLEKRRRLGDR	SLKQIES-----HEIKKKVTVRRGVG	1335
sp F4HW04 DPOE1_ARATH	KSNVYQGWLELKKRKKWVLEKRRRLGDLR	SSNQVDT-----HEINQKVGGRGGVG	1282
tr D7KI06 D7KI06_ARALL	KSNVYQGWLELKKRKKWVLEKRRRLGDLR	SPNQSDA-----HEINQKVGGRGGVG	1299
tr AOA8I6WFC8 AOA8I6WFC8_HORVV	RSTDYQGWLEAARKKWKVYREKRRRLGAAA	SSEGFSSNNLF--SARNQSQLHGNRNRS	1319
tr AOA452YAR6 AOA452YAR6_AEGTS	RSTDYQGWLEAARKKWKVYREKRRRLGAAA	SSEGFSSNNLF--SARNVSLHGNRNRS	1259
tr AOA3B5XXC3 AOA3B5XXC3_WHEAT	RSTDYQGWLEAARKKWKVYREKRRRLGAAA	SSEGFSSNNLF--SARNDSQLHGNRNRS	1314
tr AOA1D6H8Z0 AOA1D6H8Z0_MAIZE	KGTDYQGWLDARKKWKVYREKRRRLGAAA	FFDDP-NALL--SARHANQLPVNSRNRS	1293
tr AOA835B357 AOA835B357_9POAL	RSDDYQGWLDARKKWKVYREKRRRLGAAA	FFDGPNTALL--SSRNANQLPGNSRNRS	1307
tr AOA2S3GPC0 AOA2S3GPC0_9POAL	RSTDYQGWLDARKKWKVYREKRRRLGAAA	FFDGPNTALL--SSRNVSQPLPGNSRNRS	1312
tr AOA368PL62 AOA368PL62_SETIT	RSTDYQGWLDARKKWKVYREKRRRLGAAA	FFDGPNTALL--SSRNVSQPLPGNSRNRS	1316
tr AOA7I8KHB8 AOA7I8KHB8_SPIIN	RNVDYQGWLDARKKWKVYREKRRRLGAMD	SSSQFVAMAGNHESMTSNKHNIAKNGAV	1317
tr AOA6I9QIG1 AOA6I9QIG1_ELAGV	RNVDYQGWLEVKRRKWKVYREKRRRLGITK	MSQQSAGAALKPASFNFYRRHQDRNGVS	1301
tr AOA8B8JBC2 AOA8B8JBC2_PHODC	RNVDYQGWLEVKRRKWKVYREKRRRLGITK	MSQQSAGAALKPASFNFYRRHQDRSGVS	1301
tr AOA9Q0FIP5 AOA9Q0FIP5_9ROSI	RNVDYQGWLVVKKRKKWKTLEKRRRLGSLG	FSRGSDFGAHEHLSLGTKEAQRKTGVG	1327
tr AOA2C9VYJ6 AOA2C9VYJ6_MANES	RNVDYQGWLELKKRKKWVLEKRRRLGSLR	NSNRANGASEPLGSLINNKKAQHRRTVG	1308
tr AOA7J7C034 AOA7J7C034_TRIWF	KNKDYQGWLELKKRKKWVLEKRRRLGSSR	PHRADGASEVMEGMISKRGGQAKTGVG	1301
tr AOA2N9F976 AOA2N9F976_FAGSY	RNVDYQGWLELKKRKKWVLEKRRRLGSSR	PPHRGNGVSDLLGGVTNGKDTQGRSGVG	1298
tr AOA7N2KME6 AOA7N2KME6_QUELO	RNVDYQGWLELKKRKKWVLEKRRRLGSSR	PPRRKGKVLVGLGVDVTHKDDTQGRSGVS	1302
tr AOA4W5MAK2 AOA4W5MAK2_9TELE	TQEARLVWLRVYHKKKWLQLEKRRRLGSSR	L-----DGEVQAMGGVIRDAGPATGLG	1318
tr AOA8C7Q9V4 AOA8C7Q9V4_ONCMY	TQEARLVWLRVYHKKKWLQLEKRRRLGSSR	L-----DGEVQAMGGVIRDAGPATGLG	1280
tr AOA6P7J2Q5 AOA6P7J2Q5_9TELE	TKEERLVWLRVYHKKKWLQLEKRRRLGSSR	L-----DGEAQPVGGGVIRD-GPTTGLG	1316
tr AOA6P8SZE0 AOA6P8SZE0_GYMCA	SREERLVWLRVYHKKKWLQLEKRRRLGSSR	L-----DGEAQPVGGGVIRDGPTTGLG	1316
tr AOA8J0QX44 AOA8J0QX44_XENTR	TKEERLVWLRVYHKKKWLQLEKRRRLGSSR	L-----DGDVAPGAGGVIRE-TQAAGLG	1315
tr AOA4X2K1K8 AOA4X2K1K8_VOMUR	TKEERLVWLRVYHKKKWLQLEKRRRLGSSR	L-----TREGVLGS-GVIRD-GPATGLG	1301
tr AOA5F4D2S5 AOA5F4D2S5_CANLF	TQEEWLVWLRVYHKKKWLQLEKRRRLGSSR	L-----VAEGEPLP-GAIRE-RPATGLG	1351
tr AOA7J7RQ84 AOA7J7RQ84_RHIFE	TQEEWLVWLRVYHKKKWLQLEKRRRLGSSR	L-----GAEGAPQP-GAIRD-GPSAGLG	1289
tr AOA6P6D0R3 AOA6P6D0R3_PTEVA	TQEEWLVWLRVYHKKKWLQLEKRRRLGSSR	L-----TAEGAPQP-GAIRE-GPATGLG	1308
tr AOA2K6CI58 AOA2K6CI58_MACNE	TQEEWLVWLRVYHKKKWLQLEKRRRLGSSR	L-----SAEGVLRP-GAIRD-GPATGLG	1293
tr F6QAQ1 F6QAQ1_MACMU	TQEEWLVWLRVYHKKKWLQLEKRRRLGSSR	L-----SAEGVLRP-GAIRD-GPATGLG	1318
tr G3RQP2 G3RQP2_GORGO	TQEEWLVWLRVYHKKKWLQLEKRRRLGSSR	L-----SAEGVLRP-GAIRD-GPATGLG	1295
sp Q07864 DPOE1_HUMAN	SQEEWLVWLRVYHKKKWLQLEKRRRLGSSR	L-----SAEGVLRP-GAIRD-GPATGLG	1316
tr AOA2I3S482 AOA2I3S482_PANTR	TQEEWLVWLRVYHKKKWLQLEKRRRLGSSR	L-----SAEGVLRP-GAIRD-GPATGLG	1316
tr F6Z911 F6Z911_HORSE	TQEEWLVWLRVYHKKKWLQLEKRRRLGSSR	L-----VAEGAPRP-GAIRD-RPTTGLG	1316
tr AOA5G2RB90 AOA5G2RB90_PIG	TQEEWLVWLRVYHKKKWLQLEKRRRLGSSR	L-----VAEGVPRP-GAIRE-GFSTGLG	1289
tr AOA420PL83 AOA420PL83_FUSOX	ASENYEAFLLMYQKQKWKIQKARIRRRQ	L-----GDRRGGAV-NNLQ	1271
tr AOA1V6PGE7 AOA1V6PGE7_PENDC	MSEDEYEFLLKYQKQKWKIQKARIRRRQ	L-----GERTNVAT-DSLS	1308
tr AOA0G4NU82 AOA0G4NU82_PENCA	MSENYEGFLKYQKQKWKIQKARVRRRQ	L-----GERTNVAS-DSLS	1308
tr AOA1V6TET5 AOA1V6TET5_9EURO	MSENYEGFLKYQKQKWKIQKARIRRRQ	L-----GERTNVAS-DSLS	1308
tr AOA167WJ50 AOA167WJ50_PENCH	MSENYEGFLKYQKQKWKIQKARIRRRQ	L-----GERTNVAS-DSLS	1308
tr AOA3A2Z9P9 AOA3A2Z9P9_9EURO	ITEDYVGFLLKYQKQKWKIQKARVRRRQ	L-----GDRANVAT-DSLS	1309
tr AOA401L0U3 AOA401L0U3_ASPAW	MADDYVGFLLKYQKQKWKIQKARIRRRQ	L-----GERANAGG-DSLS	1312
tr AOA317VH96 AOA317VH96_ASPAC	MADDYVGFLLKYQKQKWKIQKARIRRRQ	L-----GERANAGG-DSLS	1308
tr AOA117E1M7 AOA117E1M7_ASPNG	MEDDYVGFLLKYQKQKWKIQKARIRRRQ	L-----GERANAGG-DSLS	1312
tr AOA1D8PTD0 AOA1D8PTD0_CANAL	MTEDYQGFLLYQKQKWKIQKARIRRRQ	L-----GANSSESSQRSTVG	1304
tr C5M3R9 C5M3R9_CANTT	MLDDYQGFLLYQKQKWKIQKARIRRRQ	L-----GANSSESSQRSTVG	1299
sp Q6FNY7 DPOE_CANGA	MEEDYVSWLSYQKIKWKIQKARIRRRQ	L-----GKSGEFTNSRSVLG	1304
sp P21951 DPOE_YEAST	MEDDYVGFLLKYQKQKWKIQKARIRRRQ	L-----GNTNSRSRYSKALG	1247
tr AOA7H9HLU1 AOA7H9HLU1_9SACH	LDEYVYKVLQYQKIKWKIQKARRRRAQ	L-----GDMNSSAGRSALG	1296
sp Q6CUS7 DPOE_KLULA	MLDDYVGFLLQYQKTKWKIQKIDRKKREK	L-----GKTSRASDRSALG	1217
sp Q752B8 DPOE_ASHGO	IDEDYVGFLLNYQKIKWLQLEKRRRLGSSR	L-----GSSSTLNDRSALG	1212

