

Biotechnology Journal International

20(3): 1-35, 2017; Article no.BJI.38632 ISSN: 2456-7051 (Past name: British Biotechnology Journal, Past ISSN: 2231–2927, NLM ID: 101616695)

Single Subunit RNA Polymerases: An Insight into their Active Sites and Catalytic Mechanism

P. Palanivelu^{1*}

¹Department of Molecular Microbiology, School of Biotechnology, Madurai Kamaraj University, Madurai – 625 021, India (Retd.).

Author's contribution

The sole author designed, analyzed and interpreted and prepared the manuscript.

Article Information

DOI: 10.9734/BJI/2017/38632 <u>Editor(s):</u> (1) Sonal S. Joshi, Department of Biological Sciences, Wayne State University, Detroit, Michigan, USA. <u>Reviewers:</u> (1) Michael G. Mauk, Drexel University, College of Engineering, USA. (2) Yehia A. Osman Ellazeik, Mansoura University, Egypt. (3) Roumiana Todorova, Bulgaria. (4) Katharina Semrad, University of Vienna, Austria. Complete Peer review History: <u>http://www.sciencedomain.org/review-history/22801</u>

Original Research Article

Received 4th November 2017 Accepted 15th January 2018 Published 20th January 2018

ABSTRACT

Aim: To analyze various single subunit DNA dependent RNA polymerases and identify conserved motifs, active site regions among them and propose a plausible mechanism of action for these polymerases using the T7 RNA polymerase as a model system.

Study Design: Bioinformatics, Biochemical, Site-directed mutagenesis and X-ray crystallographic data were analyzed.

Place and Duration of Study: Department of Molecular Microbiology, School of Biotechnology, Madurai Kamaraj University, Madurai – 625 021, India, from 2010 to 2013.

Methodology: The advanced version of Clustal Omega was used for protein sequence analysis of various SSU DNA dependent RNA polymerases from viruses, mitochondria and chloroplasts. Along with the conserved motifs identified by the bioinformatics analysis and with the data obtained by X-ray crystallographic, biochemical and site-directed mutagenesis were also used to confirm the possible amino acids involved in the active sites and catalysis of these RNA polymerases.

Results: Multiple sequence analyses of various single subunit (SSU) DNA dependent RNA polymerases from different sources showed only a few highly conserved motifs among them, except chloroplast RNA polymerases where a large number of highly conserved motifs were found.

Possible catalytic regions in all these polymerases consist of a highly conserved amino acid K and a 'gate keeper' YG pair. In addition to, these polymerases also use an invariant R at the -4 position from the YG pair and an invariant S/T, adjacent to the YG pair. Furthermore, two highly conserved Ds are implicated in the metal binding site and thus might participate in the catalytic process. The YG pair appears to be specific for DNA templates as it is not reported in RNA dependent RNA polymerases.

Conclusion: The highly conserved amino acid K, the 'gate keeper' YG pair and an invariant R which are reported in all DNA polymerases, are also found in these DNA dependent RNA polymerases. Therefore, these RNA polymerases might be using the same catalytic mechanism like DNA polymerases. The catalytic amino acid K could act as the proton abstractor and generate the necessary nucleophile at the 3'-OH and the YG pair, R and the S/T might involve in the template binding and selection of nucleoside triphosphates (NTPs) for polymerization reactions. The two highly conserved Ds could act as the ' NTP charge shielder' and orient the alpha phosphate of incoming NTPs for reaction at the 3'-OH growing end.

1. INTRODUCTION

RNA polymerases (EC 2.7.7.6) are one of the key enzymes that participate in the flow of genetic information in all organisms and they play vital role in copying DNA sequences into RNA sequences, which are subsequently translated into proteins which are the final players in the cellular processes. The process of copying the DNA into RNA by RNA polymerases is known as transcription. Though RNA polymerases are found in all species, their number and composition vary across taxa. For instance, viruses contain mainly two types of RNA polymerases, viz. DNA dependent RNA polymerases and RNA dependent RNA polymerases depending upon their genetic material. Bacteria contain a single type of RNA polymerase, a multi-subunit enzyme composed of 6 subunits, while eukaryotes contain five distinct types RNA polymerases which are also multi-subunit (made up of up to 12 subunits) enzymes. In spite of such differences, there are similarities among transcriptional strikina mechanisms by these polymerases.

1.1 Discovery of RNA Polymerase

RNA polymerase which makes mRNAs in the cells was discovered independently by Charles Loe, Audrey Stevens, and Jerard Hurwitz in 1960 [1]. The Nobel Prize in physiology or medicine was awarded (1959) to Severo Ochoa 'for his

discovery of the mechanisms in the biological synthesis of RNA' and in chemistry was awarded (2006) to Roger D. Kornberg 'for his studies of the molecular basis of eukaryotic transcription'.

1.2 Dynamics of RNA Polymerization

RNA polymerases belong to the Main class 'Transferases' and are involved in the transfer of ribonucleoside triphosphates (NTPs/rNTPs) (Fig. 1a). Although the transcribed RNA contains the same genetic information of its DNA template, yet it is not an identical copy of the DNA segment. i.e., its sequence is only complementary to the DNA template and all the thymine residues are replaced by uracil residues in the RNA sequences (Fig. 1b) which helps the ribosomes to read the genetic code during the translation process.

RNA polymerases bind to the 3' end of a gene (promoter) and read the template DNA from 3' to 5' direction and thus a new strand is synthesized in the 5' to 3' direction. RNA polymerases direct initiation (usually initiate with a G) and catalyze further elongation at the 3'-end of an RNA by one nucleotide at a time (Figs. 1a and 1b). Unlike DNA polymerases they can initiate a chain 'de novo' (i.e.), they do not require a primer. The overall reaction catalyzed by an RNA polymerase may be written as,

DNA/RNA Template_n-3'OH + NTPs $\xrightarrow{RNA \text{ polymerase}}$ RNA _{n+1}-3'OH + PP_i Mg²⁺



Keywords: Single subunit DNA dependent RNA polymerases; viral RNA polymerases; Mitochondrial RNA polymerases; chloroplast RNA polymerases; clustal omega; conserved motifs; polymerase active site; RNA polymerase mechanism.

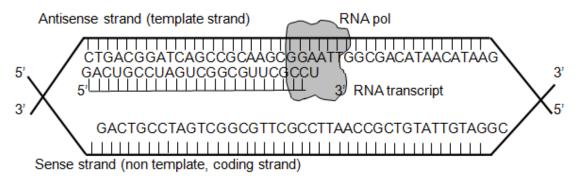


Fig. 1b. Process of RNA transcription using the template strand

Figure legends 1a: In an NTP, the strong negative charges on the phosphate groups repel each other and hence weakens the P—O bond. The hydrolysis of P—O bond results in the release of large negative free energy, which is utilized in the formation of the phosphodiester bond involving large positive free energy in DNA and RNA polymerases in general.

The RNA synthesis involves three steps, viz. initiation, elongation and termination. The newly formed RNA copies of the gene serve as blueprints for protein synthesis during the next step of translation. The basic transcription unit is the distance between the sites of Transcription Start Site (TSS) and Termination site, and may have one or more genes, e.g., mono or polycistronic.

As the prokaryotic and eukaryotic enzymes are multi-subunit enzymes and more complex, in this communication only the SSU (SSU) DNA dependent RNA polymerases are analyzed.

1.3 Types of SSU DNA Dependent RNA Polymerases

There are at least 3 different SSU DNA dependent RNA polymerases. They are:

- 1) SSUDNA dependent RNA polymerases of viruses (T7, T3, SP6, K11, etc)
- SSU DNA dependent RNA polymerases of chloroplast
- SSU DNA dependent RNA polymerases of mitochondria

In this communication, these three different SSU RNA polymerases are analyzed for their conserved motifs, active sites, metal binding sites and from these findings, a plausible mechanism of action is proposed for these types of enzymes.

1.3.1 Viral RNA polymerase

Depending upon the genome, the viruses are classified into two major types, viz. DNA and

RNA viruses. Thus, they use DNA dependent RNA polymerases and RNA dependent RNA polymerases, respectively.

Many of these viruses use a single-subunit DNAdependent RNA polymerase or RNA dependent RNA polymerases. The single-subunit DNAdependent RNA polymerases especially from T7, T3, SP6 and K11 are structurally and mechanistically similar to the single-subunit RNA polymerases of eukaryotic chloroplasts and mitochondria, and are closely related to DNA polymerases (EC 2.7.7.7.) and reverse transcriptases (EC 2.7.7.49) [2].

1.3.2 Mitochondrial RNA polymerases

Mitochondria contain a single type of DNAdependent RNA polymerases and they are single-subunit enzymes which are structurally and mechanistically very similar to the singlesubunit viral DNA-dependent RNA polymerases.

1.3.3 Chloroplast RNA polymerases

Chloroplasts contain two types of DNAdependent RNA polymerases. For example, plastids in photosynthetic higher plants use two different RNA polymerases. A multi-subunit one, very similar to bacterial RNA polymerases which is composed of α -, β -, β '-, and β "-subunits encoded bv rpoA, rpoB, rpoC1, and rpoC2 genes, and is referred to as plastid-encoded polymerase (PEP). The second enzyme is referred to as the nucleus-encoded polymerase (NEP). The NEPs is structurally and mechanistically unrelated to PEP but belong to the "single-subunit RNA polymerases" protein family. Interestingly, the NEPs are very similar to the viral RNA polymerases of T3, T7, SP6, K11, etc.

2. MATERIALS AND METHODS

A large number of RNA polymerases from various organisms have been isolated, purified, characterized, cloned and sequenced [3 and references therein]. Complete nucleic acid and protein sequence data are available for many of these enzymes from different species. Thus, these data have become valuable tools in analyzing and understanding the structurefunction relationships of these enzymes. This communication presents the results obtained from the protein sequence analysis of these enzymes, which are supported by biochemical, site-directed mutagenesis experiments and X-ray studies data on these enzymes.

The bacteriophage T7 DNA-dependent RNA polymerase is used as the model system for delineating the polymerization mechanism. Particular features of this enzyme, viz. the singlesubunit composition, relatively low molecular weight and large amount of data on biochemical, site-directed mutagenesis and X-ray analyses make this enzyme the most convenient model for investigating the physicochemical aspects of transcription. For multiple sequence analysis (MSA) of various RNA polymerases, the sequences were retrieved from SWISS-PROT and PUBMED sites and analyzed using Clustal Omega, an accurate, fast and widely accepted algorithm, available on their website.

3. RESULTS AND DISCUSSION

Figs. 2-7 show the MSA of various polymerases and their combinations (only the relevant and highly conserved regions are shown).

3.1 MSA of SSU RNA Polymerases from Different Sources

Fig. 2 shows the multiple sequence alignment and conserved motifs in SSU viral RNA polymerases such as T3, T7, SP6, K11, etc. There are large numbers of conserved motifs and amino acids among them. The catalytic, template and substrate binding motifs are highlighted. The YG 'gate keeper' motif and the catalytic K are strictly conserved (including distance conservation) DNA dependent RNA from the viruses. polymerases Similar observations were made in DNA dependent DNA polymerases also [4]. This strongly suggests that the DNA and RNA polymerases use the same set of amino acids for template, substrate binding and catalysis establishing a structure-function relationship among the DNA and RNA polymerases. The immediate downstream amino acid in DNA polymerases is usually a G or A [4] but in viral RNA polymerases it is a K or R. Interestingly, an R is found (4th amino acid downstream from the catalytic K) as the invariant amino acid in both the DNA and RNA polymerases. Another interesting observation is RNA polymerases from that the the enterobacteriophages possess one more YG 'gate keeper' pair exactly at the same distance but from the downstream of the catalytic K (The SP6 polymerase slightly deviates from others and uses TG). This suggests that the two YG pairs might be recognizing and binding on both the coding and non-coding templates of the DNA (please note that the DNA polymerases use only one template and shows one YG pair and whereas the catalytic K uses a primer) positioning in the middle might be catalyzing the NTP addition. In fact, these RNA polymerases require a double-stranded DNA for transcription as no activity was found when the T7 RNA polymerase was assaved on single-stranded DNA as substrate [5].

CLUSTAL O (1.2.4) MSA of DNA dependent RNA polymerases from enterobacteriophages like T3, T7, K11, SP6 , λ , etc

sp P06221 RPOL BPSP6	MQDLHAIQLQEEEMFNGGIRRFEADQQRQI	31
AAZ72968.1	-MSVISIDKHDFSDVSNAIEPFNLLADHYGQDLAVKQLQLEHEAYTEGERRFIKNLERQT	59
YP 009044255.1	-MSVISIDKHDFSDVSNAIEPFNLLADHYGQDLAVKQLQLEHEAYTEGERRFIKNLERQT	59
AEH41021.1	-MNALNIARNDFSEIELAAIPYNILSEHYGDRLAREQLALEHEAYELGEQRFLKMLERQV	59
sp P18147 RPOL_BPK11	-MNALNIGRNDFSEIELAAIPYNILSEHYGDQAAREQLALEHEAYELGRQRFLKMLERQV	59
ACY75835.1	-MNTINIAKNDFSDIELAAIPFNTLADHYGERLAREQLALEHESYEMGEARFRKMFERQL	59
AC057213.1	-MNTINIAKNDFSDIELAAIPFNTLADHYGERLAREQLALEHESYEMGEARFRKMFERQL	59
tr C6ZCU5 C6ZCU5 LAMBD	-MNTINIAKNDFSDIELAAIPFNTLADHYGERLAREQLALEHESYEMGEARFRKMFERQL	59
CAC86264.1	MNIIENIEKNDFSEIELAAIPFNTLADHYGSALAKEQLALEHESYELGERRFLKMLERQA	60
	** ** * ** **	

80

112

sp|P06221|RPOL_BPSP6 AAGSESD TAWNERLISEL TAPMAEGTOAYKEEYEGKKGRAPRALAFLOC-------AAZ72968.1 ERGELADNQVAKPLMQTLVPKI AQAVKEWHEGPDGKLSTSRPSVAFTML-----STEE YP 009044255.1 AEH41021.1 sp|P18147|RPOL BPK11 ACY75835.1 AC057213.1 tr|C6ZCU5|C6ZCU5_LAMBD CAC86264.1 sp|P06221|RPOL BPSP6 AAZ72968.1 YP 009044255.1 AEH41021.1 sp|P18147|RPOL BPK11 ACY75835.1 AC057213.1 tr|C6ZCU5|C6ZCU5_LAMBD CAC86264.1 sp|P06221|RPOL BPSP6 AAZ72968.1 YP 009044255.1 AEH41021.1 sp|P18147|RPOL BPK11 ACY75835.1 AC057213.1 AC057213.1 tr|C62CU5|C62CU5_LAMBD CAC86264.1 :*:* . *. sp|P06221|RPOL BPSP6 AAZ72968.1 YP 009044255.1 AEH41021.1 sp|P18147|RPOL BPK11 ACY75835.1 AC057213.1 tr|C6ZCU5|C6ZCU5_LAMBD CAC86264.1 sp|P06221|RPOL_BPSP6 AAZ72968.1 YP_009044255.1 AEH41021.1 sp|P18147|RPOL BPK11 ACY75835.1 AC057213.1 tr|C6ZCU5|C6ZCU5_LAMBD CAC86264.1 sp|P06221|RPOL_BPSP6 AAZ72968.1 YP 009044255.1 AEH41021.1 sp|P18147|RPOL BPK11 ACY75835.1 AC057213.1 tr|C6ZCU5|C6ZCU5 LAMBD CAC86264.1 .** * : : . . sp|P06221|RPOL_BPSP6 AAZ72968.1 AA2/2968.1 YP 009044255.1 AEH41021.1 sp|P18147|RPOL BPK11 ACY75835.1 AC057213.1 tr|C6ZCU5|C6ZCU5 LAMBD CAC86264.1 *: .* :* :. * *:

ERGELADNQVAKPLMQTLVPKI AQAVKEWHEGPDGKLSTSRPSVAFTML-----STEE 112 KAGEFADNVAAKPLVLTLHPQLTKRIDDWKEEQANARGKKPRAYYPIKHGVASELALSMG 119 KAGEFADNAAAKPLVLTLHPQLTKRIDDWKEEQANARGKKPRAYYPIKHGVASELAVSMG 119 KAGEVADNAAAKPLITTLLPKMIARINDWFEEVKAKRGKRPTAFOFLOE------108 KAGEVADNAAAKPLITTLLPKMIARINDWFEEVKAKRGKRPTAFQFLQE------108 KAGEVADNAAAKPLITTLLPKMIARINDWFEEVKAKRGKRPTAFQFLQE------108 KAGEIADNAAAKPLLATLLPKLTTRIVEWLEEYASKKGRKPSAYAPLQL------109 *. :*. : *: * : : : * . : -----VENEVAAYITMKVVMDMLNT--DATLQAIAMSVAERIEDQVRFSKLEGHAA 129 RAVKDRSLRISCESAAVIILKVILSKLVKPEGIPIT PMASAIGRTLEDEIRFGRIRDKEK 172 KAVKDRSLRISCESAAVIILKVILSKLVKPEGIPITPMASAIGRTLEDEIRFGRIRDKEQ 172 AEVLNEKRGVSSEAIALLTIKVVLGTLTDASKATIQQVSSQLGKALEDEARFGRIREQEA 179 AEVLKEKRGVSSEAIALLTIKVVLGNAHRPLKGHNPAVSSQLGKALEDEARFGRIREQEA 179 -----IKPEAVAYITIKTTLACLTSADNTTVQAVASAIGRAIEDEARFGRIRDLEA 159 -----IKPEAVAYITIKTTLACLTSADNTTVQAVASAIGRAIEDEARFGRIRDLEA 159 -----IKPEAVAYITIKTTLACLTSADNTTVOAVASAIGRAIEDEARFGRIRDLEA 159 -----LKPEASAFITLKVILASLTSTNMTTIQAAAGMLGKAIEDEARFGRIRDLEA 160 ...* * . .*. . KYFEKVKKS-LKASRTKSYRHAHNVAVVAEKSVAEKDADFDRWEAWPKETQLQIGTTLLE 188 EHFKKAI ADNLNKRAGASYKKAY-MOAVEASMLEOGOLE-DAWGTWSPTEAVHVGIKMLE 230 EHFKKAIAENLNKRAGASYKKAY-MQAVETSMLEQGQLE-DAWGTWSPTEAVHVGIKMLE 230 SYFKKNVADOLDKRVGHVYKKAF-MOVVEADMISKGMLGGDNWSSWKTDE OMHVGTKLLE 238 AYFKKNVADQLDKRVGHVYKKAF-MQVVEADMISKGMLGGDNWASWKTDEQMHVGTKLLE 238 KHFKKNVEEOLNKRVGHVYKKAF-MOVVEADMLSKGLLGGEAWSSWHKEDSIHVGVRCIE 218 KHFKKNVEEQLNKRVGHVYKKAF-MQVVEADMLSKGLLGGEAWSSWHKEDSIHVGVRCIE 218 KHFKKNVEEQLNKRVGHVYKKAF-MQVVEADMLSKGLLGGEAWSSWHKEDSIHVGVRCIE 218 KHFKKHVEEQLNKRHGQVYKKAF-MQVVEADMIGRGLLGGEAWSSWDKETTMHVGIRLIE 219 *::*. : .* . : . : * :* :::* :* ILEGSVFYNGEPVFMRAMRTYGGKTIYYLQTSESVGQWI---SAFKEHVAQLSPAYAPCV 245 IVIQSTQLVE---LKRYGAGNAAD---VEMVHLSDFWVKKMAQRGFSLAGIAPVYDPC IVIQSTQLVE---LKRYGAGNAATD---VEMVHLSDFWVKKMAQRGFSLAGIAPVYDPC 284 284 LLIEGTGLVE---MTKNKMADGSDDVTSMOMVQLAPAFVELLSKRAGALAGISPMYQPCV 295 LLIEGTGLVE---MTKNKMADGSDDVTSMOMVQLAPAFVELLSKRAGALAGISPMHQPCV 295 MLIESTGMVS---LHRQNAGVVGQD---SETIELAPEYAEAIATRAGALAGISPMFQPCV 272 MLIESIGMV3---LHRQNAGVVGQD--SETIELAPEYAEAIATRAGALAGISPMFDPCV 272 MLIESTGMVS---LHRONAGVVGOD---SETIELAPEYAEAIATRAGALAGISPMFOPCV 272 MLIESTGLVE---LORHNAGNAGSD---HEALOLAQEYVDVLAKRAGALAGISPMFOPC 273 :* ::* . *** I PPRPWR TPFNGGFHTEKVASR IRLVKGNREHVRKLTQKQMPKVYKAINALQNTQWQINK VPFKPWTGVVGGGYWAKGRRPLPLIRLGSKSAVARYEDVYMPEVYEAVNIIQNTPWKVNK VPFKPWTGVVGGGYWAKGRRPLPLIRLGSKSAVARYEDVYMPEVYEAVNIIQNTPWKVNK 305 344 344 VPPKPWVETVGGGYWSVGRRPLALVRTHSKKALRRYEDVHMPEVYKAVWLAQNTPWKVNK 355 VPPKPWVETVGGGYWSVGRRPLALVRTHSKKALRRYADVHMPEVYKAVALAONTPWKVNK VPPKPWTGITGGGYWANGRRPLALVRTHSKKALMRYEDVYMPEVYKAINIAONTAWKINK 355 332 332 332 333 DVLAVIE EVIRLDLGYGVPSFKPLIDKENKPANPVPVEFOHLRGRELKEMLSPEOWOOFI 365 KVLDVVNMVEKLNNTP--IDDI PQMEPL----KP--EAYA-----GETEEELK 384 KVLDVVNMVEKLNNTP--IDDI POMEPL----KP--EDYA-----GETEEELK 384 KVLAVVNEIINWKHCP--VGDVPAIEREELPPRP--DD-I-----DTNEVARK 398 KVLAVVNEIVNWKHCP--VGDVPAIEREELPPRP--DD-I-----DTNEVARK 398 KVLAVANVITKWKHCP--VEDI PAIEREELPMKP--ED-I----DMNPEALT 375 KVLAVANVITKWKHCP--VEDI PAIEREELPMKP--ED-I-----DMNPEALT 375 KVLAVANVITKWKHCP--VEDIPAIEREELPMKP--ED-I----DMNPEALT 375 KVLAVVNEIVNWKNCP--VADI PSLERQELPPKP--DD-I----DTNEAALK 376 * :: NWKGECARLYTAETKRGSKSAAVVRMVGQARKYSAFESIYFVYAMDSRSRVYVQSSTLSP 425 AWKKAAAGIYRREKARQSRRLSLSFIVNQANKFSQFKAIWFPYNMDWRGRVYAV-PMFNP 443 AWKKAAAGIYRREKARQSRRLSLSFIVNQANKFSQFKAIWFPYNMDWRGRVYAV-PMFNP 443 AWRKEAAAVYRKDKAROSRRLSMEFMVAOANKFANHKAIWFPYNMDWRGRVYAV-SMFNP 457 AWRKEAAAVYRKDKAROSRRCRCEFMVAOANKFANHKAIWFPYNMDWRGRVYAV-SMFNP 457 AWKRAAAAVYRKDKARKSRRISLEFMLEQANKFANHKAIWFPYNMDWRGRVYAV-SMFNP 434 AWKRAAAAVYRKDKARKSRRISLEFMLEOANKFANHKAIWFPYNMDWRGRVYAV-SMFNP 434 AWKRAAAAVYRKDKARKSRRISLEFMLEQANKFANHKAIWFPYNMDWRGRVYAV-SMFNP 434 EWKKAAAGIYRLDKARVSRRISLEFMLEQANKFASKKAIWFPYNMDWRGRVYAV-PMFNP 435 :: **.*:: ::*:* * ** * * * * . . *

sp P06221 RPOL BPSP6	QSNDLGKALLRFTEGRPVNGVEALKWFCINGANLWGWDKKTFDVRVSNVLDEEFQDMCRD	485
AAZ72968.1	QGNDMQKGLLTLAVGKPI-GADGFKWLKVHGANCAGVDKVTFEERIKWVEDNHDNIMA	500
YP 009044255.1	QGNDMQKGLLTLAVGKPI-GADGFKWLKVHGANCAGVDKVTFEERIKWVEDNHDNIMA	500
AEH41021.1	QGNDMTKGMLTLAKGKPI-GLDGFYWLKIHGANCAGVDKVPFPERIKFIEENEANILA	514
sp P18147 RPOL_BPK11	QGNDMTKGSLTLAKGKPI-GLDGFYWLKIHGANCAGVDKVPFPERIKFIEENEGNILA	514
ACY75835.1	QGNDMTKGLLTLAKGKPI-GKEGYYWLKIHGANCAGVDKVPFPERIKFIEENHENIMA	491
AC057213.1	QGNDMTKGLLTLAKGKPI-GKEGYYWLKIHGANCAGVDKVPFPERIKFIEENHENIMA	491
tr C6ZCU5 C6ZCU5_LAMBD	QGNDMTKGLLTLAKGKPI-GKEGYYWLKIHGANCAGVDKVPFPERIKFIEENHENIMA	491
CAC86264.1	QGNDMTKGLLTLAKGKPI-GEEGFYWLKIHGANCAGVDKVPFPERIAFIEKHVDDILA	492
	*.**: *. * :: *:*: * :. *: <mark>::***</mark> * ** * *: :	
sp P06221 RPOL BPSP6	IAADPLT F-TQWAKADAPYEFLAWCFEYAQYLDLVDEGRADEFRTHLPVHQDGSCSGIQH	544
AAZ72968.1	AAKAPMDSIEWWGKLDSPFOFLAFCFEYACVMHHGLSYSCSLPIAFDGSCSGIOH	555
YP 009044255.1	AAKAPMDSIEWWGRLDSFCFLAFCFEIAGVMHHGLSISCSLFIAFDGSCSGIGH	555
AEH41021.1	SAADPLNN-TWWTQQDSPFGFLAFCFEYAGVKHHGLNYNCSLPLAFDGSCSGIQH	568
sp P18147 RPOL BPK11	SAADPLNN-TWWTOODSPFOFLAFCFEYAGVKHHGLNYNCSLPLAFDGSCSGIOH	568
ACY75835.1	CAKSPLEN-TWWAEQDSPF0FLAFCFEYAGVOHHGLSYNCSLPLAFDQSCSGIQH	545
AC057213.1	CAKSPLEN-TWWAEQDSPFGFLAFCFEYA¢VQHHGLSYNCSLPLAFDqSCSGIQH	545
tr C6ZCU5 C6ZCU5 LAMBD	CAKSPLEN-TWWAEQDSPFGFLAFCFEYA¢VQHHGLSYNCSLPLAFDqSCSGIQH	545
CAC86264.1	CAKDPINN-TWWAEQDSPFGFLAFCFEYAGVTHHGLSYNCSLPLAFDGSCSGIQH	546
Choodadiii	* *: * *: ***: ***:**** . :. :: **: ********	010
sp P06221 RPOL BPSP6	YSAMLRDEVGAKAVNLKPSDABOIYGAVAQVVIKKNALYMDADDATTFT	594
AAZ72968.1	FSAMLRDHIGGHAVNLTPSGKVODIYRIVSDRIEEELKVLLVNGTDNEMVTHEDKKTGEI	615
YP 009044255.1	FSAMLRDHIGGHAVNLTPSGKVOLITRIVSDRIEEELKVLLVNGTDNEMVTHEDKKTGEI	615
AEH41021.1	FSAMLRDSIGGRAVNLLPSDTVOLIYHIVADKVNEVLHOHVINGSOTVVEQIADKETGEF	628
sp P18147 RPOL BPK11	FSAMLRDSIGGRAVNLLPSDIVODIYKIVADKVNEVLHOHAVNGSOTVVEQIADKEIGEF	628
ACY75835.1 T7	FSAMLRDEVGGRAVNLLPSETVOLIYGIVAKKVNEI LOADAINGTDNEVVTVTDENTGEI	605
AC057213.1	FSAMLRDEVGGRAVNLLPSETVOLIYGIVAKKVNEILOADAINGTDNEVVTVTDENTGEI	605
tr C6ZCU5 C6ZCU5 LAMBD	FSAMLRDEVGGRAVNLLPSETVOLIYGIVAKKVNEILOADAINGTDNEVVTVTDENTGEI	605
CAC86264.1	FSAMLRDEVGGRAVNLLPSETVOLIVGIVAOKVNEILKODAINGTPNEMITVTDKDTGEI	606
	:***** :* :**** ** ** ** *: : : *. *	
sp P06221 RPOL_BPSP6	SGSVTLSGTELRAMASAWDS <mark>IGITR</mark> SLTKKPVMTLBYG\$TRLTCRESVIDYIVDLEEKEA	654
AAZ72968.1	TERLKLGTRELARQWLTYGM\$RKVTKRSVMTLAYG\$KEYGFADQVYEDIVMP	667
YP_009044255.1	TERLKLGTRELARQWLTYGM\$RKVTKRSVMTLAYG\$KEYGFADQVYEDIVMP	667
AEH41021.1	REKVMLGESVLAAQWLQYGVTRKVTKRSVMTLAYGSKEFGFRQQVLEDTIQP	680
sp P18147 RPOL_BPK11	HEKVTLGESVLAAQWLQYGVIRKVIKRSVMTLAYG\$KESLVRQQVLEDTIQP	680
ACY75835.1 T7	SEKVKLGTKALAGQWLAYGVTRSVTKRSVMTLAYGSKEFGFRQQVLEDTIQP	657
AC057213.1	SEKVKLGTKALAGOWLA <mark>YG</mark> VTRSVTKRSVMTLA <mark>YG</mark> \$KEFGFRQQVLEDTIQP SEKVKLGTKALAGOWLA <mark>YG</mark> VTRSVTKRSVMTLA <mark>YG</mark> \$KEFGFRQQVLEDTIQP	657
tr C62CU5 C62CU5_LAMBD CAC86264.1	SEKVKLGTKALAGOWLA <mark>YG</mark> VTRSVTKRSVMTLA <mark>YG</mark> \$KEFGFRQQVLEDTIQP SEKLKLGTSTLAQQWLA <mark>YG</mark> VTRSVTKRSVMTLA <mark>YG</mark> \$KEFGFRQQVLDDTIQP	657 658
CAC00204.1	: :* * * *::*: **** ****: :**:	000
sp P06221 RPOL BPSP6	QKAVAEGRTANKVHPFEDDRQDYLTPGAAYNYMTALIWPSISEVVKAPIVAMKMIRQLAR	714
AAZ72968.1	AIDSGSGAMFTEPSQASRFMAKMIWEAVSVTVVAAVDAMKWLQGAAK	714
YP_009044255.1	AIDSGSGAMFTEPSQASRFMAKMIWEAVSVTVVAAVDAMKWLQGAAK	714
AEH41021.1	AIDNGEGLMFTHPNQAAGYMAKLIWDAVTVTVVAAVEAMNWLKSAAK	727
sp P18147 RPOL_BPK11	AIDNGEGLMFTHPNQAAGYMAKLIWDAVTVTVVAAVEAMNWLKSAAK	727
ACY75835.1	AIDSGKGLMFTQPNQAAGYMAKLIWESVSVTVVAAVEAMNWLKSAAK	704
AC057213.1	AIDSGKGLMFTQPNQAAGYMAKLIWESVSVTVVAAVEAMNWLKSAAK	704
tr C6ZCU5 C6ZCU5_LAMBD	AIDSGKGLMFTQPNQAAGYMAKLIWESVSVTVVAAVEAMNWLKSAAK	
CAC86264.1	AIDSGKGLMFTQPNQAAGYMAKLIWDAVSVTVVAAVEAMNWLKSAAK	705
	: . : *. * :*: :** ::: .* * : **: :: *:	
sp P06221 RPOL BPSP6	FAAKRNEGLMYTLPTGFILEQKIMATEMLRVRTCLMGDIKMSLQVETD	762
AAZ72968.1	LLAAEVKDKKTGEILKPCLPVHWVTPDGFPVWQEYRKKDTTRLNLMFLGS FNLQPTVNKG	774
YP_009044255.1	LLAAEVKDKKTGETLKPCLPVHWVTPDGFPVWQEYRKKDTTRLNLMFLGS FNLQPTVNKG	774
AEH41021.1	LLAAEVKDKKTKEVLRKRCAIHWVTPDGFPVWOEYRKONOARLKLVFLGOANVKMTYNTG	787
sp P18147 RPOL_BPK11	LLAAEVKDKKTKEVLRKRCAIHWVTPDGFPVWQEYRKQNQARLKLVFLGQANVKMTYNTG	787
ACY75835.1	LLAAEVKDKKTGEILRKRCAVHWVTPDGFPVWQEYKKPIQTRLNLMFLGQFRLQPTINTN	764
AC057213.1	LLAAEVKDKKTGEILRKRCAVHWVTPDGFPVWQEYKKPIQTRLNLMFLGQFRLQPTINTN	764
tr C6ZCU5 C6ZCU5_LAMBD	LLAAEVKDKKTGEILRKRCAVHWVTPDGFPVWQEYKKPIQTRLNLMFLGQFRLQPTINTN	764
CAC86264.1	LLAAEVKDKKTKEILRHRCAVHWTTPDGFPVWQEYRKPLQKRLDMIFLGQFRLQPTINTL	765
	: * : : * ** : *: *: ::*. :. :.	

sp P06221 RPOL_BPSP6	IVDEAAMMGAAAPNFVHGHDASHLILTVCEL-VDKGVTSIAVIHDSFGTHADNTLTL 8	18
AAZ72968.1	TKKELDKHKQESGISPNFVHSQD¢SHLRKTVVHTHRKYGVMSFAVIHDSFGTIPADAEYL 8	34
YP 009044255.1	TKKELDKHKQESGISPNFVHSQD¢SHLRKTVVHTHRKYGVMSFAVIHDSFGTIPADAEYL 8	34
AEH41021.1	KDSEIDAHKQESGIAPNFVHSQDGSHLRMTVVHANEVYGIDSFALIHDSFGTIPADAGNL 8	47
sp P18147 RPOL BPK11	KDSEIDAHKQESGIAPNFVH5QD¢SHLRMTVVHANEVYGIDSFALIHDSSGTIPADAGNL 8	47
ACY75835.1	KDSEIDAHKQESGIAPNFVH5QD¢SHLRKTVVWAHEKYGIESFALIHDSFGTIPADAANL 8	24
AC057213.1	KDSEIDAHKQESGIAPNFVH5QD¢SHLRKTVVWAHEKYGIESFALIHDSFGTIPADAANL 8	24
tr C6ZCU5 C6ZCU5 LAMBD	KDSEIDAHKQESGIAPNFVH5QD¢SHLRKTVVWAHEKYGIESFALIHDSFGTIPADAANL 8	24
CAC86264.1	KDSGIDAHKQESGIAPNFVH5QDCSHLRMTVVYAHEKYGIESFALIHDSFGTIPADAGKL 8	25
	:* :*****.:* *** ** *: *:* <mark>***</mark> ** :: *	
sp P06221 RPOL BPSP6	RVALKGOMVAMYIDGNALOKLLEEHEVRWMVDTGIEVPEQGEFDLNEIMDSEYVFA 8	74
AAZ72968.1	• • • • • • • • • • • • • • • • • • • •	93
YP 009044255.1		93
AEH41021.1		06
sp P18147 RPOL BPK11		06
ACY75835.1		83
AC057213.1		83
tr C6ZCU5 C6ZCU5 LAMBD		83
CAC86264.1		84
CAC00204.1		04
	.:: ** * . :.: .: .: . *. :* :*.:::.:*: <mark>.*::.</mark> *:.	

Fig. 2. MSA of SSU RNA polymerases from enterobacteria phages like T3, T7, SP6, K11, λ, etc

sp|P06221|RPOL_BPSP6 DNA-directed RNA polymerase OS=Enterobacteria phage SP6 AAZ72968.1 RNA polymerase [Enterobacteria phage K1F] YP_009044255.1 RNA polymerase [Escherichia phage PE3-1] AEH41021.1 RNA polymerase [Escherichia phage K30] sp|P18147|RPOL_BPK11 DNA-directed RNA polymerase OS=Enterobacteria phage K11 ACY75835.1 T7 RNA polymerase [Enterobacteria phage T7] ACO57213.1 RNA polymerase [Enterobacteria phage T7] tr|C6ZCU5|C6ZCU5_LAMBDA DNA-directed RNA polymerase OS=Escherichia phage CAC86264.1 RNA polymerase [Enterobacteria phage T3]

Fig. 3 shows the MSA and conserved motifs in SSU chloroplast RNA polymerases. As compared to mitochondrial RNA polymerases, there are large regions of conserved regions among chloroplast RNA polymerases; they are about 90% homologous. The catalytic, template and substrate binding motifs are highlighted. The YG gate keeper motif and the catalytic K is strictly conserved (including distance conservation) in SSU chloroplast RNA polymerases also. This strongly suggests that the DNA and RNA polymerases might be using the same set of amino acids for template, substrate binding and catalysis. The immediate downstream amino acid in DNA polymerases is usually a G or A [4] but in these RNA polymerases, it is a Q. Here also an R is found as the invariant amino acid at -4 position from the catalytic K. Another interesting feature in these RNA polymerases is that a YG pair is present like the viral RNA polymerases but much upstream from the catalytic K.

CLUSTAL O(1.2.4) MSA of SSU RNA polymerases from chloroplasts

	MASAAAASPSLSLNPTSHFQHQTSLVTW GGTPPDCFSQHFFLFFKCSLDLIFYIFLHLPSMASAAAASPSLSLNQSSHFKHQTSLITW	
TR A0A1J3IJ06 A0A1J3IJ06_NOCCA	QHFFLFFKCSLDLIFYIFLHLPSMASAAAASPSLSLNQSSHFKHQTSLITW	51
UPI00053999E5	MASAAAASPSLSLHQTSHFQHQTALFTW	28
UPI00053A373F	MASAAAASPSLSLNQTSHFQHQTSLFTC	28
	MAASAAAASPSISLNQTSHFQHQTSLFTW	
	MASAAAAFPSLSLNQSSHFQHQTSLVTW	
TR D7LGR7 D7LGR7_ARALL	MASAAAASPSLSLNQTSHFQHQTSLVTW	28
UPI000859C935	MASPAAAASPSLSLNQTSLFHHQTSLITW	29
TR A0A087GS25 A0A087GS25_ARAAL	MASATAASPSLSLNQSAHFQHHITF	
TR M4FDQ9 M4FDQ9_BRAR P	MASP-AAPSPSLSIYQTSLFHPQTSLVTW	28
UPI0006AAEE50	MASP-AAPSPSLSLYQTSLFHPQTSLVTW	28
	: :* **:*: :: *: : .*	

LKPPPSS--ALFRRKTLPFFERHSLPIS--ASS-SSS--SSSTSLSVHEKPISNSVHFH 81 SPI024600|RPOT3 ARATH TR|A0A1J3GXF0|A0A1J3GXF0 NOCCA LKPPSSS--ALFRRKILPLSSPVR---RLSLPISASSSS-SSSTSLSVSEKPTANSVHFH 114 UPI00053999E5 UPI00053A373F 83
 UP100053A373F
 LKPPSSF-ALFRKKILPFFQKR5LFIS-AS5-55555551515VRLKF15N5VRLF15N5VRLF1

 TR|V4L7M1|V4L7M1_EUTSA
 LKPPSS--ALFRKKILPFFDPSSPDKRISLPP-ISASSSSSASLSVSEKP--TVHFH

 TR|00H96|ROHH96_9BRAS
 LKPPSS--ALFRKKILPFFERHSLPIS-AS5-SS--SS-SSSISLSVHEKPISNSVHFH

 TR|07LGR7|D7LGR7_ARALL
 LKPPSS--ALFRKKILPFFERHSLPIS-ASS-SS--SS-SSISLSVHEKPISNSVHFH

 UP1000859C935
 LKPPSSSALFRKATKRLL-----PPI-SAASSS-SSISLSV--TTEKPTVHFH
 TR|A0A087GS25|A0A087GS25_ARAAL LKPPTSS--TLLRRKTLPFSVKR-----ISASSSSSSSSSSSSSSSSSSSSSFLSVTEKPTSNSVHFH 75 IRIMATOO9IM4FD09_BRARP IKPSS-SALFRRKPTKRLL-----PPI-SAASSSSSTSLSL-TEKPTTVHFH 74 **** * *** **:***: . :**** . GNLIESFENQDSSYAGTIKGASLIEELENPVERNGLSGRRRLFMQDPPWISALFLKGLSK 141 SP|024600|RPOT3 ARATH TR | A0A1J3GXF0 | A0A1J3GXF0 NOCCA GNLIESFENQD-SFAGSINGTSLIDELENFVQRNGISGRRRLFMQDPFWISALFLKGLSK 173 TR|A0A1J3IJ06|A0A1J3IJ06_NOCCA GNLIESFENQD-SFAGSINGTSLIDELENPVQRNGISGRRRLFMQDPFWISALFLKGLSK 165 UPT00053999E5 GNLIESFENQDSSYAGTIKGASLVEELENPVERNGLSGRRRLFMQDPPWISALFLKGLSK 143 GNLIESFENQDSSYAGAIKGASLVEELENPVERNGLSGRRRLFMQDPPWISALFLKGLSK 143 UPI00053A373F
 UPI00053A373F
 GNLIESFENQUSSIAGAIKGASLVELELENFVERNGLSGARREFNQDFFWIGALINGUS
 III

 TR|V4L7M1|V4L7M1_EUTSA
 GNLIESFENQD-SFAGTINGTSLIEELENPVERNGLSGRRRFMQDPPWISALFLKGLSK
 141

 TR|R0HH96]9BRAS
 GNLIESFENQDSSYAGTIKGASLIEELENPVERNGLSGRRRFMQDPPWISALFLKGLSK
 139

 TR|D7LGR7|D7LGR7_ARALL
 GNLIESFENQDSSYAGTINGASLIEELENPVERNGLSGRRRFMQDPPWISALFLKGLSK
 138

 UPI000859C935
 GNLIESFENQTSTIKGATF----AGTIKGATF---TDNPVERNELSARKRFTQDPPWISALFLKGITK
 129
 TR | A0A087GS25 | A0A087GS25 _ ARAAL GNLIDSFENOSG ---- TIKGATL --- IENPVERSELSGRRRLFMODP FWISALFLKGLTK 128 MV-DQTLKIERKDIDKRKFDSLRRRQVKEETEAWERMVDEYRDLEKEMCEKNLAPNLPYV 200 SP|024600|RPOT3 ARATH TR | AOA1J3GXF0 | AOA1J3GXF0 NOCCA MV-DQTLKIERKDIDKRKFDSLRRRQVKEETEAWERMVDEYRDLEKEMCEKNLAPNLPYV 232 TR | A0A1J3IJ06 | A0A1J3IJ06 NOCCA MV-DQTLKIERKDIDKRKFDSLRRQVKEETEAWERMVDEYRDLEKEMCEKNLAPNLPYV 224 MV-DQTVKIEHKDIDKRKFDSLRRRQVKEETEAWEKMVDEYRDLEKEMCEKNLAPNLPYV 202 UPI00053999E5
 0P10005399925
 MV-DQIVKIERKDIDKRKFDSLRRRQVKEETEAWEKMVDEIRDEKEMCEKNLAPNLFYV 202

 UP100053A373F
 MV-DQIVKIERKDIDKRKFDSLRRQVKEETEAWEKMVDEYRDLEKEMCEKNLAPNLPYV 202

 TR|V4L7M1|V4L7M1_EUTSA
 MV-DQIVKIERKDIDKRKFDSLRRQVKEETEAWEKMVDEYRDLEKEMCEKNLAPNLPYV 200

 TR|R0HH96|R0HH96_9BRAS
 MV-DQIVKIERKDIDKRKFDSLRRQVKEETEAWEKMVDEYRDLEKEMCEKNLAPNLPYV 198

 TR|D7LGR7|D7LGR7_ARALL
 MV-DQIVKIERKDIDKRKFDSLRRQVKEETEAWEKMVDEYRDLEKEMCEKNLAPNLPYV 197

 UP1000859C935
 MAADQIVKIERKDIDKRKFDSLRRQVKEETEAWERMVDEYRDLEKEMCEKSLAPSLPYV 189
 TR | A0A087GS25 | A0A087GS25_ARAAL MV-DQTFQIERKDIDKRKFDLLRRROVKEETEAWEKMVDEYRDLEKEMCEKNLAPNLPYV 187 TR | M4FDQ9 | M4FDQ9_BRAR P M----TVKIERKDIDKRKFDSLRRRQVKEETEAWERMVEEYRDLEKEMCEKSLAPNLPYV 186 UPI0006AAEE50 M----TVKIERKDIDKRKFDSLRRRQVKEETEAWERMVEEYRDLEKEMCEKSLAPNLPYV 186 * TR | A0A1J3GXF0 | A0A1J3GXF0 NOCCA KHMFLGWFQPLKDVIEREQKLQKNKSKKVRAAYAPHIELLPADKMAVIVMHKMMGLVMSG 292 TR | AOA1J3IJ06 | AOA1J3IJ06 NOCCA KHMFLGWFOPLKDVIEREOKLOKNKSKKVRAAYAPHIELLPADKMAVIVMHKMMGLVMSG 284 UPI00053999E5 KHMFLGWFQPLKDVIEREQKLQKNKSKKVRAAYAPHIELLPADKMAVIVMHKMMGLVMSG 262 UPI00053A373F KHMFLGWFQPLKDVIEREQKLQKNKSKKVRAAYAPHIELLPADKMAVIVMHKMMGLVMSG 262
 OPI00053A373F
 KRMFLGWFQFLKDVIEREQKLQKNKSKKVRAATAFHIELLFADRMAVIVMHKMMGLVMSG
 202

 TR|V4L7M1|V4L7M1_EUTSA
 KHMFLGWFQPLKDVIEREQKLQKNKSKKVRAATAFHIELLPADKMAVIVMHKMMGLVMSG
 260

 TR|R0HH96|R0HH96_9BRAS
 KHMFLGWFQPLKDVIEREQKLQKNKSKKVRAATAFHIELLPADKMAVIVMHKMMGLVMSG
 258

 TR|D7LGR7|D7LGR7_ARALL
 KHMFLGWFQPLKDVIEREQKLQKNKSKKVRAATAFHIELLPADKMAVIVMHKMMGLVMSG
 257

 UPI000859C935
 KHMFLGWFQPLKEVIEREQKLQKNKSKKVRAATAFHIELLPADKMAVIVMHKMMGLVMSG
 247
 TR|A0A087GS25|A0A087GS25_ARAAL KHMFLGWFQPLKDVIEREQKLQKNKSKKVRAAYAPHIELLPADKMAVIVMHKMMGLVMSG 247 TR|M4FDQ9|M4FDQ9_BRARP KHMFLGWFQPLKEVIEREQRLQKNKSKKVRAAYAPHIELLPADKMAVIVMHKMMGLVMSG 246 KHMFLGWFQPLKEVIEREQRLQKNKSKKVRAAYAPHIELLPADKMAVIVMHKMMGLVMSG 246 UPI0006AAEE50 SP|024600|RPOT3 ARATH HEDGCIQVVQAAVSIGIAIEQEVRIHNFLKRTRKNNAGDSQEELKEKQLLRKRVNSLIRR 320 TRIA0A1J3GXF0IA0A1J3GXF0 NOCCA HEDGCIOVVOAAVSIGVAIEOEVRIHNFLKRTRKNNEGDSPEELKDKOLLRKRVNSLIRR 352 TR | A0A1J3IJ06 | A0A1J3IJ06 NOCCA HEDGCIQVVQAAVSIGVAIEQEVRIHNFLKRTRKNNEGDSPEELKDKQLLRKRVNSLIRR 344 UPI00053999E5 HEDGCIQVVQAAVSIGIAIEQEVRIHNFLKKTRKNNAGDSQEELKEKQLLRKRVNSLIRR 322 UPT00053A373F HEDGCIQVVQAAVSIGIAIEQEVRIHNFLKRTRKNNAGDSQEELKEKQLLRKRVNSLIRR 322
 TR|V4L7M1|V4L7M1_EUTSA
 HEDGCIQVVQAAVSIGIAIEQEVRIHNFLKRTRKNNAGDSEEELKDKOLLRKRVNSLIRR
 320

 TR|R0HH96|R0HH96_9BRAS
 HEDGCIQVVQAAVSIGIAIEQEVRIHNFLKRTRKNNAGDSQEELKEKOLLRKRVNSLIRR
 318

 TR|D7LGR7|D7LGR7_ARALL
 HEDGCIQVVQAAVSIGIAIEQEVRIHNFLKRTRKNNAGDSQEELKEKOLLRKRVNSLIRR
 317

 UP1000859C935
 HEDGCIQVVQAAVSIGIAIEQEVRIHNFLKRTRKNNAGDSQEELKEKOLLRKRVNSLIRR
 309
 TR|A0A087GS25|A0A087GS25 ARAAL HEDGCIQVVQAAVSIGIAIEHEVRIHNFLKRTRKNNGGDTEEELKDKQLLRKRVNGLIRR 307 TR | M4FDQ9 | M4FDQ9_BRARP HEDGCIQVVQAAVSIGIAIEHEVRIHNFLKRTRKNNAGDSQEELKDKQLLRKRVNSLIRR 306 HEDGCIQVVQAAVSIGIAIEHEVRIHNFLKRTRKNNAGDSQEELKDKQLLRKRVNSLIRR 306

TR AOA1J3IJ06 AOA1J3IJ06_NOCCA UPI00053999E5 UPI00053A373F TR V4L7M1 V4L7M1_EUTSA TR ROHH96 ROHH96_9BRAS TR D7LGR7 D7LGR7_ARALL UPI000859C935	KRIIDALKVVKSEGTKPWGRATQAKLGSRLLELLIEAAYVQPPLTQSGDSIPEFRPAFRH 3 KRMIDALKVVKCEGIKPWGRATQAKLGSRLLELLIETAYVQPPLTQSGDSIPEFRPAFRH 4 KRMIDALKVVKSEGTKPWGRATQAKLGSRLLELLIETAYVQPPLTQSGDSIPEFRPAFRH 3 KRIIDALKVVKSEGTKPWGRATQAKLGSRLLELLIETAYVQPPLTQSGDSIPEFRPAFRH 3 KRIIDALKVVKSEGTKPWGRATQAKLGSRLLELLMETAYVQPPLTQSGDSIPEFRPAFRH 3				
SP 024600 RPOT3_ARATH TR A0A1J3GXF0 AOA1J3GXF0_NOCCA TR A0A1J3IJ06 A0A1J3IJ06_NOCCA UPI00053999E5 UPI00053A373F TR V4L7M1 V4L7M1_EUTSA TR R0HH96 R0HH96_9BRAS TR D7LGR7 D7LGR7_ARALL UPI000859C935 TR A0A087GS25 A0A087GS25_ARAAL TR M4FDQ9 M4FDQ9_BRARP UPI0006AAEE50	KFKTVTKYPGSKLVR TFKTVTKYPGSKLVR TFKTVTKYPGSKLVR KFKTVTKYPGSKLVR KFKTVTKYPGSKLVR KFKTVTKYPGSKLVR KFKTVTKYPGSKLVR KFKTVTKYPGSKLVR KFKTVTKYPGSKLVR	VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL VIECDSLLLAGLDKSAKHMLIPYVPMLVPPKRWKGYDKGGYL	472 464 442 442 440 438 437 429 427 426		
TR A0A1J3IJ06 A0A1J3IJ06_NOCCA UPI00053999E5 UPI00053A373F TR V4L7M1 V4L7M1_EUTSA TR R0HH96 R0HH96_9BRAS TR D7LGR7 D7LGR7_ARALL UPI000859C935	FLPS YIMRTHGSKKQQDJ FLPS YIMRTHGSKKQQDJ FLPS YIMRTHGSKKQQDJ FLPS YIMRTHGSKKQQDJ FLPS YIMRTHGSKKQQDJ FLPS YIMRTHGSKKQQDJ FLPS YIMRTHGSKKQQDJ FLPS YIMRTHGSKKQQDJ FLPS YIMRTHGSKKQQDJ FLPS YIMRTHGSKKQQDJ	ALKDISHKTAHRVFEALDTLGNTKWRVNRN ILDVVERLWADGG ALKDISSKTAHRVFEALDTLGNTKWRVNRK ILDVVEKLWADGG ALRDISSKTAHRVFEALDTLGNTKWRVNRK ILDVVEKLWADGG ALRDISSKTAHRVFEALDTLGNTKWRVNRK ILDVVERLWADGG ALRDISSKTAHRVFEALDTLGNTKWRVNRK ILDVVERLWADGG ALKDISSKTAHRVFEALDTLGNTKWRVNRK ILDVVERLWADGG ALKDISSKTAHRVFEALDTLGNTKWRVNRK ILDVVERLWADGG ALKDISSKTAHRVFEALDTLGNTKWRVNRK ILDVVERLWADGG ALKDISSKTAHRVFEALDTLGNTKWRVNRK ILDVVERLWADGG ALKDISSKTAHRVFEALDTLGNTKWRVNRK ILDVVERLWADGG	532 524 502 502 498 497 489 487 486		
TR A0A1J3IJ06 A0A1J3IJ06_NOCCA UPI00053999E5 UPI00053A373F TR V4L7M1 V4L7M1_EUTSA TR R0HH96 R0HH96_9BRAS TR D7LGR7 D7LGR7_ARALL UPI000859C935	NIAGLVNREDVPIPEKP NIAGLVNREDVPIPEKP NIAGLVNREDVPIPEKP NIAGLVNREDVPIPEKP NIAGLVNREDVPIPEKP NIAGLVNREDVPIPEKP NIAGLVNREDVPIPEKP NIAGLVNREDVPIPEKP NIAGLVNREDVPIPEKP NIAGLVNREDVPIPEKP	SSEDPEELQSWKWSAR KANKINRERHSLRC DVELKLSVARKMK ISEDPEEMQSWKWSAR KANKINRERHSLRC DVELKLSVARKMK ISEDPEEMQSWKWSAR KANKINRERHSLRC DVELKLSVARKMK SSEDPDEIQAWKWSVR KANKINRERHSLRC DVELKLSVARKMK SSEDPEEIQSWKWSVR KANKINRERHSLRC DVELKLSVARKMK SSEDPEELQSWKWSVR KANKINRERHSLRC DVELKLSVARKMK SSEDPEEIQSWKWSVR KANKINRERHSLRC DVELKLSVARKMK SSEDPEEIQSWKWSVR KANKINRERHSLRC DVELKLSVARKMK SSEDPEEIQSWKWSVR KANKINRERHSLRC DVELKLSVARKMK SSEDPEEIQSWKWSVR KAKTNRERHSLRC DVELKLSVARKMK SSEDPEEIQSWKWSVR KAKKTNRERHSLRC DVELKLSVARKMK SSEDPEEIQSWKWSVR KAKKTNRERHSLRC DVELKLSVARKMK SSEDPEEIQSWKWSVR KAKKTNRERHSLRC DVELKLSVARKMK	592 584 562 562 560 558 557 549 547 546		
TR A0A1J3IJ06 A0A1J3IJ06_NOCCA UPI00053999E5 UPI00053A373F TR V4L7M1 V4L7M1_EUTSA TR R0HH96 R0HH96_9BRAS TR D7LGR7 D7LGR7_ARALL UPI000859C935	 DEEG FYYPHNLDFRGRAY 	YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLHWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKQGLYWLKIHLANLF YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLHWLKIHLANLF YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLHWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLYWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLHWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLHWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLHWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLYWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLYWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLYWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLYWLKIHLANLY YPMHPHLNHLSSDLCRGTLEFAEGRPLGKSGLYWLKIHLANLY	652 644 622 622 620 618 617 609 607 606		

TD LIVE DWA LIVE DWA FUTCA		000
TR V4L7M1 V4L7M1_EUTSA	KDSSKDPESNPTAALAKILINQVI <mark>P</mark> KLV <mark>KQ</mark> TVMTSVYGVIYVGAREQIKRRLEEKGVISD {	
TR ROHH96 ROHH96_9BRAS	KDSSKDPESNPTAALAKILITQVI <mark>R</mark> KLV <mark>KQ</mark> TVMTSV <mark>YGVT</mark> YVGAREQIKRRLEEKGVITD '	
TR D7LGR7 D7LGR7_ARALL	KDSSKDPESNPTAALAKILITQVI <mark>R</mark> KLV <mark>KQ</mark> TVMTSV <mark>YGVT</mark> YVGAREQIKRRLEEKGVITD '	
UPI000859C935	KDSNKDPESNPTAALAKILINQVD <mark>R</mark> KLV <mark>KQ</mark> TVMTSVYGVTYVGAREQIKRRLEEKGVISD	
TR A0A087GS25 A0A087GS25_ARAAL		
TR M4FDQ9 M4FDQ9 BRAR P	KDSSKDPESNPTAALAKILINQVIN <mark>R</mark> KLV <mark>KQ</mark> TVMTSVYGVTYVGAREQIKRRLEEKGVITD	786
UPI0006AAEE50	KDSSKDPESNPTAALAKILINQVORKLVKQTVMTSVYGVTYVGAREQIKRRLEEKGVITD	786
	*** **********************************	
SP 024600 RPOT3_ARATH	${\tt ERML} \texttt{FAAACYSAKVTLAALGEIFEAARAIMSWLGDCAKIIASDNHPVRWITPLGLPVVQP}$	
TR A0A1J3GXF0 A0A1J3GXF0_NOCCA	ERMLFAAACYSAKVTLAALGEIFEAARAIMSWLGDCAKIIASDNHPVRWITPLGLPVVQP	892
TR A0A1J3IJ06 A0A1J3IJ06 NOCCA	ERMLFAAACYSAKVTLAALGEIFEAARAIMSWLGDCAKIIASDNHPVRWITPLGLPVVQP	884
UPI00053999E5	ERMLFAAACYSAKVTLAALGEIFEAARAIMSWLGDCAKIIASDNHPVRWITPLGLPVVQP	862
UPI00053A373F	ERMLFAAACYSAKVTLAALGEIFEAARAIMSWLGDCAKIIASDNHPVRWITPLGLPVVQP	862
TR V4L7M1 V4L7M1 EUTSA	ERMLFSAACYAAKVTLAALGEIFEAARAIMSWLGDCAKIIASDNHPVRWITPLGLPVVQP	860
TR ROHH96 ROHH96 9BRAS	ERMLFAAACYSAKVTLAALGEIFEAARAIMSWLGDCAKIIASDNHPVRWITPLGLPVVQP	858
TR D7LGR7 D7LGR7 ARALL	ERML FAAACYSAKVTLAALGEI FEAARAIMSWLGDCAKII ASDNHPVRWITPLGLPVVQP	857
UPI000859C935	ERML FAAACYSAKVTLAALGEI FEAARAIMSWLGDCAKI IASDNHPVRWTTPLGLPVVQP	849
TR A0A087GS25 A0A087GS25 ARAAL	ERML FAAACYSAKVTLAALGEI FEAARAIMSWLGDCAKI IASDNHPVRWTTPLGLPVVQP	847
TR M4FDQ9 M4FDQ9 BRARP	ERMLFSAACYSAKVTLAALGEIFEAARAIMSWLGDCAKIIATDNHPVRWTTPLGLPVVQP	846
UPI0006AAEE50	ERMLFSAACYSAKVTLAALGEIFEAARAIMSWLGDCAKIIATDNHPVRWTTPLGLPVVOP	846

SP 024600 RPOT3 ARATH	YCRSERHLIRTSLOVLALOREGNTVDVRKORTA FPPNFVHSLDGTHMMMTAVACREAGLN	920
TR A0A1J3GXF0 A0A1J3GXF0 NOCCA	YCRSERHLIRTSLOVLALOREGNTVDVRKORTAFPPNFVHSLDGTHMMMTAVACREAGLN	952
TRIA0A1J3IJ06 A0A1J3IJ06 NOCCA	YCRSERHLIRTSLOVLALOREGNTVDVRKORTAFPPNFVHSLDGTHMMMTAVACREAGLN	944
UPI00053999E5	YCRSERHLIRTSLOVLALOREGNTVDVRKORTAFPPNFVHSLDGTHMMMTAVACREAGLN	922
UPI00053A373F	YCRSERHLIRTSLOVLALOREGNTVDVRKORTAFPPNFVHSLDGTHMMMTAVACREAGLN	922
TR/V4L7M1/V4L7M1 EUTSA	YCRSERHLIRTSLOVLALOREGNTVDVRKORTAFPPNFVHSLDGTHMMMTAVACREAGLN	920
TR ROHH96 ROHH96 9BRAS	YCRSERHLIRTSLOVLALOREGNTVDVRKORTAFPPNFVHSLDGTHMMMTAVACREAGLN	
TR D7LGR7 D7LGR7 ARALL	YCRSERHLIRTSLOVLALOREGNTVDVRKORTA FPPNFVHSLDGTHMMMTAVACREAGLN	917
UPI000859C935	YCRSERHLIRTSLOVLALOREGNTVDVRKORTAFPPNFVHSLDGTHMMMTAVACREAGLN	
	YCRNERHLIRTSLOVLALOREGNTVDVRKORTA FPPNFVHSLDGTHMMMTAVACREAGLN	
TR M4FDQ9 M4FDQ9 BRARP	YCRSERHLIRTSLOVLALOREGNTVDVRKORTA FPPNFVHSLDGTHMMMTAVACREAGLN	
UPI0006AAEE50	YCRSERHLIRTSLOVLALOREGNTVDVRKORTA FPPNFVHSLDGTHMMMTAVACREAGLN	
	_********************************	200
	•	

UPI0006AAEE50							AGEKPADVYSEISLRVHEIMK	726
	** ******* <mark>****</mark> *******	**:	***	**	*****	****	**:********** ******	
SP 024600 RPOT3_ARATH	KDSSKDPESNPTAALAKILITQVI	R	κτν	KQ	TVMTSV	YGV.	YVGAREQIKRRLEEKGVITD	800
TR A0A1J3GXF0 A0A1J3GXF0_NOCCA	KDSNKDPESNPTAALAKIL INQV	B R	κLV	KQ	TVMTSV	YGV.	YVGAREQIKRRLEEKGVITD	832
TR A0A1J3IJ06 A0A1J3IJ06_NOCCA	KDSNKDPESNPTAALAKIL INQV	0RI	κLV	ΚQ	TVMTS	YGV.	YVGAREQIKRRLEEKGVITD	824
UPI00053999E5	KDSSKDPESNPTAALAKILITQV	B R	κLV	KQ	TVMTS	YGV.	YVGAREQIKRRLEEKGVITD	802
UPI00053A373F	KDSSKDPESNPTAALAKIL ITQV	B R	κLV	ΚQ	TVMTS	YGV.	YVGAREQIKRRLEEKGVITD	802
TR V4L7M1 V4L7M1_EUTSA	KDSSKDPESNPTAALAKIL INQV	D RI	κLV	ΚQ	TVMTS	YGV.	YVGAREQIKRRLEEKGVISD	800
TR ROHH96 ROHH96 9BRAS	KDSSKDPESNPTAALAKILITQVI	B R	κLV	KQ	TVMTS	YGV.	YVGAREQIKRRLEEKGVITD	798
TR D7LGR7 D7LGR7 ARALL	KDSSKDPESNPTAALAKILITQVI	B R	κLV	ΚQ	TVMTS	YGV.	YVGAREQIKRRLEEKGVITD	797
UPI000859C935	KDSNKDPESNPTAALAKIL INQV	0RI	κLV	ΚQ	TVMTS	YGV.	YVGAREQIKRRLEEKGVISD	789
TR A0A087GS25 A0A087GS25_ARAAL	KDSSKDPESHPTAALAKILINQVI	P R	κLV	ΚQ	TVMTS	YGV.	YVGAREQIKRRLEEKGVITD	787
TR M4FDQ9 M4FDQ9_BRARP	KDSSKDPESNPTAALAKIL INQV	P R	κLV	ΚQ	TVMTS	YGV.	YVGAREQIKRRLEEKGVITD	786
UDT000633FF50	KDSSKDDFSNDTAATAKTT TNOUT	holt	αv	R O	TWATER	VCV7	VUCADEO TEDDI FERCUTTO	786

UPI0006AAEE50	AGGVEKLSHEGRLSFVENHLDDIMDSAENAIHGRRWWLKAEDPFQCLAACVVLAQALKSP	666

SP 024600 RPOT3_ARATH	SPYSVISHLPI <mark>HQDG</mark> SCNGLQHYAALGRDSFEAAAVNLVAGEKPADVYSEISRRVHEIMK	740
TR A0A1J3GXF0 A0A1J3GXF0_NOCCA	SPSSVISHLPI <mark>HQD¢</mark> SCNGLQHYAALGRDSFEAAAVNLVAGEKPADVYSEISLRVHEIMK	772
TR A0A1J3IJ06 A0A1J3IJ06_NOCCA	SPSSVISHLPI <mark>HQD¢</mark> SCNGLQHYAALGRDSFEAAAVNLVAGEKPADVYSEISLRVHEIMK	764
UPI00053999E5	SPYSVISHLPI <mark>HQD¢</mark> SCNGLQHYAALGRDSFEAAAVNLVAGDKPADVYSEISRRVHEIMK	742
UPI00053A373F	SPYSVISHLPI <mark>HQD¢</mark> SCNGLQHYAALGRDSFEAAAVNLVAGDKPADVYSEISRRVHEIMK	742
TR V4L7M1 V4L7M1_EUTSA	SPYSVISHLPI <mark>HQD¢</mark> SCNGLQHYAALGRDSFEAAAVNLVAGEKPADVYSEISLRVHEIMK	740
TR ROHH96 ROHH96_9BRAS	SPYSVISHLPI <mark>HQD¢</mark> SCNGLQHYAALGRDSFEAAAVNLVAGEKPADVYSEISRRVHEIMK	738
TR D7LGR7 D7LGR7 ARALL	SPYSVISHLPI <mark>HQD¢</mark> SCNGLQHYAALGRDSFEAAAVNLVAGEKPADVYSEISRRVHEIMK	737
UPI000859C935	SPYSVISHLPI <mark>HQD¢</mark> SCNGLQHYAALGRDSFEAAAVNLVAGEKPADVYSEISLRVHEIMK	729
TR A0A087GS25 A0A087GS25_ARAAL	SPYSVISHLPI <mark>HQDG</mark> SCNGLQHYAALGRDSFEAAAVNLVAGEKPADVYSEISLRVHEIMK	727
TR M4FDQ9 M4FDQ9_BRARP	SPYSVISHLPI <mark>HQDG</mark> SCNGLQHYAALGRDSFEAAAVNLVAGEKPADVYSEISLRVHEIMK	726
UPI0006AAEE50	SPYSVISHLPI <mark>HQDG</mark> SCNGLQHYAALGRDSFEAAAVNLVAGEKPADVYSEISLRVHEIMK	726
	· · · · · · · · · · · · · · · · · · ·	

SP 024600 RPOT3 ARATH	AGGVEKLSHDARLAFVENHLDDIMDSAENPIHGKRWWLKAEDPFQCLAACVILTQALKSP	680
TR A0A1J3GXF0 A0A1J3GXF0_NOCCA	AGGVEKLSHDGRLAFVENHLDDIMESAENPVHGKRWWLKAEDPFQCLAACVTLTQALKSP	712
TR A0A1J3IJ06 A0A1J3IJ06_NOCCA	AGGVEKLSHDGRLAFVENHLDDIMESAENPVHGKRWWLKAEDPFQCLAACVILTQALKSP	
UPI00053999E5	AGGVEKLSHDARLAFVENHLDDIMDSAENTIHGKRWWLKAEDPFQCLAACVILTQALKSP	682
UPI00053A373F	AGGVEKLSHDARLAFVENHLDDIIDSAENTIHGKRWWLKAEDPFQCLAACVILTQALKSP	682
TR V4L7M1 V4L7M1 EUTSA	AGGVEKLSHDGRLAFVENHLDNIMDSAENPIHGQRWWLKAEDPFQCLAACVILTQALKSP	680
TR ROHH96 ROHH96 9BRAS	AGGVEKLSHDARLAFVETHLDDVMDSAENPIHGKRWWLKAEDPFQCLAACVILTQALKSP	678
TR D7LGR7 D7LGR7 ARALL	AGGVEKLSHDARLAFVENHLDDIMDSAENPIHGKRWWLKAEDPFQCLAACVILTQALRSP	677
UPI000859C935	AGGVEKLSHDGRLAFVENHLDDIIDSAENAIHGKRWWLKAEDPFQCLAACVILGQALKSP	669
TR A0A087GS25 A0A087GS25 ARAAL	AGGVEKLSHDGRLAFVENHLDVIIDSAENPIHGKRWWLKAEDPFQCLAACVILTQALKSP	667
TR M4FDQ9 M4FDQ9_BRARP	AGGVEKLSHEGRLSFVENHLDDIMDSAENAIHGRRWWLKAEDPFQCLAACVVLAQALKSP	666
	A COLUMN STREAM AND A DATE OF A DATE	c

SP 024600 RPOT3_ARATH		CDVDTMNRILREKFVELYNTPILEDLLQSFQESYPNLVFPPVPKRGDF	980
TR A0A1J3GXF0 A0A1J3GXF0_NOCCA	FAGVHDSYWTHAC	CDVDTMNRILREKFVELYNTPILEDLLQSFQESYPNLVFPPVPKRGNF	1012
TR A0A1J3IJ06 A0A1J3IJ06 NOCCA	FAGVHDSYWTHAC	COVDTMNRILREKFVELYNTPILEDLLQSFQESYPNLVFPPVPKRGNF	1004
UPI00053999E5	FAGVHDSYWTHAC	COVDTMNRILREKFVELYNTPILEDLLQSFQDAYPNLVFPPVPKRGDF	982
UPI00053A373F	FAGVHDSYWTHAC	CDVDTMNRILREKFVELYNTPILEDLLQSFQEAYPNLVFPPVPKRGDF	982
TR V4L7M1 V4L7M1 EUTSA	FAGVHDSYWTHAC	CDVDTMNRILREKFVELYNTPILEDLLQSFQESYPNLVFPPVPKRGDF	980
TR ROHH96 ROHH96 9BRAS	FAGVHDSYWTHAC	CDVDTMNRILREKFVELYNTPILEDLLQSFQESYPNLVFPPVPKRGDF	978
TR D7LGR7 D7LGR7_ARALL	FAGVHDSYWTHAC	CDVDTMNRILREKFVELYNTPILEDLLQSFQESYPNLVFPPVPKRGDF	977
UPI000859C935	FAGVHDSYWTHAC	CDVDTMNRILREKFVELYSTPILEDLLQSFQESYPNLVFPPVPKRGDF	969
TR A0A087GS25 A0A087GS25 ARAAL	FAGVHDSYWTHAC	CDVDTMNRILREKFVELYNTPILENLLQSFEESFPNLEFPPVPKRGDF	967
TR M4FDQ9 M4FDQ9_BRARP	FAGVHDSYWTHAC	CDVDTMNRILREKFVELYSTPILEDLLQSFQESYPNLVFPPVPKRGGF	966
UPI0006AAEE50		CDVDTMNRILREKFVELYSTPILEDLLQSFQESYPNLVFPPVPKRGGF	966
	**** <mark>***</mark> *****	***************************************	
		1	
SP 024600 RPOT3 ARATH	DLKEVLKSQYFFI	993	
TR A0A1J3GXF0 A0A1J3GXF0 NOCCA	DLKEVLRSQYFFN	1025	
TR A0A1J3IJ06 A0A1J3IJ06 NOCCA	DLKEVLESQYFFN	1017	
UPI00053999E5	DLKEVLKSOYFFN	995	
UPI00053A373F	DLKEVLKSQYFFN	995	
TR V4L7M1 V4L7M1 EUTSA	DLKEVLKSQYFFN	993	
TR ROHH96 ROHH96 9BRAS	DLKEVLKSQYFFN	991	
TR D7LGR7 D7LGR7 ARALL	DLKEVLKSQYFFN	990	
UPI000859C935 -	DLKEVLKSHYFFN	982	
TR A0A087GS25 A0A087GS25_ARAAL	DIKEVIKSQYFFN	980	
TR M4FDQ9 M4FDQ9_BRARP	DIKEVIKSQYFFN		
UPI0006AAEE50	DLKEVLKSQYFFN	979	
	*****	•	
		-	

Fig. 3. MSA of various SSU chloroplast RNA polymerases

SP|O24600|RPOT3_ARATH, Arabidopsis thaliana
TR|A0A1J3GXF0|A0A1J3GXF0_NOCCA, Noccaea caerulescens
TR|A0A1J3IJ06|A0A1J3IJ06_NOCCA, Noccaea caerulescens (Alpine penny-cress) (Thlaspi caerulescens)
UP100053999E5, Capsella rubella
UP100053A373F, Arabidopsis lyrata
TR|V4L7M1|V4L7M1_EUTSA, Eutrema salsugineum (Saltwater cress)
TR|R0HH96|R0HH96_9BRAS, Capsella rubella
TR|D7LGR7|D7LGR7_ARALL, Arabidopsis lyrata subsp. lyrata (Lyre-leaved rock-cress)
UP1000859C935, Raphanus sativus (Radish)
TR|A0A087GS25|A0A087GS25_ARAAL, Arabis alpina (Alpine rock cress)
TR|M4FDQ9|M4FDQ9_BRARP, Brassica rapa subsp. pekinensis (Chinese cabbage)
UP10006AAEE50, Brassica napus (Rape)
Fig. 4 shows the MSA and conserved motifs in RNA polymerases also This strongly suggests SSU mitochondrial RNA polymerases from that all these RNA polymerases might be using

SSU mitochondrial RNA polymerases from different sources like plants and fungi. It was found that the N terminal and C- terminal regions are devoid of many conserved motifs. However, the middle region towards the C terminal region shows strong alignment and showing many conserved motifs among them. The catalytic, template and substrate binding motifs are highlighted. The YG gate keeper motif and the catalytic K is strictly conserved (including distance conservation) in SSU mitochondrial RNA polymerases also This strongly suggests that all these RNA polymerases might be using same set of amino acids for template, substrate binding and catalysis. The immediate downstream amino acid in DNA polymerases is usually a G or A [4] but in these RNA polymerases, it is mostly a Q. like chloroplast RNA polymerases (The brown alga uses G and the *Schizosaccharomyces* uses P). Interestingly, here also the 4th amino acid, R, is the invariant amino acid suggesting a possible role in substrate binding and /or catalysis.

CLUSTAL O(1.2.4) MSA and conserved motifs in mitochondrial RNA polymerases from plant and fungi.

