

Replicative δ Polymerases from Plants and Animals Possess Very Similar Polymerase, Proofreading and Regulatory Domains

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Abstract

In eukaryotes, genome replication starts with the initiation of replication by the primases, followed by the synthesis of the leading- and lagging-strands by two different replicative DNA polymerases (pols), viz. ϵ and δ , respectively. The polymerase and proofreading (PR) active sites of the δ pols are analyzed from various animal and plant sources by multiple sequence alignment (MSA). The animal and plant δ pols are found to possess almost identical polymerase and PR domains. However, the BLASTp analysis has shown only 56.57% identity between the plant (*Arabidopsis thaliana*) and animal (human) δ pols. The template-binding pair (-YG-), the catalytic amino acid (K) and the nucleotide selection amino acid (Q) are found to be the same in both plant and animal δ pols. The δ pols from plant and animal sources contain a typical Mg^{2+} -binding motif, (-YGD₂D-) in the polymerase domain and 2 possible Zn^{2+} -binding motifs (ZBMs) in their carboxy terminal domain (CTD). One of the ZBMs binds to the 4Fe-4S cluster and is suggested to be involved in the regulation of replication. Interestingly, the invariant -SLYPS- and -YGD₂D- motifs which are found in the δ pols are not found in the other replicative pol ϵ . Furthermore, both animal and plant δ pols use the same PR exonuclease active site amino acids, and thus, belong to the DEDD(Y)-superfamily of exonucleases, as found in other DNA pols. Besides, many specialized, conserved sequence motifs are also identified and discussed.

Keywords: Eukaryotic genome replication; DNA polymerases δ ; δ DNA polymerase active site; Proofreading exonucleases; Proofreading exonuclease active sites; *Arabidopsis thaliana*; *Homo sapiens*

1. Introduction

Duplication of genomes is an indispensable activity in the life-cycle of all living organisms to preserve and maintain the blueprint of life in all living cells. Therefore, high-fidelity genome replication is fundamental to all life forms. The genome of each organism encodes several DNA pols which are involved in genome replication as well as repair mechanisms. To date, five different DNA pols have been characterized in *Escherichia coli*, eight in *Saccharomyces cerevisiae*, and as many as 16 in humans [1]. However, only three DNA pols, viz. α , δ and ϵ , also known as replicative polymerases, are involved in the duplication of the nuclear genome in all eukaryotes [2]. Whereas the pol α is involved in the synthesis of the primers to initiate the genome replication process, the other two replicative pols, viz. pol δ and pol ϵ faithfully replicate the whole genome and make an exact copy of the original genome. All three replicative polymerases belong to B-family pols (B pols) which are involved not only in replication but also in repair of any error occurring during the replication process [3]. The B-family DNA pols are reported from both prokaryotes and eukaryotes, e.g., pol II, pol B, pol α , pol ϵ , pol δ , pol ζ . The B-family DNA pols, in addition to polymerization, exhibit 3'→5' PR function [4]. The structural and functional aspects of these pols from animals, yeasts and higher fungi have been extensively analyzed and reported by Palanivelu [5, 6]. Even though more than a dozen different DNA pols are reported from plant cells to perform various replicative and repair functions, detailed properties about them are still very limited. All the replicative pols have an efficient PR function. However, mutations that escape during the replication process, but rarely, generate the most important new genetic variants in animals and plants.

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Though the replication process is highly conserved in all domains of life, it is much more complex in eukaryotes [7]. Genome replication in eukaryotes is incredibly more sophisticated and is performed by a highly coordinated series of molecular events. The replication process, apart from the replicative DNA pols, depends on the participation of many 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, the proper function of all these enzymes is critical to maintaining the genome stability.

Initiation, the very first-step in the replication process in both prokaryotes and eukaryotes, is accomplished by a multi-structural enzyme-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, etc. [5]. After successful priming of replication, the replication process is taken over by the replisomes by the next multi-protein complex. The replisome is mainly composed of two different replicative DNA pols in eukaryotes, viz. pol δ and pol ϵ . In this step, the DNA primers synthesized by DNA pol α (pol1) at the initiation step, are further extended to completion by these replicative pols. In prokaryotes and eukaryotes, the crucial step of the initiation of replication is performed by an RNA primase, but an additional DNA primase is required for eukaryotic replications which is synthesized by the DNA pol α . The leading-strand is synthesized by DNA pol ϵ (pol2), and the lagging-strand is synthesized by DNA pol δ (pol3). In contrast to the continuous leading strand synthesis, the lagging strand is synthesized discontinuously in ~ 200 nucleotides (nt)-long Okazaki fragments, which are then ligated to form the contiguous lagging strand [8].

1.1. Various Activities of the DNA pol δ during Genome Replication

The DNA pol δ is a high-fidelity enzyme, catalyzing the nucleotidyl transfer reaction with an error frequency of 1/22,000 [9]. Replication is initiated by pol α , priming on both strands. On the lagging strand, the priming is repeated at multiple points, whereas only once on the leading strand. During the synthesis of the lagging-strand, pol δ synthesizes a large number of Okazaki fragments (OFs) right up to the 5'-end of a preceding RNA primer, whereupon it is recycled to a new primer terminus, leaving behind a nick or a short gap. Pol δ is also responsible for maturation of the previously synthesized OFs by gradually removing the RNA primers (one at a time from the 5'-end) by a proliferating cell nuclear antigen (PCNA)-bound Flap endonuclease 1 (FEN1) which are gradually filled in the same order with dNTPs to produce ligatable links which are ligated by a ligase to make the continuous lagging strand. In addition to its function in DNA replication, pol δ has been shown to play important roles in DNA mismatch repair and recombination events also [10]. Thus, the multifunctional nature of DNA pol δ appears to be a crucial determinant of the overall fidelity of the DNA replication process in eukaryotes [11]. Even though the DNA pols δ have been extensively studied from yeasts, higher fungal and animal sources, not much information is available from plant sources.

1.2. Subunit Composition and Structural Features of human and plant δ Pols

DNA pol δ (pol3) has been extensively studied from the yeast, *S. cerevisiae*, and humans. In addition to its role in chromosomal DNA replication (as mentioned earlier where it performs the lagging-strand synthesis), it is also involved in DNA repair, DNA/RNA primer removal and recombination functions as mentioned above. Pol δ is a multi-subunit protein complex, composed of a catalytic subunit and 3 accessory subunits. The latter subunits play a critical role in the regulation of pol δ functions. The catalytic subunit of human pol δ (polD1) is one of the most well-studied. It is composed of 1107 amino acid residues and harbours the polymerase and PR exonuclease domains. Both the domains are separated by ~ 45 Å [12]. The human DNA pol δ is a heterotetramer, structurally very similar to the DNA pol ϵ (Fig. 1a). (In the budding yeast *S. cerevisiae*, the enzyme is made up of only three subunits; the p12 kDa subunit was not found [13].

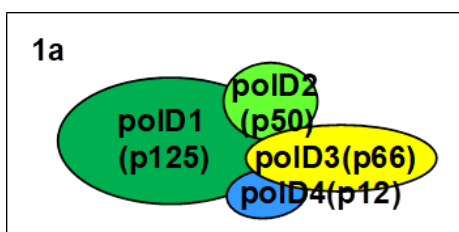


Figure 1a Subunit structure of the DNA pol δ from humans

Adapted from [6, 13].

The numbers in brackets denote the approximate molecular mass of the subunits.

Fig. 1b shows the organization of various domains of the pol δ from humans.

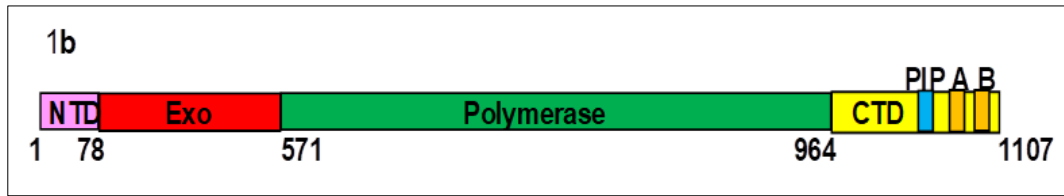


Figure 1b A schematic diagramme showing the domain organization of the DNA pol δ of animals (The numberings are from the human enzyme)

NTD, N-Terminal Domain; Exo, PR Exonuclease domain; PIP, PCNA Interacting Peptide (During elongation, the PCNA (the replication clamp) increases the pol δ catalytic rate by >30-fold. In fact, pol δ shows little activity in the absence of PCNA); A and B are CysA and CysB ZBMs.

Pol δ from *Arabidopsis*, like animals and fission yeast, is composed of four subunits (POLD1–POLD4) [10]. The POLD1 catalytic subunit harbours both the polymerase and PR exonuclease domains and it is highly stimulated by the PCNA. The other subunits in the complex are involved not only in the stabilization of the polymerase complex, but also in its interactions with the PCNA. In *Arabidopsis*, as in other eukaryotes, the deletion of *POLD1* and *POLD2* genes is found to be lethal. The subunit structure of the plant, *A. thaliana*, is shown in Fig. 2a. These data confirm that the subunit composition of the replicative pol δ is highly conserved in plants and is very similar to animal enzymes.

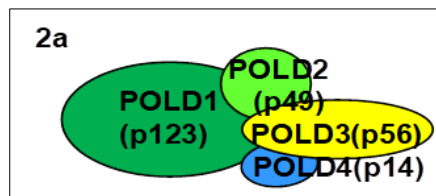


Figure 2a Subunit structure of the DNA pol δ from plants (*A. thaliana*). The numbers in brackets denote the approximate molecular mass of the subunits. NB: Rice has two *POLD4* genes.

Fig. 2b shows a tentative arrangement of various domains on the catalytic subunit, POLD1.

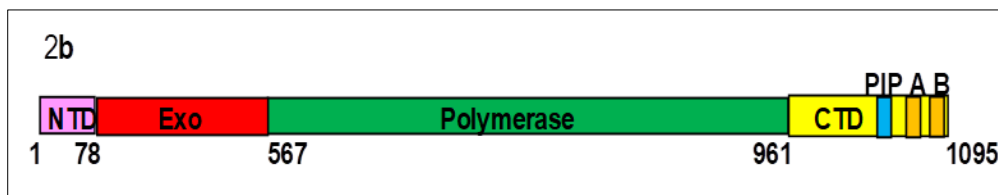


Figure 2b A schematic diagramme showing the domain organization of DNA pol δ from *A. thaliana*

PIP, PCNA Interacting Peptide (During elongation, the PCNA (the replication clamp) increases the pol δ catalytic activity several folds; A and B are CysA and CysB ZBMs.

1.3. Genome Replication in Plant Cells

Replication defects in plants may affect various functions like genome stability, plant growth, flowering, pollination, yield, etc. Our knowledge of DNA replication in plant cells is mostly derived from yeasts and animals. As in animals, the genome replication in plants is accomplished by a large multi-protein complex system known as the replisome. Some of the equivalent replisome proteins and enzymes that have already been characterized from plant sources are the minichromosome maintenance protein complex (MCM), replicative helicase, cell division cycle protein 45 (CDC45), proliferating cell nuclear antigen (PCNA), replication factor C (RFC), replication protein A (RPA), flap endonuclease, ligase, etc. [14]. It is interesting to note that in *Arabidopsis*, the knockout mutants of the main subunits of these two replicative pols (pols ϵ and δ) are found to be lethal.

The primase (DNA pol α) and the other replicative pols ϵ and δ from animal sources have been analyzed and reported by this author [5, 6]. In this communication, the DNA replicative pol δ from plant sources is analyzed and reported.

2. Material and methods

The protein sequence data of animal and plant DNA δ pols 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 from the data already available from biochemical, SDM, cryo-EM and X-ray crystallographic analyses on the replicative polymerase are used to identify the possible amino acids at the active sites of the plant replicative pol δ and their polymerase and PR functions.

3. Results and discussion

3.1. MSA Analysis of DNA Polymerase δ from Plant Sources

Figure 3 shows the MSA of DNA pols δ from various plant sources. (Only the required regions for the discussions are shown). The *A. thaliana* sequence is used as the standard and highlighted. The N-terminal region (~ 300 amino acids) shows small and large gaps in the alignment (data not shown), which is followed by the highly conserved PR exonuclease domain. The PR exonuclease domain contains the typical and completely conserved active site amino acids (highlighted in light blue) as reported in other PR DNA pols. The PR exonuclease domain is followed by the pol domain which is also highly conserved in all. The completely conserved pol active site amino acids are highlighted in yellow. The characteristic -SLYPS- and -YGD TDS- motifs of δ pol are found before and after the proposed pol active site, respectively, and their possible functions are discussed elsewhere. A polybasic, highly conserved, hexapeptide (highlighted in light violet) is found between them. Dx D types of metal-binding motifs are also observed in the PR and polymerase domains. The C-terminal region shows only a few gaps and consists of the three important regulatory motifs, viz. a PCNA interacting peptide (PIP), a ZBM and a Fe-S-ZBM, which are found to be very similar to animal δ pols [6]. Interestingly, all the three eukaryotic replicative DNA pols (pol α , ϵ and δ) contain two such conserved Cys-rich metal-binding motifs in their C-terminal domains of their catalytic subunits and are named CysA and CysB. The CysA is the regular ZBM whereas in the CysB motif, a Zn^{2+} binds to a 4Fe-4S cluster [15]. The PIP is highlighted in light magenta and its role in replication is discussed elsewhere. It is interesting to note that all δ pols invariably end in an aromatic amino acid, F/W/Y (highlighted) as in animal δ pol. The ζ pol, an error-prone polymerase specialized in translesion DNA synthesis, which is also classified under B-family pols, possesses similar catalytic core amino acids (-²⁷¹⁹RQ-⁴LGLK¹LIANVTF⁸GYT-) and the characteristic -²⁶¹⁶SYLPS- and -²⁷⁷⁸YGDTS- motifs suggesting not only that the δ pols could also perform translesion synthesis, but also their common origin of evolution.