tr AOA3P5YCF9 AOA3P5YCF9_BRACM	S	FFRRPEEALTSSSHWOI-----IQLVPS-PQ	1360
sp F4HW04 DPOE1_ARATH	S	YFRRPEEALTSSSHWOI-----IQLVPS-PQ	1307
tr D7KI06 D7KI06_ARALL	S	YFRRPEEALTSSSHWOI-----IQLVPS-PQ	1327
tr AOA8I6WFC8 AOA8I6WFC8_HORVV	T	FFQKQELSLFRSHWQ-----IIQLAPS-TM	1344
tr AOA452YAR6 AOA452YAR6_AEGTS	T	FFQKQELSLFRSHWQ-----IIQLAPS-TL	1284
tr AOA3B5XXC3 AOA3B5XXC3_WHEAT	T	FFQKQELSLFRSHWQ-----IIQLAPS-TL	1339
tr AOA1D6H8Z0 AOA1D6H8Z0_MAIZE	T	FFQKQELALFRSHWQACVFCYLLCSVALVYHLFFALLMIVNSIYCPHQIQLASS-TV	1352
tr AOA835B357 AOA835B357_9POAL	T	FFQKQELALFRSHWQ-----IIQLASS-TT	1332
tr AOA2S3GPC0 AOA2S3GPC0_9POAL	T	FFQKQELALFRSHWQ-----IIQLASS-TT	1337
tr AOA368PL62 AOA368PL62_SETIT	T	FFQKQELALFRSHWQ-----IIQLDSS-TT	1341
tr AOA7I8KHB8 AOA7I8KHB8_SPIIN	S	FFRRQELLLVHNHWQ-----IIQFVPS-AK	1342
tr AOA6I9QIG1 AOA6I9QIG1_ELAGV	S	FFRRQELALVQSHWQ-----IIQLVPS-TQ	1326
tr AOA8B8JBC2 AOA8B8JBC2_PHODC	S	FFRRQELALVQSHWQ-----IIQLNPS-TQ	1326
tr AOA9Q0FIP5 AOA9Q0FIP5_9ROSI	S	YFTRPEVVLTRCHWQ-----IIQLLPS-SL	1352
tr AOA2C9VYJ6 AOA2C9VYJ6_MANES	S	YFATHIELSLTRCHWQ-----IIQLLPS-SH	1333
tr AOA7J7C034 AOA7J7C034_TRIWF	S	YFRRHEVALTRCHWQ-----IIQLVPG-SQ	1326
tr AOA2N9F976 AOA2N9F976_FAGSY	S	YFRRQELALTRCHWQ-----IIQLVPS-SE	1323
tr AOA7N2KME6 AOA7N2KME6_QUELO	S	YFKRHEASLTRCHWQ-----IIQLVPS-S-	1326
tr AOA4W5MAK2 AOA4W5MAK2_9TELE	S	FLRRTARSILDMPWQ-----IVQIAET-SH	1346
tr AOA8C7Q9V4 AOA8C7Q9V4_ONCMY	S	FLRRTARSILDMPWQ-----IVQIAET-SH	1305
tr AOA6P7J2Q5 AOA6P7J2Q5_9TELE	S	FLRRTARSILDMPWQ-----IVQIAET-SH	1341
tr AOA6P8SZE0 AOA6P8SZE0_GYMCA	S	FLRRTARSILDMPWQ-----IVQIAET-SH	1341
tr AOA8J0QX44 AOA8J0QX44_XENTR	S	FLRRTARSILDMPWQ-----IVQIGES-SQ	1340
tr AOA4X2K1K8 AOA4X2K1K8_VOMUR	H	FLRRTARSILDLPWQ-----VVQISET-NQ	1326
tr AOA5F4D2S5 AOA5F4D2S5_CANLF	G	FLRRTARSILDLPWQ-----IVQISET-SQ	1376
tr AOA7J7RQ84 AOA7J7RQ84_RHIFE	G	FLRRTARSILDLPWQ-----IVQISET-TQ	1314
tr AOA6P6D0R3 AOA6P6D0R3_PTEVA	G	FLRRTARSILDLPWQ-----IVQISET-SQ	1333
tr AOA2K6CI58 AOA2K6CI58_MACNE	S	FLRRTARSILDLPWQ-----IVQISET-SQ	1318
tr F6QAQ1 F6QAQ1_MACMU	S	FLRRTARSILDLPWQ-----IVQISET-SQ	1343
tr G3RQP2 G3RQP2_GORGO	S	FLRRTARSILDLPWQ-----IVQISET-SQ	1320
sp Q07864 DPOE1_HUMAN	S	FLRRTARSILDLPWQ-----IVQISET-SQ	1341
tr AOA2I3S482 AOA2I3S482_PANTR	S	FLRRTARSILDLPWQ-----IVQISET-SQ	1341
tr F6Z911 F6Z911_HORSE	G	FLRRTARSILDLPWQ-----IVQISET-SQ	1341
tr AOA5G2RB90 AOA5G2RB90_PIG	G	FLRRTARSILDLPWQ-----IVQISET-SQ	1314
tr AOA420PL83 AOA420PL83_FUSOX	Q	TFMKQAHTYMSNSWQ-----VLHLKAT-ET	1296
tr AOA1V6PGE7 AOA1V6PGE7_PENDC	H	FFRNQAQLLYISTWQ-----VLQLCET-GR	1333
tr AOA0G4NU82 AOA0G4NU82_PENCA	N	FFRNQAQLMYISTWQ-----VLQLCET-GV	1333
tr AOA1V6TET5 AOA1V6TET5_9EURO	N	FFRNQAQLMYISTWQ-----VLQLCET-GV	1333
tr AOA167WJ50 AOA167WJ50_PENCH	N	FFRNQAQLMYISTWQ-----VLQLCET-GV	1333
tr AOA3A2Z9P9 AOA3A2Z9P9_9EURO	N	YFRNQAELLYINTWQ-----VLQLRET-GR	1334
tr AOA401L0U3 AOA401L0U3_ASPAW	N	LFRNQAELLYINTWQ-----VLQLRET-GR	1337
tr AOA317VH96 AOA317VH96_ASPAC	N	LFRNQAELLYINTWQ-----VLQLRET-GR	1333
tr AOA117E1M7 AOA117E1M7_ASPNG	N	LFRNQAELLYINTWQ-----VLQLRET-GR	1337
tr AOA1D8PTD0 AOA1D8PTD0_CANAL	G	MFRKRAENIAGTNSWE-----ILEYKLDPTK	1330
tr C5M3R9 C5M3R9_CANTT	G	MIRKRAENIAGTNSWE-----ILEYKDPDSK	1325
sp Q6FNY7 DPOE_CANGA	S	MIRKQAEEMFANGSWE-----VLQYRDN-YE	1329
sp P21951 DPOE_YEAST	S	MIRKQAEYSANSTWE-----VLQYKDS-GE	1272
tr AOA7H9HLU1 AOA7H9HLU1_9SACH	G	MIRKQAEYVANSWE-----ILQYKPS-AQ	1321
sp Q6CUS7 DPOE_KLULA	N	LIRKHVESYADKSWE-----ILQCKPS-ID	1242
sp Q752B8 DPOE_ASHGO	N	IKKHAESYANSWE-----ILQYKNS-SE	1237