NP 150421.1	IRTTNYLCLSDEWVEVAKQYENTFTCI.PMLCPPLTWELQET	256
tr Q9GZ07 Q9GZ07 PLAFA	IHSYVWKNNNWYGVIHMRECCANYLLNNAI-NSHIPLNYIPMICKPKRWENFEG	902
sp 000411 RPOM HUMAN	YHVYSFRNVOOIGILKPHPAYVOLLEKAAE PTLTFEAVDVPMLCPPLPWTSPHS	673
sp P92969 RPOT1 ARATH	KONFRIVILENTKISRRYGCIECDPLVLKGLDKS-ARHMVIPYLPMLIPPONWIGYDO	419
sp Q93Y94 RPOT1 NICSY	VHTLKTVETMKGSRRYGVIOCDPLVRKGLDKT-ARHMVIPYMPMLVPPOSWLGYDK	445
sp P38671 RPOM NEUCR	SHVMOLRKGKKIGTIIPNKAVVELLVREPVPDFLARHIPMVTPDDWVSFEK	642
sp 013993 RPOM_SCHPO	VHTYQYSNGRKVGMIVPHVEFYKLLSRDIE-KPHLHPQLIPMLVTPKPWTSWID	563
sp P13433 RPOM_YEAST	AHGYQYHNGSKLGVLKIHKTLIRQLNGERL-IASVQPQLIPMLVEPKPWVNWRS	687
NP 150421.1	NPYNKIESIIQGINLRGGGYLTDSEIQKNKTALLKNATAMYVVCHSEESKDNLNYIQ	313
tr Q9GZ07 Q9GZ07 PLAFA	GMLLLKNSFIPCNIKPLFNLNVCNLNRIKNIVSEIG	938
sp 000411 RPOM HUMAN	GAFLLSPTKLMRTVEGATQHQEL-LETCPPTALHGALDALTQLG	716
sp P92969 RPOT1 ARATH	GAHFELP SYVMRTHG-AKQQRT-VMKRTPKEQLE PVYEALDTLG	461
sp 093Y94 RPOT1 NICSY	GAYLFLP SYIMRTHG-AKQQRE-AVKRVPKKQLE PVFQALDTLG GAYLFLP SYIMRTHG-AKQQRE-AVKRVPKKQLE PVFQALDTLG	487
	GATLELESTIGATLELESTI	686
sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO	GAILEIRIPVREKKNGEREORLIILAAIARGDMDQVFRGLDVLG GGYYYSROPLVRLKG-ALEOVDYIMKASENGOLDELFKAVSSLG	
sp P13433 RPOM_SCHPO	GGIIIISKQFLVRLKG-ALEQVDILMKASENGQLDELFRAVSSLG GGYHYTQSTLLRTKD-SPEQVAYLKAASDNGDIDRVYDGLNVLG	606 730
SDIF13433 [KFOM_ILASI	GGINIIQSILLKIKD-SPEQVAILKAASDNGDIDKVIDGLAVLG	/30
	• • • • • • • • • • • • • • • • • • • •	
NP 150421.1	SLGFRINNDLLKIIKENKLLIPNYKESYMVAQQTRKEYCGSMF	356
tr Q9GZ07 Q9GZ07 PLAFA	NVGWKINKEILHYIEYAYIHGIT-IGKIPLYK-NYTLPKYINLKEONN-EEIKKYLLLK-	994
sp 000411 RPOM HUMAN	NCAWRVNGRVLDLVLQLFQAKGCPQLGVPAPPSEAPQPPEAHLPHSAAPARKAELRREL-	775
sp P92969 RPOT1 ARATH	NTKWKINKKVLSLVDRIWANGGR-IGGLVDREDVPIPEEPEREDQEKFKNWRWES-	515
sp Q93Y94 RPOT1 NICSY	NTKWRLNRKVLGIVDRIWASGGR-LADLVDREDVPLPEEPDAEDEAQIRKWKWKV-	541
sp P38671 RPOM NEUCR	KTGWKINSPVFKVMLDVWNSGKQ-VANIPPLDPIFDLPPEPASTEDPTVKRAWLKEI-	742
sp 013993 RPOM_SCHPO	KVSWRINORLFNVLIRIWNSGEK-FLSIPPREVKCDMPPYPKNSINPRDKVIWHTRR-	662
sp P13433 RPOM_SCHPO	RTPWTVN RKVFDVVSQVWNKGE G-FLDI PGAQDEMVLPPAPPKNSDPS ILRAWKLQV-	786
Sp(P10400) RPON_IEADI	: :* :: : :	100
NP_150421.1	KTRRAEEHDSATNYLAETDFAIDIADKLQGL-DLHFAVRHDGRGRIYTIAYPISPISANY	415
tr Q9GZ07 Q9GZ07_PLAFA	-EEINRLNKCLISERPTFLQKLAVAKTFKDNDIIYFPHNID <mark>FRGR</mark> MYPLSPHLHHMSDDI	1053
sp 000411 RPOM_HUMAN	-AHCQKVAREMHSLRAEALYRLSLAQHLRDR-VFWLPHNMD <mark>FRG</mark> RTYPCPPHFNHLGSDV	833
sp P92969 RPOT1_ARATH	-KKAIKQNNERHSQRCDIELKLEVARKMKDEEGFYYPHNVDF <mark>RG</mark> RAYPIH PYLNHLGSDL	574
sp Q93Y94 RPOT1_NICSY	-KGVKKENCERHSQRCDIELKLAVARKMKDEDGFYYPHNLDFRGRAYPMHPYLNHLGSDL	600
sp P38671 RPOM_NEUCR	-KVIENERSGLHSQRCFMNFQLEIARAYRDQ-TFYFPHNVDF <mark>RG</mark> FAYPIPPYLNHMGADH	800
sp 013993 RPOM_SCHPO	-KELAALKTGAHSQRCDFNYKLEIARAFLNE-KFYFPHSLDF <mark>RG</mark> FAYPLSSHLHHVSNDV	720
sp P13433 RPOM_YEAST	-KTIANKFSSDRSNRCDTNYKLEIARAFLGE-KLYFPHNLDFRGRAYPLSPHFNHLGNDM	844
	. ::* . : * <mark>**</mark> * * ::.:	
NP 150421.1	MRSILTCKEDYYFSKKTDRENWESLVLKLTKDIMGNN-TKKSVELFK	461
tr Q9GZ07 Q9GZ07 PLAFA	CRSLITFAEQKEIGNKGLFWLKIHLANTFGK-DKLSFQKRIQWVDQNINNIKKL	1106
sp 000411 RPOM HUMAN	ARALLEFAQGRPLGPHGLDWLKIHLVNLTGLKKREPLRKRLAFAEEVMDDILDS	887
sp P92969 RPOT1 ARATH	CRGILEFCEGKPLGKSGLRWLKIHIANLYAGGV-DKLAYEDRIAFTESHLEDIFDS	629
sp/P92909/RPOIL_ARAIN	CRGILEFAEGRPLGKSGLRWLKIHLANVYGGGV-DKLSYEGRVAFSENHVEDIFDS	655
sp P38671 RPOM_NEUCR	VRGLMLFAKGKPLGESGLRWLKVHLANVYGF-DKASLQERQDFADENIENIRDS	853
sp 013993 RPOM SCHPO	CRGLLEF STGKPLGPKGLNWLKVHLANLFGI-SKKDFATROAFVDDNMOEVFDS	773
sp P13433 RPOM YEAST	SRGLLIFWHGKKLGPSGLKWLKIHLSNLFGF-DKLPLKDRVAFTESHLODIKDS	897
	* *	
NP_150421.1	KNPGRAFDKALSDVEVIDDFSLHALKDIFINEGGQTSQLIG <mark>LD</mark> VTA	507
tr Q9GZ07 Q9GZ07_PLAFA	TQQPFDNIEFWNMAEKPWQALAVAIDLKNALESPNASKYKSSIPIQQDGTC	1157
sp 000411 RPOM_HUMAN	ADQPLTGRKWWMGAEEPWQTLACCMEVANAVRASDPAAYVSHLPVHQDGSC	938
sp P92969 RPOT1 ARATH	SDRPLEGKRWWLNAEDPFQCLAACINLSEALRSPFPEAAISHIPIHQDGSC	680
sp Q93Y94 RPOT1 NICSY	AERPLEGKRWWLGAEDPFQCLATCINIAEALRSPSPETAISYMPIHQDGSC	706
sp P38671 RPOM_NEUCR	VNNPLNGNQWWLQAEDPWQCLATCFELAAALELEDPTKYVSHLPIHQDGTC	904
sp 013993 RPOM_SCHPO	ADRPLDGNKWWSKADDPFQALAACFEIAEAVRSGDHESYISHIPIQQDGTC	824
sp P13433 RPOM YEAST	AENPLTGDRWWTTADKPWQALATCFELNEVMKMDNPEEFISHQPVHQDGTC	948
	:: .:. :: : : : : : <mark></mark> :.	
	SGLQIMGLITRCTKALEMTQVFDQNETNSAVDIYHAIQKHVVKK	551
NP_150421.1		1214
tr Q9GZ07 Q9GZ07_PLAFA	NGLQHYAALGKDKYGGKAVNIIPSDEPQDIYSVVLDIVISKIKNDLMNISNGHHNNI	
tr Q9GZ07 Q9GZ07_PLAFA sp 000411 RPOM_HUMAN	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR	989
tr Q9GZ07 Q9GZ07_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN	989 735
tr]Q9GZ07 Q9GZ07_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTLGAAAVNLVAGDKPADVYSG IAARVLDIMKRDAAKDPANDPN	989 735 761
tr]Q9GZ07 Q9GZ07_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTLGAAAVNLVAGDKPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE	989 735 761 955
trTQ9GZ07 Q9GZ07_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTLGAAAVNLVAGDKPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDIEGAKQVNLWPSDHPSDVYEAVAEIVRGFLKKDAE AGDE	989 735 761 955 875
tr]Q9GZ07 Q9GZ07_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTLGAAAVNLVAGDKPADVYSG IAARVLDIMKRDAA KDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDIEGAKQVNLWPSDHPSDVYEAVAE IVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDKPQDVYAHVARLVQKRLE IAAE KGDE	989 735 761 955
tr]Q9GZ07 Q9GZ07_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTLGAAAVNLVAGDKPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDIEGAKQVNLWPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVGATQVNLVPSDKPQDVYAHVARLVQKRLEIAAE KGDE ***	989 735 761 955 875 999
tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST NP_150421.1	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTLGAAAVNLVAGDKPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDIEGAKQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE .**** : : : *:* : *	989 735 761 955 875 999 564
tr[Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST NP_150421.1 tr[Q9G207 Q9G207_PLAFA	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTG IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTUGAAAVNLVAGDKPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDIEGAKQVNLWPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVCATQVNLVPSDKPQDVYAHVARLVQKREIAAE KGDE .*** :: * YPIVQEMIRKTYK ISFSINENIKTNKKYNNNINNNINNNNNNNNSNVNKNELASYCFKFDLLKRKVKK	989 735 761 955 875 999 564 1274
tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT_ARATH sp 093Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST NP_150421.1 tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTUGAAAVNLVAGDKPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDIEGAKQVNLVPSDHPSDVYEAVAEIVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDKPQDVYAAVAEIVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDKPQDVYAAVAEIVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNVPSDKPQDVYAAVAEIVRGFLKKDAE KGDE YPIVQEMIRKTYK ISFSINENIKTNKKYNNNINNNINNYNNNHNRNSN SNVNKNELASYCFKFDLLKRKVVK	989 735 761 955 875 999 564 1274 1004
tr Q9G207 Q9G207 PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST NP_150421.1 tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTLGAAAVNLVPGDRPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDIEGAKQVNLVPSDHPSDVYEAVAEIVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDKPQDVYAHVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNLVPSDKPQDVYAHVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNVPSDKPQDVYAHVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNVVPSDKPQDVYAHVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNVVPSDKPQDVYAHVARLVQKRLEIAAE KGDE '*** : : : *:* : 	989 735 761 955 875 999 564 1274 1004 752
tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST NP_150421.1 tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTLGAAAVNLVPGDRPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDIEGAKQVNLVPSDHPSDVYEAVAEIVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDKPQDVYAHVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNLVPSDKPQDVYAHVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNVPSDKPQDVYAHVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNVVPSDKPQDVYAHVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNVVPSDKPQDVYAHVARLVQKRLEIAAE KGDE '*** : : : *:* : 	989 735 761 955 875 999 564 1274 1004 752 778
tr Q9G207 Q9G207 PLAFA sp 000411 RPOM_HUMAN sp 92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST NP_150421.1 tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVYGEKPADVYTG IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTUGAAAVNLVYGDKPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDIEGAKQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVQKRLE IAAE KGDE .*** : : : *:* : * 	989 735 761 955 875 999 564 1274 1004 752
tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST NP_150421.1 tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVYGEKPADVYTG IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTUGAAAVNLVYGDKPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDIEGAKQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVRGFLKKDAE AGDE NGLQHYAALGGDVEGATQVNLVPSDHPSDVYEAVAELVQKRLE IAAE KGDE .*** : : : *:* : * 	989 735 761 955 875 999 564 1274 1004 752 778 970
tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST NP_150421.1 tr Q9G207 Q9G207_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_SCHPO	NGLQHYAALGRDSVGAASVNLEPSDVPQDVYSGVAAQVEVFRRQDAQRGMR NGLQHYAALGRDKLGADAVNLVTGEKPADVYTE IAARVLKIMQQDAE EDPETFPN NGLQHYAALGRDTLGAAAVNLVPGDRPADVYSG IAARVLDIMKRDAAKDPANDPN NGLQHYAALGGDTWGAQQVNLVPGDRPADVYSAVAKLVIKGIEDDLAKDNE NGLQHYAALGGDTEGAKQVNLVPSDHPSDVYEAVAEIVRGFLKKDAE AGDE NGLQHYAALGGDTEGAKQVNLVPSDKPQDVYAVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNLVPSDKPQDVYAVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNLVPSDKPQDVYAVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNVPSDKPQDVYAVARLVQKRLEIAAE KGDE NGLQHYAALGGDVEGATQVNVVPSDKPQDVYAVARLVQKRLEIAAE KGDE '*** : : : : : : : : : : : : : : : : : :	989 735 761 955 875 999 564 1274 1004 752 778 970 890

NP_150421.1 tr[Q9GZ07 Q9GZ07_PLAFA sp[000411 RPOM_HUMAN sp[P92969 RPOT1_ARATH sp[Q93Y94 RPOT1_NICSY sp[P38671 RPOM_NEUCR sp[013993]RPOM_SCHPO sp[P13433]RPOM_YEAST	GIMRMS YGEGVYSRKKTLYEYLKTLENEEFKKNKNKGTLLLDMAKAYDQAIYKEF QTIMTICYGVTSIGAKNQVKGKIQTMIGKELDKNIINKLSQYIANYIFESISEIF QTVMTVVYGVTRYGGRLQIEKRLRELSDFPQEFVWEASHYLVRQVFKSLQEMF QTVMTSVYGVIYSGARDQIKKRLKERGFTEDDSLTFHASCYAAKITLKALEEMF QTVMTSVYGVIYIGARDQIKKRLKERGVIEDDNELFAAACYAAKITLTALGEMF QTVMTNVYGVIYUGARKQVLKQIEAAYPNITAESGIEAALLASYVTQHIFRAMSTMF PTVMTNVYGVIYUGARKQISEKLENIDGMEKLKVADYANYLTKKVFEALRSLF QTVMTNVYGVIYUGATFQIAKQLSPIFDDRKESLDFSKYLTKHVFSAIRELF **	620 1329 1057 806 832 1027 943 1066
NP_150421.1 tr Q9GZ07 Q9GZ07_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST	PKFKTFTDQADKIVSIRTKLNLG	643 1347 1075 824 850 1087 971 1096
NP_150421.1 tr[Q9GZ07]Q9GZ07_PLAFA sp[000411]RPOM_HUMAN sp[P92969]RPOT1_ARATH sp[Q93Y94]RPOT1_NICSY sp[03394]RPOM_NEUCR sp[013993]RPOM_SCHPO sp[P13433]RPOM_YEAST	: : INFNISNIFKTNQYYNMDKATTYSFRDFDGKSKRITMYIPEKITSSQYERYEAKP ELNIPITWISPIGLPCEQPYRL-GNR-ILVNTPL-QSISVISYKNSQL HMGSVVEWVTPLGVPVIQPYRL-DSKVKQIGGGI-QSITYTHNGDISRKP SENNAVCWTTPLGLPVVQPYRK-PGR-HLVKTTL-QVLTLSRETDKV MENHPVRWTTPLGLPVVQPYRK-LGR-HLIKTSL-QILTLQRETDKV NDEILNNFQSTIIWTTPLRMPVVQPYRK-HGT-KTVSTCM-QDLVMT-IPERSDPV GIKDELTPVVWTTLLNLPIVQPYRN-YKS-RQIRTNL-QTVFIE-ERDRTATV KNGNKPDFMSSVIWTTPLGLPIVQPYRE-ESK-KQVETNL-QTVFIS-DPFAVNPV :: : : : : : : : : : :	698 1392 1123 868 894 1139 1020 1148
NP_150421.1 tr Q9GZ07 Q9GZ07_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHPO sp P13433 RPOM_YEAST	NTRKIKRATIENEIHHIDSLLAHLVIKEF-RKELKPLFTVHLAFYVRLIDMAFLKEAYFQ HKNKQRLGFPNEVHSLDASHLMMTAEKMVIQNNFSFAAVHDSYWAHACNVDIMNQFIRE NTRKQKNGFFPNEHHSLDSSHMMLTALHC-YRKGLTFVSVHDCYWHAADVSVMNQVCRE MARRQMTAFAPNEHHSLDGSHMMTAVAC-NRAGLSFAGVHDSFWHACDVDVMNTILRE MVKRQRTAFFPNEVHSLDGSHMMTAIAC-KESGLSFAGVHDSFWHASDVDQMNKILRE NRRKQLQAFFPNEHHSLDASHMILSALHC-DELGLTFAAVHDSFWTHASDIDSMNAVLRD QPHKQATAFFPNEHHSLDASHMILSALHC-DELGLTFAAVHDSFWTHASDIDSMNAVLRD NARRQKAGLFPNEHHSLDASHMLLSAAEC-GKQGLDFASVHDSYWTHASDIDTMNVVLRE .: . ***:*:*:::::::::::::::::::::::::::	757 1452 1182 927 953 1198 1079 1207
NP_150421.1 tr Q9GZ07 Q9GZ07_PLAFA sp 000411 RPOM_HUMAN sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NICSY sp P38671 RPOM_NEUCR sp 013993 RPOM_SCHP0 sp P13433 RPOM_YEAST	FATKIPSS PEQGELDISMVKDSLYFFS FATKIPSS PEQGELDISMVKDSLYFFS FPDISFPPL PERGDFDLRVVLSS TYFFN FPDLQFPPL PERGDFDLREVLSS PYFFN TNHFALSQKRAKASIASGGKQKHYLDIWLPLVFPPI PEKGDFDVRSLKDSTYFFS KAK FGNKSYIPLEFPPL PARGALDLKKVLSSKYFFS LDALELENGGDEN SGMSVLLPLRLPEI PPKGDFDVTVLRISQYFFS	824 1503 1243 976 1002 1423 1154 1351

Fig. 4. MSA of mitochondrial RNA polymerases from plants and fungi

*The N terminal motifs are different from plant RNA polymerases and the amino acids are marked in green

NP_150421.1, *Pylaiella littoralis* (Sea weed, brown alga) tr|Q9GZ07|Q9GZ07_PLAFA, *Plasmodium falciparum* (Malarial parasite) sp|O00411|RPOM_HUMAN, *Homo sapiens* sp|P92969|RPOT1_ARATH, *Arabidopsis thaliana* sp|Q93Y94|RPOT1_NICSY, *Nicotiana sylvestris* sp|P38671|RPOM_NEUCR, *Neurospora crassa* sp|O13993|RPOM_SCHPO, *Schizosaccharomyces pombe* sp|P13433|RPOM_YEAST, *Saccharomyces cerevisiae*

Fig. 5 shows the MSA and conserved motifs in SSU RNA polymerases exclusively from fungal mitochondria. It is clear that there are no highly

conserved motifs in the N-terminal and Cterminal regions. However, the middle region towards the C terminal shows large regions of conservation including the catalytic K, YG pair and an invariant R. The catalytic, template and substrate binding motifs are highlighted. The YG gate keeper motif and the catalytic K is strictly conserved (including distance conservation) in all DNA dependent RNA polymerases from fungal mitochondria. This strongly suggests that all these RNA polymerases might be using same set of amino acids for template, substrate binding and catalysis. The immediate downstream amino acid in DNA polymerases is usually a G or A [4] but in these out of 49 sequences analyzed, 39 RNA polymerases uses Q. (Six use R and three use P and one uses G). Interestingly, here also the 4th amino acid, R, is the invariant amino acid in all the 49 sequences, suggesting an important role in substrate binding and /or catalysis. All these fungal mitochondrial RNA polymerases end in '**SxYFFS**,' and its role is not known as of now. Identical sequences were seen in *Plasmodium* and human mitochondrial polymerases but the plant mitochondrial polymerases slightly vary (Fig. 5). This 6-amino acid sequence is found in RNA binding protein of the fungus, *Ustilago maydis* and primarily involve in RNA transports [6].

CLUSTAL O(1.2.4) MSA various SSU mitochondrial RNA polymerases from fungi

tr B6K333 B6K333_SCHJY	AASD SGQLK DLLEGL TALGN VGWKVNRKVYDMLVKIWNTGE SFLSIP SAN-TTLDIQEMP	653
5p 013993 RPOM_SCHPO	KASENGOLDELFKAV SSLGKVSWRINORLFNVLIRIWNSGEKFLSIP PRE-VKCDMPP YP	646
tr 390008 390008_3CHOY	EASHKGHLKKIYNAL SALGDVDWRINRFTFDVIVKIWNSGEGMLSIPPKN-VEVNLPPYP	660
tr 39X2W4 39X2W4_3CHCR	EASRKGHLKKVYGAL SALGDVSWRINRFTFDVIVKIWNSGEGMLSIPPKN-VEVNLPPYP	659
tr A0A1E303C6 A0A1E303C6_LIPST	EACR RNDLE SVYEGL DVLGS AAWIINTRVFE VLAKVWNTGE EFLEIPTRYEG DINFPLEP	741
tr A0A167E4J0 A0A167E4J0_9A3C0	AASDRGTLDQVYEGLNVLGNTAWTINKDIFEVILKVWNTGEEFLEIPRRVEIQPELPPAP	511
tr A0A1E3PUP0 A0A1E3PUP0_9ASCO	EASK RGAMN EVFEGL NVLGN TSWTINKDIFK VVMQLWNTGK PFLDIPGIS-DDVELPTEP	716
tr A0A0H5C7R0 A0A0H5C7R0_CYBJA	ASSDKIGKVYEGLNVLGSTAWTVNERVFNVMSQVWNTGEEFLDIPKLQ-DKIELPPQP	684
tr A0A1E3P5W0 A0A1E3P5W0_WICAO	ASTDRLDLVYEGLNVLGETAWTVNERVYKVMSEIWNTGETFLDIPKDQ-EEMNVPDAP	693
tr KOKTX3 KOKTX3_WICCF	ASSDKLDKVYDGLNVLGNTAWTVNERVFKVMSKIWNTGDEFLDIPKAH-ESLELPEVP	720
tr W6MIL2 W6MIL2_9ASCO	AASKRGDLDKVFKGLNVLGNTQWTPNKRILEIVTQVWNSGEEMLEIPAHI-SELKLPDPP	721
tr A0A1E30PI7 A0A1E30PI7_9ASCO	AASENGSLASVYKGLTVLGDTPWTVNRKIYDIVSQVWNTGESFLDIAGVQ-DELELPPPP	706
tr A0A1D2V948 A0A1D2V948_9ASCO	AASENGDLE GVYDGLNVLGVTAWTINKKILDLVTEAWNSGE EFLDIPKHE-KELILPPKP	746
tr A0A1B75ME0 A0A1B75ME0_9A5C0	TAAIKGKMDTVLQALNNLGSTAWTVNKEVLKVMIQVWNTGEEFLDIPKFR-ETLNLPPQP	393
tr Q6CRZ5 Q6CRZ5_KLULA	AVSEQGSIDNVYEGLNVLGNTPWTINEKLFNIVSEVWNTGEGFLDIPPVL-DNFEFPPQP	684
tr WOTGI8 WOTGI8_KLUMA	AVSEQGSIQNVYEGLNVLGNTAWTINEKLFNVISEVWNTGEEFLDIPPLQ-DKLELPAQP	683
tr A0A109UWS1 A0A109UWS1_9SACH	AVSDKLDNVYKGMNVLGDTPWTVNKTMLNIISTIWNSGEGFLDIPPQK-EDVELPPRP	694
tr G8JMS2 G8JMS2_ERECY	AVTG KGAVN NIYQGLNVLGD TAWTV NKPLFT ILSKI WNSGE EYLDIP PQE-DDCQLPP KP	724
tr Q75BP7 Q75BP7_ASHGO	AVTG KGVVQNVYKGLNVLGE TAWTVNKNMLHIISKVWNSGT EFLDIP PQQ-DELLLPA KP	717
tr R9XDF6 R9XDF6_ASHAC	AVTG KGAVQNVYNGL NVLGE TAWTVNKNMLH IVSKVWNSGS EFLDI P PQQ-DELLL PP RP	717
tr H2ASJ8 H2ASJ8_KAZAF	AASN VQALD KVYDGL NVLGD TAWTVNRRIFE IIS KVWNKGG SFLEIPGIQ-QESEFLPPP	702
tr J757Y3 J757Y3_KAZNA	AASN SNAID KVYDGL NVLGN TAWTVNRNIFN VVSKVWNEGK PFLEIP GTQ-EILELLP PP	695
tr GOVD01 GOVD01_NAUCC	AVSDADVIPDVYTGLNALGETAWTINKKVFDVISQVWNTGDEFLEIPEIQ-HDMNLLPPP	748
tr GOWE72 GOWE72_NAUDC	AVSDKEAIDDVYNGLNALGKTAWTVNKRLFEIISKVWNEGIEFLDIPQIQ-YDMQLIPPP	776
tr Q6FLX9 Q6FLX9_CANGA	AVSD SGAIDKIYDGLNVLGE TAWTVNRKVFDVVSKVWNEGTNFLEIPGIQ-DELKLLPPP	746
tr G8B354 G8B354 TETPH	AVSDAGAIDRVYHGLNVLGSTPWTVNRKIFNVISEVWNTGKPFLDIPGIQ-NTLNLLPPP	744
tr AOAOL 8RKW5 AOAO L8RKW5 _ SACEU	AASENGDIDRVYDGLNVLGDTPWTVNRKVFDVVSQVWNNGEGFLDIPSSQ-DEMILPPAP	771
tr AOAOL 8VRU3 AOAOL 8VRU3 9SACH	AASDNGDIDRVYDGLNVLGRTPWTVNRKVFDVVSQVWNKGEGFLDIPGAQ-DEMVLPPAP	770
tr J8PP58 J8PP58 SACAR	AASENGDIDRVYDGLNVLGNTPWTVNRKVFDVVSQVWNKREGFLDIPGAQ-DEMVLPPAP	770
tr A0A0C7MY71 A0A0C7MY71 95ACH	AVSD SGAIDNVYHGLNVLGE TPWTVNRKMFD IMSHVWNTGK AFLDIPGNQ-SKLILTPQP	716
tr C5DNP3 C5DNP3 LACTC	AVSDAGAIDNVYRGLNVLGETPWTVNRKMFNVMSQVWNSGK PFLDIPGIQ-EKLTLTPQP	711
tr C5DX79 C5DX79 ZYGRC	AVSDATAINTVYDGLNVLGETPWTVNRPLFEVMSKVWNSGKPFLDIPGVQ-EKLTLLPPP	732
tr G8ZR00 G8ZR00 TORDC	AVSNAGAIDTVYQGLNVLGETAWTVNRRVFDVMSEVWNSGKDFLEIPGIQ-EKLDLLPAP	742
tr A0A1E 4ROF7 A0A1E4ROF7 9ASCO	ASSNRISGVYDGLNVLGETPWTINRKVFEVITHYWNTGKOFLDIPPVS-EEINYPEPV	737
tr A0A0L0P4K6 A0A0L0P4K6 9A5C0	AASDAHNLDEVYKGLNILGETAWTVNSKVLDVISRCWNTGEOFLDIP PVA-EEPKLPP PL	725
tr A0A1A0HGT7 A0A1A0HGT7 9ASCO	AASD SGRLDGVYAGLNVLGKTAWSVNAKVLEVISHYWNTGNEFLDIP PIV-EEPKLPE PL	728
tr C4Y8E3 C4Y8E3 CLAL4	AASE ANNLD DVYRGLNVLGHTPWTINAKVLE VISOYWNTGE AFLDIP PVV-DEPELPP PL	731
tr G3B4C1 G3B4C1 CANTC	AASORGDLDKVYDGLNVLGNTPWTVNRKVLEVMTKFWNTGDEFLDIPPVV-DEPELPEPV	703
tr A3LX46 A3LX46 PICST	KAADLGNLNEVYDGLNVLGKTPWTVNRRVFEIITRYWNSGEEFLDIPPIM-EEPNLPEPL	677
tr AOA1E 45MT6 AOA1E45MT6 9A5CO	AASEMGNLDEIYQGLNVLGNTAWTVNRRVLDVITKHWNTGKEFLDIPPII-EEPNLPKAI	678
tr A5DN8 2 A5DN82 PICGU	AASDMGNLDOVYEGLNVLGETCWTINHEVFDVISHYWNSGEKFLDIPSIV-EELDIPPPP	723
tr B5RTF6 B5RTF6 DEBHA	AASDLONLE-IYDGLNVLGDTAWTVNRNVFNIISKFWNTGEKFLDIPPIV-EEPELPKOL	732
tr G3AEY0 G3AEY0 SPAPN	TAARNGNLDQVYAGLNVLGNTAWTVNKDIFKVISHYWNTGKEFLDIPGVL-DKPILPPKP	713
tr G8B7X1 G8B7X1 CANPC	AAAKRGNLKEVFDGLNVLGTTAWTINKKVFDIISHYWNKGEEFLSIPPVL-ETAOFPAKL	718
tr H8X1L6 H8X1L6 CANO9	AAAKRGNLOEVFDGLNVLGTTAWTINKKVFDVISHYWNKGDEFLTIPFVL EIAQFPAKL	717
tr B9W6L5 B9W 6L5 CANDC	AARERGALQEVEDGLAVLGETAWITMERVEDVISHTWARGDEFLITPFVL-ESAQEPFRL AANERGNLKAVFEGLNVLGKTAWIVNKKVFNVISHYWNSGEEFLSIPPVS-EEPRLPKDV	726
tr C4YFJ1 C4YFJ1 CANAW	AANERGNLEAVELGENVLGNEAWEVNNVENVESHEWNSGEEELSEPPVS-EEPOLPODI AANERGNLTGVFEGLNVLGNEAWEVNKKVFNVESHEWNSGEEFLSEPPVS-EEPOLPODI	706
tr C5ME71 C5ME71 CANTT	AARERGALIGVILGLAVLGAIAWIVARAVINVISHIWASGLEELSIPPVS-LEPQLPQDI AASKRGNLDOVFDGLAVLGAIAWIVARAVIPVISHYWAKGEEFLSIPPVS-LEPQLPQDI	706
tr M3IK19 M3IK19 CANNX	AASKRGNLDUVEDGLUVLGNIAWIVNRKVEDVISHIWNRGEEELSIPPVM-EEREPERE AASKRGNLDEVERGLUVLGSTPWTVNSKVEDVISHYWNIGEEELSIPPVL-NEAKEPSEL	721
PE INGINI A INGINIA CHNNY		123
	: : .: ** . * * :: ** **	

tr | B6K333 | B6K333 SCHJY sp|013993|RPOM_SCH01 tr|39Q0Q8|39Q0Q8_SCH0Y tr|39X2W4|39X2W4_SCHCR tr | S9X2W 4 | S9X2W 4 | SCHCR tr | A0A1E SQ3C6 | ADA1E SQ3C6 _ LIPST tr | A0A1E SQ3C6 | ADA1E SQ3C6 _ LIPST tr | A0A1E SPUPO | A0A1E SPUPO _ SASCO tr | A0A1E SPUPO | A0A1E SPUPO _ SASCO tr | A0A1E SPSWO | A0A1E SPSWO _ WICAO tr | KORTX3 | KORTX3 _ WICCF tr | KOMIL2 | WGMIL2 _ SASCO - A0A1E SOFOTO | ADA2E _ SASCO P-K-P-R-K-LP tr |AOALE 3QPI7 |AOALE3QPI7 _9ASCO tr |AOALE 3QPI7 |AOALE3QPI7 _9ASCO tr |AOALE2V948 |AOALE2V948 _9ASCO tr |AOALE7SME0 |AOALE7SME0 _9ASCO P-R-D-R-S-Ttr|Q6CR25|Q6CR25_KLULA tr|W0TGI8|W0TGI8_KLUMA tr|A0A109UWS1|A0A109UWS1_9SACH A-R-P-R-P-Rtr | G8 JM3 2 | G8 JM32 _ ERECY tr | Q75BP7 | Q75BP7_A3HG0 tr | R9XDF6 | R9XDF6_A3HAC tr | H2A3J8 | H2A3J8_KAZAF P-R-R-GE K-GE P-Ktr|J757Y3|J757Y3_KAZNA tr|G0VD01|G0VD01_NAUCC tr|G0WE72|G0WE72_NAUDC P-K-P-R-P-Rtr |Q6FLX9|Q6FLX9_CANGA tr |G8B354|G8B354_TETPH P-R-A-Rtr |AOAOL 8RKW5 |AOAOL 8RKW5 SACEU tr |AOAOL 8VRW5 |AOAOL 8RKW5 SACEU tr |AOAOL 8VRU3 |AOAOL 8VRU3 _98ACH tr |J8PP58 |J8PP58_SACAR P-R-P-R-P-Rtr | A0A0C7MY71 | A0A0C7MY71_9SACH P-Rtr|C5DNP3|C5DNP3_LACTC tr|C5DX79|C5DX79_ZYGRC tr|G8ZR00|G8ZR00_TORDC P-R-P-R-P-Rtr |AOALE 4RQF7 |AOALE4RQF7_9ASCO tr |AOALE 4RQF7 |AOALE4RQF7_9ASCO tr |AOALE 0HGT7 |AOALE4RQF7_9ASCO A-F-P-S-P-Ktr|C4Y8E3|C4Y8E3_CLAL4 tr|G3B4C1|G3B4C1_CANTC tr|A3LX46|A3LX46_PIC3T P-L-P-S-P-Vtr | AOA1E4SMT6 | AOA1E4SMT6 9ASCO P-Ltr|A5DN82|A5DN82_PICGU tr|B5RTF6|B5RTF6_DEBHA P-Iр-мtr|G3AEY0|G3AEY0_SPAPN tr|G8B7X1|G8B7X1_CANPC E-R-S-Ptr |H8X1L6|H8X1L6_CANO9 tr |B9W6L5|B9W6L5_CANDC tr |C4YFJ1|C4YFJ1_CANAW S-P-P-D-P-Gtr | C5ME71 | C5ME71 CANTT P-Atr |M3IK19|M3IK19_CANMX P-Etr|B6K333|B6K333 SCHJY FRGR FRGR FRGI FRGE FRGE

=p|013993|RPOM_3CHPO tr|39Q0Q8|39Q0Q8_3CHOY tr|39X2W4|39X2W4_3CHCR tr |A0A1E3Q3C6 |A0A1E3Q3C6 _LIPST tr |A0A1E3Q3C6 |A0A1E3Q3C6 _LIPST tr |A0A1E7E4J0 |A0A167E4J0 _9A3C0 tr |A0A1E3PUP0 |A0A1E3PUP0 _9A3C0 tr |A0A0H5C7R0 |A0A0H5C7R0 _CYEJA tr |AOAOHSC7R0 |AOAOHSC7R0 _CYEJA tr |AOALSS5500 |AOADHSC7R0 _CYEJA tr |AOALSS5500 |AOALS25500 _WICAO tr |KOKIX3 | KOKIX3 _WICCP tr |W6MIL2 |W6MIL2 _9ASCO tr |AOALD2V948 |AOALD2V948 _9ASCH tr |W0TG18 |W0TG18 _KLUMA tr |W0TG18 |W0TG18 _LONGW83 | 9ASCH tr | A0A109UWS1 | A0A109UWS1 95ACH tr |G8JM32|G8JM32_ERECY tr |Q75BP7|Q75BP7_A3HGO tr |R9XDF6|R9XDF6_A3HAC tr | H2ASJ8 | H2ASJ8 | KAZAF tr | J7S7Y3 | J7S7Y3 | KAZAF tr | G0VD0 1 | G0VD01_NAUCC tr | G0WE72 | G0WE72_NAUDC tr|Q6FLX9|Q6FLX9_CANGA tr|G8E354|G8E354_TETPH tr|A0A0L8RKW5|A0A0L8RKW5_SACEU tr | AOAOL SVRU3 | AOAO LSVRU3 95ACH tr | J80PD50139 | J80PD5 | SACAR tr | J80PD50 | J80PD5 | SACAR tr | A0AOC7MY71 | A0AOC7MY71 _ 93ACH tr | C5DN73 | C5DN73 _ LACTC tr | C5DX79 | C5DX79 _ ZYGRC tr |622R0 0|682R00_TORDC tr |A0A1E 4RQF7 |A0A1E 4RQF7 _9ASCO tr |A0A0L0P4K6 |A0A0L0P4K6 _9ASCO tr |A0A1A0HGT7 |A0A1A0HGT7 _9ASCO tr|C4Y8E3|C4Y8E3_CLAL4 tr|G3B4C1|G3B4C1_CANTC tr|A3LX46|A3LX46_PIC3T tr | AOA1E 45MT6 | AOA1E45MT6 9ASCO tr |A5DN82|A5DN82|FICGU tr |A5DN82|A5DN82|FICGU tr |B5RTF6|B5RTF6_DEBHA tr |G3AEY0|G3AEY0_SPAPN tr |G8B7X1|G8B7X1_CANFC tr | H8X1L6 | H8X1L6 CANO9 tr | B9W6L5 | B9W 6L5_CANDC tr | C4YFJ1 | C4YFJ1_CANAW tr | C5ME71 | C5ME71_CANTT tr |M3IK19|M3IK19 CANMX