CLUSTAL O (1.2.4) MSA of the δ polymerases from various plant sources.

tr U5H8M8 U5H8M8_USTV1	RNDN---DDDKNVNFESILKGLNEEVATDSSDQK	↑ PR Exo →	WNRPALPP--IDPDTDALIFQQIELEE	140
tr C1E609 C1E609_MICCC	HPSDPRI PDGVFPARAPRRSQVNVANDAEREH		WKRKPAPT--LDASKDNLCFQQQLDIDY	135
tr Q33BV0 Q33BV0_AUXPY	-----EVDEGLTGEAGKN		WPRPPPPQ--LNPASTSLVFQQLEVDY	88
sp Q9LVN7 DPOD1_ARATH	-----LIL-----RDIEERE---SRSSA		WARPPLSPAYLS-NSQSIIFQQLEIDS	104
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	-----LIL-----RDMEEREALSARSST		WARPPLSPAYLA-NSQSIIFQQLEIDY	99
tr A0A397Z0B4 A0A397Z0B4_BRACM	-----LIL-----RDMEEREALSARSST		WARPPLSPAYLA-NSQSIIFQQLEIDY	99
tr A0A078I2E2 A0A078I2E2_BRANA	-----LIL-----RDMEEREALSARSST		WARPPLSPAYLA-NSQSIIFQQLEIDY	99
tr A0A287NEC0 A0A287NEC0_HORVV	-----LLL-----DRDEALASRLSR		WKRPALPADLVSGCSRSVAFQQQLDIDY	130
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	-----LLL-----DRDEALASRLSR		WKRPALPADLVSGCSRSVAFQQQLDIDY	110
tr A0A453HJ27 A0A453HJ27_AEGTS	-----LLL-----DRDEALASRLSR		WKRPALPADLVSGCSRSVAFQQQLDIDY	125
tr A0A6G1C319 A0A6G1C319_9ORYZ	-----LLL-----DRDEALASRLSR		WKRPALPADLVSGCSRSVAFQQQLDIDY	114
sp Q9LRE6 DPOD1_ORYSJ	-----LLL-----DRDEALASRLSR		WRRPALPADLVSGCSRSVAFQQLEIDY	112
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	-----LLL-----DRDEALASRLSR		WKRPALPADLVSGCSRSVAFQQLEIDY	114
tr A0A5J9USA3 A0A5J9USA3_9POAL	-----QLL-----QRDEALASRLSR		WKRPPPADLVAGCSRAVAFQQLEIDY	107
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	-----LML-----QRDEALASRLSR		WKRPAIPTDLAAGCSRTVAFQQLEIDY	110
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	-----LML-----QRDEALASRLSR		WKRPALPADLVAGCSRSVAFQQLEIDY	110
tr K3ZGZ6 K3ZGZ6_SETIT	-----LMI-----QRDEALASRLSR		WKRPPPADLVAGCSRTVAFQQLEIDY	112
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	-----VLR-----VRRQVLASRLAK		WRRPPLSGAYLS-QSQSITFQQLEMDY	98
tr A0A0S3RFB6 A0A0S3RFB6_PHAAN	-----ILR-----D-IEQRHALAARLSK		WTRPPLSDDYVA-QSRGVVVFQQLEIDY	93
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	-----ILR-----D-IEEREAIVARLAR		WARPALSDDYLS-QAKNIFLQQLEMDY	94
tr A0A200Q8R4 A0A200Q8R4_9MAGN	-----LIQ-----DEEDRRQLLASRLSK		WKRPTSSPCN-----LITRIDY	60
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	-----ILR-----D-SEGRQSLASRLTR		WARPPLSDAYKS-ASKSILFQQLEIDY	98
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	-----ILR-----D-SEGRQSLASRLSK		WSRPPLSDAYVS-QRSRILFQQLEIDY	94
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	-----ILR-----D-IEERQSLASRLTK		WARPSISHAYSS-ASRSIAFQQLEIDY	94
tr A0A5E4G6B6 A0A5E4G6B6_PRUDU	-----ILR-----D-IEERQSLASRLTK		WARPSISHAYSS-ASRSIAFQQLEIDY	94
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	-----ILR-----D-IEERQSLASRLTK		WARPSISHAYIS-ASRSIAFQQLEIDY	94
			* * * * * :	

tr U5H8M8 U5H8M8_USTV1	LSEKVSNCQLELEIKHDDLLISHAPEGGWSHIAPLRVLSFDIECAGRKGIFPEAEIDFVQ	356
tr C1E609 C1E609_MICCC	S-QKQSMCQYECDFVDFKVVSHPPGQYKSLAPFRILSVDIECAGRKGHFPDADHDFVQ	373
tr Q33BV0 Q33BV0_AUXPY	POSKQTHCQLEAHLHFSKLVSHPAEGEWAKMAPFRILSVDIECQGRKGHFPEDKDFVQ	320
sp Q9LVN7 DP0D1_ARATH	A-RTLSYQCLEFHCLYSDLISHAEEGEYSKMAPFRVLSFDIECAGRKGHFEAKHDFVQ	332
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	A-RTSSYQCLEFHCLYSDLISHAPEGEYSKMAPFRVLSFDIECAGRKGHFEAKHDFVQ	327
tr A0A397Z0B4 A0A397Z0B4_BRACM	A-RTLSYQCLEFHCLYSDLISHAPEGEYSKMAPFRVLSFDIECAGRKGHFEAKHDFVQ	327
tr A0A078I2E2 A0A078I2E2_BRANA	A-RTLSYQCLEFHCLYSDLISHAPEGEYSKMAPFRVLSFDIECAGRKGHFEAKHDFVQ	327
tr A0A287NEC0 A0A287NEC0_HORVV	T-RVMSYQCLELDCLYSDLVSHAPEGEYSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	358
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	T-RVMSYQCLELDCLYSDLVSHAPEGEYSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	338
tr A0A453HJ27 A0A453HJ27_AEGTS	T-RVMSYQCLELDCLYSDLVSHAPEGEYSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	353
tr A0A6G1C319 A0A6G1C319_9ORYZ	-----SDLVSHAAEAGEHSMKAPFRILSVFDIECAGRKGHFEPTHDFVQ	324
sp Q9LRE6 DP0D1_ORYSJ	A-RIMSYQCLELDCLYSDLVSHAAEAGEHSMKAPFRILSVFDIECAGRKGHFEPTHDFVQ	340
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	-----SDLVSHAAEAGEHSMKAPFRILSVFDIECAGRKGHFEPTHDFVQ	324
tr A0A5J9USA3 A0A5J9USA3_9POAL	A-RVMSYQCLELDCLYSDLVSHAAEAGEYSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	335
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	A-CIMSYQCLELDCLYSDLVSHAAEAGEYSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	338
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	A-RVMSYQCLELDCLYSDLVSHAAEAGEYSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	338
tr K3ZGZ6 K3ZGZ6_SETIT	A-RVMSYQCLELDCLYSDLVSHAAEAGEYSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	340
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	S-RNLVSHCQLELDCLYSDLVSHAPEGEFSKMGPFILSVFDIECAGRKGHFEPTHDFVQ	327
tr A0A0S3RFB6 A0A0S3RFB6_PHAAN	V-KLSYQCLEFDCLYSDLISHAPEGEYSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	321
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	A-KNSSYQCLEFDCLYSDLISHVPEGEFSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	322
tr A0A200Q8R4 A0A200Q8R4_9MAGN	T-KTISYQCLEFDCLYSSELISHPEGEFSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	288
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	A-KSTSYQCLEFNCLYSDLISHAPEGEFSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	325
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	A-KNLSYQCLEFDCLYSSELISHTPEGEFSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	322
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	A-KHSSYQCLEFDCLFSDLISHAPEGEFSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	321
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	A-KHSSYQCLEFDCLFSDLISHAPEGEFSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	321
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	A-KHSSYQCLEFDCLYSDLISHAPEGEFSKMAPFRILSVFDIECAGRKGHFEPTHDFVQ	321
	...:*** ** :...*:**..**** ** ** *	

tr U5H8M8 U5H8M8_USTV1	IANVTRQGETKPFIRNVTILNTGSHIVGTDVIEFEKEADLLTRWREFVDEVDLIIIGY	416
tr C1E609 C1E609_MICCC	IATMTCQGGDRPFIKAIWTLDTGAPVIGADVLSFKDERELLSRWGKFLRSTDDLLIIGY	433
tr Q33BV0 Q33BV0_AUXPY	VASIVTEFGKATPTVRNIMTLKSCAPISGAEVMSFEHEKDLLLRWRDLVLETDLIIIGY	380
sp Q9LVN7 DP0D1_ARATH	IANVTLQGEDEHPFVRNVTILKSCAPVIGVDVMSFETEREVLLAWRDLIRVDVDDIIIGY	392
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	IANVTLQGEDEHPFVRNVTILKSCAPVIGVDVMSFETERKVLAWKDFVRVDVDDIIIGY	387
tr A0A397Z0B4 A0A397Z0B4_BRACM	IANVTLQGEDEHPFVRNVTILKSCAPVIGVDVMSFETERKVLAWKDFVRVDVDDIIIGY	387
tr A0A078I2E2 A0A078I2E2_BRANA	IANVTLQGEDEHPFVRNVTILKSCAPVIGVDVMSFETERKVLAWKDFVRVDVDDIIIGY	387
tr A0A287NEC0 A0A287NEC0_HORVV	IANLLTQGEAQPFVRNVTILKSCSPVIGVDVMSFDTERDILLAWRDLIREADVDDIIIGY	418
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	IANLLTQGEAQPFVRNVTILKSCSPVIGVDVMSFDTERDILLAWRDLIREADVDDIIIGY	398
tr A0A453HJ27 A0A453HJ27_AEGTS	IANLLTQGEAQPFVRNVTILKSCSPVIGVDVMSFDTERDILLAWRDLIREADVDDIIIGY	413
tr A0A6G1C319 A0A6G1C319_9ORYZ	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTERDILLAWRDLIREADVDDIIIGY	384
sp Q9LRE6 DP0D1_ORYSJ	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTERDILLAWRDLIREADVDDIIIGY	400
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTERDILLAWRDLIREADVDDIIIGY	384
tr A0A5J9USA3 A0A5J9USA3_9POAL	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFETERDILLAWRDLIREADVDDIIIGY	395
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFETERDILLAWRDLIREADVDDIIIGY	398
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTERDILLAWRDLIREADVDDIIIGY	398
tr K3ZGZ6 K3ZGZ6_SETIT	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTERDILLAWRDLIREADVDDIIIGY	400
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	VANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFETERKELLAWRDLIREADVDDIIIGY	387
tr A0A0S3RFB6 A0A0S3RFB6_PHAAN	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTEREVLLAWRDLIREADVDDIIIGY	381
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTEREVLLAWRDLIREADVDDIIIGY	382
tr A0A200Q8R4 A0A200Q8R4_9MAGN	VANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTEREVLLAWRDLIREADVDDIIIGY	348
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	VANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTEREVLLAWRDLIREADVDDIIIGY	385
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	VANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTEREVLLAWRDLIREADVDDIIIGY	382
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTEREVLLAWRDLIREADVDDIIIGY	381
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	IANVTLQGEDEHPFVRNVTILKSCSPVIGVDVMSFDTEREVLLAWRDLIREADVDDIIIGY	381
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	IANVTLQGENEHPFVRNVTILKSCSPVIGVDVMSFDTEREVLLAWRDLIREADVDDIIIGY	381
	:*:*** ** :...*:**..**** ** ** *	

tr U5H8M8 U5H8M8_USTV1	FDLQVMDQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	536
tr C1E609 C1E609_MICCC	FDLLQAVQRDHLKSSYSLNSVSAHFLGSEQEDVHHSITSELQAGTAETRRLAVYDIFDA	553
tr Q33BV0 Q33BV0_AUXPY	FDLLQAIQRDHLKSSYSLNSVSAHFLGSEQEDVHHSITSKLQDNGNAETRRLAVYDIFDA	500
sp Q9LVN7 DP0D1_ARATH	FDLLQAIHRDHLKSSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	512
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	FDLLQAIHRDHLKSSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	507
tr A0A397Z0B4 A0A397Z0B4_BRACM	FDLLQAIHRDHLKSSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	507
tr A0A078I2E2 A0A078I2E2_BRANA	FDLLQAIHRDHLKSSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	507
tr A0A287NEC0 A0A287NEC0_HORVV	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	538
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	518
tr A0A453HJ27 A0A453HJ27_AEGTS	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	533
tr A0A6G1C319 A0A6G1C319_9ORYZ	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	504
sp Q9LRE6 DP0D1_ORYSJ	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	520
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	504
tr A0A5J9USA3 A0A5J9USA3_9POAL	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	515
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	518
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	518
tr K3ZGZ6 K3ZGZ6_SETIT	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	520
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	507
tr A0A0S3RFB6 A0A0S3RFB6_PHAAN	FDLLQVMDQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	501
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	FDLLQAIQRDHLKSSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	502
tr A0A200Q8R4 A0A200Q8R4_9MAGN	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNSETRRLAVYDIFDA	468
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	FDLLQVMDQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	505
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	FDLLQAVQRDHLKSSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	502
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	501
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	501
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	FDLLQAMQRYKLSYSLNSVSAHFLGSEQEDVHHSITDQLQNGNAETRRLAVYDIFDA	501
	:*:*** ** :...*:**..**** ** ** *	

tr U5H8M8 U5H8M8_USTV1	YLPQRIMDKLMCFINYIEMARVTGIPFNYSLLSRGQIKVISQLFRKAQDNTNLY	PR Exo	PAFRSE	596
tr C1E609 C1E609_MICCC	YLPQRLLDKLMYMYNYIEMARVTGVPLSFLLRGQSIKVLSQLRKAQKQGLLV		PHIAKK	613
tr Q33BV0 Q33BV0_AUXFY	YLPQRLLVDKLMIMYNYIEMARVTGVPMPSYLLLRGQSIKVLSQLRKBRTKGLVV		PNNKRG	560
sp Q9LVN7 DPOD1_ARATH	YLPQRLLDKLMFIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKGQKQNLVL		PNAKQS	572
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	YLPQRLLDKLMCIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNMVL		PNAKQS	567
tr A0A397Z0B4 A0A397Z0B4_BRACM	YLPQRLLDKLMCIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNMVL		PNAKQS	567
tr A0A078I2E2 A0A078I2E2_BRANA	YLPQRLLDKLMCIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNMVL		PNAKQS	567
tr A0A287NEC0 A0A287NEC0_HORVV	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKGQ	598
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKGQ	578
tr A0A453HJ27 A0A453HJ27_AEGTS	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKGQ	593
tr A0A6G1C319 A0A6G1C319_9ORYZ	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKGQ	564
sp Q9LRE6 DPOD1_ORYSJ	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKGQ	580
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKGQ	564
tr A0A5J9USA3 A0A5J9USA3_9POAL	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKGQ	575
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKGQ	578
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKGQ	578
tr K3ZGZ6 K3ZGZ6_SETIT	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKGQ	580
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	YLPQRLLDKLMFIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKGLVI		PNVKQA	567
tr A0A0S3RFB6 A0A0S3RFB6_PHAAN	YLPQRLLDKLMFIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNVKQV	561
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNVKQA	562
tr A0A200Q8R4 A0A200Q8R4_9MAGN	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PSVRKQ	528
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	YLPQRLLDKLMFIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNVKQA	565
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	YLPQRLLDKLMFIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKGLVI		PNVKHA	562
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNIKQA	561
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNVKQA	561
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	YLPQRLLDKLMYIYNYVEMARVTGVPI SFLLRGQSIKVLSQLRKAQKQNLVI		PNVKQA	561