tr A0A3P5YCF9 A0A3P5YCF9_BRACM	LHRYMCKV	FALLLTDLRR	LGATIIFADFSKVIDT	GKFDLSAAKAYCDSLLTAVGNSDIF	1866
sp F4HW04 DPOE1_ARATH	LHRYMCKV	FALLLTDLRR	LAIIYADFVKVITD	TKFDLSAAKAYCESLLTVRNSDIF	1847
tr D7K106 D7K106_ARALL	LHRYMCKV	FALLLTDLRR	LGANVIFANFSKII	IDTGVKFDLSAAKAYCESLLTQTRDLF	1865
tr A0A816WFC8 A0A816WFC8_HORVU	LHNVMKVF	FALLLAEFRK	LGANVIFANFSKII	IDTGVKFDLPSARAYCDSLLTQTRDLF	1879
tr A0A452YAR6 A0A452YAR6_AEGTS	LHNVMKVF	FALLLAEFRK	LGANVIFANFSKII	IDTGVKFDLPSARAYCDSLLTQTRDLF	1819
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	LHNVMKVF	FALLLAEFRK	LGANVIFANFSKII	IDTGVKFDLPSARAYCDSLLTQTRDLF	1874
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	LHNVMKVF	FALLLAEFRK	LGANVIFANFSKII	IDTGVKFDLPSARAYCDSLLTQTRDLF	1887
tr A0A835B357 A0A835B357_9POAL	LHNVMKVF	FALLLAEFRK	LGANVIFANFSKII	IDTGVKFDLPSARAYCDSLLTQTRDLF	1865
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	LHNVMKVF	FALLLAEFRK	LGANVIFANFSKII	IDTGVKFDLPSARAYCDSLLTQTRDLF	1872
tr A0A368PL62 A0A368PL62_SETIT	LHNVMKVF	FALLLAEFRK	LGANVIFANFSKII	IDTGVKFDLPSARAYCDSLLTQTRDLF	1876
tr A0A718KHB8 A0A718KHB8_SFIIN	LHKLMRKF	FALLLSELRK	LGATIVFANFPKI	IVDTGKTDLPAARAYCDDLKALQARDLL	1874
tr A0A619QIG1 A0A619QIG1_ELAGV	LHKVMKVF	FALLLAEFRK	LGATIFANFSKVIDT	GKIDLSAARAYCDDLKALQARDLL	1864
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	LHKVMKVF	FALLLAEFRK	LGATIFANFSKVIDT	GKIDLSAARAYCDDLKALQARDLL	1867
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	LHKVMKVF	FALLLAEFRK	LGATIFANFSKVIDT	GKIDLSAARAYCDDLKALQARDLL	1907
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	LHKVMKVF	FALLLAEFRK	LGATIFANFSKVIDT	GKIDLSAARAYCDDLKALQARDLL	1874
tr A0A7J7C034 A0A7J7C034_TRIWF	LHKVMKVF	FALLLAEFRK	LGATIFANFSKVIDT	GKIDLSAARAYCDDLKALQARDLL	1866
tr A0A2N9F976 A0A2N9F976_FAGSY	LHKVMKVF	FALLLAEFRK	LGATIFANFSKVIDT	GKIDLSAARAYCDDLKALQARDLL	1864
tr A0A7N2KME6 A0A7N2KME6_QUELO	LHKVMKVF	FALLLAEFRK	LGATIFANFSKVIDT	GKIDLSAARAYCDDLKALQARDLL	1867
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	LHNMMKVF	LQLVAEFRK	LGSTVVYGNFNRI	LLCTKKRRIDDAIGYVEYITNSIHSREIF	1902
tr A0A8C7Q9V4 A0A8C7Q9V4_ONCMY	LHNMMKVF	LQLVAEFRK	LGSTVVYGNFNRI	LLCTKKRRIDDAIGYVEYITNSIHSREIF	1864
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	LHNMMKVF	LQLVAEFRK	LGSTVVYGNFNRI	LLCTKKRRIDDAIGYVEYITNSIHSREIF	1900
tr A0A6P8SZE0 A0A6P8SZE0_GYMCA	LHNMMKVF	LQLVSEFRK	LGSTVVYGNFNRI	LLCTKKRRIDDAIGYVEYITNSIHSREIF	1900
tr A0A8J0QX44 A0A8J0QX44_XENTR	LHNMMKVF	LQLVSEFRK	LGSTVVYGNFNRI	LLCTKKRRIDDAIGYVEYITNSIHSREIF	1898
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1885
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1935
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1873
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1892
tr A0A2K6C1S8 A0A2K6C1S8_MACNE	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1877
tr F6QAQ1 F6QAQ1_MACMU	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1902
tr G3RQP2 G3RQP2_GORGO	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1879
sp Q07864 DPOE1_HUMAN	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1900
tr A0A2I3S482 A0A2I3S482_PANTR	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1900
tr F6Z911 F6Z911_HORSE	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1900
tr A0A5G2RB90 A0A5G2RB90_PIG	LHNSMVKVF	LQLVAEFRK	LGSSVYANFNRI	LLCTKKRRIDDAIAYVEYITNSIHSREIF	1873
tr A0A420PL83 A0A420PL83_FUSOX	VQMSRRAE	FQQLMAEFRF	GVSNVIFANANRL	LQTTKAEVGNAYAYSEYIIRKSKPLF	1847
tr A0A1V6PGE7 A0A1V6PGE7_PENDC	VFLLSRKS	FORLMAEFRF	GVSNVIFASPT	RLRLQTTKTEVGNAYAYSQVVLKIRANPSF	1885
tr A0A0G4NU82 A0A0G4NU82_PENCA	VFLLSRKS	FORLMAEFRF	GVSNVIFASPT	RLRLQTTKTEVGNAYAYSQVVLKIRANPSF	1884
tr A0A1V6TET5 A0A1V6TET5_9EURO	VFLMSRKS	FORLMAEFRF	GVSNVIFASPT	RLRLQTTKTEVGNAYAYSQVVLKIRANPSF	1884
tr A0A167WJ50 A0A167WJ50_PENCH	VFLMSRKS	FORLMAEFRF	GVSNVIFASPT	RLRLQTTKTEVGNAYAYSQVVLKIRANPSF	1884
tr A0A3A2Z9P9 A0A3A2Z9P9_9EURO	VFLMSRKS	FORLMAEFRF	GVSNVIFASPT	RLRLQTTKTEVGNAYAYSQVVLKIRANPSF	1887
tr A0A401L0U3 A0A401L0U3_ASPAW	VFLMSRKS	FORLMAEFRF	GVSNVIFASPT	RLRLQTTKTEVGNAYAYSQVVLKIRANPSF	1891
tr A0A317VH96 A0A317VH96_ASPEC	VFLMSRKS	FORLMAEFRF	GVSNVIFASPT	RLRLQTTKTEVGNAYAYSQVVLKIRANPSF	1887
tr A0A117E1M7 A0A117E1M7_ASPNG	VRLMSRKS	FORLMAEFRF	GVSNVIFASPT	RLRLQTTKTEVGNAYAYSQVVLKIRANPSF	1891
tr A0A1D8PTD0 A0A1D8PTD0_CANAL	VHNLTKKAL	LQLVSEFRK	MGQVIFANRNK	MLIQTSKISVENSAYGQYLKAAARSKPLF	1877
tr C5M3R9 C5M3R9_CANTT	VHNLTKKAL	LQLVSEFRK	MGQVIFANRNK	MLIQTSKISVENSAYGQYLKAAARSKPLF	1872
sp Q6FNY7 DPOE_CANGA	IHNLTAKS	LQLVSEFRK	MGQVIFANRNK	MLIQTSKISVENSAYGQYLKAAARSKPLF	1891
sp P21951 DPOE_YEAST	VHNLTKKAL	LQLVSEFRK	MGQVIFANRNK	MLIQTSKISVENSAYGQYLKAAARSKPLF	1835
tr A0A7H9HLU1 A0A7H9HLU1_9SACH	IHNLTAKS	LQLVSEFRK	MGQVIFANRNK	MLIQTSKISVENSAYGQYLKAAARSKPLF	1882
sp Q6CUS7 DPOE_KLULA	IHNLTAKS	LQLVSEFRK	MGQVIFANRNK	MLIQTSKISVENSAYGQYLKAAARSKPLF	1798
sp Q752B8 DPOE_ASHGO	VNMLTKAL	LQLVSEFRK	MGQVIFANRNK	MLIQTSKISVENSAYGQYLKAAARSKPLF	1793