FRGRAYPLS PHFNHLGNDLS RGLLI FWKGKKLGPDGL WLK HCANL YOMDK IPFTER IQ 991 FRGRAYPLS PHFNHLGNDLS RSLLI FWKGKRLGPDGL WLK VHLSNI YOUNK SIEDRVK 869 FRGRAYPLS PHFNHLGNDMS RGLLI FWKGKRLGPDGL WLK VHLSNI YEVDKASLEDRVK 869 FRGRAYPLS PHFNHLGNDMS RGLLI FWKGKRLGSSGL WLK VHLSNI YEVDKASLEDRVK 869 FRGRAYPLS PHFNHLGNDMS RGLLI FWKGKRLGSSGL WLK VHLSNI YEVDKASLEDRVK 865 FRGRAYPLS PHFNHLGNDMS RGLLI FWKGKRLGSSGL WLK VHLSNI FEVDKASLEDRVK 865 FRGRAYPLS PHFNHLGNDMS RGLLT FWKGKRLGSGL WLK VHLSNI FEVDKASLEDRVK 865 FRGRAYPLS PHFNHLGNDMS RGLLF FWKGKRLGSGGL WLK VHLSNI FEVDKASLEDRVK 862 FRGRAYPLS PHFNHLGNDLT SLFL FWKGKRLGSGGL WLK VHLSNI FEVDKASLEDRVK 862 FRGRAYPLS PHLNHLGNDLT RSLFL FWKGKRLGSGELWLK VHLSNI FEVDKASLEDRVK 864 FRGRAYPLS PHLNHLGNDLT RSLFL FWKGKRLGSGELGERGLWLK VHLSNI FEVDKASLEDRVK 864 FRGRAYPLS PHLNHLGNDLT RSLFL FWEGKELGERGLEWLK HLANT YONKASLERVC 943 FRGRAYPLS PHLNHLGNDLT RSLFL FWEGKELGERGLWKK HLANT YONKASLERVC 943 FRGRAYPLS PHFNHLGNDLT RSLFL FWEGKELGERGLWKK KHLANT YONKASLERVC 946						
K-C ALIMPENDAY SPYCE BINKES REPORTANES DEC. PLANT LE ANSY VLANEE AVEPTRENED 718 K-C TAME AND AND DE DIALY OF DESIGN AND AND AND AND AND AND AND AND AND AN	E-KSIDPSARAEWLRMLKERSLDFASQHS	RCEFN	TYT LE	AKA FI	HET FYFPHNVD	708
F-C TALE PRIME AT DELEMENT HUMAN ALSO NOT THE LAND FURSE THEOREM 114 F-C TALE PRIME AT THE LANCE THE LANCE THE LAND FURSE THEOREM 714 F-C TALE PRIME AT THE LANCE THE LANCE THE LAND FURSE THEOREM 714 F-C TALE PRIME AT THE LANCE THE LANCE THE LAND FURSE THEOREM 714 F-C TALE PRIME AT THE LANCE THE LANCE THE LANCE THE LAND FURSE THE LANCE	K-NSINPRDEVIWHTRREELAALETGAHS	RC DEN	YF LE	ARA FI	NEK FYFPHS LD	
P.H. — D. D.D.PAYARB MAY GULAI HERAT SHORE O'NATH III AN FLOER LIPPINID ??66 P.H. — D.D.D.PAYARB MAY GULAI HERAT SHORE O'NATH III AN LIGER TEPRINID ??66 P.H. — T.T.E.FOYLI SHAR O'NEAD MET NO. ANTOL III AND FLOER TEPRINID ??66 P.H. — T.T.E.FOYLI SHAR O'NEAD MET NO. ANTOL III AND FLOER TEPRINID ??66 P.H. — T.T.E.FOYLI SHAR O'NEAD MET NO. ANTOL III AND FLOER TEPRINID ??66 P.H. — T.S.D.PAYLIEKEN KUKALO DEVIA DE THE CANTY II AND FLOER TEPRINID ??61 P.H. — T.D.D.PAYARB MAYALA DE TERT THE RECONNEL III AND FLOER TEPRINID ??61 P.H. — T.D.D.PAYLIEKEN KORGON DET NO. ANTOL III AND FLOER TEPRINID ??61 P.H. — T.D.D.PAYLIEKEN KORGON DET NO. ANTOL III AND FLOER TEPRINID ??61 P.H. — T.D.D.PAYLIEKEN KORGON DET NO. ANTOL III AND FLOER TEPRINID ??61 P.H. — T.D.D.PAYLIEKEN KORGON DET NO. ANTOL III AND FLOER TEPRINID ??61 P.H. — T.D.D.PAYLIEKEN KORGON DET NO. ANTOL III AND FLOER TEPRINID ??61 P.H. — T.D.D.PAYLIEKEN KORGON DET NO. ANTOL III AND FLOER TEPRINID ??61 P.H. — T.D.D.PAYLIEKEN KORGON DET NO. ANTOL III AND FLOER TEPRINID ??61 P.H. — T.D.D.PAYLIEKEN KORGON DET NO. ANTOL III AND FLOER TEPRINID ??61 P.H. — T.D.D.PAYLIEKEN KORGON DET NO. ANTOL III AND FLOER TEPRINID ??61	K-QALNPNDRV SWYSLRDKLS REKATAHS	ORCIPEN	VHLE:	ANSYL	NEK FYFPHNMD	
P=R						
CBK ————————————————————————————————————	P-RDADPSVRRDWLRQCRLIVNENQALYS	RCDIN	YF LE:	ARAFI	GERFYLPHNLD	566
P=R	A-RNVDPAIRR DWLRE CRAIVNRNQADHS	RCDIN	YF LE:	ARA FI	GER LYFPHNMD	
RE.PCTVALDPERAAURAKENZAAURAAURAAURAAURAAURAAURAAURAAURAAURAAU						
RE.PCTVALDPERAAURAKENZAAURAAURAAURAAURAAURAAURAAURAAURAAURAAU	P-RSSDPSVLNEWKIKVKALODKYATDRS	RCDAN	TYRLE	ARAFI	GEKFYFPHNLD	
P.B						
D=B	P-RDADPVVRRDWSRRVKALADEFSTRRS	RCDSN	YF LE:	ARGLI	GEKIYFPHNID	761
A-BSEDDLILEKNIK CRUSSERGERSEN LEARNE LEARAFLEKEYFPHIND 738 P-BSEDDLILKINKE CRUTHEREGERSEN LEARE SINK LEARAFLEKEYFPHIND 738 P-B	D-RGE DPSVKT EWQTI SKQKS YEYYAN RS	QRCIPTN	VYR LE:	ARA FV	GEK FYFPHN LD	
P=R						
P=R	P-RSADPLVLKEWRNKCROLTNEFKGFKS	TRCDSN	TYRLE	ARAFI	GEKFYFPHNMD	
R-CEOGEGE E D'ULE MKKQC CHELA AE YQCH RENC AAN'N LE JAA FLGEK FYFFNHOD F-CRADES'LIE MKKQC CHELA AE YQCH RENC AAN'N LE JAA FLGEK FYFFNHOD F-CRADES'LIE MKKQC CHELA AE YQCH RENC AAN'N LE JAA FLGEK FYFFNHOD F-C	P-RDADPLILKHWRNECKFKTLEFRSDRS	RCDSN	YF LE	ARAFI	GER FYFPHS LD	
K-OENGGEPETULKKKQDCALLSAFYQHRBARCLANY LEAAAFJGEK FYFPHNLD 776 F-KNADSTULEKKINNELIANYISJNESKCLANY LEAAAFJGEK FYFPHNLD 780 F-K	P-RES DPLELK RWRND CRFKN IEYRGN RA	RCDSN	YF LE:	ARA FI	GEK FYFPHNMD	
P=RNADSTUTENTKNILAINTSSNESSECLATYLESAAFLGEKYTENHUD 750 P=RSDDSTIENTKNINSULSUESANTSNESTELATYLESAAFLGEKYTENHUD 831 P=RNDSDSTIENTKNINSULSUESANTSNESTELATYLESAAFLGEKYTENHUD 831 P=RNDSDSTIENTKSINSULSUESANTSNESTELATYLESAAFLGEKYTENHUD 831 P=RNDSDSTIENTKSINSUSSANTSNESTELATYLESAAFLGEKYTENHUD 831 P=RNDSDTIENTKSINSUSSANTSOLATYLESAAFLGEKYTENHUD 831 P=RNDSDTIENTKSINSUSSANTSOLATYLESAAFLGEKYTENHUD 835 P=RNDSDTIENTKSINSUSSANTSOLATYLESAAFLGEKYTENHUD 835 P=RNDSDTIENTKSINSUSSANTSOLATYLESAAFLGEKYTENHUD 766 P=RNDSDSTIENTKEINTELANETSONSUSSANTSOLATYLESAAFLGEKYTENHUD 777 P=RNDSDSTIENTKEINTELANETSONSUSSANTSOLATYLESAAFLGEKYTENHUD 777 P=RNDSDSTIENTKEINTELANETSONSUSSANTSOLATYLESAAFLGEKYTENHUD 778 P=RNDSDSTIENTKKEINTELANETSONSUSSANTSOLATYLESAAFLGEKYTENHUD 778 P=RNDSDSTIENTKKEINTELANETSONSUSSANTSOLATYLESAAFLGEKYTENHUD 778 P=RNDSDSTIENTKKEINTELANETSONSUSSANTSOLATYLESAAFLGEKYTENHUD 778 P=RNDSDSTIENTKKEINTELANETSONSUSSANTSOLATYLESAAFLGEKYTENHUD 778 P=RNDSDSTIENTKKEINTELANETSONSUSSANTSOLATYLESAAFLGEKYTENHUD 780 P=RNDSDSTIENTKKEINTELANETSONSUSSANTSOLATYLE						
P=RG D DAVITEMENT NYLS METSAN RANCCI TYY LEAA AFLGEK FYFPHNLD 750 P=RND DESTER MKLD NELLANK SINNE RECTIVY LEAAA FLGEK FYFPHNLD 831 P=RND DESTER MKLD NELLANK SINNE RECTIVY LEAAA FLGEK FYFPHNLD 831 A-RE						
P=RDS DP 2ETR KWLLQWELLANK ISDN 3F WC TTYYLLZ AAR LLGEK FYPENILD 6031 P=RBS DP ILR KWLLQWELLANK ISDN 3F WC TTYYLL AAR LLGEK FYPENILD 6031 P=RBS DP ILR WWLLWICZIANK ISDN 3F WC TTYYLL AAR LLGEK FYPENILD 6031 P=RBS DP ILR WWLLWICZIANK ISDN 3F WC TTYYLL AAR LLGEK FYPENILD 6031 P=RBS DP ILR WWLLWICZIANK ISDN 3F WC TTYYLL AAR LLGEK FYPENILD 625 P=RBS DP ILR WWLLWICZIANK ISDN 3F WC TTYYLL AAR LLGEK FYPENILD 750 P=RBA DP JILR WWLLWICZIANK ISDN 3F WC TTYYLL AAR LLGEK FYPENILD 761 P=RBA DP JILR WWLLWICZIANK ISDN 3F WC TTYYLL AAR LLGEK FYPENILD 771 P=RBA DP JUR WWLLWICZIANK ISDN 3F WC DIYYLL AAR LLGEK FYPENILD 797 P=R						
P=R	P-RDS DPSEFR KWKLQNKELANKISKN RS	RCDIN	TYP LE:	ARAFI	GERFYFPHNLD	
A-EDADSTIR.WKLUKULINKESDNASTKOTIYYLL AAATLGEKIYFENILD 799 P-ENSDSTIR.WKLUKULINKESDNASTKOTIYYLL AAATLGEKIYFENILD 226 P-ENSDSTIR.WKLUKULINKESDNASTKOTIYYLL AAATLGEKIYFENILD 225 P-ENSDSTIR.WKLUKULINKESDNASTKOTIYYLL AAATLGEKIYFENILD 225 P-EDADSTIR.WKLUKULINKESDNASTKOTIYYLL AAATLGEKIYFENILD 225 P-EDADSTIR.WKLUKULINKESDNASTKOTIYYLL AAATLGEKIYFENILD 771 P-EDADSTIR.WKLUKULINKESDNASTKOTIYYLL AAATLGEKIYFENILD 772 P-EDADSTUREWKLUKUELINKESDNASTKOTIYLL AAATLGEKIYFENILD 772 P-E						
P=RNS DF71LRAWLQVKTIANKESDBASHCCTNYLLZ AAR LOGKLYFFENID 825 P=RNS DF71LRAWLQVKTIANKESDBASHCCTNYLLZ AAR LOGKLYFFENID 771 P=RDAD951LRWKLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 771 P=RLAD97URBEWLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 771 P=RLAD97URBEWLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 780 P=READ97URBEWLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 780 P=READ97URBEWLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 780 P=RKADE97URBEWLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 780 P=RNAEPEAREVORALOGAVLKAANSEGAC TYTYLLZ AAR LOGKLYFFENID 780 P=LNAEPELEKVQAKLRGALNAAASASSGAC TYTYLG AAR LOGKLYFFENID 780 P=LNAEPEKFEYQKKURGALNAAASASSGAC TYTYLG AAR LOGKLYFFENID 780 P=LDADFLOKTOQUKRLRGALNAASASSGAC TYTYLG AAR LOGKLYFFENID 780 P=LDADFLOKTOQUKRLRGALNAASASSGAC TYTYLG AAR LOGKLYFFENID 780 P=LDADFLKFYQKKURGALNAASASSGAC TYTYLG AAR LOGKLYFFENID 773 P=LDADFLKFYQKKURGALNAASASSGAC TYTYLG AAR LOGKLYFFENID 778	P-RSSDPTVIREWKLKNKELANKYSSDKS	RCDLN	YYP LE	ARAFI	GEKFYFPHNLD	
P=RNS DF71LRAWLQVKTIANKESDBASHCCTNYLLZ AAR LOGKLYFFENID 825 P=RNS DF71LRAWLQVKTIANKESDBASHCCTNYLLZ AAR LOGKLYFFENID 771 P=RDAD951LRWKLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 771 P=RLAD97URBEWLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 771 P=RLAD97URBEWLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 780 P=READ97URBEWLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 780 P=READ97URBEWLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 780 P=RKADE97URBEWLKHELANFESGASACAANYLLZ AAR LOGKLYFFENID 780 P=RNAEPEAREVORALOGAVLKAANSEGAC TYTYLLZ AAR LOGKLYFFENID 780 P=LNAEPELEKVQAKLRGALNAAASASSGAC TYTYLG AAR LOGKLYFFENID 780 P=LNAEPEKFEYQKKURGALNAAASASSGAC TYTYLG AAR LOGKLYFFENID 780 P=LDADFLOKTOQUKRLRGALNAASASSGAC TYTYLG AAR LOGKLYFFENID 780 P=LDADFLOKTOQUKRLRGALNAASASSGAC TYTYLG AAR LOGKLYFFENID 780 P=LDADFLKFYQKKURGALNAASASSGAC TYTYLG AAR LOGKLYFFENID 773 P=LDADFLKFYQKKURGALNAASASSGAC TYTYLG AAR LOGKLYFFENID 778	D-DNSDDSTIDTWEIOUETTANEFSSDDS	TRCDTN	TVETE	ARATI	GERITEPHNLD	
P=R	P-KNSDFTILRAWKLOVKTIANKFSSDRS	RCDIN	TYRLE	ARAFI	GEKLYFPHNLD	
P=R	P-RNSDPSILRTWKLEVKTIANKFSSDRS	RCDIN	TYR LE:	ARAFI	GEKLYFPHNLD	
P=R	P-RDADPSIHRKWKLKNKELANEFSSGRS	ARC DAN	VYR LE:	I ARA FI	.GEK FYFPHN LD	
P=R	P-RDADPSVHREWKLKNKELANEFSGNRS	ARCDAN	YELE:	ARA FI	GEK FYFPHN LD	
A-PWALEPEARLEYQRELEYQRULLASAMIS®C TIYLEZAR OFLOEKLEFENID 792 P-SWALEPEARLYQREVURULINAASFRSØK CIYLLEZAR VUGKMETENSD 780 P-SWALEPUERVURUKUNALASASFRSØK CIYLLEZAR VUGKMETENSD 780 P-LNALEPUERVURUKUNALASASFRSØK CIYLLEZAR VUGKMETENSD 780 P-LNALEPUERVURUKURUKUNALASARSØK CIYLLEZAR VUGKMETENSD 780 P-LDALEPARTEYQRKURUKURUKUNALASARSØK CIYLLEZAR FLOEKVETENSD 732 P-LDALEPARTEYQRKURUKURUKUNALASARSØK CIYLLEZAR FLOEKVETENSD 738 P-LDALEPARTEYQRKURUKURUKUNALASARSØK CIYLLEZAR FLOEKLIFTENSD 786 P-MDALEPARTEYQRKUNGURUKURUKASARSØK CIYLLEZAR FLOEKLIFTENSD 787 P-MDALEPERKURTARVOLTUGUKURUKURUKASARSØK CIYLLEZAR FLOEKLIFTENSD 788 P-MDALEPERKURTARVOLTUGUKURUKURUKURUKURUKURUKUKURUKURUKURUKUR	P-RES DPSVHR EWKLK NKETA NKF99N D91	VBCDSN	TYRLE	TARAFI	GEKEYEPHNID	
P=R	A-FNAEPEAKKEYQKRLKQAVLEASAMNS	RCDIN	YELE:	ARGFI	GEKLFFPHNID	
P=R	P-SNAEPSOKSEYIKQVKQILNEAAGHRS	DRCDIN	YELE:	ARAFV	GERMFFPHSVD	780
P-UDAEPAQEFYQRKLESALNEAASLESGCTNYKLEJARGFLGEKLYFFFHNUD P-LDAEPKEFYGYGKVENQALNAASLESGCTNYKLEJARGFLGEKLYFFFHNUD 732 P-LDADEJGKTYYGRKUKAMALASSLESGCTNYKLEJARGFLGEKLYFFHNUD 778 P-MNEDFFKAFYGKVENKAMALASSLESGCTNYKLEJARGFLGEKLYFFHNUD 778 5-PDADFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 773 5-PDADFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 773 5-PDADFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARGKLYKSLEFASSRSSGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARGKLYKSLEFASSRSSGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARGKLYKSLEFASSRSSGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDFSTRFHARGKLYKSLEFASSRSSGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDFSTRFHARGKLYKSLEFASSRSSGCYNKKULANT FRGRAYFISSHLHYNDYCRGLLEFAGERFLGEGFYNLKULANT FRGRAYFISSHLHYNDYCRGLEFFEGRELGFFDKLKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFFEGFEGEFFFEFFE FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFFEFFE FRGRAYFISSHLHYNDYCRGRUGHFFEGFEGEFFFE FRGRAYFISSHLHYNDYCRGRUGHFFEGFEGEFFFE FRGRAYFISSHLHYNDYCRGRUGHFFEGFEGEFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	P-KNAEPLEKVQYAKKVRNALNQAASFRS	DRCDTN	VYELE:	ARA YV	GEKMYFPHNVD	
P-UDAEPAQEFYQRKLESALNEAASLESGCTNYKLEJARGFLGEKLYFFFHNUD P-LDAEPKEFYGYGKVENQALNAASLESGCTNYKLEJARGFLGEKLYFFFHNUD 732 P-LDADEJGKTYYGRKUKAMALASSLESGCTNYKLEJARGFLGEKLYFFHNUD 778 P-MNEDFFKAFYGKVENKAMALASSLESGCTNYKLEJARGFLGEKLYFFHNUD 778 5-PDADFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 773 5-PDADFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 773 5-PDADFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARATTKAVRFSSBASGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARGKLYKSLEFASSRSSGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARGKLYKSLEFASSRSSGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDDFSTRFHARGKLYKSLEFASSRSSGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDFSTRFHARGKLYKSLEFASSRSSGCYNYKLEJARGFLGEKLYFFHNUD 776 P-CNDFSTRFHARGKLYKSLEFASSRSSGCYNKKULANT FRGRAYFISSHLHYNDYCRGLLEFAGERFLGEGFYNLKULANT FRGRAYFISSHLHYNDYCRGLEFFEGRELGFFDKLKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGREFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFEGFUGNSLWIKKULANT FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFFEGFEGEFFFEFFE FRGRAYFISSHLHYNDYCRGLEFFEGFEGEFFFEFFE FRGRAYFISSHLHYNDYCRGRUGHFFEGFEGEFFFE FRGRAYFISSHLHYNDYCRGRUGHFFEGFEGEFFFE FRGRAYFISSHLHYNDYCRGRUGHFFEGFEGEFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	P-1NAEPLEKVEYQRKVRHVLNEAAAYRS	DRCDTN	VELE:	ARAF	GERMFFPHNVD	
P-L	P-VDAEPAOKFEYORKLRSALNEAASLRS	DRCDTN	TYRLE	TARGET	GERVFFPHNVD	
P-M	P-LDAEPNEKFEYQKKVRQAINDAASAKS	RCDIN	TYRLE	ARGFI	GEKLFFPHNVD	
E-RSDDP3TRFHARATTRAVDEP53R39GCDAVYLTELAAR FIGEKLYFPHNLD 763 S-PDADP3TRFHARATTRAVDEF53R39GCVYVTLELAAGFIGEKLYFPHNLD 773 S-PDADPEVLINTTATIKAVTEF53R39GCVYVTLELAAGFIGEKLYFPHNLD 773 S-PDADPEVLINTTSFRALDEVSNES9GCVYVTLELAAGFIGEKLYFPHNLD 771 S-DNDDPQLAKLDNSIALYKGLREFASDRS9GCVYVTLELAAGFIGEKLYFPHNLD 761 S-ADADPAEKLENSLVYKSLREFASDRS9CVYVTLELAAGFIGEKLYFPHNLD 776 S-ANADPAEKLENSLVYKSLREFASDRS9CVYVTLELAAGFIGEKLYFPHNLD 776 S-ANADPAEKLENSLVYKSLREFASDRS9CVYVTLELAAGFIGEKLYFPHNLD 778 S-ANADPAEKLENSLVYKSLREFASDRS9CVYVTLELAAGFIGEKLYFPHNLD 778 S-CNADPAEKLENSLVYKSLREFASDRS9CVYNTLELAAGFIGEKLYFPHNLD 778 S-CNADPAEKLENSLVYKSLREFASDRS9CVYNTLELAAGFIGEKLYFPHNLD 778 S-CNADPAEKLENSLVYKSLREFASDRS9CVYNTLELAAGFIGEKLYFPHNLD 778 S-CNADPAEKLENSLVYKSLREFASDRS9CVYNTLELAAGFIGEKLYFPHNLD 778 S-CNADPAEKLENSLVYKSLREFASDRS9CVYNTLELAAGFIGEKLYFPHNLD 778 S-CNADPAEKLENSLVYKSLREFASDRS9CVYNTLELAAGFIGEKLYFPHNLD 778 S-CNADPAEKLENSLVYKSLREFASDRS9C 779 S-C	P-IDADPLOKT DYORR LROLMNDAASARS	DRCDIN	YELE:	ARAFI	GEKLYFSHNVD	
3-PDADSERVIDHTRATIKAVEFSSERSQRCYNYKLEIARGFIGEKLYFPHNLD 778 9-DNDDFVLLHMTGKFRALDEVISNKSQRCNNYKLEIARFIGEKLYFPHNLD 778 P-ADADPGAKLINGKISKUKSQRCNNYKLEIARFIGKLYFPHNLD 776 9-BNDDFVKLYKLERFASSRSQRCNNYKLEIARFIGKLYFPHNLD 776 9-ENDDFVKLYKLERFASSRSQRCNNYKLEIARFIGKLYFPHNLD 776 9-ENDDFVKLYKLERFASSRSQRCNNYKLEIARFIGKLYFPHNLD 776 9-ENDDFVKLYKLERFASSRSQRCNNYKLEIARFGYKLYFPHNLD 776 9-ENDDFVKLYKLERFASSRSQRCNNYKLEIARFGYKLYFPHNLD 776 9-RORAVEDSKILERSKLYKSLREFASSRSQRCNNYKLEIARFGYKLYFPHNLD 776 9-RORAVEDSKILFYKLERFASSRSQRCNNYKLEIARFGYKLYFPHNLD 776 9-RORAVEDSKILFYKLERFASSRSQRCNNYKLEIARFGYKLYFPHNLD 776 9-RORAVEDSKILFYKLERFASSRSQRCNNYKLYFFNXLD 776 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSHLNNKGNDFCRSLEFSCHUEFGUEGGUEWKKWLHANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLEFASSRSQRCNWKLWLANT 9-	P-MNAEPFEKAEYQRKVRKAMNEAASARS	DRCDIN	YELE:	ARGFI	GEKLFFPHNVD	
3-PDADSERVIDHTRATIKAVEFSSERSQRCYNYKLEIARGFIGEKLYFPHNLD 778 9-DNDDFVLLHMTGKFRALDEVISNKSQRCNNYKLEIARFIGEKLYFPHNLD 778 P-ADADPGAKLINGKISKUKSQRCNNYKLEIARFIGKLYFPHNLD 776 9-BNDDFVKLYKLERFASSRSQRCNNYKLEIARFIGKLYFPHNLD 776 9-ENDDFVKLYKLERFASSRSQRCNNYKLEIARFIGKLYFPHNLD 776 9-ENDDFVKLYKLERFASSRSQRCNNYKLEIARFIGKLYFPHNLD 776 9-ENDDFVKLYKLERFASSRSQRCNNYKLEIARFGYKLYFPHNLD 776 9-ENDDFVKLYKLERFASSRSQRCNNYKLEIARFGYKLYFPHNLD 776 9-RORAVEDSKILERSKLYKSLREFASSRSQRCNNYKLEIARFGYKLYFPHNLD 776 9-RORAVEDSKILFYKLERFASSRSQRCNNYKLEIARFGYKLYFPHNLD 776 9-RORAVEDSKILFYKLERFASSRSQRCNNYKLEIARFGYKLYFPHNLD 776 9-RORAVEDSKILFYKLERFASSRSQRCNNYKLYFFNXLD 776 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSHLNNKGNDFCRSLEFSCHUEFGUEGGUEWKKWLHANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLERFASSRSQRCNWKLWLANT 9-RORAVEDSKILFYKLEFASSRSQRCNWKLWLANT 9-	E-RSDDPSIKYKYRKLVTQLKSEFSTMRS(S-DDLDDSTDFFHLKLTTKLVDDFSSSDS(DRC DAN	TYRLE:	TARAFI	GERLYFPHNLD	
P-DNB DEPCLINTMESTRALDEYMSNESGRC NNYKE LETARAFIGEK LYFENNLD 781 P-GNB DEPCKLINTTS RYQALDEYISNESGRC NNYKE LETARAFIGEK LYFENNLD 776 P-CNADDEPCKLINTS RYGALDEYISNESGRC NNYKE LETARAFIGEK LYFENNLD 776 P-CNADDEPCKLIERSKLUYKSLREFASISSBOC NYNKE LETARAFIGEK LYFENNLD 776 P-CNADDEPCKLIERSKLUYKSLREFASISSBOC NYNKE LETARAFIGEK LYFENNLD 776 P-CNADPKEKLERSKLUYKSLREFASISSBOC NYNKE LETARAFIGEK LYFENNLD 776 P-CNADPKEKLERSKLUYKSLREFASISSBOC NYNKE LETARAFIGEK LYFENNLD 776 P-RORAYEJSHLHYNSDECRSLLIFSEGREF NYKE VOLANT FENKNESTIGER D 786 FRORAYEJSHLHYNSDECRSLLFFSGREF LØFERG LWIKE VOLANT FENKNESTIGER D 786 FRORAYEJSHLHNUSDECRSLLFFSGREF LØFERG LWIKE VOLANT FENKNESTIGER D 786 FRORAYEJSHLNINGSDER GELIFFERGREF LØFERG LWIKE VOLANT FENKNESTIGER D 786 FRORAYEJSHLNINGSDER GELIFFERGREF LØFERG LWIKE VOLANT FENKNESTIGER D 786 FRORAYEJSHNINGSDER GELIFFERGREF LØFERG LWIKE VOLANT FENKNESTIGER D 806 FRORAYEJSHNINGSDER GELIFFERGREF LØFERG LWIKE VOLANT FENKNESTIGER D 800 FRORAYEJSHNINGSDER SKLIFFERGREF LWIKER LINKNE LETARAFIERDER I 800 FRORAYEJSHNINGSDER SKLIFFERGREF LWIKER LINKNE FENKNESTIGER D 801 FRORAYEJSHNINGSDER SKLIFFERGREF LWIKER LINKNE LETARAFIERDER I 800 FRORAYEJSHNIN	S-PDADPSERYDHTKATIKAVREFSSSRS	DRCDYN	TYRLE	TARGET	GEKLYFPHNLD	
P-ADADPCAKLDNSIALIXGLRETAGNRSØRCYNVELELARGFIGERLYFFHNID 776 P-ENADPKEKLERSKLVYKSLREFASSRSØRCYNVELELARGFIGERLYFFHNID 778 FRGRAYPLSSHLHVSKLRESKLVYKSLREFASSRSØRCHNVELELARGFIGERLYFFHNID 778 FRGRAYPLSSHLHVSNDYRSLEFASSRSØRCHNVELELARGFIGERLYFFHNID 778 FRGRAYPLSSHLHVSNDYRSDERGLEFAGERFIGERGLØVLKVLANLFFSTØRKDFATRQA 761 FRGRAYPLSSHLHVSNDYRCKLLFFSTGFFLGERGLØVLKVLANLFFSTØRVDYASRQK 775 FRGRAYPLSSHLHHVSNDYCRGLLFFSTGFFLGERGLØVLKVLANLFFSTØRVDYASRQK 775 FRGRAYPLSSHLHVSNDYRCKJLFFYGREFLGERGLØVLKVLANLFFSTØRVDYASRQK 775 FRGRAYPLSSHLHVSNDYRCKJLFFYGREFLGERGLØVLKVLANLFFSTØRNFUDASRQK 766 FRGRAYPLSSNTHLGNDLSSGLLFFWEGRELGERGLØVLKVLKVLANUF FUNKASPHDERVQ 866 FRGRAYPLSSNTHLGNDLSSGLLFFWEGRELGEGGLØVLKVLKVLANUF FUNKASPHDERVQ 800 FRGRAYPLSSNTHLGNDLSSGLLFFWEGRELGEGGLØVLKVLKVLANUF FUNKASPHDERVQ 800 FRGRAYPLSSNTHLGNDLSSGLLFWEGRELGEGGLØVLKVLKVLANUF FUNKASPHDERVQ 800 FRGRAYPLSSNTHLGNDLSSGLLFWEGRELGEGGLØVLKVLKVLANUF FUNKASPHDERVQ 800 FRGRAYPLSSNTHLGNDLSSGLLFWEGRELGEGGLØVLKVLKVLANUF FUNKASPHDERVQ 800 FRGRAYPLSSNTHLGNDLSSGLLFWEGRELGEGGLØVLKVLKVLANUF FUNKASPHDERVX 801 FRGRAYPLSSHTHLGNDLSSGLLFWEGRELGEGGLØVLKVLKVLANUF FUNKASPHDERVX 801 FRGRAYPLSSHFNHLGNDLSSGLLFWEGRELGEGGLØVLKVLHLANUF FUNKASPHDERVX <td>P-DNS DPEVLL NYTMS KFRAL DEYMSNKS</td> <td>RCDNN</td> <td>YRLE:</td> <td>ARAFI</td> <td>GEKLYFPHNLD</td> <td></td>	P-DNS DPEVLL NYTMS KFRAL DEYMSNKS	RCDNN	YRLE:	ARAFI	GEKLYFPHNLD	
FRGR AYPLP SHLHHVNSDFCRSLLIFAEGKPLGEEG FWLKLVQLANL FKNKSTIQER ID 768 FRGR AYPLS SHLHHVNSDFCRSLLFFSTGKPLGEKGLWULKVHLANLFSTSKNFATRQA 761 FRGR YYPISAHLHHVNDFCRGLLFFSTGKPLGEKGLWULKVHLANLFSTSKNFATRQA 761 FRGR YYPISAHLHHVNDFCRGLLFFSTGKPLGEKGLWULKVHLANLFSTSKNFATRQA 774 FRGR YYPISAHLHHVNDFCRSLLFFSGKPLGENGLWULKVHLANLFSTSKNFATRQA 774 FRGR YSPISAHLHVNDFCRGLLFFSGKPLGENGLWULKVHLANLFSTSKNFATRQA 774 FRGR YSPISHLMHLGNDLS SGLLFWERAPLGEGGLWULKTHLANTG SYNKADF38VQ 866 FRGR YSPISHHNHGNDLS GLLFWERAPLGEGGLWULKTHLANT FSTEDR IA 866 FRGR YSPISHNHMGNDLS GLLFWERAPLGEGGLWULKTHLANT FSTEDR IA 861 FRGR YSPISHNHMGNDLS GLLFWEGKPLGEGGLWULKTHLANT FSTENKAPLHERVQ 808 FRGR YSPISHNHMGNDLS GLLFWEGKPLGEGGELWULKTHLANT FSTENKAPLHERVQ 808 FRGR YSPISHNHGNDLS GLLFWEGKPLGAQGIAWLKTHLANT FSTENKAPLHERE 835 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAQGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAGGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAGGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAGGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKELGEGEGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKELGEGEGIAWLKTHLANT FSTEDKAPLEREN 840	P-GNS DPOKLL HHTTS KYQAL DEYISN KS	DRCDNN	AAB TE:	ARAFI	GERLFFPHNLD	
FRGR AYPLP SHLHHVNSDFCRSLLIFAEGKPLGEEG FWLKLVQLANL FKNKSTIQER ID 768 FRGR AYPLS SHLHHVNSDFCRSLLFFSTGKPLGEKGLWULKVHLANLFSTSKNFATRQA 761 FRGR YYPISAHLHHVNDFCRGLLFFSTGKPLGEKGLWULKVHLANLFSTSKNFATRQA 761 FRGR YYPISAHLHHVNDFCRGLLFFSTGKPLGEKGLWULKVHLANLFSTSKNFATRQA 774 FRGR YYPISAHLHHVNDFCRSLLFFSGKPLGENGLWULKVHLANLFSTSKNFATRQA 774 FRGR YSPISAHLHVNDFCRGLLFFSGKPLGENGLWULKVHLANLFSTSKNFATRQA 774 FRGR YSPISHLMHLGNDLS SGLLFWERAPLGEGGLWULKTHLANTG SYNKADF38VQ 866 FRGR YSPISHHNHGNDLS GLLFWERAPLGEGGLWULKTHLANT FSTEDR IA 866 FRGR YSPISHNHMGNDLS GLLFWERAPLGEGGLWULKTHLANT FSTEDR IA 861 FRGR YSPISHNHMGNDLS GLLFWEGKPLGEGGLWULKTHLANT FSTENKAPLHERVQ 808 FRGR YSPISHNHMGNDLS GLLFWEGKPLGEGGELWULKTHLANT FSTENKAPLHERVQ 808 FRGR YSPISHNHGNDLS GLLFWEGKPLGAQGIAWLKTHLANT FSTENKAPLHERE 835 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAQGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAGGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAGGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAGGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKELGEGEGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKELGEGEGIAWLKTHLANT FSTEDKAPLEREN 840	P-ADADPQAKLDNSIALYKGLREFAGNRS	DRCDYN	YYRLE:	ARGFI	GERLYFPHNLD	
FRGR AYPLP SHLHHVNSDFCRSLLIFAEGKPLGEEG FWLKLVQLANL FKNKSTIQER ID 768 FRGR AYPLS SHLHHVNSDFCRSLLFFSTGKPLGEKGLWULKVHLANLFSTSKNFATRQA 761 FRGR YYPISAHLHHVNDFCRGLLFFSTGKPLGEKGLWULKVHLANLFSTSKNFATRQA 761 FRGR YYPISAHLHHVNDFCRGLLFFSTGKPLGEKGLWULKVHLANLFSTSKNFATRQA 774 FRGR YYPISAHLHHVNDFCRSLLFFSGKPLGENGLWULKVHLANLFSTSKNFATRQA 774 FRGR YSPISAHLHVNDFCRGLLFFSGKPLGENGLWULKVHLANLFSTSKNFATRQA 774 FRGR YSPISHLMHLGNDLS SGLLFWERAPLGEGGLWULKTHLANTG SYNKADF38VQ 866 FRGR YSPISHHNHGNDLS GLLFWERAPLGEGGLWULKTHLANT FSTEDR IA 866 FRGR YSPISHNHMGNDLS GLLFWERAPLGEGGLWULKTHLANT FSTEDR IA 861 FRGR YSPISHNHMGNDLS GLLFWEGKPLGEGGLWULKTHLANT FSTENKAPLHERVQ 808 FRGR YSPISHNHMGNDLS GLLFWEGKPLGEGGELWULKTHLANT FSTENKAPLHERVQ 808 FRGR YSPISHNHGNDLS GLLFWEGKPLGAQGIAWLKTHLANT FSTENKAPLHERE 835 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAQGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAGGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAGGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKPLGAGGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKELGEGEGIAWLKTHLANT FSTENKAPLEREN 840 FRGR YSPISHNHGNDNT SSLLFWEGKELGEGEGIAWLKTHLANT FSTEDKAPLEREN 840	P-LNADPRERLERSKLVIRSLREFASSRS	a a a a	ATALL.	ARGE .	GERLIPPINLD	778
FRGRAYPLS SHLHHVSNDVC RGLLE FSTGKP LGPKG LWRLVHLANT FJSK KDPATRQA FRGRAYPLS SHLHHVSNDCC RGLLE FSTGKP LGPKG LWRLVHLANT FJSK KDPATRQK 715 FRGRAYPLS SHLHHVSNDCC RGLLE FSEGKP LGPKG LWRLK HLANT FGSKK UDYATRQK 714 FRGRAYPLS FHLSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGSKK UDYATRQK 716 FRGRAYPLS FHLSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGSKK SFEDRIA 626 FRGRAYPLS FHLSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGSKK SFEDRIA 626 FRGRAYPLS FNTSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGSKK SFEDRIA 626 FRGRAYPLS FNTSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGINKAPLHERV 800 FRGRAYPLS PNTSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGINKAPLHERV 800 FRGRAYPLS HFNHLGNDT SLLF FWEGKP LGPKG LWRLK HLANT FGINK VSLDDRVK 801 FRGRAYPLS HFNHLGNDT SLLF FWEGKP LGPKG LWRLK HLANT FGINK VSLDDRVK 802 FRGRAYPLS HFNHLGNDT SLLF FWEGKR LGPKG LWRLK HLANT FWERK SSTEERVA 809 FRGRAYPLS HFNHLGNDT SLLF FWEGKR LGPKG LWRLK HLANT FWERK SSTEERVA 800 FRGRAYPLS HFNHLGNDT SLLF FWEGKR LGPKG LWRLK HLANT FWERK SSTEERVA 800 FRGRAYPLS HFNHLGNDT SSLLF FWEGKR LGPGG LWRLK HLANT FORK SSTEERVA 800 FRGRAYPLS HFNHLGNDT SSLLF FWEGKR LGPGG LWRLK HLANT FORK SSLEERVA 800 FRGRAYPLS HFNHLGNDT SSLLF FWEGKR LGPGG L				1		
FRGRAYPLS SHLHHVSNDVC RGLLE FSTGKP LGPKG LWRLVHLANT FJSK KDPATRQA FRGRAYPLS SHLHHVSNDCC RGLLE FSTGKP LGPKG LWRLVHLANT FJSK KDPATRQK 715 FRGRAYPLS SHLHHVSNDCC RGLLE FSEGKP LGPKG LWRLK HLANT FGSKK UDYATRQK 714 FRGRAYPLS FHLSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGSKK UDYATRQK 716 FRGRAYPLS FHLSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGSKK SFEDRIA 626 FRGRAYPLS FHLSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGSKK SFEDRIA 626 FRGRAYPLS FNTSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGSKK SFEDRIA 626 FRGRAYPLS FNTSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGINKAPLHERV 800 FRGRAYPLS PNTSHLGNDLS RGLLF FWEGKP LGPKG LWRLK HLANT FGINKAPLHERV 800 FRGRAYPLS HFNHLGNDT SLLF FWEGKP LGPKG LWRLK HLANT FGINK VSLDDRVK 801 FRGRAYPLS HFNHLGNDT SLLF FWEGKP LGPKG LWRLK HLANT FGINK VSLDDRVK 802 FRGRAYPLS HFNHLGNDT SLLF FWEGKR LGPKG LWRLK HLANT FWERK SSTEERVA 809 FRGRAYPLS HFNHLGNDT SLLF FWEGKR LGPKG LWRLK HLANT FWERK SSTEERVA 800 FRGRAYPLS HFNHLGNDT SLLF FWEGKR LGPKG LWRLK HLANT FWERK SSTEERVA 800 FRGRAYPLS HFNHLGNDT SSLLF FWEGKR LGPGG LWRLK HLANT FORK SSTEERVA 800 FRGRAYPLS HFNHLGNDT SSLLF FWEGKR LGPGG LWRLK HLANT FORK SSLEERVA 800 FRGRAYPLS HFNHLGNDT SSLLF FWEGKR LGPGG L	FRGRAVPIPSHLHHVNSDFCRSLLIFAEGKPLG	EEGEO	WLEVO	LANI	KNK ST TOER TO	
FRGR VYPIS AHLHHVINDEC GOLLE FAEGKPIGENG LWILK VHLANT FORK VDYATROK 774 FRGR VYBIS AHLHHVINDEC GOLLE FAEGKPIGENG LWILK VHLANT FORK VDYATROK 774 FRGR VYPIS AHLHHVINDEC GOLLE FEGGEVE LGENG LWILK VHLANT FORK VDYATROK 774 FRGR VYPIS PHLNHL GNDES GOLL FWEGKPIGE LGENG LWILK VHLANT FORK VDYATROK 774 FRGR VYPIS PHLNHL GNDES GOLL FWEGKPIGE LGENG LWILK VHLANT FORK ADPORVQ 566 FRGR VPIS PHLNHL GNDES GOLL FWEGKPIGE LGENG LWILK VHLANT FORK APLEER V0 600 FRGR VPIS PNENHM GNDES GOLL FWEGKPIGE LGEDG LWILK VHLANT FEIDKAPLHERVQ 600 FRGR VPIS PNENHL GNDES GOLL FWEGKPIGE LGEDG LWILK VHLANT FEIDKAPLHERVQ 600 FRGR VPIS PNENHL GNDES GOLL FWEGKPIGEG LWILK VHLANT FEIDKAPLHERVQ 600 FRGR VPIS PNENHL GNDES GOLL FWEGKPIGEG LWILK VHLANT FEIDKAPLHERVQ 600 FRGR VPIS PNENHL GNDES GOLL FWEGKPIGEG LWILK INLANT FEIDKAPLHERV 611 FRGR VPIS PNENHL GNDES GOLL FWEGKPIGEG LWILK INLANT FEIDK VSILGRVK 611 FRGR VPIS PNENHL GNDES GOLL FWEGKPIGEG LWILK INLANT FEIDK VSILGRVK 611 FRGR VPIS PNENHL GNDES GOLL FWEGKPIGEG LWILK INLANT FEIDK VSILGRVK 611 FRGR VPIS PNENHL GNDES GOLL FWEGKPIGEG LWILK INLANT FENDER VSILG VSILG VXILG 700 FRGR VPIS PHENHL GNDES GOLL FWEGKPIGEG LWILK INTON FEIDE VX 608 FRGR VSILS PHENHL GNDES GOLL FWEGKPIGEG LWILK INTON FEIDE VX 609 FRGR VSILS PHENHL GNDES GOLL FWEGKPIGEG LWILK INTON FEIDE VX 609 FRGR VSILS PHENHL GNDES GOLL FWEGKPIGEG LWILK INTON VSILG VXILG 809 FRGR VSILS PHENHL GNDES GOLL FWEGKRIGEG LWILK INTON VSILG VXILG 809 FRGR VSILS PHENHL GNDES GOLL FWEGKRIGEG LWILK INTON VSILG VXILG 809 FRGR VSILS PHENHL GNDES GOLL FWEGKRIGEG LWILK INTON VSILG VXILG 809 FRGR VSILS PHENHL GNDES SGLLIF FWEGKRIGEG LWILK INTON VSILG VXILG 809 FRGR VSILS PHENHL GNDES GOLL FWEGKRIGEG LWILK INTON VSILG VXILG 809 FRGR VSILS PHENHL GNDES GOLL FWEGKRIGEG LWILK INTON VSILG VXILS 809 FRGR VSILS PHENHL GNDES GOLL FWEGKRIGEG LWILK INTON VSILG VXILS 809 FRGR VSILS PHENHL GNDES GOLL FWEGKRIGEG LWILK INTON VSILG VXILS 809 FRGR VSILS PHENHL GNDES GOLL FWEGKRIGEG LWILK INTON VSILG VXILS 809 FRGR VSILS PHENHL GNDES GOLL FWEGKRIGEG LWILK INTON VSILG VXILS 809 FRGR	EDCDA VDI 2 2VI HUI 2VIDUODOT I D DOCOTO C					768
FRGRAYDE PHLNHL GNDCK BGLLFYWGRKE LGEBG LWILK HLANT GYDR ADFORV Q FRGRAYDE SHLNHL GNDLS BGLLFYWGRE LGEBG LWILK HLANT GYDR ADFORV G FRGRAYDE SHLNHL GNDLS BGLLFYWGRE LGEDG LWILK HLANT GYDR ADFORV FRGRAYDE SHNFNHGNDLS RGLLFYWGRE LGEDG LWILK HLANT FEDKAPENERK 811 FRGRAYDE SHNFNHGNDLS GLLFYWGRE LGEDG LWILK HLANT FEDKAPENERK 808 FRGRAYDE SHNFNHGNDLS GLLFYWGRE LGEDG LWILK HLANT FEDKAPENERA 808 FRGRAYDE SHNFNHG NDLS GLLFYWGRE LGEDG LWILK HLANT FEDKAPENERA 809 FRGRAYDE SHNFNHG NDLS SGLLFYWGRE LGEDG LWILK HLANT FENK LFDDRVA 809 FRGRAYDE SHNFNHG NDLS SGLLFYWGRE LGEDG LWILK HLANT FENK LFDDRVA 809 FRGRAYDE SHNFNHG NDLS SGLLFYWGRE LGEDG LWILK HLANT Y GHRK SFEERVA 918 FRGRAYDE SHNFNHG NDLS SGLLFYWGRE LGENG LWILK HLANT Y GHRK SFEERVA 918 FRGRAYDE APHYNHG NDLS SGLLFYWGRE LGENG LWILK HLANT Y GHRK SFEERVA 918 FRGRAYDE APHYNHG NDMT RSLLFYWGRE LGENG LWILK HLANT Y GHRK SFEERVA 918 FRGRAYDE APHYNHG NDMT RSLLFYWGRE LGENG LWILK HLANT Y GHRK SFEERVA 918 FRGRAYDE APHYNHG NDMT RSLLFYWGRE LGENG LWILK HLANT Y GHRK SFEERVA 918 FRGRAYDE APHYNHG NDMT RSLLFYWGRE LGENG LWILK HLANT Y GHRK SFEERVA 918 FRGRAYDE APHYNHG NDMT RSLLFYWGRE LGENG LWILK HLANT Y GHRK SFEERVA 919 FRGRAYDE APHYNHG NDMT RSLLFYWGRE LGENG LWILK HLANT Y GHRK SFEERVA 910 FRGRAYDE SHFNHL GNDR SGLLFYWGRE LGENG LWILK HLANT Y GHRK SFEERVA 910 FRGRAYDE SHFNHL GNDR SGLLFYWGRE LGENG LWILK HLANT Y GHRK SFEERVA 910 FRGRAYDE SHFNHL GNDR SGLLFYWGRE LGENG LWILK HLANT Y GURK YELDRUN 910 FRGRAYDE SHFNHL GNDR SGLLFYWGRE LGENG LWILK HLANT Y GURK SFEERVA 910 FRGRAYDE SHFNHL GNDR SGLLFYWGRE LGENG LWILK HLANT Y GURK SELDRUN 955 FRGRAYDE SHFNHL GNDR SGLLFYWGRE LGENG LWILK HLANT Y GURK SELDRUN 955 FRGRAYDE SHFNHL GNDR SGLLFYWGRE LGENG LWILK HLANT Y GURK AFLDERVY 950 FRGRAYDE SHFNHL GNDR SGLLFYWGRE LGERG LWILK HLANT Y GURK AFLDERVY 951 FRGRAYDE SHFNHL GNDR	ERGENIFLS SALARY SNDVCRGLLEFSTGKPLG	PKGLN	WLKVH	LANI, F	ISKKDFATRQA	
<pre>FRGRAYPLS PHTNHLGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREK 830 FRGRAYPLS PNFNHLGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDERVQ 800 FRGRAYPLS PNFNHGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDERVA 805 FRGRAYPLS PNFNHGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREA 855 FRGRAYPLS PNFNHGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREA 855 FRGRAYPLS AHFNHLGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREA 855 FRGRAYPLS AHFNHLGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREA 855 FRGRAYPLS AHFNHLGNDT SALLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREEA 855 FRGRAYPLS AHFNHLGNDT SALLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREEA 855 FRGRAYPLS AHFNHLGNDT RSLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREE 855 FRGRAYPLA PHFNHLGNDT RSLLTPWGERE LGEDG LWLTK HILSNIT FILKASPHDEREE 855 FRGRAYPLA PHFNHLGNDT RSLLTPWGERE LGEDG LWLTK HILSNIT FILKASPHDEREE 855 FRGRAYPLA PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT FILKASPHDEREE 855 FRGRAYPLA PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 18 FRGRAYPLA PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 18 FRGRAYPLA PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 18 FRGRAYPLA PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 18 FRGRAYPLS PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 18 FRGRAYPLS PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDT SGLLTPWRGER LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDS SGLLTPWRGER LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDS SGLLTPWRGER LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDS SGLLTPWRGER LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDS SGLLTPWRGER LGEDG LWLTK HILSNIT FFORKASLEERUR 20 FRGRAYPLS PHFNHLGNDS SGLLTPWRGER LGERG LWLTK HILSNIT FFORKASLE</pre>	FRGRVYPISAHLHHVNNDFCRGLLEFAEGKPLG	PNGLN	WLRVH WLRVH	LANI <mark>, F</mark> LANI, F	ISKKDFATRQA ISKVDYASRQK	761 775
<pre>FRGRAYPLS PHTNHLGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREK 830 FRGRAYPLS PNFNHLGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDERVQ 800 FRGRAYPLS PNFNHGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDERVA 805 FRGRAYPLS PNFNHGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREA 855 FRGRAYPLS PNFNHGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREA 855 FRGRAYPLS AHFNHLGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREA 855 FRGRAYPLS AHFNHLGNDLS RGLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREA 855 FRGRAYPLS AHFNHLGNDT SALLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREEA 855 FRGRAYPLS AHFNHLGNDT SALLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREEA 855 FRGRAYPLS AHFNHLGNDT RSLLTPWRGERE LGGE LWLTK HILSNIT FILKASPHDEREE 855 FRGRAYPLA PHFNHLGNDT RSLLTPWGERE LGEDG LWLTK HILSNIT FILKASPHDEREE 855 FRGRAYPLA PHFNHLGNDT RSLLTPWGERE LGEDG LWLTK HILSNIT FILKASPHDEREE 855 FRGRAYPLA PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT FILKASPHDEREE 855 FRGRAYPLA PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 18 FRGRAYPLA PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 18 FRGRAYPLA PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 18 FRGRAYPLA PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 18 FRGRAYPLS PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 18 FRGRAYPLS PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDT RALLTPWGERE LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDT SGLLTPWRGER LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDS SGLLTPWRGER LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDS SGLLTPWRGER LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDS SGLLTPWRGER LGEDG LWLTK HILSNIT YGDER SPEEDER 10 FRGRAYPLS PHFNHLGNDS SGLLTPWRGER LGEDG LWLTK HILSNIT FFORKASLEERUR 20 FRGRAYPLS PHFNHLGNDS SGLLTPWRGER LGERG LWLTK HILSNIT FFORKASLE</pre>	FRGRVYPISAHLHHVNNDFCRGLLEFAEGKPLG FRGRVYPMSAHLHHVNNDFCRGLLEFSEGKPLG	PNG LN PNG LN	WLKVH WLKVH WLKVH	LANI, F LANI, F LANI, F	SISKKDFATRQA SISKVDYASRQK SNSKVDYATRQK	761 775 774
FRGA YPLS PNFNHM GNDLS BGLLT FWKGRE LGDEG LWILK LINNI FOIN APLNERE VA FRGA YPLS PNFNHM GNDLS BGLLT FWKGRE LGDG LWILK LINNI FOIN APLNERE VA SS FRGR YPLS PNFNHL GNDLS GLLT FWKGRE LGDG LWILK LINNI FOIN APLNERE VA FRGR YPLS PNFNHL GNDLS GLLT FWKGRE LGDG LWILK LINNI FOIN APLNERE VA FRGR YPLS PNFNHL GNDLS GLLT FWKGRE LGDG LWILK LINNI FONK USJEDR VK SG FRGR YPLS PNFNHL GNDLS GLLF FWGKE LGDG LWILK LINNI FONK USJEDR VK SG FRGR YPLS PHFNHL GNDT RSLLF FWGKE LGDG LWILK LINNI Y GNEK SPEER VA FRGR YPLS PHFNHL GNDT RSLLF FWGKE LGDG LWILK LINNI Y GNEK SPEER VA SG FRGR YPLS PHFNHL GNDT RSLLF FWGKE LGDG LWILK LINNI Y GNEK SPEER VA SG FRGR YPLS PHFNHL GNDT RSLLF FWGCR LGDG LWILK LINNI Y GNEK SPEER VA SG FRGR YPLS PHFNHL GNDT RSLLF FWGCR LGDG LWILK LINNI Y GNEK SPEER VA SG FRGR YPLS PHFNHL GNDT RSLLF FWGCR LGDG LWILK LINNI Y GNEK SPEER VA SG FRGR YPLS PHFNHL GNDT RSLLF FWGCR LGDG LWILK LINNI Y GNEK SPEER VA SG FRGR YPLS PHFNHL GNDT RSLLF FWGCR LGDG LWILK VHLANI Y GNEK SPEER VA SG FRGR YPLS PHFNHL GNDT RSLLF FWGCR LGDG LWILK VHLANI Y GNEK SPEER VA SG FRGR YPLS PHFNHL GNDT RSLLF FWGCR LGDG LWILK VHLSNI Y GVDEK VPLEER N SG FRGR YPLS PHFNHL GNDS SGLLF FWKGK LGDG LWILK VHLSNI Y GVDEK VPLEDR VA SG FRGR YPLS PHFNHL GNDS SGLLF FWKGK LGDG LWILK VHLSNI Y GVDEK VPLEDR VA SG FRGR YPLS PHFNHL GNDS SGLLF FWKGK LGDG LWILK VHLSNI Y GVDEK VPLEDR VK SG FRGR YPLS PHFNHL GNDS SGLLF FWKGK LGDG LWILK VHLSNI Y GVDEK VPLEDR VK SG FRGR YPLS PHFNHL GNDS SGLLF FWKGK LGDG LWILK VHLSNI F GVDEK VPLEDR VK SG FRGR YPLS PHFNHL GNDS SGLLF FWKGK LGDG LWILK VHLSNI F GF FRGR YPLS PHFNHL GNDS SGLLF FWKGK LGDG LWILK VHLSNI F GF FRGR YPLS PHFNHL GNDS SG FRGR YPLS PHFNHL GN	FRGRVYPISAHLHHVNNDFCRGLLEFAEGKPLG FRGRVYPMSAHLHHVNNDFCRGLLEFSEGKPLG	PNG LN PNG LN	WLKVH WLKVH WLKVH	LANI, F LANI, F LANI, F	SISKKDFATRQA SISKVDYASRQK SNSKVDYATRQK	761 775 774 856
FRGRAYD15 PNFNHMGDLS RGLLF PWGGRE IGEG LWILK IHLANI FEIDKAPLMEREA FRGRAYD15 SHFNHLGNDLS GGLLFWGGRE IGEG LWILK IHLANI FEIDKAPLMEREA FRGRAYD15 AHFNHLGNDLS RGLLFWGGRE IGEG LWILK IHLANI FENK VSLOPRAF FRGRAYD15 AHFNHLGNDLS RGLLFWGGRE IGEG LWILK IHLANI FENK VSLOPRAF FRGRAYD15 PNFNHLGNDLS RGLLFWGGRE IGEG LWILK IHLANI FENK SLEDDRVK 508 FRGRAYD15 PHFNHLGNDLS RGLLFWGGRE IGEG LWILK IHLANI FENK SLEDDRVK 508 FRGRAYD15 PHFNHLGNDT RSLLFWNGKU IGEG LWILK IHLANI FENK SSFERVA 798 FRGRAYD15 PHFNHLGNDT RSLLFWNGKU IGEG LWILK IHLANI FENK SSFERVA 798 FRGRAYD15 PHFNHLGNDT RSLLFWNGKU IGEG LWILK IHLANI FENK SSFERVA 798 FRGRAYD15 PHFNHLGNDT RSLLFWGGRE IGEG LWILK IHLANI FENK SSFERVA 798 FRGRAYD15 PHFNHLGNDT RSLLFWGGRE IGEG LWILK IHLANI FENK SSFERVA 798 FRGRAYD15 PHFNHLGNDT RSLLFWGGRE IGEG LWILK IHLANI FENK SSFERVA 839 FRGRAYD15 PHFNHLGNDT RSLLFWGGRE IGEG LWILK IHLANI FENK SSFERVA 836 FRGRAYD15 PHFNHLGNDT RSLLFWGGRE IGEG LWILK IHLANI FENK SSFERVA 836 FRGRAYD15 PHFNHLGNDT RSLLFWGGRE IGEG LWILK IHLANI FENK SFERVA 836 FRGRAYD15 PHFNHLGNDT RSLLFWGGRE IGEG LWILK IHLANI FENK SFERVA 836 FRGRAYD15 PHFNHLGNDT RSLLFWGGRE IGEG LWILK IHLSNI FENK SFERVA 836 FRGRAYD15 PHFNHLGNDT RSLLFWGGRE IGEG LWILK IHLSNI FENK SFERVA 836 FRGRAYD15 PHFNHLGNDS GGLLFWKGKU IGGD LWILK IHLSNI FENK SFERVA 840 FRGRAYD15 PHFNHLGNDS SGLLFWKGKU IGGD LWILK IHLSNI FENK SFERVA 840 FRGRAYD15 PHFNHLGNDS SGLLFWKGKU IGGD LWILK IHLSNI FENK SFERVA 840 FRGRAYD15 PHFNHLGNDS SGLLFWKGKU IGGG LWILK IHLSNI FENK ASLEDRV 850 FRGRAYD15 PHFNHLGNDS SGLLFWKGKU IGGG LWILK IHLSNI FENK ASLEDRV 851 FRGRAYD15 PHFNHLGNDS SGLLFFWKGKU IGGG LWILK IHLSNI FENK ASLEDRV 840 FRGRAYD15 PHFNHLGNDS SGLLFFWHGKK IGGG LWILK IHLSNI FENK ASLEDRV 840 FRGRAYD15 PHFNHLGNDS SGLLFFWHGKK IGGG LWILK IHLSNI FENK ASLEDRV 840 FRGRAYD15 PHFNHLGNDS SGLLFFWHGKK IGGG LWILK IHLSNI FENK ASLEDRV 840 FRGRAYD15 PHFNHLGNDS SGLLFFWGGRE IGERG LWILK IHLSNI FENK ASLEDRV 840 FRGRAYD15 PHFNHLGNDT SSTELFFWGGRE IGERG LWILK IHLANI YNK ASLEDRV 840 FRGRAYD15 PHFNHLGNDT SSTELFFWGGRE IGERG LWILK IHLANI YNK ASLEDRV 840 FRGRAYD15 PHFNHLGNDT SSTELFFWGGRE IG	FRGRVYPISAHLHHVNNDFCRGLLEFAEGKPLG FRGRVYFMSAHLHHVNNDFCRGLLEFSECKPLG FRGRAYAIPPHLNHLGNDMCRGLLMFWEGKPLG FRGRAYPLSPHLNHLGNDLSRGLLKFWEARELG	PNGLNV PNGLNV ERGLRV EHGLNV	WLKVH WLKVH WLKVH WLKIH WLKVH	LANI, F LANI, F LANI, F LANVC CANVF	SISKKDFATRQA SISKVDYASRQK SNSKVDYATRQK SYDKADFQSRVQ SHNKFSFEDRIA	761 775 774 856 626
FRGR YPLS PHFNHLGNDLS BGLLI FWKGRK LGDNG LWLK HLANN F SLDK V9LQEN AZ 940 FRGR YPLS HFNHLGNDLS BGLLI FWKGKK LGDNG LWLK HLANN F SLDK V9LQEN VA 821 FRGR YPLS HFNHLGNDLS BGLLI FWKGKK LGESG FWLK HLANN F SHDK IS FDRAVA 821 FRGR YPLS HFNHLGNDLS BGLLI FWKGKK LGESG FWLK HLANN F SHDK V9LDR VK 861 FRGR YPLS HFNHLGNDLS BGLLK FWKGKK LGESG FWLK HLANN F SHDK V9LDR VK 861 FRGR YPLS HFNHLGNDT RALLF FWKGKK LGESG LWLK HLANN F SHDK V9LDR VK 99 FRGR YPLA HFNHLGNDT RALLF FWKGKK LGENG LWLK HLANN F SHDK X5 FFER VK 99 FRGR YPLA HFNHLGNDT RALLF FWGCRK LGENG LWLK HLANN F SHDK X5 FFER VK 99 FRGR YPLA HFNHLGNDT RALLF FWGCRK LGENG LWLK HLANN F SHDK AF FFDR IK 99 FRGR YPLA FHFNHL GNDT RALLF FWGCRK LGEKG LWLK HMGN V GLDK QT FFAR VA 36 FRGR YPLA FHFNHL GNDT RALLF FWGCRK LGEKG LWLK HMGN V GUDK QT FFAR VA 36 FRGR YPLA FHFNHL GNDT RALLF FWGCRK LGEKG LWLK HMGN V GUDK QT FFAR VA 36 FRGR YPLA FHFNHL GNDT RALLF FWGCRK LGEKG LWLK HMAN V GUDK V9 LDDR VA 310 FRGR YPLA FHFNHL GNDS SGLLF FWKGKK LGENG LWLK HMAN V GUDK V9 LDDR VA 310 FRGR YPLA FHFNHL GNDS SGLLF FWKGKK LGENG LWLK HLANN V GUDK V9 LDDR VA 360 FRGR YPLA FHFNHL GNDS SGLLF FWKGKK LGENG LWLK VHAN V SUN KASTELER VA 361 FRGR YPLA FHFNHL GNDS SGLLF FWKGKK LGENG LWLK VHAN V SUN KASTELER VA <	FRGRVYFISAHLHHVNNDFCRGLLEFAGGRFLG FRGRVYFMSAHLHHVNNDFCRGLLEFAGGRFLG FRGRAYAIPHLNHLGNDLRGLLMFWEGRFLG FRGRAYFLSPHLNHLGNDLRGLLMFWEGRFLG FRGRAYFLSPHLNHLGNDLRGLLMFWGREVG FRGRAYFLSPHFNHLGNDLRGLLIFWEGRELG	PNGLN PNGLN ERGLN EHGLN ARGFN EDGLN	WLKVH WLKVH WLKIH WLKIH WLKIQ WLKVH	LANI, F LANI, F LANI, F LANVC CANVF LANVF LANVF	SISK KDFATRQA SISK VDYASRQK SNSK VDYATRQK SYDKADFQSRVQ SHNKFSFEDRIA SFDKASFNDREK SIDKAPLHERVQ	761 775 774 856 626 831 800
<pre>FRGRAYPLS AHFNHL GNDAT BALLV FWEGKP LGAQG LWILK THLANT FEHRK IF FDARVA 221 FRGRAYPLS PNFNHL GNDLS BGLLF WKKKK LGGS FWLK THVCNI WFFKLSLDDRVK 261 FRGRAYPLA PHTNHL GNDLS BGLLF WKKKK LGGS FWLK THVCNI WFFKLSLDDRVK 508 FRGRAYPLA PHTNHL GNDAT BALLT FWNGKR LGAGG LWILK THVANT WFFKLSLDDRVK 508 FRGRAYPLA PHTNHL GNDAT BALLT FWNGKR LGAGG LWILK THVANT WFFKLSLDDRVK 508 FRGRAYPLA PHTNHL GNDAT BALLT FWNGKR LGAGG LWILK THVANT WFFKLSTERVA 798 FRGRAYPLA PHTNHL GNDAT BALLT FWGCKR LGAGG LWILK THVANT WFFKR SFEERVA 798 FRGRAYPLA PHTNHL GNDAT BALLT FWGCKR LGAGG LWILK THVANT WFFKR FFEDR IK 899 FRGRAYPLA PHTNHL GNDAT BALLT FWGCKR LGAGG LWILK THVANT WFFKR FFEDR IK 899 FRGRAYPLA PHTNHL GNDAT BALLT FWEGKR LGAGG LWILK THVANT WFFFEDR IK 899 FRGRAYPLA PHTNHL GNDAT BALLT FWEGKR LGAGG LWILK THVANT WFICK OFFEARVA 536 FRGRAYPLS PHTNHL GNDAT BALLT FWEGKR LGAGG LWILK THVANT WFICK OFFEARVA 536 FRGRAYPLS PHTNHL GNDAT BALLT FWRGKR LGAGG LWILK THVANT WFICK AFPERVR 663 FRGRAYPLS PHTNHL GNDAT BALLT FWRGKR LGAGG LWILK VHJSNI TY VDK V9LLDR WF 663 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY VDK V9LLDR WF 663 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS PEDER VN 663 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS PEDER VN 663 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS PEDER VN 663 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS PEDER VN 664 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS PEDER VN 664 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS PEDER VN 655 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS LGEVR 640 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS LERVY 640 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS LERVY 640 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS LERVY 640 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS LERVY 640 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG LWILK VHJSNI TY FOKAS LERVY 640 FRGRAYPLS PHTNHL GNDAS BGLLT FWRGKR LGAGG L</pre>	FRGRUYFISAHLHWINDFCRGLLEFAEGKFLG FRGRUYNDSAHLHWINDFCRGLLEFAEGKFLG FRGRAYAIPPHLNHLGNDCRGLLKFWEGKFLG FRGRAYFLSPHLNHLGNDLSRGLLKFWEARELG FRGRAYFLSPHLNHLGNDLSRGLLIFWEGKELG FRGRAYFLSPHTNHLGNDLSRGLLIFWEGKELG	PNGLNV PNGLNV ERGLRV EHGLNV ARGFRV EDGLRV DEGLRV	WLKVH WLKVH WLKIH WLKIQ WLKVH WLKIQ	LANL F LANL F LANL F LANV C CANV F LANV F LANV F LSNL F	SISK KDFATRQA SISK VDYASRQK SNSK VDYATRQK SYDKADFQSR VQ SHNK FSFEDRIA SFDKASFNDREK SIDKAPLHERVQ SIDKAPLEERVA	761 775 774 856 626 831 800 808
FRGRAYDLA PHFNHL GNDLS BGLLF FWNGKG LGEG LJWLK LHUCHLWG FDK LSLDDRVK 508 FRGRAYDLA PHFNHL GNDMT RSLLI FWNGKR LGENG LWLK LHLANL Y GMCK CSFEER VE 799 FRGRAYDLA PHFNHL GNDMT RSLLI FWNGKR LGENG LWLK LHLANL Y GMCK CSFEER VA 798 FRGRAYDLA PHFNHL GNDMT RSLLI FWNGKR LGENG LWLK LHLANL Y GMCK RSFEER VA 798 FRGRAYDLA PHFNHL GNDMT RSLLI FWNGKR LGENG LWUK LHLANL Y GMCK RSFEER VA 798 FRGRAYDLA PHFNHL GNDMT RSLLI FWGCKR LGENG LWUK LHLANL Y GMCK RSFEER VA 830 FRGRAYDLA PHFNHL GNDMT RSLLI FWGCKR LGENG LWUK LHANL Y GMCK RSFEER VA 836 FRGRAYDLA PHFNHL GNDMT RSLLI FWGCKR LGENG LWUK LHANL Y GUCK UFFLAR VA 836 FRGRAYDLA PHFNHL GNDMT RSLLI FWGCKR LGENG LWUK LHANL Y GUCK UFFLAR VA 836 FRGRAYDLS PHFNHL GNDK SGLLI FWRGKK LGENG LWUK LHANN Y GUCK UFFLAR VA 836 FRGRAYDLS PHFNHL GNDLS BGLLI FWRGKK LGENG LWUK LHANN Y GUCK VSLDDR VA 810 FRGRAYDLS PHFNHL GNDLS BGLLI FWRGKK LGENG LWUK LHLSNI Y GUCK VSLDDR VA 810 FRGRAYDLS PHFNHL GNDLS BGLLI FWRGKK LGENG LWUK LHLSNI Y GUCK VSLDDR VA 810 FRGRAYDLS PHFNHL GNDLS BGLLI FWRGKK LGENG LWUK LHLSNI Y GUCK VSLDDR VA 861 FRGRAYDLS PHFNHL GNDLS BGLLI FWRGKK LGENG LWUK LHLSNI Y GUCK VSLDDR VA 861 FRGRAYDLS PHFNHL GNDS GGLLI FWRGKK LGENG LWUK LHLSNI Y GUCK SSLDER VK 861 FRGRAYDLS PHFNHL GNDS SGLLI FWRGKK LGENG LWUK LHLSNI Y GUCK SSLDER VK 865 FRGRAYDLS PHFNHL GNDS SGLLI FWRGKK LGENG LWUK LHLSNI F GUCK SLLDER VA 865 FRGRAYDLS PHFNHL GNDS SGLLI FWRGKK LGENG LWUK LHLSNI F GUCK SLLDER VA 865 FRGRAYDLS PHFNHL GNDS SGLLI FWRGKK LGENG LWUK LHLSNI F GUCK SLLDER VA 865 FRGRAYDLS PHFNHL GNDS SGLLI FWRGKK LGENG LWUK LHLSNI F GUCK SLLDER VA 865 FRGRAYDLS PHFNHL GNDS SGLLI FWRGKK LGENG LWUK LHLSNI F GUCK SLLDER VA 865 FRGRAYDLS PHFNHL GNDS SGLLI FWRGKK LGENG LWUK LHLSNI F GUCK SLLDER VA 865 FRGRAYDLS PHFNHL GNDS SGLLI FWRGKK LGENG LWUK LHLSNI F GUCK SLLDER VA 865 FRGRAYDLS PHFNHL GNDS SGLLI FWRGKK LGENG LWUK LHLSNI F GUCK SLLDER VA 860 FRGRAYDLS PHFNHL GNDT SLLF FWGCK LGERG LWUK LHLSNI F GUCK SLLDER VA 860 FRGRAYDLS PHFNHL GNDT SLF FFWGCK LGERG LWUK LHLSNI F GUCK SLLDER VA 860 FRGRAYDLS PHFNHL G	FRGRVYFISAHLHHVNNDFCRGLLEFAEGKFLG FRGRVYFMSAHLHHVNNDFCRGLLEFAEGKFLG FRGRÀYFLSPHLNHLGNDLSRGLLFWEGKFLG FRGRÀYFLSPHLNHLGNDLSRGLLFWEGKFLG FRGRÀYFLSPHLNHLGNDLSRGLLIFWEGKFLG FRGRÀYFLSPHNHMGNDLSRGLLIFWEGKFLG FRGRÀYFLSPHNHMGNDLSRGLLIFWEGKFLG	PNGLW PNGLW ERGLR EHGLW ARGFR EDGLR DEGLR EEGLR	WLKVH WLKVH WLKVH WLKVH WLKVH WLKUH WLKIH WLKIH	LANL F LANL F LANU F LANU F CANU F LANU F LSNL F LSNL F	SISK KDFATRQA SISKVDYASRQK SNSKVDYATRQK SYDKADFQSRVQ SHNKFSFEDRIA SFDKASFNDREK SIDKAPLHERVQ SIDKAPLERVA SIDKAPLNEREA	761 775 774 856 626 831 800 808 835
<pre>FRGRAYPLA PHFNHL ONDMT BALLT FWNORK LIGT 5G LWILK LIHLANI Y SMDK C3FEERVA 798 FRGRAYPLA PHFNHL ONDMT BALLT FWNORK LIGT 6G LWILK LIHLANI Y SMDK C3FEERVA 798 FRGRAYPLA PHFNHL ONDMT BALLT FWORK LIGENG LWILK LIHLANI Y SMDK AFFEDR IK 809 FRGRAYPLA PHFNHL ONDMT BALLT FWORK LIGENG LWILK LIHLANI Y SMDK KFFEDR IK 809 FRGRAYPLA PHFNHL ONDMT RALLT FWORK LIGENG LWILK LIHLANI Y SMDK KFFEDR IK 809 FRGRAYPLA PHFNHL ONDMT RALLT FWORK LIGENG LWILK LIHLANI Y SMDK KFFEDR IK 809 FRGRAYPLA PHFNHL ONDMT RALLT FWORK LIGENG LWILK LIHLANI Y SMDK KFFEDR IK 836 FRGRAYPLA PHFNHL ONDMT RALLT FWORK LIGENG LWILK LIHLANI Y SMDK KFFEDR IK 836 FRGRAYPLA PHFNHL ONDMT SGLLT FWRGKK LIGENG LWILK LIHLANI Y SMDK AFFEDR IK 84 FRGRAYPL3 PHFNHL ONDS SGLLT FWRGKK LIGENG LWILK LIHLSNI Y SVDK V9LLER EN 817 FRGRAYPL3 PHFNHL ONDLS RGLLT FWRGKK LIGENG LWILK LIHLSNI Y SVDK V9LLER EN 817 FRGRAYPL3 PHFNHL ONDLS SGLLT FWRGKK LIGENG LWILK LIHLSNI Y SVDK V9LEDR IK 859 FRGRAYPL3 PHFNHL ONDLS SGLLT FWRGKK LIGENG LWILK LIHLSNI Y SVDK V9LEDR IK 859 FRGRAYPL3 PHFNHL ONDLS SGLLT FWRGKK LIGENG LWILK LIHLSNI Y SVDK V9LEDR IK 859 FRGRAYPL3 PHFNHL ONDS SGLLT FWRGK LIGENG LWILK LIHLSNI Y SVDK V9LEDR IK 859 FRGRAYPL3 PHFNHL ONDS SGLLT FWRGK LIGENG LWILK LIHLSNI Y SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDS SGLLT FWRGK LIGENG LWILK LIHLSNI Y SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDS SGLLT FWRGK LIGENG LWILK LIHLSNI Y SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDS SGLLT FWRGK LIGENG LWILK LIHLSNI F SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDS SGLLT FWRGK LIGENG LWILK LIHLSNI F SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDS SGLLT FWRGK LIGENG LWILK LHLSNI F SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDS SGLLT FWRGK LIGENG LWILK LHLSNI F SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDS SGLLT FWRGK LIGENG LWILK LHLSNI F SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDT SGLLT FWRGK LIGENG LWILK LHLSNI F SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDT SGLLT FWRGK LIGENG LWILK LHLSNI F SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDT SGLLT FWRGK LIGENG LWILK LHLSNI F SFDK ASLEDD IV 85 FRGRAYPL3 PHFNHL ONDT SGLLT FWRGK LIGENG LWILK LHLSNI F SFDK A</pre>	FRGRVYFISAHLHHVINDFCRGLLEFABGKPLG FRGRVYFMSAHLHHVINDFCRGLLEFABGKPLG FRGRAYAIPPHLINHLGNDLRGLLMFWEGKPLG FRGRAYFLSPHLINHLGNDLRGLLMFWEGKPLG FRGRAYFLSPHINHLGNDLRGLLIFWEGKELG FRGRAYFLSPHFNHMGNDLRGLLIFWEGKELG FRGRAYFLSPHFNHMGNDLRGLLIFWEGKELG FRGRAYFLSPHFNHLGNDLRGLLIFWEGKELG	PNGLN PNGLN ERGLN EHGLN ARGFN EDGLN DEGLN EEGLN DNGLN	WLKVH WLKVH WLKVH WLKVH WLKVH WLKIQ WLKVH WLKIH WLKIH	LANL F LANL F LANU C CANV F LANV F LANU F LSNL F LANL F LANL F	SISK KDFATRQA SISK VDYASRQK SNSK VDYATRQK SYDKADFQSRVQ SHNK FSFEDRIA SFDKASFNDREK SIDKAPLHERVQ SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERA	761 775 774 856 626 831 800 808 835 840
FRGRAYPLS PHFNHL ONDER SILLT FWOCKELGENG LWILK LINLANI Y SMDK SSPEER VA FRGRAYPLA PHFNHL ONDER CSILLT FWOCKELGENG LWILK VHLANI Y SMDK SSPEER VA SSP FRGRAYPLA PHFNHL ONDER SALLT FWOCKELGENG LWILK VHLANI Y SMDK KPFEDR IK SSP FRGRAYPLS PHFNHL ONDER TSILT FWECKELGENG LWILK VHLANI Y SUDK CFFEAR VA SSP FRGRAYPLS PHFNHL ONDER SALLT FWECKELGENG LWILK VHLSNI Y SUDK VFLEEREN FRGRAYPLS PHFNHL ONDER SALLT FWECKELGENG LWILK VHLSNI Y SUDK VFLEEREN FRGRAYPLS PHFNHL ONDER SALLT FWECKELGENG LWILK VHLSNI Y SUDK VFLEEREN FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI Y SUDK VFLEEREN FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI Y SUDK VFLEEREN FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI Y SUDK VFLEDR VR SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI Y SUDK VFLEDR VR SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI Y SUDK VFLEDR VR SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK VFLEDR VR SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK VFLEDR VR SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK VFLEDR VR SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK SS FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK SALLER VR SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK SS FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK ASLEER VC SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK ASLEER VC SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK ASLEER VC SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK ASLEER VC SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK ASLEER VC SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK ASLEER VC SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK ASLEER VC SG FRGRAYPLS PHFNHL ONDES SALLT FWECKELGENG LWILK VHLSNI F SUDK ASLEER VC SG FRGRAYPLS PHFNHL ONDES TRALFF FWECKELGENG LWILK VHLSNI F SUDK ASLEER VC SG FRGRAYPLS PHFNHL ONDET TRALFF FWECKELGE	FRGRVYFISAHLHHVNNDFCRGLLEFAEGKFLG FRGRVYFMSAHLHHVNNDFCRGLLEFAEGKFLG FRGRAYAIPHLNHLGNDCRGLLMFWEGRFLG FRGRAYFLSPHLNHLGNDLSRGLLFWEGRELG FRGRAYFLSPHLNHLGNDLSRGLLIFWEGKELG FRGRAYFLSPHNHLGNDLSRGLLIFWEGKELG FRGRAYFLSPHFNHLGNDLSRGLLIFWEGKELG FRGRAYFLSPHFNHLGNDLSRGLLIFWEGKELG FRGRAYFISPHFNHLGNDLSRGLLIFWEGKELG FRGRAYFISPHFNHLGNDLSRGLLIFWEGKELG	PNGLN PNGLN ERGLN EHGLN ARGFN EDGLN DEGLN EEGLN DNGLN AQGLN ESGFN	WLKVH WLKVH WLKVH WLKVH WLKVH WLKIA WLKIH WLKIH WLKIH WLKIH	LANI F LANI F LANI F LANV C CANV F LANV F LANI F LANI F LANI F LANI F LANI F	ISK KDFATRQA SISK VDYASRQK SMSK VDYASRQK SYDKADFQSRVQ HNK FSFEDRIA FDKASFNDREK SIDKAPLHERVQ SIDKAPLHERVA SIDKAPLMEREA SIDK VSLQERAE HDK IJFDARVA	761 775 774 856 626 831 808 835 840 821 861
FRGRAYPIA PHFNHL GNDMC BALLI FWOGRE LGPEG LWILK THLANI Y SMDK AP FEDR IK 809 FRGRAYPIA PHFNHL GNDMT BALLI FWOGRE LGPEG LWILK THLANI Y SMDK AP FEDR IK 839 FRGRAYPIA PHFNHL GNDMT BALLI FWOGRE LGPEG LWILK THLANI Y SMDK AP FEDR IK 839 FRGRAYPIA PHFNHL GNDMT BALLI FWOGRE LGPEG LWILK THLANI Y SMDK AP FEDR IK 836 FRGRAYPIA PHFNHL GNDMT BALLI FWEGRE LGREG LWILK THLANI Y SUDK (JT FEAR VA 836 FRGRAYPIA PHFNHL GNDMT BALLI FWEGRE LGPEG LWILK THLANI Y SUDK (JT FEAR VA 836 FRGRAYPIA PHFNHL GNDMS GLLI FWEGRE LGPEG LWILK THLANI Y SUDK V9 LLER EN 817 FRGRAYPIA PHFNHL GNDS SGLLI FWEGRE LGPEG LWILK THLANI Y SUDK V9 LLER EN 863 FRGRAYPIA PHFNHL GNDLS RGLLI FWEGRE LGPEG LWILK THLANI Y SUDK V9 LLER EN 863 FRGRAYPIA PHFNHL GNDS SGLLI FWEGRE LGPEG LWILK THLANI Y SUDK V9 LLER EN 859 FRGRAYPIA PHFNHL GNDS SGLLI FWEGRE LGPEG LWILK THLANI Y SUDK V9 LLER EN 855 FRGRAYPIA PHFNHL GNDMS SGLLI FWHGKE LGPEG LWILK THLANI Y SUDK PEDR KASLED EN 855 FRGRAYPIA PHFNHL GNDMS SGLLI FWHGKE LGPEG LWILK THLANI FFOR KAPLED EN 855 FRGRAYPIA PHFNHL GNDMS SGLLI FWHGKE LGPEG LWILK THLANI FFOR KAPLED EN 855 FRGRAYPIA PHFNHL GNDMS SGLLI FWHGKE LGPEG LWILK THLANI Y SUDK APLADEN T 826 FRGRAYPIA PHFNHL GNDMS SGLLI FWEGRE LGPEG LWILK THLANI Y SUDK APLADEN T 826 FRGRA	FRGRUYFISAHLHWINDFCRGLLE FAEGKFLG FRGRUYNDSAHLHWINDFCRGLLE FSEGKFLG FRGRAYAI P PHLNHL GNDLS RGLLK FWEARELG FRGRAYFLS PHLNHL GNDLS RGLLL FWEARELG FRGRAYFLS PHLNHL GNDLS RGLLL FWEGKELG FRGRAYFLS PHYNHL GNDLS RGLLL FWEGKELG FRGRAYFLS PHYNHL GNDLS RGLLL FWEGKELG FRGRAYFLS PHYNHL GNDLS RGLLL FWEGKELG FRGRAYFLS HFNHL GNDLS RGLLL FWEGKELG FRGRAYFLS HFNHL GNDLS RGLLL FWEGKELG FRGRAYPUS PHYNHL GNDLS RGLLL FWEGKELG FRGRAYPUS PHYNHL GNDLS RGLLL FWEGKELG	PNGLN PNGLN ERGLN EHGLN ARGFN EDGLN DEGLN DEGLN DNGLN AQGLN ESGFN EEGLN	WLKVH WLKVH WLKVH WLKVH WLKIQ WLKVH WLKIH WLKIH WLKIH WLKIH WLKIH	LANI FILANI FILANI CANV FULANV FULANV FULANI FULANI FULANI FULANI FULANI FULANI FULANI FULANI FULANI FULANI FULANI FULANI FULANI	ISK KDFATRQA SISK VDYASRQK SNSK VDYASRQK SYDK ADFQSR VQ ENNK FSFEDRIA FDK ASFNDREK SIDK APLHER VQ SIDK APLHER VQ SIDK APLHER VQ SIDK APLER VA SIDK VSLQER AE SHDK VSLEDR VK EFDK LSLDDR VK	761 775 774 856 626 831 800 808 835 840 821 861 821 8508
FRGRAYPLS PHFNHL GNDAT BALLT FWEGRK LGREG LWILK HANNI YGLDK (TFEARVA FRGRAYPLS PHFNHL GNDAT BALLT FWEGRK LGREG LWILK HANNI YGLDK (TFEARVA 56 FRGRAYPLS PHFNHL GNDAT BALLT FWEGRK LGREG LWILK VHLSNI YGVDK VPLLER EN 517 FRGRAYPLS PHFNHL GNDAS BGLLI FWKGKK LGPLG LWILK VHLSNI YGVDK VPLLER EN 517 FRGRAYPLS PHFNHL GNDAS BGLLI FWKGKK LGPLG LWILK VHLSNI YGVDK VPLLER EN 518 FRGRAYPLS PHFNHL GNDAS BGLLI FWKGKK LGPLG LWILK VHLSNI YGVDK VPLLER EN 519 FRGRAYPLS PHFNHL GNDAS BGLLI FWKGKK LGPLG LWILK VHLSNI YGVDK VPLLER VK 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWKGKK LGPLG LWILK VHLSNI YGVDK VPLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWKGKK LGPLG LWILK VHLSNI YGVDK VPLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWKGKK LGPLG LWILK VHLSNI YGVDK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWHGKK LGSSG LWILK VHLSNI YGVDK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWHGKK LGSSG LWILK HLSNI FGTK LRLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWHGKK LGSSG LWILK VHLSNI FGTK LRLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWHGKK LGSSG LWILK VHLSNI FGTK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWHGKK LGSSG LWILK VHLSNI FGTK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWHGKK LGSG LWILK VHLSNI FGTK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWHGKK LGSG LWILK VHLSNI FGTK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWHGKK LGSG LWILK VHLSNI FGTK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWKGKK LGGRG LWILK VHLSNI FGTK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BGLLI FWKGKK LGGRG LWILK VHLSNI FGTK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BLLI FWKGKK LGGRG LWILK VHLSNI FGTK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BLLI FWKGKK LGGRG LWILK VHLSNI FGTK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BLLI FWKGKK LGGRG LWILK VHLSNI FGTK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BLLI FWKGKK LGGRG LWILK VHLSNI FYDK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS BLLI FWKGKK LGGRG LWILK VHLSNI FYDK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS RALF FWKGKE LGGRG LWILK VHLSNI FYDK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS RALF FWKGKK LGGRG LWILK VHLSNI FYDK ASLED EN 510 FRGRAYPLS PHFNHL GNDAS R	FRGRUYPISAHLHHUNDFCRGLLEFAGGKPIG FRGRUYPISAHLHHUNDFCRGLLEFSGGKPIG FRGRAYPISPHINHIGNDERGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG FRGRAYPISPHINHIGNDSRGLLFWEGKPIG	PNGLN PNGLN ERGLN EHGLN EHGLN EDGLN DEGLN DEGLN DNGLN AQGLN ESGFN EEGLN TSGLQ	WLKVH WLKVH WLKVH WLKVH WLKIQ WLKVH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH	LANI FLANI FLANI CANU CANU FULANU CANU FULAN	ISK KDFATRQA SISK VDVASRQK MSK VDVATRQK VDKADFQSRVQ HNK FSFEDRIA SFDKASFNDREK SIDKAPLHERVQ SIDKAPLHERVQ SIDKAPLHERVA SIDKAPLHERVA SHOK VSLEDRVK SHOK VSLEDRVK SFDK LSLDDRVK	761 775 774 856 626 831 800 808 835 840 821 861 508 799
FRGRAYPLS PHFNHL ONDER SGLLI FWEGERLGKEG LWILK LTHCANI YCLDK OFFER VA FRGRAYPLS PHFNHL ONDES GGLLI FWEGERLGKEG LWILK VHLSNI YCUDK V9LLEREN FRGRAYPLS PHFNHLGNDES GGLLI FWEGERLGKEG LWILK VHLSNI YCUDK V9LLEREN FRGRAYPLS PHFNHLGNDES GGLLI FWEGERLGEGG LWILK VHLSNI YCUDK V9LLEREN FRGRAYPLS PHFNHLGNDES GGLLI FWEGERLGEGG LWILK VHLSNI YCUDK V9LEDERVE FRGRAYPLS PHFNHLGNDS GGLLI FWEGERLGEGG LWILK VHLSNI YCUDK V9LEDERVE S1 FRGRAYPLS PHFNHLGNDS GGLLI FWEGERLGEGG LWILK VHLSNI FORKAPLEDERVE S1 FRGRAYPLS PHFNHLGNDT BSLIF FWEGERLGEGG LWILK VHLSNI FORKAPLEDERVE S1 FRGRAYPLS PHFNHLGNDT SGLLI FWEGERLGERG LWILK VHLSNI FORKAPLEDERVE S1 FRGRAYPLS PHFNHLGNDT SGLLI FWEGERLGERG LWILK VHLSNI FORKAPLEDERVE S1 FRGRAYPLS PHFNHLGNDT SGLLI FWEGERLGERG LWILK VHLSNI FORKAPLEDERVE S1 FRGRAYPLS PHFNHLGNDT SGLIF FWEGERLGERG LWILK VHLSNI FORKAPLERVE S1 FRGRAYPLS PHFNHLGNDT SGLIF FWEGERLGERG LWILK VHLSNI V0DK V9LRAPLERVE S1 FRGRAYPLS PHFNHLGNDT SGLIF FWEGERLGERG LWILK VLSNI V9DK V9LRAPLERVE S1 FRGRAYPLS PHFNHLGNDT SGLIF FWEGERLGERG LWILK V1LANI YVDK V9LRAPLERVE S1 FRGRAYPLS PHFNHLGNDT SGLIF FWEGERLGERG LWILK V1LANI YVDK V9LRAPLERVE S1 FRGRAYPLS PHFNHLGNDT SGLIF FWEGERLGERG LWILK V1LANI YVDK V9LRAPLEREN S1 FRGRAYPLS PHFNHLGNDT SGLIF FWEGERLGERG LWIL	FRGRUYFISAHLHWUNDFCRGLLE FAEGKFLG FRGRUYNDSAHLHWUNDFCRGLLE F3EGKFLG FRGRAYAID PHLNHLGNDCRGLLA FWEGKFLG FRGRAYFLS PHLNHLGNDLSRGLLA FWEGKFLG FRGRAYFLS PHLNHLGNDLSRGLLI FWEGKFLG FRGRAYFLS PHTNHLGNDLSRGLLI FWEGKFLG FRGRAYFLS PHTNHLGNDLSRGLLI FWEGKFLG FRGRAYFLS PHTNHLGNDLSRGLLFWEGKFLG FRGRAYFLS PHTNHLGNDLSRGLLFWEGKFLG FRGRAYFLS PHTNHLGNDLSRGLLFWEGKKLG FRGRAYFLA PHTNHLGNDLSRGLLFWEGKKLG FRGRAYFLA PHTNHLGNDLSRGLLFWEGKKLG FRGRAYFLA PHTNHLGNDTRSLLI FWEGKFLG	PNGLAW PNGLAW ERGLAW ERGLAW ARGFAW EDGLAW DEGLAW DEGLAW AQGLAW EEGGAW TSGLQW ENGLAW	WLKVH WLKVH WLKVH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH	LANI P LANI P	SISKUDFATRQA SISKUDYATRQK NJSKUDYATRQK VDKADFQ3RVQ HNKFSFEDRIA SFDKASFNDREK SIDKAPLHERVQ SIDKAPLHERVQ SIDKAPLHERVQ SIDKAPLGERAF HDK VSLORVK SFDKLSLDDRVK SFDKLSLDDRVK SFDKLSLDDRVK	761 775 856 826 831 800 808 835 840 821 841 861 508 799 798