tr U5H8M8 U5H8M8_USTV1	GS-----DEQYEGATVIEPEKGYDVPDIATLDFASLYPS	IMQAHNLCYTTLLDAKIAEA	650
tr C1E609 C1E609_MICCC	GGGEQADGGVAYEGATVLDKAGYEMPVATLDFASLYPS	IMMAHNLCTSLVPRDRV--	671
tr Q33BV0 Q33BV0_AUXFY	GD---AGEGVAYEGATVLEPRAGYDPRVATLDFASLYPS	IMMAHNLCTTLPLPKGQ---	615
sp Q9LVN7 DPOD1_ARATH	GS-----EQGTYEGATVLEARTGFYEKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	627
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	GS-----EQGTFEAGATVLEARTGFYEKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	622
tr A0A397Z0B4 A0A397Z0B4_BRACM	GS-----EQGTFEAGATVLEARTGFYEKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	622
tr A0A078I2E2 A0A078I2E2_BRANA	GS-----EQGTFEAGATVLEARTGFYEKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	622
tr A0A287NEC0 A0A287NEC0_HORVV	SS-----GQDTFEAGATVLEARAGFYKPIATLDFASLYPS	IMMAHNLCTLVPPEDVRK	653
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	SS-----GQDTFEAGATVLEARAGFYKPIATLDFASLYPS	IMMAHNLCTLVPPEDVRK	633
tr A0A453HJ27 A0A453HJ27_AEGTS	SS-----GQDTFEAGATVLEARAGFYKPIATLDFASLYPS	IMMAHNLCTLVPPEDVRK	648
tr A0A6G1C319 A0A6G1C319_9ORYZ	GS-----GQDTFEAGATVLEARAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVPPEDVRK	619
sp Q9LRE6 DPOD1_ORYSJ	AS-----GQDTFEAGATVLEARAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVPPEDARK	635
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	AS-----GQDTFEAGATVLEARAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVPPEDARK	619
tr A0A5J9USA3 A0A5J9USA3_9POAL	GS-----GQDTFEAGATVLEARAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVPPEDARK	630
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	GS-----GQDTFEAGATVLEARAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVPPEDARK	633
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	GS-----GQDTFEAGATVLEASAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVPPEDARK	633
tr K3ZGZ6 K3ZGZ6_SETIT	GS-----GQDTFEAGATVLEARAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVPPEDARK	635
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	GS-----EQGTYEGATVLEAKAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	622
tr A0A0S3RFB6 A0A0S3RFB6_PHAAN	GS-----EQGTFEAGATVLEARAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	616
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	GS-----EQGTYEGATVLEAKAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	617
tr A0A200Q8R4 A0A200Q8R4_9MAGN	GS-----GEGTFEAGATVLEARTGFYEKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	583
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	GS-----EQGTYEGATVLEAKAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVRSSEVRK	620
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	GS-----EQGTYEGATVLEARAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	617
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	GS-----EQGTYEGATVLEAKAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	616
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	GS-----EQGTYEGATVLEAKAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	616
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	GS-----EQGTYEGATVLEAKAGFYKPIATLDFASLYPS	IMMAYNLCYCTLVTPEDVRK	616

tr U5H8M8 U5H8M8_USTV1	LNLKEGVYVTRPNNDLFVKSEKRGLLPIILEDLLSARKRARAELKKETDFFKRAVLGD	710
tr C1E609 C1E609_MICCC	QFMAS-EDVTRTPCGDFTVFKSHKKGILPEILTELLSARKRKAADLKEAKDPLEKAVLDG	730
tr Q33BV0 Q33BV0_AUXFY	KMFPS-EHLTFPNNDFVFKPSLQKQILPEILEELITARKRKAADLKEAKDPLEKAVLDG	674
sp Q9LVN7 DPOD1_ARATH	LNLPP-EHVTKTPSGETFFVKQTLQKQILPEILEELITARKRKAADLKEAKDPLEKAVLDG	686
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	LNLPP-EHINKTPSGETFFVKQTLQKQILPEILEELITARKRKAADLKEAKDPLEKAVLDG	681
tr A0A397Z0B4 A0A397Z0B4_BRACM	LNLPP-EHINKTPSGETFFVKQTLQKQILPEILEELITARKRKAADLKEAKDPLEKAVLDG	681
tr A0A078I2E2 A0A078I2E2_BRANA	LNLPP-EHINKTPSGETFFVKQTLQKQILPEILEELITARKRKAADLKEAKDPLEKAVLDG	681
tr A0A287NEC0 A0A287NEC0_HORVV	LNLPP-ESLYKTPSGEIFVKPELQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	712
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	LNLPP-ESLYKTPSGEIFVKPELQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	692
tr A0A453HJ27 A0A453HJ27_AEGTS	LNLPP-ESLYKTPSGEIFVKPELQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	707
tr A0A6G1C319 A0A6G1C319_9ORYZ	LNLPP-ESLNKTPSGETFFVKPELQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	678
sp Q9LRE6 DPOD1_ORYSJ	LNLPP-ESVNTTPSGETFFVKPDVQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	694
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	LNLPP-ESVNTTPSGETFFVKPEVQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	678
tr A0A5J9USA3 A0A5J9USA3_9POAL	LNLPP-ESLNRTPSGEIFVKPELQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	689
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	LNLPP-EFVNTTPSGEIFVKPELQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	692
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	LNLPP-ESLNKTPSGEIFVKPDQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	692
tr K3ZGZ6 K3ZGZ6_SETIT	LNLPP-ESLNKTPSGEIFVKPELQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	694
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	LNLPP-ECVNTTPSGETFFVKSTLQKQILPEILEELITARKRKAADLKEAKDPLEKAVLDG	681
tr A0A0S3RFB6 A0A0S3RFB6_PHAAN	LNIPI-ESLNKTPSGETFFVKSQKQILPEILEELITARKRKAADLKEAKDPLEKAVLDG	675
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	LNLPP-ECVNTTPSGEMFVKPNLQKQILPEILEELITARKRKAADLKEAKDPLEKAVLDG	676
tr A0A200Q8R4 A0A200Q8R4_9MAGN	LNLPP-ECVNTTPSGETFFVKSQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	642
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	LNLPP-ECVNTTPSGETFFVKNLQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	679
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	LNLPP-ECVNTTPSGETFFIKSNLQKQILPEILEELITARKRKAADLKEAKDPLEKAVLDG	676
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	LNIPI-EFVNTTPSGETFFVKSQKQILPEILEELITARKRKAADLKEAKDPLEKAVLDG	675
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	LNIPI-EFVNTTPSGETFFVKSQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	675
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	LNIPI-EFVNTTPSGETFFVKSQKQILPEILEELLAARKRKAADLKEAKDPLEKAVLDG	675

tr U5H8M8 U5H8M8_USTV1	ROLALKVSANSVYFTGATVGLPCLEI	QI SMSVTAYGRQMIERTKQEVQDRYNTANGYEYD	770
tr C1E609 C1E609_MICCC	ROLALKVSANSVYFTGATVGLPCLEI	ISSSTTAFGREMIDHTKAMVEKRYTTANGYKAN	790
tr Q33BV0 Q33BV0_AUXPY	ROLALKVSANSVYFTGATVGLPCLEI	ISSSVTSFGREMIMETRRRVQERYCKANGYSHD	734
sp Q9LVN7 DPOD1_ARATH	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	746
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	741
tr A0A397Z0B4 A0A397Z0B4_BRACM	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	741
tr A0A078I2E2 A0A078I2E2_BRANA	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	741
tr A0A287NEC0 A0A287NEC0_HORVV	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	772
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	752
tr A0A453HJ27 A0A453HJ27_AEGTS	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	767
tr A0A6G1C319 A0A6G1C319_9ORYZ	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	738
sp Q9LRE6 DPOD1_ORYSJ	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	754
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	738
tr A0A5J9USA3 A0A5J9USA3_9POAL	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	749
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	752
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	752
tr K3ZGZ6 K3ZGZ6_SETIT	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	754
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	741
tr A0A0S3RFB6 A0A0S3RFB6_PHAAN	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	735
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	736
tr A0A200Q8R4 A0A200Q8R4_9MAGN	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	702
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	739
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	736
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	735
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	735
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	ROLALKISANSVYFTGATVGLPCLEI	ISSSVTSYGRQMIETQKKLVEDKFTTLGGYEYN	735

tr U5H8M8 U5H8M8_USTV1	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	830
tr C1E609 C1E609_MICCC	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	850
tr Q33BV0 Q33BV0_AUXPY	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	794
sp Q9LVN7 DPOD1_ARATH	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLINKRR	806
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLINKRR	801
tr A0A397Z0B4 A0A397Z0B4_BRACM	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLINKRR	801
tr A0A078I2E2 A0A078I2E2_BRANA	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLINKRR	801
tr A0A287NEC0 A0A287NEC0_HORVV	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLINKRR	832
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	812
tr A0A453HJ27 A0A453HJ27_AEGTS	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	827
tr A0A6G1C319 A0A6G1C319_9ORYZ	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	798
sp Q9LRE6 DPOD1_ORYSJ	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	814
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	798
tr A0A5J9USA3 A0A5J9USA3_9POAL	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	809
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	812
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	812
tr K3ZGZ6 K3ZGZ6_SETIT	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	814
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	801
tr A0A0S3RFB6 A0A0S3RFB6_PHAAN	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	795
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	796
tr A0A200Q8R4 A0A200Q8R4_9MAGN	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	762
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	799
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	796
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	795
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	795
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	AEVLYGDTDSVMVQFVGVDDVAAAMQLGREAAEYISGTFIKPIKLEFEKVIYFPYLLISKRR	795

tr U5H8M8 U5H8M8_USTV1	YAGLWTKPEKYDKMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	890
tr C1E609 C1E609_MICCC	YAGLWTKPEKYDKMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	910
tr Q33BV0 Q33BV0_AUXPY	YAGLWTKPEKYDKMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	854
sp Q9LVN7 DPOD1_ARATH	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	866
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	861
tr A0A397Z0B4 A0A397Z0B4_BRACM	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	861
tr A0A078I2E2 A0A078I2E2_BRANA	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	861
tr A0A287NEC0 A0A287NEC0_HORVV	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	892
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	872
tr A0A453HJ27 A0A453HJ27_AEGTS	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	887
tr A0A6G1C319 A0A6G1C319_9ORYZ	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	858
sp Q9LRE6 DPOD1_ORYSJ	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	874
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	858
tr A0A5J9USA3 A0A5J9USA3_9POAL	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	869
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	872
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	872
tr K3ZGZ6 K3ZGZ6_SETIT	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	874
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	861
tr A0A0S3RFB6 A0A0S3RFB6_PHAAN	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	855
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	856
tr A0A200Q8R4 A0A200Q8R4_9MAGN	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	822
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	859
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	856
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	855
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	855
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	YAGLWLTNPQKFKDMDTKGIETVRRDNC	LLVKNLVTECLHKILVDRDPVGAEEYVKNTIS	855

U5H8M8_USTV1 DNA polymerase, *Microbotryum lychnidis-dioicae* (an obligate biotrophic plant parasite)
 C1E609_MICCC DNA polymerase, *Micromonas commode* (a eukaryotic, photosynthetic microbe)
 Q33BV0_AUXPY DNA polymerase, *Auxenochlorella pyrenoidosa* (Chlorella)
 Q9LVN7|DPOD1_ARATH DNA polymerase, *Arabidopsis thaliana*
 A0A3P6BBX0_BRAOL DNA polymerase, *Brassica oleracea*
 A0A397Z0B4_BRACM DNA polymerase, *Brassica campestris*
 A0A078I2E2_BRANA DNA polymerase, *Brassica napus*
 A0A287NEC0_HORVV DNA polymerase, *Hordeum vulgare subsp. Vulgare*
 A0A3B6JHK9_WHEAT DNA polymerase, *Triticum aestivum*
 A0A453HJ27_AEGTS DNA polymerase, *Aegilops tauschii subsp. Strangulate*
 A0A6G1C319_9ORYZ DNA polymerase, *Oryza meyeriana var. granulate*
 Q9LRE6|DPOD1_ORYSJ DNA polymerase, *Oryza sativa subsp. Japonica*
 A0A0E0MDA8_ORYPU DNA polymerase, *Oryza punctate*
 A0A5J9USA3_9POAL DNA polymerase, *Eragrostis curvula*
 A0A1D6QLT8_MAIZE DNA polymerase, *Zea mays*
 A0A2S3ICY2_9POAL DNA polymerase, *Panicum hallii*
 K3ZGZ6_SETIT DNA polymerase, *Setaria italic*
 A0A2P2KVG9_RHIMU DNA polymerase, *Rhizophora mucronata*
 A0A0S3RFB6_PHAAN DNA polymerase, *Vigna angularis var. angularis*
 A0A7J7DZR4_TRIWF DNA polymerase, *Tripterygium wilfordii*
 A0A200Q8R4_9MAGN DNA polymerase, *Macleaya cordata*
 A0A2P6RSP9_ROSCH DNA polymerase, *Rosa chinensis*
 A0A2I4F7Z3_JUGRE DNA polymerase, *Juglans regia*
 A0A6J5U1U4_PRUAR DNA polymerase, *Prunus armeniaca*
 A0A5E4GBB6_PRUDU DNA polymerase, *Prunus dulcis*
 A0A6P5S1M3_PRUAV DNA polymerase, *Prunus avium*

Figure 4 shows the 'Mix and Match' MSA of the plant and animal δ pols (only the required regions for the discussions are shown). The plant sequences are highlighted in green and the animal sequences in black. There are large and small gaps in the N-terminal domains (data not shown). The PR exonuclease domain shows many conservations in both δ pols, but much higher conservations are observed at the end of the PR domain. It is interesting to note that the PR exonuclease active site amino acids (highlighted in light blue) are completely conserved in both plant and animal δ pols (Fig. 4). However, the second domain, i.e., the pol domain is highly conserved throughout. The polymerase active site amino acids are also completely conserved in both the δ pols (highlighted in yellow). The -DxD- metal-binding motifs are highly conserved in both and highlighted in dark green. The characteristic motifs found in the δ pols, viz. -SYLPS- and YGDTD- are completely conserved in both δ pols and their significance is discussed elsewhere. The highly conserved polybasic peptide is found in both pols and placed in between them (highlighted in light violet). However, the larger conserved peptide carrying the -SYLPS- motif shows marked differences in four amino acids, -FYEKPIATLDFASLYPS- (from plant sources, *A. thaliana*) and -YYDVPIATLDFSSLYPS- (from animal sources, humans). However, the BLASTp analysis has shown only 56.57% identity between the plant (*A. thaliana*) and animal (human) δ pols. The pI values of *A. thaliana* and human δ pols showed a marked difference, 8.00 and 6.64, respectively. Apart from the conserved Cs of the ZBMs in the CTD, there are other completely conserved C residues in both pols (highlighted in orange) which could possibly play a role in disulphide bond formation. The PIP heptapeptide is found in both the δ pols in the CTD and is highlighted in magenta. Even though the PIPs are conserved in both plants and animals, but small variations are observed between them as shown: -S/GGIMKFA- (from plant sources) and -GLLAFA- (from animal sources). Interestingly, both plant and animal δ pol sequences almost end in an aromatic amino acid (**F** in plants and **W** in animals). The significance of such similar endings in all δ pol sequences is not clear now.