tr A0A3P5YCF9 A0A3P5YCF9_BRACM	-----	ILFLKLCFAVMKRNLLKY	INVKEFAAAEFLDPG	PSFILPNVA	SNCDAYD	2082
sp F4HW04 DPOE1_ARATH	-----	VMRKSLLYIKVKECAAAE	FLDPGPSFILPNVA	SNCDAYD	LL	2048
tr D7K106 D7K106_ARALL	-----	LISGNLVLETMFTNRV	MKGLLKYIKVKECAAAE	FLDPGPSFILPNVA	SNCDAYD	2128
tr A0A816WFC8 A0A816WFC8_HORVU	-----	-----	RMKRLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2110
tr A0A452YAR6 A0A452YAR6_AEGTS	-----	-----	RMKRLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2050
tr A0A3B5XXC3 A0A3B5XXC3_WHEAT	-----	-----	RMKRLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2105
tr A0A1D6H8Z0 A0A1D6H8Z0_MAIZE	-----	-----	RMKRLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2113
tr A0A835B357 A0A835B357_9POAL	-----	-----	RMKRLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2095
tr A0A2S3GPC0 A0A2S3GPC0_9POAL	-----	-----	RMKRLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2100
tr A0A368PL62 A0A368PL62_SETIT	-----	-----	RMKRLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2104
tr A0A718KHB8 A0A718KHB8_SFIIN	-----	-----	RMKRLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2105
tr A0A619QIG1 A0A619QIG1_ELAGV	-----	-----	RMKRLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2099
tr A0A8B8JBC2 A0A8B8JBC2_PHODC	-----	-----	RMKRLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2102
tr A0A9Q0FIP5 A0A9Q0FIP5_9ROSI	-----	-----	VMRNLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2147
tr A0A2C9VYJ6 A0A2C9VYJ6_MANES	-----	-----	VMRNLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2113
tr A0A7J7C034 A0A7J7C034_TRIWF	-----	-----	VMRNLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2093
tr A0A2N9F976 A0A2N9F976_FAGSY	-----	-----	VMRNLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2056
tr A0A7N2KME6 A0A7N2KME6_QUELO	-----	-----	VMRNLKLVVRKEFAPEAQ	FDPQPCASFILPNVI	SYGNDCRD	2096
tr A0A4W5MAK2 A0A4W5MAK2_9TELE	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2166
tr A0A8C7Q9V4 A0A8C7Q9V4_ONCMY	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2134
tr A0A6P7J2Q5 A0A6P7J2Q5_9TELE	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2171
tr A0A6P8SZE0 A0A6P8SZE0_GYMCA	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2171
tr A0A8J0QX44 A0A8J0QX44_XENTR	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2168
tr A0A4X2K1K8 A0A4X2K1K8_VOMUR	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2149
tr A0A5F4D2S5 A0A5F4D2S5_CANLF	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2154
tr A0A7J7RQ84 A0A7J7RQ84_RHIFE	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2137
tr A0A6P6D0R3 A0A6P6D0R3_PTEVA	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2164
tr A0A2K6C1S8 A0A2K6C1S8_MACNE	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2145
tr F6QAQ1 F6QAQ1_MACMU	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2170
tr G3RQP2 G3RQP2_GORGO	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2147
sp Q07864 DPOE1_HUMAN	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2168
tr A0A2I3S482 A0A2I3S482_PANTR	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2168
tr F6Z911 F6Z911_HORSE	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2168
tr A0A5G2RB90 A0A5G2RB90_PIG	-----	-----	KLKRDLLRLVDVGEFSEEAQ	FRDPCRSYILPEVI	HSNFCRD	2139
tr A0A420PL83 A0A420PL83_FUSOX	-----	-----	LLRKEALLLFEVREFSKDGT	FTNPSLRLPQISDSTMMR	DL	2065
tr A0A1V6PGE7 A0A1V6PGE7_PENDC	-----	-----	LLRKEALLLFEVREFSKDGT	FTNPSLRLPQISDSTMMR	DL	2112
tr A0A0G4NU82 A0A0G4NU82_PENCA	-----	-----	LLRKEALLLFEVREFSKDGT	FTNPSLRLPQISDSTMMR	DL	2110
tr A0A1V6TET5 A0A1V6TET5_9EURO	-----	-----	LLRKEALLLFEVREFSKDGT	FTNPSLRLPQISDSTMMR	DL	2110
tr A0A167WJ50 A0A167WJ50_PENCH	-----	-----	LLRKEALLLFEVREFSKDGT	FTNPSLRLPQISDSTMMR	DL	2110
tr A0A3A2Z9P9 A0A3A2Z9P9_9EURO	-----	-----	LLRKEALLLFEVREFSKDGT	FTNPSLRLPQISDSTMMR	DL	2111
tr A0A401L0U3 A0A401L0U3_ASPAW	-----	-----	LLRKEALLLFEVREFSKDGT	FTNPSLRLPQISDSTMMR	DL	2114
tr A0A317VH96 A0A317VH96_ASPEC	-----	-----	LLRKEALLLFEVREFSKDGT	FTNPSLRLPQISDSTMMR	DL	2110
tr A0A117E1M7 A0A117E1M7_ASPNG	-----	-----	LLRKEALLLFEVREFSKDGT	FTNPSLRLPQISDSTMMR	DL	2114
tr A0A1D8PTD0 A0A1D8PTD0_CANAL	-----	-----	ILKKEALLLFDVDRD	SKDPTFRDPCRSYILPEVI	HSNFCRD	2108
tr C5M3R9 C5M3R9_CANTT	-----	-----	ILKKEALLLFDVDRD	SKDPTFRDPCRSYILPEVI	HSNFCRD	2104
sp Q6FNY7 DPOE_CANGA	-----	-----	ILKKEALLLFDVDRD	SKDPTFRDPCRSYILPEVI	HSNFCRD	2114
sp P21951 DPOE_YEAST	-----	-----	ILKKEALLLFDVDRD	SKDPTFRDPCRSYILPEVI	HSNFCRD	2058
tr A0A7H9HLU1 A0A7H9HLU1_9SACH	-----	-----	ILKKEALLLFDVDRD	SKDPTFRDPCRSYILPEVI	HSNFCRD	2108
sp Q6CUS7 DPOE_KLULA	-----	-----	ILKKEALLLFDVDRD	SKDPTFRDPCRSYILPEVI	HSNFCRD	2022
sp Q752B8 DPOE_ASHGO	-----	-----	ILKKEALLLFDVDRD	SKDPTFRDPCRSYILPEVI	HSNFCRD	2017