<pre>FRGRAYPLS PHFNHL ONDMS BGLLT FWKGKK LGKEG LWLK VHLSNIL YCVDK VPLLERENN 11 FRGRAYPLS PHFNHL ONDMS BGLLT FWKGKK LGPHG LWLK HLSNIL YCVDK VPLLDR VR 643 FRGRAYPLS PHFNHL ONDLS BGLLT FWKGKK LGPHG LWLK HLSNIL YCVDK VPLDDR VR 645 FRGRAYPLS PHFNHL ONDLS BGLLT FWKGKK LGPHG LWLK HLSNIL YCVDK VPLDDR VR 646 FRGRAYPLS PHFNHL ONDLS BGLLT FWKGKK LGPHG LWLK HLSNIL YCVDK VPLDDR VR 647 FRGRAYPLS PHFNHL ONDLS BGLLT FWKGKK LGPHG LWULK VHLSNIL YCVDK VPLDDR VR 648 FRGRAYPLS PHFNHL ONDS BGLLT FWHGKK LGPSG LWULK VHLSNIL YCVDK VPLDDR VR 646 FRGRAYPLS PHFNHL ONDS BGLLT FWHGKK LGPSG LWLK VHLSNIL YCVDK LGLDR VR 646 FRGRAYPLS PHFNHL ONDS BGLLT FWHGKK LGPSG LWLK VHLSNIL YCVDK LGLDR VR 645 FRGRAYPLS PHFNHL ONDS BGLLT FWHGKK LGPSG LWLK VHLSNIL FORKAPLDR VR 645 FRGRAYPLS PHFNHL ONDS BGLLT FWHGKK LGPSG LWLK VHLSNIL FORKAPLDR VR 647 FRGRAYPLS PHFNHL ONDS BGLLT FWHGKK LGPSG LWLK VHLSNIL FORKAPLDR VR 647 FRGRAYPLS PHFNHL ONDS BGLLT FWHGKK LGPGG LWLK VHLSNIL FORKAPLDR VR 647 FRGRAYPLS PHFNHL ONDS BGLLT FWRGKK LGPGG LWLK VHLSNIL FORKAPLDR VR 647 FRGRAYPLS PHFNHL ONDS BGLLT FWRGKK LGPGG LWLK VHLSNIL FORKAPLDR VR 646 FRGRAYPLS PHFNHL ONDS BGLLT FWRGK LGPGG LWLK VHLSNIL FORKAPLDR VR 648 FRGRAYPLS PHFNHL ONDS BGLLT FWRGK LGPGG LWLK VHLSNIL FORKAPLDR VR 648 FRGRAYPLS PHFNHL ONDT RSLFL FWRGK LGPGG LWLK VHLSNIL FORKAPLDR VR 649 FRGRAYPLS PHFNHL ONDT RSLFL FWRGK LGERG LWLK VHLANIL YVR KRAPLER VR 640 FRGRAYPLS PHFNHL ONDT RSLFL FWRGK LGERG LWLK VHLANIL YVR KRAPLER VR 643 FRGRAYPLS PHFNHL ONDT RSLFL FWRGK LGERG LWLK VHLANIL YVR KRAPLER VR 745 FRGRAYPLS PHFNHL ONDT RSLFL FWRGK LGERG LWLK VHLANIL YVR KRAPLER VR 745 FRGRAYPLS PHFNHL ONDT RSLFL FWRGK LGERG LWLK VHLANIL YVR KRAPLER VR 745 FRGRAYPLS PHFNHL ONDT RSLFL FWRGK LGERG LWLK VLANIL YVR KRAPLER VR 745 FRGRAYPLS PHFNHL GODT RSLFL FWRGK LGERG LWLK VLANIL YVR KRAPLER VR 745 FRGRAYPLS PHFNHL GODT RSLFL FWRGK LGERG LWLK VLANIL YVR KRAPLER VR 745 FRGRAYPLS PHFNHL GODT RSLFL FWRGK LGERG LWLK VLANIL YVR KRAPLER VR 745 FRGRAYPLS PHFNHL GODT RSLFL FWRGK LGERG LWLK VLANIL YVR KRAPLER VR 745 FRGRAYPLS PHFNHL GODT R</pre>	FRGRVYFISAHLHHVINDFCRGLLEFAEGKFLG FRGRVYFMSAHLHHVINDFCRGLLEFAEGKFLG FRGRAYELSPHLINHLGNDLSRGLLFWEARFLG FRGRAYELSPHLINHLGNDLSRGLLFWEARFLG FRGRAYELSPHLINHLGNDLSRGLLIFWEGKELG FRGRAYELSPHINHLGNDLSRGLLIFWEGKELG FRGRAYELSPHINHLGNDLSRGLLIFWEGKELG FRGRAYELSPHINHLGNDLSRGLLIFWEGKELG FRGRAYELSPHINHLGNDLSRGLLIFWEGKELG FRGRAYELSPHINHLGNDLSRGLLFWEGKELG FRGRAYELSPHINHLGNDLSRGLLFWEGKELG FRGRAYELSPHINHLGNDTRSLLFWEGKELG FRGRAYELSPHINHLGNDTRSLLFWEGKELG FRGRAYELAPHENHLGNDTRSLLFWEGKELG	PNGLAW PNGLAW ERGLAW ARGFRU EDGLEW EEGLAW DNGLRU AQGLAW ESGFRU EEGLAW TSGLQU ENGLEW PEGLEW	WLKVH WLKVH WLKVH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH	LANI LANI LANI PULANU COANU PULANU PULANU PULANU PULANU PULANU PULANU VONIMU LANU VULANU	SISKUDFATRQA SISKUDYATRQK SNSKUDYATRQK SNSKUDYATRQK SUDKADFQSRUQ SIDKASFNDREK SIDKASFNDREK SIDKASFNDREK SIDKASLERVA SIDKASLERVA SHDKUSEDRVK SFDKLSLDDRVK SFDKLSLDDRVK SFDKLSLDDRVK MDKKSFEERVA MDKKSFEDRIK	761 775 856 826 831 800 808 835 840 821 861 508 799 798 809 839
FRGRAYPLS PHFNHLGNDMS BGLLT FWKGKKLGSIG LWLK VHLSNI YGVDK V3LDDRVA 610 FRGRAYPLS PHFNHLGNDLS RGLLT FWKGKKLGSDG LWLK VHLSNI YGVDK V3LDDRVA 663 FRGRAYPLS PHFNHLGNDLS RGLLT FWKGKKLGSDG LWLK VHLSNI YGVDK VPLDDRVK 661 FRGRAYPLS PHFNHLGNDLS RGLLT FWKGKKLGSDG LWLK VHLSNI YGVDK VPLDDRVK 663 FRGRAYPLS PHFNHLGNDLS RGLLT FWKGKLGSDG LWLK VHLSNI YGVDK VPLDDRVK 663 FRGRAYPLS PHFNHLGNDS RGLLT FWKGKLGSG LWLK VHLSNI YGVDK VPLDRVK 655 FRGRAYPLS PHFNHLGNDS RGLLT FWHGKKLGSG LWLK VHLSNI YGVDK VPLDRVK 665 FRGRAYPLS PHFNHLGNDS RGLLT FWHGKKLGSG LWLK VHLSNI YGVDK VPLDRVK 865 FRGRAYPLS PHFNHLGNDS RGLLT FWHGKKLGSG LWLK VHLSNI FGFDK LPLKDRVA 865 FRGRAYPLS PHFNHLGNDS RGLLT FWHGKKLGSG LWLK VHLSNI FGFDK APLDRVK 865 FRGRAYPLS PHFNHLGNDS RGLT FWHGKKLGSG LWLK VHLSNI FGFDK APLLDRVK 865 FRGRAYPLS PHFNHLGNDS RGLT FWHGKKLGSG LWLK VHLSNI FGFDK APLLDRVK 865 FRGRAYPLS PHFNHLGNDS RGLLF FWGKRLGSG LWLK VHLSNI FGFDK APLLDRVK 865 FRGRAYPLS PHFNHLGNDLT RSLFL FWMGKE LGGG LWLK VHLSNI FGFDK APLLDRVK 865 FRGRAYPLS PHFNHLGNDLT RSLFL FWGKRLGGG LWLK VHLSNI FGFDK APLLAND V 865 FRGRAYPLS PHLNHLGNDLT RSLFL FWGKR LGGG LWLK VHLSNI FGFDK APLLAND V 865 FRGRAYPLS PHFNHLGNDLT RSLFL FWGCK LGGRG LWLK HLANN YGVDK APLLAND V 865 F	FRGRVYFISAHLHFUNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNDFCRGLLE FSEGKFLG FRGRAYELS PHINHI GNDER GGLLK FWEARPLG FRGRAYELS PHINHI GNDLS RGLLT FWEGKFLG FRGRAYELS PHINHI GNDLS RGLLI FWEGKFLG FRGRAYELS PHINHI GNDLS RGLLI FWEGKFLG FRGRAYELS PHINHI GNDLS RGLLI FWEGKFLG FRGRAYELS AHFINHI GNDLS RGLLL FWEGKFLG FRGRAYELS AHFINHI GNDLS RGLLI FWEGKFLG FRGRAYELS AHFINHI GNDLS RGLLI FWEGKFLG FRGRAYELS AHFINHI GNDER RSLLI FWEGKFLG FRGRAYELS HFINHI GNDER RSLLI FWEGKFLG FRGRAYELS HFINHI GNDER RSLLI FWEGKFLG FRGRAYELS HFINHI GNDER RSLLI FWEGKFLG FRGRAYELS HFINHI GNDER RSLLI FWEGKFLG	PNGLAW PNGLAW ERGLAW ERGLAW EDGLKW DEGLAW DEGLAW DNGLAW DNGLAW ESGFAW ESGFAW ESGFAW EEGLAW TSGLOW PEGLKW PEGLAW KEGLAW	WLKVH WLKVH WLKVH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH	LANI LANI FILANI CANF CANF CANF CANF CANF CANF CANF CANF	ISK KDFATRQA SISK VDYATRQK SYDK ADFQSRVQ SYDK ADFQSRVQ SYDK ADFQSRVQ SIDK APLHERVA SIDK APLHERVQ SIDK APLHERVA SIDK APLERVA SIDK SIZQERAE SHDK IPFDARVA SHDK VSLEDRVK SYDK LSLDDRVK SMDK CSFEERVA SMDK APFEDRIK SMDK KPFEDRIK SLDRQTFEARVA	761 775 774 856 626 831 800 835 840 821 861 508 799 798 809 839 839
FRGRAYPLS PHFNHLGNDLS RGLLT FWKGKKLGPHG LWLK LKLSNL YMDK APFDERVR FRGRAYPLS PHFNHLGNDLS RGLLT FWKGKKLGPGG LWLK LKLSNL YMDK APFDERVR FRGRAYPLS PHFNHLGNDLS RGLLT FWKGKKLGPGG LWLK LKLSNL YFUKASLEDRVK FRGRAYPLS PHFNHLGNDKS RGLLT FWKGKKLGPSG LWLK LKLSNL YFUKASLEDRVK FRGRAYPLS PHFNHLGNDKS RGLLT FWHGKKLGPSG LWLK LKLSNL FFUKASLEDRVK FRGRAYPLS PHFNHLGNDKS RGLLT FWHGKKLGPSG LWLK LKLSNL FFUKASLEDRVK FRGRAYPLS PHFNHLGNDKS RGLLT FWHGKKLGPSG LWLK LKLSNL FFUKASLEDRVK FRGRAYPLS PHFNHLGNDKS RGLLT FWHGKKLGPGG LWLK LKLSNL FFUKASLEDRVK FRGRAYPLS PHFNHLGNDKS RGLLT FWHGKKLGPGG LWLK LKLSNL FFUKASLEDRVK FRGRAYPLS PHFNHLGNDKS RGLLT FWHGKRLGPGG LWLK LKLSNL FFUKASLEDRVK FRGRAYPLS PHFNHLGNDLT RSLFL FWGKEV LGGSG LWLK LKLANT YVKASLEDRVV FRGRAYPLS PHFNHLGNDLT RSLFL FWGCRE LGGRG LWLK LKLANT YVKASLEDRVV FRGRAYPLS SHFNHLGNDLT RSLFL FWGCRE LGGRG LWLK LKLANT YVKASLEDRVV FRGRAYPLS SHFNHLGNDLT RSLFL FWGCRE LGGRG LWLK LKLANT YVKASLEDRVV FRGRAYPLS SHFNHLGNDLT RSLFL FWGCRE LGGRG LWLK LKLANT YVKASLEDRVV FRGRAYPLS SHFNHLGDLT RSLFL FWGCRE LGGRG LWLK LKLANT YVKASLEDRVV FRGRAYPLS SHFNHLGDLT RSLFL FWGCRE LGGRG LWLK LKLANT YVKASLESLTKVV	FRGRVYFISAHLHFUNDFCRGLLEFAEGKFLG FRGRVYMSAHLHFUNDFCRGLLEFSEGKFLG FRGRAYELSPHLNHLGNDERGGLLFWEGKFLG FRGRAYELSPHLNHLGNDLSRGLLFWEGKFLG FRGRAYELSPHLNHLGNDLSRGLLFWEGKFLG FRGRAYELSPHYNHLGNDLSRGLLFWEGKFLG FRGRAYELSPHYNHLGNDLSRGLLFWEGKFLG FRGRAYELSPHYNHLGNDLSRGLLFWEGKFLG FRGRAYELSAHFNHLGNDLSRGLLFWEGKFLG FRGRAYELSAHFNHLGNDLSRGLLFWEGKFLG FRGRAYELSPHYNHLGNDLSRGLLFWEGKFLG FRGRAYELSPHYNHLGNDLSRGLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG FRGRAYELSPHYNHLGNDTRSLLFWEGKFLG	PNGLA PNGLA PNGLA ERGLA ELGLA ELGLA ELGLA ELGLA DNGLA AQGLA AQGLA ELGLA ELGLA ELGLA PEGLA ELGLA FEGLA KEGLA	WLKVH WLKVH WLKVH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH	LANI P LANI P LANU P LANU P LANU P LANU P LANU P LANU P LANI P LANI P LANI P LANI P LANI P LANI Y LANI Y LANI Y LANI Y MGNI Y MANI Y	SISKUPATRQA SISKUPASRQK SYSKADFQSRVQ YDKADFQSRVQ FUNKFSFEDRIA SFDKASFNDREK SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVA SIDKUSLORVK SFDKLSLDRVK SFDKLSLDRVK SFDKLSLDRVK SFDKLSLDRVK STDKSSFERVA MDKASFERVE MDKKSFEDRIK MDKKFPEDRIK SLDKQTFEARVA	761 775 774 856 826 831 808 825 840 821 840 821 840 799 798 809 839 839 836 839
FRGRAYELS PHFNHLGNDLS BALLT FWRGKELGEDG LWILK LYHLSNL FEVDK VPLEDRVK 661 FRGRAYELS PHFNHLGNDMS GALLT FWRGKELGSGLKWLK IHLSNL FEVDK NAALDRVK 669 FRGRAYELS PHFNHLGNDMS GALLT FWRGKELGSGLKWLK IHLSNL FEFDK ICLEDR IA 866 FRGRAYELS PHFNHLGNDS BALLT FWRGKELGSGLKWLK IHLSNL FEFDK ICLEDR IA 866 FRGRAYELS PHFNHLGNDS GALLT FWRGKELGSGLKWLK IHLSNL FEFDK ILLEDRVN 865 FRGRAYELS PHFNHLGNDS GALLT FWRGKELGSGLKWLK IHLSNL FEFDK APLDERVN 865 FRGRAYELS PHFNHLGNDS GALLT FWRGKELGSGLKWLK IHLSNL FEFDK APLDERVN 865 FRGRAYELS PHFNHLGNDS GALLT FWRGKELGSGLKWLK IHLSNL FEFDK APLDERVN 826 FRGRAYELS PHFNHLGNDS GALLT FWRGKELGSGLKWLK INLSNL FEFDK APLDERVN 826 FRGRAYELS PHFNHLGNDS GALLT FWRGKELGSGLKWLK INLSNL FEFDK APLDERVN 826 FRGRAYELS PHFNHLGNDLT BALLT FWRGKELGSGLKWLK INLSNL FEFDK APLDERVN 826 FRGRAYELS PHFNHLGNDLT RALFLFWRGKELGSGLGKLK INLSNL FEFDK APLDERVN 840 FRGRAYELS PHFNHLGNDLT RALFLFWRGKELGSGLGLWLK INLSNL Y VYKVPLKDR IE 852 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSGLGUKUK INLSNL Y VYKVPLKDR IE 852 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSGLGUKUK INLSNL Y VYKVPLKDR IE 852 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSGLGWLK INLANU Y VYKARALSLEERVN 840 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSGLGUKUK INLANU Y VYKARALSLEERVN 840 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSRGLWKK INLANU Y VYKARALSLEERVN 840 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSRGLWKK INLANU Y VYKARALSLEERVN 840 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSRGLWKK INLANU Y VYKARALKERVN 992 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSRGLWKK INLANU Y VYKARALKERVN 993 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSRGLWKK INLANU Y VYKARALKERVN 993 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSRGLWKK INLANU Y VYKARALKERVN 993 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSRGLWKK INLANU Y VYKARALKERVN 932 FRGRAYELS PHNNHLGNDLT RALFLFWRGKELGSRGLWKK INLANU Y VYKARALKERVN 932 FRGRAYELS PHNNHLGDLT RALFLFWRGKELGSRGLWKK VLANU Y VYKARALKERVN 933 FRGRAYELS PHNNHLGDLT RALFLFWRGKELGSRGLWKK VLANU Y VYKARALKERSL 943 FRGRAYELS PHNNHLGDLT RALFLFWRGKELGSRGLWKK VLANU Y VYKARALKERSL 943 FRGRAYELS PHNNHLGDLT RALFLFWRGKELGSGLWKKK VLANU Y FVKARALSLKRVC 933 FRGRAYELS PHNNHLGDLT RALFLFWRGK	FRGRVYFISAHLHFUNNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNNDFCRGLLE FSEGKFLG FRGRAYELSPHLNHLGNDER GGLLE FSEGKFLG FRGRAYELSPHLNHLGNDER GGLLE FWEARLG FRGRAYELSPHLNHLGNDER GGLLFFWEGKELG FRGRAYELSPHTNHLGNDER GGLLFFWEGKELG FRGRAYELSPHTNHLGNDER SGLLFFWEGKELG FRGRAYELSPHTNHLGNDER SGLLFFWEGKELG FRGRAYELSAHFNHLGNDER SGLLFFWEGKELG FRGRAYELSAHFNHLGNDER SGLLFFWEGKELG FRGRAYELSAHFNHLGNDER SSLLFFWEGKELG FRGRAYELSAHFNHLGNDER SSLLFFWEGKELG FRGRAYELSHFNHLGNDER SSLLFFWEGKELG	PNGLW PNGLW ERGLW ERGLW ARGFW EDGLW DEGLW DEGLW ESGFW DNGLW ESGFW DNGLW ESGFW TSGLQ ESGFW TSGLQ ESGFW ESGLW KEGLW KEGLW KEGLW	WLKVH WLKVH WLKVH WLKIH WLKIQ WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH	LANI P LANI P LANG Y LANG Y Y LANG Y Y LANG Y Y LANG Y Y LANG Y Y LANG Y Y LANG Y Y LANG Y Y LANG Y Y Y LANG Y Y Y Y Y X Y Y Y Y Y Y Y Y Y Y Y Y Y Y	SISKUPATRQA SISKUPASRQK SYDKADFQSRVQ HNKFSFEDRIA STDKADFQSRVQ SIDKADFLERVQ SIDKADFLERVQ SIDKADFLERVQ SIDKADFLERVA HDKIJEDRVK STDKIJEDRVK SFDKLSLDDRVK SFDKLSLDDRVK SIDKQFFERVE SUDKQFFERVA SUDKUFFERVA SUDKUFFERVA SVDKVFLEREN	761 775 774 856 826 831 808 841 861 850 850 850 850 850 850 850 850 850 850
FRGRAYELS PHFNHL ONDS BGLLT FWRGKQLGASG LWILK LYHLSNI YETRASLEDRVR FRGRAYELS PHFNHL ONDS BGLLT FWHGKKLGSG LWILK LHLSNI FFOR ICLEDR IA 866 FRGRAYELS PHFNHL ONDS BGLLT FWHGKKLGSG LWILK LHLSNI FFOR LRLEDRVA 865 FRGRAYELS PHFNHL ONDS RGLLT FWHGKKLGSG LWILK LHLSNI FFOR APLOERVT 811 FRGRAYELS PHFNHL ONDS BGLLT FWHGKKLGSG LWILK LHLSNI FFOR APLOERVT 811 FRGRAYELS PHFNHL ONDS BGLLT FWHGKKLGSG LWILK LHLSNI FFOR APLOERVT 817 FRGRAYELS PHFNHL ONDS BGLLT FWHGKKLGSG LWILK LHLSNI FFOR APLOERVT 817 FRGRAYELS PHFNHL ONDS BGLLT FWHGKKLGSG LWILK LWILSNI FFOR APLOERV 817 FRGRAYELS PHFNHL ONDS BGLLT FWHGKKLGSG LWILK LWILSNI FFOR APLOERV 810 FRGRAYELS PHFNHL ONDS BGLLT FWHGKKLGSG LWILK LWILSNI FFOR APLOERV 810 FRGRAYELS PHFNHL ONDT RSILF FWHGKKLGGRG LWILK LWILSNI FFOR APLOERV 840 FRGRAYELS PHILHI ONDT RSILF FWHGKE LGERG LWILK LHLAWY VOR KAPLOERV 840 FRGRAYELS PHILHL ONDT RSIFT FWHGKE LGERG LWILK LHLAWY VOR KAPLOERV 840 FRGRAYELS PHFNHL ONDT RSIFT FWEGRE LGERG LWILK LHLAWY VOR KAPLOERV 840 FRGRAYELS PHFNHL ONDT RSIFT FWEGRE LGERG LWILK LHLAWY VOR KAPLOERV 840 FRGRAYELS PHFNHL ONDT RSIFT FWEGRE LGERG LWILK LHLAWY VOR KAPLOERV 840 FRGRAYELS PHFNHL ONDT RSIFT FWEGRE LGERG LWILK LHLAWY VOR KAPLOERV 840 FRGRAYELS PHFNHL ONDT RSIFT FWEGRE LGERG LWILK LHLAWY VOR KAPLOERV 840 FRGRAYELS PHFNHL ONDT RSIFT FWEGRE LGERG LWILK LHLAWY VOR KAPLOERV 840 FRGRAYELS PHFNHL ONDT RSIFT FWEGRE LGERG LWILK LHLAWY VOR KAPLOERV 840 FRGRAYELS PHFNHL ONDT RSIFT FWEGRE LGERG LWILK LHLAWY VOR KAPLERV 942 FRGRAYELS PHFNHL ONDT RSIFT FWEGRE LGERG LWILK LWILAWY VOR KAPLERV 943 FRGRAYELS PHFNHL ONDT RSIFT FWEGRE LGERG LWILK LWILAWY VOR KAPLERV 945 FRGRAYELS PHFNHL GDUT RSIFT FWEGRE LGERG LWILK LWILAWY VOR KAPLERV 946 FRGRAYELS PHFNHL GDUT RSIFT FWEGRE LGERG LWILK LWILAWY VOR KAPLERV 947 FRGRAYELS PHFNHL GDUT RSIFT FWEGRE LGERG LWILK VOLAWY VOR KAPLERV 941 FRGRAYELS PHFNHL GDUT RSIFT FWEGRE LGERG LWILK VOLAWY VOR KAPLERV 941 FRGRAYELS PHFNHL GDUT RSIFT FWEGRE LGERG LWILK VOLAWY VOR KAPLERV 941 FRGRAYELS PHFNHL GD	FRGRVYFISAHLHVUNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHVUNDFCRGLLE FSEGKFLG FRGRAYAIP PHLNHLGNDCRGLLA FWEGKFLG FRGRAYFLSPHLNHLGNDLSRGLLA FWEGKFLG FRGRAYFLSPHLNHLGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHLGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHLGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHLGNDLSRGLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLAPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKKFLG FRGRAYFLSPHTNHLGNDTRSLLFWEGKKFLG	PNGLA PNGLA PNGLA ERGLA EDGLA EDGLA DEGLA EGLA DNGLA AQGLA ESGFA EEGLA TSGLQ ENGLA FSGLQ ENGLA KEGLA KEGLA KEGLA SLGLA	WLKVH WLKVH WLKVH WLKVH WLKVH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH	LANI F LANI F LANI F LANI C CANU F LANI F LANI F LANI F LANI F LANI F LANI F LANI F LANI F LANI Y LANI Y	SISKUDFATRQA SISKUDYATRQK SNSKUDYATRQK SNSKUDYATRQK SUDKADFQSRUQ SIDKASFNDREK SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKASLORVA HDKVSLDDRVK SHDKVSFERVA SUDKVSFERVA SUDKUFFERVA SUDKUFFERVA SUDKUFFERVA	761 775 774 856 626 831 808 835 840 821 869 799 809 798 809 836 836 817 810 863
FRGRAYPLS PHFNHLGNDMS RGLLT FWHGKKLGSSG LWILK LHISNI FFORK ICLEDR IA FRGRAYPLS PHFNHLGNDMS RGLLT FWHGKKLGSG LWILK LHISNI FFORK ICLEKORVA FRGRAYPLS PHFNHLGNDMS RGLLT FWHGKKLGSG LWILK LHISNI FFORKAPLERVT SSS FRGRAYPLS PHFNHLGNDMS RGLTFWHGKKLGSG LWILK LHISNI FFORKAPLERVT SSS FRGRAYPLS PHFNHLGNDMS RGLTFWHGKRLGSG LWILK LHISNI FFORKAPLERVT SSS FRGRAYPLS PHFNHLGNDMS RGLTFWHGKRLGSG LWILK LHISNI FFORKAPLERVT SSS FRGRAYPLS PHFNHLGNDMS GGLTFWHGKRLGSG LWILK LHISNI FFORKAPLERV SSS FRGRAYPLS PHFNHLGNDLT RSILFFWHGKRLGSG LWILK LHISNI FFORKASLLERVQ SSS FRGRAYPLS PHFNHLGNDLT RSILFFWHGKRLGSG LWILK LHISNI FFORKASLERVQ SSS FRGRAYPLS PHINHLGNDLT RSILFFWHGKRLGSG LWILK LHISNI FFORKASLERVQ SSS FRGRAYPLS PHINHLGNDLT RSILFFWHGKRLGSG LWILK LHISNI FFORKASLERVX SSS FRGRAYPLS PHFNHLGNDLT RSILFFWHGKRLGSG LWILK LHISNI FFORKAPLERVX SSS FRGRAYPLS PHFNHLGNDLT RSILFFWHGKRLGSG LWILK LHISNI FFORKAPLERVX SSS FRGRAYPLS PHFNHLGNDT RSILFFWHGKRLGSG LWILK LHISNI FFORKAPLERVX SSS FRGRAYPLS PHFNHLGNDT RSILFFWHGKRLGSG LWILK LHISNI FFORKAPLERVX SSS FRGRAYPLS SHTNHLGNDT RSILFFWHGKRLGSG LWILK LHISNI FFORKAPLERVX SSS FRGRAYPLS SHTNHLGNDT RSILFFWHGKRLGSG LWILK LHISNI FFORKAPLERVX SSS FRGRAYPLS SHTNHLGDDT RSILFFWHGKRLGSG LWILK LWILK FWILK FFORKAPLERVX SSS FRGRAYPLS SHTNHLGDDT RSILFFWHGKRLGSG LWILK VLANN FFORKAPLEST SSS FRGRAYPLS SHTNHLGDLT RSILF	FRGRVYFISAHLHFUNNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNNDFCRGLLE FSEGKFLG FRGRÀYELSHLINH GNDLRGLLMFWEGKPLG FRGRÀYELSHLINH GNDLRGLLFWEGKLG FRGRÀYELSHLINH GNDLRGLLFWEGKLG FRGRÀYELSHNINH GNDLRGLLFWEGKLG FRGRÀYELSHTNHGNDLSRGLLFWEGKLG FRGRÀYELSAHFNHLGNDLRGLLFWEGKLG FRGRÀYELSAHFNHLGNDLRGLLFWEGKLG FRGRÀYELSAHFNHLGNDLRGLLFWEGKLG FRGRÀYELSHFNHGNDT RSLLFWEGKLG FRGRÀYELSHFNHLGNDM RGLLFWEGKLG FRGRÀYELSHFNHLGNDM RGLLFWEGKLG FRGRÀYELSHFNHLGNDM RGLLFWEGKLG FRGRÀYELSHFNHLGNDM RGLLFWEGKLG	PNGLAW PNGLAW ERGLAW ERGLAW EDGLKW DDGLEW EEGLAW DNGLAW AQGLAW EEGLAW TSGLQW EEGLAW FEGLAW FEGLAW KEGLSW KEGLSW SLGLKW PPGLW PDGLW	WLKVH WLKVH WLKUH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH	LANI FLANI YLANI Y	ISKDPATRQA SISKUDYATRQK NJSKUDYATRQK NJSKUDYATRQK NJSKUDYSRUQ SIDKAPLERDRIA SFDKASFNDREK SIDKAPLERTVA SIDKAPLERTVA SIDKUSLQERAE SHDK IPFDARVA SHDKVSLEDRVK SFDKLSLDDRVK SMDKCSFEERVE MDKKPFEDRIK SUDKUFEARVA SUDKUFEARVA SUDKUSLDDRVK SUDKUSLDDRVK SUDKUSLDDRVK SUDKUSLDDRVA SUDKUSLDDRVA SUDKUSLDDRVA	761 775 774 856 626 831 800 835 840 821 861 508 799 839 839 839 839 839 839 839 836 810 810
FRGAYELS PHFNHLONDS BGLLT FWHCKLGPSG LWILK HISNI FFOR LELKDRVA FRGAYELS PHFNHLONDS BGLLT FWHCKLGPSG LWILK HISNI FFOR LELKDRVS S55 FRGRYELS PHFNHLONDS BGLMT FWHCKLGPSG LWILK VHLSNI FFOR APLDER VT S11 FRGRYELS PHFNHLONDS BGLMT FWHCKLGPSG LWILK VHLSNI FFOR APLDER VT S12 FRGRYELS PHFNHLONDS BGLMT FWHCKLGPSG LWILK VHLSNI FFOR APLDER VT S12 FRGRYELS PHFNHLONDS BGLLT FWHCKLGPSG LWILK VHLSNI FFOR APLDER VT S12 FRGRYELS PHFNHLONDS BGLLT FWHCKLGPSG LWILK VHLSNI FFOR APLDER VT S12 FRGRYELS PHFNHLONDT S12LT FWHCKLGPSG LWILK VHLSNI FFOR APLDER VT S12 FRGRYELS PHFNHLONDT S12LT FWHCKLGPSG LWILK VHLSNI FFOR APLDER VT S12 FRGRYELS PHFNHLONDT S12LT FWHCKLGPSG LWILK VHLANT VYNK APLDER VT S12 FRGRYELS PHFNHL GNDT S12LT FWHCKLGPSG LWILK VHLANT VYNK APLDER VT S12 FRGRYELS PHFNHL GNDT S12LT FWHCKT LGRAG LWILK VHLANT VYNK APLDER VT S12 FRGRYELS PHFNHL GNDT S12LT FWHCKT LGRAG LWILK VHLANT VYNK APLDER VT S12 FRGRYELS PHFNHL GDDT S12LT FWHCKT LGRAG LWILK VLANT VYNK APLDER VT S13 FRGRYELS PHFNHL GDDT S12LT FWHCKT LGRAG LWILK VLANT VYNK APLDER VT S13 FRGRYELS PHFNHL GDDT S12LT FWHCKT LGRAG LWILK VLANT VYNK APLDER VT S13 FRGRYELS PHFNHL GDDT S12LT FWHCKT LGRAG LWILK VLANT VYNK APLDER VT S13 FRGRYELS PHFNHL GDDT S12LT FWHCKT LGRAG LWILK VLANT VYNK APLDER VT S13 FRGRYELS PHFNHL GDDT S12LT FWHCKT LGRAG LWILK VLANT VYNK APLDER VT S13 FRGRYELS PHSHLH LGDLT S12LT FWHCKT LGRAG LWILK VLANT VYNK APLDER VT S14 FRGRYELS PHSHLHLGDLT S12LT FWHCKT LGRAG LWILK VLANT VYNK APLDER VT S15 FRGRYELS PHSHLK FLCOLT S12LT FWHCKT LGRAG L	FRGRVYFISAHLHFUNDFCRGLLEFAGGKFLG FRGRVYMSAHLHFUNDFCRGLLEFSGGKFLG FRGRAYFLSPHLNHLGNDCRGLLMFWEGKFLG FRGRAYFLSPHLNHLGNDSRGLLFWLGKFLG FRGRAYFLSPHLNHLGNDSRGLLFWLGKFLG FRGRAYFLSPHFNHLGNDSRGLLFWLGKFLG FRGRAYFLSPHFNHLGNDSRGLLFWLGKFLG FRGRAYFLSPHFNHLGNDTRSLLFWLGKFLG FRGRAYFLSHFNHLGNDTRSLLFWLGKFLG FRGRAYFLSHFNHLGNDTRSLLFWLGKFLG FRGRAYFLSHFNHLGNDTRSLLFWLGKFLG FRGRAYFLSHFNHLGNDTRSLLFWLGKFLG FRGRAYFLSHFNHLGNDTRSLLFWLGKFLG FRGRAYFLSHFNHLGNDTRSLLFWLGKFLG FRGRAYFLSHFNHLGNDTRSLLFWLGKFLG FRGRAYFLSHFNHLGNDTRSLLFWLGKFLG FRGRAYFLSHFNHLGNDTRSLLFWLGKKLG FRGRAYFLSHFNHLGNDTRSLLFWLGKKLG FRGRAYFLSHFNHLGNDTRSLLFWLGKKLG FRGRAYFLSHFNHLGNDTRSLLFWLGKKLG FRGRAYFLSHFNHLGNDTRSLLFWLGKKLG FRGRAYFLSHFNHLGNDTRSLLFWLGKKLG FRGRAYFLSHFNHLGNDTRSLLFWLGKKLG FRGRAYFLSHFNHLGNDTRSLLFWLGKKLG FRGRAYFLSHFNHLGNDTRSLLFWLGKKLG FRGRAYFLSHFNHLGNDSRGLLFWLGKKLG FRGRAYFLSHFNHLGNDSHGNLFWLGKLG FRGRAYFLSHFNHLGNDSHFLGFUNGKLG FRGRAYFLSHFNHLGNDSHF	PNGLAW PNGLAW PNGLAW EHGLAW ARGFAN EDGLKW DEGLAW EEGLAW DNGLAW AQGLAW ESGFAW ESGFAW ESGFAW ESGFAW ESGFAW EEGLAW KEGLAW KEGLAW KEGLAW SILGLAW PHGLAW	WLKVH WLKVH WLKVH WLKVH WLKVH WLKUH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKUH WLKUH WLKUH	LANL FLAND	SISKUDFATRQA SISKUDYATRQK SNSKUDYATRQK VIDKADFQSRUQ SIDKADFQSRUQ SIDKADFLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVA MIDKASFERVE MIDK SSFEERVA MIDKASFEERVE MIDK SSFEERVA MIDKAFFEDRIK SIDKQTFEARVA SUDKUPLEREN SUDKUPLEREN MIDKAPFEDRIK SUDKUPLEREN MIDKAPFEDRIK	761 775 776 856 826 831 808 835 840 821 860 821 860 821 860 839 839 839 839 839 839 839 839 839 839
FRGRAYPLS PHFNHLGNDMS RGLLT FWHGKRLGPSGLWUK KILSNI FFOR KLRLEDNS FRGRAYPLS PHFNHLGNDMS GALT FWHGKRLGPGLWUK KILSNI FFOR APLDERVT S1 FRGRAYPLS PHFNHLGNDMS RGLMF FWHGKRLGPGGLWUK VHLSNI FFOR APLDERVT S2 FRGRAYPLS PHFNHLGNDMS RGLLF FWHGKRLGPGGLWUK VHLSNI FFOR APLERV S7 FRGRAYPLS PHFNHLGNDMS RGLLF FWHGKRLGPGGLWUK VHLSNI FFOR APLERV S4 FRGRAYPLS PHFNHLGNDT RSLFLFWHGKRLGPGGLWUK VHLSNI FFOR APLERV S4 FRGRAYPLS PHFNHLGNDT RSLFLFWHGKRLGPGGLWUK VHLSNI FFOR APLERV S4 FRGRAYPLS PHFNHLGNDT RSLFLFWHGKRLGPGGLWUK VHLANV VKNA APLDERVK S4 FRGRAYPLS PHFNHLGNDT RSLFLFWHGKRLGPGGLWUK VHLANV VKNA APLDERV S4 FRGRAYPLS PHFNHLGNDT RSLFLFWHGKRLGPGGLWUK VHLANV VKNA APLDERV S4 FRGRAYPLS PHFNHLGNDT RSLFLFWHGKRLGPGGLWUK VHLANV VKNA APLAKKVE 792 FRGRAYPLS PHFNHLGNDT RSLFLFWHGKRLGPGGLWUK VHLANV VKNA APLAKKVE 793 FRGRAYPLS PHFNHLGNDT RSLFLFWHGKRLGPGGLWUK VHLANV VVNA APLAKKVE 794 FRGRAYPLS PHFNHLGDT RSLFLFWHGKRLGPGGLWUK VHLANV VVNA APLAKKVE 795 FRGRAYPLS PHFNHLGDT RSLFLFWHGKRLGPGELWUK VLANV VVNA APLSERIQ 333 FRGRAYPLS PHFNHLGDT RSLFLFWHGKLGPGGLWUK VLANV VVNA APLSERIQ 343 FRGRAYPLS PHFNHLGDT RSLFLFWHGKLGPGGLWUK VLANV VVNA FJISERIQ 344 FRGRAYPLS PHFNHLGDT RSLFLFWHGKRLGPGGLWUK VLANV VVNA FJISERIQ 345 FRGRAYPLS PHFNHLGDT RSLFLFWHGKRLGPGGLWUK VLANV VVNA FJISERIV 346 FRGRAYPLS PHFN	FRGRVYFISAHLHVUNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHVUNDFCRGLLE FSEGKFLG FRGRAYAD SHLHVUNDFCRGLLE FSEGKFLG FRGRAYELS PHINHLGDLS RGLLK FWEARDLG FRGRAYELS PHINHLGDLS RGLLL FWEGKLG FRGRAYELS PHINHLGDLS RGLLL FWEGKLG FRGRAYELS PHYNHLGDLS RGLLL FWEGKLG FRGRAYELS PHYNHLGNDLS RGLLL FWEGKLG FRGRAYELS PHYNHLGNDLS RGLLL FWEGKLG FRGRAYELS PHYNHLGNDLS RGLLL FWEGKLG FRGRAYELS PHYNHLGNDLS RGLLL FWEGKLG FRGRAYELS PHYNHLGNDMT RSLLL FWEGKLG FRGRAYELS PHYNHLGNDMT RSLL FWEGKLG FRGRAYELS PHYNHLGNDMS RGLL FWEGKLG FRGRAYELS PHYNHLGNDS RGLL FWEGKKLG FRGRAYELS PHYNHLGNDS SGLL FWEGKKLG FRGRAYELS PHYNHLGNDLS RGLL FWEGKLG FRGRAYELS PHYNHLGNDLS FRGLL FWEGKLG FRGRAYELS PHYNHLGNDS FRGL FWEGKLG FRGRAYELS PHYNHLG FRGRAYELS FRGRAYELS FRGAXELS FRGAXELS	PNGLIN PNGLIN ERGIN ERGIN EDGIN EDGIN EDGIN EGIN ESGFN ESGFN ESGFN ESGFN ESGFN ESGFN ESGFN ESGFN EGIN KEGIN KEGIN KEGIN KEGIN FIGIN FIGIN	WLKVH WLKVH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH WLKIH	LANI F LANI F LANI F LANI C LANI F LANI F LSNI F LSNI F LANF F LANF F LANF F LANF F LANF F LANF Y LANI Y LANI Y LANI Y LANI Y LANI Y LANI Y LANI Y LANI Y LSNI Y LSNI Y LSNI F LSNI F	ISKDPATRQA SISKUDYATRQK SYDKADFQSRVQ SYDKADFQSRVQ SYDKADFQSRVQ SYDKASFNDREK SIDKAPLEREVQ SIDKAPLEREVQ SIDKAPLEREVQ SIDKAPLEREVA SHDK IFFDARVA SHDK USLDRVK SFDKLSLDDRVK SHDK SFERVA SHDK SFERVA SHDK YFLEREN SUDK QIFEARVA SUDK VJLEREN SYDK VSLDDRVA SHDK SIDDRVA SHDK SEDRIK SYDK VSLDDRVA SHDK SEDRY	761 775 774 856 626 831 800 835 840 821 861 862 809 799 809 836 836 836 836 837 810 862 891 862
FRGRAYPLS PHFNHLGNDMS RGLLMF FWHCKRLGSTG LWULK VHLSNI FFORKAPLERVQ 847 FRGRAYPLS PHFNHLGNDMS RGLLLFWNGKRLGSG LWULK VHLSNI FFORKASLERVQ 847 FRGRAYPLS PHFNHLGNDMS RGLLF WNGKRLGSG LWULK VHLSNI FFORKASLERVQ 843 FRGRAYPLS PHFNHLGNDLT RSLFLFWNGKRLGSG LWULK VHLSNI FFORKAPLERVQ 843 FRGRAYPLS PHFNHLGNDLT RSLFLFWNGKRLGSG LWULK VHLSNI FFORKAPLERVQ 843 FRGRAYPLS PHFNHLGNDLT RSLFLFWNGKRLGSG LWULK VHLSNI FFORKAPLERVQ 843 FRGRAYPLS PHFNHLGNDLT RSLFLFWEGKRLGSG LWULK VHLSNI FFORKAPLERVQ 843 FRGRAYPLS PHFNHLGNDLT RSLFLFWEGKRLGSG LWULK VHLSNI FFORKAPLERVQ 843 FRGRAYPLS PHFNHLGNDLT RSLFLFWEGKRLGSG LWULK VHLSNI FFORKAPLAGRAQ 846 FRGRAYPLS PHFNHLGNDLT RSLFLFWEGKRLGSG LWULK VHLSNI FFORKAPLAGRAQ 848 FRGRAYPLS PHFNHLGNDLT RSLFLFWEGKRLGSG LWULK VHLSNI FFORKAPLAGRAQ 848 FRGRAYPLS PHFNHLGNDT RSLFLFWEGKRLGSG LWULK VHLSNI FFORKAPLAGRAQ 848 FRGRAYPLS PHFNHLGNDT RSLFLFWEGKRLGSG LWULK VHLSNI FFORKAPLER 10 847 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGSG LWULK VQLSNI FFORKAPFFORK 828 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGGE LWULK VQLSNI FVOKAPFFORK 828 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGEGG LWULK VQLSNI FVOKAPFFORK 828 FRGRAYPLS PHNHLGDTT RSLFLFWEGKRLGEGG LWULK VQLSNI FVOKAPFFORK 828 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGEGG LWULK VQLSNI FVOKAPFFORK 828 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGEGG LWULK VQLSNI FVOKAPISER 10 833 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGEGG LWULK VQLSNI FVOK SLKRVF 841 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGEGG LWULK VQLSNI FVOK SLKRVF 841 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGEGG LWULK VQLSNI FVOK SLKRVF 841 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGEGG LWULK VQLSNI FSLGRVF 845 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGEGG LWULK VQLSNI FSLGRVF 845 FRGRAYPLS PHFNHLGDTT RSLFLFWEGKRLGEGG LWULK FLANT FSL	FRGRVYFISAHLHVUNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHVUNDFCRGLLE FSEGKFLG FRGRAYAI P PHLNHLGNDCRGLLA FWEGKFLG FRGRAYFLS PHLNHLGNDLSRGLL FWEGKFLG FRGRAYFLSPHLNHLGNDLSRGLLI FWEGKFLG FRGRAYFLSPHINHGNDLSRGLLI FWEGKFLG FRGRAYFLSPHYNHGNDLSRGLLI FWEGKFLG FRGRAYFLSPHYNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHYNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHYNHLGNDLSRGLLFWEGKFLG FRGRAYFLSPHYNHLGNDLSRGLLFWEGKFLG FRGRAYFLAPHYNHLGNDM TRSLLFWEGKFLG FRGRAYFLAPHYNHLGNDM TRSLLFWEGKFLG FRGRAYFLAPHYNHLGNDM TRSLLFWEGKFLG FRGRAYFLAPHYNHLGNDM TRSLLFWEGKFLG FRGRAYFLAPHYNHLGNDM TRSLLFWEGKFLG FRGRAYFLAPHYNHLGNDM TRSLLFWEGKFLG FRGRAYFLAPHYNHLGNDM TRSLLFWEGKFLG FRGRAYFLAPHYNHLGNDM TRSLLFWEGKFLG FRGRAYFLAPHYNHLGNDM TRSLLFWEGKFLG FRGRAYFLAPHYNHLGNDM TRSLLFWEGKFLG FRGRAYFLSPHYNHLGNDM SRGLLFWEGKFLG FRGRAYFLSPHYNHLGNDSRGLLFWEGKFLG FRGRAYFLSPHYNHLGNDSRGLLFWEGKFLG FRGRAYFLSPHYNHLGNDSRGLLFWEGKFLG FRGRAYFLSPHYNHLGNDM SRGLLFWEGKFLG FRGRAYFLSPHYNHLGNDM SRGLFWEGKFLG	PNGLAW PNGLAW PNGLAW EHGLAW ARGFAW EHGLAW DEGLAW DEGLAW DEGLAW EEGLAW EEGLAW EEGLAW FEGLAW KEGLAW KEGLAW KEGLAW FHGLW PHGLW PHGLW PHGLW PHGLW PHGLW	MIK HH MIK HH M MIK HH MIK HH MIK HH MIK HH MIK HH MIK HH MIK HH MIK HH MIK HH	LANI PLANI P	SISKUDFATRQA SISKUDYATRQK SYDKADFQ3RVQ SYDKADFQ3RVQ SYDKADFQ3RVQ SIDKADFDRIERVQ SIDKADFLERVQ SIDKADFLERVQ SIDKADFLERVA SIDKUDCRAF HDKUSFDRVK SYDKUSFDRVK SUDKUSFDRVK SUDKUSFDRVK SUDKUFFLRVA SUDKUFFLRVA SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK SYDKUSFDRVK	761 775 856 826 831 808 835 840 821 840 821 840 821 840 821 840 836 817 810 836 836 836 836 845 859 886 885
FRGRAYPLS PHFNHLGNDMS BGLLL FWNGKELGPGGLWULKUHLSNI FFEDKASLLERVQ 847 FRGRAYPLS PHFNHLGNDMS BGLLL FWKGKELGPGLWULKUHLSNI FFEDKASLLENV 857 FRGRAYPLS PHLNHLGNDLT RSLFLFWKGKELGPGLWULKUHLSNI FFEDKASLLERVK 852 FRGRAYPLS PHLNHLGNDLT RSLFLFWNGKE LGERGLWULK IHLSNI FFEDKASLLERVK 843 FRGRAYPLS PHLNHLGNDLT RSLFLFWNGKE LGERGLWULK IHLSNI FFEDKASLERVK 843 FRGRAYPLS PHLNHLGNDLT RSLFLFWNGKE LGERGLWULK IHLSNI FYDKASLERVK 843 FRGRAYPLS PHLNHLGNDLT RSLFLFWEGRE LGERGLWULK IHLSNI FYDKASLERVK 843 FRGRAYPLS PHTNHLGNDLT RSLFLFWEGRE LGERGLWULK IHLSNI FYDKASLERVK 843 FRGRAYPLS PHTNHLGNDLT RSLFLFWEGRE LGERGLWULK IHLSNI FYDKARLERVK 943 FRGRAYPLS PHTNHLGNDLT RSLFLFWEGRE LGERGLWULK IHLSNI FYDKARLERVK 945 FRGRAYPLS PHTNHLGNDLT RSLFLFWEGRE LGERGLWULK IHLSNI FYDKARLERVK 945 FRGRAYPLS PHTNHLGNDLT RSLFLFWEGRE LGERGLWULK IHLSNI FYDKARLERVK 938 FRGRAYPLS PHTNHLGNDT RSLFLFWEGRE LGERGLWULK INLANI FYDKAPLHERV 938 FRGRAYPLS PHTNHLGNDT RSLFLFWEGRE LGERGLWULK INLANI FYDKAPFDERVK 228 FRGRAYPLS HHNHLGDLT RSLFLFWEGRE LGERGLWULK INLANI FYDKAPFDERVK 288 FRGRAYPLS HHNHLGDLT RSLFLFWEGRE LGERGLWULK INLANI FYDKAPFDERVK 288 FRGRAYPLS HHNHLGDLT RSLFLFWEGRE LGERGLWULK INLANI FYDKAPFDERVK 283 FRGRAYPLS HHNHLGDLT RSLFLFWE	FRGRVYFISAHLHFUNNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNNDFCRGLLE FSGRFLG FRGRAYELSPHLNHLGNDERGGLLFWEGKFLG FRGRAYELSPHLNHLGNDLSGLLFWEGKELG FRGRAYELSPHLNHLGNDLSGLLFWEGKELG FRGRAYELSPHTNHLGNDLSGLLFWEGKELG FRGRAYELSPHTNHLGNDLSGLLFWEGKELG FRGRAYELSAFINHLGNDLSGLLFWEGKELG FRGRAYELSAFINHLGNDLSGLLFWEGKELG FRGRAYELSAFINHLGNDKRSLLFWEGKELG FRGRAYELSAFINHLGNDKRSLLFWEGKELG FRGRAYELSAFINHLGNDKRSLLFWEGKELG FRGRAYELSPHTNHLGNDKRSLLFWEGKELG FRGRAYELSPHTNHLGNDKRSLLFWEGKELG FRGRAYELSPHTNHLGNDKRSLLFWEGKELG FRGRAYELSPHTNHLGNDKRSLLFWEGKELG FRGRAYELSPHTNHLGNDKRSLLFWEGKELG FRGRAYELSPHTNHLGNDKRSLLFWEGKELG FRGRAYELSPHTNHLGNDKRSLLFWEGKELG FRGRAYELSPHTNHLGNDKRSLLFWEGKELG FRGRAYELSPHTNHLGNDKRSLLFWEGKELG FRGRAYELSPHTNHLGNDKSSL	PNGLIN PNGLIN PNGLN EHGLIN ARGF20 EHGLIN DEGLIN DEGLIN EGGIN AQGLIN EGGIN TSGLQ ENGLN FEGLQ FDGLN FEGLS SLGLS FDGLS FDGLS FDGLS FDGLS FDGLS FDGLS FDGLS	MINE H MINE H MI	LANI P LANI Y LANI Y	SISKUDFATRQA SISKUDYASRQK SYDKADFQSRVQ HNK FSFEDRIA SFDKASFNDREK SIDKAPLERRVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ HDK IJFDARVA HDK VJEDRVK SFDK LSLDDRVK SFDK LSLDDRVK SUDK VFLERVQ NDK SSFERV2 MDK SSFERV2 MDK SSFERV2 SUDK VFLERVA SUDK VFLERVA SUDK VFLERVA SUDK VFLERVA SUDK VFLERVA SUDK VFLERVA SUDK VFLERVA STOK LFLERVA	761 775 626 831 808 825 840 825 840 821 860 821 840 840 840 840 840 840 840 840 840 840
FRGRAYPLS PHTNHL GNDET RSLLF FWGGER LGERG LWILK UHLSNI FSTDKAPLADE IA FRGRAYPLS PHTNHL GNDLT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLDER VK 552 FRGRAYPLS PHTNHL GNDLT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLDER VK 543 FRGRAYPLS PHTNHL GNDLT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLDER VC 546 FRGRAYPLS PHTNHL GNDLT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLAGRAQ 546 FRGRAYPLS PHTNHL GNDLT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLAGRAQ 547 FRGRAYPLS PHTNHL GNDLT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLAGRAQ 548 FRGRAYPLS PHTNHL GNDLT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLAGRAQ 548 FRGRAYPLS PHTNHL GNDLT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLMER VC 548 FRGRAYPLS PHTNHL GNDT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLMER VC 548 FRGRAYPLS PHTNHL GNDT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLMER VC 549 FRGRAYPLS PHTNHL GNDT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLMER VC 549 FRGRAYPLS PHTNHL GDDT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLMER VC 543 FRGRAYPLS PHTNHL GDDT RSLFLFWGGER LGERG LWILK UHLSNI FSTDKAPLMER VC 543 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK UMLSNI FSTDKAPLMER VC 543 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPLBER IQ 543 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPLBER IQ 543 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPLBER IQ 544 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPLBER IQ 545 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPLBER IQ 545 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPLBER IQ 545 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPLBER IZ 545 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPLBER IZ 545 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPLBER IZ 545 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPL FSTDKAPL 546 FRGRAYPLS PHTNHL GDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPL FSTDKAPL 546 FRGRAYPLS PHTNHLGDLT RSLFLFWGGER LGERG LWILK VC JLSNI FSTDKAPL 546 FRGRAYPLS PHTNHLGDLT RSL	FRGRVYFISAHLHVUNDFCRGLLEFAEGKFLG FRGRVYFNSAHLHVUNDFCRGLLEFAEGKFLG FRGRAYAIPPHLNHLGNDCRGLLKFWEAKFLG FRGRAYFLSPHLNHLGNDLSRGLLKFWEAKFLG FRGRAYFLSPHLNHLGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLAPHTNHGNDTSRLLFWEGKFLG FRGRAYFLAPHTNHGNDTSRLLFWEGKFLG FRGRAYFLAPHTNHGNDTSRLLFWEGKFLG FRGRAYFLAPHTNHGNDTSRLLFWEGKFLG FRGRAYFLAPHTNHGNDTSRLLFWEGKFLG FRGRAYFLAPHTNHGNDTSRLLFWEGKFLG FRGRAYFLAPHTNHGNDTSRLLFWEGKFLG FRGRAYFLSPHTNHGNDTSRLLFWEGKFLG FRGRAYFLSPHTNHGNDTSRLLFWEGKFLG FRGRAYFLSPHTNHGNDTSRLLFWEGKFLG FRGRAYFLSPHTNHGNDTSRLLFWEGKFLG FRGRAYFLSPHTNHGNDTSRLLFWEGKFLG FRGRAYFLSPHTNHGNDTSRLLFWEGKFLG FRGRAYFLSPHTNHGNDTSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG FRGRAYFLSPHTNHGNDSSGLFFWEGKFLG	PNGLIN PNGLIN PNGLIN EHGLIN AKG FAN EDGL KU DEGLIN EEGLAN EEGLAN EEGLAN TSGLQ EEGLAN TSGLQ EENGLK PEGLAN KEGLS SLGLK PHGLS PDGLN PHGLS SSGLK PSGLK	MITEAN MI	LAND P LAND P LAND P CANUE CANUE CANUE CANUE CANUE CANUE F LAND P LAND P LAND P LAND P LAND P LAND P LAND P LAND Y LAND Y	SISK KDFATRQA SISK VDYATRQK SNSK VDYATRQK SNSK VDYATRQK SNSK VDYATRQK SIDKADFQSRVQ SIDKASTHDREK SIDKASTHDREK SIDKAPLEERVA SIDKAPLERVA SIDKAPLERVA SHDK VSLOERAE MDK SSFEERVA MDK SSFEERVA MDK SSFEERVA SVDK VPLLEREN SUDK VFLEREN SUDK VFLEREN SVDK VSLODRVA SVDK VSLODRVA SVDK VSLODRVA SFOK ASLEDRVK SFOK ASLEDRVK SFOK ASLEDRVK SFOK ASLEDRVA SFOK LELEDRVA SFOK LELEDRVA	761 775 856 826 831 808 835 840 821 863 840 821 863 809 799 839 836 836 836 837 810 863 891 863 855 885
FRGRAYPLS PHINHLGNDLT RSLFLFWNORKE UGERGLWILK LHLSNU YEVDK VPLKDRIE 850 FRGRAYPLS PHINHLGNDLT RSLFLFWOCKE LGERGLWILK LHLANU YENDK APLDERVK 850 FRGRAYPLS PHINHLGNDLT RSLFLFWOCKE LGERGLWILK LHLANU YENDKAPLOERVK 850 FRGRAYPLS PHINHLGNDLT RSLFLFWOCKE LGERGLWILK LHLANU YENDKAPLOERVK 950 FRGRAYPLS PHINHLGNDLT RSLFLFWOCKE LGERGLWILK LHLANU YEVDKAPLAERVQ 952 FRGRAYPLS PHINHLGNDT RSLFLFWOCKE LGERGLWILK LHLANU YEVDKAPLAERVQ 952 FRGRAYPLS PHINHLGNDT RSLFLFWOCKE LGERGLWILK LHLANU YEVDKAPLAERVQ 953 FRGRAYPLS PHINHLGNDT RSLFLFWOCKE LGERGLWILK LHLANU YEVDKAPLAERVQ 953 FRGRAYPLS PHINHLGNDT RSLFLFWOCKE LGERGLWILK LHLANU YEVDKAPLERIQ 833 FRGRAYPLS PHINHLGNDT RSLFLFWOCKE LGERGLWILK LHLANU YEVDKAPIDERIQ 833 FRGRAYPLS PHINHLGDTT RSLFLFWOCKE LGERGLWILK LOLANU YEVDKAPIDERIQ 841 FRGRAYPLS PHIS PHINHLGDTT RSLFLFWCKE LGERGLWILK LOLANU YEVDKAPIDERIK 841 FRGRAYPLS PHINHLGDTT RSLFLFWCKE LGERGLWILK LOLANU YEVDKAPISEN 841 FRGRAYPLS PHIS PHINHLGDTT RSLFLFWCKE LGERGLWILK LOLANU YEVDKAPISEN 841 FRGRAYPLS PHIS PHINHLGDTT RSLFLFWCKE LGERGLWILK LOLANU YEVDKAPISEN 842 FRGRAYPLS PHIS PHINHLGDTT RSLFLFWCKE LGERGLWILK LOLANU YEVDKAPISEN 843 FRGRAYPLS PHIS PHINHLGDTT RSLFLFWCKE LGERGLWICK LGLANU YEVDKAPISEN 84	FRGRVYFISAHLHFUNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNDFCRGLLE FSEGKFLG FRGRAYELSHLHHLGNDCRGLLMFWEGKFLG FRGRAYELSHLNHLGNDLSRGLLFWEGKRLG FRGRAYELSHLNHLGNDLSRGLLFWEGKRLG FRGRAYELSHNHLGNDLSRGLLFWEGKRLG FRGRAYELSHTNHLGNDLSRGLLFWEGKRLG FRGRAYELSHTNHLGNDLSRGLLFWEGKRLG FRGRAYELSHTNHLGNDLSRGLLFWEGKRLG FRGRAYELSHTNHLGNDLSRGLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTRSLLFWEGKRLG FRGRAYELSHTNHLGNDTSSLLFWEGKRLG FRGRAYELSHTNHLGNDSSCLFWEGKLG FRGRAYELSHTNHLGNDSSCLFWEGKLG FRGRAYELSHTNHLGNDSSCLFWEGKLG FRGRAYELSHTNHLGNDSSCHTFWEGKLG FRGRAYELSHTNHLGNDSSCHTFWEGKLF	PNGLW PNGLW PNGLW PNGLW PNGLW EDGLW EDGLW EDGLW EDGLW PEGLW FSGLW FSGLW FSGLW FSGLW FSGLW FSGLW FSGLW FSGLW FSGLW FSGLW FSGLW FSGLW FSGLW	MIKAN MIKANI	LANI P LIANI P	SISKUDFATRQA SISKUDYASRQK SYDKADFQSRVQ HNK FSFEDRIA SFDKASFNDREK SIDKAPLERRVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ HDK VSLEDRVK SFDK LSLDDRVK SHOK SSFEERVA SHOK ASFEDRIK SHOK AFFEDRIK SHOK VFLERNVA SUDK QIFEARVA SUDK QIFEARVA SUDK QIFEARVA SUDK VFLERNVA SHOK SPEDRIK SHOK SPEDRIK SHOK VFLERNVA SFDK LEDRVK SFDK LEDRVA SFDK LEDRVA SFDK AFLERVS	761 775 774 856 626 831 800 835 840 821 861 862 809 799 809 836 836 836 836 837 810 862 862 863 845 885 831 826
FRGRAYPL PHLINHL GNDLT RSLFV FWEGVE LGESG LEWLK THLANT Y EVDK ASLEERVQ 843 FRGRAYPL PHLINHL GNDLT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK ASLEERVQ 846 FRGRAYPLS PHENHL GNDLT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK AFLAERAQ 818 FRGRAYPLS PHENHL GNDLT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK AFLAERAQ 818 FRGRAYPLS PHENHL GNDLT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK AFLAERVQ 793 FRGRAYPLS PHENHL GNDLT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK AFLAERVQ 793 FRGRAYPLS PHENHL GNDLT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK AFLAERVQ 838 FRGRAYPLS HENNHL GNDT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK AFLAERVQ 838 FRGRAYPLS HENNHL GNDT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK AFLAEFDERVK 828 FRGRAYPLS HENNHL GNDT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK AFLAEFDERVK 828 FRGRAYPLS HENNHL GNDT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK AFLAEFDERVK 828 FRGRAYPLS HENNHL GNDT RSLFL FWEGRE LGERG LWLK THLANT Y GNDK AFLSER IQ 833 FRGRAYPLS HENNHL GNDT RSLFL FWEGRE LGERG LWLK TOLANT Y GNDK AFLSER IQ 834 FRGRAYPLS HENNHL GNDT RSLFL FWEGRE LGERG LWLK TOLANT Y GNDK ESLKRVE 841 FRGRAYPLS HENNHL GNDT RSLFL FWEGRE LGERG LWLK TOLANT Y GNDK ESLKRVE 841 FRGRAYPLS HENNHL GNDT RSLFL FWEGRE LGERG LWLK TOLANT Y GNDK ESLKRVE 841 FRGRAYPLS HENNHL GNDT RSLFL FWEGRE LGERG LWLK T	FRGRVYFISAHLHFUNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNDFCRGLLE FSGRFLG FRGRAYALSPHLNHLGNDER GGLLK FWGARELG FRGRAYELSPHLNHLGNDLSRGLLK FWGARELG FRGRAYELSPHLNHLGNDLSRGLLIFWGRKELG FRGRAYELSPHLNHLGNDLSRGLLIFWGRKELG FRGRAYELSPHTNHLGNDLSRGLLFWGRKELG FRGRAYELSPHTNHLGNDLSRGLLFWGRKELG FRGRAYELSPHTNHLGNDLSRGLLFWGRKELG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDTRSLLFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRAYELSPHTNHLGNDSSGLFFWGRKEG FRGRA	PNGLIM PNGLIM ERGLAD ERGLAD ERGLAD ERGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD EFGLAD	MIF AMPRATES AND	LANI P. LANI P	ISKUDFATRQA SISKUDYATRQK SYDKADFQ3RVQ SYDKADFQ3RVQ SYDKADFQ3RVQ SYDKADFQ3RVQ SIDKADFDRIERVQ SIDKADFLERVQ SIDKADFLERVQ SIDKADFLERVQ SYDKUSLDDRVK SFORLSLDDRVK SFORLSLDDRVK SYDKVSLDDRVK SUDKVSLDDRVK SUDKVSLDDRVA SYDKVSLDDRVA SYDKVSLDDRVA SYDKVSLDDRVA SYDKVSLDDRVA SFORLFERVQ SYDKVSLDDRVA SFORLFERVQ SFORAJEDRVA SFORLFERVQ SFORAJEDRVA SFORLEDRVA SFORLEDRVA SFORLEDRVA SFORLADERVA	761 775 856 826 831 808 835 840 821 840 821 840 821 840 821 840 836 836 836 836 836 836 836 836 836 847 859 863 864 859 885 885
FRGRAYPLP PHINHL GNDLT R3LFL FWEGRE LGERG LWRLKHLANT YWMTKAPLAQRAQ 846 FRGRAYPM S PHFNHLGNDLT R3LFL FWEGRE LGERG LWRLK HLANT YWDK PLPERAQ 618 FRGRAYPM S PHFNHLGNDLT R3LFL FWEGRE LGERG LWRLK HLANT YWDKAPLNERVQ 792 FRGRAYPLS PHFNHLGNDLT R3LFL FWEGRE LGERG LWRLK HLANT YWDKAPLNERVQ 792 FRGRAYPLS PHFNHLGNDLT R3LFL FWEGRE LGERG LWRLK HLANT YSTDKAPLNERVQ 838 FRGRAYPLS PHFNHLGNDT R3LFL FWEGRE UGDEG LWRLK HLANT YSTDKAPLHERVQ 838 FRGRAYPLS PHFNHLGNDT R3LFL FWEGRE UGDEG LWRLK HLANT YSTDKAPLHERVQ 848 FRGRAYPLS PHFNHLGDDT R3LFL FWEGRE UGDEG LWRLK HLANT YSTDKAPLHERVQ 838 FRGRAYPLS PHFNHLGDDT R3LFL FWEGRE LGERG LWRLK ULANT YSTDKAPLHERVQ 843 FRGRAYPLS PHFNHLGDDT R3LFL FWEGRE LGERG LWRLK ULANT YSTDKAPLHERVQ 843 FRGRAYPLS PHFNHLGDDLT R3LFL FWEGRE LGERG LWRLK ULANT YSTDKAPISER IQ 833 FRGRAYPLS PHNNHLGDLT R3LFL FWEGRE LGERG LWRLK ULANT YSTDKAPISER IQ 843 FRGRAYPLS PHFNHLGDLT R3LFL FWEGRE LGERG LWRLK ULANT YSTDKAPISER IQ 841 FRGRAYPLS PHFNHLGDLT R3LFL FWEGRE LGERG LWRLK ULANT YSTDKAPISER INF 841 FRGRAYPLS PHFNHLGDLT R3LFL FWEGRE LGERG LWRLK ULANT YSTDKAPISER INF 841 FRGRAYPLS PHFNHLGDLT R3LFL FWEGRE LGERG LWRLK ULANT YSTDK PSLRKVE 841 FRGRAYPLS PHFNHLGDLT R3LFL FWEGRE LGERG LWRLK ULANT YSTDK PSLRKKVE 841 <td>FRGRVYFISAHLHFUNNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNNDFCRGLLE FSGGKFLG FRGRAYELSPHINHLGNDFCRGLLFFWEGKFLG FRGRAYELSPHINHLGNDSRGLLFFWEGKEG FRGRAYELSPHINHLGNDSRGLLFWEGKEG FRGRAYELSPHINHLGNDSRGLLFWEGKEG FRGRAYELSPHINHLGNDSRGLLFWEGKEG FRGRAYELSAFINHLGNDSRGLLFWEGKEG FRGRAYELSAFINHLGNDSRGLLFWEGKEG FRGRAYELSAFINHLGNDSRGLLFWEGKEG FRGRAYELSAFINHLGNDSRGLLFWEGKEG FRGRAYELSAFINHLGNDSRGLLFWEGKEG FRGRAYELSPHINHLGNDSRGLFFWEGKEG FRGRAYELSPHINHLGNDS</td> <td>PNGLIM ERGIAN</td> <td>MIF AN ANY ANY ANY ANY ANY ANY ANY ANY ANY</td> <td>LANI P LIANI P</td> <td>SISKUDFATRQA SISKUDYASRQK SYDKADFQSRVQ SYDKADFQSRVQ SYDKADFQSRVQ SIDKASTHDREK SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SHOKVSLEDRVK SFDKLSLDDRVK SFDKLSLDDRVK STDKQTFEARVA SUDKVFLEREN MDK SFFERVA SUDKVFLEREN MDK SFFERVA SUDKVFLEREN MDK SFFERVA SUDKVFLEREN MDK IPFTERIQ SVDKVPLEDRVK SFDKASLEDRVK SFDKASLEDRVS SFDKASLEDRVS SFDKASLERVQ SFDKASLERVQ SFDKASLERVQ SFDKASLERVQ SFDKASLERVQ</td> <td>761 775 626 831 808 808 825 840 821 860 821 860 839 798 839 839 839 839 839 839 839 839 839 8</td>	FRGRVYFISAHLHFUNNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNNDFCRGLLE FSGGKFLG FRGRAYELSPHINHLGNDFCRGLLFFWEGKFLG FRGRAYELSPHINHLGNDSRGLLFFWEGKEG FRGRAYELSPHINHLGNDSRGLLFWEGKEG FRGRAYELSPHINHLGNDSRGLLFWEGKEG FRGRAYELSPHINHLGNDSRGLLFWEGKEG FRGRAYELSAFINHLGNDSRGLLFWEGKEG FRGRAYELSAFINHLGNDSRGLLFWEGKEG FRGRAYELSAFINHLGNDSRGLLFWEGKEG FRGRAYELSAFINHLGNDSRGLLFWEGKEG FRGRAYELSAFINHLGNDSRGLLFWEGKEG FRGRAYELSPHINHLGNDSRGLFFWEGKEG FRGRAYELSPHINHLGNDS	PNGLIM ERGIAN	MIF AN ANY ANY ANY ANY ANY ANY ANY ANY ANY	LANI P LIANI P	SISKUDFATRQA SISKUDYASRQK SYDKADFQSRVQ SYDKADFQSRVQ SYDKADFQSRVQ SIDKASTHDREK SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SHOKVSLEDRVK SFDKLSLDDRVK SFDKLSLDDRVK STDKQTFEARVA SUDKVFLEREN MDK SFFERVA SUDKVFLEREN MDK SFFERVA SUDKVFLEREN MDK SFFERVA SUDKVFLEREN MDK IPFTERIQ SVDKVPLEDRVK SFDKASLEDRVK SFDKASLEDRVS SFDKASLEDRVS SFDKASLERVQ SFDKASLERVQ SFDKASLERVQ SFDKASLERVQ SFDKASLERVQ	761 775 626 831 808 808 825 840 821 860 821 860 839 798 839 839 839 839 839 839 839 839 839 8
FRGRAYPIS PHTNHL ONDLT RSLFL FWECKELGERG LWLK LHLANU YGVDK APLMERVQ 792 FRGRAYPIS PHTNHL ONDLT RSLFL FWECKELGERG LWLK LHLANU YGVDK APLMERVQ 793 FRGRAYPIS PHTNHL ONDT RSLFL FWECKELGERG LWLK HLANU YGVDK APLMERVQ 838 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE VGDEGL LWLK HLANU YGVDK APLMERIQ 847 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK APIDERVK 828 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK APIDERIQ 833 FRGRAYPIS PHLNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK APIDERIQ 843 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK APIDERIQ 843 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK ESLKRVE 841 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK ESLKRVE 841 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGEEG LWLK LQLANU YGVDK ESLKRVE 841 FRGRAYPIS PHTNHL GDLT RSLFL FWEGRE LGEEG LWLK LQLANU YGVDK ESLKRVE 841	FRGRVYFISAHLHFUNNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNNDFCRGLLE FSEGKFLG FRGRAYALSPHLNHLGNDLSRGLLFWEGKFLG FRGRAYFLSPHLNHLGNDLSRGLLFWEGKFLG FRGRAYFLSPHLNHLGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDLSRGLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDTRSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSLLFWEGKFLG FRGRAYFLSPHTNHGNDSSCLFFWEGKFLG FRGRAYFLSPHTNHGNDSSCLFFWEGKFLG FRGRAYFLSPHTNHGNDSSCLFFWEGKFLG FRGRAYFLSPHTNHGNDSSCLFFWEGKFLG FRGRAYFLSPHTNHGNDSSCLFFWEGKFLG FRGRAYFLSPHTNHGNDSSCLFFWEGKFLG FRGRAYFLSPHTNHGNDSSCLFFWEGKFLG FRGRAYFLSPHTNHGNDSSCLFFW	PNGLIM ERGLAS ERGLAS ALGENAL ALGENAL ALGENAL ALGENAL ERGLAS ALGENAL ERGLAS ERGL	MIF (A) MIF (A	LANI P LANI P LA	SISKUDFATRQA SISKUDYATRQK SNSKUDYATRQK SNSKUDYATRQK SUDKADFQSRUQ SIDKADFQSRUQ SIDKASFNDREK SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA MOK SSFEERVA MOK SSFEERVA MOK SSFEERVA SUDKUPLEREN SUDKUPLEREN SUDKUPLEREN SUDKUPLEREN SUDKUPLEREN SUDKUPLEREN STOKASLEDRVK SFORASLEDRVK	761 775 776 856 826 831 808 835 840 821 868 835 826 836 836 836 836 836 836 836 836 836 83
FRGRAYPIS PHTNHL ONDLT RSLFL FWECKELGERG LWLK LHLANU YGVDK APLMERVQ 792 FRGRAYPIS PHTNHL ONDLT RSLFL FWECKELGERG LWLK LHLANU YGVDK APLMERVQ 793 FRGRAYPIS PHTNHL ONDT RSLFL FWECKELGERG LWLK HLANU YGVDK APLMERVQ 838 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE VGDEGL LWLK HLANU YGVDK APLMERIQ 847 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK APIDERVK 828 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK APIDERIQ 833 FRGRAYPIS PHLNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK APIDERIQ 843 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK APIDERIQ 843 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK ESLKRVE 841 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGERG LWLK LQLANU YGVDK ESLKRVE 841 FRGRAYPIS PHTNHL GODT RSLFL FWEGRE LGEEG LWLK LQLANU YGVDK ESLKRVE 841 FRGRAYPIS PHTNHL GDLT RSLFL FWEGRE LGEEG LWLK LQLANU YGVDK ESLKRVE 841	FRGRVYFISAHLHFUNNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNNDFCRGLLE FSGGRFLG FRGRÀYELS PHINNI GNDLS RGLLK FWEARLG FRGRÀYELS PHINNI GNDLS RGLLI FWEGKLG FRGRÀYELS PHINNI GNDLS RGLLI FWEGKLG FRGRÀYELS PHYNNI GNDLS RGLLI FWEGKLG FRGRÀYELS PHYNNI GNDLS RGLLI FWEGKLG FRGRÀYELS ANFINI GNDM RSLLI FWEGKLG FRGRÀYELS PHYNNI GNDM RGLLI FWEGKLG FRGRÀYELS PHINNI GNDM	PNGLIM PNGLIM ERGIA ERGIA DNGLOS ELGIAN ELGIA EL	MIE (NA MIE (N	LANE P LIANE P	ISKUDFATRQA SISKUDYASRQK SYDKADFQSRVQ HNK FSFEDRIA SFDKASFNDREK SIDKAPLERRVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ HDK IJFDARVA HDK VJEDRVK SFDK LSLDDRVK SFDK LSLDDRVK SFDK LSLDDRVK SUDK VFLERVA NDK AFFEDRIK SUDK VFLERVA SVDK VFLERVA SVDK VFLERVQ SVDK VFLEDRVK SFDKASLEDRVK SFDKASLEDRVK SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR	761 775 626 821 808 825 840 821 840 821 840 821 840 821 840 840 840 840 840 840 840 840 840 840
FRGRAYPLS PHFNHLGNDLT RSLFLFWEGKE IGENG LWIK LHLANU FSIDK APLARVE 793 FRGRAYPLS PHFNHLGNDLT RSLFLFWOGKKUGARG LWIK HLANU YSIDK APLHERVQ 838 FRGRAYPLS AHLMHLGNDLT RSLFLFWOGKKUGARG LWIK LWLANU YSIDK APLHERVQ 847 FRGRAYPIS PHFNHLGGDLT RSLFLFWEGKE LGERG LWIK VQLANU YSIDK APIDER VK 838 FRGRAYPIS PHLNHLGGDLT RSLFLFWEGKE LGERG LWIK VQLANU YSUDKAPISER IQ 839 FRGRAYPIS PHLNHLGGDLT RSLFLFWEGKE LGERG LWIK VQLANU YSUDKAPISER IQ 841 FRGRAYPIS PHFNHLGGDLT RSLFLFWEGKE LGERG LWIK VQLANU YSUDKAPISER IQ 841 FRGRAYPIS PHFNHLGGDLT RSLFLFWEGKE LGERG LWIK VQLANU YSUDKAPISER IX 841 FRGRAYPIS PHFNHLGDLT RSLFLFWEGKE LGERG LWIK VQLANU YSUDKE SLARVE 841 FRGRAYPIS PHFNHLGDLT RSLFLFWEGKE LGERG LWIK VQLANU YSUDKE SLARVE 841	FRGRVYFISAHLHFUNNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHFUNNDFCRGLLE FSGGRFLG FRGRÀYELS PHINNI GNDLS RGLLK FWEARLG FRGRÀYELS PHINNI GNDLS RGLLI FWEGKLG FRGRÀYELS PHINNI GNDLS RGLLI FWEGKLG FRGRÀYELS PHYNNI GNDLS RGLLI FWEGKLG FRGRÀYELS PHYNNI GNDLS RGLLI FWEGKLG FRGRÀYELS ANFINI GNDM RSLLI FWEGKLG FRGRÀYELS PHYNNI GNDM RGLLI FWEGKLG FRGRÀYELS PHINNI GNDM	PNGLIM PNGLIM ERGIA ERGIA DNGLOS ELGIAN ELGIA EL	MIE (NA MIE (N	LANE P LIANE P	ISKUDFATRQA SISKUDYASRQK SYDKADFQSRVQ HNK FSFEDRIA SFDKASFNDREK SIDKAPLERRVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ HDK IJFDARVA HDK VJEDRVK SFDK LSLDDRVK SFDK LSLDDRVK SFDK LSLDDRVK SUDK VFLERVA NDK AFFEDRIK SUDK VFLERVA SVDK VFLERVA SVDK VFLERVQ SVDK VFLEDRVK SFDKASLEDRVK SFDKASLEDRVK SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR SFDKASLEDRVR	761 775 626 821 808 825 840 821 840 821 840 821 840 821 840 840 840 840 840 840 840 840 840 840
FRGRAYPLSAHLMHLGNDMT RSLFLFWEGRE VGDEGLMUK IHLANU YSIDKAPLMERIQ 847 FRGRAYPLSHFNHLGGDMT RSLFLFWOCKELGERGLBWLK VQLANU YSVDKAPLSERIQ 833 FRGRAYPIS PHLNHLGGDLT RSLFLFWEGKELGERGLBWLK VQLANU YSVDKAPISERIQ 833 FRGRAYPIS PHLNHLGGDLT RSLFLFWEGKELGERGLBWLK VQLANU YSVDKAPISERIQ 841 FRGRAYPIS PHNNHLGGDLT RSLFLFWEGKELGERGLBWLK VQLANU YSVDKESLARKVE 841 FRGRAYPIS PHNNHLGGDLT RSLFLFWEGKELGERGLBWLK VQLANU YSVDKESLARKVE 841 FRGRAYPIS PHNNHLGGDLT RSLFLFWEGKELGERGLBWLK VQLANU YSVDKESLARKVE 841	FRGR VYPES AHLHRV NNDFC ROLLE FABGRE IG FRGR VYPES AHLHRV NNDFC ROLLE FABGRE IG FRGR VALS SHILHRV NNDFC ROLLE FSGRE IG FRGR AYELS PHINHL GNDLS ROLLE FWEARE IG FRGRAYELS PHINHL GNDMT RSLLI FWEARE IG FRGRAYELS PHINHL GNDMS RGLI FWEARE IG FRGRAYELS PHINHL GNDT RSLEI FWEARE	PNGLIM PNGLIM ERGLAS LEGING ANGFAN EDGLKA EDGLKA EDGLKA EDGLKA EDGLKA EDGLKA EDGLKA EDGLKA EDGLKA EDGLKA EDGLKA EDGLKA EDGLKA EN	MIE (NHE HAR) MIE (NHE HAR) MI	LANI P LIANI P	SISKUDFATRQA SISKUDYAJRQK SYSKUDYAJRQK SYSKUDYAJRQK SYDKAJFQSRUQ SYDKAJEQSRUQ SIDKAJELERVQ SIDKAJELERVQ SIDKAJELERVQ SIDKAJELERVQ SIDKAJELERVA MICKSFEDRIK SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKUSLERVU SYDKAJELERVU SYDKAJELERVU SYDKAJELERVU SYDKASLERVU SYDKAJELERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU SYDKASLERVU	761 775 836 826 831 808 835 840 821 840 839 798 839 839 839 839 839 839 839 839 839 8
FRGRAYPI3 PHINHLGGDIT RSLFI FWEGKELGERGLEWLKVQLANVYSVDKAPI3ERIQ 832 FRGRAYPI3 PHFNHLGGDIT RSLFI FWDGKELGEEGLEWLKIQLANVYSVDKESITKRVE 841 FRGRAYPI3 PHFNHLGGDIT RSLFI FWDGKELGEEGLEWLKIQLANVYSVDKESIAKRVE 821 FRGRAYPI3 PHFNHLGGDIT RSLFI FWEGKOLGEEGLEWLKIQLANVYSVDKESIGRVK 836	FRGRVYFISAHLHVUNDFCRGLLE FAEGKFLG FRGRVYFNSAHLHVUNDFCRGLLE FAEGKFLG FRGRAYELSHHLHLGNDFCRGLLE FSEGKFLG FRGRAYELSHLNHLGNDSRGLLFWUGRKLG FRGRAYELSHLNHLGNDSRGLLFWUGRKLG FRGRAYELSHLNHLGNDSRGLLFWUGRKLG FRGRAYELSHTNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDTRSLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLLFWUGRKLG FRGRAYELSHFNHLGNDSRGLFWUGRKLG FRGRAYELSHFNHLGNDSRGLFWUGRKLG FRGRAYELSHFNHLGNDSRGLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDFSFC FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFWUGRKLG FRGRAYELSHFNHLGNDSRCLFFWUGRKLG FRGRAYELSHFNHLGNDFSFC FRGRAYELSHFNHLGNDFSFC FRGRAYELSHFNHLGNDFSFC FRGRAYELSHFNHLGNDFF	PNGLIM PNGLIM ERGIA RAGFA ALGENA ERGIA ERGIA ALGENA ALGENA ERGIA PRGLIM	WIE VIE WEEVE	LANI P LIANI P LIANI P LIANI P LIANI C CCANY P LIANI P	SISKUDFATRQA SISKUDYAJRQK NYSKUDYAJRQK YDKADFQSRVQ HNK FSFEDRIA SFDKAJFNDREK SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ HDK VJEDRVK HDK VJEDRVK MDK SSFEERVA MDK SSFEERVA MDK SSFEERVA SUDK VJEDRVK SUDK VJEDRVK SUDK VJEDRVK SUDK VJEDRVK SUDK VJEDRVK SFDKALEDRV SFDKAJEDRV SFDKAJEDRVA SFDKALEDRVS SFDKAJEDRVR SFDKAJEDRVR SFDKAJEDRVR SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY SFDKAJERVY	761 775 856 826 831 808 8421 808 8421 861 861 861 863 856 836 810 863 856 856 836 857 852 840 857 852 840 846 857 852 840 846 840 857 852 840 857 852 840 857 852 840 857 852 840 855 852 855 855 855 855 855 855 855 855
FRGRAYPI3 PHINHLGGDIT RSLFI FWEGKELGERGLEWLKVQLANVYSVDKAPI3ERIQ 832 FRGRAYPI3 PHFNHLGGDIT RSLFI FWDGKELGEEGLEWLKIQLANVYSVDKESITKRVE 841 FRGRAYPI3 PHFNHLGGDIT RSLFI FWDGKELGEEGLEWLKIQLANVYSVDKESIAKRVE 821 FRGRAYPI3 PHFNHLGGDIT RSLFI FWEGKOLGEEGLEWLKIQLANVYSVDKESIGRVK 836	FRGR VYPES AHLHRV NNDFC ROLLE FAEGKPLG FRGR VYPES AHLHRV NNDFC ROLLE FAEGKPLG FRGR VALS AHLHRV NNDFC ROLLA FWEGKPLG FRGR VALS PHINHL GNDLS ROLLA FWEGKRLG FRGR VALS PHINHL GNDLS ROLLA FWEGKRLG FRGR VALS PHINHL GNDMT RSLLI FWEGKRLG FRGR VALS PHINHL GNDT RSLFL FWEGKRLG FRGR VA	PNG LIM PNG LIM PNG LIM PNG LIM PNG LIM PNG LIM PNG LIM PNG LIM PEG LIM PEG LIM PEG LIM PNG LI	MIE (NHE MIE) MIE (NHE MIE) MI	LANI P LIANI P LIANI P LIANI C CONV P LIANI P	SISK DFATRQA SISK UDYAIRQK SYSK VDYAIRQK SYSK VDYAIRQK SYDK VDYAIRQK SYDK VDYAIRQK SIDK ADFQSRVQ SIDK ADFQSRVQ SIDK ADFLERVA SIDK ADFLERVA SIDK ADFLERVA SIDK ADFLERVA MOK ASFEERVE MOK SSFEERVA MOK ASFEERVE MOK ASFEERVE MOK ASFEERVE SIDK QTFLARVA SUDK VFLLEREN MOK APFDER IK SIDK QTFLARVA SYDK VFLEREN SIDK ADFLERVA SFOK ILLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SYDK VJLEREN SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SYDK VJLEREN SFOK ADFLERVA SYDK VJLEREN SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA	761 775 836 826 831 808 835 840 821 860 839 798 839 839 839 839 839 839 839 839 839 8
FRGRAYPI3 PHINHLGGDIT RSLFI FWEGKELGERGLEWLKVQLANVYSVDKAPI3ERIQ 832 FRGRAYPI3 PHFNHLGGDIT RSLFI FWDGKELGEEGLEWLKIQLANVYSVDKESITKRVE 841 FRGRAYPI3 PHFNHLGGDIT RSLFI FWDGKELGEEGLEWLKIQLANVYSVDKESIAKRVE 821 FRGRAYPI3 PHFNHLGGDIT RSLFI FWEGKOLGEEGLEWLKIQLANVYSVDKESIGRVK 836	FRGR VYPES AHLHRV NNDFC ROLLE FAEGKPLG FRGR VYPES AHLHRV NNDFC ROLLE FAEGKPLG FRGR VALS AHLHRV NNDFC ROLLA FWEGKPLG FRGR VALS PHINHL GNDLS ROLLA FWEGKRLG FRGR VALS PHINHL GNDLS ROLLA FWEGKRLG FRGR VALS PHINHL GNDMT RSLLI FWEGKRLG FRGR VALS PHINHL GNDT RSLFL FWEGKRLG FRGR VA	PNG LIM PNG LIM PNG LIM PNG LIM PNG LIM PNG LIM PNG LIM PNG LIM PEG LIM PEG LIM PEG LIM PNG LI	MIE (NHE MIE) MIE (NHE MIE) MI	LANI P LIANI P LIANI P LIANI C CONV P LIANI P	SISK DFATRQA SISK UDYAIRQK SYSK VDYAIRQK SYSK VDYAIRQK SYDK VDYAIRQK SYDK VDYAIRQK SIDK ADFQSRVQ SIDK ADFQSRVQ SIDK ADFLERVA SIDK ADFLERVA SIDK ADFLERVA SIDK ADFLERVA MOK ASFEERVE MOK SSFEERVA MOK ASFEERVE MOK ASFEERVE MOK ASFEERVE SIDK QTFLARVA SUDK VFLLEREN MOK APFDER IK SIDK QTFLARVA SYDK VFLEREN SIDK ADFLERVA SFOK ILLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SYDK VJLEREN SFOK ADFLERVA SFOK ADFLERVA SFOK ADFLERVA SYDK VJLEREN SFOK ADFLERVA SYDK VJLEREN SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA SYDK ADFLERVA	761 775 836 826 831 808 835 840 821 860 839 798 839 839 839 839 839 839 839 839 839 8
FRGRAYFIS PHFNHLGGDLT RSLFLFWDGKELGEEG LWILK IOLANV VEVDKESLTKRVE 841 FRGRAYFIS PHFNHLGGDLT RSLFLFWDGKELGEEG LWILK IOLANV VEVDKESLTKRVE 821 FRGRAYFIS PHFNHLGGDLT RSLFLFWEGKOLGEEG LWILK VOLANV VEVDKESIDGRVK 836	FRGRVYFISAHLHVUNDFCRGLLE FAEGKFLG FRGRVYFSAHLHVUNDFCRGLLE FAEGKFLG FRGRAYALSPHLNHLGNDERGLLFWEGKFLG FRGRAYELSPHLNHLGNDERGLLFWEGKFLG FRGRAYELSPHLNHLGNDERGLLFWEGKFLG FRGRAYELSPHTNHGNDESGLFFWEGKFLG FRGRAYELSPHTNHGNDESGLFFWEGKFLG FRGRAYELSPHTNHGNDESGLFFWEGKFLG FRGRAYELSPHTNHGNDESGLFFWEGKFLG FRGRAYELSPHTNHGNDESGLFFWEGKFLG FRGRAYELSPHTNHGNDESGLFFWEGKFLG FRGRAYELSPHTNHGNDESGLFFFWEGKFLG FRGRAYELSPHTNHGNDESGLFFFWEGKFLG FRGRAYELSPHTNHGNDESGLFFFFWEGKFLG FRGRAYELSPHTNHGNDESGLFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	PNGLIM ERGLAS ELGLIM EL	MIEKON MI	LANI P. LIANI P. LIANI P. LIANI P. LIANI P. LIANI P. LIANI P. LIAN	ISK NDFATRQA SISK VDYATRQK SISK VDYATRQK SYDK ADFQSRVQ SYDK ADFQSRVQ SYDK ADFQSRVQ SIDK ADFLERVQ SIDK ADFLERVQ SIDK ADFLERVQ SIDK ADFLERVQ SIDK ADFLERVQ MOK SSFEERVA MOK SSFEERVA MOK SSFEERVA SYDK VDLEDRVK SYDK VDLEDRVK SYDK VSLDDRVA SYDK VSLDRVA SYDK VSLDRVA SYDK VSLDRVA SYDK VSLDRVA SYDK ASLERVQ SYDK AFLERVQ SYDK AFLERVA SYDK AFLERVA SYDK ASLERVQ SYDK ASLERVQ SYDK ASLERVQ SYDK AFLERVA SYDK ASLERVQ SYDK ASLERVQ SYDK ASLERVQ SYDK ASLERVQ SYDK ASLERVQ SYDK ASLERVQ SYDK ASLERVQ SYDK ASLERVQ SYDK ASLERVQ SIDK ASLEVC SIDK ASLEVC	761 775 856 826 831 808 835 840 821 840 835 840 835 840 835 840 837 840 837 840 836 837 840 836 837 850 855 855 855 857 852 846 857 852 846 857 857 852 846 857 857 857 857 857 857 857 857 857 857
FRGRAYPISPHFNHLGGDLTRSLFLFWEGKOLGEEGLRWLKWOLANVYEVDKESIDGRVK 836	FRGRVYFISAHLHVUNDFCRGLLE FAEGKFLG FRGRVYFSAHLHVUNDFCRGLLE FSGGEFLG FRGRAYESAHLHVUNDFCRGLLE FSGGEFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRSLFFWEGKFLG FRGRAYESPHINHLGNDSRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFSC FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFFEGKEGFFG FRGRAYESPHINHLGNDTRSLFFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFFEGKEGFFFG FRGRAYESPHINHLGN	PNGLIM PNGLIM ERGIA ALGENA ERGIA ALGENA ALGE	MIEKO MIEKO	LIANE P LIANE P LIA	ISKDPATRQA SISKUPASRQK SYCKADFQSRVQ HNKFSFEDRIA SFDKASFNDREK STDKAPLERRVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ HDK IJFDARVA HDK VILEDRVK SFDK LSLDDRVK SFDK LSLDDRVK STDKAPEDRIK MDR SFFERVA MDR SFFERVA SUDK VILEDRVK SFDKALEDRVK SFDKALEDRVR SFDKALEDRVR SFDKALEDRVR SFDKALERVQ SFDKAPLEVQ SFDKAPLEVQ SFDK	761 775 856 826 831 808 825 820 821 821 821 821 821 821 821 821 821 839 839 839 839 836 837 859 836 855 831 855 835 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 845 845 845 845 845 845 845 845 845
FRGRAYPIS PHFNHLGGDLTRSLFLFWEGROLGEHGLDWLKVOLANUY VOVDKLSLAGRIQ 838	FRGRVYFISAHLHVUNDFCRGLLE FAEGKFLG FRGRVYFSAHLHVUNDFCRGLLE FSGGEFLG FRGRAYESAHLHVUNDFCRGLLE FSGGEFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDTRSLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRGLLFWEGKFLG FRGRAYESPHINHLGNDSRSLFFWEGKFLG FRGRAYESPHINHLGNDSRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFSC FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFFEGKEGFFG FRGRAYESPHINHLGNDTRSLFFFWEGKFLG FRGRAYESPHINHLGNDTRSLFFFFEGKEGFFFG FRGRAYESPHINHLGN	PNGLIM PNGLIM ERGIA ALGENA ERGIA ALGENA ALGE	MIEKO MIEKO	LIANE P LIANE P LIA	ISKDPATRQA SISKUPASRQK SYCKADFQSRVQ HNKFSFEDRIA SFDKASFNDREK STDKAPLERRVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ SIDKAPLERVQ HDK IJFDARVA HDK VILEDRVK SFDK LSLDDRVK SFDK LSLDDRVK STDKAPEDRIK MDR SFFERVA MDR SFFERVA SUDK VILEDRVK SFDKALEDRVK SFDKALEDRVR SFDKALEDRVR SFDKALEDRVR SFDKALERVQ SFDKAPLEVQ SFDKAPLEVQ SFDK	761 775 856 826 831 808 825 820 821 821 821 821 821 821 821 821 821 839 839 839 839 836 837 859 836 855 831 855 835 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 840 845 845 845 845 845 845 845 845 845 845
·····	FRGR VYPES ALLHRV NNDFC ROLLE FABGRE IG FRGR VYPES ALLHRV NNDFC ROLLE FABGRE IG FRGR VALS PHINHL GNDLS ROLL FWEARE IG FRGR AYPLS PHINHL GNDLS ROLL FWEARE IG FRGR AYPLA PHINHL GNDMT RSLL FWEARE IG FRGR AYPLS PHINHL GNDMS RGLL FWEARE IG FRGR AYPLS PHINHL GNDT RSLFL FWEARE IG FRGR AYPLS PHINHL	PNGLIM PNGLIM ERGLAS ALGENA ENGLIM EN	MUEKNO MU	LANI, P. LIANI,	ISKDPATRQA SISKUPASRQK SYDKADFQSRVQ SYDKADFQSRVQ SYDKADFQSRVQ SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLERVA SIDKAPLERVA SIDKAPLERVA SIDKAPLERVA MOK SSFEERVA MOK SSFEERVA MOK APFDRIK SUDK YELERVA SYDK VFLERVA SYDK VFLERVA SYDK VFLEDRVK SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA STDKAPLA	761 775 856 826 831 808 835 840 821 840 839 798 839 839 839 839 839 839 839 839 839 8
	FRGR VYPES ALLHRV NNDFC ROLLE FABGRE IG FRGR VYPES ALLHRV NNDFC ROLLE FABGRE IG FRGR VALS PHINHL GNDLS ROLL FWEARE IG FRGR AYPLS PHINHL GNDLS ROLL FWEARE IG FRGR AYPLA PHINHL GNDMT RSLL FWEARE IG FRGR AYPLS PHINHL GNDMS RGLL FWEARE IG FRGR AYPLS PHINHL GNDT RSLFL FWEARE IG FRGR AYPLS PHINHL	PNGLIM PNGLIM ERGLAS ALGENA ENGLIM EN	MUEKNO MU	LANI, P. LIANI,	ISKDPATRQA SISKUPASRQK SYDKADFQSRVQ SYDKADFQSRVQ SYDKADFQSRVQ SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLERVA SIDKAPLERVA SIDKAPLERVA SIDKAPLERVA MOK SSFEERVA MOK SSFEERVA MOK APFDRIK SUDK YELERVA SYDK VFLERVA SYDK VFLERVA SYDK VFLEDRVK SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA STDKAPLA	761 775 856 826 831 808 835 840 821 840 839 798 839 839 839 839 839 839 839 839 839 8
	FRGR VYPES ALLHRV NNDFC ROLLE FABGRE IG FRGR VYPES ALLHRV NNDFC ROLLE FABGRE IG FRGR VALS PHINHL GNDLS ROLL FWEARE IG FRGR AYPLS PHINHL GNDLS ROLL FWEARE IG FRGR AYPLA PHINHL GNDMT RSLL FWEARE IG FRGR AYPLS PHINHL GNDMS RGLL FWEARE IG FRGR AYPLS PHINHL GNDT RSLFL FWEARE IG FRGR AYPLS PHINHL	PNGLIM PNGLIM ERGLAS ALGENA ENGLIM EN	MUEKNO MU	LANI, P. LIANI,	ISKDPATRQA SISKUPASRQK SYDKADFQSRVQ SYDKADFQSRVQ SYDKADFQSRVQ SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLERVA SIDKAPLERVA SIDKAPLERVA SIDKAPLERVA MOK SSFEERVA MOK SSFEERVA MOK APFDRIK SUDK YELERVA SYDK VFLERVA SYDK VFLERVA SYDK VFLEDRVK SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA STDKAPLA	761 775 856 826 831 808 835 840 821 840 839 798 839 839 839 839 839 839 839 839 839 8
	FRGR VYPES ALLHRV NNDFC ROLLE FABGRE IG FRGR VYPES ALLHRV NNDFC ROLLE FABGRE IG FRGR VALS PHINHL GNDLS ROLL FWEARE IG FRGR AYPLS PHINHL GNDLS ROLL FWEARE IG FRGR AYPLA PHINHL GNDLS ROLL FWEARE IG FRGR AYPLA PHINHL GNDLS ROLL FWEARE IG FRGR AYPLA PHINHL GNDMT RSLLI FWEARE IG FRGR AYPLS PHINHL GNDMS RGLLI FWEARE IG FRGR AYPLS PHINHL GNDT RSLFL FWEA	PNGLIM PNGLIM ERGLAS ALGENA ENGLIM EN	MUEKNO MU	LANI, P. LIANI,	ISKDPATRQA SISKUPASRQK SYDKADFQSRVQ SYDKADFQSRVQ SYDKADFQSRVQ SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLEERVA SIDKAPLERVA SIDKAPLERVA SIDKAPLERVA SIDKAPLERVA MOK SSFEERVA MOK SSFEERVA MOK APFDRIK SUDK YELERVA SYDK VFLERVA SYDK VFLERVA SYDK VFLEDRVK SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA SFDK AFLERVA STDKAPLA	763 777 854 822 800 800 800 800 800 800 800 800 800