CLUSTAL O (1.2.4) MSA of δ pols from animal and plant sources

		NTD ← SRS		→ EXO		
sp Q9LVN7 DP0D1_ARATH	-----LILRDIKERE--SRS	WARPPPLSPAYL--SNSQSIIFQO	LEIDSITIAESHK	111		
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	-----LILRDMEREALSARSST	WARPPPLSPAYL--ANSQSIIFQO	LEIDYVVIKEIHK	106		
tr A0A397Z0B4 A0A397Z0B4_BRCM	-----LILRDMEREALSARSST	WARPPPLSPAYL--ANSQSIIFQO	LEIDYVVIKEIHK	106		
tr A0A153A927 A0A153A927_BRANA	-----LILRDMEREALSARSST	WARPPPLPADLVSGCSRVAFQO	LEIDYVIGESHK	117		
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	-----LLL--DRDEALASRLSR	WARPPALPADLVSGCSRVAFQO	LEIDYVIGESHK	117		
tr A0A287NEC0 A0A287NEC0_HORVV	-----LLL--DRDEALASRLSR	WARPPALPADLVSGCSRVAFQO	LEIDYVIGESHK	117		
tr A0A661C319 A0A661C319_9ORYZ	-----LLL--DRDEALASRLSR	WARPPALPADLVSGCSRVAFQO	LEIDYVIGESHK	121		
sp Q9LRE6 DP0D1_ORYSJ	-----LLL--DRDEALASRLSR	WARPPALPADLVSGCSRVAFQO	LEIDYVIGESHK	119		
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	-----LLL--DRDEALASRLSR	WARPPALPADLVSGCSRVAFQO	LEIDYVIGESHK	121		
tr A0A5J9USA3 A0A5J9USA3_9POAL	-----QLL--QRDEALASRLSR	WARPPALPADLVSGCSRVAFQO	LEIDYVIGESHK	114		
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	-----LML--QRDEALASRLSR	WARPPALPADLVSGCSRVAFQO	LEIDYVIGESHK	106		
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	-----LML--QRDEALASRLSR	WARPPALPADLVSGCSRVAFQO	LEIDYVIGESHK	117		
tr K3ZGZ6 K3ZGZ6_SEITIT	-----LMI--QRDEALASRLSR	WARPPALPADLVSGCSRVAFQO	LEIDYVIGESHK	119		
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	-----VREQVLAASRLAK	WARPPALSGAYL--SQSQSITFQO	LEMDYVVGESHK	105		
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	-----ILRD--IEEREAIVASRLAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	101		
tr A0A200QBR4 A0A200QBR4_9MAGN	-----ILQDEEDRQLASRLSR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	67		
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	-----ILRD--SEQRQSLASRLTR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	105		
tr A0A214F7Z3 A0A214F7Z3_JUGRE	-----ILRD--SEQRQSLASRLTR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	101		
tr A0A63JULU4 A0A63JULU4_PRUAR	-----ILRD--IEERQSLASRLTR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	101		
tr A0A5E4QBB6 A0A5E4QBB6_PRUDU	-----ILRD--IEERQSLASRLTR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	101		
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	-----ILRD--IEERQSLASRLTR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	101		
tr A0A6P5I296 A0A6P5I296_PHACI	EEEEELH--LPP--EGAEGHFTSAWDR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	146		
sp P52431 DP0D1_MOUSE	EEEEELQ--PPEGVGGQFSTADIDPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	107		
sp O54747 DP0D1_RAT	EEEEELQ--PPEGVGGQFSTADIDPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	105		
tr G3V8M1 G3V8M1_RAT	EEEEELQ--PPEGVGGQFSTADIDPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	105		
tr A0A1S3A927 A0A1S3A927_ERIEU	EEE--ALQVSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	107		
tr H0V251 H0V251_CAVPO	EEE--ELQSAALGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	107		
tr A0A619JZ04 A0A619JZ04_CHRAS	EEE--ELQSAALGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	110		
tr A0A7J7SK29 A0A7J7SK29_RHIFE	EEE--ELQSAALGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	112		
sp P28340 DP0D1_HUMAN	EEE--ELQSVLEGVADGQVPSAIDPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr A0A2K6D6G8 A0A2K6D6G8_MACNE	EEE--ELQSVLEGVADGQVPSAIDPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr A0A0A0MW23 A0A0A0MW23_PAPAN	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr A0A6P7EPG1 A0A6P7EPG1_SHEEP	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	108		
sp P28339 DP0D1_BOVIN	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	108		
tr E1BNZ6 E1BNZ6_BOVIN	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	108		
tr A0A383ZY66 A0A383ZY66_BALAS	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr A0A2Y9P989 A0A2Y9P989_DELLE	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr F7DXU3 F7DXU3_HORSE	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr A0A5G2QET9 A0A5G2QET9_FIG	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr A0A6J1X8L4 A0A6J1X8L4_ACTIJB	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr M3VUJ4 M3VUJ4_FELCA	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr E2R5W5 E2R5W5_CANLF	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr G1M3J7 G1M3J7_AILME	EEE--ELQSALEGA--DGFQSLTADAR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr A0A2U3ZRE1 A0A2U3ZRE1_ODORO	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr A0A6J2WZ66 A0A6J2WZ66_CHACN	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		
tr Q2KNE0 Q2KNE0_DANRE	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	103		
tr A0A6P6JVN6 A0A6P6JVN6_CARAU	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	103		
tr A0A6P6JG77 A0A6P6JG77_CARAU	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	103		
tr A0A673JF13 A0A673JF13_9TELE	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	103		
tr A0A498LX53 A0A498LX53_LABRO	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	103		
tr COHA77 COHA77_SALSA	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	103		
tr A0A6P7IUM6 A0A6P7IUM6_9TELE	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	102		
tr A0A3Q3E049 A0A3Q3E049_HIPCM	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	103		
tr A0A4W3I8L4 A0A4W3I8L4_CALMI	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	103		
tr DOVEW7 DOVEW7_XENLA	EQGAGHDVIP---VGDLFSA--DLNPR	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	104		
tr A0A6J1U352 A0A6J1U352_9SAUR	EAQLSSDAIP---LGNLFSS--IHNP	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	108		
tr A0A619XX64 A0A619XX64_9SAUR	EAQLSSDAIP---LGNLFSS--IHNP	WARPPALSDYL--SQAKNITFQO	LEMDYVVGESHK	109		

sp Q9LVN7 DP0D1_ARATH	-----RTLSYCOLEFHCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	328
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	-----RTSSYCOLEFHCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	323
tr A0A397Z0B4 A0A397Z0B4_BRCM	-----RTLSYCOLEFHCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	323
tr A0A078I2E2 A0A078I2E2_BRANA	-----RTLSYCOLEFHCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	323
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	-----RVMSYCOLELDCLYSDLVSHAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	324
tr A0A287NEC0 A0A287NEC0_HORVV	-----RVMSYCOLELDCLYSDLVSHAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	354
tr A0A661C319 A0A661C319_9ORYZ	-----SILVSHAAPEGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	320
sp Q9LRE6 DP0D1_ORYSJ	-----SILVSHAAPEGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	320
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	-----SILVSHAAPEGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	320
tr A0A5J9USA3 A0A5J9USA3_9POAL	-----RVMSYCOLELDCLYSDLVSHAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	331
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	-----RVMSYCOLELDCLYSDLVSHAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	334
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	-----RVMSYCOLELDCLYSDLVSHAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	334
tr K3ZGZ6 K3ZGZ6_SEITIT	-----RVMSYCOLELDCLYSDLVSHAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	336
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	-----RNLSHCQLEFDCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	323
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	-----KNSSYCOLEFDCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	318
tr A0A200QBR4 A0A200QBR4_9MAGN	-----KTISSYCOLEFDCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	284
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	-----KTISSYCOLEFDCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	321
tr A0A214F7Z3 A0A214F7Z3_JUGRE	-----RNLSYCOLEFDCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	318
tr A0A63JULU4 A0A63JULU4_PRUAR	-----KHSSYCOLEFDCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	317
tr A0A5E4QBB6 A0A5E4QBB6_PRUDU	-----KHSSYCOLEFDCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	317
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	-----KHSSYCOLEFDCLYSDLISHAAPGEYSKMAPFRVLSFDIECA	---GRKGHFPEAKHD	317
tr A0A6P5I296 A0A6P5I296_PHACI	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	366
sp P52431 DP0D1_MOUSE	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	330
sp O54747 DP0D1_RAT	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	328
tr G3V8M1 G3V8M1_RAT	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	328
tr A0A1S3A927 A0A1S3A927_ERIEU	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr H0V251 H0V251_CAVPO	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr A0A619JZ04 A0A619JZ04_CHRAS	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	334
tr A0A7J7SK29 A0A7J7SK29_RHIFE	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	340
sp P28340 DP0D1_HUMAN	-----EKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr A0A2K6D6G8 A0A2K6D6G8_MACNE	-----KKTTCQLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr A0A0A0MW23 A0A0A0MW23_PAPAN	-----KKTTCQLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr A0A452F6S3 A0A452F6S3_CAPHI	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	331
tr A0A6P7EPG1 A0A6P7EPG1_SHEEP	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	331
sp P28339 DP0D1_BOVIN	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	331
tr E1BNZ6 E1BNZ6_BOVIN	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	331
tr A0A383ZY66 A0A383ZY66_BALAS	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr A0A2Y9P989 A0A2Y9P989_DELLE	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr F7DXU3 F7DXU3_HORSE	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr A0A5G2QET9 A0A5G2QET9_FIG	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr A0A6J1X8L4 A0A6J1X8L4_ACTIJB	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr M3VUJ4 M3VUJ4_FELCA	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr E2R5W5 E2R5W5_CANLF	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr G1M3J7 G1M3J7_AILME	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr A0A2U3ZRE1 A0A2U3ZRE1_ODORO	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	332
tr A0A6J2WZ66 A0A6J2WZ66_CHACN	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	336
tr Q2KNE0 Q2KNE0_DANRE	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	336
tr A0A6P6JVN6 A0A6P6JVN6_CARAU	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	336
tr A0A6P6JG77 A0A6P6JG77_CARAU	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	336
tr A0A673JF13 A0A673JF13_9TELE	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	331
tr A0A498LX53 A0A498LX53_LABRO	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	336
tr COHA77 COHA77_SALSA	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	336
tr A0A6P7IUM6 A0A6P7IUM6_9TELE	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	335
tr A0A3Q3E049 A0A3Q3E049_HIPCM	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	336
tr A0A4W3I8L4 A0A4W3I8L4_CALMI	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	338
tr DOVEW7 DOVEW7_XENLA	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	336
tr A0A6J1U352 A0A6J1U352_9SAUR	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	339
tr A0A619XX64 A0A619XX64_9SAUR	-----GKATLCOLEADVWLSVSHHPPEGEWQRTAPLRVLSFDIECA	---GRKGHFPEAKHD	342

sp Q9LVN7 DPOD1_ARATH	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	508
tr AOA3P6BBX0 AOA3P6BBX0_BRAOL	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	503
tr AOA397Z0B4 AOA397Z0B4_BACRM	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	503
tr AOA078I2E2 AOA078I2E2_BRANA	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	503
tr AOA3B6JHK9 AOA3B6JHK9_WHEAT	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	514
tr AOA287NEC0 AOA287NEC0_HORVY	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	514
tr AOA6G1C319 AOA6G1C319_9ORYZ	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	500
sp Q9LRE6 DPOD1_ORYSJ	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	516
tr AOA0E0MDA8 AOA0E0MDA8_ORYPU	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	500
tr AOA5J9USA3 AOA5J9USA3_9POAL	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	511
tr AOA1D6QLT8 AOA1D6QLT8_MAIZE	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	514
tr AOA2S3ICV2 AOA2S3ICV2_9POAL	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	514
tr K3ZGZ6 K3ZGZ6_SETIT	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	516
tr AOA2P2KV69 AOA2P2KV69_RHIMU	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	503
tr AOA7J7DZ4 AOA7J7DZ4_TRIWF	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	498
tr AOA200Q8R4 AOA200Q8R4_9MAGN	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	464
tr AOA2P6RSP9 AOA2P6RSP9_ROSCH	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	501
tr AOA2I4F7Z3 AOA2I4F7Z3_JUGRE	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	498
tr AOA6J5U1U4 AOA6J5U1U4_PRUAR	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	497
tr AOA5E4GBB6 AOA5E4GBB6_PRUDU	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	497
tr AOA6P5S1M3 AOA6P5S1M3_PRUAV	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	497
tr AOA6P5I296 AOA6P5I296_PHACI	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	546
sp P52431 DPOD1_MOUSE	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	510
sp O54747 DPOD1_RAT	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	508
tr G3V8M1 G3V8M1_RAT	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	508
tr AOA1S3A927 AOA1S3A927_ERIEU	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	510
tr HOV251 HOV251_CAVPO	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	510
tr AOA6I9J204 AOA6I9J204_CHRAS	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	514
tr AOA7J7SK29 AOA7J7SK29_RHIFE	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	520
sp P28340 DPOD1_HUMAN	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr AOA2K6D6G8 AOA2K6D6G8_MACNE	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr AOA0A0MW23 AOA0A0MW23_PAPAN	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr AOA452F6S3 AOA452F6S3_CAPHI	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	511
tr AOA6P7EPG1 AOA6P7EPG1_SHEEP	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	511
sp P28339 DPOD1_BOVIN	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	511
tr E1BNZ6 E1BNZ6_BOVIN	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	511
tr AOA383ZY66 AOA383ZY66_BALAS	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr AOA2Y9P989 AOA2Y9P989_DELLE	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr F7DXU3 F7DXU3_HORSE	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr AOA5G2QET9 AOA5G2QET9_PIG	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr AOA6J1XK42 AOA6J1XK42_ACIBJ	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr M3VUJ4 M3VUJ4_FELCA	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr E2R5W5 E2R5W5_CANLF	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr G1M3J7 G1M3J7_AILME	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr AOA2U3ZRE1 AOA2U3ZRE1_ODORO	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr AOA6J2WZ6 AOA6J2WZ6_CHACN	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	512
tr Q2KNE0 Q2KNE0_DANRE	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	516
tr AOA6P6JVN6 AOA6P6JVN6_CARAU	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	516
tr AOA6P6JG77 AOA6P6JG77_CARAU	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	516
tr AOA673JF13 AOA673JF13_9TELE	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	516
tr AOA498LX53 AOA498LX53_LABRO	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	511
tr COHA77 COHA77_SALSA	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	516
tr AOA6P7IUM6 AOA6P7IUM6_9TELE	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	515
tr AOA3Q3E049 AOA3Q3E049_HIPCM	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	516
tr AOA4W3I8L4 AOA4W3I8L4_CALMI	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	518
tr DOVEW7 DOVEW7_XENLA	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	516
tr AOA6J1U352 AOA6J1U352_9SAUR	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	519
tr AOA6I9XX64 AOA6I9XX64_9SAUR	GRVQFDLQAIHRDHKLSYSLNSVSAHFLSEQKEDVHHSITDQLONGNAETRRRLAVYC	522