Accession	Gene	Protein	Sequence	Position
tr A0A3P5YCF9 A0A3P5YCF9	BRACM	I GRDPALLT-----	←EKEWQADISCGSKIYDREQMENSLLQMVRRQERMYHMDDLV	2132
sp F4HW04 DPOE1	ARATH	I CRDPALLT-----	EKEWQADISCGSKIYDREQMESSLLEVMRQERMYHMDDV	2098
tr D7KI06 D7KI06	ARALL	I CRDPALLT-----	EKEWQADISCGSKIYDREQMESSLLEVMRQERMYHMDDLV	2178
tr A0A8I6WFC8 A0A8I6WFC8	HORVV	I CRDSTLQ-----	GHEWRRQAVPCCGQPYHREEMENALLQIVRQERLYHLQDVL	2159
tr A0A452YAR6 A0A452YAR6	ABGTS	I LCRDSTLQ-----	GHEWRRQAVPCCGQPYHREEMENALLQIVRQERLYHLQDVL	2099
tr A0A3B5XXC3 A0A3B5XXC3	WHEAT	I LCRDSTLQ-----	GHEWRRQAVPCCGQPYHREEMENALLQIVRQERLYHLQDVL	2159
tr A0A1D6H8Z0 A0A1D6H8Z0	MAIZE	I LCRDSTLQ-----	GHEWRRQAVPCCGQPYHREEMENALLQIVRQERLYHLQDVL	2162
tr A0A835B357 A0A835B357	9POAL	I LCRDSTLQ-----	GHEWRRQAVPCCGQPYHREEMENALLQIVRQERLYHLQDVL	2144
tr A0A2S3GPC0 A0A2S3GPC0	9POAL	I LCRDSTLQ-----	GHEWRRQAVPCCGQPYHREEMENALLQIVRQERLYHLQDVL	2149
tr A0A368PL62 A0A368PL62	SETIT	I LCRDSTLQ-----	GHEWRRQAVPCCGQPYHREEMENALLQIVRQERLYHLQDVL	2153
tr A0A7I8KHB8 A0A7I8KHB8	SPIIN	I LSRDSALL-----	EQEWRRAVPPCCGQPYDRGQMESALLQIVRQERLYHLQDVL	2154
tr A0A6I9QIG1 A0A6I9QIG1	ELAGV	I LCRDSALS-----	DNEWRRQAVPCCGQSYNREQMENSLLQIVRQERLYHLQDVL	2148
tr A0A8B8JBC2 A0A8B8JBC2	PHODC	I LCRDSALS-----	DSWRRQAVPCCGQSYNREQMENSLLQIVRQERLYHLQDVL	2151
tr A0A9Q0FIP5 A0A9Q0FIP5	9ROSI	I LCRDSTALL-----	SQWRRQAVPCCGQPYDREVMENALLQIVRQERLYHLQDVL	2196
tr A0A2C9VYJ6 A0A2C9VYJ6	MANES	I LCRDSTALL-----	AQWRRQAVPCCGQPYDREVMENALLQIVRQERLYHLQDVL	2162
tr A0A7J7C034 A0A7J7C034	TRIFW	I LCRDSALL-----	AHEWRRQAVPCCGQPYDREVMENALLQIVRQERLYHLQDVL	2142
tr A0A2N9F976 A0A2N9F976	FAGSY	I LCRDSALL-----	AQWRRQAVPCCGQPYDREVMENALLQIVRQERLYHLQDVL	2105
tr A0A7N2KME6 A0A7N2KME6	QUELO	I LCRDSTALL-----	AQWRRQAVPCCGQPYDREVMENALLQIVRQERLYHLQDVL	2145
tr A0A4W5MAK2 A0A4W5MAK2	9TELE	I LCKDPSVAQDG-----	SVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2218
tr A0A8C7Q9V4 A0A8C7Q9V4	ONCMY	I LCKDPSVAQDG-----	SVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2186
tr A0A6P7J2Q5 A0A6P7J2Q5	9TELE	I LCKDPSVAQDG-----	SVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2223
tr A0A6P8SZE0 A0A6P8SZE0	GYMAC	I LCKDPSVAQDG-----	SVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2223
tr A0A8J0XQ44 A0A8J0XQ44	XENTR	I LCKDPAINQDG-----	SVLPQWFL--TNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2220
tr A0A4X2K1K8 A0A4X2K1K8	VOMUR	I LCKDPAINQDG-----	SILPQWFL--TNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2201
tr A0A5F4D2S5 A0A5F4D2S5	CANLF	I LCKEFAFSQDG-----	AVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2206
tr A0A7J7RQ84 A0A7J7RQ84	RHIFE	I LCRDPSVQDG-----	AVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2189
tr A0A6P6D0R3 A0A6P6D0R3	PTEVA	I LCRDPSVQDG-----	AVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2216
tr A0A2K6C158 A0A2K6C158	MACNE	I LCKDSSFSQDG-----	AVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2197
tr F6QAQ1 F6QAQ1	MACMU	I LCKDSSFSQDG-----	AVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2222
tr G3RQP2 G3RQP2	GORGO	I LCKDSSFSQDG-----	AVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2199
sp Q07864 DPOE1	HUMAN	I LCKDSSFSQDG-----	AVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2220
tr A0A2I3S482 A0A2I3S482	PANTR	I LCKDSSFSQDG-----	AVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2220
tr F6Z911 F6Z911	HORSE	I LCKDPSFSQDG-----	AVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2220
tr A0A5G2RB90 A0A5G2RB90	PIG	I LCKEFSFSQDG-----	AVLPQWFL--SNQIAYDSSVIEEMALVEALQKLLMAFTLQDVL	2191
tr A0A420PL83 A0A420PL83	FUSOX	I LCRDEDLDFGE-----	GAWRRQAVPCCGQTEYDRLAQEEILLIGQIQGYIVGWQTDLK	2114
tr A0A1V6PGE7 A0A1V6PGE7	PENDC	I LCRDEDVLPDPG-DTSK-TPKFWR	PECHAEYDRLAQEEILLIGQIQGYIVGWQTDLK	2168
tr A0A0G4NU82 A0A0G4NU82	PENCA	I LCRDEDVLPDASAEASK-STQFWR	PECHAEYDRLAQEEILLIGQIQGYIVGWQTDLK	2167
tr A0A1V6TET5 A0A1V6TET5	9EURO	I LCRDEDVLPDASAEASK-STQFWR	PECHAEYDRLAQEEILLIGQIQGYIVGWQTDLK	2167
tr A0A167WJ50 A0A167WJ50	PENCH	I LCRDEDVLPDASAEASK-STQFWR	PECHAEYDRLAQEEILLIGQIQGYIVGWQTDLK	2167
tr A0A3A2Z9P9 A0A3A2Z9P9	9EURO	I LCRDEDVLPDPSGSDVT-TTKFWL	PECHAEYDRLAQEEILLIGQIQGYIVGWQTDLK	2168
tr A0A401L0U3 A0A401L0U3	ASPAW	I LCRDEDVLPDPSGSDVT-TTKFWL	PECHAEYDRLAQEEILLIGQIQGYIVGWQTDLK	2172
tr A0A317VH96 A0A317VH96	ASFEC	I LCRDEDVLPDPSGSDVT-TTKFWL	PECHAEYDRLAQEEILLIGQIQGYIVGWQTDLK	2168
tr A0A117E1M7 A0A117E1M7	ASPNG	I LCRDEDVLPDPSGSDVT-TTKFWL	PECHAEYDRLAQEEILLIGQIQGYIVGWQTDLK	2172
tr A0A1D8PTD0 A0A1D8PTD0	CANAL	I LCREE-----	INWNR--LNRKRAYNKIALEEEIINQFNKLFVKFYQDVK	2153
tr C5M3R9 C5M3R9	CANTT	I FCCQNE-----	ESVWNR--SNCHKPYDKSAIEEGIISQLNKLKFKVYQDVK	2149
sp Q6FNY7 DPOE	CANGA	I LCRDGL-----	DGKFC--PDKSINDSLLEQHEMIQNLAETQYITQDRL	2159
sp P21951 DPOE	YEAST	I FCKAAP-----	ESIFSC--VRCRKAFAFQVLLQEHLLQKLRSDIESYLLQDLK	2103
tr A0A7H9HLU1 A0A7H9HLU1	9SACH	I FCRDNF-----	STIFCC--SNCHKELNKRGLLQERLIHNIYVEIESYLLQDVK	2153
sp Q6CUS7 DPOE	KLULA	I ICRESM-----	ERVFTC--QSNRSLNKNLIEEHVIERLQAVQVATYITQDVK	2067
sp Q752B8 DPOE	ASHGO	I ICMSDL-----	RSMFKC--SKCYRTLKRPFIENLIQKLRQTLQATYITQDRL	2062

Accession	Gene	Protein	Sequence	Position
tr A0A3P5YCF9 A0A3P5YCF9	BRACM	C FCRNQVKAHHLTEQ	CGSFRCKESGS-----	2161
sp F4HW04 DPOE1	ARATH	C FCRNQVKAHHLTEQ	CGSFRCKESGS-----	2127
tr D7KI06 D7KI06	ARALL	C FCRNQVKAHHLTEQ	CGSFRCKESGS-----	2207
tr A0A8I6WFC8 A0A8I6WFC8	HORVV	C VCRQVKAHHLVSEQ	CGSFRCKEEAP-----	2188
tr A0A452YAR6 A0A452YAR6	ABGTS	C VCRQVKAHHLVSEQ	CGSFRCKEEAP-----	2128
tr A0A3B5XXC3 A0A3B5XXC3	WHEAT	C VCRQVKAHHLVSEQ	CGSFRCKEEAP-----	2183
tr A0A1D6H8Z0 A0A1D6H8Z0	MAIZE	C VCRQVKAHHLVSEQ	CGSFRCKEEAP-----	2191
tr A0A835B357 A0A835B357	9POAL	C LCRQVKAHHLSEQ	CGSFRCKEES-----	2173
tr A0A2S3GPC0 A0A2S3GPC0	9POAL	C LCRQVKAHHLSEQ	CGSFRCKEES-----	2178
tr A0A368PL62 A0A368PL62	SETIT	C LCRQVKAHHLSEQ	CGSFRCKEES-----	2182
tr A0A7I8KHB8 A0A7I8KHB8	SPIIN	C KCRGVKADHLAEQ	CGSFGCKEESSA-----	2183
tr A0A6I9QIG1 A0A6I9QIG1	ELAGV	C LCRQVKAHHLAEQ	CGSFRCKEDSF-----	2177
tr A0A8B8JBC2 A0A8B8JBC2	PHODC	C LCRQVKAHHLAEQ	CGSFRCKEDSF-----	2180
tr A0A9Q0FIP5 A0A9Q0FIP5	9ROSI	C LCRQVKAHHLAEQ	CGSFRCKEDSF-----	2225
tr A0A2C9VYJ6 A0A2C9VYJ6	MANES	C LCRQVKAHHLAEQ	CGSFRCKEDSF-----	2191
tr A0A7J7C034 A0A7J7C034	TRIFW	C LCRQVKAHHLTEQ	AGSFRCKEDVS-----	2171
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tr A0A6P6D0R3 A0A6P6D0R3	PTEVA	C LKCRGVKETHMSVYC	CAGDFALTIHTK-----	2245
tr A0A2K6C158 A0A2K6C158	MACNE	C LKCRGVKETSMLVYC	CAGDFALTIHTQ-----	2226
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tr A0A5G2RB90 A0A5G2RB90	PIG	C VCRQVKAHHLVSEQ	CAGDFALTIHTK-----	2220
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tr A0A167WJ50 A0A167WJ50	PENCH	C SFCKSGLKVSDFMEHC	CGAWTATVDRK-----	2196
tr A0A3A2Z9P9 A0A3A2Z9P9	9EURO	C SFCKGNLQVSEFMEHC	CGAWVETIDRA-----	2197
tr A0A401L0U3 A0A401L0U3	ASPAW	C SFCKGTLKVSDFMEHC	CGVWVETMDRK-----	2197
tr A0A317VH96 A0A317VH96	ASFEC	C SFCKGTLKVSDFMEHC	CGVWVETMDRK-----	2201
tr A0A117E1M7 A0A117E1M7	ASPNG	C SKCKGTLKVSDFMEHC	CGVWVETMDRK-----	2201
tr A0A1D8PTD0 A0A1D8PTD0	CANAL	C NKCKNQIRQNNMDLHC	CGNWIETVDYH-----	2182
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sp Q6FNY7 DPOE	CANGA	C CKCKHTVKRDLDMSTNC	CGNWCCTTKPE-----	2188
sp P21951 DPOE	YEAST	C SRCKHKVRRDYSACPC	CAGAEGLFLPRE-----	2132
tr A0A7H9HLU1 A0A7H9HLU1	9SACH	C FCKCNKVKQDNMSDYC	CGSNVGLISKH-----	2182
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sp Q752B8 DPOE	ASHGO	C AKCKRKIKSDTMSAYC	CGKVVQITISKD-----	2091