P. Palanivelu; BJI, 20(3): 1-35, 2017; Article no.BJI.38632

tr B6K333 B6K333_SCHJY
sp 013993 RPOM SCHPO
tr 39Q0Q8 39Q0Q8_3CHOY tr 39X2W4 39X2W4_3CHCR
tr A0A1E3Q3C6 A0A1E3Q3C6_LIPST
tr A0A167E4J0 A0A167E4J0_9A3C0 tr A0A1E3PUP0 A0A1E3PUP0_9A3C0
tr A0A0H5C7R0 A0A0H5C7R0 CYBJA
tr A0A1E3P5W0 A0A1E3P5W0_WICAO
tr KOKTX3 KOKTX3_WICCF tr W6MIL2 W6MIL2_9ASCO
tr A0A1E3QPI7 A0A1E3QPI7_9ASCO
tr A0A1D2V948 A0A1D2V948_9A3C0 tr A0A1B7SME0 A0A1B7SME0_9A3C0
tr Q6CR25 Q6CR25 KLULA
tr WOTGI 8 WOTGI 8 KLUMA
tr A0A109UWS1 A0A109UWS1_9SACH tr G8JMS2 G8JMS2_ERECY
tr Q75BP7 Q75BP7_ASHGO
tr R9XDF 6 R9XDF 6_A SHAC tr H2ASJ 8 H2A SJ 8_KAZAF
tr J757Y3 J757Y3 KAZNA
tr GOVD01 GOVD01_NAUCC tr GOWE72 GOWE72_NAUDC
tr Q6FLX9 Q6FLX9_CANGA
tr G8B354 G8B354 TETPH
tr A0A0L8RKW5 A0A0L8RKW5_SACEU tr A0A0L8VRU3 A0A0L8VRU3_9SACH
tr J8PP58 J8PP58_SACAR
tr A0A0C7MY71 A0A0C7MY71 _9SACH
tr C5DNP3 C5DNP3 LACTC tr C5DX7 9 C5DX79_2 YGRC tr G8ZR0 0 G8ZR00_TORDC
tr G8ZR00 G8ZR00_TORDC
tr A0A1E 4RQF7 A0A1E4RQF7 _ 9ASCO
tr A0A1E4RQF7 A0A1E4RQF7_9A3CO tr A0A0L0P4K6 A0A0L0P4K6_9A3CO tr A0A1A0HGT7 A0A1A0HGT7_9A3CO
FICHIDES CHIDES_CLARA
tr G3B4C1 G3B4C1_CANTC tr A3LX46 A3LX46_PICST
tr A0A1E4SMT6 A0A1E4SMT6_9ASCO
tr A5DN82 A5DN82_PICGU tr B5RTF6 B5RTF6_DEBHA
tr G3AEY0 G3AEY0 SPAPN
tr G8B7X1 G8B7X1_CANPC
tr H8X1L6 H8X1L6_CANO9 tr B9W6L5 B9W6L5_CANDC
tr C4YFJ1 C4YFJ1_CANAW
tr C5ME71 C5ME71_CANTT tr M3IK19 M3IK19_CANMX
tr B6K333 B6K333_SCHJY
tr B6K333 B6K333_SCHJY sp 013993 RP0M_SCHP0
- tr B6K333 B6K333_SCHJY =p 013993 RPOM_SCHPO tr S9Q0Q8 S9Q0Q8_SCHOY tr S9X274 4 S9X274_SCHCR
- ====================================
L B6R333 B6R333 SCHJY =p 013993 RF0M SCHF0 tr 39Q0Q8 39Q0Q8 SCHOY tr 39X2W4 39X2W4 SCHCR tr A0A1E 3Q3C6 LIPST tr A0A167E4J0 A0A1 E32U6 LIPST tr A0A167E4J0 A0A1 E32UF0 9A3C0 tr A0A16SCTR0 A0A0HSCTR0_CYEJA
L 66K333 66K333 SCHJY =p 013993 RPOM_SCHPO tr 99Q028 39Q026 SCHOY tr 99X2K 4 39X2K4 SCHCR tr A0A1F3Q3C6 A0A1F3Q3C6_LIPST tr A0A1F3Q3C6 A0A1F3Q3C6_LIPST tr A0A1F3PUPO A0A1F3PUPO_9ASCO tr A0A1F3PUPO A0A1F3PUPO_SCHO_ tr A0A1F3PUPO A0A1F3PUPO_WICAO
L B6K333 B6K333 SCHJY =p 013993 RFOM_SCHF0 tr 99008 39008 SCHOY tr 99008 39008 SCHOY tr 99008 39008 SCHOY tr 30018 20306 A0A1230306 LIPST tr A0A167E470 A0A167E470 9A3C0 tr A0A16307H0 A0A163057R0 CYBJA tr A0A16357R0 A0A16357R0 CYBJA tr A0A163557R0 A0A16357R0 WICA0 tr R0KIX3 KOKIX3 WICCF
L B6K333 B6K333 SCHJY =p 013993 RFOM_SCHF0 tr 99008 39008 SCHOY tr 99008 39008 SCHOY tr 99008 39008 SCHOY tr 30018 20306 A0A1230306 LIPST tr A0A167E470 A0A167E470 9A3C0 tr A0A16307H0 A0A163057R0 CYBJA tr A0A16357R0 A0A16357R0 CYBJA tr A0A163557R0 A0A16357R0 WICA0 tr R0KIX3 KOKIX3 WICCF
L B6K333 B6K333 SCHJY =p 013993 RF0M_SCHF0 tr 99Q08 39Q0Q8 SCHOY tr 99Q08 39Q0Q8 SCHOY tr 30A1E3Q3C6 A0A1E3Q3C6 _ LIPST tr A0A1E3Q3C6 A0A1E3Q3C6 _ LIPST tr A0A1E3PT00 A0A1E3Q5C7 _ QASC0 tr A0A1E3P500 A0A1E3Q5C7 _ QASC0 tr A0A1E3Q5T7 A0A1E3Q5T7 _ QASC0 tr A0A1E2Q5T4 A0A1E75M50 _ QASC0 tr A0A1E75M50 A0A1E75M50 _ QASC0 tr A0A1E75M50 A0A1E75M50 _ QASC0
L 66K333 66K333 SCHJY =p 013993 RPOM_SCHPO tr 89Q008 39Q008 SCHOY tr 99X2K 4 95X2W4 SCHCR tr 40A1E3Q3C6 A0A1E3Q3C6 _ LIPST tr A0A1E3Q3C6 A0A1E3Q3C6 _ LIPST tr A0A1E3DFD0 A0A1E3PHD0 _ 9A3CO tr A0A1E3DFD0 A0A1E3QPI7 _ 9A3CO tr A0A1E3QPI7 B0A1E7SHD0 _ 9A3CO tr A0A1E3B B0TGE KLUDA
Lr 56K333 56K333 SCHJY =p 013993 RPOM SCHPO tr 59X2W 4 59X2W 4 SCHCY tr 30X2W 4 59X2W 4 SCHCY tr 30X1E 303C6 A0A1E303C6 _ LIPST tr 30A1E 3PUFO A0A1E302W05 _ 538CO tr 30A1E 3PUFO A0A1E302W0 _ 538CO tr 30A1E 3PUFO A0A1E302W0 _ WICAO tr 30A1E 3PUFO A0A1E302W0 _ WICAO tr 30A1E302W7 30A1E302W7 _ 538CO tr 30A1E302FT 30A1E302W7 _ 538CO tr 40A1E302FT 40A1E302W7 _ 538CO tr 40A1E302FT 40A1E302W7 _ 538CO tr 40A1E302FT 40A1E302W7 _ 538CO tr 40A1E302W7 40A1E302W7 _ 538CO tr 40A1E302W7 40A1E302W7 _ 538CO tr 40A1E302W7 50A1E302W7 _ 538CO tr 40A1E302W7 _ 548W7 _ 548W7
Lr 56K333 56K333 SCHJY =p 013993 RPOM SCHPO tr 59X2W 4 59X2W 4 SCHCY tr 30X2W 4 59X2W 4 SCHCY tr 30X1E 303C6 A0A1E303C6 _ LIPST tr 30A1E 3PUFO A0A1E302W05 _ 538CO tr 30A1E 3PUFO A0A1E302W0 _ 538CO tr 30A1E 3PUFO A0A1E302W0 _ WICAO tr 30A1E 3PUFO A0A1E302W0 _ WICAO tr 30A1E302W7 30A1E302W7 _ 538CO tr 30A1E302FT 30A1E302W7 _ 538CO tr 40A1E302FT 40A1E302W7 _ 538CO tr 40A1E302FT 40A1E302W7 _ 538CO tr 40A1E302FT 40A1E302W7 _ 538CO tr 40A1E302W7 40A1E302W7 _ 538CO tr 40A1E302W7 40A1E302W7 _ 538CO tr 40A1E302W7 50A1E302W7 _ 538CO tr 40A1E302W7 _ 548W7 _ 548W7
L 36K333 36K333 SCHJY =p 013933 RF0M_SCHJY tr 390008 390008 SCH0Y tr 390008 390008 SCH0Y tr 39008 390008 SCH0Y tr 30018 30008 30018 2000 9A3C0 tr 30018 30700 30018 20100 9A3C0 tr 30018 20700 30018 20100 9A3C0 tr 30018 20700 30018 20100 WICAO tr 30018 20700 30018 20100 WICAO tr 30018 20701 30018 20100 WICAO tr 30018 20171 30018 20177 9A3C0 tr 30018 20171 30018 20177 9A3C0 tr 30018 20171 30018 20177 9A3C0 tr 30018 75ME0 30018 20197 9A3C0 tr 30018 30076 KLUMA tr 30310 9UW31 3031 9UW31 93ACH tr 63JM32 65JM32 ERECY tr 075BF7 075BF7 35H00 tr R9XDF6 R9XDF6 38XDF tr R9XDF6 83XDF6 38XAC
L 66K333 66K333 SCHJY =p 013993 RPOM_SCHPO tr 99Q026 59Q026_SCHOY tr 99Q026 59Q026_SCHOY tr 99Q244 59X244 SCHCR tr A0A1E3Q3C6 A0A1E3Q3C6_LIPST tr A0A1E3Q3C6 A0A1E3Q4D0_9A3CO tr A0A1E3PTV0 A0A1E3PHD0_9A3CO tr A0A1E3PTV0 A0A1E3PHD0_9A3CO tr A0A1E3PTV0 A0A1E3PHD0_9A3CO tr A0A1E3PSV0 A0A1E3PHD0_9A3CO tr A0A1E3PSV0 A0A1E3PHD0_9A3CO tr A0A1E3PTV A0A1E3QPI7_9A3CO tr A0A1E3PTV A0A1E3QPI7_9A3CO tr A0A1E3PHD4 A0A1E3YHE0_9A3CO tr A0A1E3VH20 A0A1E7SHE0_9A3CO tr A0A1E3VH20 A0A1E3VH20 A0A1E7SHE0_9A3CO tr A0A1E3VH20 A0A1E3VH20 A0A1E3VH20 tr A0A1E3VH20 A0A1E3VH20 tr A0A15XH20 A0A1E3VH20 tr A0A15XH20 A0A15XH20 tr A0A15XH20 A0A15XH20 tr A0A15XH2
L T B6K333 B6K333 SCHJY T B6K333 B6K333 SCHJY T 90008 390008 SCHOY L 39208 390008 SCHOY L 39208 392008 SCHOY L 30112 30266 A0A1230366 LIPST L A0A12 SPUE A0A1252400 SASCO L A0A12 SPUE A0A1252400 SASCO L A0A12 SPUE A0A1252400 SASCO L A0A12 SPSW A0A1252400 WICAO L A0A12 SPSW A0A1252400 WICAO L A0A12 SPSW A0A1252400 WICAO L A0A12 SPSW A0A1252400 SASCO L A0A12 SPSW A0A1252400 SASCO L A0A12 SPSW A0A1252400 SASCO L A0A12 SPSW A0A1252400 SASCO L A0A12 SPSW A0A125240 SASCO L A0A12 SPSW A0A125240 SASCO L A0A12 SWE A0A125240 SASCO L A0A12 SWE A0A125240 SASCO L A0A12 SWE A0A125240 SASCO L A0A12 SWE A0A1252 SKLUAA L A0A10 SUMS1 A0A10 SUM51 SASCO L A0A12 SI 26 SJM32 ERECY L A0A125 H2A SJS KAZAP L J7S7Y3 J7S7Y3 KAZNA L GOWD1 GOVD01 NAUCC L GOWD2 GOWCZ NAUCC
tr B6K333 B6K333 SCHJY p 013993 RPOM_SCHPO tr B9Q028 S9Q028 SCHOY tr B9Q028 S9Q028 SCHOY tr B9Q028 S9Q028 SCHOY tr B9Q124 S9X244 SCHCR tr A0A16 3Q3C6 A0A16 2Q3C6 _ LIPST tr A0A16 3Q2C6 A0A16 2Q3C6 _ LIPST tr A0A16 3PUPO A0A16 2P400 _ 9A3CO tr A0A16 SOFTO A0A1829ENO WICAO tr A0A12 SPSN0 A0A1829ENO WICAO tr A0A12 SPSN0 A0A1829ENO WICAO tr A0A12 SPSN0 A0A1829ENO WICAO tr A0A12 SQE17 A0A1829ENO WICAO tr A0A12 SQE17 A0A1829ENO WICAO tr A0A18 SQE17 A0A1829ENO WICAO tr A0A18 SQE17 A0A1829ENO WICAO tr A0A187 SME0 A0A187 SME0 SASCO tr A0A187 SME0 SASCO tr A0A187 SME0 SASCO tr A0A19 SUMS1 A0A19UMS1 _ SASCO tr
tr B6K333 B6K333 SCHJY p 013993 RPOM_SCHPO tr B9Q0Q8 S9Q0Q8 SCROY tr B9Q0Q8 S9Q0Q8 SCROY tr B9Q0Q8 S9Q0Q8 SCROY tr B9Q0Q8 S9Q0Q8 SCROY tr B9Q0X4 S9X2W4 SCRCR tr A0A16 3Q2C6 A0A162Q3C6 _ LIPST tr A0A16 2Q2C6 A0A162Q5C6 _ LIPST tr A0A16 2Q2C6 A0A162Q5C6 _ LIPST tr A0A16 2Q4C6 A0A162Q5C6 _ LIPST tr A0A16 SCRON A0A16295W0 _ WICAO tr A0A16 SCRON A0A16295W0 _ WICAO tr ROKIX3 KOKIX3 W ICCF tr A0A16 ZQ5T7 A0A162Q5T7 9ASCO tr A0A16 ZQ5T7 A0A187 SME0 _ 9A3CO tr IAOA18 ZQ5T7 A0A187 SME0 _ 9A3CO tr A0A19 SUM31 A0A195 SME0 _ 9A3CO tr IAOA19 SUM31 _ JOA109 SUM31 _ 9AACH tr A0A10 SUM31 A0A192 ERECY tr A0A19 SUM31 _ A0A192 ERECY tr A0A19 SUM31 _ SAACH tr IAOA19 SUM31 _ SAACH tr IAOA19 SUM31 _ SAACH tr IAOA19 SUM31 _ S
tr B6K333 B6K333 SCHJY p 013993 RPOM_SCHPO tr B9Q028 S9Q028 SCHOY tr B9Q028 S9Q028 SCHOY tr B9Q028 S9Q028 SCHOY tr B9Q124 S9X244 SCHCR tr A0A16 3Q3C6 A0A16 2Q3C6 _ LIPST tr A0A16 3Q2C6 A0A16 2Q3C6 _ LIPST tr A0A16 3PUPO A0A16 2P400 _ 9A3CO tr A0A16 SOFTO A0A1829ENO WICAO tr A0A12 SPSN0 A0A1829ENO WICAO tr A0A12 SPSN0 A0A1829ENO WICAO tr A0A12 SPSN0 A0A1829ENO WICAO tr A0A12 SQE17 A0A1829ENO WICAO tr A0A12 SQE17 A0A1829ENO WICAO tr A0A18 SQE17 A0A1829ENO WICAO tr A0A18 SQE17 A0A1829ENO WICAO tr A0A187 SME0 A0A187 SME0 SASCO tr A0A187 SME0 SASCO tr A0A187 SME0 SASCO tr A0A19 SUMS1 A0A19UMS1 _ SASCO tr
L 66K333 66K333 SCHJY =p 013933 RPOM_SCHPO tr 99206 59006_SCHOY tr 99206 59006_SCHOY tr 90206 59006_SCHOY tr 802K4 592 244 SCHCR tr 802K4 592 244 SCHCR tr 802K4 592 244 SCHCR tr 802K1529U0 A0A1 529U0_9ASCO tr A0A1529U0 A0A1 529U0_9ASCO tr A0A1529U0 A0A1 529U0_9ASCO tr A0A1529U7 A0A1 529U0_9ASCO tr A0A1529U7 A0A1 529U7_9ASCO tr A0A152 G5JM32_ERCY tr G5B57 Q75BP7_A3BGO tr B02052 G5JM32_ERCY tr G75U7 3 J773Y3_KA2NA tr G00E72 G0WE72_NAUDC tr G0EX54 G6B554 TETPH tr A0A015RKW5 A0A104RW5_SACH tr A0A015RKW5 A0A104RW5_SACH tr A0A015RKW5 A0A104RW5_SACH tr A0A015RKW5 A0A015VRU3_93ACH tr A0A015RKW5 A0A015VRU3_93ACH
tr B6K333 B6K333 SCHJY p 013993 RPOM_SCHPO tr B9Q008 S9Q008 SCHOY tr B9Q008 S9Q008 SCHOY tr B9Q204 S9X2W4 SCHCR tr A0A16 20266 LIPST tr A0A16 72430 A0A16240266 LIPST tr A0A16 72430 A0A1672430 9A3C0 tr A0A16 20266 LIPST tr A0A16 20266 LIPST tr A0A16 20276 A0A162900 9A3C0 tr A0A16 20570 A0A1629500 WICA0 tr KOM12 20577 A0A1629500 WICA0 tr A0A16 20577 A0A1629577 9A3C0 tr A0A17 57ME0 A0A1879ME0 9A3C0 tr A0A17 57ME0 A0A1879ME0 9A3C0 tr A0A1879ME0 19A0189ME1 9A3ACH
tr 86K333 86K333_SCHJY =p 013933 RPOM_SCHPO tr 89Q0Q8 88Q0Q8_SCHOY tr 89Q0Q8 88Q0Q8_SCHOY tr 89Q0Q8 88Q0Q8_SCHOY tr 80A1E3Q3C6 A0A1E3Q3C6_LIPST tr A0A1E3Q3C6 A0A1E3Q3C6_LIPST tr A0A1E3PTV0 A0A1E3Q3C6_LIPST tr A0A1E3PTV0 A0A1E3Q8C6_CIPST tr A0A1E3PTV0 A0A1E3Q8C6_CIPST tr A0A1E3PTV0 A0A1E3Q8C7 tr A0A1E3PSTV0 A0A1E3Q8C7 tr A0A1E3PSTV0 A0A1E3Q8T7_9A3C0 tr A0A1E3Q8T7 A0A1E3Q8T7_9A3C0 tr A0A1E3Q8T7 A0A1E3Q8T7_9A3C0 tr A0A1E3Q8T7 A0A1E3Q8T7_9A3C0 tr A0A1E3Q8T7 A0A1E3Q8T7_9A3C0 tr A0A157ME0 A0A1B73ME0 SA3C0 tr A0A157ME0 A0A1B73ME0 SA3C0 tr A0A109UW31 A0A109UW31_9A3C0 tr A0A109UW31 A0A109UW31_9SACH tr A0A109UW31 A0A109UW31_9SACH tr A0A109UW31 A0A109UW31_9SACH tr A0A109UW31 A0A109UW31_9SACH tr A0A108VD3 RA2AF tr 737Y3 J737Y3_KA2NA tr G0UD31 G0UD01 NAUCC tr G0WB72 G0W872_NAUDC tr G0WB72 G0W872_NAUDC tr G0WB73 G0A01EVTW3_SACEU tr A0A018VT03 A0A01EVTW3_SACEU tr A0A018VT03 A0A01EVTW3_SACEU tr A0A0C7MY71 A0A0CTMY71_9SACH tr C5DX79 C5DX79_ZYGRC tr C5DX79 C5DX79_ZYGRC
tr 186K333 [86K333 SCHJY p[013993]RPOM_SCHPO tr 1890008 [390008 SCHOY tr 1892008 [390008 SCHOY tr 18041 E39200 [A0A1 E39260 [JAN1 E39500 [MICAO tr 18041 E39500 [A0A1 E39500 [MICAO tr 18041 E3950 [A0A1 E39500 [MICAO tr 18041 E3950 [A0A1 E39500 [MICAO tr 18041 E3950 [A0A1 E39500 [MICAO tr 18041 E39571 [A0A1 E3950 [MICAO tr 18041 E39571 [A0A1 E3950 [MICAO tr 18050 [MICAO tr 18041 E3950 [MICAO tr 18050 [MICAO </td
tr 186K333 [86K333 SCHJY p[013993]RPOM_SCHPO tr 1890008 [390008 SCHOY tr 1892008 [390008 SCHOY tr 18021 [392008 [30008 SCHOY tr 18021 [39200 [3021 [2020 [2020 [3020 [20200 [20200 [20200 [20200 [20200 [20200 [2020 [2020 [2020 [2020 [20
<pre>L 66K333 86K333 SCHJY =p 013993 RPOM_SCHPO tr 89Q008 39Q008 SCHOY tr 89Q008 39Q008 SCHOY tr 89X14 39X244 SCRCR tr A0A1E 3Q206 A0A1E3Q306 _ LIPST tr A0A1E 3UPUO A0A1E3QUD0_9ASCO tr A0A1E 3UPUO A0A1E3UU0_9ASCO tr A0A1E 3UPUT A0A1E3UU7_9ASCO tr A0A1E 3UU0_1 A0A1U0U001_9ASCC tr G0M23 GBJM32 ERECY tr G0M23 GBJM32 ERECY tr G0M23 GBJM32 ERECY tr G0M23 GBJM32 ERECY tr G0M21 G0M01_0 NAUCC tr G0M23 GBJM32 ERECY tr G0M25 G0M27_2 NAUDC tr G0M25 G0M27_2 NAUDC tr G0M25 G0M27_2 NAUDC tr G0M25 G0M27_2 NAUDC tr G0M25 GDM25 CAM6A tr A0A01E8VR03 A0A01E8VR5 SACEU tr A0A01E8VR03 A0A01E8VR5 SACEU tr A0A01E8VR03 A0A01E8VR5 SACEU tr CSDNP3 CSDNP3 LACTC tr CSDNP3 CSDNP3 LACTC tr CSDNP3 CSDNP3 LACTC tr G0A01E0PT A0A1E40PT _ 9ASCO tr A0A01E0PT A0A1D40FT _ 9ASCO tr A0A1L0HCT A0A1L0HCT + A0A1CHCT tr CSDNF3 CSDNF3 _ CLAL4 TR CSTRES CLAL4 TR CSTRES CLAL4 TR CSTRES CAM2 Tr CSTRES CAM2 Tr CSTRES CAM2 Tr CSTRES CAM4 TR CSTRES CAM2 TR CSTRES CAM4 TR CSTRES CSTRES CAM4 TR CSTRES CST</pre>
L B6K333 B6K333 SCHJY =p 013993 RPOM_SCHPO tr 99Q028 39Q026 SCHOY tr 99X2K 19X2K SCHCR tr 30X1K 19X2K SCHCR tr 30A1F3Q3C6 A0A1F3Q3C6 LIPST tr A0A1F3Q3C6 A0A1F3Q3C6 LIPST tr A0A1F3Q3C6 A0A1F3Q3C0 SASCO tr A0A1F3Q5K A0A1F3PHO_9ASCO tr A0A1F3PHO A0A1F3PHO_9ASCO tr C6CR25 C6CR25_KLULA tr C6TB1 WOTG1E KLUMA tr A0A10 9UW31 A0A1579HO_9ASCO tr B3XDF7 C75BF7 A3HGO tr C6CR25 C6CR25_KLULA tr C6TLS 00CF12_NAUDC tr C6FLX C6FLX5_CANGA tr C6BE354 GBE354 TETPH tr A0A01BKWS A0A01BVRWS SACH tr C6BE354 C6BE354 TETPH tr A0A01BKWS A0A01BVRWS SACH tr C5DNF3 C5DNF3_LACTC tr C5DNF3 C5DNF3_LACTC tr C5DNF3 C5DNF3_LACTC tr C5DNF3 C5DNF3_LACTC tr C6DRC7 CAD1F4RCF7 SASCO tr A0A100P4K6 A0A100F77 SASCO tr A0A100P4K6 A0A100F7 SASCO tr A0A110P4K6 A0A100F7 SASCO tr A0A110P4K6 A0A100F7 SASCO tr A0A110P4K6 A0A100F7 SASCO tr A0A110P4K6 A0A10F7 SASCO tr A0A110P4K6 A0A10F7 SASCO tr A0A110F4 C4B2C CALH tr C3BHC1 C3BHC1 CANTC tr C4D116 C4D126 CANTC SASCO tr A0A110F4 C4B2C CALH tr C3BHC1 C3BHC1 CANTC SASCO tr A0A14 C4B24 CALTC TETFH tr A344 C4 SASLX4C_ANTC tr A344 C4 SASLX4C_ANTC SASCO tr A0A14 C4 SASLX4C_ANTC SAS
<pre>L L L L L L L L L L L L L L L L L L L</pre>
<pre>tr 86K333 86K333 SCHJY p 013933 RPOM_SCHPO tr 89Q008 39Q008_SCHOY tr 89Q008 39Q008_SCHOY tr 89Q008 39Q008_SCHOY tr 80A182Q3C6 A0A183Q3C6_LIPST tr A0A183Q3C6 A0A183Q3C6_LIPST tr A0A183DT0P A0A183PH0_9A3C0 tr A0A183DT0P A0A183PH0_9A3C0 tr A0A183DF00 A0A183PH0_9A3C0 tr A0A183DF00 A0A183PH0_9A3C0 tr A0A183DF00 A0A183PH0_9A3C0 tr A0A183DF00 A0A183PH0_9A3C0 tr A0A183DF00 A0A1873MD0_9A3C0 tr A0A183DF00 A0A1873MD0_9A3C0 tr A0A183DF01 A0A183DF1_9A3C0 tr A0A183DF10 A0A1873MD0_9A3C0 tr A0A183DF17 A0A183DF1_9A3C0 tr A0A183DF10 A0A1873MD0_9A3C0 tr A0A183DF10A183DF1_9A3C0 tr A0A183DF10A183DF1_9A3C0 tr A0A183DF1_9A3C0 tr A0A184DF1_1A0A184DF7_9A3C0 tr A0A184DF7_1A0A184DF7_9A3C0 tr </pre>
J J T J J T J SCR33 J T J SCR3 J T SCR3 J SCR3 J SCR3 J
J J T J J T J SCR33 J T J SCR3 J T SCR3 J SCR3 J SCR3 J
br B6K333 B6K333 SCHJY br B6K333 B6K333 SCHJY br B39006 S9006 SCHOY tr B39006 S9006 SCHOY tr B39206 A0A123026 LIPST tr BA024 S9224 SCHCR tr IA0A123026 A0A1230206 _ LIPST tr IA0A123026 A0A1230200 _ SCHOY tr IA0A123026 A0A1230200 _ SASCO tr IA0A1230207 A0A1230207 _ SASCO tr IA0A1230207 A0A1230207 _ SASCO tr IA0A1230207 A0A1230207 _ SASCO tr IA0A1230207 A0A12000000 _ SASCO tr IA0A11230207 A0A120000000000000000000000000000000000
br br br <tdbr< td=""> br <t< td=""></t<></tdbr<>
J J T J J T J SCRUY T J SCRUY T J SCRUY T J SQ008 SCRUY T J SQ008 SCRUY T J SQ206 SCRUY T J SQ206 J T J J J T J J J T J J J J T J J J J T J J J J J T J J J J J T J J J

FVDNHLQDI FNSVDK PLDGE - QFWT KADDPFQALAV CFEIADAIRSG DP3SF ISHVP	100 827
FVDDNMQEV FDSADR PLDGN-KWWS KADDPFOALAA CFEIAEAVRSGDHESY ISHIP	100 820
FVDNHLQDIFNSVDKPLDGE-QFWTKADDFOALAVCFEIADAIRSGDPSSFISHVP FVDDNMQEVFDSADRFLDGN-KWWSKADDFQALAACFEIAEAVRSGDHESYISHIP FVDDNILLFDSYDHFLGR-KWWSSEDFQALAAIELRAIRSGPESYCCHVP FVDDNILEFYDSYDRPLDGR-KWWTSEDFQALAAIELKAIRSENPETYCCHVP	TOD 834
YADDNIEEV FDSYDR PLDGR - KWWT SAEDPF OALAA IAEIAKATRSENPETY VCHVP YADDKIGEI FDSADC PLDGR - RWWMOASDPWOCLAA CFELADALBSP DPYAF BSBLP	VQD 833 VHD 915
FADE NMEKILDSANS PMEGO-KWWOEAESPWOALAT CIEIRNAMNLE DPSKYKCRLP	VH4 685
FADNHIKDIYDSAEKPLDGQ-KWWMTADDPWQALAVCMELSKAYSMDDPTKFVSRLP	1HQ 890
FVDDNIEEVFD3YDR PLDGR - KWWT SAEDP CALAAIAEIARATRSENPETYVCHVP YADDNIGEIFD3ADC PLDGR - RWWMQASDF QCLAACFELADALRSP DFYAFRSKLP FADENMEKILD3ANS PMEGQ - KWWMQASDF QCLAACFELADALRSP DFYAFRSKLP FADENMEKILD3ANS PMEGQ - KWWMTADDF QALAYCHLSRAYMDD PTKFVSKDP FADENLENIKTAAD DHGG - KWWTADDF QALAYCHLSRAYMDD PTKFVSKDP FADENLENIKTAAD DHGR - EFWIKADKF QALAYIYDLADAYKLE DFTKVSKDP FADENLENIKTAAD DHANQ - EFWIKADKF QALAYIYDLADAYKLE DFTKVSKDP FADENLENIKTAAD DHANQ - EFWIKADKF QALAYIYDLADAYKLE DFTKVSKDP FADAHVAEIMESARD PLAGQ - RWWKKADKF QALAYIYDLADAYKLE DFTKVSKDP FADAHVAEIMESARD DHGA - GWWKKADKF QALAYIFLAANNLE DFTKISHOP FADAHVAEIMESARD DHGA - GWWKKADKF QALAYIFLAANNLE DFTFISHOP FADAHVAEIMESARD DHGA - GWWKKADKF QALAYIFLE QALKKLDPTFISHOP FADAHVAEIMESARD DHGA - GWWKKADKF QLAYICLEN EALKLDNPENFISHOP FADAHVAEIMESAEN DLGG - RWWTKADKF QLAYICLEN EALKLDNPENFISHOP FADAHLKEIRESAEN PLGG - RWWTKADKF QLAYICLEN EALKLDNPENFISHOP FADAHLKEIRESAEN PLGGK - RWWTKADKF QLAYICLEN EALKLDNPENFISHOP FTEENLEDIKDSAEN PLGGK - GWWKKADKF QCLAYICLEN EAKKLDNFEPFISHOP FTEELEINE HENSEN PLHOK - GWWKKADKF QCLAYICLEN EAKKLDNFEPFISHOP FTEELEDIKD KDSAEN PLHOK - GWWKKADKF QCLAYICLEN EAKKLDNFEPFISHOP FTEELHEDIKDSAEN PLHOK - GWWKKADKF QCLAYICLEN EAKKLDNFEPFISHOP FTEELHEDIKDSAEN PLHOK - GWWKKADKF QCLAYICLEN EAKKLDNFEPFISHOP FTEELHEDIKDSAEN PLHOK - GWWKKADKF QCLAYICLEN EAKKLDNFEPFISHOP FTEAHLEDIKDSAEN PLHOK - GWWKKADKF QCLAYICLEN EAKKLDNFEPFISHOP FTEAHLEDIKDSAEN PLHOK - GWWKKADKF QCLAYICLEN EAKKLDNFEPFISHOP FTEAHLEDIKDSAEN PLHOK - GWWKKADKF QCLAYICLEN EAKKLSNFEPJYSHOP FTEAHLEDIKDSAEN PLHOK - GWWKKADKF QCLAYICHEN EAKKLSNFEPJYSHOP FTEAHLEDIKDSAEN PLHOK - GWWKKADKF QCLAYICHEN EAKKLSNFEPJYSHOP	7HD 859 7HD 867
FVNDNIELVKRAAED PMANQ-EWWT KADKPWQALAT IIDLA DALKLP DPTKH ISHQP	VHQ 894
FTEKHLEDIRDSARDPLGGQ-RWWMKADKPWQALATCFELEAAFNLEDPTQFISHQP	<mark>үн</mark> о 899
FADAHVAEIMESARD PLHGA-GWWK SADKPW QALST IFELS EALQMA DPTQY VSHQP FTFNNYFNI HESAFN DOLLD-LWWEKADE ON LT IFELS CALE IN DETFFISION	VHD 880 VHD 920
YVDDHLDEI FESARD PLGGS - RMWYKADKPW QFLAS AMELE QAFRLP DPTKF ISHQP	VHQ 567
FADT HLKEI RESAEH PLDGT - RWWT KADKPW OFLAT CIELN EALKLDNPENFISHOP	<mark>үн</mark> о 858
FANA HFDDI KDSAEN PLGGK-RWWT KADKPWQLLAT CIELN EAMKLDNPEDF ISHQP	VHO 857
FTEE HLEDI KDSAEN PLNGK-GWWKKADKPWOCLAT CLELN EAYKLENPEDF VSHOP FTEE HLEDI KDSAEN PLHGN-GWWKKADKPWOCLAT CMELR DAYKLENPEDF I SHOP	VHO 868 VHO 898
FTEAHLEDIKDSAEN PLNGK-GWWKKADKPWQCLATCMEINNAYKLSNPEDYVSHQP	VHQ 895
FTEAHLEDI KESAEN PLNGK-GWWKKADKPWQCLAT CMELNNAYKLSNPEDYVSHQP	VHD 895
FIDDHLEEIKDSAENPLNGKYLWWQKADKPWQALATCIELNEALKLENPEDFISHOP FIESQLDEVKDSAEDPLNGR-GWWKKADKPWQALATCMELNEALKLDNPEDFVSHOP	VHO 877 VHO 869
FVEDHLOEIKESAENPLTTG-KWWKDADKPWOCLATCIELTEALKLDNPEEFISHOP	THD 922
FIEDHIEDV KDTAEN PLDGK-GWWK KADKPWQLLAT CIELNEALKLDNPEDFISHOP FTECHIEDI KDSAEN PLNGK-GWWKTADKPWQALAT CMELNEALKLDNPEDYISHOP	<mark>үн</mark> о 950
FTECHIEDIKDSAEN PLNGK-GWWKTADKPWQALAT CMELNEALKLDNPEDYISHQP FAEENMENIKDSAEN PLNGK-GWWKSADKPWQALST CIELNEAFKLENPEDFISHQP	VHD 920 VHD 918
FTESHLKDI KDSAEN PLTGD-RWWT TADKPWQALAT CFELNEVLKMDNPEEFVSHQP	
FTESHLODI KDSAEN PLTGD-RWWT TADKPWOALAT CFELNEVMKMDNPEEF ISHOP	VHD 944
FTES HLEDIKDSAEN PLTGG-GWWKTADKEWUALAT CFELNEVWRMDNEEDFISHOP FTES HLEDIKDSAEN PLDGK-GWWKQADKEWQALAT CMELNEALKLDNPCDFISHOP FAEDHIDDIRDSAEN PLDGK-CWWKEADKEWQALAT CMELNEALKMSNPDDFVSHOP	HD 944
FAEDHIDDIRDSAEHPLOGK-GWWKGADKPWGALATCMELNEALKLDNPCDFISHVP FAEDHIDDIRDSAEHPLOGK-CWWKEADKPWGALATCMELNEALKMSNPDDFVSHOP	HO 890 HO 885
FADE HIDDI KOSAOD PLKED - AWWM KAEKPW OALAT CMELN DAMKLDNPEDF ISHOP	0HQ 906
YAEAHLKDVKRSAEDPLAGD-GWWMKADKPWQALATCIEINEAYKLPNPEDFISHQP	0 916 916
FANKNIENIKAVAKD PYQ-N-QWWVKGDKPWQILGICYELAEAYTLE DPTKFVSHFP FVEE NMDKV FQTARD PLGED-RWWIKGDKPWQVLSVCFELNEAYKLE DPTKYVSYIP	
FVDDNLENI CKVAEN PIANE - EWWS KADKPWQVLSV CFELNEAHKLS DPRLYVSYIP	v <mark>HQ</mark> 902
FVDDNLEHV FESARD PTGGS-KWWT KGEKPW QVLSV CFELLEAYKLD DPTKY VSHVP	<mark>ино</mark> 905
FTET HLDKI RESAET PFDKD-AWWT KGEKPWQVLAC CFELNEAYKLE DPTQYVSHVP	VHO 877 THO 851
FVNDNLENV FESARN PYDTD-AWWKKAEKP QALGV CFELE EAYKLENPTQY VSHIP. FVNENLENI FQSAQN PYDPQ-AWWLKGEKPWQVLSV CFELNEAYKMS DPTKFVSHIP	VHQ 852
FVDDNLHHI IESAKN PLAED-AWWK KAEKPW QVLGV CFELK RAYDLE DPTEH ISHLP	1 <mark>HQ</mark> 897
FVDDNLENI LECARN PINGS - GWWKKGEKP QVLSVCFELNEAFQLDDPTKFVSHIP	VHO 906 VHO 887
FVDDNLENILLEARN FINSD-GWARNER OULSVCTELLEAR (ULDDFIR VSDIF FVEDNLQW FESARN FNSD-AWKRADER® (QLSVCTELLEARLPDFTRVSDIAN FATDHLQEAIRSAED FLN-H-KWWTRAERF (QLSVCTELLEARLPDFTRVSVIP FATDHLEEAIRSAED FLN-Y-KWWTRAERF (QLSVCTELLEARLPDFTRVSVIP FVDDNLERVFSSAAD FLASN-AWWQRAERF (QLSVCTELLEARLDDFTRFVSNIP) FVDENLERVIESAAD FFATD-AWWQRAERF (QLSVCTELLEARLDDFTRFVSNIP)	VHQ 891
FATDHIEEA IKSAED PLE-Y-KWWT KAEKPWQALSVCFELAEAYKLPDPTKFVSYLP	оев ону
FVDANLEKV FASAAD PLASN-AWWQKAEKPWQALSVCFELAEAYKLDDPTKFVSHLP	00e 0H
FIDDNIENVIASAKD PYAPD - AWWORAEKPWOALSVCFELGEAVOLDDFTKFVSHLP	VHO 880 VHO 895
FVND SMDKV IESAAD PLAED - AWWK KAEKPW QALSV CFELA EASKMD DFTKFVSHLP	V <mark>HQ</mark> 897
FIDDNIENVIASAKD PYAPD - AWWQRAEKEW QALSVCFELGEAYQLDDFKFVSHLP FVND SMDKVIESAAD PLAED - AWWKKAEKEW QALSVCFELAEASKMDDFKFVSHLP :	
DGTCHGLOH YAALGG DPEGA REVNLEPSNRPNDVYA AVAAR VISILKKEA AAGDPM DGTCNGLOH YAALGG DIEGA REVNL MPSDHPSDVYE AVAE IVRGFLKKDAERGOEM DGTCNGLOH YAALGR DPDGA HEVNL SPNDRPKDVYD AVAKI VISRLE QES AKGDEV DGTCNGLOH YAALGR DPDGA HEVNISPNDRPKDVYD AVAKI VISRLE HESMKGDEW	AE 885 AN 878 AS 892 AS 891
DETCHSLOH YAALGC DPEGA REVNEP PENRE NDVVA AVAR VISILKKE – A AAGDEM DETCNGLOH YAALGG DIEGA REVNLWPSDHP SDVYE AVAEI VRGFLKKD – A BAGDEM DETCNGLOH YAALGR DPDGA REVNLSPHDRF KDVVD AVAKI VISRLE QE – S AKGDEV DETCNGLOH YAALGR DPDGA REVNLSPHDRF KDVVD AVAKI VISRLE HE – SMKGDEM DETCNGLOH YAALGR DEDGA REVNLSPHDRF KDVVD AVAKI VISRLE HE – SMKGDEM	AE 885 AN 878 AS 892 AS 891 AK 973
DSTC MGLOH YAALGG DPEGA REVNDE PSNRP NDVYA AVAAR VISILKKE A AAGDPM DSTC NGLOH YAALGG DIEGA REVNLWP SDHP SDVYE AVAE I VRGFLKKD A EAGDEM DSTC NGLOH YAALGR DPGA REVNLSPNDR FLOVYD AVAKI VISRLE QE SARGDEV DSTC NGLOH YAALGR DPGA HEVNLSPNDRP KDVYD AVAKI VISRLE HE SMRGDEM DSTC NGLOH YAALGG DIEGA REVNLSPNDRP KDVYD AVAKI VISKLE HE SMRGDEM DSTC NGLOH YAALGG DIEGA REVNLSPNDRP KDVYD AVAKI VISKLE HE SMRGDEM DSTC NGLOH YAALGG DIEGA REVNLSPNDRP KDVYD YSVLEI VURVEVE DD AENGHEV DSSC NGLOH YAALGG DIEGA REVNLSPNSRP KDVYS SVLEI VURVEVE DD ATKGHKE	AE 885 AN 878 AS 892 AS 891 AK 973 AK 743
LOTC MGLOH YAALGG DPEGA REVIND EP SNR P NDVYA AVAAR VISILKKE A AAGDPM DGTC NGLOH YAALGG DIEGA RÜVNLWP SDHP SDVYE AVAE I VRGFLKKD A EAGDEM DGTC NGLOH YAALGR DPGGA REVINIS PNDR F NDVYD AVAKI VISRLE (E SAKGDEM DGTC NGLOH YAALGR DPGGA REVINIS PNDR F KDVYD AVAKI VISRLE (E SAKGDEM DGTC NGLOH YAALGR DFGA REVINIS PNDR F KDVYD AVAKI VISRLE (E SAKGDEM DGTC NGLOH YAALGG DIEGA REVINIS PNDR F KDVYD AVAKI VISRLE (E A ENGREK DGSC NGLOH YAALGG DVEGA AEVNI VPSSKP ODVYS RVLEI VRVRVE ED A TKGHKE DGSC NGLOH YAALGG DIEGA REVINI P PASRP ODVYS FVANI VRARINND F ENGRET DGSC NGLOH YAALGG DIEGA REVINI F PASRP ODVYS FVANI VRARINND F ENGRET	AE 885 AN 878 AS 892 AS 891 AK 973 AK 948 AI 917
LGTC MGLQH YAALGG DPEGA REVNDEPSNRPNDVYA AVAAR VISILKKEA AAGDPM DGTC NGLQH YAALGG DIEGA REVNDEPSNRPNDVYE AVAEI VRGFLKKDAEAGDEM DSTC NGLQH YAALG PDGA REVNL SPNDRFRDVYD AVAKI VISRLE QESARGDEV DGTC NGLQH YAALG NDEGA REVNL SPNDRFRDVYD AVAKI VISRLE QESARGDEV DSTC NGLQH YAALGG DIEGA REVNL VFSNRPQDVYS RVLEI VVNTVE DEAENGREFV DSSC NGLQH YAALGG DIEGA REVNL VFSNRPQDVYS RVLEI VVNTVE DEAENGREFU DSSC NGLQH YAALGG DIEGA REVNL VFSNRPQDVYS RVLEI VVNTVE DEAENGREFU DSSC NGLQH YAALGG DIEGA REVNL IFSNRPQDIYS EVANI VRARTINNDFENGNET DSTC NGLQH YAALGG DVEGA REVNL IFSNRPQDVYT FVANL VKERLDKLAEGDEL DSTC NGLQH YAALGG DVEGA REVNL VFADER QDVYT FVANL VKERLDKLARGBER	AE 885 AN 878 AS 891 AK 973 AK 743 AA 948 AI 917 AE 925
LOT CHSLCH YAALG DPEGA REVNED PSNRP NDVYA XVARV Y SILKKE A AGGDPM DGTCNGLCH YAALG DPEGA REVNED PSDHP SDVYE AVAAR VY SILKKE A AGGDPM DGTCNGLCH YAALG PDEGA REVNEJ SPNDRP RDVYD AVAKI VI SRLE (E SAKGDEV DGTCNGLCH YAALG PDEGA REVNEJ SPNDRP RDVYD AVAKI VI SRLE HE SMKGDEV DGTCNGLCH YAALG DPEGA REVNEJ SPNDRP RDVYD AVAKI VI SRLE HE SMKGDEV DGTCNGLCH YAALG DVEGA REVNEJ SPNDRP RDVYD AVAKI VI SRLE HE SMKGDEV DGTCNGLCH YAALG DVEGA REVNEJ SPNDRP RDVYS RVLEI VENRVE ED A ENGHEV DGTCNGLCH YAALG DVEGA REVNEJ I SPSNP CDVYS RVLEI VENRVE ED A ENGHEV DGTCNGLCH YAALG DVEGA REVNEJ PSNP CDVYS RVLEI VENRVE ED A ENGHEV DGTCNGLCH YAALG DVEGA REVNEJ PSNP CDVYS RVLEI VENRVE ED A ENGHEV DGTCNGLCH YAALG DVEGA REVNEJ PSNP CDVYT FVANL VERELDKEL A LEGDEL DSTCNGLCH YAALG DVEGA TEVNEJ PSNP CDVYT FVANL VERELDKEL A A AKGDEM DSTCNGLCH YAALG DVEGA TEVNEJ PSDR PCOVYT HVAGU VERKEL A A AKGDEM	AE 885 AN 878 AS 891 AK 973 AK 948 AI 917 AE 925
LOTCINGLON YAAL GO DPEGA REVNEP PONRP NOVYA AVAR VISILKKE A ASGDEM DGTCNGLON YAAL GO DIEGA REVNEP PONRP NOVYE AVAE I VRGFLKKD A EAGDEM DGTCNGLON YAAL GR DPDGA NEVNI SPNDRP KDVYD AVAKI VISRLE QE SAKGDEV DGTCNGLON YAAL GR DPDGA NEVNI SPNDRP KDVYD AVAKI VISRLE HE SMKGDEM DGTCNGLON YAAL GO DVEGA REVNI SPNDRP KDVYD AVAKI VISRLE HE SMKGDEM DGTCNGLON YAAL GO DVEGA REVNI SPNDRP KDVYD AVAKI VISRLE HE SMKGDEM DGTCNGLON YAAL GO DVEGA REVNI SPNDRP KDVYD KULEI VKNRVE ED A TRGHKE DGTCNGLON YAAL GO DVEGA REVNI I PSDRP QDVYS RVLEI VKNRVE ED A TRGHKE DGTCNGLON YAAL GO DVEGA REVNI I PSDRP QDVYT FVANL VKRELDKL A LEGDEL DGTCNGLON YAAL GO DVEGA TEVNI APSDRP QDVYT HVARL VKRLE AA A AKGDEM DGTCNGLON YAAL GO DVEGA TEVNI APSDRP QDVYT HVARL VKRLE AA A AKGDEM DGTCNGLON YAAL GO DVEGA TEVNI APSDRP QDVYT HVARL VKRLE AA A AKGDEM DGTCNGLON YAAL GO DVEGA TEVNI I PSDRP QDVYT HVARL VKRLE AA A AKGDEM DGTCNGLON YAAL GO DVEGA TEVNI I PSDRP QDVYT HVARL VKRLE AA A AKGDEM	AE 885 AN 878 AS 892 AS 891 AK 973 AK 948 AI 947 AI 942 AI 917 AE 925 AN 957 AA 935
LOTCINGLON YAALOG DPEGA REVIND EP SINE PIDUYA AVAAR VISILKKE A AAGDEM DGTCINGLON YAALG DIEGA RÜVNL WP BIHS SDUYE AVAE I VRGFLKKD A EAGDEM DGTCINGLON YAALG DEDGA REVILS SPIDDER KDUYD AVAKI VISILE HE SAKGDEM DGTCINGLON YAALG DEDGA REVILS PPIDER KDIYD AVAKI VISILE HE SIKGOEM DGTCINGLON YAALG DIEGA RÜVNL EP GDREP GDIYS EVANI VUSIKLE HE SIKGOEM DGTCINGLON YAALG DIEGA RÜVNL EP GDREP GDIYS EVANI VRARINND FENGRET DGTCINGLON YAALG DIEGAR WINL IF SDREP GDIYS EVANI VRARINND FENGRET DGTCINGLON YAALG DIEGAR WINL IF SDREP GDIYS EVANI VRARINND FENGRET DGTCINGLON YAALG DIEGAR WINL IF SDREP GDIYS EVANI VRARINND FENGRET DGTCINGLON YAALG DIEGAR WINL IF SDREP GDIYT FIVARS VIKERLIKE A ARGDEM DGTCINGLON YAALG DIEGAR WINL IF SDREP GDIYT FIVARS VIKERLIKE A ARGDEM DGTCINGLON YAALG DIYEGAT WINL SPIDER POUYT HVARL VRARLE AA A ARGDEM DGTCINGLON YAALG DIYEGAT WINL SPIDER POUYT HVARL VRARLE AA A ARGDEM DGTCINGLON YAALG DIYEGAT WINL SPIDER POUYT HVARL VRARLE AA A ARGDEM DGTCINGLON YAALG DIYEGAT WINL SPIDER POUYT HVARL VRARLE AA A ARGDEM DGTCINGLON YAALG DIYEGAT WINL SPIDER POUYT HVARL VRARLE AA A ARGDEM DGTCINGLON YAALG DIYEGAT WINL SPIDER POUYT HVARL VRARLE AA A ARGDEM DGTCINGLON YAALG DIYEGAT WINL SPIDER POUYT HVARL VRARLE AA A DOFM	AE 885 AN 878 AS 892 AS 891 AK 973 AK 743 AA 948 AI 917 AE 925 AR 952 AN 935 AA 9378
LOTCINGLON YAAL GO DEGA REVNE PENRE NUVYA AVAR VISILKKE A ASGDEM DGTCNGLON YAAL GO DEGA KEVNE PENRE NUVYA AVAR VISILKKE A BAGDEM DGTCNGLON YAAL GO DEGA KEVNE SPNDRE KDVYD AVAKI VISRLE QE S AKGDEV DGTCNGLON YAAL GO DEGA KEVNE SPNDRE KDVYD AVAKI VISRLE HE SMKGDEM DGTCNGLON YAAL GO DEGA KEVNE SPNDRE KDVYD AVAKI VISRLE HE SMKGDEM DGTCNGLON YAAL GO DEGA KEVNE SPNDRE KDVYD AVAKI VISRLE HE SMKGDEM DGTCNGLON YAAL GO DEGA KEVNE SPNDRE KDVYD AVAKI VISRLE HE AKGGDEM DGTCNGLON YAAL GO DEGA KEVNE I SPNDRE VOYS SVLEI VKNRVE ED ATKGHKE DGTCNGLON YAAL GO DEGA KEVNE I SPNDRE VOYS SVLEI VKNRVE ED ATKGHKE DGTCNGLON YAAL GO DEGA KEVNE I SPNDRE VOYS VLEI VKNRVE ED ATKGHKE DGTCNGLON YAAL GO DEGA KEVNE VAN VAN VKNEL DKL AL BODEL DGTCNGLON YAAL GO DEGA KEVNE VAN VAN VKNEL VKNEL EA AAKGDEM DGTCNGLON YAAL GO DEGA KEVNE VAN VAN VKNEL VKNEL EA AAKGDEM DGTCNGLON YAAL GO DEGA KEVNE I SPLEKE OD VYT HVARL VKREL EA AAKGDEM DGTCNGLON YAAL GO DEGA KEVNE I SPLEKE OD VYT HVARL VKREL KKE AAKGDEM	AE 885 AN 878 AS 892 AS 891 AK 973 AK 948 AI 917 AE 925 AR 952 AN 9357 AA 925 AR 925 AR 925 AR 925 AR 925 AR 625
LOTCINGLON YAALOG DPEGA REVINDEP SINE PIDUYA AVAAR VISILKE A AAGDEM DSTCINGLON YAALOG DIEGA RÜVNLWP SINE SDUYE AVAE I VRGFLKKD A EAGDEM DSTCINGLON YAALOG DIEGA RÜVNLSPINDEP SDUYE AVAE I VRGFLKKD A EAGDEM DSTCINGLON YAALOG DDEGA REVINLSPINDEP KDVYD AVAKI VISRLE (PE SAKGGEM DSTCINGLON YAALOG DIEGA RÜVNLEP GDKP QDIYT HVASR VHDYVK QD A ENGHEV DSTCINGLON YAALOG DIEGA RÜVNLIP SDKP QDIYS RÜVLI VKRUVE (DE A KIGHKE DSTCINGLON YAALOG DIEGA RÜVNLIP SDKP QDIYS RÜVLI VKRUVE (DE A KIGHKE DSTCINGLON YAALOG DUEGA RÜVNLIP SDKP QDIYS RÜVLI VKRUVE (DE A KIGHKE DSTCINGLON YAALOG DUEGA RÜVNLIP SDKP QDIYS RÜVLI VKRUT (DE A KIGHKE DSTCINGLON YAALOG DUEGA RÜVNLIP SDKP QDIYT FUANLUKERLD KL A LEGDEL DSTCINGLON YAALOG DUEGA RÜVNLIP SDKP QDUYT HVARLUKERLD A A ANGDEM DSTCINGLON YAALOG DUEGA RÜVNLIP SDKP QDIYT HVARLUKRAKLE AA A ANGDEM DSTCINGLON YAALOG DUEGA RÜVNLIS PLEKP QDIYT HVARLUKRAKLE AA A ANGDEM DSTCINGLON YAALOG DUEGA RÜVNLIS PSUKFNDIYT HVARLUKRAKLAAS DDDM DSTCINGLON YAALOG DIEGA RÜVNLIS PSUKFNDIYT HVARLUKRKLAAS DDEM DSTCINGLON YAALOG DIEGAR RÜVNLIS PSUKFNDIYT SVIALUKKRLAAS UKINGKOG DSTCINGLON YAALOG DIEGAR RÜVNLIS PSUKFNDIYT HVARLUKKRLAAS LKAGDEEQ DSTCINGLON YAALOG DIEGAR RÜVNLIVPADRP QDIYT HVARLUKKRLAAS LKAGDEG DSTCINGLON YAALOG DIEGAR RÜVNLIVPADRP QDIYT HVARLUKKRLAAS AARODEQ DSTCINGLON YAALOG DIEGAR RÜVNLIVPADRP QDIYT HVARLUKKRLAAS	AE 885 AN 878 AS 892 AS 891 AK 973 AK 948 AI 948 AI 948 AI 952 AN 935 AA 935 AA 978 AK 625 AA 916 AL 915
LOT CHGLCH YAALGC DPEGA REVNED PSNRP NDVYA VVARV VJSILKKE A AAGDEM DGTCNGLCH YAALGG DIEGA REVNED PSNRP NDVYA VVARI VJSILKKE A BAGDEM DGTCNGLCH YAALGR DPDGA REVNEJ SPNDRP RDVYD AVAKI VJSRLE QE S AKGDEV DGTCNGLCH YAALGR DPDGA REVNEJ SPNDRP RDVYD AVAKI VJSRLE QE S AKGDEV DGTCNGLCH YAALG NDEGA REVNEJ SPNDRP RDVYD AVAKI VJSRLE HE SMKGDEM DGTCNGLCH YAALGG DIEGA REVNEJ EPGDKP QDIYJ RVVAD VHDYNK QD AENGHEV DGTCNGLCH YAALGG DVEGA REVNEJ PSNRP QDVYS RVLEI VHRVVE ED AENGHEV DGTCNGLCH YAALGG DVEGA REVNEJ TPARPP QDVYS RVLEI VHRVVE ED AENGHEV DGTCNGLCH YAALGG DVEGA REVNEJ TPARPP QDVYT FVANL VKRELDKEI ALEGDEL DGTCNGLCH YAALGG DVEGA REVNEJ PARPP QDVYT FVANL VKRELDKEI ALEGDEL DGTCNGLCH YAALGG DVEGA TEVNEJ APSDRP QDVYT HVAGU VTRKLE AA AAKGDEM DGTCNGLCH YAALGG DEGAR ZVNEJ SPLEKF QDVYT HVAGU VTRKLE AA AAKGDEM DGTCNGLCH YAALGG DEGAR ZVNEJ SPLEKF QDVYT HVAGU VTRKLE AA AAKGDEM DGTCNGLCH YAALGG DEGAR ZVNEJ SPLEKF QDVYT HVARU VERKELAS AAKGDEM DGTCNGLCH YAALGG DLEGAR ZVNEJ SPLEKF QDVYT HVARU VERKELKER AAKGDEM DGTCNGLCH YAALGG DLEGAR ZVNEJ VPADRP BDVYT HVARL VERKELKE AAKGDEM DGTCNGLCH YAALGG DLEGAR ZVNEJ VPADRP BDVYT HVARL VERKELKE AAKGDED DGTCNGLCH YAALGG DLEGAR ZVNEJ VPADRP BDVYT HVARL VERKELKE AAKGDED DGTCNGLCH YAALGG DLEGAR ZVNEJ VPADRP BDVYT HVARL VERKEL SD DERGLED DGTCNGLCH YAALGG DLEGAR ZVNEJ VPADRP DDVYT HVARL VERKEN AAKGDED DGTCNGLCH YAALGG DLEGAR ZVNEJ VPADRP DDVYT HVARL VERKEN AAKGDED DGTCNGLCH YAALGG DLEGAR ZVNEJ VPBERP DDVYAFVARL VTERLEKA AEAGDES DGTCNGLCH YAALGG DLEGAR ZVNEJ VPSEKR MDVYK HVAKL VTERLEKA AEAGDES DGTCNGLCH YAALGG DLEGAR ZVNEJ VPSEKR MDVYK HVAKL VTERLEKA AEAGDES	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 948 AI 947 AL 925 AR 952 AN 948 AI 935 AA 978 AK 625 AN 916 AI 926
DETCIGLON YAALGG DEGAR EVINE PENRE NUVVA VAAR VISILKKE AAAGDEM DETCIGLON YAALGG DEGAR EVINE PENRE NUVVA VAAR VISILKKE AAAGDEM DETCIGLON YAALGG DEGAR EVILS PHORE ROVVD AVAKI VISILE (E SAKGDEV DETCIGLON YAALGG DEGAR EVILS PHORE ROVVD AVAKI VISILE (E SAKGDEV DETCIGLON YAALGG DEGAR EVILS PHORE ROVVD AVAKI VISILE (E SAKGDEV DETCIGLON YAALGG DEGAR EVILS PHORE ROVVD AVAKI VISILE (E SAKGDEV DETCIGLON YAALGG DEGAR EVILS PHORE ROVVD AVAKI VISILE (E SAKGDEV DETCIGLON YAALGG DEGAR EVILS PHORE ROVVD AVAKI VISILE (E AFKGHE DETCIGLON YAALGG DEGAR EVIL I PENER POIVTS EVILS I VERIVE ED AFKGHE DETCIGLON YAALGG DEGAR EVIL I PENER POIVTS EVILS I VERIVE ED AFKGHE DETCIGLON YAALGG DEGAR EVIL I PENER POIVT FVANL VERELDKL ALEGOEL DETCIGLON YAALGG DEGAR EVIL I PADRE POIVT FVANL VERELDKL ALEGOEL DETCIGLON YAALGG DEGAR EVIL I SPLER POIVT HVAGL VERKILE AA AAKGDEM DETCIGLON YAALGG DEGAR EVIL I SPLER POIVT HVARL VERKLE EA AAKGDED DETCIGLON YAALGG DEGAR EVIL SPLER POIVT HVARL VERKILKE AARGDED DETCIGLON YAALGG DIEGAR EVIL SPLER POIVT FVARL VERKILKE DE DEGEE DETCIGLON YAALGG DIEGAR EVIL VERDRE BOIVT HVARL VERKURKEN DE DEGEE DETCIGLON YAALGG DIEGAR EVIL VERDRE POIVTA FVARL VERKILKEN AARGDED DETCIGLON YAALGG DIEGAR EVIL VERDRE POIVTA FVARL VERKURKA AEAGDES DETCIGLON YAALGG DIEGAR EVIL VERDRE POIVTA FVARL VERKURKA AEAGDES DETCIGLON YAALGG DIEGAR EVIL VERDRE RDIVTK HVARL VERKILN AEAGDES DETCIGLON YAALGG DIEGAR EVIL VERDRE RDIVTK HVARL VERKILNA AEAGDES DETCIGLON YAALGG DIEGAR EVIL VERDRE RDIVTK HVARL VERKILNA AEAGDES DETCIGLON YAALGG DIEGAR EVIL VERDRE RDIVTK HVARL VERKILA AEAGDES DETCIGLON YAALGG DIEGAR EVIL VERDRE RDIVTK HVARL VERKILA AEAGDES DETCIGLON YAALGG DIEGAR EVIL VERDRE RDIVTK HVARL VERKILKA AEAGDES DETCIGLON YAALGG DIEGAR EVIL VERDRE RDIVTK HVARL VERKILKA AEAGDES DETCIGLON YAALGG DIEGAR EVIL VERDRE RDIVTK HVARL VERKILKA AEAGDES	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 948 AI 946 AI 917 AE 952 AR 952 AA 948 AI 947 AE 952 AN 953 AA 978 AR 625 AA 916 AI 915 AI 926 AE 953
LOTCINGLON YAALGG DPEGA RUVNL PPSNR PNDVYA AVAAR VISILKKE A AAGDPM LGTCINGLON YAALGG DIEGA RUVNL WPSDNP SDVYE AVAEI VINGFLKKD A EAGDEM GSTCINGLON YAALGR DPGGA RUVNL SPNDR F RDVYD AVAKI VISRLE (P= SAKGGDEM GSTCINGLON YAALGR DPGGA RUVNL SPNDR F RDVYD AVAKI VISRLE (P= SAKGGDEM GSTCINGLON YAALGR DPGGA RUVNL PPGDRP CDVYS RVLEI VRUDYK QD A ENGHEV GSTCINGLON YAALGG DVEGA RUVNL IPSDRP CDVYS RVLEI VRUDYK QD A ENGHEV GSTCINGLON YAALGG DVEGA RUVNL IPSDRP CDVYS RVLEI VRUDYK QD A ENGHEV GSTCINGLON YAALGG DVEGA RUVNL IPSDRP CDVYS RVLEI VRURVK PED A ENGHEV GSTCINGLON YAALGG DVEGA RUVNL IPSDRP CDVYT FVANL VRARINND FENGNET GSTCINGLON YAALGG DVEGA RUVNL IPSDRP CDVYT FVANL VRARINND A ENGHEV GSTCINGLON YAALGG DVEGA RUVNL IPSDRP CDVYT FVANL VRARINND A ENGHEV GSTCINGLON YAALGG DVEGA RUVNL SPSDRP CDVYT HVARL VRARLE AA AAKGGDEM GSTCINGLON YAALGG DVEGA RUVNL SPSDRP CDVYT HVARL VRARLE AA AAKGGDEM GSTCINGLON YAALGG DJEGA RUVNL SPLEKP QDVYA FVAEL VKKRLAAS DDPM GSTCINGLON YAALGG DIEGAR RUVNL SPSDRP CDVYA FVAEL VKKRLAAS DDPM GSTCINGLON YAALGG DIEGAR RUVNL SPSDRP CDVYA FVAEL VKKRLAAS AKGGDES GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVAEL VKKRLAAS AAKGGDES GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVAEL VKKRLAS AAKGGDES GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVARL VTKRLE NS AAAGGDE GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVARL VTERLIK AS AAAGGDES GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVARL VTERLIK AS AAAGGDES GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVARL VTERLIK AS AAAGGDES GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVARL VTERLIK AS AAAGGDES GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVARL VTERLIK AS AAAGGDES GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVARL VTERLIK AS AAAGGDES GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVARL VTERLIK AS AAAGGDES GSCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVARL VTERLIK AS AAAGDEK DSTCINGLON YAALGG DIEGAR RUVNL VPSDRP CDVYA FVARL VTERLIK AS ALAGGDEN	AE 885 AN 878 AS 892 AS 891 AK 973 AK 948 AI 917 AE 925 AN 952 AN 953 AL 916 AL 916 AL 956 AA 953
DETCIGLON YAALG DEGA RUVIL PENRE NUVYA VVAR VISILKKE A AAGDEM DETCIGLON YAALG DEGA KUVIL WEDDH SDVYE AVAEI VIGELKKE A AAGDEM DETCIGLON YAALG DEGA KUVIL SPHDRE KDVYD AVAKI VISILE (E SAKGDEV DETCIGLON YAALG DEGA RUVIL SPHDRE KDVYD AVAKI VISILE (E SAKGDEV DETCIGLON YAALG DEGA RUVIL EGORK POLYD AVAKI VISILE (E SAKGDEV DETCIGLON YAALG DEGA RUVIL EFORK POLYD AVAKI VISILE HE SAKGDEV SCIGLON YAALG DEGA RUVIL FEGORK POLYS RULEI VKRVE ED ATKGHKE DETCIGLON YAALG DVEGA RUVIL I SPHDRE NDYYD AVAKI VISILE HE ALKGDEN DETCIGLON YAALG DVEGA RUVIL I SPHDRE POLYS FVANL VKRATINDA FLIGHEL STCIGLON YAALG DVEGA RUVIL I SPHDRE POLYT FVANL VKRATINDA ALKGDEN DETCIGLON YAALG DVEGA RUVIL I SPHDRE POLYT HVARU VKRATLEA AAKGDEN DETCIGLON YAALG DVEGA RUVIL SPHDRE POLYT HVARU VKRALLEA AAKGDEN DETCIGLON YAALG DVEGA RUVIL SPHDRE POLYT HVARU VKRALLEA AAKGDEN DETCIGLON YAALG DVEGA RUVIL SPHDRE POLYT HVARU VKRALLEA AAKGDEN DETCIGLON YAALG DLEGA RUVIL SPHDRE POLYT HVARU VKRALLEA ALKGDEN DETCIGLON YAALG DLEGA RUVIL SPHDRE POLYA FVARL VKRALLAS DDEM DETCIGLON YAALG DLEGA RUVIL VARDKE POLYT HVARU VKRAL POL-L RAGLEE STICHGLON YAALG DLEGA RUVIL VARDKE POLYTA VAKL VKRALAS	AE 885 AN 878 AS 892 AS 891 AK 973 AK 743 AA 948 AI 917 AE 925 AN 935 AA 936 AK 723 AR 952 AN 935 AA 916 AL 915 AI 925 AA 952 AA 935 AK 925 AA 916 AL 915 AI 952 AA 953 AK 953
LOTCINGLON YAALOG DPEGA RUVNL EP SINE PIDUYA AVAAR VISILKKE A AAGDEM DGTCINGLON YAALOG DIEGA RUVNL WP SDH9 SDUYE AVAE I VIAGFLKKD A EAGDEM GTCINGLON YAALOG DEIGAR EVNI SPHDRE RUVD DAVAKI VISILE HE SAKGDEM GTCINGLON YAALOG DEIGAR EVNI SPHDRE RUVD AVAKI VISILE HE SIKGOEM GTCINGLON YAALOG DIEGAR EVNI SPHDRE RUVD AVAKI VISILE HE SIKGOEM GTCINGLON YAALOG DIEGAR EVNI SPHDRE RUVD AVAKI VISILE HE SIKGOEM GTCINGLON YAALOG DIEGAR EVNI SPHDRE RUVD AVAKI VISILE HE SIKGOEM GTCINGLON YAALOG DIEGAR EVNI PEORE POUYS EVNI VIARINND FENGHEV DSCINGLON YAALOG DIEGAR EVNI TPAERE POUYT EVNI VEREID KI A ENGHEV GTCINGLON YAALOG DIEGAR EVNI PABRE POUYT EVNI VEREID KI ALGOEM GTCINGLON YAALOG DVEGAT EVNI PABRE POUYT EVNI VEREID KI ALGOEM STCINGLON YAALOG DVEGAT EVNI PABRE POUYT EVNI VEREID KI ALGOEM GTCINGLON YAALOG DVEGAT EVNI SPHERE PENDEVT HVARL VEREID KI ALGOEM STCINGLON YAALOG DVEGAT EVNI SPHERE POUYT HVARL VERALE AA ALGOEM STCINGLON YAALOG DEIGAR EVNI SPHERE POUYT HVARL VERALE AA ALGOEM STCINGLON YAALOG DIEGAR EVNI SPHERE POUYTA FVALL VIKRLE AA ALGOEM STCINGLON YAALOG DIEGAR EVNI SPHERE POUYTA FVALL VIKRLE AA ALGOEM STCINGLON YAALOG DIEGAR EVNI VPSDRE POUYA FVALL VIKRLE AA ALGOEM STCINGLON YAALOG DIEGAR EVNI VPSDRE POUYA FVALL VIKRLE AA ALGOEM STCINGLON YAALOG DIEGAR EVNI VPSDRE POUYA FVALL VIKRLE KA ALGOEM STCINGLON YAALOG DIEGAR EVNI VPSDRE POUYA FVALL VIERLIKKA ALAGOEM STCINGLON YAALOG DIEGAR EVNI VPSDRE POUYA FVALL VIERLIK KA ALAGOEM STCINGLON YAALOG DIEGAR EVNI VPSDRE POUYA FVALL VIERLIK KA ALGODEM STCINGLON YAALOG DIEGAR EVNI VPSDRE POUYA FVALL VIERLIK KA ALGODEM STCINGLON YAALOG DIEGAR EVNI VPSDRE POUYA FVALL VIERLIK KA ALGODEM	AE 885 AN 878 AS 892 AS 891 AK 973 AK 743 AA 948 AI 917 AE 925 AN 935 AA 916 AI 916 AI 953 AA 953 AA 953 AA 953 AK 926 AF 953 AK 927
LOTCHGLCH YAALG DPEGA REVNEPEPSNEPSNEPSNEA NUVYA VAAR UTSILKKE A AAGDPM DGTCNGLCH YAALG DPEGA REVNEPSNEPSNEPSNEF KUVYA VAAR UTSILKKE A EAGDPM DGTCNGLCH YAALG NPEGA REVNESPNEPSNEPSNEF KUVYD AVAKI VISKLEHE SAKGDEM DGTCNGLCH YAALG NPEGA REVNESPNEPSNEPSNEPSNEF KUVYD AVAKI VISKLEHE SAKGDEM DGTCNGLCH YAALG DIEGA REVNESPNEPSNEPSNEPSNEF KUVYD AVAKI VISKLEHE SAKGDEM DGTCNGLCH YAALG DUEGA REVNESPNEPSNEPSNEF KUVYD AVAKI VISKLEHE ALNGGEN DGTCNGLCH YAALG DUEGA REVNESPNEPSNEPSNEF KUVYD AVAKI VISKLEHE ALNGGEN DGTCNGLCH YAALG DUEGA REVNESPNEPSNEPSNEF KUVYS KULEI VKNEV ED ALNGHEV DGTCNGLCH YAALG DUEGA REVNESPNEPSNEF KUVYS KULEI VKNEV ED ALNGHEV DGTCNGLCH YAALG DUEGA REVNESPNEPSNEF KUVYS KULEI VKNEV ED ALNGGEN DGTCNGLCH YAALG DUEGA REVNESPNEF KUVYS KULEI VKNEV ED ALNGGEN DGTCNGLCH YAALG DUEGA REVNESPNEF KUVYS VVAGU VARKELEA ALNGGEN DGTCNGLCH YAALG DEGA REVNESPNEF KUVYS VVAGU VARKELEA ALNGGEN DGTCNGLCH YAALG DIEGA REVNESPNEF KUVYS VVAGU VARKEV ES AANGEDEN DGTCNGLCH YAALG DIEGA REVNESPNEF KUVYS VVAGU VARKEV SEN DEF DGTCNGLCH YAALG DIEGA REVNESPNEF KUVYS VVAGU VARKEV SEN AANGDEE DGTCNGLCH YAALG DIEGA REVNESPNEF KUVYS VVAGU VARKEV SEN AANGDEE DGTCNGLCH YAALG DIEGA REVNESPNEF KUVYS VVAGU VARKENS AANGDEE DGTCNGLCH YAALG DIEGA REVNESPNEF KUVYS VVAGU VARKENS AANGDEE DGTCNGLCH YAALG DIEGA REVNESPNEF KUVYS VVAGU VARKENSEN AANGDEE DGTCNGLCH YAALG DIEGA REVNESPNEF KUVYS VVAKU VERELKKA ALNGDEF DGTCNGLCH YAALG DEGA REVNESPNEF KUVYS VVAKU VERELKKA ALNGDEF DGTCNGLCH YAALG DEGA REVNESPNEF KUVYS VVAKU VERELKKA ALGODHME DGTCNGLCH YAALG DEGA REVNESPNEF KUVYS VVAKU VERELKKA ALGODHME DGTCNGLCH YAALG DEGA REVNESPNEF KUVYS VVAKU VERELKKA ALGODHME DGTCNGLCH YAALG DEGA REVNESSEN KUVYS VVAKU VERELKKA ALGODHME DGTCNGLCH YAALG DE	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 925 AR 952 AN 948 AI 917 AE 925 AA 978 AK 625 AA 916 AL 915 AA 952 AA 953 AA 953 AA 953 AK 925 AK 928 AK 928 AK 928 AE 1008