sp Q9LVN7 DPOD1_ARATH	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	567
tr AOA3P6BBX0 AOA3P6BBX0_BRAOL	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	562
tr AOA397Z0B4 AOA397Z0B4_BACRM	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	562
tr AOA078I2E2 AOA078I2E2_BRANA	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	573
tr AOA3B6JHK9 AOA3B6JHK9_WHEAT	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	593
tr AOA287NEC0 AOA287NEC0_HORVY	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	559
tr AOA6G1C319 AOA6G1C319_9ORYZ	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
sp Q9LRE6 DPOD1_ORYSJ	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
tr AOA0E0MDA8 AOA0E0MDA8_ORYPU	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	570
tr AOA5J9USA3 AOA5J9USA3_9POAL	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	573
tr AOA1D6QLT8 AOA1D6QLT8_MAIZE	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	573
tr AOA2S3ICV2 AOA2S3ICV2_9POAL	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
tr K3ZGZ6 K3ZGZ6_SETIT	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
tr AOA2P2KV69 AOA2P2KV69_RHIMU	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	562
tr AOA7J7DZ4 AOA7J7DZ4_TRIWF	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	557
tr AOA200Q8R4 AOA200Q8R4_9MAGN	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	523
tr AOA2P6RSP9 AOA2P6RSP9_ROSCH	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	560
tr AOA2I4F7Z3 AOA2I4F7Z3_JUGRE	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	557
tr AOA6J5U1U4 AOA6J5U1U4_PRUAR	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	556
tr AOA5E4GBB6 AOA5E4GBB6_PRUDU	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	556
tr AOA6P5S1M3 AOA6P5S1M3_PRUAV	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	556
tr AOA6P5I296 AOA6P5I296_PHACI	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	605
sp P52431 DPOD1_MOUSE	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	569
sp O54747 DPOD1_RAT	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	567
tr G3V8M1 G3V8M1_RAT	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr AOA1S3A927 AOA1S3A927_ERIEU	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr HOV251 HOV251_CAVPO	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	569
tr AOA6I9J204 AOA6I9J204_CHRAS	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	573
tr AOA7J7SK29 AOA7J7SK29_RHIFE	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	579
sp P28340 DPOD1_HUMAN	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr AOA2K6D6G8 AOA2K6D6G8_MACNE	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr AOA0A0MW23 AOA0A0MW23_PAPAN	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr AOA452F6S3 AOA452F6S3_CAPHI	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	570
tr AOA6P7EPG1 AOA6P7EPG1_SHEEP	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	570
sp P28339 DPOD1_BOVIN	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	570
tr E1BNZ6 E1BNZ6_BOVIN	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	570
tr AOA383ZY66 AOA383ZY66_BALAS	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr AOA2Y9P989 AOA2Y9P989_DELLE	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr F7DXU3 F7DXU3_HORSE	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr AOA5G2QET9 AOA5G2QET9_PIG	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr AOA6J1XK42 AOA6J1XK42_ACIBJ	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr M3VUJ4 M3VUJ4_FELCA	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr E2R5W5 E2R5W5_CANLF	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr G1M3J7 G1M3J7_AILME	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr AOA2U3ZRE1 AOA2U3ZRE1_ODORO	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	571
tr AOA6J2WZ6 AOA6J2WZ6_CHACN	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
tr Q2KNE0 Q2KNE0_DANRE	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
tr AOA6P6JVN6 AOA6P6JVN6_CARAU	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
tr AOA6P6JG77 AOA6P6JG77_CARAU	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
tr AOA673JF13 AOA673JF13_9TELE	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
tr AOA498LX53 AOA498LX53_LABRO	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	570
tr COHA77 COHA77_SALSA	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
tr AOA6P7IUM6 AOA6P7IUM6_9TELE	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	574
tr AOA3Q3E049 AOA3Q3E049_HIPCM	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	574
tr AOA4W3I8L4 AOA4W3I8L4_CALMI	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	578
tr DOVEW7 DOVEW7_XENLA	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	575
tr AOA6J1U352 AOA6J1U352_9SAUR	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	578
tr AOA6I9XX64 AOA6I9XX64_9SAUR	LKDAYLPLRLLERLMVNVNAMEMARVTVGVPISYLLSRGQSKVLSQQLRQAMRQGLLVP	581

sp Q9LVN7 DP0D1_ARATH	NAKQSGSQGTTEGATVLEARTG-----FYEKPIATLDFAS	SLYPS	607
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	NAKQSGSQGTTEGATVLEARTG-----FYEKPIATLDFAS	SLYPS	602
tr A0A397Z0B4 A0A397Z0B4_BRACM	NAKQSGSQGTTEGATVLEARTG-----FYEKPIATLDFAS	SLYPS	602
tr A0A0781Z2E A0A0781Z2E_BRANA	NAKQSGSQGTTEGATVLEARTG-----FYEKPIATLDFAS	SLYPS	602
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	NIKQSSGQDTTEGATVLEARAG-----FYEKPIATLDFAS	SLYPS	613
tr A0A287NEC0 A0A287NEC0_HORVV	NIKQSSGQDTTEGATVLEARAG-----FYEKPIATLDFAS	SLYPS	633
tr A0A6G1C319 A0A6G1C319_9ORYZ	NIKQSSGQDTTEGATVLEARAG-----FYEKPIATLDFAS	SLYPS	599
sp Q9LRE6 DP0D1_ORYSJ	NIKQSSGQDTTEGATVLEARAG-----FYEKPIATLDFAS	SLYPS	615
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	NIKQSSGQDTTEGATVLEARAG-----FYEKPIATLDFAS	SLYPS	599
tr A0A5J9USA3 A0A5J9USA3_9POAL	NIKQSSGQDTTEGATVLEASAG-----FYEKPIATLDFAS	SLYPS	610
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	NIKQSSGQDTTEGATVLEASAG-----FYEKPIATLDFAS	SLYPS	613
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	NIKQSSGQDTTEGATVLEARAG-----FYEKPIATLDFAS	SLYPS	613
tr K3ZGZ6 K3ZGZ6_SETIT	NIKQSSGQDTTEGATVLEARAG-----FYEKPIATLDFAS	SLYPS	615
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	NVKQAGSQGTTEGATVLEAKAG-----FYEKPIATLDFAS	SLYPS	602
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	NVKQAGSQGTTEGATVLEAKAG-----FYEKPIATLDFAS	SLYPS	597
tr A0A200Q8R4 A0A200Q8R4_9MAGN	NVKQAGSQGTTEGATVLEARTG-----FYEKPIATLDFAS	SLYPS	563
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	NVKQAGSQGTTEGATVLEAKAG-----FYEKPIATLDFAS	SLYPS	600
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	NVKHAGSQGTTEGATVLEAKAG-----FYEKPIATLDFAS	SLYPS	597
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	NVKQAGSQGTTEGATVLEAKAG-----FYEKPIATLDFAS	SLYPS	596
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	NVKQAGSQGTTEGATVLEAKAG-----FYEKPIATLDFAS	SLYPS	596
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	NVKQAGSQGTTEGATVLEAKAG-----FYEKPIATLDFAS	SLYPS	596
tr A0A6P5I296 A0A6P5I296_PHACI	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	643
sp P52431 DP0D1_MOUSE	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	607
sp O54747 DP0D1_RAT	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	605
tr G3V8M1 G3V8M1_RAT	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	605
tr A0A1S3A927 A0A1S3A927_ERIEU	NVKAEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr H0V251 H0V251_CAVEO	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	607
tr A0A6I9JZ04 A0A6I9JZ04_CHRAS	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	611
tr A0A7J7SK29 A0A7J7SK29_RHIFE	NVKTEGG--EDYTGATVIEPLKGVRR-----SLTPFPGRYVDVPIATLDFAS	SLYPS	630
sp P28340 DP0D1_HUMAN	NVKSEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr A0A2K6D6G8 A0A2K6D6G8_MACNE	VVRSEGG--EDYTGATVIEPLKGLGAVCTSW---TPRRGAPCRYVDVPIATLDFAS	SLYPS	626
tr A0A0A0MW23 A0A0A0MW23_PAPAN	VVRSEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr A0A452F6S3 A0A452F6S3_CAPHI	HTWVFP---SFFPGAAD---ARGEDDGT-----AEGAGQGYVDVPIATLDFAS	SLYPS	617
tr A0A6P7EPG1 A0A6P7EPG1_SHEEP	VVKT-----EGGE-----DYTGA-----TVIEPLKGYVDVPIATLDFAS	SLYPS	608
sp P28339 DP0D1_BOVIN	VVKT-----EGGE-----DYTGA-----TVIEPLKGYVDVPIATLDFAS	SLYPS	608
tr E1BNZ6 E1BNZ6_BOVIN	VVKT-----EGGE-----DYTGA-----TVIEPLKGYVDVPIATLDFAS	SLYPS	608
tr A0A383ZY66 A0A383ZY66_BALAS	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr A0A2Y9P989 A0A2Y9P989_DELLE	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr F7DXU3 F7DXU3_HORSE	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr A0A5G2QET9 A0A5G2QET9_PIG	NVKTEGG--EDYTGATVIEPLKGLDGAAGAVAGLPVLTPTPRARYVDVPIATLDFAS	SLYPS	629
tr A0A6J1XK42 A0A6J1XK42_ACIBJ	NVKTEGV--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr M3VUJ4 M3VUJ4_FELCA	NVKTEGV--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr E2R5W5 E2R5W5_CANLF	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr G1M3J7 G1M3J7_AILME	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr A0A2U3ZRE1 A0A2U3ZRE1_ODORO	NVKTEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	609
tr A0A6J2WZ6 A0A6J2WZ6_CHACN	NVKTEGG--EDYTGATVIEPEKG-----YVDVPIATLDFAS	SLYPS	613
tr Q2KNE0 Q2KNE0_DANRE	NVKTEGG--EDYTGATVIEPEKG-----YVDVPIATLDFAS	SLYPS	613
tr A0A6P6JVN6 A0A6P6JVN6_CARAU	NVKTEGG--EDYTGATVIEPEKG-----YVDVPIATLDFAS	SLYPS	613
tr A0A6P6JG77 A0A6P6JG77_CARAU	NVKTEGG--EDYTGATVIEPEKG-----YVDVPIATLDFAS	SLYPS	613
tr A0A673JFI3 A0A673JFI3_9TELE	NVKTEGG--EDYTGATVIEPEKG-----YVDVPIATLDFAS	SLYPS	613
tr A0A498LX53 A0A498LX53_LABRO	NVKTEGG--EDYTGATVIEPEKG-----YVDVPIATLDFAS	SLYPS	608
tr COHA77 COHA77_SALSA	NVKPEGG--EDYTGATVIEPEKG-----YVDVPIATLDFAS	SLYPS	613
tr A0A6P7IUM6 A0A6P7IUM6_9TELE	NVKSQGG--EDYTGATVIEPEKG-----YVDVPIATLDFAS	SLYPS	612
tr A0A3Q3E049 A0A3Q3E049_HIPCM	NVKSQGG--EDYTGATVIEPEKG-----YVDVPIATLDFAS	SLYPS	613
tr A0A4W3I8L4 A0A4W3I8L4_CALMI	IVLAI DA--IDYCPWKT I--RPS-----YVDVPIATLDFAS	SLYPS	614
tr D0VEW7 D0VEW7_XENLA	VVRSEGG--EDYTGATVIEPLK-----YVDVPIATLDFAS	SLYPS	613
tr A0A6J1U352 A0A6J1U352_9SAUR	NVKTEGG--EDYAGATVIEPLK-----YVDVPIATLDFAS	SLYPS	616
tr A0A6I9XX64 A0A6I9XX64_9SAUR	NVKTEGG--EDYAGATVIEPLK-----YVDVPIATLDFAS	SLYPS	619
	::: **::****: *****		
sp Q9LVN7 DP0D1_ARATH	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		667
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		662
tr A0A397Z0B4 A0A397Z0B4_BRACM	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		662
tr A0A0781Z2E A0A0781Z2E_BRANA	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		662
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	IMMAHNLCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		662
tr A0A287NEC0 A0A287NEC0_HORVV	IMMAHNLCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		693
tr A0A6G1C319 A0A6G1C319_9ORYZ	IMMAHNLCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		673
sp Q9LRE6 DP0D1_ORYSJ	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		675
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		659
tr A0A5J9USA3 A0A5J9USA3_9POAL	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		670
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		673
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		673
tr K3ZGZ6 K3ZGZ6_SETIT	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		675
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		662
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		657
tr A0A200Q8R4 A0A200Q8R4_9MAGN	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		623
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		660
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		660
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		656
tr A0A5E4GBB6 A0A5E4GBB6_PRUDU	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		656
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	IMMAYNLCYCTLVPEPDRKLNLPPEHVNKTPSGETFVKQTLQKGLIPEILEELLTARKR		656
tr A0A6P5I296 A0A6P5I296_PHACI	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		703
sp P52431 DP0D1_MOUSE	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		667
sp O54747 DP0D1_RAT	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		665
tr G3V8M1 G3V8M1_RAT	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		665
tr A0A1S3A927 A0A1S3A927_ERIEU	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		669
tr H0V251 H0V251_CAVEO	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		667
tr A0A6I9JZ04 A0A6I9JZ04_CHRAS	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		671
tr A0A7J7SK29 A0A7J7SK29_RHIFE	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		690
sp P28340 DP0D1_HUMAN	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		669
tr A0A2K6D6G8 A0A2K6D6G8_MACNE	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		686
tr A0A0A0MW23 A0A0A0MW23_PAPAN	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		669
tr A0A452F6S3 A0A452F6S3_CAPHI	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		677
tr A0A6P7EPG1 A0A6P7EPG1_SHEEP	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		668
sp P28339 DP0D1_BOVIN	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		668
tr E1BNZ6 E1BNZ6_BOVIN	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		668
tr A0A383ZY66 A0A383ZY66_BALAS	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		669
tr A0A2Y9P989 A0A2Y9P989_DELLE	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		667
tr F7DXU3 F7DXU3_HORSE	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		669
tr A0A5G2QET9 A0A5G2QET9_PIG	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		689
tr A0A6J1XK42 A0A6J1XK42_ACIBJ	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		669
tr M3VUJ4 M3VUJ4_FELCA	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		669
tr E2R5W5 E2R5W5_CANLF	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		669
tr G1M3J7 G1M3J7_AILME	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		669
tr A0A2U3ZRE1 A0A2U3ZRE1_ODORO	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		669
tr A0A6J2WZ6 A0A6J2WZ6_CHACN	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		673
tr Q2KNE0 Q2KNE0_DANRE	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		673
tr A0A6P6JVN6 A0A6P6JVN6_CARAU	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		673
tr A0A6P6JG77 A0A6P6JG77_CARAU	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		673
tr A0A673JFI3 A0A673JFI3_9TELE	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		673
tr A0A498LX53 A0A498LX53_LABRO	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		668
tr COHA77 COHA77_SALSA	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		673
tr A0A6P7IUM6 A0A6P7IUM6_9TELE	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		673
tr A0A3Q3E049 A0A3Q3E049_HIPCM	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		673
tr A0A4W3I8L4 A0A4W3I8L4_CALMI	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		673
tr D0VEW7 D0VEW7_XENLA	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		674
tr A0A6J1U352 A0A6J1U352_9SAUR	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		676
tr A0A6I9XX64 A0A6I9XX64_9SAUR	IMMAHNLCTVTLRPGAAQKLGLEDQFIKPTGDEFVKT SVRKGGLLPQILENLLSARKR		679
	****:***: **:		