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tr|A0A8I6WFC8|A0A8I6WFC8_HORVV    -- 2224
tr|A0A452YAR6|A0A452YAR6_AEGTS    -- 2160
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tr|A0A2C9VYJ6|A0A2C9VYJ6_MANES    -- 2223
tr|A0A7J7C034|A0A7J7C034_TRIWF    -- 2203
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tr|A0A4X2K1K8|A0A4X2K1K8_VOMUR    -- 2267
tr|A0A5F4D2S5|A0A5F4D2S5_CANLF    -- 2319
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tr|A0A2K6CI58|A0A2K6CI58_MACNE    -- 2263
tr|F6QAQ1|F6QAQ1_MACMU             -- 2288
tr|G3RQP2|G3RQP2_GORGO             -- 2265
sp|Q07864|DPOE1_HUMAN              -- 2286
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tr|F6Z911|F6Z911_HORSE             -- 2286
tr|A0A5G2RB90|A0A5G2RB90_PIG      -- 2257
tr|A0A420PL83|A0A420PL83_FUSOX    -- 2175
tr|A0A1V6PGE7|A0A1V6PGE7_PENDC    -- 2229
tr|A0A0G4NU82|A0A0G4NU82_PENCA    -- 2228
tr|A0A1V6TET5|A0A1V6TET5_9EURO    -- 2228
tr|A0A167WJ50|A0A167WJ50_PENCH    -- 2228
tr|A0A3A2Z9P9|A0A3A2Z9P9_9EURO    -- 2229
tr|A0A401L0U3|A0A401L0U3_ASPAW    -- 2233
tr|A0A317VH96|A0A317VH96_ASPEC    -- 2229
tr|A0A117E1M7|A0A117E1M7_ASPNG    -- 2233
tr|A0A1D8PTD0|A0A1D8PTD0_CANAL    -- 2211
tr|C5M3R9|C5M3R9_CANTT             -- 2207
sp|Q6FNY7|DPOE_CANGA               -- 2217
sp|P21951|DPOE_YEAST               -- 2162
tr|A0A7H9HLU1|A0A7H9HLU1_9SACH    -- 2212
sp|Q6CUS7|DPOE_KLULA               -- 2125
sp|Q752B8|DPOE_ASHGO               -- 2120
    
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From PLANTS

A0A3P5YCF9_BRACM, *Brassica campestris*
 D7KI06_ARALL, *Arabidopsis lyrata*
 A0A452YAR6_AEGTS, *Aegilops tauschii*
 A0A1D6H8Z0_MAIZE, *Zea mays*
 A0A2S3GPC0_9POAL, *Panicum hallii*
 A0A7I8KHB8_SPIIN, *Spirodela intermedia*
 A0A8B8JBU2_PHODC, *Phoenix dactylifera*
 A0A2C9VYJ6_MANES, *Manihot esculenta*
 A0A2N9F976_FAGSY, *Fagus sylvatica*

From ANIMALS

A0A6P7J2Q5_9TELE, *Parambassis ranga*
 A0A6P7J2Q5_9TELE, *Hucho hucho*
 A0A8J0QX44_XENTR, *Xenopus tropicalis*
 A0A5F4D2S5_CANLF, *Canis lupus familiaris*
 A0A6P6D0R3_PTEVA, *Pteropus vampyrus*
 F6QAQ1_MACMU, *Macaca mulatta*
 Q07864|DPOE1_HUMAN, *Homo sapiens*
 F6Z911_HORSE, *Equus caballus*

From YEASTS and HIGHER FUNGI

A0A420PL83_FUSOX, *Fusarium oxysporum*
 A0A0G4NU82_PENCA, *Penicillium camemberti*
 A0A167WJ50_PENCH, *Penicillium chrysogenum*
 A0A401L0U3_ASPAW, *Aspergillus awamori*
 A0A117E1M7_ASPNG, *Aspergillus niger*
 C5M3R9_CANTT, *Candida tropicalis*
 P21951|DPOE_YEAST, *Saccharomyces cerevisiae*
 Q6CUS7|DPOE_KLULA, *Kluyveromyces lactis*

F4HW04|DPOE1_ARATH, *Arabidopsis thaliana*
 A0A8I6WFC8_HORVV, *Hordeum vulgare* subsp. *Vulgare*
 A0A3B5XXC3_WHEAT, *Triticum aestivum*
 A0A835B357_9POAL, *Digitaria exilis*
 A0A368PL62_SETIT, *Setaria italic*
 A0A6I9QIG1_ELAGV, *Elaeis guineensis* var. *tenera*
 A0A9Q0FIP5_9ROSI, *Turnera subulata*
 A0A7J7C034_TRIWF, *Tripterygium wilfordii*
 A0A7N2KME6_QUELO, *Quercus lobata*

A0A8C7Q9V4_ONCMY, *Oncorhynchus mykiss*
 A0A6P8SZE0_GYMAC, *Gymnodraco acuticeps*
 A0A4X2K1K8_VOMUR, *Vombatus ursinus*
 A0A7J7RQ84_RHIFE, *Rhinolophus ferrumequinum*
 A0A2K6CI58_MACNE, *Macaca nemestrina*
 G3RQP2_GORGO, *Gorilla gorilla*
 A0A2I3S482_PANTR, *Pan troglodytes*
 A0A5G2RB90_PIG, *Sus scrofa*

A0A1V6PGE7_PENDC, *Penicillium decumbens*
 A0A1V6TET5_9EURO, *Penicillium flavigenum*
 0A3A2Z9P9_9EURO, *Aspergillus sclerotialis*
 A0A317VH96_ASPEC, *Aspergillus eucalypticola*
 A0A1D8PTD0_CANAL, *Candida albicans*
 Q6FNY7|DPOE_CANGA, *Candida glabrata*
 A0A7H9HLU1_9SACH, *Torulaspora* sp.
 Q752B8|DPOE_ASHGO, *Ashbya gossypii*

Figure 5 Mix and Match MSA of all the four eukaryotic ε DNA polymerase catalytic subunits

3.3. ZBM's and their role(s) in eukaryotic replicative polymerases

All the three eukaryotic replicative DNA pols (α, ε and δ) invariably possess the two completely conserved ZBM's at the CTDs of their catalytic subunits, and are known as CysA and CysB, suggesting an important role(s) in eukaryotic genome replication and regulation. In pol ε, the CysA (-Cx₂Cx_nCx_{2/4}C-) site is the regular ZBM, where a Zn²⁺ binds, but a [4Fe-

4S]²⁺ binds to the CysB (-Cx₂Cx₁₁CxC-) site. The [4Fe-4S]²⁺ cluster is implicated in the redox signaling and regulation of the replication process in eukaryotes. In fact, the CysB motif is present in all the four yeast's B-family DNA pols which include the DNA mutagenesis enzyme pol ζ [22]. Interestingly, the ε pols contain an additional ZBM within the pol domain which is also shown to bind an [4Fe-4S]²⁺ cluster. Based on spectroscopic and other data, Jain *et al.* [23] suggested that the three highly conserved C residues (C⁶⁶⁵, C⁶⁶⁸, C⁶⁷⁷ and C⁷⁶³) in yeast ε pol's pol domain are involved in binding to [4Fe-4S] cluster (Fig. 3). This was based on their observation that the wild-type yeast pol ε's catalytic core was yellowish-brown, but a mutant in which all the three residues (C⁶⁶⁵, C⁶⁷⁷ and C⁷⁶³) were mutated, the mutant enzyme was colourless and its UV-Vis spectrum lacked the broad peak centered at 400 nm. Besides, they also found that this triple mutant was deficient only in the DNA pol activity, but not in the PR exonuclease activity, suggesting a link between the pol activity and the [4Fe-4S] cluster suggesting its possible involvement in the eukaryotic genome replication and regulation. Thus, the additional ZBM found exclusively in the ε pols suggests that ε pols are more sensitive to oxidative stress than the other two replicative pols [23]. Furthermore, Pinto *et al.* [24] have shown that the [4Fe-4S]²⁺ cluster of yeast DNA polymerase ε is redox active and can undergo DNA-mediated signaling. A double cysteine-to-serine mutant (C⁶⁶⁵→S and C⁶⁶⁸→S) of Pol2_{COREEXO}, which lacked the [4Fe-4S] cluster, showed no redox signal upon oxidation as the wildtype enzyme. Significantly, protein oxidation yielded a sharp decrease in polymerization, while rereduction restored the activity almost to the level of the untreated enzyme.

It is interesting to note that pol δ also possesses two ZBMs at its CTD, viz. CysA (-Cx₂CnCx₂C-) and CysB (-Cx₂Cx₉Cx₄C-) [2]. Similar SDM experiments on pol δ by Netz *et al.* [22] have shown that the CysB motif was bound to [4Fe-4S] cluster and involved in the formation of the pol active complexes. For example, the loss of [4Fe-4S] cluster binding by Cys-ligand mutagenesis of pol δ, destabilized the CTD and abolished interactions between the polD1 and polD2 subunits. They found that the conversion of the C residues in the CysB site, viz. C¹⁰⁵⁶, C¹⁰⁵⁹, C¹⁰⁶⁹, C¹⁰⁷⁴ to A residues abolished the [4Fe-4S] binding [22]. Furthermore, a lethal double mutation C¹⁰⁵⁹→S/C¹⁰⁷⁴→S in CysB site of pol δ disrupted its binding to both polD1 and polD2. However, in marked contrast, a lethal double mutation in CysA site (C¹⁰¹²→S/C¹⁰²⁷→S) did not alter the subunit composition of the purified pol δ complex, and also did not affect the pol δ interactions with the subunits as evidenced from a yeast two hybrid analysis. However, the double mutation severely decreased PCNA-dependent replication processivity, suggesting the utmost importance of this metal centre for polymerase function. Thus, the CysA (PCNA-binding) and CysB (subunits interactions) motifs play distinct roles in the eukaryotic replicative pols.