LOTCINGLON YAALGG DPEGA RUVNL PPSNR PNDVYA AVAAR VISILKKE A AAGDPM LGTCINGLON YAALGG DIEGA RUVNL WPSDNP SDVYE AVAEI VINGFLKKD A EAGDEM GTCINGLON YAALG DDEGA RUVNL SPNDR F RDVYD AVAKI VISRLE (P= SAKGGDEM GTCINGLON YAALG PDGA RUVNL SPNDR F RDVYD AVAKI VISRLE (P= SAKGGDEM GTCINGLON YAALGG DIEGA RUVNL PPGDRP CDIVY FUVANUTYKDUYWE DD A ENGHEV GSCINGLON YAALGG DVEGA RUVNL VPSDRP CDIVY SVLEI VRUDYWE DD A ENGHEV GSCINGLON YAALGG DVEGA RUVNL VPSDRP CDIVY SVLEI VRUDYWE DD A ENGHEV GSCINGLON YAALGG DVEGA RUVNL VPSDRP CDIVY SVLEI VRUDYWE DD A ENGHEV GSCINGLON YAALGG DVEGA RUVNL VPSDRP CDIVY FUVANU VRARINND F ENGNET GSCINGLON YAALGG DVEGA RUVNL VPSDRP CDIVT FUVANU VRARINND F ENGNET GSCINGLON YAALGG DVEGA RUVNL SPSDRP CDIVT FUVANU VRARINND F ENGNET GSCINGLON YAALGG DVEGA RUVNL SPSDRP CDIVT FUVANU VRARIL AA AAKGGDEM GSCINGLON YAALGG DVEGA RUVNL SPSLEKP QDVYA FVAEL VKKRLAAS ANGGDEN GSCINGLON YAALGG DLEGA RUVNL SPLEKP QDVYA FVAEL VKKRLAAS DDPM GSCINGLON YAALGG DLEGA RUVNL SPSLEKP QDVYA FVAEL VKKRLAAS DDPM GSCINGLON YAALGG DLEGA RUVNL SPSLEKP QDVYA FVAEL VKKRLAS AANGGDEN GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VKKRLAS AAAGGDE GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VKKRLAS AAAGGDE GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VKREL KA ALAGGDES GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VTKRLE NS AAAGGDE GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VTREL KA ALAGGDES GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VTERL KA ALAGGDES GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VTERL KA ALAGGDES GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VTERL KA ALAGGDES GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VTERL KA ALAGGDEN GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VTERLE KA ALAGGDEN GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VTERLE KA ALAGGDEN GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VTERLE KA ALAGGDEN GSCINGLON YAALGG DLEGA RUVNL VPSDRP CDVYA FVAEL VTERLE KA ALAGGDEN GSCINGLON YAALGG DUEGA RUVNL VPSDRP CDVY	AE 885 AN 878 AS 892 AS 891 AK 973 AK 743 AA 948 AI 917 AE 925 AN 957 AA 935 AA 916 AL 915 AA 953 AA 953 AA 953 AK 926 AL 978 AK 926 AA 953 AA 953 AK 928 AK 928 AK 928 AK 928 AK 978
LOTCHGLCH YAALGG DPEGA RUWL PEDNRE NDUYA AVAAR VISILKKE A AAGDEM LGTCNGLCH YAALGG DIEGA RUWL WEDHP SDUYE AVAEI VRGFLKKD A EAGDEM GTCNGLCH YAALGR DEGA RUWL SPHDRE RDUYD AVAKI VISRLE (PE SAKGOEV LSTCNGLCH YAALGR DEGA RUWL SPHDRE RDUYD AVAKI VISRLE (PE SAKGOEV STCNGLCH YAALG DIEGA RUWL SPHDRE RDUYD AVAKI VISRLE (PE SAKGOEV LSTCNGLCH YAALG DUEGA RUWL IPSDRE PODYS RULEI VRUEVK ED A TNGHKE STCNGLCH YAALG DUEGA RUWL VPSRE QDUYS RULEI VRUEVK ED A TNGHKE STCNGLCH YAALG DUEGA RUWL IPSDRE QDIYS EVANI VRARINND FENGNET LSTCNGLCH YAALG DUEGA RUWL IPSDRE QDUYT HVASU VIKRLE AA AAKGOEM STCNGLCH YAALG DUEGA RUWL SPHDRE QDUYT HVASU VIKRLE AA AAKGOEM STCNGLCH YAALG DUEGA RUWL SPHDRE QDUYT HVASU VIKRLE AA AAKGOEM STCNGLCH YAALG DUEGA RUWL SPHDRE QDUYT HVASU VIKRLE AA AAKGOEM STCNGLCH YAALG DUEGA RUWL SPHDRE QDUYT HVASU VIKRLE AA AAKGOEM STCNGLCH YAALG DUEGA RUWL VPSDRE QDUYT HVASU VIKRLE AA AAKGOEM STCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIKRLE AA AAKGOEM STCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIKRLE AA AAKGOEM STCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIKRLE AA AAKGOEM STCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIKRLE NA AAKGOES SSCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIKRLE NA AAKGOES SSCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA AAKGOER STCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA ALAGDES SSCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA ALAGDES STCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA ALAGDES STCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA ALAGDES STCNGLCH YAALG DIEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA ALAGDER STCNGLCH YAALG DUEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA ALAGDER STCNGLCH YAALG DUEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA ALAGDER STCNGLCH YAALG DUEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA ALAGDER STCNGLCH YAALG DUEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA ALAGDER STCNGLCH YAALG DUEGA RUWL VPSDRE QDUYA FVAL VIERLIK KA ALAGDER STCNGLCH YAALG DUEGA RUWL VPSDRE QDUYA FVAL VIERLE KA ALAGDER STCNGLCH YAALG DUEGA RUWL V	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 948 AI 917 AE 925 AN 957 AA 948 AI 917 AE 952 AN 957 AA 953 AA 953 AA 953 AK 928 AK 920 AE 1008 AE 1008
DETCIGLON YAALGG DEGAR EVINE PENRE PLOVYA AVAR VISILKKE A AAGDEM DETCIGLON YAALGG DEGAR EVINE PENRE PLOVYA AVAR VISILKKE A AAGDEM DETCIGLON YAALGG DEGAR EVINE SPHDRE RDVYD AVAKI VISILE (E SAKGDEV DETCIGLON YAALGG DEGAR EVINE SPHDRE RDVYD AVAKI VISILE (E SAKGDEV DETCIGLON YAALGG DEGAR EVINE SPHDRE RDVYD AVAKI VISILE (E SAKGDEV DETCIGLON YAALGG DEGAR EVINE SPHDRE RDVYD AVAKI VISILE (E SAKGDEV DETCIGLON YAALGG DEGAR EVINE SPHDRE RDVYD AVAKI VISILE (E SAKGDEV DSTCIGLON YAALGG DEGAR EVINE JEGDRE POLYS EVILE I VENRVE ED ATKGHKE DSTCIGLON YAALGG DEGAR EVINE I PENER POLYS EVILE I VENRVE ED ATKGHKE DSTCIGLON YAALGG DEGAR EVINE I PENER POLYT FVANL VERELDKE ALGOREL DSTCIGLON YAALGG DEGAR EVINE I PENER POLYT FVANL VERELDKE ALGOREL DSTCIGLON YAALGG DEGAR EVINE I SPEER POLYT FVANL VERELDKE ALGOREL DSTCIGLON YAALGG DEGAR EVINE SPEER POLYT FVANL VERELDKE ALGOREL DSTCIGLON YAALGG DEGAR EVINE SPEER POLYT FVANL VERELE A ALGOREL DSTCIGLON YAALGG DEGAR EVINE SPEER POLYT FVANL VERKEL AS DEPG DSTCIGLON YAALGG DEGAR EVINE VERDRE POLYTA FVALE VERKELAS DEPG DSTCIGLON YAALGG DEGAR EVINE VERDRE POLYAF VALE VERKELAS DEPG DSTCIGLON YAALGG DEGAR EVINE VERDRE POLYAF VALE VERKELAS DEPG DSTCIGLON YAALGG DEGAR EVINE VERDRE POLYAF VALE VERKEL AS ALGOREL DSTCIGLON YAALGG DEGAR EVINE VERDRE POLYAF VALE VERKELAS ALEGOREL DSTCIGLON YAALGG DEGAR EVINE VERDRE POLYAF VALE VERELE KA ALGOREL DSTCIGLON YAALGG DEGAR EVINE VERDRE POLYAF VALE VERELE KA ALGOREL DSTCIGLON YAALGG DEGAR EVINE VERDRE POLYAF VALE VERELE KA ALGOREL DSTCIGLON YAALGG DEGAR EVINE VERDRE POLYAF VALE VERELE KA ALGOREL DSTCIGLON YAALGG DEGAR EVINE VERDRE POLYAF VALE VERELE KA ALGOREL DSTCIGLON YAALGG DEGAR EVINE VERER ENDVYK HVALE VERELE KA ALGOREL DSTCIGLON YAALGG DEGAR EVINE VERER POLYAF VALE VERELE KA ALGOREL DSTCIGLON YAALGG DEGAR EVINE VERER ENDVYK HVAL VERELE KA ALGOREL DSTCIGLON YAALGG DEGAR EVINE VERER ENDVYK HVAL VERELE KA ALGOREN DSTCIGLON YAALGG DEGAR EVINE VERER ENDVYK HVAL VERELE KA ALGOR	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 917 AL 948 AI 949 AI 925 AR 952 AN 978 AL 935 AA 916 AI 915 AI 926 AE 953 AA 953 AK 927 AK 928 AK 926 AL 953 AL 937 AK 928 AK 926 AK 937 AK 928 AK 976 AK 976 AK 1002
DETCIGLEN YAALG DEGA REVNE PENRE NUVYA VAAR VISILKKE AAAGDEM DETCIGLEN YAALG DEGA REVNE PENRE NUVYA VAAR VISILKKE AAAGDEM DETCIGLEN YAALG DEGA REVNE SPHDRE REVVED AVAKI VISRLE (E SAKGDEV DETCIGLEN YAALG DEGA REVNE SPHDRE REVVED AVAKI VISRLE (E SAKGDEV DETCIGLEN YAALG DEGA REVNE SPHDRE REVVED AVAKI VISRLE (E SAKGDEV DETCIGLEN YAALG DEGA REVNE SPHDRE REVVED AVAKI VISRLE HE SAKGDEV DETCIGLEN YAALG DEGA REVNE SPHDRE REVVED AVAKI VISRLE HE SAKGDEV DETCIGLEN YAALG DEGA REVNE SPHDRE REVVED YAKI VISRLE HE SAKGDEV DETCIGLEN YAALG DEGA REVNE I SPHDRE REVVED YS EVAN VERATINDA- FENGHET DETCIGLEN YAALG DEGA REVNE I SPHDRE REVVED YS EVAN VERATINDA- FENGHET DETCIGLEN YAALG DEGA REVNE I SPHDRE REVVET VANE VERALE AA AAKGDEM DETCIGLEN YAALG DEGA REVNE I SPHERE REVVET HVARU VERALE AA AAKGDEM DETCIGLEN YAALG DEGA REVNE I SPHERE REVVET HVARU VERELE AA AAKGDEM DETCIGLEN YAALG DEGA REVNE SPHERE REVVET HVARU VERELE AA AAKGDEM DETCIGLEN YAALG DEGA REVNE SPHERE REVVET HVARU VERELKKE AAEGDEV DETCIGLEN YAALG DEGA REVNE VEREN SPHERE REVVER HVARU VERSTE DE DEDM DETCIGLEN YAALG DEGA REVNE VEREN SPHERE REVVER HVARU VERSTE DE DE LEAGLEE DETCIGLEN YAALG DEGA REVNE VEREN SPHERE REVVER HVARU VERSTE DE DE LEAGLEE DETCIGLEN YAALG DEGA REVNE VEREN REVVER HVARU VERSTE DE LEAGLEE DETCIGLEN YAALG DEGA REVNE VEREN REVVER HVARU VERSTE DE AEAGDES DESCIGLEN YAALG DEGA REVNE VEREN REVVER HVARU VERELE NA ALAGDER DETCIGLEN YAALG DEGA REVNE VEREN REVVER HVARU VERELE KA ALAGDER DETCIGLEN YAALG DEGA REVNE VEREN REVYEN HVARU VERELE KA ALAGDER DETCIGLEN YAALG DEGA REVNE VEREN REVYEN VARU VERELE KA ALAGDER DETCIGLEN YAALG DEGA REVNE VEREN REVYEN VARU VERELE KA ALAGDER DETCIGLEN YAALG DEGA REVNE VEREN REVYEN VARU VERELE KA ALAGDER DETCIGLEN YAALG DEGA REVNE VEREN REVYEN VARU VERELE KA ALAGDER DETCIGLEN YAALG DEGA REVNE VEREN REVYEN VARU VERELE KA ALAGDER DETCIGLEN YAALG DEGA REVNE VEREN REVYEN VARU VERELE KA ALAGDER DETCIGLEN YAALG DEGA REVNE VEREN VEREN VEREN VEREN REV ALAGDER DETCIGLEN YAALG DEVEGA REVNE	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 948 AI 947 AL 925 AN 957 AA 948 AI 925 AN 952 AN 953 AL 915 AI 953 AA 953 AA 953 AK 928 AK 928 AK 926 AL 978 AK 928 AK 928 AK 926 AL 978 AK 928 AK 926 AK 908 AK 976 AE 1002 AE 948
LOTCHGLCH YAALG DPEGA REVNE PENRE NUVYA VAAR VISILKKE A AAGDEM DGTCNGLCH YAALG DPEGA REVNE PENRE NUVYA VAAR VISILKKE A AGGDEM GTCNGLCH YAALG NEDGA REVNE SPHDRE RUVYD AVAKI VISILE (E SAKGGEV DGTCNGLCH YAALG NEDGA REVNE SPHDRE RUVYD AVAKI VISILE (E SAKGGEV GTCNGLCH YAALG NEDGA REVNE SPHDRE RUVYD AVAKI VISILE (E SAKGGEV DGTCNGLCH YAALG DVEGA REVNE SPHDRE RUVYD AVAKI VISILE (E SAKGGEV DGTCNGLCH YAALG DVEGA REVNE SPHDRE RUVYD AVAKI VISILE (E SAKGGEV DSTCNGLCH YAALG DVEGA REVNE SPHDRE RUVYD AVAKI VISILE (E ALGGEL DSTCNGLCH YAALG DVEGA REVNE VPSSRP ODVYS RULEI VKNEVE ED ATNGHEV DSTCNGLCH YAALG DVEGA REVNE VPSSRP ODVYS RULEI VKNEVE ED ATNGHEN DSTCNGLCH YAALG DVEGA REVNE VPSSRP ODVYT FVANL VKARLE AA AAKGDEM DSTCNGLCH YAALG DVEGA REVNE VPSSRP ODVYT FVANL VKARLE AA AAKGDEM DSTCNGLCH YAALG DVEGA REVNE VPSSRP ODVYT FVANL VKRELLAS AAKGDEM DSTCNGLCH YAALG DEGA REVNE VPSSRP ODVYT FVANL VKRELLAS AAKGDEM DSTCNGLCH YAALG DLEGAR ZVNE VPSSRP ODVYA FVAL VKRELLAS AAKGDEM DSTCNGLCH YAALG DLEGAR ZVNE VPSSRP ODVYA FVAL VKRELLAS AAKGDEM DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VVSSRP DD VKNGRSQ DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTSRLE NS AAAGDEE DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTSRLE NS AAAGDEE DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA AAAGDEE DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA AAAGDEE DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA AAAGDEE DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA ALGGOEN DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP DDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP DDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP DDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP DDVYA FVAL VVAL VEKRE E KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 925 AR 952 AN 948 AI 917 AE 925 AN 935 AA 935 AA 935 AK 625 AN 953 AA 953 AK 953 AK 928 AK 980 AE 1008 AE 1008 AE 1002 AK 1002 AK 1002 AE 943
LOTCHGLCH YAALG DPEGA REVNE PENRE NUVYA VAAR VISILKKE A AAGDEM DGTCNGLCH YAALG DPEGA REVNE PENRE NUVYA VAAR VISILKKE A AGGDEM GTCNGLCH YAALG NEDGA REVNE SPHDRE RUVYD AVAKI VISILE (E SAKGGEV DGTCNGLCH YAALG NEDGA REVNE SPHDRE RUVYD AVAKI VISILE (E SAKGGEV GTCNGLCH YAALG NEDGA REVNE SPHDRE RUVYD AVAKI VISILE (E SAKGGEV DGTCNGLCH YAALG DVEGA REVNE SPHDRE RUVYD AVAKI VISILE (E SAKGGEV DGTCNGLCH YAALG DVEGA REVNE SPHDRE RUVYD AVAKI VISILE (E SAKGGEV DSTCNGLCH YAALG DVEGA REVNE SPHDRE RUVYD AVAKI VISILE (E ALGGEL DSTCNGLCH YAALG DVEGA REVNE VPSSRP ODVYS RULEI VKNEVE ED ATNGHEV DSTCNGLCH YAALG DVEGA REVNE VPSSRP ODVYS RULEI VKNEVE ED ATNGHEN DSTCNGLCH YAALG DVEGA REVNE VPSSRP ODVYT FVANL VKARLE AA AAKGDEM DSTCNGLCH YAALG DVEGA REVNE VPSSRP ODVYT FVANL VKARLE AA AAKGDEM DSTCNGLCH YAALG DVEGA REVNE VPSSRP ODVYT FVANL VKRELLAS AAKGDEM DSTCNGLCH YAALG DEGA REVNE VPSSRP ODVYT FVANL VKRELLAS AAKGDEM DSTCNGLCH YAALG DLEGAR ZVNE VPSSRP ODVYA FVAL VKRELLAS AAKGDEM DSTCNGLCH YAALG DLEGAR ZVNE VPSSRP ODVYA FVAL VKRELLAS AAKGDEM DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VVSSRP DD VKNGRSQ DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTSRLE NS AAAGDEE DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTSRLE NS AAAGDEE DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA AAAGDEE DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA AAAGDEE DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA AAAGDEE DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA ALGGOEN DSTCNGLCH YAALG DLEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP QDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP DDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP DDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP DDVYA FVAL VTERLE KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP DDVYA FVAL VVAL VEKRE E KA ALGOEN DSTCNGLCH YAALG DVEGAR ZVNE VPSDRP	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 925 AR 952 AN 948 AI 917 AE 925 AN 935 AA 935 AA 935 AK 625 AN 953 AA 953 AK 953 AK 928 AK 980 AE 1008 AE 1008 AE 1002 AK 1002 AK 1002 AE 943
LOTCHGLCH YAALG DPEGA REVNE PENRE NUVYA VVAR VISILKKE A AAGDEM DGTCNGLCH YAALG DPEGA REVNE PENRE NUVYA VVARI VISILKKE A AAGDEM GTCNGLCH YAALG DPEGA REVNE SPHDRE RUVD AVAKI VISILE (E SAKGBEV DGTCNGLCH YAALG NEDGA REVNE SPHDRE RUVD AVAKI VISILE (E SAKGBEV DGTCNGLCH YAALG DPEGA REVNE SPHDRE RUVD AVAKI VISILE (E SAKGBEV DGTCNGLCH YAALG DPEGA REVNE SPHDRE RUVD AVAKI VISILE (E SAKGBEV DSTCNGLCH YAALG DVEGA REVNE SPHDRE RUVD AVAKI VISILE (E SAKGBEV DSTCNGLCH YAALG DVEGA REVNE SPHDRE RUVD AVAKI VISILE (E ALRGHEV DSTCNGLCH YAALG DVEGA REVNE VPSSRE ODVYS RULEI VKNEVE ED ATKGHEV DSTCNGLCH YAALG DVEGA REVNE VPSSRE ODVYS RULEI VKNEVE ED ATKGHEV DSTCNGLCH YAALG DVEGA TEVNE VPSSRE ODVYT FVANL VKARLE AA ALRGDEM DSTCNGLCH YAALG DVEGA TEVNE VPSSRE ODVYT FVANL VKARLE AA ALRGDEM DSTCNGLCH YAALG DVEGA TEVNE VPSSRE ODVYT FVANL VKARLE AA ALRGDEM DSTCNGLCH YAALG DEGAR ZWNE JPSSRE POUVT FVANL VKRELL AA ALRGDEM DSTCNGLCH YAALG DLEGAR ZWNE VPSSRE VDVY TVAKE VKRELAS ALRGDEM DSTCNGLCH YAALG DLEGAR ZWNE VPSSRE POUVA FVALE VKRELAS ALRGDEM DSTCNGLCH YAALG DLEGAR ZWNE VPSDRE POUVA FVALE VKRELAS DAGDED DSTCNGLCH YAALG DLEGAR ZWNE VPSDRE POUVA FVALE VTERLE KA ALRGDES DSTCNGLCH YAALG DLEGAR ZWNE VPSDRE POUVA FVALE VTERLE KA ALRGDES DSTCNGLCH YAALG DLEGAR ZWNE VPSDRE POUVA FVALE VTERLE KA ALRGDES DSTCNGLCH YAALG DLEGAR ZWNE VPSDRE POUVA FVALE VTERLE KA ALRGDES DSTCNGLCH YAALG DLEGAR ZWNE VPSDRE POUVA FVALE VTERLE KA ALGODEN DSTCNGLCH YAALG DUEGAR ZWNE VPSDRE POUVA FVALE VTERLE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZWNE VPSDRE POUVA FVALE VTERLE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZWNE VPSDRE POUVA FVALE VTERLE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZWNE VPSDRE POUVA FVALE VTERLE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZWNE VPSDRE POUVA FVALE VERRE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZWNE VPSDRE POUVA FVALE VERRE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZWNE VPSDRE POUVA FVALE VERRE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZWNE VPSDRE POUVA FVALE VERRE KA ALGODEN DSTCNGLCH YAALG DVEGAT	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 925 AR 952 AN 948 AI 917 AE 925 AA 978 AR 925 AA 935 AA 935 AA 935 AK 926 AE 953 AA 953 AK 928 AK 928 AK 928 AE 976 AE 1002 AE 943 AK 964 AB 964 AB 974
LGTCNGLCH YAALG DPEGA REVNE PENRE PIDVYA VVAR VISILKKE A AGDEM DGTCNGLCH YAALG DPEGA REVNE PENRE PIDVYA VVAR VISILKKE A AGDEM DGTCNGLCH YAALG DPEGA REVNE SPNDRE RDVYD AVAKI VISRLE (E SAKGEV DGTCNGLCH YAALG DPEGA REVNE SPNDRE RDVYD AVAKI VISRLE HE SAKGEV DGTCNGLCH YAALG DPEGA REVNE SPNDRE RDVYD AVAKI VISRLE HE SAKGEV DGTCNGLCH YAALG DPEGA REVNE SPNDRE RDVYD AVAKI VISRLE HE SAKGEV DSTCNGLCH YAALG DVEGA REVNE SPNDRE RDVYD AVAKI VISRLE HE SAKGEV DSTCNGLCH YAALG DVEGA REVNE I PENER DDVYS RVLEI VKRVK ED ATKGHKE DSTCNGLCH YAALG DVEGA REVNE I PENER DDVYT FVANL VKRELDKE ALGOREL DSTCNGLCH YAALG DVEGA REVNE I PENER DDVYT FVANL VKRELDKE ALGOREL DSTCNGLCH YAALG DVEGA REVNE I PABRE DDVYT HVAGL VKREL BA ALGOREL DSTCNGLCH YAALG DVEGA REVNE I SPLEKE DDVYT HVAGL VKREL BA ALGOREL DSTCNGLCH YAALG DVEGA REVNE I SPLEKE DDVYT HVAGL VKREL BA ALGOREL DSTCNGLCH YAALG DVEGA REVNE I SPLEKE DDVYT HVARL VKREL BA ALGOREL DSTCNGLCH YAALG DLEGAR ZVNE I SPLEKE DDVYT HVARL VKREL BA ALGOREL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYT HVARL VKREL KKE ALGOREL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTRKER N ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTRKEL NKA ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTRELKKA ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VYRKLE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VYRKLE KA ALGODEL DSTCNGLCH YAA	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 917 AF 925 AR 952 AN 948 AI 917 AE 952 AN 953 AA 916 AI 915 AI 926 AE 953 AA 953 AA 953 AK 926 AE 960 AE 1008 AL 978 AK 920 AE 943 AK 1002 AE 943 AM 964 AM 964 AM 9643 AM 9643 AM 9643 AM 96457
LETCHSLCH YAALG DPEGA REVNE PENRE NDVYA VVAR VISILKKE A AAGDEM DETCHSLCH YAALG DPEGA REVNE PENRE NDVYA VVAR VISILKKE A AAGDEM DETCHSLCH YAALG DPEGA REVNE SPHDRE RDVYD AVAKI VISRLE HE SAKGDEM DETCHSLCH YAALG DPEGA REVNE SPHDRE RDVYD AVAKI VISRLE HE SAKGDEM DETCHSLCH YAALG DPEGA REVNE SPHDRE RDVYD AVAKI VISRLE HE SAKGDEM DETCHSLCH YAALG DPEGA REVNE SPHDRE RDVYD AVAKI VISRLE HE SAKGDEM DETCHSLCH YAALG DVEGA REVNE SPHDRE RDVYD AVAKI VISRLE HE SAKGDEM DETCHSLCH YAALG DVEGA REVNE SPHDRE RDVYD AVAKI VISRLE HE ALNGENE DSTCHSLCH YAALG DVEGA REVNE I PEGBRE POLYS RULEI VREVVE ED ATNGHKE DSTCHSLCH YAALG DVEGA REVNE I PEGBRE POLYS RULEI VREVUE ED ATNGHKE DSTCHSLCH YAALG DVEGA REVNE I PERBE POLYT FVANL VRERLDK ALEGDEL DSTCHSLCH YAALG DVEGA REVNE I PERBE POLYT FVANL VRERLDK ALEGDEL DSTCHSLCH YAALG DVEGA REVNE I SPLERE POLYT HVAGU VIRKEL AA AAKGDEM DSTCHSLCH YAALG DLEGAR REVNE SPLERE POLYT HVAGU VIRKEL AA AAKGDEM DSTCHSLCH YAALG DLEGAR REVNE SPLERE POLYT HVARL VIRKEL AS AAKGDEM DSTCHSLCH YAALG DLEGAR REVNE SPLERE POLYTA FVALL VREKSEV 200 LEAGLEE DSTCHSLCH YAALG DLEGAR REVNE VPADRE SDUYT HVALL VIRKEL NA AAKGDEE DSTCHSLCH YAALG DIEGAR REVNE VPADRE SDUYTA FVALL VIRKEL NA AAKGDEE DSTCHSLCH YAALG DIEGAR REVNE VPADRE SDUYTA FVALL VIRKEL NA AAKGDEE DSTCHSLCH YAALG DIEGAR REVNE VPADRE POLYA FVALL VIRKEL NA AAKGDEE DSTCHSLCH YAALG DIEGAR REVNE VPADRE POLYA FVALL VIRKEL NA AAKGDEE DSTCHSLCH YAALG DIEGAR REVNE VPADRE POLYA FVALL VIRKEL KA ALGGDEH DSTCHSLCH YAALG DUEGAR REVNE VPADRE POLYA FVALL VIRKEL KA ALGGDEH DSTCHSLCH YAALG DVEGAR ZEVNE VPADRE POLYA FVALL VIRKEL KA ALGGDEH DSTCHSLCH YAALG DVEGAR ZEVNE VPADRE POLYA FVALL VIRKEL KA ALGGDEH DSTCHSLCH YAALG DVEGAR ZEVNE VPADRE POLYA FVALL VIRKEL KA ALGGDEH DSTCHSLCH YAALG DVEGAR ZEVNE VPADRE POLYA FVALL VIRKEL KA ALGGDEH DSTCHSLCH YAALG DVEGAR ZEVNE VPADRE POLYA FVALL VIRKEL KA ALGGDEH DSTCHSLCH YAALG DVEGAR ZEVNE VPADRE POLYA FVALL VERLE KA ALGGDEH DSTCHSLCH YAALG DVEGAR ZEVNE VPADRE POLYA HVARL VRARLE	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 948 AI 917 AE 925 AN 952 AN 935 AA 926 AL 915 AN 925 AN 926 AL 916 AL 926 AN 953 AN 953 AN 928 AK 960 AL 976 AE 10003 AK 1002
LGTCNGLCH YAALG DPEGA REVNE PENRE PIDVYA VVAR VISILKKE A AGDEM DGTCNGLCH YAALG DPEGA REVNE PENRE PIDVYA VVAR VISILKKE A AGDEM DGTCNGLCH YAALG DPEGA REVNE SPNDRE RDVYD AVAKI VISRLE (E SAKGEV DGTCNGLCH YAALG DPEGA REVNE SPNDRE RDVYD AVAKI VISRLE HE SAKGEV DGTCNGLCH YAALG DPEGA REVNE SPNDRE RDVYD AVAKI VISRLE HE SAKGEV DGTCNGLCH YAALG DPEGA REVNE SPNDRE RDVYD AVAKI VISRLE HE SAKGEV DSTCNGLCH YAALG DVEGA REVNE SPNDRE RDVYD AVAKI VISRLE HE SAKGEV DSTCNGLCH YAALG DVEGA REVNE I PENER DDVYS RVLEI VKRVK ED ATKGHKE DSTCNGLCH YAALG DVEGA REVNE I PENER DDVYT FVANL VKRELDKE ALGOREL DSTCNGLCH YAALG DVEGA REVNE I PENER DDVYT FVANL VKRELDKE ALGOREL DSTCNGLCH YAALG DVEGA REVNE I PABRE DDVYT HVAGL VKREL BA ALGOREL DSTCNGLCH YAALG DVEGA REVNE I SPLEKE DDVYT HVAGL VKREL BA ALGOREL DSTCNGLCH YAALG DVEGA REVNE I SPLEKE DDVYT HVAGL VKREL BA ALGOREL DSTCNGLCH YAALG DVEGA REVNE I SPLEKE DDVYT HVARL VKREL BA ALGOREL DSTCNGLCH YAALG DLEGAR ZVNE I SPLEKE DDVYT HVARL VKREL BA ALGOREL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYT HVARL VKREL KKE ALGOREL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTRKER N ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTRKEL NKA ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTRELKKA ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DLEGAR ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEL DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VTERLE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VYRKLE KA ALGODEN DSTCNGLCH YAALG DVEGAT ZVNE VPADRE PDVYA FVARL VYRKLE KA ALGODEL DSTCNGLCH YAA	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 917 AL 948 AI 917 AE 925 AN 978 AL 915 AL 915 AL 953 AA 953 AL 978 AL 903 AL 978 AL 978 AL 976 AL 902 AL 964 AL 964 AQ 957
DETCINGLON YAALGG DPEGA RUVNL PPSNR PNDVYA AVAAR VISILKKE A AAGDEM DETCINGLON YAALG DDEGA RUVNL SPNDR RUVVD AVAKI VISILKKE A AAGDEM GETCINGLON YAALG PDGA RUVNL SPNDR RUVVD AVAKI VISILE HE SAKGGOEM DETCINGLON YAALG DDEGA RUVNL SPNDR RUVVD AVAKI VISILE HE SAKGGOEM DETCINGLON YAALG DDEGA RUVNL SPNDR RUVVD AVAKI VISILE HE SAKGGOEM DETCINGLON YAALG DDEGA RUVNL SPNDR RUVVD AVAKI VISILE HE SAKGGOEM DETCINGLON YAALG DVEGA RUVNL VPSNR DOVYS RULEI VRUVVR ED A TNGHKE DETCINGLON YAALG DVEGA RUVNL VPSNR DOVYS RULEI VRURVKE DD A TNGHKE DETCINGLON YAALG DVEGA RUVNL VPSNR DOVYS RULEI VRURVKE DD A TNGHKE DETCINGLON YAALG DVEGA RUVNL VPSNR DOVYT FVANI VRARINND FENGNET DETCINGLON YAALG DVEGA RUVNL SPSNR DOVYT FVANI VRARINND FENGNET DETCINGLON YAALG DVEGA RUVNL SPSNR DOVYT FVANI VRARINND ALGODEL DETCINGLON YAALG DVEGA RUVNL SPSNR DOVYT FVANI VRARILE AA AARGOEM DETCINGLON YAALG DLEGA RUVNL SPLEKP DOVYT FVANI VRARILE AA AARGOEM DETCINGLON YAALG DLEGA RUVNL SPLEKP DOVYT FVANI VRARILE AA AARGOEM DETCINGLON YAALG DLEGA RUVNL SPLEKP DOVYA FVARL VRARILE AA AARGOEM DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIRKEL AS AARGOEM DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIRKEL NA AARGOER DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIRKEL NA AARGOER DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIRELIK A ALGODES DESCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIERLIK A ALGODES DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIERLIK A ALGODES DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIERLIK A ALGODES DETCINGLON YAALG DUEGA RUVNL VPSDR POUVA FVARL VIERLIK A ALGODES DETCINGLON YAALG DUEGA RUVNL VPSDR POUVA FVARL VIERLIK EA ALGODES DETCINGLON YAALG DUEGA RUVNL VPSDR POUVA FVARL VIERLIK EA ALGODES DETCINGLON YAALG DUEGA RUVNL VPSDR POUVA FVARL VIERLE KA ALGODES DETCINGLON YAALG DVEGA TUVNL VPSDR POUVA HVARL VIRKEL EA ALGODES DETCINGLON YAALG DUEGA TUVNL VPSDR POUVA HVARL VIRKEL EA ALGODES DETCINGLON YAALG DUEGA TUVNL VPSDR POUVA HVARL VIRKEL EA A	AE 885 AN 878 AS 892 AS 891 AK 973 AK 743 AA 948 AI 917 AE 925 AN 957 AA 948 AI 917 AE 925 AN 957 AA 948 AI 917 AE 952 AN 957 AA 953 AA 953 AK 928 AK 928 AK 928 AK 900 AE 1002 AE 1002 AE 1002 AF 943 AM 9443 AM 9443 AM 9464 AE 976 AI 9663 AV 960
LGTCNGLCH YAALG DPEGA REVNE PENRE NUVYAVARUS ILKKE AAGDEM DGTCNGLCH YAALG DPEGA REVNE PENRE NUVYAVARUS INGELKKE AAGDEM DGTCNGLCH YAALG NEDGA REVNE SPHDRE NUVYAVARUS INSELE (E SAKGDEV DGTCNGLCH YAALG NEDGA REVNE SPHDRE NUVYAVARUS INSELE (E SAKGDEV DGTCNGLCH YAALG NEDGA REVNE SPHDRE NUVYAVARUS INSELE (F SAKGDEV DGTCNGLCH YAALG NEGA REVNE PENDER DUVYA VARUS INSELE (F SAKGDEV DGTCNGLCH YAALG DVEGA REVNE SPHDRE NUVYAVARUS INSELE (F SAKGDEV DGTCNGLCH YAALG DVEGA REVNE I PENDER DUVY SVLEI VURVE ED ATKGHEV DGTCNGLCH YAALG DVEGA REVNE I PENDER DUVY FVANE VERALTDEK ALRGDEL DGTCNGLCH YAALG DVEGA REVNE I PENDER DUVYT FVANE VERALTDEK ALRGDEN DGTCNGLCH YAALG DVEGA REVNE I PADREP QUVYT FVANE VERALTDEK ALRGDEN DGTCNGLCH YAALG DVEGA REVNE I SPELER POUVT FVANE VERKEL AA AANGDEN DGTCNGLCH YAALG DVEGA REVNE SPELER POUVA FVALE VERKELAS ANGDEN DGTCNGLCH YAALG DEGA REVNE SPELER POUVA FVALE VERKELAS ANGDEN DGTCNGLCH YAALG DIEGAREVNE VERDER DUVY HVAGL VERKEL EA AANGDEN DGTCNGLCH YAALG DIEGAREVNE VERDER DUVYA FVALE VERKELAS	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 917 AL 948 AI 925 AR 952 AN 948 AI 915 AI 916 AI 915 AI 926 AP 953 AA 953 AA 953 AK 926 AP 953 AK 953 AK 926 AF 910 AL 978 AK 928 AK 928 AK 926 AE 1002 AK 1002 AK 1002 AK 964 AD 957
DETCINGLON YAALGG DPEGA RUVNL PPSNR PNDVYA AVAAR VISILKKE A AAGDEM DETCINGLON YAALG DDEGA RUVNL SPNDR RUVVD AVAKI VISILKKE A AAGDEM GETCINGLON YAALG PDGA RUVNL SPNDR RUVVD AVAKI VISILE HE SAKGGOEM DETCINGLON YAALG DDEGA RUVNL SPNDR RUVVD AVAKI VISILE HE SAKGGOEM DETCINGLON YAALG DDEGA RUVNL SPNDR RUVVD AVAKI VISILE HE SAKGGOEM DETCINGLON YAALG DDEGA RUVNL SPNDR RUVVD AVAKI VISILE HE SAKGGOEM DETCINGLON YAALG DVEGA RUVNL VPSNR DOVYS RULEI VRUVVR ED A TNGHKE DETCINGLON YAALG DVEGA RUVNL VPSNR DOVYS RULEI VRURVKE DD A TNGHKE DETCINGLON YAALG DVEGA RUVNL VPSNR DOVYS RULEI VRURVKE DD A TNGHKE DETCINGLON YAALG DVEGA RUVNL VPSNR DOVYT FVANI VRARINND FENGNET DETCINGLON YAALG DVEGA RUVNL SPSNR DOVYT FVANI VRARINND FENGNET DETCINGLON YAALG DVEGA RUVNL SPSNR DOVYT FVANI VRARINND ALGODEL DETCINGLON YAALG DVEGA RUVNL SPSNR DOVYT FVANI VRARILE AA AARGOEM DETCINGLON YAALG DLEGA RUVNL SPLEKP DOVYT FVANL VRARILE AA AARGOEM DETCINGLON YAALG DLEGA RUVNL SPLEKP DOVYT FVANL VRARILE AA AARGOEM DETCINGLON YAALG DLEGA RUVNL SPLEKP DOVYA FVARL VRARIL SF DDMM DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIRKEL NA AARGOER DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIRKEL NA AARGOER DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIRKEL NA AARGOER DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIERLIK AA ALGODES DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIERLIK AA ALGODES DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIERLIK AA ALGODES DETCINGLON YAALG DLEGA RUVNL VPSDR POUVA FVARL VIERLIK AA ALGODES DETCINGLON YAALG DUEGA RUVNL VPSDR POUVA FVARL VIERLIK AA ALGODES DETCINGLON YAALG DVEGA RUVNL VPSDR POUVA FVARL VIERLIK AA ALGODES DETCINGLON YAALG DVEGA RUVNL VPSDR POUVA FVARL VIERLIK EA ALGODES DETCINGLON YAALG DVEGA RUVNL VPSDR POUVA FVARL VIERLE KA ALGODES DETCINGLON YAALG DVEGA RUVNL VPSDR POUVA HVARL VIRKEL EA ALGODES DETCINGLON YAALG DVEGA RUVNL VPSDR POUVA HVARL VIRKEL EA ALGODES DETCINGLON YAALG DVEGA RUVNL VPSDR POUVA HVARL VIRKLE F	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 948 AI 917 AE 925 AN 952 AN 935 AA 926 AL 915 AN 925 AN 926 AL 916 AL 916 AL 953 AA 953 AK 927 AK 928 AK 937 AK 928 AK 960 AL 976 AE 10003 AK 1002 AE 974 AM 943 AM 9443 AM 943 AQ 957 AV 935
LGTCNGLCH YAALG DPEGA REVNE PENRE PIDVYA VVAR VISILKKE A AGDEM DGTCNGLQH YAALG DPEGA REVNE SPHDRE RDVVD AVAKI VISILKKE A EAGDEM GTCNGLQH YAALG DPEGA REVNE SPHDRE RDVVD AVAKI VISILE HE SMGGDEM GTCNGLQH YAALG DPEGA REVNE SPHDRE RDVVD AVAKI VISILE HE SMGGDEM GTCNGLQH YAALG DPEGA REVNE SPHDRE RDVVD AVAKI VISILE HE SMGGDEM GTCNGLQH YAALG DVEGA REVNE SPHDRE RDVVD AVAKI VISILE HE SMGGDEM GTCNGLQH YAALG DVEGA REVNE SPHDRE RDVVD AVAKI VISILE HE SMGGDEM GTCNGLQH YAALG DVEGA REVNE SPHDRE RDVVD YND YND YND YND YND AENGHEV GSCNGLQH YAALG DVEGA REVNE I PSDRE QDVYT FVANL VKREILDKE ALEGDEL GTCNGLQH YAALG DVEGA TEVNE JPSDRE QDVYT FVANL VKREILDKE ALEGDEN GTCNGLQH YAALG DVEGA TEVNE JPSDRE QDVYT FVANL VKREIL AA AARGDEM GTCNGLQH YAALG DEGAR ZWNE JPSDRE QDVYT HVAGU VFRALK EA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE JPSDRE PQUVYT FVANL VKRELL AA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE JPSDRE PQUVYA FVALE VKRELA AS AARGDEM GTCNGLQH YAALG DLEGAR ZWNE JPSDRE PQUVYA FVALE VKRELA AS AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KE AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM DFTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODE	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 925 AR 952 AN 948 AI 917 AE 925 AR 925 AA 935 AA 935 AA 935 AA 926 AK 926 AE 953 AA 953 AA 953 AK 928 AK 980 AE 1008 AE 1002 AE 1002 AE 943 AM 964 AE 974 AI 960 AI 963 AV 935 AV 935
LICHNICLE YAALG DEGA REVNE PENRE NUVYA VAAR UTSILKKE AAAGDEM DITCNGLQH YAALG DEGA REVNE SPHDRE KDVYD AVAKI VISULE (E SAKGDEV DITCNGLQH YAALG DEGA REVNE SPHDRE KDVYD AVAKI VISULE (E SAKGDEV DITCNGLQH YAALG DEGA REVNE SPHDRE KDVYD AVAKI VISULE (E SAKGDEV DITCNGLQH YAALG DEGA REVNE SPHDRE KDVYD AVAKI VISULE (E SAKGDEV DITCNGLQH YAALG DEGA REVNE SPHDRE KDVYD AVAKI VISULE (E SAKGDEV DITCNGLQH YAALG DEGA REVNE SPHDRE KDVYD AVAKI VISULE (E SAKGDEV DITCNGLQH YAALG DEGA REVNE SPHDRE KDVYD AVAKI VISULE (E SAKGDEV DITCNGLQH YAALG DEGA REVNE I SPHDRE KDVYD YVLE I VKRUE ED ATKGHKE DITCNGLQH YAALG DVEGA REVNE I SPHDRE KDUYT FVANL VKREIDKI ALGGDEL DITCNGLQH YAALG DVEGA REVNE I SPHDRE KDUYT HVAGL VKREIDKI ALGGDEN DITCNGLQH YAALG DVEGA REVNE I SPHERE KDUYT HVAGL VKREIDKI ALGGDEN DITCNGLQH YAALG DVEGA REVNE I SPHERE KDUYT HVAL VKREIDKI ALGGDEN DITCNGLQH YAALG DEGA REVNE SPHERE KDUYT HVAL VKREIL AA AANGDEN DITCNGLQH YAALG DEGA REVNE SPHERE KDUYT HVAL VKREIL AA ALGGDEN DITCNGLQH YAALG DIEGAR ZVNE VPADRE PDUYA FVAL VKREIL AA ALGGDEN DITCNGLQH YAALG DIEGAR ZVNE VPADRE PDUYA FVAL VKREIN S DEDME DITCNGLQH YAALG DIEGAR ZVNE VPADRE PDUYA FVAL VKREIN S ALGGDEN DITCNGLQH YAALG DIEGAR ZVNE VPADRE PDUYA FVAL VKREIN S ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DIEGAR ZVNE VPBDRE QDUYA FVAL VTERLE KA ALGGDER DITCNGLQH YAALG DEGAR ZVNE VPBDRE QDUYA FVAL	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 973 AK 917 AL 948 AI 917 AR 925 AN 957 AL 935 AA 948 AI 916 AL 915 AL 915 AL 953 AA 953 AA 953 AL 956 AL 956 AL 976 AK 980 AL 976 AL 964 AL 964 AL 963 AV 963 AV 963 AV 963 AV 963
LGTCNGLCH YAALG DPEGA REVNE PENRE PIDVYA VVAR VISILKKE A AGDEM DGTCNGLQH YAALG DPEGA REVNE SPHDRE RDVVD AVAKI VISILKKE A EAGDEM GTCNGLQH YAALG DPEGA REVNE SPHDRE RDVVD AVAKI VISILE HE SMGGDEM GTCNGLQH YAALG DPEGA REVNE SPHDRE RDVVD AVAKI VISILE HE SMGGDEM GTCNGLQH YAALG DPEGA REVNE SPHDRE RDVVD AVAKI VISILE HE SMGGDEM GTCNGLQH YAALG DVEGA REVNE SPHDRE RDVVD AVAKI VISILE HE SMGGDEM GTCNGLQH YAALG DVEGA REVNE SPHDRE RDVVD AVAKI VISILE HE SMGGDEM GTCNGLQH YAALG DVEGA REVNE SPHDRE RDVVD YND YND YND YND YND AENGHEV GSCNGLQH YAALG DVEGA REVNE I PSDRE QDVYT FVANL VKREILDKE ALEGDEL GTCNGLQH YAALG DVEGA TEVNE JPSDRE QDVYT FVANL VKREILDKE ALEGDEN GTCNGLQH YAALG DVEGA TEVNE JPSDRE QDVYT FVANL VKREIL AA AARGDEM GTCNGLQH YAALG DEGAR ZWNE JPSDRE QDVYT HVAGU VFRALK EA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE JPSDRE PQUVYT FVANL VKRELL AA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE JPSDRE PQUVYA FVALE VKRELA AS AARGDEM GTCNGLQH YAALG DLEGAR ZWNE JPSDRE PQUVYA FVALE VKRELA AS AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KE AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA AARGDEM GTCNGLQH YAALG DLEGAR ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM GTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODM DFTCNGLQH YAALG DVEGAT ZWNE VPSDRE PQUVA FVALE VFRELK KA ALEGODE	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 973 AK 925 AA 948 AI 925 AA 948 AI 925 AA 948 AI 925 AA 935 AA 935 AA 948 AI 926 AE 953 AA 953 AA 953 AK 953 AK 960 AE 1008 AL 976 AE 1002 AK 1002 AK 960 AL 963 AV 963 AV 963 AV 964
LGTCNGLCH YAALG DPEGA REVNE PSNRP NDVYA VAAR VISILKE — AAGDEM DGTCNGLCH YAALG DPEGA REVNI SPNDRP RDVYD AVAKI VISRLE (R— AAGDEM DGTCNGLCH YAALG NDPGA REVNI SPNDRP RDVYD AVAKI VISRLE (R— SAKGDEV DGTCNGLCH YAALG NDPGA REVNI SPNDRP RDVYD AVAKI VISRLE (R— SAKGDEV DGTCNGLCH YAALG NDFGA REVNI SPNDRP RDVYD AVAKI VISRLE (R— SAKGDEV DGTCNGLCH YAALG DVEGA REVNI SPNDRP RDVYD AVAKI VISRLE (R— SAKGDEV DSTCNGLCH YAALG DVEGA REVNI PSNRP QDVYT RVARI VNBARINDFF PSNRFF DSTCNGLCH YAALG DVEGA REVNI IPSNRP QDVYT FVANL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DVEGA REVNI IPSNRP QDVYT HVAGL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DVEGA REVNI IPSNRP QDVYT HVAGL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DVEGA REVNI SPLKRP QDVYT HVAGL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DVEGA REVNI SPLKRP QDVYT HVAGL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DVEGA REVNI SPLKRP QDVYT HVAGL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DLEGAREVNI SPLKRP QDVYT HVAGL VKRLIZAS — DDPM DSTCNGLCH YAALG DLEGAREVNI SPLKRP QDVYT HVARL VKRLIZAS — DDPM DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VKRLIZAS — DDAM DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VKRLIZAS — AANGDEN DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VTRELK NA — AAAGDEE DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VTRELKA — ALGGDEI DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VTRELKA — ALGGDEN DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VTRELK KA — ALGGDEN DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VTRELK KA — ALGGDEN DSTCNGLCH YAALG DVEGATEVNI VPSDRP QDVYA FVARL VTRELK KA — ALGGDEN DSTCNGLCH YAALG DVEGATEVNI VPSDRP QDVYA FVARL VTRELK KA — ALGGDEN DSTCNGLCH YAALG DVEGATEVNI VPSDRP QDVYA FVARL VTRELK KA — ALGGDEN DSTCNGLCH YAALG DVEGATEVNI VPSDRP QDVYA FVARL VVARLE KA — ALGGDEN DSTCNGLCH YAALG DVEGATEVNI VPSDRP QDVYA FVARL VVARLE KA — ALGGDEN DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VVARLE KA — ALGGDEN	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 973 AK 973 AK 925 AA 948 AI 925 AA 978 AR 952 AA 978 AA 935 AA 916 AI 915 AI 926 AE 953 AA 953 AA 953 AK 926 AE 908 AE 900 AE 1008 AI 926 AE 1002 AK 902 AK 1002 AK 902 AI 963 AV 909 AI 964
LGTCNGLCH YAALG DPEGA RYNL PPBNR PNDYYA VVAR VISILKKE A AGDEM GTCNGLCH YAALG DPEGA RYNL PPBNR PNDY AVARI VIGFLKKD A EAGDEM GTCNGLCH YAALG PDGA RYNL SPNDR FNDYD AVARI VISRLE HE SAKGDEM GTCNGLCH YAALG DPEGA RYNL SPNDR FNDYD AVARI VISRLE HE SAKGDEM GTCNGLCH YAALG DPEGA RYNL SPNDR FNDYD AVARI VISRLE HE SAKGDEM GTCNGLCH YAALG DIEGA RYNL PPBNR PDYD AVARI VISRLE HE SAKGDEM GTCNGLCH YAALG DVEGA RYNL IPBCRP QDYY SVLEI VWRVYE ED ATNGHKE GTCNGLCH YAALG DVEGA RYNL IPBCRP QDYY FVANL VRARIND FENGNET GTCNGLCH YAALG DVEGA RYNL IPBCRP QDYT FVANL VRARIND FENGNET GTCNGLCH YAALG DVEGA RYNL IPBCRP QDYT FVANL VRARILE AA AAKGDEM GTCNGLCH YAALG DVEGA RYNL IPBCRP QDYT HVAG VIKALE AA AAKGDEM GTCNGLCH YAALG DEGAR YNL IPBCRP QDYT HVAG VIKALE AA AAKGDEM GTCNGLCH YAALG DLEGAR YNL SPLKFP QDYT HVAG VIKKLE AA AAKGDEM GTCNGLCH YAALG DLEGAR YNL YBDRP QDYTA FVAL VKRLLAS AANGDEN GTCNGLCH YAALG DLEGAR YNL YBDRP QDYYA FVAL VKRLLAS AAKGDEM GTCNGLCH YAALG DLEGAR YNL YBDRP QDYYA FVAL VKRLLAS AAKGDEM GTCNGLCH YAALG DLEGAR YNL YBDRP QDYYA FVAL VIKKLI NS AAKGDEM GTCNGLCH YAALG DLEGAR YNL YBDRP QDYYA FVAL VIKKLI NS AAKGDEM GTCNGLCH YAALG DLEGAR YNL YBDRP QDYYA FVAL VIKKLI NS AAKGDEM GTCNGLCH YAALG DLEGAR YNL YBDRP QDYYA FVAL VIKKLI NS AAKGDEM GTCNGLCH YAALG DLEGAR YNL YBDRP QDYYA FVAL VIKKLI KA ALAGDES GSCNGLCH YAALG DLEGAR YNL YBDRP QDYYA FVAL VIKRLI KA ALAGDEM GTCNGLCH YAALG DLEGAR YNL YBDRP QDYYA FVAL VIKRLI KA ALAGDEM GTCNGLCH YAALG DUEGAR YNL YBDRP QDYYA FVAL VIKRLI KA ALAGDEM GTCNGLCH YAALG DUEGAR YNL YBDRP QDYYA FVAL VIKRLI KA ALAGDEM GTCNGLCH YAALG DUEGAR YNL YBDRP QDYYA FVAL VIKRLI KA ALAGDEM GTCNGLCH YAALG DUEGAR YNL YBDRP QDYYA FVAL VIKRLI KA ALAGDEM GTCNGLCH YAALG DVEGAR YNL YBDRP QDYYA FVAL VIKRLI KA ALAGDEM GTCNGLCH YAALG DVEGAR YNL YBDRP QDYYA FVAL VIKRLE KA ALAGDEM GTCNGLCH YAALG DVEGAR YNL YBDRP QDYYA FVAL VIKRLE KA ALAGDEM GTCNGLCH YAALG DVEGAR YNL YBDRP QDYYA HVAL VIKRLE KA ALAGDEM DTCNGLCH YAALG DVEGAR YNL YBDRP QDYYA HVAL VI	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 948 AI 917 AE 925 AN 957 AR 952 AN 935 AA 948 AI 917 AE 925 AN 935 AA 935 AA 916 AL 915 AL 953 AK 926 AE 900 AL 976 AE 10003 AK 1002 AE 974 AI 968 AQ 957 AI 960 AI 960 AI 961 AI 962 AV 935
LGTCNGLCH YAALG DPEGA REVNE PSNRP NDVYA VAAR VISILKE — AAGDEM DGTCNGLCH YAALG DPEGA REVNI SPNDRP RDVYD AVAKI VISRLE (R— AAGDEM DGTCNGLCH YAALG NDPGA REVNI SPNDRP RDVYD AVAKI VISRLE (R— SAKGDEV DGTCNGLCH YAALG NDPGA REVNI SPNDRP RDVYD AVAKI VISRLE (R— SAKGDEV DGTCNGLCH YAALG NDFGA REVNI SPNDRP RDVYD AVAKI VISRLE (R— SAKGDEV DGTCNGLCH YAALG DVEGA REVNI SPNDRP RDVYD AVAKI VISRLE (R— SAKGDEV DSTCNGLCH YAALG DVEGA REVNI PSNRP QDVYT RVARI VNBARINDFF PSNRFF DSTCNGLCH YAALG DVEGA REVNI IPSNRP QDVYT FVANL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DVEGA REVNI IPSNRP QDVYT HVAGL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DVEGA REVNI IPSNRP QDVYT HVAGL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DVEGA REVNI SPLKRP QDVYT HVAGL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DVEGA REVNI SPLKRP QDVYT HVAGL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DVEGA REVNI SPLKRP QDVYT HVAGL VKRLIDKI — ALGGDEI DSTCNGLCH YAALG DLEGAREVNI SPLKRP QDVYT HVAGL VKRLIZAS — DDPM DSTCNGLCH YAALG DLEGAREVNI SPLKRP QDVYT HVARL VKRLIZAS — DDPM DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VKRLIZAS — DDAM DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VKRLIZAS — AANGDEN DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VTRELK NA — AAAGDEE DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VTRELKA — ALGGDEI DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VTRELKA — ALGGDEN DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VTRELK KA — ALGGDEN DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VTRELK KA — ALGGDEN DSTCNGLCH YAALG DVEGATEVNI VPSDRP QDVYA FVARL VTRELK KA — ALGGDEN DSTCNGLCH YAALG DVEGATEVNI VPSDRP QDVYA FVARL VTRELK KA — ALGGDEN DSTCNGLCH YAALG DVEGATEVNI VPSDRP QDVYA FVARL VTRELK KA — ALGGDEN DSTCNGLCH YAALG DVEGATEVNI VPSDRP QDVYA FVARL VVARLE KA — ALGGDEN DSTCNGLCH YAALG DVEGATEVNI VPSDRP QDVYA FVARL VVARLE KA — ALGGDEN DSTCNGLCH YAALG DLEGAREVNI VPSDRP QDVYA FVARL VVARLE KA — ALGGDEN	AE 885 AN 878 AS 892 AS 891 AK 973 AK 973 AK 973 AK 948 AI 917 AE 925 AN 957 AR 952 AN 935 AA 948 AI 917 AE 925 AN 935 AA 935 AA 916 AL 915 AL 953 AK 926 AE 900 AL 976 AE 10003 AK 1002 AE 974 AI 968 AQ 957 AI 960 AI 960 AI 961 AI 962 AV 935