sp Q9LVN7 DPOD1_ARATH	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	727
tr AOA3P6BBX0 AOA3P6BBX0_BRAOL	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	722
tr AOA39720B4 AOA39720B4_BRACM	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	722
tr AOA07812E2 AOA07812E2_BRANA	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	722
tr AOA3B6JHK9 AOA3B6JHK9_WHEAT	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	733
tr AOA287NEC0 AOA287NEC0_HORVV	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	753
tr AOA6G1C319 AOA6G1C319_9ORYZ	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	719
sp Q9LRE6 DPOD1_ORYSJ	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	735
tr AOA0E0MDA8 AOA0E0MDA8_ORYPU	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	719
tr AOA5J9USA3 AOA5J9USA3_9POAL	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	730
tr AOA1D6QLT8 AOA1D6QLT8_MAIZE	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	733
tr AOA2S3ICY2 AOA2S3ICY2_9POAL	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	733
tr K3ZGZ6 K3ZGZ6_SEITIT	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	735
tr AOA2P2KV69 AOA2P2KV69_RHIMU	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	722
tr AOA7J7DZR4 AOA7J7DZR4_TRIWF	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	717
tr AOA200Q8R4 AOA200Q8R4_9MAGN	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	683
tr AOA2P6RSP9 AOA2P6RSP9_ROSCH	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	720
tr AOA2I4F7Z3 AOA2I4F7Z3_JUGRE	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	717
tr AOA6J5U1U4 AOA6J5U1U4_PRUAR	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	716
tr AOA5E4GBB6 AOA5E4GBB6_PRUDU	AKADLKEAKDPLEKAVLDGRLALKIKSANSVYGF	GTGATVGGQLF	CLEISSSVTSYGRQMT	716
tr AOA6P5I1M3 AOA6P5I1M3_PRUAV	AKAELARETDPFLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	716
tr AOA6P5I1Z96 AOA6P5I1Z96_PHACT	AKAELARETDPFLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	763
sp P52431 DPOD1_MOUSE	AKAELAQETDPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	727
sp O54747 DPOD1_RAT	AKAELAQETDPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	725
tr G3V8M1 G3V8M1_RAT	AKAELAQETDPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	725
tr AOA1S3A927 AOA1S3A927_ERIEU	AKAELAQETDPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr HOV251 HOV251_CAVPO	AKAELAQETDPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	727
tr AOA6I9JZ04 AOA6I9JZ04_CHRAS	AKAELAQETDPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	731
tr AOA7J7SK29 AOA7J7SK29_RHIFE	AKAELAQETDPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	750
sp P28340 DPOD1_HUMAN	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr AOA2K6D6G8 AOA2K6D6G8_MACNE	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	746
tr AOA0A0MW23 AOA0A0MW23_PAPAN	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr AOA452F6S3 AOA452F6S3_CAPHI	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	737
tr AOA6P7EPG1 AOA6P7EPG1_SHEEP	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	728
sp P28339 DPOD1_BOVIN	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	728
tr E1BNZ6 E1BNZ6_BOVIN	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	728
tr AOA383ZY66 AOA383ZY66_BALAS	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr AOA2Y9P989 AOA2Y9P989_DELLE	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr F7DXU3 F7DXU3_HORSE	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr AOA5G2QET9 AOA5G2QET9_PIG	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	749
tr AOA6J1XK42 AOA6J1XK42_ACIBJ	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr M3VUJ4 M3VUJ4_FELCA	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr E2R5W5 E2R5W5_CANLF	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr G1M3J7 G1M3J7_ODORO	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr AOA2U3ZRE1 AOA2U3ZRE1_ODORO	AKAELAKE'DPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	729
tr AOA6J2WZ6 AOA6J2WZ6_CHACN	AKAELKKE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	733
tr Q2KNE0 Q2KNE0_DANRE	AKAELKKE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	733
tr AOA6P6JVN6 AOA6P6JVN6_CARAU	AKAELKKE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	733
tr AOA6P6JG77 AOA6P6JG77_CARAU	AKAELKKE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	733
tr AOA673JF13 AOA673JF13_9TELE	AKAELKKE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	733
tr AOA498LX53 AOA498LX53_LABRO	AKAELKKE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	728
tr COHA77 COHA77_SALSA	AKAELKNE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	733
tr AOA6P7IUM6 AOA6P7IUM6_9TELE	AKAELKKE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	733
tr AOA3Q3E049 AOA3Q3E049_HIPCM	AKAELKKE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	732
tr AOA4W3I8L4 AOA4W3I8L4_CALMI	AKTELKNE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	734
tr DOVEW7 DOVEW7_XENLA	AKTELKNE'DPFFKQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	733
tr AOA6J1U352 AOA6J1U352_9SAUR	AKLELQETDPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	736
tr AOA6I9XX64 AOA6I9XX64_9SAUR	AKLELQETDPLRRQVLDGRLALKIKSANSVYGF	GTGAQVQKLE	CLEISSSVTGFGRQMT	739

sp Q9LVN7 DPOD1_ARATH	QTKKLVEDKFTTLGGYEHNAEVI	YGD	TD	SVMVQF	GVSV	VEAAMN	LGREAA	EHI	ISGFT	FKP	787				
tr AOA3P6BBX0 AOA3P6BBX0_BRAOL	QTKKLVEDKFTTLGGYEHNAEVI	YGD	TD	SVMVQF	GVSD	VEAAMT	LGREAA	EYI	ISGFT	FKP	782				
tr AOA39720B4 AOA39720B4_BRACM	QTKKLVEDKFTTLGGYEHNAEVI	YGD	TD	SVMVQF	GVSD	VEAAMT	LGREAA	EYI	ISGFT	FKP	782				
tr AOA07812E2 AOA07812E2_BRANA	QTKKLVEDKFTTLGGYEHNAEVI	YGD	TD	SVMVQF	GVSD	VEAAMT	LGREAA	EYI	ISGFT	FKP	782				
tr AOA3B6JHK9 AOA3B6JHK9_WHEAT	QTKKLVEDKFTTLGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	793				
tr AOA287NEC0 AOA287NEC0_HORVV	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	813				
tr AOA6G1C319 AOA6G1C319_9ORYZ	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	779				
sp Q9LRE6 DPOD1_ORYSJ	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	795				
tr AOA0E0MDA8 AOA0E0MDA8_ORYPU	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	779				
tr AOA5J9USA3 AOA5J9USA3_9POAL	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	790				
tr AOA1D6QLT8 AOA1D6QLT8_MAIZE	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	793				
tr AOA2S3ICY2 AOA2S3ICY2_9POAL	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	793				
tr K3ZGZ6 K3ZGZ6_SEITIT	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	795				
tr AOA2P2KV69 AOA2P2KV69_RHIMU	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	782				
tr AOA7J7DZR4 AOA7J7DZR4_TRIWF	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	777				
tr AOA200Q8R4 AOA200Q8R4_9MAGN	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	743				
tr AOA2P6RSP9 AOA2P6RSP9_ROSCH	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	777				
tr AOA2I4F7Z3 AOA2I4F7Z3_JUGRE	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	780				
tr AOA6J5U1U4 AOA6J5U1U4_PRUAR	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	776				
tr AOA5E4GBB6 AOA5E4GBB6_PRUDU	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	776				
tr AOA6P5I1M3 AOA6P5I1M3_PRUAV	HTKKLVEDKFTTLVGGYEHNAEVI	YGD	TD	SVMVQF	GVST	VEDAMK	LGREAA	EYI	ISGFT	FKP	776				
tr AOA6P5I1Z96 AOA6P5I1Z96_PHACT	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	823				
sp P52431 DPOD1_MOUSE	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	787				
sp O54747 DPOD1_RAT	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	785				
tr G3V8M1 G3V8M1_RAT	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	785				
tr AOA1S3A927 AOA1S3A927_ERIEU	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr HOV251 HOV251_CAVPO	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	787				
tr AOA6I9JZ04 AOA6I9JZ04_CHRAS	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	791				
tr AOA7J7SK29 AOA7J7SK29_RHIFE	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	810				
sp P28340 DPOD1_HUMAN	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr AOA2K6D6G8 AOA2K6D6G8_MACNE	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	806				
tr AOA0A0MW23 AOA0A0MW23_PAPAN	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr AOA452F6S3 AOA452F6S3_CAPHI	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	797				
tr AOA6P7EPG1 AOA6P7EPG1_SHEEP	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	788				
sp P28339 DPOD1_BOVIN	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	788				
tr E1BNZ6 E1BNZ6_BOVIN	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr AOA383ZY66 AOA383ZY66_BALAS	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	788				
tr AOA2Y9P989 AOA2Y9P989_DELLE	RTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr F7DXU3 F7DXU3_HORSE	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr AOA5G2QET9 AOA5G2QET9_PIG	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr AOA6J1XK42 AOA6J1XK42_ACIBJ	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	809				
tr M3VUJ4 M3VUJ4_FELCA	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr E2R5W5 E2R5W5_CANLF	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr G1M3J7 G1M3J7_ODORO	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr AOA2U3ZRE1 AOA2U3ZRE1_ODORO	KTKQLVESKYTVBNGYTSARVV	YGD	TD	SVMCRF	GVSS	VAEAMN	LGREAA	DW	SGHF	FPP	789				
tr AOA6J2WZ6 AOA6J2WZ6_CHACN	QTKQLVESRYTISNGYQADAKVI	YGD	TD	SVMVKL	GVAT	VQEA	AMN	LGK	EA	AW	VS	SH	F	VP	793
tr Q2KNE0 Q2KNE0_DANRE	QTKQLVESRYTISNGYQADAKVI	YGD	TD	SVMVKL	GVAT	VQEA	AMN	LGK	EA	AW	VS	SH	F	VP	793
tr AOA6P6JVN6 AOA6P6JVN6_CARAU	QTKQLVESRYTISNGYQADAKVI	YGD	TD	SVMVKL	GVAT	VQEA	AMN	LGK	EA	AW	VS	SH	F	VP	793
tr AOA6P6JG77 AOA6P6JG77_CARAU	QTKQLVESRYTISNGYQADAKVI	YGD	TD	SVMVKL											

sp Q9LVN7 DP0D1_ARATH	KILIDRDVPGAENVKKTISDLLMNRDLSLLVITKGLTKTGDDYEVKSAHGELAERMRRK	906
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	KILIDRDVQGAAYEVKNTIADLLMNRDLSLLVITKGLTKTGDDYEVKSAHGELAERMRRK	901
tr A0A39720B4 A0A39720B4_BRACM	KILIDRDVQGAAYEVKNTIADLLMNRDLSLLVITKGLTKTGDDYEVKSAHGELAERMRRK	901
tr A0A07812E2 A0A07812E2_BRANA	KILIDRDVQGAAYEVKNTIADLLMNRDLSLLVITKGLTKTGDDYEVKSAHGELAERMRRK	901
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	912
tr A0A287N9C0 A0A287N9C0_HORVV	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	932
tr A0A6G1C319 A0A6G1C319_9ORYZ	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	898
sp Q9LRE6 DP0D1_ORYSJ	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	914
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	909
tr A0A5J9USA3 A0A5J9USA3_9POAL	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	912
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	912
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	912
tr K3ZGZ6 K3ZGZ6_SEITIT	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	914
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	901
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	862
tr A0A200Q8R4 A0A200Q8R4_9MAGN	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	896
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	899
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	896
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	895
tr A0A5E4GBB6 A0A5E4GBB6_PRUUD	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	895
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	KILIDRDVPGAQVYVYKNTISDLLMNRDLSLLVITKGLTKTGDDYAVKAAHVLAERMRRK	895
tr A0A6P5I296 A0A6P5I296_PHACI	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	943
sp P52431 DP0D1_MOUSE	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	907
tr O54747 DP0D1_RAT	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	905
tr G3V8M1 G3V8M1_RAT	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	905
tr A0A1S3A927 A0A1S3A927_ERIEU	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	909
tr H0V251 H0V251_CAVPO	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	907
tr A0A6I9J204 A0A6I9J204_CHRAS	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	911
tr A0A7J7SK29 A0A7J7SK29_RHIFE	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	930
sp P28340 DP0D1_HUMAN	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	906
tr A0A2K6D6G8 A0A2K6D6G8_MACNE	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	929
tr A0A0A0MW23 A0A0A0MW23_PAPAN	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	907
tr A0A452F6S3 A0A452F6S3_CAPHI	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	919
tr A0A6P7EPG1 A0A6P7EPG1_SHEEP	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	908
sp P28339 DP0D1_BOVIN	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	908
tr E1BNZ6 E1BNZ6_BOVIN	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	908
tr A0A383ZY66 A0A383ZY66_BALAS	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	909
tr A0A2Y9P989 A0A2Y9P989_DELLE	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	909
tr F7DXU3 F7DXU3_HORSE	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	909
tr A0A5G2QET9 A0A5G2QET9_PIG	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	929
tr A0A6J1XK42 A0A6J1XK42_ACIBJ	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	909
tr M3VUJ4 M3VUJ4_FELCA	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	909
tr E2R5W5 E2R5W5_CANLF	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	909
tr G1M3J7 G1M3J7_AILME	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	909
tr A0A2U3ZRE1 A0A2U3ZRE1_ODORO	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	909
tr A0A6J2WZ6 A0A6J2WZ6_CHACN	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	913
tr Q2KNE0 Q2KNE0_DANRE	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	913
tr A0A6P6JVN6 A0A6P6JVN6_CARAU	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	913
tr A0A6P6JG77 A0A6P6JG77_CARAU	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	913
tr A0A673JF13 A0A673JF13_9TELE	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	913
tr A0A498LX53 A0A498LX53_LABRO	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	908
tr COHA77 COHA77_SALSA	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	913
tr A0A6P7IUM6 A0A6P7IUM6_9TELE	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	912
tr A0A3Q3E049 A0A3Q3E049_HIPCM	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	913
tr A0A4W3I8L4 A0A4W3I8L4_CALMI	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	914
tr D0VEW7 D0VEW7_XENLA	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	913
tr A0A6J1U352 A0A6J1U352_9SAUR	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	916
tr A0A6I9XX64 A0A6I9XX64_9SAUR	RLLIDRDVPSGVAHAQDVISDLLCNRDISQLVITKELTRAAADYAGKQAHVLAERMRRK	919