4. Active site analyses of the DNA polymerase ε

The pol domain's active site amino acids of the pol ε from plant and animal sources is mostly arrived at from the data available on the yeast enzyme. The active sites of the yeast enzyme were analyzed by SDM, deletion mutagenesis and crystallographic studies [16, 19, 25, 26]. Pavlov *et al.* [16] found that in the yeast enzyme, the Y⁸³¹→A replacement by SDM reduces replication fidelity and its participation in chromosomal replication suggesting its involvement in the pol active site. Interestingly, the present study shows that the Y⁸³¹ (highlighted in dark blue in Table 1) is in the proposed and highly conserved template-binding -Y⁸³¹G- pair of the yeast pol ε.

Kesti *et al.* [20] found that a yeast strain with an N-terminal deletion, which deletes the pol domain of the pol ε (*pol2*) gene, but retaining the C-terminal region intact, grew slowly and was viable. Their in-frame deletion experiment lacked the sequence, encoding amino acids 176–1134 of the 2222-amino-acid pol ε protein containing all of the conserved motifs associated with the DNA pol and PR exonuclease functions. They found that such a large N-terminal deletion of the yeast enzyme consisting of all the known pol and PR exonuclease domains was dispensable for DNA replication, repair, and cell viability. Furthermore, such deletion of the PR and pol catalytic domains of pol ε from the NTD was not lethal and did not block chromosomal DNA replication [20]. Besides, they found that the C-terminal portion of the enzyme was both necessary and sufficient for viability and hence, suggested that another polymerase could possibly substitute for the polymerization function of pol ε in their N-terminal deletion mutant. Interestingly, the present study has shown that the presence of one more putative pol active site in the CTD (highlighted in yellow) could have possibly compensated for the pol function in their N-terminal deletion mutants. In another deletion analysis, Ohya *et al.* [27] found a pol ε deletion mutant of yeast was temperature-sensitive, exhibited severe defects in chromosomal DNA replication at the permissive temperature, and underwent premature senescence, suggesting the role of PR function in such deletion mutants as the CTD does not possess a functional PR active site in the yeast pol ε (Table 1).

The crystal structure of yeast DNA pol ε catalytic subunit has been solved by Jain *et al.* [25]. The yeast enzyme adopts the universal 'right-hand' DNA pol fold with an active site formed by a 'palm' (holding the catalytic residues for dNTP addition), a 'thumb' (that binds the template-primer duplex) and 'fingers' (interacting with incoming nucleotides) and an exonuclease domain. The enzyme's palm subdomain was found to be larger and more elaborate than that is found in pols α and δ. In the pol ε, the pol and exo active sites are separated by ~41 Å in a direction roughly perpendicular to the

DNA axis. Pol ϵ 's fidelity to a nascent Watson-Crick base-pairing was determined primarily by residues V⁸²⁵, N⁸²⁸, S⁸²⁹, Y⁸³¹ and G⁸³² from the fingers' domain (all the five amino acids are in the proposed catalytic core of the enzyme) and by Y⁶⁴⁵ from the palm domain. As discussed elsewhere, the Y⁸³¹→A replacement in pol ϵ reduced replication fidelity and its participation in chromosomal replication, but without eliminating an additional function that is essential for viability [25]. It is interesting to note that the same invariant Y⁸³¹G⁸³² pair is proposed here as the template-binding pair by sequence similarity and is in close agreement with other DdDps and DdRps. The pol active site is characterized by the catalytic metal-binding residues, D⁶⁴⁰ and D⁸⁷⁷. Both (-HVD⁶⁴⁰- and -DTD⁸⁷⁷-) are found to be completely conserved in the eukaryotic ϵ pols. The PR exonucleases active site amino acids are further confirmed by SDM and X-ray crystallographic data. When the D²⁹⁰ and E²⁹² of the first triad in the PR exonuclease were mutated to A (highlighted in dark blue in Table 1), the exonuclease activity was abolished, confirming their direct involvement in PR function [15]. The x-ray crystallographic data further confirmed that the PR exo domain was located on the opposite side of the DNA of the thumb domain and contained the catalytic residues (D²⁹⁰, E²⁹² and D⁴⁷⁷ and D²⁷⁵, E²⁷⁷ (numberings are based on the yeast and human enzymes, respectively) for PR activity [25]. A catalytic metal ion was found to be coordinated by D²⁹⁰ (D²⁷⁵ in human enzyme) (Fig. 5A). These active site amino acids are in complete agreement with the present MSA analysis (highlighted in light blue).

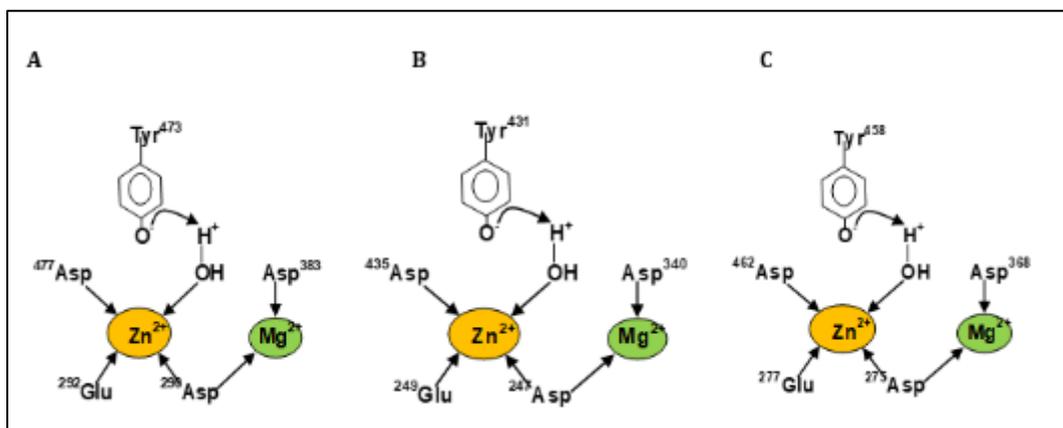
Table 1 shows a comparative account of the active site amino acids in the PR exonuclease and pol domains of the eukaryotic DNA pol ϵ from different sources from yeasts to humans. The PR exonuclease and pol active sites are almost identical in all eukaryotes from lower (yeasts and higher fungi) to higher (plants and animals) except for a small difference where the plant and animal enzymes use a -KC- pair at the proton abstraction site and the yeast and higher fungal enzymes use a -KV- pair without altering the invariant K in all. The putative second pol active site amino acids are also identified in the CTD. However, the second PR exonuclease active site in the CTD is not complete in all ϵ pols (Table 1).

Table 1 Proposed active site amino acids of PR exonuclease and pol domains of eukaryotic ϵ pols

	<i>S. cerevisiae</i>	<i>A. thaliana</i>	<i>Homo sapiens</i>
PR Exo-1 (NTD)	-D ²⁹² -FD ³⁸³ -Y ⁴⁷³ -D ⁴⁷⁷ -	-DIE ²⁴⁹ -FD ³⁴⁰ -Y ⁴³¹ -D ⁴³⁵ -	-D ²⁷⁵ -E ²⁷⁷ -F ³⁶⁷ -D ³⁶⁸ -Y ⁴⁵⁸ -D ⁴⁵⁹ -D ⁴⁶² -
Pol-1(NTD)	- ⁸¹⁶ YDSLQ ¹ LAHK ¹ VILNSFY ⁸ YV ⁸³⁴ -	- ⁷⁷⁴ YDSLQ ¹ LAHK ¹ CILNSFY ⁸ YV ⁷⁹² -	- ⁸⁰¹ YDSLQ ¹ LAHK ¹ CILNSFY ⁸ YV ⁸¹⁹ -
PR Exo-2 (CTD)	-DIE ¹²¹⁶ -?-?-?	-DIE ¹¹⁸⁰ -?-?-?	-DIE ¹⁴²⁴ -LD ¹⁵¹⁶ -Y ¹⁶³⁶ -D ¹⁶⁴⁰
Pol-2 (CTD)	- ¹⁸³⁷ HNLT ¹ KK ¹ ALLQLVNEFSAL ¹³ GS-	- ¹⁷⁸⁹ HKVMQ ¹ K ¹ VFALLTLDRRL ¹³ GA-	- ¹⁸⁴² HNNM ¹ KK ¹ LFLQLIAEFKRL ¹³ GS-

Adapted from Palanivelu [8]; Active site amino acids in dark blue are confirmed by SDM analysis; Mutations in pol ϵ PR exo active site region (highlighted in dark blue) lead to several types of cancers, e.g., D²⁷⁵ leads to endometrial, breast, glioblastoma, colorectal, lung cancers; F³⁶⁷ leads to endometrial, colon cancers; S⁴⁵⁹ leads to colon, endometrial, glioblastoma, duodenal cancers.