	_					
tr B6K333 B6K333_SCHJY					YVGARAQIEKQLKLQEDIP-KDLLRDASAFLAKRVFQ YVGARKQISEKLENIDGME-KLKVADYANYLTKKVFE	944 × 937
sp 013993 RPOM_SCHP0 tx 39Q0Q8 39Q0Q8_SCH0Y	VLKDKVL				TYVGARNQI SERLENIDGME-KLKVADIAN ILIKKVFE TYVGARNQI ISQLEKRGDI P-KDMLNNYSS YLTKMVFR	951
tr S9X2W4 S9X2W4 SCHCR	ALKDRID	RSVV	RETVMIN	Y GV	YVGAKNQI ISQLE KRGDI P-KDMLNNYSS YLTKMV FR	950
tr A0A1E303C6 A0A1E303C6_LIPST	ILVGKV		KQ SVMTN	YGV	YYI GARAQI LGQLK DTKQI D-ERDL WRCAA YLTTLV FK	1032
tr A0A167E4J0 A0A167E4J0_9ASCO tr A0A1E3PUP0 A0A1E3PUP0_9ASCO	MAVDKL LIKDHIB				FFV GARQQI SNRLS DA-GLE-QEHL YSTAG YLAKTV LG FFI GARAOI AKOIK DLPHI G-PENI FIVAS YLTINV FA	801 1007
tr A0A0H5C7R0 A0A0H5C7R0 CYBJA		REV			TYIGARAQIA KQIK DLPHIG-PLNIFIVASILIINVFA TYIGATAOIDKOLA DVFPGE-DTYKYSL YLTKHVFA	974
tr AOA1E 3P5W0 AOA1E3P5W0 WICAO	TLEDEI	RKVV	ROTVMIN	YGV	YIGATHQIHKQLQDVFDDT-ESYKLSTYLAKHVFA	982
tr KOKTX3 KOKTX3 WICCF	MLKDNIK				QVGATNQIHKQLQNVFSED-QSYKLSVYLTKVVFA	1009
tr W6MIL2 W6MIL2_9ASCO	ILKDLIA KIIPILK	I			YMGASQQI ARRLE DLGFSKDDAKLHSR YLARRV FD YI GGAEQI KKOLD AHFDD K-EAYALSR FLATHT FA	1015 992
tr A0A1E3QPI7 A0A1E3QPI7_9A5C0 tr A0A1D2V948 A0A1D2V948 9A5C0	LVQHSIK				TYLGAEQI KKQLDAHFDDK-EAYALSKFLATHTFA TYLGATQQI AKQLT DEFGKD-TAYFLSKYLAVHVFA	1035
tr A0A1B7SME0 A0A1B7SME0 9ASCO	LVKDVI				YVGARAQITKRLKDIEFDEKYMSMSSKYLTQKVFK	683
tr Q6CRZ5 Q6CRZ5_KLULA					FVGAADQIMKELDQYFDKPEESNELSRYLAKHVFA	974
tr WOTGI 8 WOTGI 8 KLUMA					FVGAADQIMKELDGYFDN PEESNELSR YLAKHVFA	973
tr A0A109UWS1 A0A109UWS1_9SACH tr G8JMS2 G8JMS2 ERECY					FFIGAAAQIDKELQDELPEDADCYALSRYLARHVFA FFVGASQQIDKELREAFPDKNESYDMARYLTRHVFA	984 1014
tr Q75BP7 Q75BP7 A3HGO					FIGATNQIDKELQDAFPDNSYDMARYLTKHVFN	1009
tr R9XDF 6 R9XDF6 A SHAC			KRTVMTN	Y GV	FIGATNQIDKELQDAFPDNSYDMARYLTKHVFD	1009
tr H2ASJ8 H2ASJ8_KAZAF	FLVDKL				LLGATLQIDKQLNDLFDDSSDSMKYSKYLARHVFA	995
tr J757Y3 J757Y3_KAZNA tr G0VD0 1 G0VD01 NAUCC	FLVDKLN ILVDKIS				LVGATLQIDKQIGDYFSDHRESLKYSKYLAKHVFA YVGATFQIEKQLSKFFPDRKECFDLSKYLTSHVFA	986 1038
tr GOWE72 GOWE72_NAUDC	LLVDKIT				TYVGATFQIEKQLSKFFFDRKECF-DLSKFLISHVFA	1066
tr Q6FLX9 Q6FLX9 CANGA	ILKGKV				YVGATFOIAKOLTAIFDDRAYSLELSKYLAKHVFA	1036
tr G8B354 G8B354_TETPH	VLQDKI				YVGATFQIDKQLSDVFENRNQSLELSKYLTRHVFM	1034
tr A0A0L8RKW5 A0A0L8RKW5_SACEU	ILKDKI				YVGATFQIAKQLSPIFDDRKESL-DFSKYLTKHVFG	1061
tr A0A0L8VRU3 A0A0L8VRU3_9SACH tr J8PP58 J8PP58 SACAR	ILKDKIT				YV GATFQI AKQLS PIFDDRKESL DFSK YLTKHV FS YV GATFQI AKQLS PIFDDRKESL DFSK YLTKHV FG	1060 1060
tr A0A0C7MY71 A0A0C7MY71 95ACH	LLETMIN				YIGATHQIEKQLSNVFDDYKRSYEMSKYLTKHVFA	1006
tr C5DNP3 C5DNP3_LACTC	LLEDRI				YYI GATHQI DKOLSTLFNDHKRSYELSK YLTKHV FA	1001
tr C5DX79 C5DX79_ZYGRC	ILKDKI				YVGATFQIDKQLSNIFEDRKYSLELSKYLTKHVFG	1022
tr G8ZR00 G8ZR00_TORDC tr A0A1E4RQF7 A0A1E4RQF7 9ASCO	TLKDKIT				YVGATFQIEKQLSHIFDDRTYSLELSK YLTKHVFA FVGALAQIKKQVIHHFGK DEDEKAKKFTK YLTSLVFD	1032
tr AOALOP4K6 AOALOP4K6 ASCO	FLRGKIT				TYVGALAQI KKQVI HHYGKDEDEKAKKYIK YLISLVYD TYVGAVAQI EKQIA SLFKGEPSDKL SIYSR YLTTHVFA	1028
tr A0A1A0HGT7 A0A1A0HGT7 9ASCO	FLKGKI				FV GAVAQIEKQLS GLFGK DDYATV QKHSR YLTSLV FA	1020
tr C4Y8E3 C4Y8E3_CLAL4	FLQGKI				FVGAVAQIEKQLGHLFEKDDYDSVTLYARYLTSLVFA	1023
tr G3B4C1 G3B4C1_CANTC	FLKDKIN				FV GAREQIKKQLKVHFDS DSEENS GEYAQYLTQHV FA	995
tr A3LX46 A3LX46_PICST tr A0A1E45MT6 A0A1E45MT6 9A5C0	FLODKIT				FVGATAQIKKQIDQYF3GEEDVADYAR YLTMHVFN FVGAAAQIKKQLDHHFTKDMEEDVVDYAR YLTLHVFA	967 970
tr A5DN8 2 A5DN82 PICGU	FLRDKIT				FVGAVAQIQKQIDQYFSKEDQDKVADYSRYLTMLVFA	1015
tr B5RTF6 B5RTF6 DEBHA	FLQDKI		KOTVMIN	YGV	FVGAVLQIQKQIDHYFDKNDTENVDEYARYLTAHVFA	1024
tr G3AEY0 G3AEY0_SPAPN					YYI GALAQVRKQLE DYFPDNQRDSL QEHAR YLTTHVFA	1005
tr G8B7X1 G8B7X1_CANPC	FFKDKIT FFKDKIK				FFV GALAQI KKQVA QHFGD EHDAH IYTK YLTKQV FA FFV GALAQI KKQVA QHFGE DQDAH IYTK YLTKQV FA	1007 1006
tr H8X1L6 H8X1L6_CANO9 tr B9W6L5 B9W6L5_CANDC	FLODKIK				FVGALAQI KKQVAQAFGLDQDAAIIIK ILIKQVFA	1016
tr C4YFJ1 C4YFJ1 CANAW	FLODKIK				FIGAIEOIRKOIIHLFPKDADHHAAARYLAVOVFA	996
tr C5ME71 C5ME71_CANTT	LLQNEI				FVGAIQQIKKQISHLVPEDNSAHLYARYLANQVFI	1011
tr M3IK19 M3IK19_CANMX	FLQDKIK				FVGAIQQIKKQVSQHFGDNDNEHLYAKYLASQVFA :*. *: .:	1013 X
tr B6K333 B6K333_3CHJY sp 013993 RFOM SCHF0					IAH SVPEEALKQKELDKMTAVVWTTPLN ITH SLPADY IKEGIK DELTPVVWTTLLN	994 987
tr 390008 390008_3CHOY	ALRSLFE	RAHE		SYL	ISNSLPAEFVKQGHKDKLTPTIWTTPLG	1001
tr 39X2W4 39X2W4 SCHCR						2002
					ISN SLPARY IEEGHKDKLTPTIWTTPLG	1000
tr A0A1E303C6 A0A1E303C6_LIPST	VVRN LFN	GAHL	IQDWLAEC	AKR	ISKSVPPTVHSDLKPNSSMTSVIWTTPLG	
tr A0A1E3Q3C6 A0Ā1E3Q3C6_LIPST tr A0A167E4J0 A0A167E4J0_9ASCO tr A0A1E3PUP0 A0A1E3PUP0_9ASCO	VVRNLFN AVRSLFE AVRSLFH	GAHL GAHL AAHL	.IQDW LAEC .IQDW LGDN .IQDW LGEC	'AKR IATR 'AKM	ISK SVPPTVHSDLKPN SSMTS VIWITPLG ISR SVRLDMGSMAT KSSKNGNRPEFMSS VIWITPLG ISK AVRIDI INRVAKNGNRPDFMSS VIWITPLG	1000 1083 859 1062
tr AOA1E3Q3C6 AOA1E3Q3C6_LIP5T tr AOA167E4J0 AOA167E4J0_9A5C0 tr AOA1E3PUP0 AOA1E3PUP0_9A5C0 tr AOA1E3PUP0 AOA1E3PUP0_9A5C0 tr AOA045C7R0 AOA045C7R0_CYBJA	VVRNLFN AVRSLFE AVRSLFH CIRELFE	GAHL GAHL AAHL GAHL	IQDW LAEC IQDW LGDN IQDW LGEC IQDW LAEC	AKR IATR AKM AKM	ISKSVPPTVHSDLKPNSSMTSVIWTTPLG ISRSVALDMGSMATKSSKNGNRPEPMSSVIWTTPLG ISRAVRIDITNRVARNGNRPDPMSSVIWTTPLG ISRSVRIDMDADEVIRS-GEKPPHMASTIWTTPLN	1000 1083 859 1062 1030
tr ADALE 302C6 ADALE 302C6 _ LIPST tr ADALE 302C6 ADAL 67E470 _ DASCO tr ADALE 3PUPO ADALE 3PUPO _ DASCO tr ADALE 3PUPO ADALE 3PUPO _ TOAD tr ADALE 3PSWO ADALE 3PSWO _ MICAO	VVRNLFN AVRSLFE AVRSLFH CIRELFE CMRELFE	GAHL GAHL AAHL GAHL GAHL	IQDW LAEC IQDW LGDN IQDW LGEC IQDW LALC IQDW LALC	'AKR IATR 'AKM 'AKM 'AKM	ISK SVPFTVH3DLKEN SSMTSVIWIT PLG ISR SVRLMGSMAR KSSNGNRP EMSSVIWIT PLG ISK AVRIDITNRVAKNGNRP DEMSSVIWIT PLG ISH SVRIMDA DEVIR 3-GEKP FIMASIWIT PLM ISR SIR IDVDI YEVINQ-KNRP AFMASVIWIT PLM	1000 1083 859 1062
tr ADALE 302C6 ADALE 302C6 _ LIPST tr ADALE 302C6 ADAL 678470 _ DASCO tr ADALE 3PUPO ADALE 3PUPO _ DASCO tr ADALE 3PUPO ADALE 3PUPO _ DASCO tr ADALE 3PSWO ADALE 3PSWO _ MICAO tr KOKTX3 KOKTX3 _ MICCF tr W6KIX2 KOKTX3 _ MICCF	VVRNLFN AVR3LFE AVR3LFH CIRELFE CMRELFE SMRELFE AVRQLFH	GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQDW LAEC IQDW LGDW IQDW LGEC IQDW LAEC IQDW LAEC IQDW LAEC IQDW LAEC	AKR IATR AKM AKM AKM AKM ADR	ISK SYPFTVH3DLKENSSMTSVIWTTPLG ISR SVRLDWGSMAR KSSNGNRPERMSSVIWTTPLG ISK AVRIDITNRVAKNGNRPDFMSSVIWTTPLG ISH SYRIDDADEVIR 3-GERPFMASTIWTTPLM ISR SIRIOVDTYEVINQ-KNRPAFMASVIWTTPLM ISK SIYNDID3YEEMGP-KKRPSFMASVIWTTPLD ISK LSYVHDD1YEELGSDMQICRSSVIWTSPLG	1000 1083 859 1062 1030 1038 1065 1069
tr ADALE 302C6 ADĀL E302C6 _ LIPST tr ADALE 3724J0 ADAL 6724J0 _ 9ASCO tr ADALE 3PUP0 ADAL E3PUP0 _ 9ASCO tr ADALE 3PUP0 ADAL E3PSW0 _ WICAO tr ADALE 3PSW0 ADAL E3PSW0 _ WICAO tr ROKIX 3 KOKIX 3 _ WICCF tr WEMIL 2 WEMIL 2 _ 9ASCO tr ADALE 302FI7 ADALE 302FI7 _ 9ASCO	VVRNLEN AVRSLFE AVRSLFH CIRELFE CMRELFE SMRELFE AVRQLFH AIRELFN	GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQDW LAEC IQDW LGDW IQDW LGEC IQDW LAEC IQDW LAEC IQDW LAEC IQDW LAES	AKR IATR IAKM IAKM IAKM IAKM IARA	ISK SVPFTVH3DLKPN SSMTSVIWTT PLG ISR SVRLDM GSMAT KSSKNGNRP EFMSSVIWTT PLG ISK AVRIDINRVARNGNRP DFMSSVIWTT PLG ISH SVRIDMDADEVIR S-GERP FMASTIWTT PLN ISR SIRIDDTYEVINQ-KNRP AFMASVIWTT PLN ISK SVRIDIDSYEEMG P-KKKP SFMASVIWTT PLD ISK SVRIDIDSDEILSDNQ ICRSSVIWTS PLG ICK AIKLDHAQRP DFMSAVIWT SPLG	1000 1083 859 1062 1030 1038 1065 1069 1040
tr AOALE 302C6 AOAL E3023C6 _ LIPST tr AOAL67E4J0 AOAL67E4J0 SASCO tr AOALE3PTP0 AOAL63PTP0 SASCO tr AOAUE3PTP0 AOAUE3PTP0 SASCO tr AOAUE3P5W0 AOAL63P5W0 WICAO tr KOKTX3 KOKTX3 WICCF tr WEMIL2 WEMIL2 SASCO tr AOAL63QE17 AOAL63QE17 SASCO tr AOAL63QE17 AOAL63QE17 SASCO tr AOAL63QE17 AOAL63QE17 SASCO	VVRNLFN AVR3LFE AVR3LFH CIRELFE CMRELFE SMRELFE AVRQLFH AIRELFN SVRELFQ	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQDW LAEC IQDW LGDW IQDW LGEC IQDW LAEC IQDW LAEC IQDW LAEC IQDW LAEC IQDW LGEC	'A KR IA TR 'A KM 'A KM 'A KM 'A KM 'A RA 'A RA 'A KR	ISK SYPFTVH3DLKENSSMTSVIWTTPLG ISR SVRLDWGSMAR KSSNGNRPERMSSVIWTTPLG ISK AVRIDITNRVAKNGNRPDFMSSVIWTTPLG ISH SYRIDDADEVIR 3-GERPFMASTIWTTPLM ISR SIRIOVDTYEVINQ-KNRPAFMASVIWTTPLM ISK SIYNDID3YEEMGP-KKRPSFMASVIWTTPLD ISK LSYVHDD1YEELGSDMQICRSSVIWTSPLG	1000 1083 859 1062 1030 1038 1065 1069
tr ADALE 302C6 ADĀL E302C6_LIPST tr ADALE 3PUPO ADAL E302C6_LIPST tr ADALE 3PUPO ADAL E3PUPO] 9ASCO tr ADALE 3PUPO ADAL E3PUPO] 9ASCO tr ADALE 3PSW0 ADAL E3PSW0 WICAO tr ADALE 3PSW0 ADAL E3PSW0 WICAO tr KOKIX 3 KOKIX 3 WICCF tr WEMIL 2 WEMIL 2 9ASCO tr ADALE 302FI ADAL E302FI 7] 9ASCO tr ADALE 305FI ADALE 75ME0] 9ASCO tr ADALE 75ME0 ADALE 75ME0] 9ASCO tr QCCR2 5 QCCR25_KLULA	VVRNLFN AVRSLFE AVRSLFE CIRELFE SMRELFE AVRQLFH AIRELFD SVRELFQ SIRELFH	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQDW LAEC IQDW LGDN IQDW LGEC IQDW LALC IQDW LALC IQDW LALC IQDW LAS IQDW LGEC IQDW LGEC IQDW LIS	AKR AKM AKM AKM AKM AKM ARA ARR AKR AKR AKR	ISK SYRDE DLNGKT SIMTSUWTP LG ISR SYRLDM GSMAT KSSKNGNRP EFMSS VIWTP LG ISR AVRID INRVARNGNRP EFMSS VIWTP LD ISK SYRDDDA DEVIR S-GERP FMAS SIWTP LN ISR SIR IDDT YEUN Q-KNRP AFMAS VIWTP LN ISK SYRLDI DS YEEMG P-KKKP SFMAS VIWTP LD ISK SVRIDI DS TEIVD PKTLKL LCMTSVIWTSP LG IGS SVRIDLKE TEIVD PKTLKL LCMTSVIWTSP LG ISK SVRID LD PGART INSS DLMTSVIWTSP LG	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029
tr ADALE 302C6 ADAL E302C6 _ LIPST tr ADALE 37440 ADAL 678470 _ 0ASCO tr ADALE 3PUPO ADAL E3PUPO _ 0ASCO tr ADALE 3PUPO ADALE 3PUPO _ 0ASCO tr ADALE 3PSW0 ADALE 305W0 _ WICAO tr KOKIX3 KOKIX3 _ WICCF tr W6MIL 2 W6MIL _ 0AALE 329W0 _ WICAO tr ADALE 30PUT ADALE 30PIT _ 0ASCO tr ADALE 30PIT ADALE 30PIT _ 0ASCO tr ADALE 75MED ADALE 75MED _ 0ASCO tr Q6CR25 0CGT85_KLUMA	VVRNLFN AVRSLFH CIRELFE SMRELFE AVRQLFH AIRELFN SVRELFQ SIRELFH SIRELFH	GAHL GAHL GAHL GAHL GAHL GAHL GAHL NAHA AAHL AAHL	IQDW LAEC IQDW LGEON IQDW LGEON IQDW LALC IQDW LALC IQDW LALC IQDW LAEC IQDW LGEO IQDW LGEO IQDW LGEO IQDW LGEO	ARR IATR ARM ARM ARM ARM ARR ARR ARR ARR ARR AR	ISK SYKPETVH3	1000 1083 859 1062 1038 1065 1069 1040 1092 733 1029 1028
tr ADALE 302C6 ADĀL E302C6_LIPST tr ADALE 3PUPO ADAL E302C6_LIPST tr ADALE 3PUPO ADAL E3PUPO] 9ASCO tr ADALE 3PUPO ADAL E3PUPO] 9ASCO tr ADALE 3PSW0 ADAL E3PSW0 WICAO tr ADALE 3PSW0 ADAL E3PSW0 WICAO tr KOKIX 3 KOKIX 3 WICCF tr WEMIL 2 WEMIL 2 9ASCO tr ADALE 302FI ADAL E302FI 7] 9ASCO tr ADALE 305FI ADALE 75ME0] 9ASCO tr ADALE 75ME0 ADALE 75ME0] 9ASCO tr QCCR2 5 QCCR25_KLULA	VVRNLFN AVRSLFE AVRSLFH CIRELFE SMRELFE AVRQLFH AIRELFD SVRELFQ SIRELFH SIRELFH	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQDW LAEC IQDW LGDN IQDW LAEC IQDW LALC IQDW LALC IQDW LAEC IQDW LGEC IQDW LGEC IQDW LGEC IQDW LGEC IQDW LGEC IQDW LGEC	AKR JATR JAKM JAKM JAKM JAKM JAKM JAKR JAKR JAKK JAKK JAKK	ISK SYPETUH3DLKEN SSMTSVIWTT PLG ISR SVRLDM GSMAT KSSKNGNRP EFMSSVIWTT PLG ISR AVRIDINRVARNGNRP EFMSSVIWTT PLG ISH SYRIDDA DEVIR 3-GERP FMASTIWTT PLN ISR SIRIDDTYEUNQ-KNRP AFMASVIWTT PLN ISR SVRIDIDS YEEMG P-KKKP SFMASVIWTT PLG ISK SVRIDIDS DEILS DNQ ICRSSVIWTSPLG ICK AIKLDHAQRP DMSAVIWTSPLG ISK SVRIDLKEQRP DMCSVIWTSPLG ISK SVRLDFDINQSKT INSS DLMTSVIWTSPLG ISK SVRLDFDLNQSKT INSS DLMTSVIWTSPLG ISK SVRLDFDLSDSKT INST DLMTSVIWTSPLG ISK SVRLDEL	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029
tr AOALE 302C6 AOĀLE302C6 _ LIPST tr AOALE 37E4J0 AOAL 67E4J0 _ 9ASCO tr AOALE 3FUPO AOAL E3FUPO _ 9ASCO tr AOALE 3FUPO AOALE3FUPO _ 9ASCO tr AOALE 3FSW0 AOALE3FW0 _ WICAO tr ROKTX3 KORTX3 _ WICCF tr WEMIL 2 WEMIL2 _ 9ASCO tr AOALE 302FI7 AOALE37WE0 _ 9ASCO tr AOALE 73WE0 AOALE75WE0 _ 9ASCO tr AOALE 75WE0 TS KLULA tr WOTE 18 WOTE 15 _ KLUMA tr AOAL0 9UWS1 AOAL0 9UWS1 _ 95ACH tr (65 JMS2 (65 JMS2 _ FRECY tr (65 JFS7 67 SFS7 _ ASHGO	VVRMLFN AVR3LFH CIRELFE CMRELFE SMRELFE AVRQLFH AIRELFN SVRELFQ SIRELFH SIRELFH SIRELFH SIRELFH	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQDW LAEC IQDW LGBCU IQDW LGBCU IQDW LALC IQDW LALC IQDW LAAS IQDW LAES IQDW LGBCU IQDW LGBCU IQDW LGBCU IQDW LGBCU IQDW LAES IQDW LAES	ARR ARM ARM ARM ARM ARM ARR ARR ARR ARR	$\label{eq:second} \begin{split} & \texttt{ISK SYRPETVH3}{=} \\ & \texttt{LSK SYRLDK GSMAR KSSKNGNRPEFNSS VIWTTPLG} \\ & \texttt{ISK AVRLDK GSMAR KSSKNGNRPEFNSS VIWTTPLG} \\ & \texttt{ISK AVRLDK TPRVLRS-GERPFMAAS VIWTTPLM} \\ & \texttt{ISK STRIDVDTYELMG P-KKRPSFNAS VIWTTPLD} \\ & \texttt{ISK STRIDVDTYELMG P-KKRPSFNAS VIWTTPLD} \\ & \texttt{ISK LSK VANDDYELMG P-KKRPSFNAS VIWTSPLG} \\ & \texttt{ISK LSK VANDDYELMG P-KKRPSFNAS VIWTSPLG} \\ & \texttt{ISK STWIDL SQKPDHMSAVIWTSPLG} \\ & \texttt{ISK STRIDJ DQKPDHMSAVIWTSPLG} \\ & \texttt{ISK SVRIDL FLQKPDHMSAVIWTSPLG} \\ & \texttt{ISK SVRDLP DIQKPDHMSAVIWTSPLG} \\ & \texttt{ISK SVRDLP DIQKSS DIMTSVIWTSPLG} \\ & \texttt{ISK SVRDLP DIQKSS DIMTSVIWTSPLG} \\ & \texttt{ISK SVRLDFDQKSKVDSSMMMTSVIWTTPLG} \\ & ISK SVRLDEL$	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1028 1039 1069
tr ADALE 302C6 ADĀL E302C6 _ LTPST tr ADALE 3700 ADAL E302C6 _ LTPST tr ADALE 3700 ADAL E37070 _ 9ASCO tr ADALE 37500 ADAL E37500 _ WICAO tr ADALE 37500 ADAL E37500 _ WICAO tr ADALE 37500 ADAL E37500 _ WICAO tr ADALE 30717 ADALE 30707 _ 9ASCO tr ADALE 30717 ADALE 30717 ADALE 30717 _ 9ASCO tr ADALE 30717 ADALE	VVENLEN AVRSLFH CIRELFE CMRELFE SMRELFE AVRQLFH AIRELFD SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQDW LAEC IQDW LGEC IQDW LGEC IQDW LALC IQDW LALC IQDW LALC IQDW LAES IQDW LGEC IQDW LGEC IQDW LGEC IQDW LAES IQDW LAES IQDW LAES	AKR AKM AKM AKM AKM AKK AKR AKR AKR AKR AKR AKR AKR AKR AKR	ISK SVRPTVH3DLKPN SSMTSVIWTT PLG ISR SVRLDM GSMAT KSSKNGNRP EFMSSVIWTT PLG ISR AVRID INRVARNGNRP EFMSSVIWTT PLG ISK AVRID INRVARNGNRP EFMSSVIWTT PLG ISR STRID DTYEUNG-KNRP AFMASVIWTT PLM ISR SVRIDI D3YEEMG P-KKKP SFMASVIWTT PLG ISK SVRIDI D3	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1028 1029 1064 1064
tr AOALE 302C6 AOĀLE302C6 _ LIPST tr AOALE 37E4J0 AOAL 67E4J0 _ 9ASCO tr AOALE 3FUPO AOAL E3FUPO _ 9ASCO tr AOALE 3FUPO AOALE3FUPO _ 9ASCO tr AOALE 3FSW0 AOALE3FW0 _ WICAO tr ROKTX3 KORTX3 _ WICCF tr WEMIL 2 WEMIL2 _ 9ASCO tr AOALE 302FI7 AOALE37WE0 _ 9ASCO tr AOALE 73WE0 AOALE75WE0 _ 9ASCO tr AOALE 75WE0 TS KLULA tr WOTE 18 WOTE 15 _ KLUMA tr AOAL0 9UWS1 AOAL0 9UWS1 _ 95ACH tr (65 JMS2 (65 JMS2 _ FRECY tr (65 JFS7 67 SFS7 _ ASHGO	VVRNLFN AVRSIFH CIRELFE CMRELFE SMRELFE AVRQLFH AIRELFN SVRELFN SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQDW LAEC IQDW LGEC IQDW LGEC IQDW LALC IQDW LALC IQDW LAAS IQDW LGEC IQDW LGEC IQDW LGEC IQDW LGEC IQDW LGEC IQDW LAES IQDW LAES IQDW LAES IQDW LAES	ARR IATR ARM IARM IARM IARM IARR IARR IARR IARR	$\label{eq:second} \begin{split} & \texttt{ISK SYRPETVH3}{=} \\ & \texttt{LSK SYRLDK GSMAR KSSKNGNRPEFNSS VIWTTPLG} \\ & \texttt{ISK AVRLDK GSMAR KSSKNGNRPEFNSS VIWTTPLG} \\ & \texttt{ISK AVRLDK TPRVLRS-GERPFMAAS VIWTTPLM} \\ & \texttt{ISK STRIDVDTYELMG P-KKRPSFNAS VIWTTPLD} \\ & \texttt{ISK STRIDVDTYELMG P-KKRPSFNAS VIWTTPLD} \\ & \texttt{ISK LSK VANDDYELMG P-KKRPSFNAS VIWTSPLG} \\ & \texttt{ISK LSK VANDDYELMG P-KKRPSFNAS VIWTSPLG} \\ & \texttt{ISK STWIDL SQKPDHMSAVIWTSPLG} \\ & \texttt{ISK STRIDJ DQKPDHMSAVIWTSPLG} \\ & \texttt{ISK SVRIDL FLQKPDHMSAVIWTSPLG} \\ & \texttt{ISK SVRDLP DIQKPDHMSAVIWTSPLG} \\ & \texttt{ISK SVRDLP DIQKSS DIMTSVIWTSPLG} \\ & \texttt{ISK SVRDLP DIQKSS DIMTSVIWTSPLG} \\ & \texttt{ISK SVRLDFDQKSKVDSSMMMTSVIWTTPLG} \\ & ISK SVRLDEL$	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1028 1039 1069
tr ADALE 302C6 ADAL F303C6 _ LTP3T tr ADALE 37440 ADAL 678470 SASCO tr ADALE 3PUPO ADAL 678470 SASCO tr ADALE 3PUPO ADALE 3PUPO SASCO tr ADALE 3PSW0 ADALE 3PSW0 WICAO tr KOKTX3 KOKTX3 WICCF tr WGML 2 WGML 2 SASCO tr ADALE 30PUT ADALE 30PUT SASCO tr ADALE 30PUT SASCO SASCO tr ADALE 30T SASCO	VURNLEN AVRSIFH CIRELFE CMRELFE SMRELFE AVRQLFH AIRELFE SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH AIRESFE AIRESFE AIRESFE	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQDW LAECO IQDW LAGO IQDW LGEC IQDW LALC IQDW LALC IQDW LALC IQDW LALC IQDW LGEC IQDW LGEC IQDW LGEC IQDW LGEC IQDW LGES IQDW LAES IQDW LGEC IQDW LGEC IQDW LGEC IQDW LGEC	ARR ARM ARM ARM ARM ARM ARR ARR ARR ARR	ISK SYVPFTVH3DLKENSSMTSVIWTTPLG ISR SVRLDMGSMAR KSSNGNRPERMSSVIWTTPLG ISR SVRLDMGSMAR KSSNGNRPERMSSVIWTTPLG ISR STRIDVDTYELMGP-KRKPSTMASVIWTTPLN ISR STRIDVDTYELMGP-KRKPSTMASVIWTTPLN ISK STVRIDIJ3YELMGP-KRKPSTMASVIWTTPLD ISK STVRIDIJ3YELMGP-KRKPSTMASVIWTSPLG ISK STVRIDIJPLDPTTLRLLCHTSVIWTSPLG ISK STVRIDID1PLDPTTLRLLCHTSVIWTSPLG ISK STVRIDTD1PLDPTTLRLLCHTSVIWTSPLG ISK STVRIDTD1PLSTKRLLCHTSVIWTSPLG ISK STVRIDTD1PLSTKRLLCHTSVIWTSPLG ISK STVRIDTD1PLSTKRLLCHTSVIWTSPLG ISK STVRIDTD1DKSRKVDSSMMTSVIWTSPLG ISK STVRLDELEKIKKLDSSMMTSVIWTSPLG ISK STRLDLELEKIKKLDSSMMTSVIWTSPLG ISK SIRLDLELEKIKKLDSSMMTSVIWTSPLG ISK SIRLDLEL	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1029 1029 1064 1050 1041 1093
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E4D ADAL 67E4J0 _ 9ASCO tr ADALE 3FUPO ADAL E3FUPO _ 9ASCO tr ADALE 3FUPO ADALE 3FUPO _ 9ASCO tr ADALE 3FSW0 ADALE 3FSW0 _ WICAD tr ADALE 3FSW0 ADALE 3FSW0 _ WICAD tr WEMIL 2 WEMIL _ 9ASCO tr ADALE 30FSW1 ADALE 3FSWE _ 9ASCO tr ADALE 30FSW1 ADALE 3FSWE _ 9ASCO tr ADALE 37SW0 ADALE 3FSWE _ 9ASCO tr ADALE 37SW0 ADALE 3FSWE _ 9ASCO tr ADALE 7SWE ADALE 3FSWE _ 9ASCO tr ADALE 7SWE ADALE 3FSWE _ 9ASCO tr ADALE 7SWE ADALE 3FSWE _ 9ASCO tr 4DALE 7SWE ADALE 3FSWE _ 9ASCO tr 4DALE 7SWE ADALE 3FSWE _ 9ASCO tr 4DALE 7SWE ADALE 3FSWE _ 9ASCO tr 65 UMS 2 65 UMS 2 _ FECY tr (75 FSF (75 FSF _ ASHGO tr H2XAS & HEAS ASE _ ASHAC tr H2XAS & HEAS ASE _ ASHAC tr H2XAS & HEAS ASE _ ASHAC tr GOVDD 1 GOVDD 1 _ NAUCC tr GOVDD 1 GOVDD _ MAUCC	VURNIEN AVRSIFE AVRSIFE CIMELFE CMRELFE SMRELFE AVROLFH AIRELFN SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH TIRELFH TIRELFH	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQOW LAPC. IQOW LAPC.	"A KR IA TR "A KM "A KM "A KM "A KM "A KR "A KR	$\begin{split} 1 \text{HS} & \text{SYPFTVH3} & \longrightarrow \text{DL} - \text{KPN} \text{SMTSVIWTPLG} \\ 1 \text{ISR} & \text{SYRLDM} \text{SMAT} \text{HS} \text{MNG} - \text{NRP} \text{PMS} \text{SVIWTPLG} \\ 1 \text{ISR} & \text{SYRLDM} \text{SMAT} \text{HS} \text{MNG} - \text{NRP} \text{PMS} \text{SVIWTPLG} \\ 1 \text{SH} & \text{SYRIDM} \text{DA} - \dots \text{DEVIR} \text{S} - \text{CRP} \text{PMAS} \text{SVIWTPLM} \\ 1 \text{ISR} & \text{STRIDV} \text{DT} - \dots \text{YEVM} \text{O} - \text{KRP} \text{FMAS} \text{VIWTPLN} \\ 1 \text{ISR} & \text{STRIDVD} - \dots \text{YEVM} \text{O} - \text{KRP} \text{FMAS} \text{VIWTPLD} \\ 1 \text{ISR} & \text{STRIDVD} - \dots \text{YEVM} \text{O} - \text{KRP} \text{SMAS} \text{VIWTSPLG} \\ 1 \text{ISR} & \text{STWIDD} \text{S} - \dots \text{YEVM} \text{O} \text{CRSSVIWTSPLG} \\ 1 \text{GS} & \text{SVRIDL} \text{R} - \dots - \dots \text{CPD} \text{DVGSVIWTSPLG} \\ 1 \text{ISR} & \text{SVRLDP} \text{D} - \dots - \text{CPD} \text{DVGSVIWTSPLG} \\ 1 \text{ISR} & \text{SVRLDP} \text{D} - \dots \text{QSRT} \text{I} - \text{NSS} \text{DLMTSVIWTSPLG} \\ 1 \text{ISR} & \text{SVRLDP} \text{D} - \dots \text{QSRT} \text{I} - \text{NSS} \text{DLMTSVIWTSPLG} \\ 1 \text{ISR} & \text{SVRLDP} \text{L} - \dots \text{QSRT} \text{I} - \text{NSS} \text{DLMTSVIWTSPLG} \\ 1 \text{ISR} & \text{SVRLDEL} - \dots \text{CRSKV} - \text{DSSMMMTSVIWTSPLG} \\ 1 \text{ISR} & \text{SVRLDEL} - \dots \text{EKRKV} - \text{DSSMMMTSVIWTSPLG} \\ 1 \text{ISR} & \text{STRLDLE} - \dots \text{EKRMC} - \text{NRT} \text{VIWTSPLG} \\ 1 \text{ISR} & \text{STRLDLE} - \dots \text{EKRMC} - \text{DSSMMTSVIWTSPLG} \\ 1 \text{ISR} & \text{STRLDLE} - \dots \text{EKRMG} - \text{DRE} \text{DTMSVIWTSPLG} \\ 1 \text{ISR} & \text{STRLDDE} - \dots \text{KSFRM} - \text{DRE} \text{DTMSVIWTSPLG} \\ 1 \text{ISR} & \text{STRLDD} \text{US} - \dots \text{KSFRM} - \text{DRE} \text{DTMSVIWTSPLG} \\ 1 \text{ISR} & \text{STRLDDVD} - \dots \text{KSFRM} - \text{DRE} \text{DTMSVIWTTPLG} \\ 1 \text{ISR} & \text{STRLDVD} - \dots \text{KSFRM} - \text{DRE} \text{DTMSVIWTTPLG} \\ 1 \text{ISR} & \text{STRLDVD} \text{UD} - \dots \text{KSFRM} - \text{DRE} \text{DMSVIWTTPLG} \\ 1 \text{ISR} & \text{STRLDVD} \text{UD} - \dots \text{KSFRM} - \text{DRE} \text{DSWSVIWTTPLG} \\ 1 \text{ISR} & \text{STRLDVD} \text{UD} - \dots \text{KSFRM} - \text{DRE} \text{DTMSVIWTTPLG} \\ 1 \text{ISR} & \text{STRLDVD} \text{UD} - \dots \text{KSFRM} - \text{DRE} \text{DMSVIWTTPLG} \\ 1 \text{ISR} & \text{STRLDVD} \text{UD} - \dots \text{KSFRM} - \text{DRE} \text{DSWSVIWTTPLG} \\ 1 \text{ISR} & \text{STRLDVD} \text{UD} - \dots \text{KSFRM} - \text{ORE} \text{DRSVIWTTPLG} \\ 1 \text{ISR} & \text{STRLDVD} \text{UD} - \dots \text{KSFRM} - \text{ORE} \text{DRSVIWTTPLG} \\ 1 \text{ISR} & \text{STRLDVD} \text{D} - \dots \text{KSFRM} - \text{MRE} \text{DSWSV} \\ 1 \text{WTTPLG} \\ 1 \text{ISR} & \text{STRLDVD} \text{UD} - \dots \text{KSFRM} - \text{MRE} \text{N} \\ 1 \text{MS} $	1000 1083 859 1062 1030 1065 1069 1065 1069 1029 1029 1069 1064 1064 1064 1050 1041 1093
tr ADALE 302C6 ADAL F302C6 _ LTP3T tr ADALE 37440 ADAL 678470 _ DASCO tr ADALE 3PUPO ADAL 678470 _ DASCO tr ADALE 3PUPO ADALE 3PUPO _ DASCO tr ADALE 3PUPO ADALE 3PUPO _ TCAO tr KOKTX3 KOKTX3 WICCF tr W6KIL 2 W6KIL 2 _ DASCO tr ADALE 30PUT ADALE 320PIT _ DASCO tr ADALE 30PUT ADALE 30PUT _ DASCO tr ADALE 30PUT _ ADALE 30PUT _ DASCO tr GOWET 2 GOWET 2 _ NAUDC tr GOWET 2 GOWET 2 _ NAUDC tr GOWET 2 GOWET 2 _ NAUDC tr GOWET 2 GOWET 2 _ NAUDC	VURNIEN AVRSIFE AVRSIFE CIMELFE SMMELFE SMMELFE SMELFH AVRQLFH AIRELFH SIRELFH SIRELFH SIRELFH SIRELFH AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQUM LAPC. IQUM LAPC. IQUM LGPX IQUM LAPC. IQUM LAPC. IQUM LAPC. IQUM LAPC. IQUM LAPC. IQUM LGPX IQUM LGPX. IQUM LGPX. IQUM LGPX. IQUM LGPX. IQUM LGPX. IQUM LGPX. IQUM LGPX. IQUM LGPX. IQUM LGPX.	"A KR IA TR "A KM "A KM "A KM "A KM "A KM "A KK "A KK "A KK "A KK "A KK "A KK "A KK "A KK "A KK "A KK	ISK SYCPTUH3	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1069 1069 1064 1050 1050 1051 1093
tr ADALE 302C6 ADALE 302CC6 _ LIPST tr ADALE 37440 ADAL 678440 SASCO tr ADALE 3PUPO ADALE 3PUPO SASCO tr ADALE 3PUPO ADALE 3PUPO SASCO tr ADALE 3PUPO ADALE 3PUPO MICAO tr KOKTX3 KOKTX3 WICCF tr WGML1 2 WGML12_ 9ASCO tr ADALE 30PUPI ADALE 32PUPI SASCO tr ADALE 30PUPI ADALE 30PIT SASCO tr ADALE 30PUT ADALE 30PIT SASCO tr ADALE 30PIT ADALE 30PIT SASCO tr GOTGI WOTGI & KLUMA tr GS MSJ GS MSJ SASCO tr GOWET 2 GOWET 2 MAUDC tr GOWET 2 GOWET 2 MAUDC tr GSBS54 GSB S54 TETPH tr ADALE 30PIT SAGOLESKWS SACEU	VURNIEN AVRSIE AVRSIE CIRELFE CIRELFE SMRELFE SMRELFE AVRQLFH AIRELFN SIRELFH SIRELFH SIRELFH SIRELFH AIRESFR TIRELFH TIRELFH AVRELFE AIRESFR	GAHI GAHI GAHI GAHI GAHI GAHI GAHI GAHI	IQUM LARC IQUM LARC IQUM LGUM IQUM LGUM IQUM LALC IQUM LALC IQUM LALC IQUM LAIC IQUM LGUM IQUM LGUM IQUM LGUM IQUM LGUM IQUM LGUM IQUM LGUM IQUM LGUM IQUM LGUM IQUM LGUM IQUM LGU IQUM LGU IQUM LGU IQUM LGU IQUM LGU IQUM LGU	"A KR IA TR "A KM "A KM "A KM "A KM "A KR "A KR	ISK SYPFTVH3DLKENSSMTSVIWTTPLG ISR SVELDMGSMAR TSSNGNRPERSSVIWTTPLG ISK SVELDMGSMAR TSSNGNRPERSSVIWTTPLG ISK STRIDUD	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1069 1064 1064 1050 1050 1064 1093 1121 1099 1116
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E470 ADAL 67E470 SASCO tr ADALE 3FUP0 ADAL 67E470 SASCO tr ADALE 3FUP0 ADALE 3FUP0 _ SASCO tr ADALE 3FUP0 ADALE 3FUP0 _ WICAO tr KOKIX 3 KOKIX 3 WICCF tr W6MIL 2 W6MIL 2 SASCO tr ADALE 30FUP1 ADALE 32SUP1 _ SASCO tr ADALE 30FU7 ADALE 32SUP1 _ SASCO tr GECR2 5 GECR25 _ KLUIAA tr GOB 2 GSUP32 _ RECY tr GSUP1 6 NOT GT8 _ KLUMA tr GSUP1 6 NOT GT8 _ KLUMA tr GSUP1 6 NSUP1 GA SHACC tr H2XD5 / H2XD5 _ SASLAF tr J737Y 3 J737Y3 _ KAZNA tr GOWE7 2 GOWE7 _ ANDCC tr GOWE7 2 GOWE7 _ NADCC tr GOWE7 2 GOWE7 _ NADCC tr GESS 4 GSB 54 _ TETPH tr ADALE SRUS ADAD LERKWS _ SACEU tr ADALE SRUS ADAD LERKWS _ SACEU	VURNIEN AVRSIFE AVRSIFE CIMELFE CMRELFE SMRELFE SMRELFN AIRELFN SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRELFH AIRELFH AIRELFH AIRELFH	GAHI GAHI GAHI GAHI GAHI GAHI GAHI AAHI A	IQUM LAPE. IQUM LGDW LGPC IQUM LGDW LGPC IQUM LALC IQUM LALC IQUM LALC IQUM LATC IQUM LGPC IQUM LGPC	"A KR IA TR "A KM "A KM "A KM "A KM "A KR "A KR "A KR "A KR "A KR "A KR "A KR "A KR "A KR "S NK "A KR "S NK	I #K SYUPFTUH3UPL-KEN SSMT SUWTT PLG I #R SVELDWGSMAR KSSMGNRP EMSSUWTT PLG I #K AVRIDI TNRVAKNGNRP DEMSSUWTT PLG I #K AVRIDI TN RVAKNGNRP DEMSSUWTT PLG I #K #K AVRDDI VELMG P-KKRP STMASUWTT PLN I #K #K XNDDD VELMG P-KKRP STMASUWTT PLG I #K #K XNDDD VELMG P-KKRP STMASUWTT PLG I #K #K XNDDD VELMG P-KKRP STMASUWTT PLG I #K #K XNDDD VELMG P-KTKRP STMASUWTT PLG I #K #K XNDD VELMG P-KTKRP STMASUWTT PLG I #K #K XNDD VELMG P-KTKRP STMASUWTT PLG I #K #K XNDD	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1029 1029 1064 1050 1041 1093 1121 1099 1121 1089
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E40 ADAL 67E4J0 _ 9ASCO tr ADALE 3FUPO ADAL E3FUPO _ 9ASCO tr ADALE 3FUPO ADALE 3FUPO _ 9ASCO tr ADALE 30FUT ADALE 3FUPO _ 9ASCO tr ADALE 30FUT ADALE 3FUPO _ 9ASCO tr ADALE 30FUT ADALE 3FUPO _ 9ASCO tr ADALE 37UPO ADALE 3FUPO _ 9ASCO tr 4DALE 37UPO ADALE 3FUPO _ 9ASCO tr 4DALE 37UPO ADALE 3FUPO _ 9ASCO tr 66 JUS 2 66 JUS 2 _ RELY tr (67 JUS 1 ADALE 3FUPO _ 9ASCO tr 60 JUS 1 ADĀL 95 JUS 1 _ 9ASCA tr 60 JUS 1 ADĀLE 7 JUPO _ 1 tr 60 JUS 1 ADĀLE 3FUPO _ 1 tr 60 JUS 1 ADĀLE 3FUPO _ 1 tr 60 JUS 1 50 JUS 1 _ 8AZAF tr 60 JUS 2 60 JUS 2 _ NAUCC tr 60 JUS 2 60 JUS 2 _ NAUCC tr 60 JUS 2 60 JUS 2 _ NAUDC tr 66 JUS 2 60 JUS 2 _ NAUDC tr 60 JUS 2 60 JUS 2 _ NAUDC tr 70 JUS 2 50 JUS 2 JUS 4 _ JUS 2 _ JUS 4 _ JUS 2 _ JUS 4 _	VURNIEM AVRSIF AVRSIF CIMELFE CMRELFE SMRELFE SMRELFE AVROLFH AIRELFN SIRELFH SIRELFH SIRELFH SIRELFH AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRELFH AIRELFH AIRELFH AIRELFH	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQUM LARC. IQUM LGDN IQUM LGDN IQUM LGDN IQUM LAIC IQUM LAIC IQUM LAIC IQUM LAIC IQUM LGDC IQUM LGDC	CARR IATR CARM CARM CARM CARM CARM CARR CARR CAR	$\begin{split} & 1 \text{SK} \text{SVPFTVH3}{$	1000 1083 859 1062 1030 1038 1065 1069 1069 1029 1029 1064 1064 1064 1064 1050 1041 1093 1121 1091 1089 1116 1115
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E4D ADAL 67E4J0 _ 9ASCO tr ADALE 3FUP0 ADAL E3FUP0 _ 9ASCO tr ADALE 3FUP0 ADALE 3FUP0 _ 9ASCO tr ADALE 3FUP0 ADALE 3FUP0 _ WICAO tr ADALE 3FUP1 ADALE 3FUP0 _ 9ASCO tr ADALE 3QPI7 ADALE 3FUP0 _ 9ASCO tr ADALE 3GUP1 / ADALE 3FUP0 _ 9ASCO tr GOTSE 1 WOTGE TE RLUMA tr GOTSEP / [075E7 _ ASHGO tr RESKDF 6 BSKDF 6 _ ASHAC tr (75FP 7 075E7 _ ASHGO tr 12A5 8 ICAS 156 & RAZAF tr 75773 3 773773 & RAZNA tr GOFEC 2 GOWE 72 _ NAUDC tr GEFLX 9 GEFLX9 _ CANGA tr GOED 1 GOVDO1 _ NAUCC tr GEFLX 9 GEFLX9 _ CANGA tr GODD 1 SADOLE SFUR5 _ SACEU tr ADALD SFUR5 ADALE SFUR5 _ SACEU tr ADALE SFUR5 ADALE SFUR5 _ 9ACH tr JBP5 8 JBP58 _ SACAR tr ADAC 7M171 ADALCC7M171 _ 9SACH tr CSENT 4 _ DATEST	VURNIEN AVRSIFE AVRSIFE CIMELFE CMRELFE SMRELFE SMRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN SVRELFE SVRELFE	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQUM LAPC. IQUM LGDW. IQUM LGDU IQUM LALC. IQUM LALC. IQUM LALC. IQUM LAIC. IQUM LAIC. IQUM LGDU IQUM LGDU	CARR CARM CARM CARM CARM CARM CARM CARR CARR	I M K JY PF T V H 3	1000 1083 859 1062 1030 1065 1069 1069 1069 1029 1029 1069 1064 1064 1064 1093 1221 1093 1221 1091 1215 1115
tr ADALE 302C6 ADAL F303C6 _ LTP3T tr ADALE 37440 ADAL 678440 SASCO tr ADALE 375W0 ADAL 678470 SASCO tr ADALE 375W0 ADALE 375W0 _ WICAO tr ADALE 375W0 ADALE 375W0 _ WICAO tr KOKIX3 KOKIX3 _ WICCF tr WGMIL 2 WGMIL 2 SASCO tr ADALE 305W0 ADALE 305W0 _ WICAO tr ADALE 305W1 ADALE 305W0 _ WICAO tr ADALE 305W1 ADALE 305W1 _ SASCO tr ADALE 305W1 ADALE 305W1 _ SASCO tr ADALE 305W1 ADALE 305W1 _ SASCO tr ADALE 305W1 = ADALE 305W1 _ SASCO tr 050W51 ADALE 305W1 _ SASCO tr 050W51 ADALE 305W1 _ SASCO tr 050W51 SASCE 505W1 _ SASCA tr 050W51 SASCE 505W1 _ SASCA tr 1737Y3 1737Y3 _ KAZAF tr 3737Y3 3737Y3 _ KAZAF tr 305D54 GBB 354 _ TEFFH tr ADALE 87W5 ADALE 5WFW3 _ SASCE U tr ADALE 87W5 ADALE 5WFW3 _ SASCE U tr ADALE 87W5 ADALE 5WFW3 _ SASCE U tr ADALE 87W7 ADALE 5WFW3 _ SASCE U tr ADALE 7W71 ADALE 5WFW3 _ SASCE U tr ADALE 7W71 ADALE 5WFW3 _ SASCE U tr CSDWF3 CSDWF3 _ LACTC tr CSDWF3 CSDWF3 _ LACTC	VURNIEN AVRSIFE AVRSIFE CIMELFE SMMELFE SMMELFE SMMELFE AVRQLFH AIRELFO SIRELFH SIRELFH SIRELFH SIRELFH AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRELFH AIRELFH AIRELFH AIRELFH AIRELFH AIRELFH AIRELFH AIRELFH AIRELFH AIRELFH AIRELFH AIRELFH	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQUM LAPE IQUM LGDW LGPC IQUM LGDW LGPC IQUM LAIC IQUM LAIC IQUM LAIC IQUM LAIC IQUM LGPC IQUM LGPC	"A KR IA TR "A KM "A KM "A KR "A KR	ISK SYPFTVH3DLKENSSMTSVIWTTPLG ISR SVELDMGSMAR TSSNGNRPERSSVIWTTPLG ISK AVRIDITNRVAKNGNRPDENSSVIWTPLD ISK STRIDTYELMGKREARASVIWTTPLD ISK STWIDID3YELMGP-KKEPSTMASVIWTTPLD ISK STWIDID3YELMGP-KKEPSTMASVIWTTPLD ISK STWIDID3YELMGP-KKEPSTMASVIWTTPLD ISK STWIDID3YELMGP-KKEPSTMASVIWTTPLD ISK STWIDID3YELMGP-KKEPSTMASVIWTTPLD ISK STWIDID3YELMGP-KKEPSTMASVIWTTPLD ISK STWIDID3YELMGP-KKEPSTMASVIWTTPLD ISK STWIDID3YELMGP-KKEPSTMASVIWTTPLD ISK STWIDID3YELMGP-KKEPSTMASVIWTSPLG ISK STWIDID1NQSKTINSS DLMTSVIWTSPLG ISK STWIDFLNQSKTINSS DLMTSVIWTSPLG ISK STWLDELDKSKKVDSSMMATSVIWTSPLG ISK STWLDELEKIKKLDSSIMATSVIWTSPLG ISK STWLDELKSFKNGNKPPENSSVIWTPLG ISK STWLDUEKSFKNGDKPMSSVIWTTPLG ISK STWLDUEKSFKNGDKPMSSVIWTTPLG ISK STRLDVDCKSFKNGDKPMSSVIWTTPLG ISK STRLDVDCKSFKNGNKPPMSSVIWTTPLG ISK STRLDVDCKSFKNGNKPDMSSVIWTTPLG ISK STRLDVDCKSFKNGNKPDFMSSVIWTTPLG ISK STRLDVDCKSFKNGNKPDFMSSVIWTTPLG ISK STRLDVDCKSFKNGNKPDFMSSVIWTTPLG ISK STRLDVDCKSFKNGNKPDFMSSVIWTTPLG ISK STRLDVDCKSFKNGNKPDFMSSVIWTTPLG ISK STRLDVDCKSFKNGNKPDFMSSVIWTTPLG ISK STRLDVDC-	1000 1083 859 1062 1038 1065 1069 1040 1092 733 1029 1069 1069 1064 1050 1050 1064 1093 1121 1091 1089 1116 1115 1061 1056
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E4D ADAL 67E4J0 _ 9ASCO tr ADALE 3FUP0 ADAL E3FUP0 _ 9ASCO tr ADALE 3FUP0 ADALE 3FUP0 _ 9ASCO tr ADALE 3FUP0 ADALE 3FUP0 _ WICAO tr ADALE 3FUP1 ADALE 3FUP0 _ 9ASCO tr ADALE 3QPI7 ADALE 3FUP0 _ 9ASCO tr ADALE 3GUP1 / ADALE 3FUP0 _ 9ASCO tr GOTSE 1 WOTGE TE RLUMA tr GOTSEP / [075E7 _ ASHGO tr RESKDF 6 BSKDF 6 _ ASHAC tr (75FP 7 075E7 _ ASHGO tr 12A5 8 ICAS 156 & RAZAF tr 75773 3 773773 & RAZNA tr GOFEC 2 GOWE 72 _ NAUDC tr GEFLX 9 GEFLX9 _ CANGA tr GOED 1 GOVDO1 _ NAUCC tr GEFLX 9 GEFLX9 _ CANGA tr GODD 1 SADOLE SFUR5 _ SACEU tr ADALD SFUR5 ADALE SFUR5 _ SACEU tr ADALE SFUR5 ADALE SFUR5 _ 9ACH tr JBP5 8 JBP58 _ SACAR tr ADAC 7M171 ADALCC7M171 _ 9SACH tr CSENT 4 _ DATEST	VURNIEN AVRSIFE AVRSIFE CIMELFE CMRELFE SMRELFE SMRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN AIRELFN	GAHL GAHL GAHL GAHL GAHL GAHL GAHL GAHL	IQUM LAPC. IQUM LGDW LGPC. IQUM LGDW LGPC. IQUM LADU IQUM LADU IQUM LADU IQUM LATU IQUM LGPC. IQUM LGPC.	CAKR CAKM CAKM CAKM CAKM CAKM CAKM CAKM CAKM	I M K JY PF T V H 3	1000 1083 859 1062 1030 1065 1069 1069 1069 1029 1029 1069 1064 1064 1064 1093 1221 1093 1221 1091 1215 1115
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E470 ADAL 67E470 SASCO tr ADALE 3FUP0 ADAL 67E470 SASCO tr ADALE 3FUP0 ADAL 12SPUP0 SASCO tr ADALE 3FUP0 ADALE 37EV0 WICAO tr KOKIX3 KOKIX3 WICCF tr WGMIL 2 WGMIL 2 SASCO tr ADALE 30FUN ADALE 32SPUT SASCO tr ADALE 30FUT ADALE 32SPUT SASCO tr GOKEZ 5 GCCR25 KLUAA tr GOK 32 GS JM32 FRECY tr G75BP7 Q75BP7 SAFA tr GVBSD7 6 BSXDF6 ASHAC tr H3XDF6 BSXDF6 ASHAC tr GSB54 GSB54 SETPH tr ADALE 37S73 XAZNA tr GOKE7 2 GOWE72 ADALCC tr GESS4 GSB54 TETPH tr ADALE SRWS ADALESRWS SACEU tr J3PF58 J3PF56 SACAR tr J3PF58 J3PF56 SACAR tr J3PF58 J3PF56 SACAR tr GSBC0 (GSZRO0 _ TORDC tr GSBC0 0 GSZRO0 _ TORDC tr GDME27 GDD 0 ADALESRWS SASCO tr ADALE 4RQC7 ADALEARCF SASCO	VURNIEN AVRSIFE AVRSIFE CIMELFE CMRELFE SMRELFE SMRELFN SURELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRELFN AVRELFE SVRELFE SVRELFE SVRELFE SVRELFE SVRELFE	GA HI GA HI	IQUM LAPE. IQUM LGDW LGPC IQUM LGDW LGPC IQUM LGPC IQUM LAPC IQUM LAPC IQUM LAPC IQUM LGPC IQUM LGPC	"A KR IA TR CA KM CA KM CA KM CA KM CA KR CA KR	I M K JY PF T V H 3	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1028 1039 1064 1050 1064 1050 1041 1093 1121 1091 1089 1116 1115 1115 1165 1056 1077 1083 1072
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E40 ADAL 67E4J0 _ 9ASCO tr ADALE 3FUP0 ADAL E3FUP0 _ 9ASCO tr ADALE 3FUP0 ADALE 3FUP0 _ 9ASCO tr ADALE 39EV0 ADALE 3FUP0 _ 9ASCO tr ADALE 39EV0 ADALE 3FUP0 _ 9ASCO tr ADALE 39EV0 ADALE 3FUP0 _ 9ASCO tr ADALE 37UP0 3FUP0 _ 3FUP0 _ 9ASCO tr ADALE 37UP0 = 189XDF6 _ 3HAC tr 12358 12358 _ 7AZAF tr 375773 373773 _ RAZNA tr 60FD7 60FUP0 _ NAUCC tr 60FD7 60FUP0 _ NAUCC tr 60FD7 65FS6 _ 3ACAR tr ADALE 8FUF58 _ 3ACAR tr ADALE 8FUF58 _ SACAR tr ADALE 8FUF58 _ SACAR tr ADALE 8FUF58 _ SACAR tr ADALE 8FUF58 _ 3ACAR tr ADALE 8FUF58 _ 3ACAR	VURNIEN AVRSIFE AVRSIFE CIMELFE CIMELFE SMRELFE SMRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE SVRELFE SVRELFE SVRELFE SVRELFE SVRELFE SVRELFE	GA HI GA HI GA HI GA HI GA HI GA HI GA HI GA HI GA HI GA HI SA HI SA HI SA HI SA HI SA HI SA HI GA HI GA HI GA HI GA HI GA HI GA HI GA HI GA HI	IQUM LAPC. IQUM LGDW. IQUM LGDW LAPC. IQUM LGDW LAPC. IQUM LAPC. IQUM LAPC. IQUM LAPC. IQUM LGPC. IQUM LGPC.	CAKR CAKM CAKM CAKM CAKM CAKR CARA CAKR CARR CARR CARR CARR CARR	19K SVPFTVH3DLKPN S3MT 3'UWTP LG 19R SVRLDM GSMAT K3SMGNRP EFNS3 VIWTP LG 19R SVRLDM GSMAT K3SMGNRP EFNS3 VIWTP LG 19R STRIDVDTYELMG O-KREA FYMAS VIWTP LN 19R STRIDVDTYELMG P-KKRP SFMAS VIWTP LN 19K SVRIDI D3YELMG P-KKRP SFMAS VIWTP LN 19K SVRIDD D3YELMG P-KKRP SFMAS VIWTP LN 19K SVRIDD D3	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1029 1029 1064 1064 1064 1064 1064 1064 1093 1121 1091 1093 1115 1115 1015 0177 1083
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E470 ADAL 67E470 SASCO tr ADALE 3FUP0 ADAL 67E470 SASCO tr ADALE 3FUP0 ADAL 12SPUP0 SASCO tr ADALE 3FUP0 ADALE 37EV0 WICAO tr KOKIX3 KOKIX3 WICCF tr WGMIL 2 WGMIL 2 SASCO tr ADALE 30FUN ADALE 32SPUT SASCO tr ADALE 30FUT ADALE 32SPUT SASCO tr GOKEZ 5 GCCR25 KLUAA tr GOK 32 GS JM32 FRECY tr G75BP7 Q75BP7 SAFA tr GVBSD7 6 BSXDF6 ASHAC tr H3XDF6 BSXDF6 ASHAC tr GSB54 GSB54 SETPH tr ADALE 37S73 XAZNA tr GOKE7 2 GOWE72 ADALCC tr GESS4 GSB54 TETPH tr ADALE SRWS ADALESRWS SACEU tr J3PF58 J3PF56 SACAR tr J3PF58 J3PF56 SACAR tr J3PF58 J3PF56 SACAR tr GSBC0 (GSZRO0 _ TORDC tr GSBC0 0 GSZRO0 _ TORDC tr GDME27 GDD 0 ADALESRWS SASCO tr ADALE 4RQC7 ADALEARCF SASCO	VURNIEN AVRSIFE AVRSIFE CIMELFE CIMELFE SMRELFE SIMELFN SIMELFN SIMELFN SIMELFN SIMELFN SIMELFN SIMELFN SIMELFN AIRESFE AIRESFE AIRESFE AIRELFN SIM	GA HI GA HI SA HI SA HI SA HI SA HI SA HI SA HI SA HI SA HI GA HI	IQUM LAPE. IQUM LGDW LGPC IQUM LGDW LGPC IQUM LGPC IQUM LAPC IQUM LAPC IQUM LAPC IQUM LGPC IQUM	"A KR KA TR KA KM "A KM "A KM "A KM "A KM "A KM "A KK "A KK "A KK "A KK "A KK "A KK "A KK "A KK "A KK	I M K JY PF T V H 3	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1028 1039 1064 1050 1064 1050 1041 1093 1121 1091 1089 1116 1115 1115 1165 1056 1077 1083 1072
tr ADALE 302C6 ADAL F303C6 _ LTP3T tr ADALE 37440 ADAL 678440 9ASCO tr ADALE 375W0 ADAL 678440 9ASCO tr ADALE 375W0 ADALE 375W0 _ WICAO tr ADALE 375W1 ADALE 375W1 _ 9ASCO tr 045W2 05W7 = 3HAC tr 05W5 2 05W7 = 3HAC tr 1737Y3 J737Y3 = KAZAF tr 05W5 4 05W5 = 7 _ 3HAC tr 05W5 4 05W5 = 7 _ 3HAC tr 05W5 4 05W1 = ADALE XW3 _ 9ASCH tr 05W5 1 50W1 = ADALE XW5 _ 3ACEU tr 05W5 4 05W1 = ADALE XW5 _ 3ACEU tr 35P7 8 J3P7 9 = 3ACAR tr 05W5 8 J5BP7 8 = 3ACAR tr 05W7 9 C5DW7 9 _ ZYGRC tr 05DW7 9 C5DW7 9 _ ZYGRC tr 05DW7 8 J5DP7 8 = 3ACCR tr 05DW7 9 C5DW7 9 _ ZYGRC tr 05DW7 9 C5DW7 9 _ ZYGRC tr 05DW7 9 C5DW7 9 _ ZYGRC tr 05DL 074K6 ADALE 474K7 _ 9ASCO tr ADAL 074K6 ADALE 474K7 _ 9ASCO tr ADAL 074K6 ADALE 474K7 _ 9ASCO tr ADAL 074K6 ADALE 474K7 _ 9ASCO tr ADALD 074K6 ADALE 474K6 _ 9ASCO tr 04788 C4Y683 _ CLAL4 tr 03B4C1 03B4C1 _ CANTC	VURNIER AVRSIFE AVRSIFE CIMELFE SMMELFE SMMELFE SMMELFE SIMELFH SIMELFH SIMELFH SIMELFH SIMELFH AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE SIMELFH SIMELFH AIRELFH AIRELFH AIRELFH SVMELFE SVMELFE SVMELFE SIMELFA SMMELFE SVMELFE SIMELFE SIMELFE	GA HI GA HI GA HI GA HI GA HI GA HI GA HI GA HI SA HI GA HI GA HI GA HI GA HI GA HI GA HI GA HI GA HI GA HI	IQUM LAPE. IQUM LGDW LGPC IQUM LGDW LGPC IQUM LGDW LADC IQUM LADC IQUM LADC IQUM LADC IQUM LGPC IQUM LGPC	CARR CARM CARM CARM CARM CARM CARM CARM	I MK SYPFTUH3DLKEN S SMT SUWTT PLG I SK SVELDMGSMAR K SSNGNRP ENSSUWTT PLG I SK AVRIDI TN RVAKNGNRP DEMSSUWTT PLG I SK AVRIDI TN RVAKNGNRP DEMSSUWT PLG I SK J SK I SK	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1064 1069 1064 1050 1064 1050 1064 1093 1121 1091 1089 1116 1115 1016 1056 1077 1083 1075 1078 1075
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E40 ADAL 67E400 9ASCO tr ADALE 3PEVPO ADAL E3PEVPO _ 9ASCO tr ADALE 3PEVPO ADAL E3PEVPO _ 9ASCO tr ADALE 37EVO ADALE 37EVPO _ 9ASCO tr ADALE 37EVO ADALE 37EVO _ VICAO tr KOKIX 3 KOKIX 3 VICCF tr WGMIL 2 WGMIL 2 9ASCO tr ADALE 30EVI ADAL E3PEVT _ 9ASCO tr ADALE 30EVI ADAL E3PEVT _ 9ASCO tr ADALE 30EVI ADAL E30EVI _ 9ASCO tr 60EVI 5 WOT GI 5E KLUMA tr 60B 216 6WSI 5E KLUMA tr 60B 216 6WSI 5E ADALE 5E ADALE 5E FOT GI 5E KUMA tr 60B 51 60F LAS 0 KAZNA tr 60WEI 2 60WEI _ AJABC tr 60B 54 66B 54 EETEH tr ADALO 8VRUS ADAL 5EVRUS _ 9ASCH tr 32BF 58 36P D55 3ACAR tr 30ED 18 SOED 18 ADALE 5ERWS - 3ACEU tr 60B 16 5DEVI _ 2 2GCC tr 60D 662 CONTYI _ 93CCH tr 75TY 3 75TY 3 CANGA tr 5DEVI 3 25DNY 3 LACTC tr 60D 662 CONTYI _ 93CCH tr ADALE 48QFT ADALE4RQFT _ 9ASCO tr ADALE 48QFT ADALE4RQFT _ 9ASCO tr ADALE 0 662 CANTC ADALE4RQFT = 9ASCO tr ADALE 48QFT ADALE4RQFT ADALE5WT 6 9ASCO tr ADALE 48QFT ADALE4SWT 6 9ASCO	VURNIEN AVRSIFE AVRSIFE CIMELFE CIMELFE SMRELFE SMRELFE SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFH AIRESFE AIRESFE AIRESFE SIRELFE SVRELFE	GAHI GAHI GAHI GAHI GAHI GAHI GAHI GAHI	IQUM LAPE. IQUM LGDW LGPC IQUM LGDW LGPC IQUM LGPC IQUM LAPC IQUM LAPC IQUM LAPC IQUM LAPC IQUM LGPC IQUM	CARR NATRA CARM CARM CARM CARM CARM CARM CARR CARR	I M K JYPFT VH3	1000 1083 859 1062 1030 1065 1069 1069 1069 1069 1069 1064 1064 1064 1064 1064 1093 1221 1093 1221 1099 1116 1115 1115 1061 1056 1077 1089 1115 1015 1089 10172 1075 1072
tr ADALE 302C6 ADAL F303C6 _ LTP3T tr ADALE 37440 ADAL 678440 9ASCO tr ADALE 375W0 ADAL 678440 9ASCO tr ADALE 375W0 ADALE 375W0 _ WICAO tr ADALE 375W1 ADALE 375W1 _ 9ASCO tr 045W2 05W7 = 3HAC tr 05W5 2 05W7 = 3HAC tr 1737Y3 J737Y3 = KAZAF tr 05W5 4 05W5 = 7 _ 3HAC tr 05W5 4 05W5 = 7 _ 3HAC tr 05W5 4 05W1 = ADALE XW3 _ 9ASCH tr 05W5 1 50W1 = ADALE XW5 _ 3ACEU tr 05W5 4 05W1 = ADALE XW5 _ 3ACEU tr 35P7 8 J3P7 9 = 3ACAR tr 05W5 8 J5BP7 8 = 3ACAR tr 05W7 9 C5DW7 9 _ ZYGRC tr 05DW7 9 C5DW7 9 _ ZYGRC tr 05DW7 8 J5DP7 8 = 3ACCR tr 05DW7 9 C5DW7 9 _ ZYGRC tr 05DW7 9 C5DW7 9 _ ZYGRC tr 05DW7 9 C5DW7 9 _ ZYGRC tr 05DL 074K6 ADALE 474K7 _ 9ASCO tr ADAL 074K6 ADALE 474K7 _ 9ASCO tr ADAL 074K6 ADALE 474K7 _ 9ASCO tr ADAL 074K6 ADALE 474K7 _ 9ASCO tr ADALD 074K6 ADALE 474K6 _ 9ASCO tr 04788 C4Y683 _ CLAL4 tr 03B4C1 03B4C1 _ CANTC	VURNIEN AVRSIFE AVRSIFE CIMELFE CIMELFE SMRELFE SMRELFE SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN AIRESFE AIRESFE AIRESFE AIRESFE AVRELFE SVRELFE SVRELFE SVRELFS SIRELFS SIRELFS SIRELFS SIRELFE	GAHIL GAHIL	IQUM LARC IQUM LGDN IQUM LGDN IQUM LGDN IQUM LGDN IQUM LATC IQUM LATC IQUM LATC IQUM LGDN IQUM L	CAKR NATRAKM CAKM CAKM NADR AAKM NADR AAKK CAKK CAKK CAKK CAKK CAKK CAKK CAK	I M K JYPFT VH3DLKPN S JMT J WITT PLG I SR VYFLUMGSMAR T SJRNGNRP ETMS J WITT PLG I SR JYRLDMGSMAR T SJRNGNRP ETMS J WITT PLG I SH JYRLDMDA DEVIR 3-GERP FIMAS I WITT PLN I SH JYRLDWDI YEEMG P-KKRP STMAS J WITT PLN I SH JYRLDWDI YEEMG P-KKRP STMAS J WITT PLN I SK JYRLDI DJ YEEMG P-KKRP STMAS J WITT PLN I SK JYRLDI DJ YEEMG P-KKRP STMAS J WITT PLN I SK JYRLDI DJ P QUT DIMSS J WITT PLG I SK JYRLDI DJ QUT DIMSS J WITT PLG I SK JYRLDI DJ QUT DIMSS J WITT PLG I SK JYRLDI DJ QUT DIMSS J WITT PLG I SK JYRLDI EL DK SKK VDS J MMT SJ WITT PLG I SK SYRLDI EL DK SKK VDS J MMT SJ WITT PLG I SK SYRLDI EL EKIKKLDS J MMT SJ WITT PLG I SK STRLDL EL EKIKKLDS J MMT SJ WITT PLG I SK STRLDU EL KFRNG DKP DIMS J WITT PLG I SK STRLDU DE KSFRNG DKP DIMS J WITT PLG I SK STRLDU DE KSFRNG DKP DIMS J WITT PLG I SK STRLDU DE KSFRNG DKP DIMS J WITT PLG I SK STRLDU DE KSFRNG DKP DIMS J WITT PLG I SK STRLDU DE KSFRNG DKP DIMS J WITT PLG I SK STRLDU DE KSFRNG DKP DIMS J WITT PLG I SK STRLDU DE KSFRNG DKP DIMS J WITT PLG I SK STRLDU DE KSFRNG DKP DIMS J WITT PLG I SK STRLDU DE KSFRNG NKP DIMS J WITT PLG I SK STRLDU DE KSFRNG NKP DIMS J WITT PLG I SK STRLDU DE KSFRNG NKP DIMS J WITT PLG I SK STRLDU DE KSFRNG NKP DIMS J WITT PLG I SK STRLDU DE KSFRNG NKP DIMS J WITT PLG I SK STRLDU DE KSFRNG NKP DIMS J WITT PLG I SK STRLDU DE KSFRNG NKP DIMS J WITT PLG I SK STRLDU DE KSFRNG NKP DIMS J WITT PLG I SK STRLDU DE KSFRNG NKP DIMS J WITT PLG I SK STRLDU DE KSFRNG NKP DIMS SV WITT PLG I SK STRLDU DE KSFRNG NKP DIMS SV WITT PLG I SK STRLDU DE KSFRNG NKP DIMS SV WITT PLG I SK STRLDU DE SG NAM NKP SH SI SV WITT PLG I SK STRLDU DE SG NAM NKP SH SV WITT PLG I SK STRLDU DE SG NAM NKP SH SV WITT PLG I SK STRLDU DE SG NAM NKP SH SU SV WITT PLG I SK SVRDY ED SG NAM NKP SH	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1064 1069 1064 1050 1064 1050 1064 1093 1121 1091 1089 1116 1115 1016 1056 1077 1083 1075 1078 1075
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E4J0 ADAL 67E4J0 _ 9ASCO tr ADALE 37EV0 ADAL 63EVP0 _ 9ASCO tr ADALE 37EV0 ADALE 37EV0 _ WICAO tr ADALE 37EV0 ADALE 37EV0 _ 9ASCO tr ADALE 37EV0 ADALE 37EV0 _ 9ASCO tr ADALE 73EV0 ADALE 72EV1 _ 9ASCO tr ADALE 91 ADALE 92EV1 _ 9ASCO tr ADALE 91 ADALE 92EV1 _ 9ASCO tr ADALE 91 ADALE 72EV1 _ 9ASCO tr ADALE 73EV1 _ ADALE 72EV1 _ 73773 = RAZNA tr GOWE72 GOWE72 _ NAUDC tr ADALE 82EV58 _ ADALE 82EV5 _ 3ACEU tr ADALE 82EV58 _ ADALE 82EV5 _ 3ACEU tr ADALE 82EV59 SADATE 72EV71 _ 9ASCA tr GOWE72 SDN79 _ ZCRC tr ADALE 48EV7 ADALE 48EV7 _ 9ASCO tr ADALE 48EV7 _ 9ASCO tr ADALE 48EV7 _ 9ASCO tr ADALE	VURNIER AVRSIE AVRSIE AVRSIE CIRELFE SMRELFE SMRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN AIRESFR TIRELFN AIRESFR AVRELFE SVRELFE SVRELFE SVRELFE SVRELFE SVRELFE SVRELFE SIRELFA SIRELF	GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL SAHIL SAHIL SAHIL SAHIL SAHIL SAHIL SAHIL SAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL MAN	IQUM LAPE IQUM LAPE	"A KR NA TR NA TR NA TR NA TA NA TA NA TA NA TA NA TA NA TR NA TR	INK SYPFTUH3DLKEN SIMT 3UMTT PLG INK SVPLTUH3	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1028 1064 1064 1064 1064 1064 1064 1064 1064
tr ADALE 302CG ADAL F2302CG _ LTP3T tr ADALE 37440 ADAL 67440 SASCO tr ADALE 3PUPO ADAL 152PUPO] SASCO tr ADALE 3PUPO ADALE 32PUPO] SASCO tr ADALE 3PUPO ADALE 32PUPO] SASCO tr ADALE 395W0 ADALE 32PUPO] SASCO tr ADALE 395W0 ADALE 32PUPO] tr KOKTX3 KOKTX3 KICCF tr KOKTX3 KOKTX3 KICCF tr KOKTX3 KOKTX3 KICCF tr ADALE 30PUT ADALE 32PUT] SASCO tr ADALE 30PUT] SASCE ASSCO tr ADALE STAPE 3 ADALESTARS] SASCE U tr ADALE ASTE ADALESTARS] SASCE U tr ADALESTARS] SASCE] SASCE O tr ADALESTARS] SASCE] SASCE O tr ADALESTARS] SASCE] SASCE O tr ADALE	VURNIEN AVRSIFE AVRSIFE CIMELFE CIMELFE SMRELFE SMRELFE SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN AIRESFE AIRESFE AIRESFE AIRESFE SIRELFN SIRELFN SIRELFN SVRELFE SVRE SVRE SVRE SVRE SVRE SVRE SVRE SVRE	GAHIL MATANA	IQUM LAPE. IQUM LGDW LGPC IQUM LGDW LGPC IQUM LGDW LGPC IQUM LATC IQUM LATC IQUM LATC IQUM LGPC IQUM LGPC	"A KR VA TR A KM "A KM "A KM "A KM "A KR "A KR""A KR "A KR""A KR""	I M K JYPFT VH3DLKPN S JMT J WITT P LG I SR VNLDMGSMAR T SJNGNRP ENS J WITT P LG I SR NYLDMGSMAR T SJNGNRP ENS J WITT P LG I SH JYRIDMDA DEVIR 3-GREP FIMAS J WITT P LN I SH JYRIDMDA DEVIR 3-GREP FIMAS J WITT P LN I SH JYRIDMDA YEEMG P-KKRP STMAS VIWIT P LN I SK JYRIDI D3 YEEMG P-KKRP STMAS VIWIT P LN I SK JYRIDI D3 YEEMG P-KKRP STMAS VIWIT P LN I SK JYRIDI D3 YEEMG P-KKRP STMAS VIWIT P LN I SK JYRIDI D3 YEEMG P-KKRP STMAS VIWIT SJ LG I SK JYRIDMD DEVIR JL LCHTS VIWIS J LG I SK JYRIDP D1 NQSKT INS DLMT SVIWIS J LG I SK SYRIDP D1 NQSKT INS JLMT SVIWIS J LG I SK SYRIDP D1 DKSKK V DS JMMT SVIWIS J LG I SK SYRIDL EL EKIKK LDS J MMT SVIWIS J LG I SK SYRIDL EL EKIKK LDS J MMT SVIWIS J LG I SK SYRIDD D2 KSFKNG DKP DMS J WITT P LG I SK SYRIDD D2 KSFKNG DKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG DKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG DKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG DKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SIRLDV D2 KSFKNG NKP DMS SVIWIT P LG I SK SVRUDY D2 KSFKNG NKP DMS SVIWIT P LG I SK SVRUDY D2 KSFKNG NKP DMS SVIWIT P LG I SK SVRUDY D2 KSFKNG NKP DMS SVIWIT P LG I SK SVRUDY D2 KSFKNG NKP DMS SVIWIT P LG I SK SVRUDY D2 KSFKNG NKP DMS SVIWIT P LG I SK SVRUDY D2 KSFKNG NKP DMS SVIWIT P LG I SK SVRUDY D2 KSFKNG NKP DMS SVIWIT P LG I SK SVRUDY D2 KSFKNG NKP	1000 1083 859 1062 1038 1065 1069 1040 1092 733 1029 1069 1069 1064 1050 1069 1064 1050 1064 1093 1121 1091 1089 1064 1093 1121 1091 1089 1066 1016 1056 1077 1083 1075 1075 1075 1079 1023 1079 1056
tr AOALE 302CG AOĀLE 302CG _ LIPST tr AOALE 37E40 AOAL 67E4J0 _ 9ASCO tr AOALE 3FEV0 AOAL 63FEVD0 _ 9ASCO tr AOALE 3FEV0 AOALE 3FEV0 _ WICAO tr AOALE 3FEV0 AOALE 3FEV0 _ WICAO tr AOALE 3FEV0 AOALE 3FEV0 _ WICAO tr KOKIX 3 KOKIX 3 _ WICCF tr WOMIL 2 WOMIL 2 _ 9ASCO tr AOALE 30EV1 AOALE 3FEV0 _ 9ASCO tr AOALE 30EV1 AOALE 3FEV0 _ 9ASCO tr AOALE 30EV1 AOALE 3FEV0 _ 9ASCO tr AOALE 7SEO AOALE 3FEVE _ 9ASCO tr AOALE 7SEO AOALE 3FEVE _ 9ASCO tr AOALE 7SEO AOALE 3FEVE _ 9ASCO tr AOALE 7SEO AOALE 7SEO _ 9ASCO tr AOALE 7SEO AOALE 7SEO _ 9ASCO tr AOALE 7SEO AOALE 7SEO _ 9ASCO tr AOALE 9W & I AOALE 7SEO _ 9ASCO tr AOALE 9W & I AOALE 7SEO _ 9ASCO tr AOALE 9W & I AOALE 7SEO _ 7ASCO tr AOALE 7SEO _ 107973 ADALE 7SEO _ 5ASCH tr GOWE 7 2 GOWE 72 _ NAUDC tr GOWE 72 GOWE 72 _ NAUDC tr AOALE 8WKS ADAD LEXKKS _ SACEU tr AOALE 8WKS ADAD LEXKKS _ SACEU tr AOALE 8WKS ADAD LEXKKS _ SACEU tr AOALE 8WKS ADAD LEXKS _ SACEU tr AOALE 8WKS ADAD LEXKS _ SACEU tr AOALE 8W & I ADALE 7W & SACAR tr GOME 7 SDN 79 _ ZYGRC tr AOALE 48WT (ADALE 48WT 6 _ 9ASCO tr AOALE 48WT 6 ADALE 48WT 6 _ 9ASCO tr AOALE 48WT 6 ADALE 48WT 6 _ 9ASCO tr ADALE 48WT 6 ADALE 48WT 6 _ 9ASCO	VURNIER AVRSIFE AVRSIFE CIMELFE CIMELFE SMRELFE SMRELFO SIRELFO SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH AIRESFE AIRESFE AIRESFE AIRELFH SIRELFE SVRELFE SVRELFE SVRELFE SVRELFE SIRELFE SMRELFE SIRELFE	GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL SAHIL SAHIL SAHIL SAHIL SAHIL SAHIL SAHIL SAHIL SAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL GAHIL MAHINAHINAHI	IQUM LAPE. IQUM LGDW LGPC IQUM LGDW LGPC IQUM LGDW LAPC IQUM LAPC IQUM LAPC IQUM LAPC IQUM LAPC IQUM LGPC IQUM LGPC	CARRA VATRA CARMA CARMA CARMA CARMA CARMA CARMA CARRA CARA CARRA C	I M K JYPFT VH3DLKPN S JMT J WITT P LG I JR K JVRLDG SMAT K 35 KINGNRP ENKS J WITT P LG I JR KJVRIDD TN RVAKNGNRP DEMS J WITT P LD I JR JYRIDM DA DEVIR 3-GREP FIMAS J WITT P LN I SR J KIND VDT YELMG P-KKRP STMAS J WITT P LN I SK J KVRIDD JS YELMG P-KKRP STMAS J WITT P LN I SK J KVRIDD JS YELMG P-KKRP STMAS J WITT P LN I SK J KVRIDD JS YELMG P-KKRP STMAS J WITT P LN I SK J KVRIDD JS YELMG P-KKRP STMAS J WITT P LN I SK J KVRIDD JS YELMG P-KKRP STMAS J WITT P LD I SK J KVRIDD JS YELMG P-KKRP STMAS J WITT P LG I SK SVRIDD DIS NQSKT INS DLMT SJ WITT P LG I SK SVRIDD DIS DUSKT INS DLMT SJ WITT P LG I SK SVRIDP DIS DUSKT INS DLMT SJ WITT P LG I SK SVRLDP LI SK SKK V DS SMMT SJ WITT P LG I SK SVRLD E LI SK SKK V DS SMMT SJ WITT P LG I SK SVRLD Z SK SKK V DS SMMT SJ WITT P LG I SK SVRLD Z SK	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1028 1064 1064 1064 1064 1064 1064 1064 1064
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E40 ADAL 67E40 SASCO tr ADALE 3FUPO ADAL 67E40 SASCO tr ADALE 3FUPO ADAL 63EVDO _ SASCO tr ADALE 37EWO ADALE 37EWO _ WICAO tr ADALE 37EWO ADALE 37EWO _ SASCO tr GECR2 5 GCCR25 _ KLUMA tr GOM 216 WOT GTA K _ LUMA tr GOM 216 WOT GTA K _ LUMA tr GOM 216 WOT GTA & LUMA tr GOM 216 WOT GTA & LUMA tr GOM 216 WOT GTA & LUMA tr GOM 216 GOW 57 _ ASHGO tr GECR 31 GEGR 35 _ ALZAF tr J737Y 3 J737Y 3 _ KAZNA tr GOWE7 2 GOW E7 _ NAUDC tr GOWE7 2 GOW E7 _ NAUDC tr GOWE7 2 GOW E7 _ NAUDC tr GOWE7 2 GOW F7 _ NAUDC tr GOWE7 2 GOW F7 _ NAUDC tr ADAL 8FKWS ADAO LEFKWS _ SACEU tr ADALE 4FKSF JDAPS = LACTC tr GOM 21 GOY DOR _ TORDC tr ADALE 4FKF7 ADAL CANTC _ SASCO tr ADALA 01677 ADAL 124FKF7 _ SASCO tr ADALA 01677 ADAL 124FK76 _ SASCO tr ADALA 01677 GADA 124FK76 _ SASCO tr ADALA 124F76 JSAF76 _ DEBHA tr GSAFY0 GAEYO 3 FAFW tr GSAFY0 GAEYO 3 FAFW tr GSAFY0 GAEYO 3 FAFW tr GSAFY0 GAEYO 3 FAFW	VURNIEN AVRSIFE AVRSIFE CIMELFE CIMELFE SMRELFE SMRELFE SIRELFN SIRELFN SIRELFN SIRELFN SIRELFN SIRELFH SIRELFH AIRESFE AIRESFE AIRESFE SVRELFE SVRELFE SVRELFE SVRELFE SVRELFE SIRELFS SIRELFE	GA HIL GA	IQUM LAPE. IQUM LGDN IQUM LGDN LGDC IQUM LGDN LAPC IQUM LGDN LAPC IQUM LGDN LAPC IQUM LAPC IQUM LGPC IQUM	LARRA VATRAKM VATRAKM VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA VAKMA	I M K JYPFT VH3DLKPN S JM T JUWT P LG I SK VYPLT VH3	1000 1083 859 1062 1030 1038 1065 1069 1069 1069 1029 1029 1069 1064 1064 1050 1041 1093 1221 1091 1115 1115 1115 1061 1077 1089 1116 1115 1015 1072 1075 1078 1079 1023 1079 1023
tr ADALE 302C6 ADAL F2302C6 _ LTP3T tr ADALE 37440 ADAL 678440 SASCO tr ADALE 375W0 ADAL 678440 SASCO tr ADALE 375W0 ADALE 375W0 _ MICAO tr ADALE 375W0 ADALE 375W0 _ MICAO tr ADALE 375W0 ADALE 375W0 _ MICAO tr KOKTX3 KOKTX3 _ WICCF tr WGMIL 2 WGMIL 2 SASCO tr ADALE 375W0 ADALE 375W0 _ MICAO tr ADALE 375W0 ADALE 375W1 _ SASCO tr ADALE 375W0 ADALE 375W1 _ SASCO tr ADALE 375W0 ADALE 375W1 _ SASCO tr ADALE 375W1 ADALE 375W1 _ SASCO tr ADALE 75W1 _ ADALE 375W1 _ SASCO tr GSW 52 GS JW3 _ RAZAF tr GSW 54 GSW 57 _ SHGO tr GSW 57 2 GOW E7 2 ADALE 475W1 _ SASCE U tr GSW 54 GSW 54 _ TLFPH tr ADALE 37W1 ADALE 7W71 _ SASCE U tr GSW 55 JGEP 55 _ SACAR tr GSW 79 CSD 79 _ Z YGRC tr CSDW 79 CSD 79 _ Z YGRC tr GSW 70 CSD 79 _ Z YGRC tr GADL 0 FKK 6 ADALE 74KCF _ SASCO tr ADALE 48QF7 ADALE 48QF7 SASCO tr ADALE 48QF7 CANTE _ SASCO tr ADALE 48QF7 CANTE _ SASCO tr ADALE 48QF7 CANTE _ SASCO tr ADALE 48QF7 SASCO _ TCHC tr HSXIL 6 HSXIL6 _ CANCO tr HSXIL6 HSXIL6 _ CANCO tr HSXIL6 HSXIL6 _ CANCO tr HSXIL6	VURNIER AVRSIFE AVRSIFE AVRSIFE CIMELFE SMRELFE SMRELFE SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE SIRELFE SVRELFE SVRELFE SIRELFE	GA HII GA HII GA HII GA HII GA HII GA HII GA HII GA HII GA HII GA HII SA	IQUM LAPE. IQUM LAPE. IQUM LGDW LGPC IQUM LGPC IQUM LGPC IQUM LATC IQUM LATC IQUM LGPC IQUM LFPC IQUM LFPC	CARRA VATRA CARMA CARMA CARMA CARMA CARMA CARRA CARA CARRA C	I HK SYPFTUH3DLKEN SSMT SUMTT PLG I SK SVELDMGSMAR H SSNGNRP ENSSUMTT PLG I SK AVRIDI TN RVAKINGNRP ENSSUMTT PLG I SK AVRIDI TN RVAKINGNRP DEMSSUMTT PLG I SK JIRUDYD YELMG P-KKRP STMASUMT PLD I SK JIRUDYD YELMG P-KKRP STMASUMT PLD I SK JIRUDND DEUIR S	1000 1083 859 1062 1030 1038 1065 1069 1040 1092 733 1029 1028 1069 1064 1064 1064 1064 1093 1121 1091 1089 1116 1115 1081 1089 1116 1115 1081 1083 1077 1083 1077 1083 1077 1083 1075 1075 1078 1023 1021 1023 1021 1023 1025 1066 1060 1056 1068
tr ADALE 302C6 ADĀLE 302C6 _ LIPST tr ADALE 37E40 ADAL 67E40 SASCO tr ADALE 3FUPO ADAL 67E40 SASCO tr ADALE 3FUPO ADAL 63EVDO _ SASCO tr ADALE 37EWO ADALE 37EWO _ WICAO tr ADALE 37EWO ADALE 37EWO _ SASCO tr GECR2 5 GCCR25 _ KLUMA tr GOM 216 WOT GTA K _ LUMA tr GOM 216 WOT GTA K _ LUMA tr GOM 216 WOT GTA & LUMA tr GOM 216 WOT GTA & LUMA tr GOM 216 WOT GTA & LUMA tr GOM 216 GOW 57 _ ASHGO tr GECR 31 GEGR 35 _ ALZAF tr J737Y 3 J737Y 3 _ KAZNA tr GOWE7 2 GOW E7 _ NAUDC tr GOWE7 2 GOW E7 _ NAUDC tr GOWE7 2 GOW E7 _ NAUDC tr GOWE7 2 GOW F7 _ NAUDC tr GOWE7 2 GOW F7 _ NAUDC tr ADAL 8FKWS ADAO LEFKWS _ SACEU tr ADALE 4FKSF JDAPS = LACTC tr GOM 21 GOY DOR _ TORDC tr ADALE 4FKF7 ADAL CANTC _ SASCO tr ADALA 01677 ADAL 124FKF7 _ SASCO tr ADALA 01677 ADAL 124FK76 _ SASCO tr ADALA 01677 GADA 124FK76 _ SASCO tr ADALA 124F76 JSAF76 _ DEBHA tr GSAFY0 GAEYO 3 FAFW tr GSAFY0 GAEYO 3 FAFW tr GSAFY0 GAEYO 3 FAFW tr GSAFY0 GAEYO 3 FAFW	VURNIER AVRSIFE AVRSIFE AVRSIFE CIMELFE SMRELFE SMRELFE SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH SIRELFH AIRESFE AIRESFE AIRESFE AIRESFE AIRESFE SIRELFE SVRELFE SVRELFE SIRELFE	GA HIL GA HIL SA HIL SA HIL GA	IQUM LAPE. IQUM LGDW LGPC IQUM LGDW LGPC IQUM LGDW LGPC IQUM LGPC IQUM LATC IQUM LGPC IQUM LFPC IQUM LFPC	LARRA UATRA LARMA LARMA LARMA LARMA LARMA LARMA LARMA LARRA	I M K JYPFT VH3DLKPN S JM T JUWT P LG I SK VYPLT VH3	1000 1083 859 1062 1030 1038 1065 1069 1069 1069 1029 1029 1069 1064 1064 1050 1041 1093 1221 1091 1115 1115 1115 1061 1077 1089 1116 1115 1015 1072 1075 1078 1079 1023 1079 1023