sp Q9LVN7 DP0D1_ARATH	IKLEFEKVFYFVYLLINPKRYAGLLWT-NPQKFDKMDTKGIETVRRDNCPLVKNLVTESLN	846
tr A0A3P6BBX0 A0A3P6BBX0_BRAOL	IKLEFEKVFYFVYLLINPKRYAGLLWT-NPQKFDKMDTKGIETVRRDNCPLVKNLVTESLN	841
tr A0A39720B4 A0A39720B4_BRACM	IKLEFEKVFYFVYLLINPKRYAGLLWT-NPQKFDKMDTKGIETVRRDNCPLVKNLVTESLN	841
tr A0A07812E2 A0A07812E2_BRANA	IKLEFEKVFYFVYLLINPKRYAGLLWT-NPQKFDKMDTKGIETVRRDNCPLVKNLVTESLN	841
tr A0A3B6JHK9 A0A3B6JHK9_WHEAT	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	852
tr A0A287N9C0 A0A287N9C0_HORVV	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	872
tr A0A6G1C319 A0A6G1C319_9ORYZ	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	852
sp Q9LRE6 DP0D1_ORYSJ	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	854
tr A0A0E0MDA8 A0A0E0MDA8_ORYPU	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	838
tr A0A5J9USA3 A0A5J9USA3_9POAL	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	849
tr A0A1D6QLT8 A0A1D6QLT8_MAIZE	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	852
tr A0A2S3ICY2 A0A2S3ICY2_9POAL	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	854
tr K3ZGZ6 K3ZGZ6_SEITIT	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	852
tr A0A2P2KVG9 A0A2P2KVG9_RHIMU	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	841
tr A0A7J7DZR4 A0A7J7DZR4_TRIWF	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	836
tr A0A200Q8R4 A0A200Q8R4_9MAGN	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	802
tr A0A2P6RSP9 A0A2P6RSP9_ROSCH	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	839
tr A0A2I4F7Z3 A0A2I4F7Z3_JUGRE	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	836
tr A0A6J5U1U4 A0A6J5U1U4_PRUAR	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	835
tr A0A5E4GBB6 A0A5E4GBB6_PRUUD	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	835
tr A0A6P5S1M3 A0A6P5S1M3_PRUAV	IKLEFEKVFYFVYLLISKKRYAGLLWT-NPEKFDKMDTKGIETVRRDNCPLVKNLVTECLH	835
tr A0A6P5I296 A0A6P5I296_PHACI	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	883
sp P52431 DP0D1_MOUSE	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	847
tr O54747 DP0D1_RAT	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	845
tr G3V8M1 G3V8M1_RAT	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	845
tr A0A1S3A927 A0A1S3A927_ERIEU	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr H0V251 H0V251_CAVPO	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	847
tr A0A6I9J204 A0A6I9J204_CHRAS	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	851
tr A0A7J7SK29 A0A7J7SK29_RHIFE	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	870
sp P28340 DP0D1_HUMAN	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr A0A2K6D6G8 A0A2K6D6G8_MACNE	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	866
tr A0A0A0MW23 A0A0A0MW23_PAPAN	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr A0A452F6S3 A0A452F6S3_CAPHI	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	857
tr A0A6P7EPG1 A0A6P7EPG1_SHEEP	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	848
sp P28339 DP0D1_BOVIN	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	848
tr E1BNZ6 E1BNZ6_BOVIN	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	848
tr A0A383ZY66 A0A383ZY66_BALAS	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr A0A2Y9P989 A0A2Y9P989_DELLE	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr F7DXU3 F7DXU3_HORSE	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr A0A5G2QET9 A0A5G2QET9_PIG	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	869
tr A0A6J1XK42 A0A6J1XK42_ACIBJ	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr M3VUJ4 M3VUJ4_FELCA	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr E2R5W5 E2R5W5_CANLF	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr G1M3J7 G1M3J7_AILME	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr A0A2U3ZRE1 A0A2U3ZRE1_ODORO	IRLEFEKVFYFVYLLISKKRYAGLLPSSRSDAHDRMDCKGLEAVRRDNCPLVANLVTSASLR	849
tr A0A6J2WZ6 A0A6J2WZ6_CHACN	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	853
tr Q2KNE0 Q2KNE0_DANRE	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	853
tr A0A6P6JVN6 A0A6P6JVN6_CARAU	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	853
tr A0A6P6JG77 A0A6P6JG77_CARAU	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	853
tr A0A673JF13 A0A673JF13_9TELE	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	853
tr A0A498LX53 A0A498LX53_LABRO	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	848
tr COHA77 COHA77_SALSA	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	853
tr A0A6P7IUM6 A0A6P7IUM6_9TELE	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	852
tr A0A3Q3E049 A0A3Q3E049_HIPCM	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	853
tr A0A4W3I8L4 A0A4W3I8L4_CALMI	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	854
tr D0VEW7 D0VEW7_XENLA	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	853
tr A0A6J1U352 A0A6J1U352_9SAUR	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	856
tr A0A6I9XX64 A0A6I9XX64_9SAUR	IKLEFEKVFYFVYLLINPKRYAGLLPSSAEBHDKMDTKGIETVRRDNCPLVANLVTSASLR	859

sp	Q9LVN7 DP0D1_ARATH	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	Pol	CTD	966
tr	AOA3P6BBX0	AOA3P6BBX0	BRAOL	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	961
tr	AOA39750B4	AOA39750B4	BRACM	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	961
tr	AOA07812E2	AOA07812E2	BRANA	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	961
tr	AOA3B67HK9	AOA3B67HK9	WHEAT	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	972
tr	AOA287NECO	AOA287NECO	HORVV	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	992
tr	AOA6G1C319	AOA6G1C319	9ORYZ	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	958
sp	Q9LRE6 DP0D1_ORYSJ	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	Pol	CTD	974
tr	AOA0E0MDA8	AOA0E0MDA8	ORYPU	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	958
tr	AOA5J9USA3	AOA5J9USA3	9FOAL	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	969
tr	AOA1D6QLT8	AOA1D6QLT8	MAI5E	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	972
tr	AOA2S3ICY2	AOA2S3ICY2	9POAL	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	972
tr	K3ZGZ6	K3ZGZ6	SETIT	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	974
tr	AOA2P2KVG9	AOA2P2KVG9	RHIMU	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	961
tr	AOA7J7D8R4	AOA7J7D8R4	TRIFW	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	956
tr	AOA200Q8R4	AOA200Q8R4	9MAGN	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	922
tr	AOA2P6RSP9	AOA2P6RSP9	ROSCH	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	959
tr	AOA2I4F7Z3	AOA2I4F7Z3	JUGRE	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	956
tr	AOA6J5U1U4	AOA6J5U1U4	PRUAR	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	955
tr	AOA5E4GBB6	AOA5E4GBB6	PRUDU	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	955
tr	AOA6P5S1M3	AOA6P5S1M3	PRUAV	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	955
tr	AOA6P5I296	AOA6P5I296	_PHACI	RDAATAPNVGDRVFPVVI IKAAKGAKAYE	SESDP	YVVLQNNI	PIDP	PKYYL	ENQISK	1003
sp	F52431 DP0D1_MOUSE	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	967			
sp	O54747 DF0D1_RAT	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	965			
tr	G3V8M1 G3V8M1_RAT	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	965			
tr	AOA1S3A927	AOA1S3A927	_ERIEU	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969	
tr	H0V251 H0V251_CAVPO	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	967			
tr	AOA6I9J204	AOA6I9J204	_CHRAS	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	971	
tr	AOA7J78K29	AOA7J78K29	_RHIFE	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	960	
sp	F28340 DP0D1_HUMAN	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969			
tr	AOA2K6D6G8	AOA2K6D6G8	_MACNE	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	966	
tr	AOA0A0MW23	AOA0A0MW23	_PAPAN	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969	
tr	AOA452P683	AOA452P683	_CAPHI	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	977	
tr	AOA6P7EPG1	AOA6P7EPG1	_SHEEP	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	968	
sp	F28339 DP0D1_BOVIN	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	968			
tr	E1BN26 E1BN26_BOVIN	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	968			
tr	AOA382Y66	AOA382Y66	_BALAS	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969	
tr	AOA2Y9P989	AOA2Y9P989	_DELLE	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969	
tr	F7DXU3 F7DXU3_HORSE	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969			
tr	AOA5G2QBT9	AOA5G2QBT9	_FIG	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969	
tr	AOA6J1XK42	AOA6J1XK42	_ACIJB	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969	
tr	M3VUJ4 M3VUJ4_FELCA	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969			
tr	E2RSW5 E2RSW5_CANLF	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969			
tr	G1M3J7 G1M3J7_AILME	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969			
tr	AOA2U32RE1	AOA2U32RE1	_ODORO	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	969	
tr	AOA6J2WZ6	AOA6J2WZ6	_CHACN	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	973	
tr	Q2KNE0 Q2KNE0_DANRE	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	973			
tr	AOA6P6JVN6	AOA6P6JVN6	_CARAU	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	973	
tr	AOA6P6JG77	AOA6P6JG77	_CARAU	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	973	
tr	AOA673JF13	AOA673JF13	_STELE	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	973	
tr	AOA498LX53	AOA498LX53	_LABRO	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	968	
tr	COHA77 COHA77_SALSA	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	973			
tr	AOA6P7IUM6	AOA6P7IUM6	_STELE	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	972	
tr	AOA3Q2D49	AOA3Q2D49	_HIPCM	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	974	
tr	AOA4W2I8L4	AOA4W2I8L4	_CALMI	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	974	
tr	DOVEW7 DOVEW7_KENLA	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	973			
tr	AOA6J1U352	AOA6J1U352	_9SAUR	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	976	
tr	AOA6I9XX64	AOA6I9XX64	_9SAUR	RDFGSAFSLGDRVFPVVI IGAAGVAAVMKSE	DFLVLEHSLP	IDTQYVLE	QQQLAK	FLMRI	979	

sp	Q9LVN7 DP0D1_ARATH	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	PIP	1022	
tr	AOA3P6BBX0	AOA3P6BBX0	BRAOL	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1017
tr	AOA39750B4	AOA39750B4	BRACM	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1017
tr	AOA07812E2	AOA07812E2	BRANA	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1017
tr	AOA3B67HK9	AOA3B67HK9	WHEAT	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1030
tr	AOA287NECO	AOA287NECO	HORVV	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1050
tr	AOA6G1C319	AOA6G1C319	9ORYZ	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1016
sp	Q9LRE6 DP0D1_ORYSJ	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	PIP	1032	
tr	AOA0E0MDA8	AOA0E0MDA8	ORYPU	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1016
tr	AOA5J9USA3	AOA5J9USA3	9FOAL	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1027
tr	AOA1D6QLT8	AOA1D6QLT8	MAI5E	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1030
tr	AOA2S3ICY2	AOA2S3ICY2	9POAL	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1030
tr	K3ZGZ6	K3ZGZ6	SETIT	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1032
tr	AOA2P2KVG9	AOA2P2KVG9	RHIMU	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1019
tr	AOA7J7D8R4	AOA7J7D8R4	TRIFW	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1014
tr	AOA200Q8R4	AOA200Q8R4	9MAGN	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	980
tr	AOA2P6RSP9	AOA2P6RSP9	ROSCH	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1017
tr	AOA2I4F7Z3	AOA2I4F7Z3	JUGRE	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1014
tr	AOA6J5U1U4	AOA6J5U1U4	PRUAR	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1013
tr	AOA5E4GBB6	AOA5E4GBB6	PRUDU	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1013
tr	AOA6P5S1M3	AOA6P5S1M3	PRUAV	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1013
tr	AOA6P5I296	AOA6P5I296	_PHACI	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1062
sp	F52431 DP0D1_MOUSE	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	PIP	1026	
sp	O54747 DF0D1_RAT	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	PIP	1024	
tr	G3V8M1 G3V8M1_RAT	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	PIP	1024	
tr	AOA1S3A927	AOA1S3A927	_ERIEU	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1028
tr	H0V251 H0V251_CAVPO	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	PIP	1026	
tr	AOA6I9J204	AOA6I9J204	_CHRAS	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1030
tr	AOA7J78K29	AOA7J78K29	_RHIFE	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1028
sp	F28340 DP0D1_HUMAN	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	PIP	1048	
tr	AOA2K6D6G8	AOA2K6D6G8	_MACNE	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1028
tr	AOA0A0MW23	AOA0A0MW23	_PAPAN	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1036
tr	AOA452P683	AOA452P683	_CAPHI	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1027
tr	AOA6P7EPG1	AOA6P7EPG1	_SHEEP	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1027
sp	F28339 DP0D1_BOVIN	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	PIP	1027	
tr	E1BN26 E1BN26_BOVIN	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	PIP	1027	
tr	AOA382Y66	AOA382Y66	_BALAS	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1028
tr	AOA2Y9P989	AOA2Y9P989	_DELLE	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1028
tr	F7DXU3 F7DXU3_HORSE	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	PIP	1028	
tr	AOA5G2QBT9	AOA5G2QBT9	_FIG	FEPVLKNA--SSELLHGSHTRS	ISITPSN	SGIMKFAKKQLS	CVGCKVPI	SN--GTL	CAAS	1048

δ Polymerase from Plant Sources

Q9LVN7|DPOD1_ARATH DNA polymerase, *Arabidopsis thaliana*
A0A3P6BBX0_BRAOL DNA polymerase, *Brassica oleracea*
A0A397Z0B4_BRACM DNA polymerase, *Brassica campestris*
A0A078I2E2_BRANA DNA polymerase, *Brassica napus*
A0A287NEC0_HORVV DNA polymerase, *Hordeum vulgare* subsp. *Vulgare*
A0A3B6JHK9_WHEAT DNA polymerase, *Triticum aestivum*
A0A6G1C319_9ORYZ DNA polymerase, *Oryza meyeriana* var. *granulate*
Q9LRE6|DPOD1_ORYSJ DNA polymerase, *Oryza sativa* subsp. *Japonica*
A0A0E0MDA8_ORYPU DNA polymerase, *Oryza punctata*
A0A5J9USA3_9POAL DNA polymerase, *Eragrostis curvula*
A0A1D6QLT8_MAIZE DNA polymerase, *Zea mays*
A0A2S3ICY2_9POAL DNA polymerase, *Panicum hallii*
K3ZGZ6_SETIT DNA polymerase, *Setaria italica*
A0A2P2KVG9_RHIMU DNA polymerase, *Rhizophora mucronata* (mangrove)
A0A7J7DZR4_TRIWF DNA polymerase, *Tripterygium wilfordii*
A0A200Q8R4_9MAGN DNA polymerase, *Macleaya cordata*
A0A2P6RSP9_ROSCH DNA polymerase, *Rosa chinensis*
A0A2I4F7Z3_JUGRE DNA polymerase, *Juglans regia*
A0A6J5U1U4_PRUAR DNA polymerase, *Prunus armeniaca*
A0A5E4G6B6_PRUDU DNA polymerase, *Prunus dulcis*
A0A6P5S1M3_PRUAV DNA polymerase, *Prunus avium*