The 3'→5' PR exonucleolytic activity is intrinsic to the replicative DNA pols ϵ and δ and is essential for the faithful replication of the genomic DNA. Figs. 6A, B and C show the proposed active site amino acids at the PR exonuclease active sites of yeast, plant and human ϵ pols, respectively, which is based on the crystallographic, SDM and MSA data.



Figures 6A, B and C. Proposed amino acids at the PR exonuclease active sites of DNA pols ϵ of *S. cerevisiae* (A), *A. thaliana* (B) and humans (C)

The proposed two-metal ion in the active site in the PR exonucleases is based on Beese and Steitz's observation of similar active site structure in the 3'→5' PR exonuclease active site in *E. coli* pol I [28] and is also further confirmed from a large number DdRps [6].

5. Conclusions

Understanding the functions of the replicative pols, viz. α , ϵ and δ , which make the replisome complex, is a prerequisite for understanding the mechanism of genome replication and maintenance of genome integrity in eukaryotes. The present study unravels striking similarities of one of the main replicative pols ϵ from lower to higher eukaryotes at the molecular level. The MSA analysis has shown that the ϵ pols in all eukaryotes contain the same template-binding pairs, catalytic and nucleotide selection amino acids and also the same catalytic metal-binding motifs. Furthermore, the two completely conserved ZBMs in the CTDs of all the three replicative pols suggest their essential roles in genome replication and regulation. A unique [4Fe-4S]²⁺ cluster-binding motif in the ϵ pol domain is implicated in the redox signaling and the regulation of the replication process in eukaryotes as this enzyme links the DNA replication machinery to S-phase checkpoint-control in eukaryotes. Moreover, the PR exonuclease active site amino acids are identical in all eukaryotic enzymes and belong to the DEDD(Y) superfamily of PR exonucleases. These findings establish that the pol, PR exonuclease and CTD domains of the ϵ pols and their roles in genome replication, maintenance of genome integrity and regulation are highly conserved across all eukaryotes, from yeasts to higher animals. The highly conserved pol, PR exonuclease and CTD domains strongly suggest a possible common evolutionary origin of the ϵ pols in eukaryotes.

Compliance with ethical standards

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Disclosure of conflict of interest

The author has declared that no competing interests exist.

References

- [1] Palanivelu P. Analyses of priming reactions and proofreading functions during initiation of replication of prokaryotic and eukaryotic genomes. *Br J Pharm Med Res.* 2022; 7:3790-7828.
- [2] Palanivelu P. Replicative δ polymerases from plants and animals possess very similar polymerase, proofreading and regulatory domains. *World J Adv Res Rev.* 2024, 23:2239–2260.
- [3] Jain R, Aggarwal AK, Rechkoblit O. Eukaryotic DNA polymerases. *Curr Opin Struct Biol.* 2018; 53:77–87.
- [4] Johansson E, Dixon N. Replicative DNA Polymerases. *Cold Spring Harb Perspect Biol.* 2013; 5: a012799, doi: 10.1101/cshperspect. a012799.
- [5] Pavlov YI, Shcherbakova PV, Rogozin IB. Roles of DNA polymerases in replication, repair, and recombination in eukaryotes. *Int Rev Cytol.* 2006; 255:41–132.
- [6] Palanivelu P. DNA polymerases – An insight into their active sites and mechanism of action, In: *Recent Advances in Biological Research*, Vol 1, Chapter 2, pp 1-39, SCIENCEDOMAIN International Book Publishers, UK, ISBN: 9788193422441, DOI: 10.9734/bpi/rabr/v1; (2019).
- [7] DePamphilis ML, Bell SD. *Genome duplication (Concepts, mechanisms, evolution and disease)*. London and New York: Garland Science; 2010.
- [8] Palanivelu P. An Insight into the Mechanism of Genome Duplication in Eukaryotes: Polymerase and Proofreading Functions by Eukaryotic DNA Replicases. *Int J Recent Sci Res.* 2022; 13:2076-2116.
- [9] Burgers PMJ, Kunkel TA. Eukaryotic DNA replication fork. *Annu Rev Biochem.* 2017; 86: 417–438.
- [10] Wintersberger U, Wintersberger E. Studies on deoxyribonucleic acid polymerases from yeast. Partial purification and properties of two DNA polymerases from mitochondria-free cell extracts. *Eur J Biochem.* 1970; 13: 11–19.
- [11] Pospiech H, Syväoja JE. DNA Polymerase epsilon - More Than a Polymerase. *Sci World J.* 2003; 3:87-104.

- [12] Garcia J-A P, De Veylder L, Raynaud C. Plant DNA polymerases. *Int J Mol Sci.* 2019; 20: 4814.
- [13] Ronceret A, Guillemot J, Lincker F, Gadea-Vacas J, Delorme V, Bechtold N, *et al.* Genetic analysis of two *Arabidopsis* DNA polymerase epsilon subunits during early embryogenesis. *Plant J.* 2005; 44:223–236.
- [14] Jenik PD, Jurkuta RE, Barton MK. Interactions between the cell cycle and embryonic patterning in *Arabidopsis* uncovered by a mutation in DNA polymerase epsilon. *Plant Cell.* 2005; 17: 3362–77.
- [15] Pavlov YI, Maki S, Maki H, Kunkel TA. Evidence for interplay among yeast replicative DNA polymerases alpha, delta and epsilon from studies of exonuclease and polymerase active site mutations. *BMC Biol.* 2004; 2:1-13.
- [16] Pavlov YI, Shcherbakova PV, Kunkel TA: *In vivo* consequences of putative active site mutations in yeast DNA polymerases, alpha, epsilon, delta, and zeta. *Genetics.* 2001; 159:47-64.
- [17] Poot RA, Dellaire G, Hulsmann BB, Grimaldi MA, Corona DFV, Becker PB, *et al.* HuCHRAC, a human ISWI chromatin remodelling complex contains hACF1 and two novel histone-fold proteins. *EMBO J.* 2000; 19: 3377–3387.
- [18] Dua R, Levy DL, Campbell JL. Role of the putative zinc finger domain of *Saccharomyces cerevisiae* DNA polymerase ϵ in DNA replication and the S/M checkpoint pathway. *J Biol Chem.* 1998; 273:30046–30055.
- [19] Yuan Z, Georgescu R, Schauer GD, O'Donnell ME, Li H. Structure of the polymerase ϵ holoenzyme and atomic model of the leading strand replisome. *Nat Commun.* 2020; 11:1-10.
- [20] Kesti T, Flick K, Keranen S, Syvaola JE, Wittenberg C: DNA polymerase epsilon catalytic domains are dispensable for DNA replication, DNA repair, and cell viability. *Mol Cell.* 1999; 3:679-685.
- [21] Palanivelu P. Eukaryotic Multi-subunit DNA dependent RNA Polymerases: An Insight into their Active Sites and Catalytic Mechanism. In: *Advances and Trends in Biotechnology and Genetics.*, Vol. 1. pp 1-38, SCIENCEDOMAIN International Book Publishers, UK, Print ISBN: 978-93-89246-59-9, DOI:10.9734/bpi/atbg/v1;2020.
- [22] Netz DJ, Stith CM, Stumpfig M, Kopf G, Vogel D, Genau HM, *et al.* Eukaryotic DNA polymerases require an iron-sulfur cluster for the formation of active complexes. *Nat Chem Biol.* 2012; 8:125–132.
- [23] Jain R, Vanamee ES, Dzikovski BG, Buku A, Johnson RE, *et al.* (2014) An Iron-Sulfur Cluster in the Polymerase Domain of Yeast DNA Polymerase epsilon. *J Mol Biol.* 2014; 426:301–308.
- [24] Pinto MN, Beek JT, Ekanger LA, Johansson E, Barton JK. The [4Fe-4S] Cluster of yeast DNA polymerase ϵ is redox active and can undergo DNA-mediated signaling. *J Am Chem Soc.* 2021: DOI: 10.1021/jacs.1c07150.
- [25] Jain R, Rajashankar KR. Buku A, Johnson RE, Prakash L, Prakash S, *et al.* Crystal structure of yeast DNA polymerase epsilon catalytic domain. *PLoS ONE.* 2014; 9:e94835. doi: 10.1371/journal.pone.0094835.
- [26] Jain R, Rice WJ, Malik R, Johnson RE, Prakash L, Prakash S, *et al.* Cryo-EM structure and dynamics of eukaryotic DNA polymerase δ holoenzyme. *Nat Struct Mol Biol.* 2019; 26:955–962.
- [27] Ohya T, Kawasaki Y, Hiraga S, Kanbara S, Nakajo K, Nakashima N, Suzuki A, Sugino A. The DNA Polymerase Domain of pol ϵ Is Required for Rapid, Efficient, and Highly Accurate Chromosomal DNA Replication, Telomere Length Maintenance, and Normal Cell Senescence in *Saccharomyces cerevisiae*. *J Biol Chem.* 2002; 277:28099–28108
- [28] Beese LS, Steitz TA. Structural basis for the 3'-5' exonuclease activity of *Escherichia coli* DNA polymerase I: a two-metal ion mechanism. *EMBO J.* 1991; 10:25–33.