δ Polymerase from Animal Sources

A0A6P5IZ96_PHACI DNA polymerase, *Phascolarctos cinereus* (koala bear)
P52431|DPOD1_MOUSE DNA polymerase, *Mus musculus*
O54747|DPOD1_RAT DNA polymerase, *Rattus norvegicus*
G3V8M1_RAT DNA polymerase, *Rattus norvegicus*
A0A1S3A927_ERIEU DNA polymerase, *Erinaceus europaeus*
H0V251_CAVPO DNA polymerase, *Cavia porcellus*
A0A6I9JZ04_CHRAS DNA polymerase, *Chrysochloris asiatica*
A0A7J7SK29_RHIFE DNA polymerase, *Rhinolophus ferrumequinum*
P28340|DPOD1_HUMAN DNA polymerase, *Homo sapiens*
A0A2K6D6G8_MACNE DNA polymerase, *Macaca nemestrina*
A0A0A0MW23_PAPAN DNA polymerase, *Papio Anubis*
A0A452F6S3_CAPHI DNA polymerase, *Capra hircus*
A0A6P7EPG1_SHEEP DNA polymerase, *Ovis aries*
A0A6P7IUM6_9TELE DNA polymerase, *Parambassis ranga*
P28339|DPOD1_BOVIN DNA polymerase, *Bos Taurus*
E1BNZ6_BOVIN DNA polymerase, *Bos Taurus*
A0A383ZY66_BALAS DNA polymerase, *Balaenoptera acutorostrata scammoni* (Minke Whale)
A0A2Y9P989_DELLE DNA polymerase, *Delphinapterus leucas*
F7DXU3_HORSE DNA polymerase, *Equus caballus*
A0A5G2QET9_PIG DNA polymerase, *Sus scrofa*
A0A6J1U352_9SAUR DNA polymerase, *Notechis scutatus* (Tiger snake)
M3VUJ4_FELCA DNA polymerase, *Felis catus*
E2R5W5_CANLF DNA polymerase, *Canis lupus familiaris*
G1M3J7_AILME DNA polymerase, *Ailuropoda melanoleuca*
A0A2U3ZRE1_ODORO DNA polymerase, *Odobenus rosmarus divergens*
A0A6J2WZW6_CHACN DNA polymerase, *Chanos chanos*
Q2KNE0_DANRE DNA polymerase, *Danio rerio*
A0A6P6JVN6_CARAU DNA polymerase, *Carassius auratus*
A0A6P6JG77_CARAU DNA polymerase, *Carassius auratus*
A0A673JFI3_9TELE DNA polymerase, *Sinocyclocheilus rhinoceros*
A0A498LX53_LABRO DNA polymerase, *Labeo rohita*
C0HA77_SALSA DNA polymerase, *Salmo salar*
A0A3Q3E049_HIPCM DNA polymerase, *Hippocampus comes*
A0A4W3I8L4_CALMI DNA polymerase, *Callorhynchus milii*
D0VEW7_XENLA DNA polymerase, *Xenopus laevis*
A0A6J1U352_9SAUR DNA polymerase, *Notechis scutatus*
A0A6I9XX64_9SAUR DNA polymerase, *Thamnophis sirtalis* (Garter snake)

3.2. Active Site Analyses of the δ DNA Polymerases

The MSA analysis of the DNA-dependent DNA pols (DdDps) from viruses, bacteria, yeasts, higher fungi, plants and animals has shown that the δ pols of eukaryotes are closer to viral and prokaryotic DNA pols in possessing the two characteristic invariant motifs, -SLYPS- and -YGD TDS-. Even though all three eukaryotic replicative pols (pols α , ϵ and δ) are classified under the B-family pols, the pol ϵ differs from others by not possessing the conserved -SLYPS- and -YGD TDS- motifs, suggesting their possible different evolutionary origins. The proposed active site amino acids at the pol and PR domains are shown in Table 1. The template-binding pair (YG), the catalytic basic amino acid (K) and nucleotide selection amino acid (Q) are completely conserved in both the replicative δ pols from plants and animals. The PR 3'→5' exonuclease belongs to the DEDD-superfamily of exonucleases reported from other DNA polymerases as well. The proposed PR exonuclease active site amino acids that are confirmed by SDM experiments are highlighted in dark blue (Table 1).

Table 1 Comparative analysis of the DNA δ pols from yeasts, plants and animals

	Yeasts (<i>S. cerevisiae</i>)	Plants (<i>A. Thaliana</i>)	Animals (Human)
PR exonuclease	-D ³²³ ...E ³²³ ...F ⁴⁰⁷ ...Y ⁵¹⁶ ...D ⁵²⁰ .	-D ^{E314} ...FD ⁴⁵⁴ ...Y ⁵⁰⁷ ...D ⁵¹¹ .	-D ³¹⁶ E ³¹⁸ ...F ⁴⁰² ...Y ⁵¹¹ ...D ⁵¹⁵ .
Pol δ	- ⁶⁸⁸ FKRDVNLNGRQ ⁴ LAL ¹ K ¹ SANSV ^Y GF ⁷¹¹ -	-EKAVLDGRQ ⁴ LAL ¹ K ¹ SANSV ^Y GF ⁷¹¹ -	- ⁶⁸¹ LRRQVLDG ⁶⁸⁵ Q ⁴ LAL ¹ K ¹ V ¹ SANSV ^Y GF ⁷¹¹ -
-YGD TDS- & -SLYPS-	- ⁶¹⁰ N ¹ SLYPS ⁶¹⁶⁻⁸ ₇₅₉ V ¹ YGD TDS ⁷⁶⁶⁻⁸ V ¹	- ⁶⁰² A ¹ SLYPS ⁶⁰⁸⁻⁸ ₇₅₀ V ¹ YGD TDS ⁷⁵⁷⁻⁸ V ¹	- ⁶⁰⁴ S ¹ SLYPS ⁶¹⁰⁻⁸ ₇₅₂ V ¹ YGD TDS ⁷⁵⁹⁻⁸ V ¹

Adapted from Palanivelu [6]. Amino acids, highlighted in dark-blue, are confirmed by SDM analysis.

Pol δ is a versatile PR enzyme. As mentioned earlier, it can correct not only its own errors but also the errors made by the other two replication enzymes, viz. DNA pol α and pol ϵ and thus, ensuring an error-free replication process. The PR active site amino acids of the δ pols, arrived at from MSA analysis by sequence similarity, were also further corroborated by SDM analysis. Simon *et al.*, [16] subjected the D and E of the first conserved triad of the PR active site of pol δ of the yeast enzyme, (i.e.), -D³²¹E³²³- to D³²¹→A/V and E³²³→A and also in the D in the dyad, FD⁴⁰⁷→A by SDM. They found that these mutations drastically reduced the exonuclease activity, suggesting their direct role in the PR function. Importantly, their SDM experiments on the above PR active site amino acids did not affect the pol activity, suggesting that both the domains are well separated. Consistent with the key role played by pol δ in DNA replication, inactivation of pol δ PR function or mutation of critical pol δ residues involved in base selection, resulted in a dramatic increase in replication errors in both yeast and mice enzymes [14 and references therein].

Figures 5A and 5B show the proposed active site of the PR exonucleases from animals and plants. The proposed two-metal ion in the active sites is based on findings of similar active site structure in the 3'→5' exonuclease active site in *E. coli* DNA pol I [17], and such similarities are also extensively analyzed and reported by this author from various sources [18]. The mechanism of Zn-mediated excision of the wrong nucleotide incorporation is explained by Palanivelu [4].

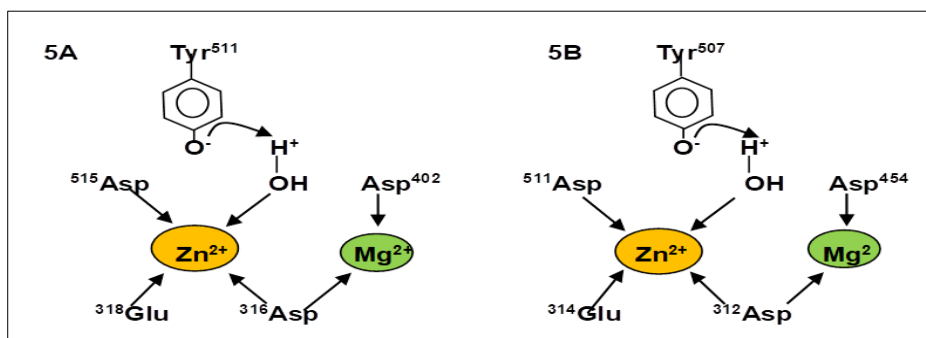


Figure 5 Proposed amino acids at the PR exonuclease active sites of the DNA pols δ from animals, **5A** (from humans) and **5B** from plants, (*A. thaliana*) (numberings are from the humans and *A. thaliana* δ pols).

3.3. The Importance of CysA, CysB and PIP in the Eukaryotic Replicative δ Polymerases

The importance of these three motifs is understood from the analysis of the replicative pols of other eukaryotes as well. All the three eukaryotic replicative pols (pol α , ϵ and δ) invariably possess two of the conserved ZBMs, viz. CysA and CysB, in the CTD of their catalytic subunits and a PIP in the δ pols, suggesting their important role(s) in eukaryotic genome replication. The CysA is the regular ZBM whereas at the CysB, another Zn²⁺ binds and forms the 4Fe-4S cluster.

The importance of these motifs is proved by SDM and X-ray crystallographic analyses. Based on spectroscopic and other experimental data, Jain et al., [19] have shown that the three highly conserved Cys residues (Cys⁶⁶⁵, Cys⁶⁷⁷ and Cys⁷⁶³) of yeast pol ϵ are involved in binding to the Fe-S cluster. This was based on their observation that the wild-type yeast pol ϵ 's catalytic core was found to be yellowish-brown, but the mutant in which all three Cs, (Cys⁶⁶⁵, Cys⁶⁷⁷ and Cys⁷⁶³) were mutated, it became colourless. Besides, they also found that a Cys triple mutant was deficient in the DNA pol activity, but not in the exonuclease activity, suggesting a link between the pol activity and the Fe-S cluster. A similar SDM experiment on pol δ by Netz et al, [20] has shown that the CysB motif was bound to [4Fe-4S] cluster to form an active pol complex. For example, the loss of the [4Fe-4S] cluster by a Cys-ligand mutagenesis in pol δ , destabilized the CTD and abolished interaction with the polD1 and polD2 subunits. This was further confirmed by SDM experiments, where the conversion of the C residues, viz. C¹⁰⁵⁶, C¹⁰⁵⁹, C¹⁰⁶⁹, C¹⁰⁷⁴ (in yeast pol δ) to Ala abolished Fe-S binding [20]. In addition to, a lethal double mutation, C¹⁰⁵⁹→S/C¹⁰⁷⁴→S in CysB of pol δ disrupted binding polD1 and polD2, but in marked contrast, a lethal double mutation of CysA (C¹⁰¹²→S/C¹⁰²⁷→S) did not alter the subunit composition of the pol δ complex, and also did not affect the pol δ interactions in the yeast two-hybrid analysis. These authors have further shown that the Zn-binding CysA motif is required for PCNA-mediated pol δ processivity. The PCNA interactions with PIP enhance the pol δ activity several folds. However, the PIP is found only in the δ pols.

3.4. The Unique -SLYPS- and -YGD TDS- Motifs of δ Polymerases

As discussed elsewhere, the -SLYPS- and -YGD TDS- are the characteristic motifs found only in the replicative pols α and δ . They are implicated in dNTP- and metal-binding, respectively. Interestingly, they are also reported from a large number of DdDps from viruses and bacteria [4,6]. For example, in addition to their presence in the eukaryotic replicative DNA pols α and δ , they are also found in the *E. coli* DNA pol II and in many viral DNA pols like pox viruses (Smallpox, Monkeypox, etc.), Vaccinia, Epstein-Barr virus, Human Cytomegalo virus, Human Herpes Simplex Viruses 1 and 2, Adeno virus 2, *E. coli* phage RB69, *Bacillus subtilis* phage Φ 29, suggesting their possible origin from viruses and prokaryotes. Interestingly, these two motifs are also completely conserved in the δ pol from various plant sources. In contrast, they are not found in the eukaryotic leading-strand synthesis enzyme, the pol ϵ . In fact, the other eukaryotic replicase enzyme, viz. pol ϵ , is closer to the prokaryotic DNA pols I, and DNA pols III (in the catalytic subunit α of the replicases), where they also do not possess these two motifs, strongly suggesting two different origins of the eukaryotic replicative pols. Thus, based on this property, DNA pols maybe broadly classified into two groups, i.e., the one having these two characteristic motifs in them, like prokaryotic DNA pol II, α , δ and ζ pols and the other group which does not possess these two motifs, like pol ϵ , prokaryotic DNA pol I, and DNA pol III (prokaryotic replicases).

SLYPS and YGD TDS motifs' role in dNTP- and metal-binding sites, respectively, has been further confirmed by SDM experiments. The conserved motif -YGD T D¹⁰⁰⁴S- in the catalytic subunit of the human DNA pol α was subjected to SDM analysis. The D¹⁰⁰⁴→N mutation produced a protein with no detectable pol activity while other SDM mutants at that site showed activities from 1 to 20% of the wild-type pol activity [21]. The second conserved motif's (-SLYPS-) involvement in dNTP-binding is also proved by similar SDM experiments using the yeast pol δ . The SDM analysis where L⁶¹²→G in the -SL⁶¹²YPS- motif of yeast pol δ , increased the rates of C-to-A transversion substitutions [22], suggesting its importance in the nucleotide selection process. Furthermore, they also reported that the substitutions at L⁶¹² of *S. cerevisiae* δ pol differentially affect viability, sensitivity to genotoxic agents, cell cycle progression, and replication fidelity.

Moreover, substitution at a residue in the conserved motif A (-SLYPS-) caused mutator phenotypes in eukaryotic DNA pol δ [23]. They have generated mice harbouring an L⁶⁰⁴→G or L⁶⁰⁴→K substitutions in the highly conserved -SL⁶⁰⁴YPS- in the active site of mice δ pol. They found that the homozygous *Pold1*^{L604G/L604G} and *Pold1*^{L604K/L604K} mice died in utero. However, heterozygous animals were viable and displayed no overall increase in disease incidence, indicative of efficient compensation for the defective mutant pol. Schmitt *et al.*, analyzed the human δ pol and found that the mutation of the highly conserved L⁶⁰⁶ in the -SL⁶⁰⁶YPS- motif induced a mutator phenotype with a biased error spectrum that would be suitable for strand-specific identification of pol δ mediated DNA transactions *in vivo* [24]. The above experiments have shown unambiguously the importance of these motifs in δ pols.

Pavlov *et al.*, 2001 [25] analyzed the crucial Y in α , δ , ϵ , and ζ in the yeast DNA pols. They replaced the Y with A in the catalytic subunits of DNA pols α , δ , ϵ , and ζ and examined the consequences *in vivo*. Strains with the Y→A substitution in

the conserved -SL/MYPS/N- motif in the pols δ and ϵ were inviable. Strains with the same substitution in Rev3, the catalytic subunit of pol ζ , were nearly UV immutable, suggesting severe loss of its function. Their experiment further suggested that the Y in the conserved -SL/MYPS/N- motif- is important for the functioning of all B-family pols.

4. Conclusion

MSA analysis has shown that one of the main replicative δ pols from plants and animals contains the same template-binding pairs, catalytic and nucleotide selection amino acids, and also very similar catalytic metal-binding motifs. The highly conserved CTDs in both pols also suggest a similar role in the regulation of the replication process. Moreover, the PR exonuclease active site amino acids are found to be identical in both plants and animals and belong to the DEDD(Y)-superfamily of PR exonucleases. These findings establish that the catalytic, PR exonuclease and CTD domains of the δ pols and their roles in genome replication are highly conserved across all eukaryotes, like yeasts, higher fungi, plants and animals. Moreover, the highly conserved pol, PR exonuclease and CTD domains in plant and animal replicative δ pols strongly suggest a possible common evolutionary origin.

Compliance with ethical standards

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Disclosure of conflict of interest

The author has declared that no competing interests exist.

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