P. Palanivelu; BJI	, 20(3): 1-35	, 2017; Article	no.BJI.38632
--------------------	---------------	-----------------	--------------

tr	B6K333 B6K333_SCHJY 013993 RP0M_SCHP0
tr	[390008 390008_3CHOY
	39X2W4 39X2W4_3CHCR A0A1E3Q3C6 A0A1E3Q3C6_LIPST
ter	1303167E4J01303167E4J0 93500
tr	AOA1E3PUPO AOA1E3PUPO 9A3CO
tr	A 0 A 0 H 5 C 7 R 0 A 0 A 0 H 5 C 7 R 0 _ CYB J A A 0 A 1 E 3 P 5 W 0 A 0 A 1 E 3 P 5 W 0 _ WI C A 0
tr	KOKTX3 KOKTX3_WICCF W6MIL2 W6MIL2_9ASCO
tr	AOA1E3QPI7 AOA1E3QPI7_9ASCO
	A0A1D2V948 A0A1D2V948_9A3C0 A0A1B7SME0 A0A1B7SME0_9A3C0
tr	Q6CRZ5 Q6CRZ5_KLULA W0TGI8 W0TGI8_KLUMA
tr	1A0A109UWS11A0A109UWS1 9SACH
tr	G8 JMS2 G8 JMS2_ERECY Q7 58 P7 Q7 58 P7_A8HGO R9XDF6 R9XDF6_A8HAC H2 A5 J8 H2 A5 J8_KAZAF
tr	R9XDF6 R9XDF6_ASHAC
tr	H2 A5 J8 H2 A5 J8_KAZ AF J7 57 Y3 J7 57 Y3_KAZ NA
tr	GOVD01 GOVD01_NAUCC GOWE72 GOWE72_NAUDC
tr	GOWE72 GOWE72_NAUDC Q6FLX9 Q6FLX9_CANGA
tr	G8BS54 G8BS54_TETPH
tr	AOAOL8RKW5 AOAOL8RKW5_SACEU AOAOL8VRU3 AOAOL8VRU3_9SACH
tr	J8 PP 58 J8 PP 58_SACAR A0 A0 C7 MY7 1 A0 A0 C7 MY7 1 _95 ACH
tr	C5DNP3 C5DNP3_LACTC
tr	C5DNP3 C5DNP3_LACTC C5DK79 C5DK79_ZYGRC G8ZR00 G8ZR00_TORDC
tr	AOA1E4ROF7 AOA1E4ROF7_9ASCO
tr	A 0 A 0 L 0 P 4K 6 A 0 A 0 L 0 P 4 K 6 _ 9 A 3 C 0 A 0 A 1 A 0 H G T 7 A 0 A 1 A 0 H G T 7 _ 9 A 3 C 0
tr	C4Y8E3 C4Y8E3_CLAL4
tr	G3B4C1 G3B4C1_CANTC A3LX46 A3LX46_PIC5T
tr	AOA1E4SMT6 AOA1E4SMT6_9ASCO
tr	A5DN82 A5DN82_PICGU B5RTF6 B5RTF6_DEBHA
tr	G3AEY0 G3AEY0_SPAPN
+	68B7X1 68B7X1_CANPC H8X1L6 H8X1L6_CANO9
tr	B9W6L5 B9W6L5 CANDC
tr	C4YFJ1 C4YFJ1_CANAW C5ME71 C5ME71_CANTT M3IK19 M3IK19_CANMK
tr	M3IK19 M3IK19_CANMX
	B6K333 B6K333_SCHJY
apl	013993 RPOM_SCHPO
ap tr tr	013993 RPOM_SCHPO 990008 99008_SCHOY 99X2W4 99X2W4_SCHCR
ap tr tr tr	013993 RPOM_SCHPO 99008 S9009_SCHOY 99X2W4 S9X2W4_SCHCR A0A1E303C6 A0A1E303C6_LIPST
ap tr tr tr tr tr	013953]RFOM_SCHOO S90008 S9008_SCHOY S9X2W4 S9X2W4_SCHCR NOALE303C6 ADALE303C6_LIPST ADALE3PUF0 ADALE3PUF0_SASCO ADALE3PUF0 ADALE3PUF0_SASCO
ap tr tr tr tr tr tr tr	013993 RPOM_SCHPO S9Q0Q8 S9Q0Q8_SCHOY S9X2W4 S9X2W4_SCHCR A0A1E3Q3C6 A0A1E3Q3C6_LIPST A0A1E5TE4J0 A0A1E3FUF0_SASCO A0A1E3FUF0 A0A1E3FUF0_SASCO A0A0HSCTR0 A0A0HSCTR0_CYEJA
ap tr tr tr tr tr tr tr tr tr	013953]RPOM_SGRPO S90008 S90008_SCHOY S9X2W4 S9X2W4_SCHCR NOALE303C6 ADALE303C6_LIPST A0A167E4J0 A0A167E4J0_SASCO A0A163PUP0 AOALE3PUP0_SASCO A0A0H5C7R0 A0A0H5C7R0_CYBJA A0ALE3PSW0 A0ALE3PSW0_WICAO KOXIX3 KOXIX3_WICCF
api tri tri tri tri tri tri	013953]RPOM_SCHOP S90008 S90008_SCHOY S9X2W4 S9X2W4_SCHCR ADAL5203C6 ADAL533C6_LIPST ADAL572470 ADAL6724J0_SASCO ADAL52PUP0 ADAL53PUP0 ADADH527R0 ADAL53PUP0 ADAL52PSW0 ADAL53PSW0_WICAD KOKTX3 KOKTX3_WICCP WEMIL2 WEMIL2 SASCO
ap tr tr tr tr tr tr tr tr tr	013933]RPOM_SCHOV S90008 S90008_SCHOY S9X2W4 S9X2W4_SCHCR ADAL5243C6 ADALB303C6_LIPST ADAL572470 ADAL574J0_SASCO ADALB3PUP0 ADALB3PUP0 SASCO ADALB3PUP0 ADALB3PUP0_SASCO ADALB3PU0 ADALB3PSM0_WICAD KOKTX3 KOKTX3_WICCP WOHLI2 WSHL2_SASCO ADALB30FT ADALB30FT_SASCO ADALB30FT ADALB30FT_SASCO
ap tr tr tr tr tr tr tr tr	013953]RPOM_SCHOV 950008 S50008_SCHOY 950208 S50204_SCHOY 35X2W4 S5X2W4_SCHCR ADAL572470 ADAL6724J0_SASCO ADAL52FUF0 ADAL52FUF0_SASCO ADAD4557R0 ADAL52FUF0_WICAO KOKTX3 KOKTX3_WICCF WEMIL2 WEMIL2_SASCO ADAL525CHIMIL2_SASCO ADAL525CO ADAL52746_SASCO ADAL57SUF0 ADAL524050_SASCO ADAL57SUF0 ADAL524050
api tri tri tri tri tri tri tri tri tri tr	013953]RPOM_SGEPO 950008 S50008_SCHOY 950208 S50208_SCHOY 55X2W4 S5X2W4_SCHCR ADAL572470 ADAL6724J0_SASCO ADAL52FUF0 ADAL59709_SASCO ADAD452700 ADAL537500_WICAO KOKTX3 KOKTX3_WICCF WEMIL2 WEMIL2_SASCO ADAL530P17 ADAL530P17_SASCO ADAL530P17 ADAL530P17_SASCO ADAL530P17 ADAL530P17_SASCO ADAL530P17 ADAL530P17_SASCO ADAL530P10 ADAL530P10_SASCO Q6CR25 Q6CR25_KLULA W07CT48 WID7CT8_KLUMA
api tri tri tri tri tri tri tri tri tri tr	013933]RPOM_SGEPO \$90028]S90028_SCHOY \$97204 \$97204_SCHOY \$97204 \$97204_SCHOY \$97204 \$97204_SCHOY \$001672470]R0016740_\$RSCO \$001827070]R00182700_VECA \$001827070]R00182700_VECA \$001827071]R00182700_VECA \$001827071]R00182700 \$001827071]R00182700 \$001827071]R00182700 \$001827071]R00182700 \$001827071]R0018700 \$00182500 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$00180000 \$00180000 \$00180000 \$00180000 \$00180000 \$001800000 \$001800000 \$0018000000 \$0018000000000 \$00180000000000000000000000000000000000
api tri tri tri tri tri tri tri tri tri tr	013933]RPOM_SGEPO \$90028]S90028_SCHOY \$97204 \$97204_SCHOY \$97204 \$97204_SCHOY \$97204 \$97204_SCHOY \$001672470]R0016740_\$RSCO \$001827070]R00182700_VECA \$001827070]R00182700_VECA \$001827071]R00182700_VECA \$001827071]R00182700 \$001827071]R00182700 \$001827071]R00182700 \$001827071]R00182700 \$001827071]R0018700 \$00182500 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$0018000 \$00180000 \$00180000 \$00180000 \$00180000 \$00180000 \$001800000 \$001800000 \$0018000000 \$0018000000000 \$00180000000000000000000000000000000000
api tri tri tri tri tri tri tri tri tri tr	013933]RPOM_SGEPO \$90008\S0008_SCHOY \$90008\S0008_SCHOY \$90208\S0204\S0206LIPST ADAL572470 R0A1633C6_LIPST ADAL572470 R0A163700_SASCO ADA1529UP0 R0A1239UP0_SASCO ADA1529FW0 R0A12395W0_WICAO KOKTX3 KOKTX3_WICCP W6MIZ1\W6WIL2_98SCO ADA1529FT7 R0A1530FI7_9ASCO ADA153WE0 R0A157ME0_9ASCO ADA1575ME0 R0A157ME0_9ASCO ADA1575ME0 R0A157ME0_9ASCO Q6CR25 Q6CR55_KULLA W07CT8 KUNAL ADA105UW31 R0A105UW31_95ACH G8JM52[G8JM52_EPCCY Q75BF7 Q75BF7_ASHGO R9XDF6 R5XDF6_SSHACH H2A538
ap) tr tr tr tr tr tr tr tr tr tr	013953]RPOM_SGRPO 950008 S50008_SCHOY 950008 S50208_SCHOY 950208 S50204]S50274_SCHCY ADAL572470 ADAL5724J0_SASCO ADAL52FUPO ADAL52FUPO_SASCO ADAL52FUPO ADAL52FUPO_SASCO ADAL52FUPO ADAL52FUPO_SASCO ADAL52FUPO ADAL52FUPO_SASCO ADAL52FUPO ADAL52FUPO KOKTX3 KOKTX3_WICCF WGML2 WGML2_SASCO ADAL52FUPO ADAL52FUPO ADAL52FUPO ADAL52FUPO ADAL52FUPO ADAL52FUPO ADAL52FUPO ADAL52FUPO ADAL52FUPO ADAL52FUPO ADAL52FUPO 0407658 WGTC58FLUDA ADAL62FUPO 0758F7 ADA150 R5%DF6 R5%DF5_ASHAC H2A536 H2A53KALFA J757Y3 J75YY3KALNA
ap) tr tr tr tr tr tr tr tr tr tr	013933]RPOM_SGEPO S90008]SS0008_SCHOY S9X2W4 S3X2W4_SCHCR ADA1672470]ADA1674J0_SASCO ADA1672470]ADA1674J0_SASCO ADA182FUPO ADA183PUPO_SASCO ADA182FUPO ADA183PUPO_SASCO ADA18275W0 ADA183PUPO_WICAO KOKTX3 KOKTX3_WICCF WEMIZ]WSUIZ_SASCO ADA1820PT7 ADA1830PUF048_SASCO ADA18279K0 ADA1875ME0_SASCO ADA1875ME0 ADA1875ME0_SASCO Q6CR25 Q6CR25_KUUAA ADA109UW31 ADA1875ME0_SASCO Q6SM28](GSM52_RECY Q75BF7 Q75BF7_ASHCO RSMDF6[SSUF5_ASHCC H2ASJ8 H2ASJ8_KAZAF H2ASJ8 H2ASJ8_KAZAF H2ASJ8 H2ASJ8_KAZAF
ap tr tr tr tr tr tr tr tr tr tr tr tr tr	013953]RPOM_SGRPO 990008 S90008_SCHOY 992008 S92008_SCHOY 992048 S9X2W4_SCHCR ADALE203C6 ADALE303C6_LIPST ADALE2FUTO ADALE3PUTO_SASCO ADALE3PUTO ADALE3PUTO_SASCO ADALE3PUTO ADALE3PUTO_SASCO ADALE3PUTO ADALE3PUTO_SASCO ADALE3PUT ADALE3OPIT_9ASCO ADALE27FT ADALE3OPIT_9ASCO ADALE3PUTO ADALE3OPIT_9ASCO ADALE3PUTO ADALE3OPIT_9ASCO ADALE3PUTO ADALE3OPIT_9ASCO ADALE3PUTO ADALE3OPIT_9ASCO ADALE3PUTO ADALE3OPIT_9ASCO ADALE3PUTO ADALE3OPIT_9ASCO ADALE3PUTO ADALE3OPIT_9ASCO Q6CR25 Q6CR25_XLULA W0TGI8 W0TGI8_KLUMA W0TGI8 W0TGI8_KLUMA W0TGI2 W0TGI8_KLUMA W0TGI8 W0TGI8_KLUMA
ap) tri tri tri tri tri tri tri tri	013933;RPOM_SGEPO \$90008;S0008_SCHOY \$90008;S0008_SCHOY \$90208;S0206;LDPST ADAL572470]ADAL5724J_SASCO ADAL572470]ADAL5724J_SASCO ADAL529UPO[ADAL23PUPO]SASCO ADAH5C7R0[ADAD45C7R0_CYEJA ADAL23P5W0]ADAL23P5W0_WICAO KUKIX2;KUKIX3_WICCF WEMIZ2;WEMIZ2_SASCO ADAL23P5W0[ADAL23P5W0_WICAO KUKIX3 KUKIX3_WICCF WEMIZ2;WEMIZ2_SASCO ADAL23P5W0[ADAL23P5W0_WICAO ADAL23P5W0[ADAL23P5W0_SASCO ADAL27948[ADAL29745_SASCO ADAL27948[ADAL29745_SASCO ADAL27948[ADAL29745_SASCO ADAL27948[ADAL29745_SASCO Q6CR25](GCR25_KUULA WOTCI8]KUMAL ADAL09UW31[ADAL09UW31_SACH GCMM22[GJMS2_ERCY_ Q75BP7[075B77_ASHGO RSXDF6[RSXDF6_SSHACH H2ASJ3]H2ASJ3_KAZAF J73773]J75733 KAZAF GVDD01_GUD01_NUNCC GOWE72[GOWE72_NAUDC Q6ESS4[GEDS4_CTEPH
api tri tri tri tri tri tri tri tri tri tr	013933;RFOM_5GFPO \$90008;S90008_SCHOY \$97204;\$97204_SCHOY \$97204;\$97204_SCHOY \$97204;\$97204_SCHOY \$97204;\$97204;\$97205 \$00152700;\$001600;\$97205 \$00152700;\$001600;\$97205 \$00152705;\$001600;\$000000
ap) tri tri tri tri tri tri tri tri	013933;RPOM_SGRPO 950008;S50008_SCHOY 950008;S50008_SCHOY 950208;S50008_SCHOY NDAL572470]ADA16724J_SASCO NOADH52700]ADA1574J_SASCO NOADH52700]ADA153PUPD SASCO NOADH52700]ADA153PUPD SASCO NOADH52700]ADA153PUPD SASCO NOADH52700]ADA153PUDO WEMIL2;WEMIL2_SASCO NOAL520PT7]ADA1530PUT_SASCO NOAL520PT7]ADA1530PUT_SASCO NOAL520PT7]ADA1530PUT_SASCO NOAL520PT7]ADA1530PUT_SASCO NOAL520PT7]ADA1530PUT_SASCO NOAL520PT7]ADA1530PUT_SASCO 0007218;WUDC28_KUUAA NOAL05UWS1]ADA105UWS1_SSACH 0735F7]C755F7_ASHCO RSXDF6;RSXDF6_ASHAC HX2AS3;RXALAF J757Y3;J757Y3_KALAF J757Y3;J757Y3_KALAF J757Y3;J757Y3_KALAF J757Y3;J757Y3_KALAF NAUDC 06FLX3;COFFLX3_CANGA 068554,CEPS4 NAUDC 06FLX3;CANGA 068554,CEPFH NOADL87KU3;ADA0L87KU5_SACEU ADA0L87KU3;ADA0L87KU5_SACH
ap) tr tr tr tr tr tr tr tr tr tr	013933;RPOM_SGRPO \$90008;S0008_SCHOY \$90008;S0008_SCHOY \$90008;S0008_SCHOY ADAL572471[20120] ADAL572470]ADAL5724J_SASCO ADAL539UP0[ADAL539UP0 SASCO ADAD452700[ADAL539UP0 SASCO ADAL539UP0[ADAL539UP0] KURIZ;KKNIZ_SASCO ADAL530FT7[ADAL530FI7_SASCO ADAL530FT7[ADAL530FI7_SASCO ADAL530FT7[ADAL530FI7_SASCO ADAL530FT7[ADAL530FI7_SASCO ADAL530FI7]ADAL530FI7_SASCO ADAL530FI7[ADAL530FI7_SASCO ADAL530FI7]ADAL530FI7_SASCO GCCR25[QCCR25_KLULA MOTCI8[MUTCI8_KLUAA ADAL030WS1[ADAL030WS1_SSACH G8JMS2[G8JMS2_ERCY G75BF7[075BF7_ASHCO G75BF7[075BF7_ASHCO G75BF7[075BF7_ASHCO G0FD21[G0WF72]KAUAC G0FD21[G0WF72]KAUAC G6FLS3[Q6FLS3_CAMCA G6B54[G5B54_TETPH ADAL68XW5[ADAL8XW5_SACEU ADAL68XW5[ADAL8XW5_SACEU ADAL68XW5[ADAL8XW5_SACEU ADAL68XW5]ADAL8XW5_SACEU ADAL68XW5[ADAL8XW5]SSACH J3FF58]J3FF58_SACAR ADADC7WY11[ADADC7W71]S3ACH
ap) tr tr tr tr tr tr tr tr tr tr	013933;RPOM_SGRPO \$90008;S0008_SCHOY \$90008;S0008_SCHOY \$90008;S0008_SCHOY ADAL572471[20120] ADAL572470]ADAL5724J_SASCO ADAL539UP0[ADAL539UP0 SASCO ADAD452700[ADAL539UP0 SASCO ADAL539UP0[ADAL539UP0] KURIZ;KKNIZ_SASCO ADAL530FT7[ADAL530FI7_SASCO ADAL530FT7[ADAL530FI7_SASCO ADAL530FT7[ADAL530FI7_SASCO ADAL530FT7[ADAL530FI7_SASCO ADAL530FI7]ADAL530FI7_SASCO ADAL530FI7[ADAL530FI7_SASCO ADAL530FI7]ADAL530FI7_SASCO GCCR25[QCCR25_KLULA MOTCI8[MUTCI8_KLUAA ADAL030WS1[ADAL030WS1_SSACH G8JMS2[G8JMS2_ERCY G75BF7[075BF7_ASHCO G75BF7[075BF7_ASHCO G75BF7[075BF7_ASHCO G0FD21[G0WF72]KAUAC G0FD21[G0WF72]KAUAC G6FLS3[Q6FLS3_CAMCA G6B54[G5B54_TETPH ADAL68XW5[ADAL8XW5_SACEU ADAL68XW5[ADAL8XW5_SACEU ADAL68XW5[ADAL8XW5_SACEU ADAL68XW5]ADAL8XW5_SACEU ADAL68XW5[ADAL8XW5]SSACH J3FF58]J3FF58_SACAR ADADC7WY11[ADADC7W71]S3ACH
ap) tr tr tr tr tr tr tr tr tr tr	013933;RPOM_SGRPO 950008;S90008_SCHOY 950008;S90008_SCHOY 950208;S90008_SCHOY NDAL572470]ADA16724J_SASCO NOADH52700]ADA1574J_SASCO NOADH52700]ADA153PUPD SASCO NOADH52700]ADA153PUPD SASCO NOADH52700]ADA153PUPD SASCO NOADH52700]ADA153PUPD SASCO NOADH52700]ADA153PUPD NOMIL2;WEMIL2;SASCO NOAL520PT7]ADA1530PU7_SASCO NOAL520PT7]ADA1530PU7_SASCO NOAL520PT7]ADA1530PU7_SASCO NOAL520PT7]ADA1530PU7_SASCO NOAL520PT7]ADA1530PU7_SASCO Q6CR25]Q6CR25_KLULA NOTCIS;WUDGTS_KLUNA NOAL05UWS1]ADA105UWS1_SSACH G8JMS2[G8JMS2_ERCY 0735F7]Q758F7_ASHCO G735F7]Q758F7_ASHCO G735F7]Q758F7_ASHCO G755F3[G0WE72]NAUCC G6WE72[G0WE72]NAUCC G6F1X5]Q6F1X5_CANGA G8554[G8554_TETPH NOADL87KW5]ADA0L87KW5_SACEU ADA0L87KW5]ADA0L87KW5_SACH NOADL87KW5]ADA0L87KW5_SACH NOADL87KW5]ADA0L87KW5_SACH NOADL87KW5]ADA0L87KW5_SACH NOADL87KW5]ADA0L87KW5_SACH NOADL87KW5]ADA0L87KW5_SACH NOADL87KW5]ADA0L87KW5_SACH NOADL87KW7]ADA0L87KW5_SACH NOADL87KW7]ADA0C7M771_SACH C5DNF3]C5DNF3_LCCC C5DNF3[C5DNF3_LCCC
	013933;RFOM_5GFPO \$90026;S90026;SHOY \$97204;S37204_SCHOY \$97204;S37204_SCHOY \$97204;S37204_SCHOY \$97204;S37204_SCHOY \$97204;S37204;S37204;S37204 \$004152704;J0041537500_SASCO \$0041527050;J0041537500_SASCO \$0041527054;J0041537500_SASCO \$0041527054;J0041537500_SASCO \$0041575050;J0041537500_SASCO \$0041575050;J0041537500_SASCO \$0041575050;J0041537500 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007615,S1004 \$007616;007515,S1004 \$007616;007515,S1004 \$007616;007515,S1004 \$007616;007515,S1004 \$007616;007515,S1004 \$007616;007515,S1004 \$007616;007515,S1004 \$007616;007515,S1004 \$007616;007515,S1004 \$007616;007515,S1004 \$007616;007515,S1004 \$007616;000505,S1004 \$007616;000505,S1004 \$007616;000505,S1004 \$007616;000505,S1004 \$007616;0005
ap tr tr tr tr tr tr tr tr tr tr	013933;RPOM_3CEPO \$90028;S90028_SCHOY \$97204;S9204_SCHOY \$97204;S9204_SCHOY \$97204;S9204_SCHOY \$97204;S9204_SCHOY \$97204;S9204,S9205 \$0012900;100129740 \$000452700;100129740 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000000;00000 \$000000;00000 \$000000;00000 \$000000;00000 \$000000;00000 \$000000;00000 \$000000;00000 \$00000;000000 \$00000;00000 \$00000;000000 \$00000;000000 \$000000;000000 \$000000;000000 \$0000000000
ap tr tr tr tr tr tr tr tr tr tr	013933;RPOM_3CEPO \$90028;S90028_SCHOY \$97204;S9204_SCHOY \$97204;S9204_SCHOY \$97204;S9204_SCHOY \$97204;S9204_SCHOY \$97204;S9204,S9205 \$0012900;100129740 \$000452700;100129740 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;0000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000502;00000 \$000000;00000 \$000000;00000 \$000000;00000 \$000000;00000 \$000000;00000 \$000000;00000 \$000000;00000 \$00000;000000 \$00000;00000 \$00000;000000 \$00000;000000 \$000000;000000 \$000000;000000 \$0000000000
ap tr tr	013933;RPOM_5GPO \$90008;S9006_SCHOY \$90008;S9006_SCHOY \$90008;S9006_SCHOY \$90208;S9006_SCHOY \$90208;S9006_SCHOY \$00152701]A0A15740_SASCO A0A1527001]A0A152700_VEJA A0A1527070]A0A153700_VEJA A0A1527500]A0A1537500_WICAO KOKTX3;KOKTX3_WICCF WEMIZ]WSHIZ_383CO A0A152777[A0A1530F1]SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO C65M23[C5M35]EECY 075557](75557_ASHOO C65M25]C5M35_ASHAC HASJ36]HAASJ36_KALAF J75773]J75733_KAZMA C0VD01_GVD01_NUNCC C60F23[C0W572_NUNCC C6FLX5]C5MA5_ASHAC HASJ36]HAASJ36_KALAF J35775]C5DN73_LACAG C65M54]C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C4065]C4065]C401545_SASCO A0A10477[A0A104077_SASCO A0
ap tr tr	013933;RPOM_5GPO \$90008;S9006_SCHOY \$90008;S9006_SCHOY \$90008;S9006_SCHOY \$90208;S9006_SCHOY \$90208;S9006_SCHOY \$00152701]A0A15740_SASCO A0A1527001]A0A152700_VEJA A0A1527070]A0A153700_VEJA A0A1527500]A0A1537500_WICAO KOKTX3;KOKTX3_WICCF WEMIZ]WSHIZ_383CO A0A152777[A0A1530F1]SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO A0A1575ME0[A0A157ME0_SASCO C65M23[C5M35]EECY 075557](75557_ASHOO C65M25]C5M35_ASHAC HASJ36]HAASJ36_KALAF J75773]J75733_KAZMA C0VD01_GVD01_NUNCC C60F23[C0W572_NUNCC C6FLX5]C5MA5_ASHAC HASJ36]HAASJ36_KALAF J35775]C5DN73_LACAG C65M54]C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C5DN73[C5DN73_LACAC C4065]C4065]C401545_SASCO A0A10477[A0A104077_SASCO A0
<pre>ap) tr tr</pre>	013933;RPOM_5GPO 559006;Ss0006_SCHOY 559006;Ss0006_SCHOY 559006;Ss0006_SCHOY 559006;Ss0006_SCHOY 559006;Ss0006_SCHOY 559006;Ss006;St007 ADA1E25900;JADA1E39UPO ADA1E25900;JADA1E39UPO ADA1E25900;JADA1E39UPO ADA1E25900;JADA1E39500_WICAO KOKTX3;KOKTX3_WICCF WEMLZ;WSULZ_582CO JOALE27944;JADA1E30F17_5ASCO JOALE27944;JADA1E30F17_5ASCO JOALE27944;JADA1E30F17_5ASCO JOALE27944;JADA1E30F17_5ASCO JOALE27944;JADA1E30F17_5ASCO JOALE27944;JADA1E30F17_5ASCO GCCR25;IGCCR25_KULTA JOAL579MED;JADA1E37MED_5ASCO GCCR25;IGCCR25_KULTA JOAL579MED;JADA1E37MED_5ASCO GCSTAS;IGS1MS2_ERCY G75BF7;IG75BF7_ASHOO RSWDF6;BXDFF_ASHOC GSVD21;GCVF1X5_CAMCA GS0V52;IGCVF1X5_CAMCA GSES54;IGBS54_TETPH JOADCHVT1;JADACTW71_5SACH CSDM73;IGSDF5_JACRC GSZR00;G2EXGO_TORCC JDAD162745;JADA1E4R0F7_SASCO JOADLEXWS;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOALLOFXK5;JADA1E4R0F7_SASCO JOADLOFXK5;JADA1E4R0F7_SASCO JOALLOFXK5;JADA1E4R0F7_SASCO JOALLOFXK5;JADA1E4R0F7_SASCO JOALLOFXK5;JADA1E4R0F7_SASCO JOALLOFXK5;JADA1E4R0F7_SASCO JOALLOFXK5;JADA1E4R0F7_SASCO JOALLOFXK5;JADA1E4R0F7_SASCO JOALL64K0F;JADA1E4R0F7_SASCO JOALL64K0F;JADA1E4R0F7_SASCO JOALL64K0F;JADA1E4R0F7_SASCO JOALL64K0F;JADA1E4R0F7_SASCO JOALE4K0F;JADA1E4R0F7_SASCO JOALE4K0F7;JADA1E4R0F7_SASCO JOALE4K0F;JADA1E4R0F7_SASCO JOALE4K0F;JADA1E4R0F7_SASCO JOALE4K0F7;JADA1E4R0F7_SASCO JOALE4K0F7;JADA1E4R0F7_SASCO JOALE4K0F7;JADA1E4R0F7_SASCO JOALE4K0F7;JADA1E4R0F7_SASCO JSDN76;JADX64;JAT46_FCST JOAD264K5;JADX64_FTCST JOAD264K5;JADX64_FTCST JOAD264K5;JADX64_FTCST JOAD264K5;JADX64_FTCST JOAD264K5;JADX64_FTCST JOAD264K5;JADX64_FTCST JOAD264K5;JADX64_FTCST JOAD264K5;JADX64_FTCST
ap tr tr tr tr tr tr tr tr tr tr	013933;RPOM_5GPO 590008;SS0008_SCHOY 590008;SS0008_SCHOY 590208;SS0008_SCHOY 590208;SS0008_SCHOY 590208;SS0008_SCHOY 590208;SS0008_SCHOY 50028;SS008 ADA1E220F10;ADA1E3PUP0_SASCO ADA1E3PUP0;ADA1E3PUP0_SASCO ADA1E3PUP0;ADA1E30FUT_SASCO ADA1E30F1;ADA1E30F17_SASCO ADA1E30F1;ADA1E30F17_SASCO ADA1E30F1;ADA1E30F17_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E37SME0;ADA1E37ME0_SASCO (GCR25;06CR25_KULTA ADA105UWS1;ADA105UWS1_SSACH GSM25;06STMS2_CHUAA ADA105UWS1;ADA105UWS1_SSACH GSM25;06F1X5_CAMCA GSM55;06F1X5_CAMCA GSM55;05F1X5_CAMCA GSM55;05F1X5_CAMCA GSM55;05F1X5_CAMCA GSM55;05F1X5_CAMCA GSM55;05F1X5_CAMCA GSM57;05DUF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C4Y8E3;C4DA1E480F7;SASCO ADA10477;IADA10477;SASCO ADA104
ap tr tr tr tr tr tr tr tr tr tr	013933;RPOM_5GPO 590008;SS0008_SCHOY 590008;SS0008_SCHOY 590208;SS0008_SCHOY 590208;SS0008_SCHOY 590208;SS0008_SCHOY 590208;SS0008_SCHOY 50028;SS008 ADA1E220F10;ADA1E3PUP0_SASCO ADA1E3PUP0;ADA1E3PUP0_SASCO ADA1E3PUP0;ADA1E30FUT_SASCO ADA1E30F1;ADA1E30F17_SASCO ADA1E30F1;ADA1E30F17_SASCO ADA1E30F1;ADA1E30F17_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E30F5ME0;ADA1E37ME0_SASCO ADA1E37SME0;ADA1E37ME0_SASCO (GCR25;06CR25_KULTA ADA105UWS1;ADA105UWS1_SSACH GSM25;06STMS2_CHUAA ADA105UWS1;ADA105UWS1_SSACH GSM25;06F1X5_CAMCA GSM55;06F1X5_CAMCA GSM55;05F1X5_CAMCA GSM55;05F1X5_CAMCA GSM55;05F1X5_CAMCA GSM55;05F1X5_CAMCA GSM55;05F1X5_CAMCA GSM57;05DUF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C5DX79;C5DXF3_LACTC C4Y8E3;C4DA1E480F7;SASCO ADA10477;IADA10477;SASCO ADA104
ap tr tr tr tr tr tr tr tr tr tr	013933;RPOM_SGEPO \$90026;S90026;SHOY \$97204;S37204_SCHOY \$97204;S37204_SCHOY \$97204;S37204_SCHOY \$97204;S37204_SCHOY \$97204;S37204;S37204 \$004182704;J0041239209_SASCO \$0041827040;J0041839209_SASCO \$0041827044;J0041839500_WICAO KOXTX3;K0KTX3_WICCF WEMIZ_\$98200 \$0041827044;J0041839500_WICAO KOXTX3;K0KTX3_WICCF \$0041827044;J0041839500_SASCO \$0041827044;J0041837040_SASCO \$0041827044;J0041873480_SASCO \$0041827044;J0041873480_SASCO \$0041827044;J0041873480_SASCO \$0041827044;J0041873480_SASCO \$0041827044;J0041873480_SASCO \$00401;G04192;J01404 \$00401;G04192;J01404 \$00401;G04192;J01404 \$00401;G04192;J01404 \$00401;G04192;J01404 \$00401;G04192;J01404 \$00401;G04192;J01404 \$00401;G04193;J0001;RX045 \$00401;G04192;J001;RX045 \$00401;G0411;J00018741;J30CC \$00512;J05145;J001874 \$0040147;J0018745;J0026 \$00402;G04823;J10401445;J026 \$00402;G04823;J026 \$0041440;G7;J0041440;G7;J030C \$0041440;G7;J0041645;J020 \$0041440;G7;J0041440;G7;J030C \$0041440;G7;J0041440;G7;J040;G7 \$0041440;G7;J0041440;G7;J0040;G7 \$0041440;G7;J0041440;G7;J0040;G7 \$0041440;G7;J0041440;G7 \$0041440;G7;J0041440;G7 \$0041440;G7;J0041440;G7 \$0041440;G7;J0041440;G7 \$0041440;G7;J0041440;G7 \$0041440;G7;J0041440;G7 \$0041440;G7 \$0041440;G7 \$0041440;G7 \$0041440;G7 \$0041440;G7 \$0041440;G7 \$0041440;G7 \$0041440;G7 \$0041440;G7
ap tr tr tr tr tr tr tr tr tr tr tr tr tr	013933;RPOM_SGRPO \$90008;S90008_SCHOY \$90008;S90008_SCHOY \$90008;S90008_SCHOY \$90008;S90008_SCHOY \$90008;S90008_SCHOY ADALE203C6[ADALE303C6_LIPST ADALE20701[ADALE3PUPD_SASCO ADALE3PUPO]ADALE3PUPD_SASCO ADALE3PUPO[ADALE3PUPD_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PT7[ADALE30PUT_SASCO ADALE30PUTGIS_KLUBA ADAL05UWS1[ADAL05UWS1_SACH GGMS2[GUMS2_RECY Q75BP7[075BP7_ASHGO RSXDF6[RSXDF6_SSHACL H2ASJ3[H2ASJ3G_KALAF J73773]J75733 FAINA COVDO1[AUACC GOWE72[GOWE72_NAUDC GOWE72[GOWE72_NAUDC GGBS54[GBS54_TETPH ADALERXWS]ADALEXRUS_SACH J8PP58[J3PF58_SACAR ADALOTMYT1[ADALEXRUS_SACH ADALEXRUS]ADALEXRUS_SACH ADALEXRUS[ADALEXRUS_SACH ADALEXRUS]ADALEXRUS_SACH ADALEXRUS]ADALEXRUS_SACH ADALEXRUS[ADALEXRUS_SACH ADALEXRUS]ADALEXRUS_SACH ADALEXRUS[ADALEXRUS_SACH ADALEXRUS]ADALEXRUS_SACH ADALEXRUS[ADALEXRUS_SACH ADALEXRUS_ACH ADALEXRUS_ACH ADALEXR

LPVVOPYRKFPSKOIT	TNLQSVYLED PDSNA PVD PRKOT TAV PPNFIHSLDATHM FMTCL	1054
LPIVOPYRNYKSROIP	TNLOTVFIEERDRTATVOPHKOATAEPPNFIHSLDATHMFMTCL	1047
	TNLQSVCIEDRDRVASVEPRKQAAAFPPNFVHSLDATHIFMTCL TNLQSVCIEDRDRVASVEPRKQAAAFPPNFVHSLDATHIFMTCL	1061 1060
LPVVQPYREIVRKQVQ	TNLOSVFISDPYAIHPVNSRKOVTAFPPNFIHSLDATHNLLSAL	1143
LPIVOPYRODIKKOVI	T SLOSVFITD PYALRGVNGRKORTA <mark>FPPNFIHSLDASHNIMSAI</mark> TNLOTVYITD PYALE PVKSRKOVSA <mark>FPPNYIHSLDATHNIMSAI</mark>	919 1122
LPIVOPYRBVERROIA	TRLCTIVIKD FFAMN PVDARKCVAA FPPNFIHSLDATHNLISAI TRLCTVFISD FFEMHQVDSRKCMAA FPPNFIHSLDATHNLISAI	1090
L P IVOPYRAVVKKOVS	TNLQTVFISDPFEMHQVDSRKQMAAEPPNFIHSLDASHNLLSAI	1098
LPIVOPYRAIVEROIO	TNLQTVFIQDPYELHQVDARKQMAA FPPNFIHSLDA SHALLSA S TNLQTVYITDPYEIHEVDRRKQIAA FPPNFVHSLDA THALKTAV	1125 1129
LPCVQPYRNDKKSQIS	TNLOTVFISDPYVAR PVDPRROOAGEPPNFIHSIDA SHMLMSA I	1100
	TTNLQS I SITD PFE INVVN AR KQYTA F PPNFIHSLDA SHALL SAV TTMQT I TIVD PYQVKRVDGR KQA 3G F PPNFIHSLDA THAVL SAN	1152 793
LEVVOPYRDLKKKOVC	TNLOTVFITDPFAINPINPRROOAGIPPNFIHSLDASHNILSAI	1089
L PVVQPYRDLKKKQVQ	TNLQTVFITD FAIN FIN FRRQQAGI PPNFIHSLDASHALLSAI	1088 1099
LPVVOPYRDIKKROIT	TNLQTVFISDPFAINAVNGRRQTAGIPPNFIHSLDASHNLLSAV TNLQTVFIADPFAVNPIDPRKQMAGIPPNFIHSLDASHNLLSAI ITNLQTVFIADPFAVNPIDPRRQMAGEPPNFIHSLDASHNLLSAI	1129
L PVVQPYRD IKKKQ IH	TNLQTVFIADPFAVNPIDPRRQMAGEPPNFIHSLDASHNLLSAI	1124
LPIVOPYROLSKKOIE	TNLQTVFIAD PFAVN PID PRROMAGE PPNFIHSLDA SHMLLSAI TNLQSVFISD PFAVNQVN ARROKAGE PPNFIHSLDA SHMLLSAS	1124 1110
LPIVQPYREVSKKQVI	TNLQTVFISDPFAVNQINARRQKAGEPPNFIHSLDASHNLLSAS	1101
	IT NLOT V FI SD P FA VNG VN ARROKAG E PPNFIHSLDA SHNILLSA I IT NLOT I FI SD P FA ING VN ARROKAG E PPNFIHSLDA SHNILLSA I	1153 1181
LPIVOPYRDAGKKOVI	TNLOSVFISDPFAINPINSRROKAGEPPNFIHSLDASHMLLSAA	1151
LPIVOPYREGSKKOVR	TNL QTVFISDPFSIN PVNAR QKAGE PPNFIHSLDA SHALLSAS	1149 1176
LPIVOPYRESKKOVE	TNLQTVFISDFAVNEVNAR QKTGIPPNFIHSLDA SHMLLSA TNLQTVFISDFAVNEVNAR QKAGIPPNFIHSLDA SHMLLSA	1175
LPIVOPYREESKKOVE	TNLQTVFISDPFAVNPVNARRQKAGIPPNFIHSLDASHNLLSAA TNLQTVFISDPFAVNPINARRQKAGEPPNFIHSLDASHNLLSAL	1175 1121
LPIVOPYRENGKKOVA	TNLOTVFISDPFAVNPINARROKAGEPPNFIHSLDASHALLSAL	1116
	TNLQTVFISDFGVNPVNARRQKAGEPPNFIHSLDA SHNLLSAA	1137
T DOT OD VD TT VD OT TD	TNLQTVFISDPFSVNPVNARRQKAGEPPNFIHSLDASHNLLSAA TNLQDISIHDPFSGSQVDARRQQTAEPPNFVHSLDATHNIMTSK	1147 1143
LPCVOPYRANROOT IT	T SLODV SI SDPFGASOVDARKOO AA EPPNFVHSLDATHNIMTAK	1132
LPCVQPYRAILNOVVS	TNLQDISISDPWKATQVDARKQQTA PPNFIHSLDATHNIMTAA	1135 1138
LPCVOPYRT IKKOI IN	II ILLOUIS IN DEFENSO VUARKOUL PENEVINS LA INICALISA I SLOVISI SO PERSO VUARKOUL PENEVINS LA INICALISA I SLOVISI SO PERSO VUARKOUL PENEVINS LA INICALISA I SLOVISI SI SO PERSO VUARKOUL PENEVINS LA INICALISA I SLOVISI SI SO PERSO VUARKOUL PENEVINS LA INICALISA I SLOVISI SI SO PERSO VUARKOUL PENEVINS LA INICALISA	1109
L PCVQPYRI SKNQL IN	TTNLQD I SI SDP FS AS QVDAR KQQAA FPPNFVHSLDATHMIMTAK TTNLQD I SI SDP FGTS QVDAR KQQAA FPPNFVHSLDATHMIMTSR	1081
LPCVOPYRVTKKOIVH	ITNLQDIVISDPFGISQVDARKQQAAF PPNFVHSLDATHMLMISK ITNLQDIVISDPFGASQVDARKQQSAF PPNFVHSLDATHMLMISK	1083
LPCVOPYRVTKKQI IS	TNLQDIVISDPFGASQVDARKQQAAFPPNYVHSLDATHMLMTAK	1139
LPCVQPYRKGTSESLA LPCVOPYRVNAHHAVR	T AVOT L T I NR I DG AGMVD GR KOVAG <mark>PPNFVHS L DA THMM</mark> TAA T SVONVSI TNP SGT ST ID SR KOQ AG <mark>PPNFI HS L DA THMIM</mark> TAT	1116 1120
LPCVOPYRVNKHHSVR	T SVODVLI SNP SGTSTID SRKOOAG FPPNFIHSLDATHMLMTAT	1119
L PCVQPYRQHKKKQLR	TAVODMHIIVPSNTSAVDSRKOONGEPPNFIHSLDATHMIMTAT TAVODLNIVMPSNTSAVDSRKOONGEPPNFIHSLDATHMIMTAT	1128 1108
LPCVOPYRIHKYROVN	T SVQSIKITAP SGTSQVDSRKQVAG FPPNFVHSLDATHMIMTAT	1121
LPCVQPYRVHKQTAVR	IT 5VQS IKITAP 3GTSQVDSRKQVAG PPNPVH3LDATHMIMTAT IT 5VQDIFISIP 3GTSAVD 3RKQQAG PPNFIHSLDATHMIMTAA * :* : : :. :. :. * . ***:**:**:*:	1126
	· · · · · · · · · · · · · · · · · · ·	
KCKKRNITFVBVHDSY	WTHAASVAELNGLLREAFVELHSRDILGDLKREFEDRYKNHYVH	1114
	WTHACDVDQMNSLLREAFVLLHSNNIMERLKQEFEERYKGFLVS	1107
	WTHACDVEQLGNLLRQAF VELHSQKIMEKLRNEFRKRYKNFMIP WTHACDVEKLGSLLREAF VELHSQKIMEKLRNEFRKRYKNYMIQ	1121 1120
	WTHAADIDRMNAILRDAFIKLHEGDLVAKLKEEFERRYAGYMOF	1203
	WTHPGDIDKMNRILRDCFIELHQVDLVDKLRIEFEQRYTGLLQY	979
	WTHAADVDDMNSILRDAFIRLHEVDLVTKLKTEFDRRYEGFLHF WTHACDVDTMNRCLRDEFIKLHEVDLIARLKDEFDERYKGFLRL	1182 1150
	WTHASDVKTMGNLLREAFIGLHEVDLVSKLKQEFDQRYHGFLQL	1158
	WTHACDVGEMSESLRETFIELHQVDLIARLKDEFDERYKGFLQL	1185
	WTHAADVDVMNKAIREEFSSMHETNLVAGLKKEFEVRYEGFVYW WTHAADVDIMNEHIRSGFVSLHGTNLVARLKREFDTRYKGFVOM	1189 1160
ECGRKELTFAAVHDSY	WTHAGDVDRMNEIIRDKFIGLHQVDLVQRLKNEFEKRYQGYLLQ	1212
	WTHASDVSVMNKILREQFIHLHTNNLIEKLDKELRMRYGKNLMV	853
OCGRAGLDFAAVHD9Y OCGRAGLDFAAVHD9Y	WTHASEVDNMNRLLROEFIKLHEVDLIERLKNEFDERYRDYLEI WTHACDVDDMNFLLROEFINLHKIDLIERLKNEFDERYRDYLEI	1149 1148
ASAKHGLRFAAVHDSY	WTHASDVDTMNNELRKEFVRMYSVDLIQRLKNEFDERYADYVEI	1159
ECGSOGLOFAAVHDSY	WSHACDISLMNKTLRNOFIKMHEVDLIORLKNEFDERYKDYLEV WTHASDVPKMNKALRNEFVKMHOVDLIORLKNEFDARYKNYLEV	
ECONDOD/FARVIDS1		1189
ECCKAGLOFANVHDSY	WTHASDIPAMNRALRNEFVKMHOVDLIORLKNEFDARIKNILEV	1184
ECHKDGLVFABVHDSY	WT HASDIPAMNRALRNEF VKMHQVDLIQRLKNEFDARYKNYLEV WT HACDVSKMNKHLREQFVKLHEVDLIERLKEEFDERYKNYVEI	1184 1184 1170
ECHKDGLVFABVHDSY KCAEEGLDFABVHDSY	WT HASDIPAMNRALRNEFVKMHQVDLIQRLKNEFDARYKNYLEV WT HACDVSKMNKHLREQFVKLHEVDLIERLKEEFDERYKNYVEI WT HACDVEKMNKHIRNEFVTLHEVDLIERLKEEFDERYRNYVQI	1184 1184 1170 1161
ECHKDGLVFASVHDSY KCAEEGLDFASVHDSY QCRANGLEFASVHDSY	WTHASDIPAMNRALRNEFVKMHQVDLIQRLKNEFDARYKNYLEV WTHACDVSKMNKHLR&QFVKLHEVDLIERLKEEFDERYKNYVEI WTHACDVEXMNKHIRNEFVTLHEVDLIERLKEEFDERYKNYVQI WTHACDIKMSVVLR&QFIDLHKVDLIERLKNEFDERYKNYVQI	1184 1184 1170
ECHKDGLVFASVHDSY KCAEEGLDFASVHDSY QCRANGLEFASVHDSY KCKENGLEFASVHDSY GCRDNGLDFASVHDSY	WT HAB DIFAMSFALISNEFVXMHQVDLIQALKWEFDARYKNYLEV WT HACDVSNOKKHLREGFVXHHEVDLIERLKEEFDERYKNYVEI WT HACDVSNOKKHLREGFVTLHEVDLIERLKEEFDERYKNYVQI WT HACDINXMSVYLREGFIDLHKVDLIERLKMEFDERYKNYVQI WT HACDVNKMSVYLREFIELHKVDLIERLKDEFDERYKNYVQI WT HACDVNKMSVYLREFIELHEVDLIGALKEEFDERYKNYLAI	1184 1184 1170 1161 1213 1241 1211
ECHKDGLVFABVHDSY KCAEEGLDFABVHDSY QCRANGLEFABVHDSY KCKENGLEFABVHDSY GCRDNGLDFABVHDSY ACGEKGLDFABVHDSY	WTHASDIPANNRALRNEFVKMHQVDLIQRLKNEFDARYKNYLEV WTHACDVSKNMKHLR&QFVKLHEVDLIRELKEFDERYKNYVEI WTHACDVSKNMKHLR&QFVTHEVDLIRELKREFDERYKNYVQI WTHACDIDKMSVYLR&QFIDLHKVDLIRELKNEFDERYKNYVQI WTHACDUNKMSVYLRDEFIELHEVDLIRELKNEFDERYKNYVQI WTHASDVDKMVVIRDEFIELHEVDLIQRLKNEFDERYKNYVQW WTHACDIDINMKALRQFVALHEVDLIQRLKNEFDERYKNYVQ	1184 1184 1170 1161 1213 1241 1211 1209
ECHKDGLVFABVHDSY KCAEEGLDFABVHDSY QCRANGLEFABVHDSY KCKENGLEFABVHDSY GCRDNGLDFABVHDSY ACGEKGLDFABVHDSY ECGKQGLDFABVHDSY	WTASDJFANNFALRNEFVXHHOVDLIGLKNEFDARYKNYLEV WTHACDVSXMKHLREGFVKHEVDLIERLKEFDERYKNYVEI WTACDVSXMKHLRUFVILHEVDLIERLKEFDERYKNYVGI WTACCDIKMSVYLREGFIDLHKVDLIERLKEFDERYKNYVGI WTACDVKMSVYLREGFILHKVDLIERLKEFDERYKNYVGI WTACDVKMNVVIRGKFIELHEVDLIGALKMEFDERYKNYVGY WTASDVDKMNVVIRGKFIELHEVDLIGALKMEFDERYKNYVGY WTASDVDKMNVVIRGKFIELHEVDLIGALKMEFDERYKNYVGY	1184 1184 1170 1161 1213 1241 1211 1209 1236
ECHKDGLVFASVEDY KCAEEGLDFASVEDY (CRANGLEFASVEDY KCKENGLEFASVEDY ACCEKGLDFASVEDY ECGKGLDFASVEDY ECGKGLDFASVEDY ECGKGLDFASVEDY	WTRABDIFAMMRALRMEFVXMHQVDLIQALKMEFDARYKNYLEV WTRACDVSKMKKHIR&GFVXLHEVDLIRALKEFDERYKNYVEI WTRACDVSKMKKHIR&FVILHEVDLIRALKEFDERYKNYVQI WTRACDVKMSVYLR&GFIDLHKVDLIRALKEFDERYKNYVQI WTRACDVKMSVYLR&FIELHEVDLIQALKEFDERYKNYVQI WTRACDIMSKALR&GFVALHEVDLIQALKEFDERYKNYVQI WTRACDIMSKALR&GFVALHEVDLIQALKEFDERYKNYVQI WTRACDIMSKALR&GFILHEVDLVRALREFTQRYKNYVXI WTRASDIDTMMVVLR&GFIKLHEVDLVRALREFTQRYKNYVXI WTRASDIDTMMVVLR&GFIKLHEVDLVLALKEFTQRYKNYVXI	1184 1184 1170 1161 1213 1241 1211 1209 1236 1235 1235
ECHKDGLVFABVFBV KCAEEGLDFABVFBV QCRANGLFFABVFBV KCKENGLEFABVFBV KCKENGLFFABVFBV ACGEKGLFFABVFBV ECGKQGLDFABVFBV ECGEKGLDFABVFBV KCGEKGLDFAVFBV	WT HADDYRAMWRALRWEFYXHHOVDLIGLKWEFDARYKNYLEY WT HADDYSMMKHLREGFVKHHEVDLIERLKEEFDERYKNYVEI WT HADDYSMMKHLREGFVTHEVDLIERLKEEFDERYKNYVGI WT HACDIKMSVYLREGFIDLHKVDLIERLKEEFDERYKNYVGI WT HACDYKMSVYLREGFILHEVDLIGRLKEEFDERYKNYVGI WT HADDYKMSVYLREGFILHEVDLIGRLKEEFDERYKNYVRI WT HADDINMSVLREGFIKHEVDLUGRLKEEFDGRYKNYVKI WT HASDVDTMSVVLREGFIKHEVDLVLRLKEEFDGRYKNYVKI WT HASDVDTMSVVLREGFIKHEVDLULRLKEEFDGRYKNYVKI WT HASDVDTMSVVLREGFIKHEVDLULRLKEEFDGRYKNYVKI WT HASDVDTMSVVLREGFIKHEVDLULRLKEEFDGRYKNYVKI	1184 1184 1170 1161 1213 1241 1211 1209 1236 1235 1235 1181
ECHKDGLVFASVEDSY KCAFEGLDFASVEDSY (CCANGLFFASVEDSY KCKENGLFFASVEDSY ACGEKGLDFASVEDSY ACGEKGLDFASVEDSY ECGKQGLDFASVEDSY ECGKGLDFASVEDSY KCGEKGLDFASVEDSY KCGEKGLDFAVEDSY	WTRABDIFAMMRALRMEFVXMHQVDLIQALKMEFDARYKNYLEV WTRACDVSKMKKHIR&GFVXLHEVDLIRALKEFDERYKNYVEI WTRACDVSKMKKHIR&FVILHEVDLIRALKEFDERYKNYVQI WTRACDVKMSVYLR&GFIDLHKVDLIRALKEFDERYKNYVQI WTRACDVKMSVYLR&FIELHEVDLIQALKEFDERYKNYVQI WTRACDIMSKALR&GFVALHEVDLIQALKEFDERYKNYVQI WTRACDIMSKALR&GFVALHEVDLIQALKEFDERYKNYVQI WTRACDIMSKALR&GFILHEVDLVRALREFTQRYKNYVXI WTRASDIDTMMVVLR&GFIKLHEVDLVRALREFTQRYKNYVXI WTRASDIDTMMVVLR&GFIKLHEVDLVLALKEFTQRYKNYVXI	1184 1184 1170 1161 1213 1241 1211 1209 1236 1235 1235
ECHKDGLYPASVEDSY KCAFEGLPFASVEDSY QCRANGLEPASVEDSY KCKENGLEPASVEDSY ACCERGLEPASVEDSY ACCERGLEPASVEDSY ECGKQGLEPASVEDSY ECGKQGLEPASVEDSY KCCERGLEPASVEDSY KCCERGLEPASVEDSY ACCERGLEPASVEDSY ACCERGLEPASVEDSY	WT HADDYRAWRALRWEFVXHHOVDLIGLKWEFDARYKNYLEY WT HACDYSKONKHLRWEFVXHHOVDLIGLKWEFDARYKNYLEY WT HACDYSKONKHLRWEFVTHEVDLIERLKWEFDERYKNYVGI WT HACDYNMSYVLRBOF IDLHKVDLIERLKWEFDERYKNYVGI WT HACDYNMSVYLRBOF IDLHKVDLIGLKWEFDERYKNYVGI WT HACDYNMSVVLRBOF ILHEVDLIGLKWEFDERYKNYVGI WT HACDYNMSVVLRDF ILHEVDLIGLKWEFDERYKNYVGY WT HADDIDIMKKLRDOF VALHEVDLIGLKWEFDERYKNYVGY WT HADDIDIMKVLRBOF IKLHEVDLVRLKWEFDERYKNYVGY WT HADDIDIMKVLRBOF IKLHEVDLVRLKEEFOGRYKNYVKI WT HADDIDIMKVLRBOF IKLHEVDLVRLKEEFOGRYKNYVKI WT HADVINMSVVLRBOF IKLHEVDLVRLKKEEFOGRYKNYVLI WT HADDIDIMKVLRBOF IKLHEVDLURLKWEFDERYKNYUGI WT HACDVINMSVLRBOF IKLHEVDLIERLKWEFDERYKNYUGI WT HACDVINMSVLRBOF IKLHEVDLIERLKWEFDERYKNYUGI WT HACDVINMSYLRBOF IKLHEVDLIERLKWEFDERYKNYUGI	1184 1184 1170 1161 1213 1241 1211 1205 1235 1235 1235 1181 1176 1197 1207
ECHKDGLVPASVEDSY KCAEEGLDPASVEDSY QCRANGLEFASVEDSY KCKENGLEFASVEDSY ACGENGLDPASVEDSY ACGEKGLDPASVEDSY ECGKQGLDPASVEDSY ECGKGLDPASVEDSY ECGEKGLDPASVEDSY KCGEKGLDPASVEDSY ACGEEGLDPASVEDSY ACGEEGLDPASVEDSY ACGEEGLPASVEDSY	WT AB DIFAMMRALEMEFVXHHQVDLIQELKMEFDARYKNYLEV WT HACDVSXMKHLRNEFVXHHQVDLIQELKMEFDARYKNYLEV WT HACDVSXMKHLRNEFVIHEVDLIRELKMEFDERYKNYVQI WT HACDIKMSVYLREQFIELHKVDLIRELKMEFDERYKNYVQI WT HACDIKMSVYLREQFIELHKVDLIQELKMEFDERYKNYVQI WT HACDIKMSVLRUFFIELHEVDLIQELKMEFDERYKNYVQI WT HACDIKMSVLRUFFIELHEVDLIQELKMEFDERYKNYVQI WT HASDIDIMMVLRUFFIELHEVDLIQELKMEFDERYKNYVQI WT HASDIDIMMVVLRUFFIKHEVDLIVMELKEFTQRYKSYVXI WT HASDIDIMMVVLRUFFIKHEVDLIVMELKEFTQRYKSYVXI WT HASDIDIMMVVLRUFFIKHEVDLIVMELKEFTQRYKSYVXI WT HASDIDIMMVVLRUFFIKHEVDLIVMELKEFTQRYKSYVXI WT HASDIDIMMVVLRUFFIKHEVDLIRELKMEFDERYKNYLQI WT HACDVDMNVVLRUFFIKHEVDLIRELKMEFDERYKNYVQI WT HACDVDMNVVLRUFFIKHEVDLIRELKMEFDERYKNYVQI WT HACDVDMNVVLRUFFIKHEVDLIRELKMEFDERYKNYVQI WT HACDVDMNVFIRUFFIKHEVDLIRELKMEFDERYKNYVQI WT HACDVDMNVFIRUFYVXHUFIKHVVQI WT HACDVDMNVFIRUFYKHYVQI WT HACDVDMNYFIKUFYVXH	1184 1184 1170 1161 1213 1241 1209 1236 1235 1235 1235 1181 1176 1197 1207
ECHKDGLVFASVRDSY KCAEFGLDFASVDDSY (CRANGLEFASVDDSY (CRANGLEFASVDDSY KCKENCLEFASVDDSY ACGEKGLDFASVDDSY ECGKGCLDFASVDDSY ECGKGLDFASVDDSY KCGEKGLDFASVDDSY KCGEKGLDFASVDDSY ACGEGGLDFASVDDSY ACGEGGLDFASVDDSY ACGEGGLDFASVDDSY ACGEGGLDFASVDDSY ACGEGGLDFASVDDSY	WT HADDIFAMMFALINEF VXHHQVDLIQLIXMEFDARYXMYLEV WT HACDVSKMKHLREGFVXHHQVDLIQLIXMEFDARYXMYLEV WT HACDVSKMKHLREGFVLHEVDLIERLKEFDERYXMYVQI WT HACDIKMSVYLREGFIDLHKVDLIERLKKEFDERYXMYVQI WT HACDIKMSVYLREGFIDLHKVDLIERLKKEFDERYXMYVQI WT HACDINMSKLRGGFVLHEVDLIQLIXMEFFERYXMYVQI WT HASDVDKMVVLRUGFILHEVDLIQLIXMEFFERYXMYVQI WT HASDVDKMVVLRUGFIKHEVDLVRLKKEFDQRYXMYVXI WT HASDIDTMMVVLRUGFIKHEVDLVRLKKEFDQRYXMYVXI WT HASDIDTMMVLRUGFIKHEVDLVRLKKEFDQRYXMYVXI WT HASDIDTMMVLRUGFIKHEVDLVRLKKEFDQRYXMYVXI WT HASDIDTMMVLRUGFIKHEVDLVRLKKEFDQRYXMYVXI WT HASDIDTMMVLRUGFIKHEVDLVRLKKEFDQRYXMYVXI WT HASDVDTMMVLRUGFIKHEVDLVRLKKEFDRYXMYVQI WT HACDVDMMVVLRUGFIKHEVDLVRLKKEFDRYXMYVQI WT HACDVDMMVVLRUGFIKHEVDLIERLKKEFDRYXMYVQI WT HACDVDTMNYLRUGFIKHEVDLIERLKKEFDRYXMYVQI WT HASDVDTMNYHIRMGFVKHQDIVIKLKDEFFHXYKCFLQV WT HASDVDMMYHIRMGFVKHQDIZKKKEFTRAYKCFLQV WT HANDVDKMVVRIGFVKHQDDIZKKKEFTRAYKCFLQV	1184 1184 1170 1161 1213 1241 1209 1235 1235 1235 1235 1181 1176 1197 1207 1203 1192 1195
ECRNCLIVEASVEDSY KCAESCLIPASVEDSY QCRANGLEFASVEDSY QCRANGLEFASVEDSY ACCERCLIPFASVEDSY ECCRCQLIPFASVEDSY ECCRCQLIPFASVEDSY ECCRCQLIPFASVEDSY KCGERCLIPFASVEDSY ACCERCLIPFASVEDSY ACCERCLIPFASVEDSY ACCERCLIPFASVEDSY ACCERCLIPFASVEDSY ACCERCLIPFASVEDSY ACCERCLIPFASVEDSY ACCERCLIPFASVEDSY ACCERCLIPFASVEDSY ACCERCLIPFASVEDSY	WT HADDIFAMMFALKMEFVXHHQVDLIQLIKMEFDARYKNYLEY WT HACDVSXMKHIRMEFVXHHQVDLIQLIKMEFDARYKNYLEY WT HACDVSXMKHIRMEFVIHEQFYLHEVDLIFALKEFDERYKNYVQI WT HACDVIKMSVILREGFILHKVDLIFALKEFDERYKNYVQI WT HADUNKMSVILREGFILHKVDLIFALKKEFDERYKNYVQI WT HADUNKMSVILREGFILHKVDLIQLIKMEFDERYKNYVQI WT HASDVDKMMVURDGFILHEVDLIQLIKMEFDERYKNYVQI WT HASDIDIMNKALRDGFILHEVDLIQLIKMEFDERYKNYVQI WT HASDIDIMNVLREGFIKHEVDLIVALKEFDQRYKNYVXI WT HASDIDIMNVLREGFIKHEVDLIVALKEFDQRYKNYVXI WT HASDIDIMNVLREGFIKHEVDLIRALKKEFDERYKNYVQI WT HASDIDIMNVLREGFIKHEVDLIERLKKEFDERYKNYVQI WT HASDIDIMNVLREGFIKHEVDLIERLKKEFDERYKNYVQI WT HASDIDIMNVLREGFIKHEVDLIERLKKEFDERYKNYVQI WT HACDVDMNVFLREGFIKHEVDLIERLKKEFDERYKNYVQI WT HASDVDMNVFLREGFIKHEVDLIERLKKEFDERYKNYVQI WT HASDVDMNSVLREGFIKHEVDLIERLKKEFDERYKNYVQI WT HASVVDNSVLKUGVKIKESFIKHEVDLIERLKKEFDERYKNYQI WT HASVVDNSVLKUGVKIKESFIKHEVDLIERLKEFTERYKGFLQV WT HASVVDNSHIKIKGVYVLKEFTERYKGFLQV	1184 1184 1170 1161 1213 1241 1209 1236 1235 1235 1181 1176 1187 1207 1203 1192 1195 1188
ECHKDGLYPASYBOY KCAEGGLPPASYBOY QCRANGLEPASYBOY QCRANGLEPASYBOY ACCERCLPPASYBOY ECGKQGLDPASYBOY ECGKQGLDPASYBOY ECGKQGLDPASYBOY KCCEKGLPPAVBOY KCCEKGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY ACGECGLPPAVBOY	WT HADDYRAWRALRWEFVXHHOVDLIGLKWEFDARYKNYLEY WTHACDVSXMNKHLRWEFVXHHOVDLIGLKWEFDARYKNYLEY WTHACDVSXMNKHLRWEFVTHEVDLIERLKWEFDERYKNYVGI WTHACDUSKMKHLRWEFVTHEVDLIERLKWEFDERYKNYVGI WTHACDUSKMKVIRBGFIELHEVDLIERLKWEFDERYKNYVGI WTHACDUSKMNVVIRBGFIELHEVDLIGLKWEFDERYKNYVGI WTHASDVDRMVVIRBGFIELHEVDLIGLKWEFDERYKNYVGY WTHASDVDRMVVIRBGFIKHEVDLIGLKWEFDERYKNYVGY WTHASDVDRMVVLRBGFIKHEVDLIGLKWEFDERYKNYVGY WTHASDVDRMVVLRBGFIKHEVDLIERLKWEFDERYKNYVGY WTHASDVDRMVVLRBGFIKHEVDLIERLKWEFDERYKNYVGY WTHASDVDRMVVLRBGFIKHEVDLIERLKWEFDERYKNYVGY WTHASDVDRMVVLRBGFIKHEVDLIERLKWEFDERYKNYVGI WTHASDVDRMVVLRBGFIKHEVDLIERLKWEFDERYKNYVGI WTHACDVDNMVVLRBGFIKHEVDLIERLKWEFDERYKNYVGI WTHACDVDNMVVLRBGFIKHEVDLIERLKWEFDERYKNYVGI WTHACDVDNMVFLRBGFIKHEVDLIERLKWEFDERYKNYVGI WTHACDVDNMVFLRBGFIKHEVDLIERLKWEFDERYKNYVGI WTHACDVDNMVFLRBGFIKHESLIVRLRWEFDERYKNYVGI WTHACDVDNMVFLRBGFIKHESLIVRLRWEFDERYKNYVGI WTHACDVDNMFYLRBGFIKHESLIVRLRWEFDERYKNYVGI WTHACDVDNMFYLRBGFIKHESLIVRLRWEFERRYKGFLGV WTHACDVDNMFYHRBGFVKHHESLIVRLRDEFERRYKGFLGV WTHALDVDNMFYHRBGFIKHESLIVRLRDEFERRYKGFLGV WTHACDVDNMSHIRBFIKGFIKHESLIVRLRDEFERRYKGFLGV WTHACDVDNMSHIRBFIKGFIKHESLIVRLRDEFERRYKGFLGV WTHACDVDNSHIFTIRNGFIKHESLIVRLRDEFERRYKGFLGV WTHACDVDNSHIFTIRNGFIKHESLIVRLRDEFERRYKGFLGV WTHACDVDNSHIFTIRNGFIKHESLIVRLRDEFERRYKGFLGV	1184 1184 1170 1161 1213 1241 1209 1235 1235 1235 1181 1176 1197 1207 1203 1192 1195 1195 1195
ECHKDGLVFASVEDSY KCAESGLFASVEDSY QCRANGLEFASVEDSY KCKENGLFFASVEDSY KCKENGLFFASVEDSY ACGERKGLFFASVEDSY ECGKQGLFFASVEDSY ECGKQGLFFASVEDSY KCGEKGLFFASVEDSY ACGECGLFFASVEDSY ACGECGLFFASVEDSY ACGECGLFFASVEDSY ACGECGLFFASVEDSY ACGECGLFFASVEDSY ACGECGLFFASVEDSY ACGECGLFFASVEDSY ACGEDALSFASVEDSY ACGEDALSFASVEDSY ACGEDALSFASVEDSY ACGEDALSFASVEDSY	WT HADDYRAWRALRWEFVXHHOVDLIQLIKNEFDARYKNYLEY WT HADDYSMMKHLRWEFVXHHOVDLIQLIKNEFDARYKNYLEY WT HADDYSMMKHLRWEFVIHEVDLIERLKEFDERYKNYVDI WT HADDYSMMKHLRWEFVIHEVDLIERLKEFDERYKNYVQI WT HADDYKMMVYLRBOF IDLHKVDLIERLKKEFDERYKNYVQI WT HADDYKMMVVIRDF IELHEVDLIQLIKEFDERYKNYVQI WT HADDYKMMVVIRDF IELHEVDLIQLIKEFDERYKNYVQI WT HADDYKMMVVIRDF IELHEVDLIQLIKEFDERYKNYVQI WT HADDYKMMVVIRDF IELHEVDLIQLIKEFDERYKNYVQI WT HADDYDKMVVIRDF IELHEVDLIQLIKEFDERYKNYVQI WT HADDYDKMVVIRDF IELHEVDLIQLIKEFDERYKNYVQI WT HADDYDKMVVIRDF IKLHEVDLVIRLKEFDQRYKNYVXI WT HADDYDMMVVIRDF IKLHEVDLURLKKEFDQRYKNYVXI WT HADDYDMMVVIRDF IKLHEVDLIERLKMEFDERYKNYVQI WT HADDYDMMVVIRDF IKLHEVDLIERLKMEFDERYKNYVQI WT HADDYDMMVVIRBOF IKLHEVDLIERLKMEFDERYKNYVQI WT HADDVDMMVFIRBOF IKLHEVDLIERLKMEFDERYKNYVQI WT HADDVDMMVFIRBOF IKLHEVDLIERLKMEFDERYKNYVQI WT HADDVDMMVFIRBOF IKLHEVDLIERLKMEFDERYKNYVQI WT HADDVDMMVFIRBOF IKLHEVDLIERLKMEFDERYKNYVQI WT HADDVDMMNFIRBOF VXLHODNLVTIKLKDEFERYKCFLQV WT HADDVDMMNKHIRBOF VXLHOVINVLIRDFFERYKCFLQV WT HADDUNMNSEITRMOF VXLHESLIVNZNOEFEKRYKCFLQV WT HADDUNMNEJTRMOF VXLHESNIVQELKEFERRYKCFLQV WT HADDUNMNEJTRMOF VXLHESNIVQELKEFERRYKCFLQV	1184 1184 1170 1161 1213 1241 1209 1236 1235 1235 1181 1176 1187 1207 1203 1192 1195 1188
ECHKDGLVFASVEDSY KCAFEGLFASVEDSY (CRANGLFASVEDSY (CRANGLFASVEDSY KCKENCLFFASVEDSY ACCEKGLDFASVEDSY ECGKQGLDFASVEDSY ECGKQGLDFASVEDSY ECGKGLDFASVEDSY KCCEKGLDFASVEDSY KCCEKGLDFASVEDSY ACCECGLFFASVEDSY ACCECGLFFASVEDSY ACCECGLFFASVEDSY ACCECGLFFASVEDSY ACCECGLSFASVEDSY ACCECGLSFASVEDSY ACCECGLSFASVEDSY ACCECGLSFASVEDSY ACCECGLSFASVEDSY ACCECGLSFASVEDSY ACCEGGLSFASVEDSY ACCEGGLSFASVEDSY ACCEGGLSFASVEDSY	WT HADDIFAMMFALMMEFVXHHQVDLIQLIKMEFDARYKNYLEV WT HACDVSXMKKHIRMEFVXHHQVDLIQLIKMEFDARYKNYLEV WT HACDVSXMKKHIRMEFVTHEQFYLHEVDLIRLIKMEFDERYKNYVQI WT HACDVKMSVYLREQFIDLHKVDLIRLIKMEFDERYKNYVQI WT HACDVKMSVYLREQFIDLHKVDLIRLIKMEFDERYKNYVQI WT HACDVKMSVYLREQFILHEVDLIQLIKMEFPERYKNYVQI WT HACDVKMSVLREQFIXHHEVDLIQLIKMEFPERYKNYVQI WT HACDVKMSVLREQFIXHHEVDLVRLREEFIQRYKNYVXI WT HASDVDKMSVVLREQFIXHHEVDLVRLREEFIQRYKNYVXI WT HASDVDKMSVVLREQFIXHHEVDLVRLKEFPQRYKNYVQI WT HASDVDKMSVVLREQFIXHHEVDLVRLKKEFQQXKNYVXI WT HASDVDKMSVLREQFIXHHEVDLVRLKKEFQQXKNYVXI WT HASDVDKMSVLREQFIXHHEVDLVRLKKEFPQRYKNYVQI WT HASDVDKMSVLREQFIXHHEVDLVRLKKEFPQRYKNYVQI WT HACDVDKMSVLREQFIXHHEVDLVRLKKEFPQRYKNYVQI WT HACDVDKMSVLREQFIXHHEVDLVRLKKEFPQRYKNYVQI WT HACDVDKMSVLREQFIXHHEVDLVRLKKEFPQRYKNYVQI WT HACDVDKMSVLREQFIXHHEVDLVRLKKEFPQRYKNYQQI WT HASDVDKMSVLREQFIXHHEVDLVRLKKEFPQRYKNYQQI WT HASDVDKMSVLREQFIXHHEVDLVRLKKEFPQRYKNYQQI WT HASDVDKMSVLREQFIXHHEVDLVRLKKEFPQRYKKFQQV WT HASDVDKMSVLREQFIXHHESULVQLKEFFRAYKKFQQV WT HASDVDKMSVLREQFIXHHSMLMQVKDEFFRAYKKFQQV WT HASDVDKMSLIRMQFVXLHSNLMVQLKEFFRAYKKCLQV WT HASDVDKMSLIRMQFVXLHSNLMVVLRDEFFRAYKKCLQV WT HASDVDKMSLIRMQFVXLHSNLMVVLRDEFFRAYKKCLQV WT HASDVDKMSLIRMQFVXLHSNLMVVLRDEFFRAYKKCLQV WT HASDVDKMSLIRMQFVXLHSNLMVVLRDEFFRAYKKCLQV WT HASDVDKMSLIRMQFVXLHSNLMVVLRDEFFRAYKKCLQV	1184 1184 1170 1161 1213 1241 1209 1235 1235 1235 1235 1235 1235 1237 1207 1207 1203 1192 1195 1198 1169 1141 1143 1150
ECREMOLIVEASVEDSY KCAESGLEFASVEDSY QCRANGLEFASVEDSY QCRANGLEFASVEDSY CCERCULPFASVEDSY ACCERCULPFASVEDSY ECCERCULPFASVEDSY ECCERCULPFASVEDSY KCCERCULPFASVEDSY KCCERCULPFASVEDSY ACCECCULPFASVEDSY ACCECCULPFASVEDSY ACCECCULFFASVEDSY	WT HADDYRAWSHIENEFVXH(VDLIQELKNEFDARYKYLEY WT HACDYSMONKHIRNEFVXH(VDLIQELKNEFDARYKYVEI WT HACDYSMONKHIRNEFVIHEVDLIRELKNEFDERYKNYVQI WT HACDYSMONKHIRNEFVIHEVDLIRELKNEFDERYKNYVQI WT HACDYNAWSVIRNEFIELHEVDLIQELKNEFDERYKNYVQI WT HADDYNNWYVRICTIELHEVDLIQELKNEFDERYKNYVQI WT HADDINNNALRDQFVALHEVDLIQELKNEFDERYKNYVQI WT HASDIDTNNVLRDQFIKLHEVDLIQELKNEFDERYKNYVQI WT HASDIDTNNVLRDQFIKLHEVDLIQELKNEFDERYKNYVQI WT HASDIDTNNVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDIDTNNVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDIDTNNVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDIDTNNVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDIDTNNVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDIDTNNVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDIDTNNVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDVDNNSVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDVDNNSVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDVDNNSVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDVDNNSVLRDQFIKLHEVDLIZELKNEFDERYKNYVQI WT HASDVDNNSHIRDQFVKLHQDSIQKLKDEFFRYKCFLQV WT HASDVDNNKIERSFVKHHESLIVNLRDEFFRYKCFLQV WT HADDVDNNKIERSFVKHHSNLINQVRDEFFRYKNCLQV WT HADDVDNNKIERSFVKHHSNLINQVRDEFFRYKNCLQV WT HADDVDNNKIERNQFVNLHSNLINQVRDEFFRYKCFLQV WT HADDVDNNKIERSFVKHHESLIVVLINDEFFRYKNCLQV WT HADDVDNNKIERSFVKHHESLIVVLINDEFFRYKNCLQV WT HADDVDNNKIERSFVKHHSNLINQVRDEFFRYKCFLQV WT HADDVDNNKIERSFVKHHSNLINQVRDEFFRYKCFLQV WT HADDVDNNKIERSFVKHHESLIVVLINDEFFRYKCFLQV WT HADDVDNNKIERSFVKHHESLIVVLINDEFFRYKCFLQV WT HADDVDNNKIERSFVKHHSNLINQVRDEFFRYKCFLQV WT HADDVDNNKIERSFVKHHSNLINQVRDEFFRYKCFLQV WT HADDVDNNKIERSFVKHESTVKHESNLINQVRDEFFRYKCFLQV WT HADDVDNNKIERSFVKHESNLINQVRDEFFRYKCFLQV WT HADDVDNNKIERSFVKHESNLINQVRDEFFRYKCFLQV WT HADDVDNNSIERSFVKHESNLINQVRDEFFRYKCFLQV WT HADDVDNNSIEFFNKHESNLINQVRDEFFRYKCFLQV	1184 1184 1170 1161 1213 1241 1209 1236 1235 1235 1235 1181 1176 1197 1203 1192 1195 1198 1169 1141 1143 1199
ECHNOLVPASVEDSY KCAPEGLEPASVEDSY QCRANGLEPASVEDSY QCRANGLEPASVEDSY QCRANGLEPASVEDSY ACCERCLEPASVEDSY ECCKQGLEPASVEDSY ECCKQGLEPASVEDSY ECCKQGLEPASVEDSY KCGEKGLEPASVEDSY ACCEPCLEPASVEDSY	WT HADDYRAWSHILWEFYXHHOVDLIQLIKHEFDARYKYLLY WT HADDYSMENKHIRWEFYXHHEVDLIGALKHEFDERYKNYVEI WT HADDYSMENKHIRWEFYTHEVDLIGALKHEFDERYKNYVQI WT HADDYSMENKHIRWEFYTILHEVDLIGALKHEFDERYKNYVQI WT HADDINNSYVIRWEFIELHEVDLIGALKHEFDERYKNYVQI WT HADDINNSVIRWEFIELHEVDLIGALKHEFDERYKNYVQI WT HADDINNSVIRWEFIELHEVDLIGALKHEFDERYKNYVQI WT HADDINNSVIRWEFIELHEVDLIGALKHEFDERYKNYVQI WT HADDINNSVIRWEFIELHEVDLIGALKHEFDERYKNYVQI WT HADDINNSVIRWEFIELHEVDLIGALKHEFDERYKNYVQI WT HADDINNSVIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDINNSVIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDINNSVIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDINNSVIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDVDNNVFIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDVDNNVFIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDVDNNVFIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDVDNNVFIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDVDNNVFIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDVDNNVFIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDVDNNVFIRWEFIKHEVDLIGALKHEFDERYKNYVQI WT HADDVDNNVFIRWEFIKHEVDLIGALKHEFDERYKNYQQI WT HADDVDNNVFIRWEFIKHEVDLIGALKHEFTERYKKELQV WT HADDVDNNVFIRWEFIKHENLIVKIRDEFFERYKKELQV WT HADDVDNNVFIRWEFIKHENLIVKIRDEFFERYKKELQV WT HADDVDNNSTINGEFFERYKKELQV WT HADDVDNNSTINGFFERNYKCELQV WT HADDVDNNSTINGEFFERNYKCELQV WT HADDVDNNSTINGEFFERNYKCELQV WT HADDVDNNSTINGEFFERNYKCELQV WT HADDVDNNSTINGEFFERNYKCELQV WT HADDVDNNSTINGEFFERNYKCELQV WT HADDVDNNSTINGEFFERNYKCELQV WT HADDVDNNSTINGEFFERNYKCELQV WT HADDVDNNSTINGFFERNYKCELQV WT HADDVDNNSTINGFFERNYKCELQV WT HADDVDNNSTINGEFFERNYKCELQV WT HADDVDNNSTINGFFERNYKCELQV WT HADDVDNNSTINGFFERNYKCELQV WT HADDVDNNSTINGFFERNYKCELQV WT HADDVDNNSTINGFFERNYKCELQV WT HADDVDNNSTINGFFERNYKCELQV WT HADDVDNNSTINGFFERNYKCELQV WT HADDVNNSTINGFFERNYKCELQV WT HADDVDNNSTINGFFERNYKCELQV WT HADDVNNNSTINGFFERNYKCELQV WT HADDVNNNSTINGFFERNYKCELQV WT HADDVNNSTINGFFERNYKCELQV WT HADDVNNNSTINGFFERNYKCELQV WT HADDVNNNSTINGFFERNYKCELQV WT HADVNNNSTINGFFERNYKCELQV WT HADVNNNSTINGFFERNYKCELVYKNCUNYLLGPFFENYKCELQV WT HADVNNNSTINGFFERNYKCELVYLLGPFFERNYKCELQV	1184 1184 1170 1161 1213 1241 1209 1235 1235 1235 1235 1235 1235 1237 1207 1207 1203 1192 1195 1198 1169 1141 1143 1150
ECHKDGLVFASVEDSY KCAESGLFFASVEDSY QCRANGLEFASVEDSY QCRANGLEFASVEDSY ACCERCLFFASVEDSY ECGKQGLDFASVEDSY ECGKQGLDFASVEDSY ECGKQGLDFASVEDSY ECGKQGLDFASVEDSY KCCEKCLFFASVEDSY ACCERCLFFASVEDSY	WT HADJERAMERALENEFVXHHOVDLIGELKMEFDARYKNYLEY WT HADJEXMEKHLENGFVXHHOVDLIGELKMEFDARYKNYLEY WT HADJEXMEKHLENGFVTHEVDLIERLKEFDERYKNYVGI WT HADJEXMEKHLENGFTDLHEVDLIERLKEFDERYKNYVGI WT HADJEXMEKVIREGFIDLHEVDLIERLKEFDERYKNYVGI WT HADJEXMENVVIREGFILHEVDLIGELKMEFDERYKNYVGI WT HADJEXMENVVIREGFILHEVDLIGELKMEFDERYKNYVGI WT HADJEXMENVVIREGFIKHEVDLIGELKMEFDERYKNYVGI WT HADJEXMENVVIREGFIKHEVDLVALKEFFGGRYKNYVKI WT HADJEXMENVVIREGFIKHEVDLVALKEFFGGRYKNYVKI WT HADJEXMENVVIREGFIKHEVDLVALKEFFGGRYKNYVKI WT HADJEXMENVIREGFIKHEVDLVIRLKEFFGRYKNYVGI WT HADJEXMENVIREGFIKHEVDLVIRLKEFFGRYKNYVGI WT HADJEXMENVIREGFIKHEVDLIERLKMEFDERYKNYVGI WT HADJEXMENVIREGFIKHEVDLIERLKMEFDERYKNYVGI WT HADJEXMENVIREGFIKHEVDLIERLKMEFDERYKNYVGI WT HADJEXMENTREGFIKHEVDLIERLKMEFDERYKNYVGI WT HADJEXMENTREGFIKHEVDLIERLKMEFDERYKNYVGI WT HADJEXMENTREGFIKHESLIVELERLKEFFERYKNYGGI WT HADJEXMENTREGFIKHESLIVELERLKEFFERYKNYGGI WT HADJEXMENTREGFIKHESLIVELERLKEFFERYKSFLQV WT HADJEXMENTREGFIKHESLIVELREFKRYKGFLQV WT HADJENNELTRNGFIKHESLIVELSEFKRYKGFLQV WT HADJENNESTIRGFIKHESLIVELSEFKRYKGFLQV WT HADJENNESTIRGFIKHESLIVELSEFKRYKGFLQV WT HADJENNESTIRGFIKHESLIVELSEFKRYKGFLQV WT HADJENNESTRNGFIKHESSIVGELKEFFERYKSFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELKEFFKRYKGFLQV WT HADJENNESTRNGFIKHESSIVJELKSEFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELKEFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELKEFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELKEFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELKSEFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELSTEFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELKSFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELKSFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELSTEFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELKSFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJELKSFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJERFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJERFFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJERFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKHSSIVJERFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKKKGFKGYVERFKRYKGFLQV WT HADJENNESTRNGFIKHEGFIKKSSIVJERFKRYKGFYKGFYKGFYGYKSJU	1184 1184 1170 1161 1213 1241 1209 1226 1225 1225 1235 1182 1176 1187 1207 1203 1182 1185 1185 1185 1185 1189 1143 1189 1143 1199 1176 1189
ECHKDGLVFASVEDSY KCAEEGLEFASVEDSY (CRANGLEFASVEDSY (CRANGLEFASVEDSY ACCERGLEFASVEDSY ACCERGLEFASVEDSY ECGKQGLFASVEDSY ECGKQGLFFASVEDSY ECGKQGLFFASVEDSY KCGEKGLFFASVEDSY KCGEKGLFFASVEDSY ACCEGENGFFASVEDSY ACCEGENGFFASVEDSY ACCEGENSFFASVEDSY ACCEGENSFFASVEDSY ACCEGENSFFASVEDSY ACCEGENSFFASVEDSY ACCEGENSFFASVEDSY ACCGGELSFFASVEDSY ACCGGELSFFASVEDSY ACCEGELSFFASVEDSY ACCEGELSFFASVEDSY ACCEGELSFFASVEDSY ACCEGELSFFASVEDSY ACCEGELSFFASVEDSY ACCEGENSFFASVEDSY ACCEGENSFFASVEDSY ACCEGENSFFASVEDSY ACCEGENSFFASVEDSY ACCEGENSFFASVEDSY ACCEGENSFFASVEDSY ACCEGENSFFASVEDSF SCCESEDLGFASVEDSF SCCESEDLGFASVEDSF	WT HADDIFAMMFALMMEFVXHMUVDLIQLIKMEFDARYKMYLEV WT HACDVSKMKKHLRWEFVXHMUVDLIQLIKEFDARYKMYVEI WT HACDVSKMKHLRWEFVIHEQFYLHEVDLIRALKKEFDERYKMYVQI WT HACDIKMSYVLRBOFIELHKVDLIRALKKEFDERYKMYVQI WT HACDVKMSVYLRBOFIELHKVDLIRALKKEFDERYKMYVQI WT HACDVKMSVILRBOFIELHKVDLIQLIKKEFDERYKMYVQI WT HACDVKMSVLRBOFIELHKVDLUQLIKEFDERYKMYVQI WT HASDVDIMMVVLRBOFIKLHEVDLUQLIKEFDERYKMYVQI WT HASDVDIMMVVLRBOFIKLHEVDLVLALKEFDQRYKMYVXI WT HASDIDTMNVVLRBOFIKLHEVDLVLALKEFDQRYKMYVXI WT HASDIDTMNVVLRBOFIKLHEVDLVLALKEFDQRYKMYVXI WT HASDIDTMNVVLRBOFIKLHEVDLVRLKEFDQRYKMYVXI WT HASDVDMMVVLRBOFIKLHEVDLVRLKEFDQRYKMYVXI WT HASDVDMMVVLRBOFIKLHEVDLVRLKKEFDQRYKMYVQI WT HASDVDMMVVLRBOFIKLHEVDLIRALKKEFDERYKMYQQI WT HACDVDMMVVLRBOFIKLHEVDLIRALKKEFDERYKMYQQI WT HACDVDMMVVLRBOFIKLHEVDLIRALKKEFDERYKMYQQI WT HACDVDMMVVLRBOFIKLHEVDLIRALKKEFDERYKMYQQI WT HASDVDMMVXLRBOFIKLHEVDLIRALKKEFDERYKMYQQI WT HASDVDMMVXLRBOFIKLHEVDLIRALKKEFDERYKMYQQI WT HASDVDMMVXLRBOFIKLHEVDLIRALKKEFDERYKKFLQV WT HASDVDMMVXLRBOFIKLHSMLINQVKDEFFRAYKKFLQV WT HASDVDMMVXLRBOFIKLHSMLINQVKDEFFRAYKKFLQV WT HASDVDMMXEIRMQFVLHSMLINQLKEFFRAYKKFLQV WT HASDVDMMSILRBOFVLHSMLINQLKEFFRAYKKFLQV WT HACDVDMMSILRBOFVLHSMLINGLKEFFRAYKKFLQV WT HASDVDMMSILRBOFVLHSMLINQLKEFFRAYKKFLQV WT HANVDMMSILRBOFVLHSMLINGLKEFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINQLKEFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINLINGLKEFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLKEFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLKEFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINULLKEFFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLLKEFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLKHFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLKHFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLKEFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLKEFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLKFFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLLKFFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLILLKFFFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLLLKFFFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLLLKFFFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGLLLKFFFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGVLUNGLLKFFFRAYKKFLQV WT HADVDMMSILRBOFVLHSMLINGVLUNGSILRFFRAYKKFLQV	1184 1184 1170 1161 1213 1241 1209 1235 1235 1235 1235 1235 1235 1197 1207 1203 1192 1199 1199 1199 1141 1143 1190 1199 1176
ECHKDGLYPASYBOY KCAPEGLPASYBOY (CRANGLEPASYBOY (CRANGLEPASYBOY (CRENGLEPASYBOY ACCEKGLPFASYBOY ECGKQGLPFASYBOY ECGKQGLPFASYBOY ECGKQGLPFASYBOY KCGEKGLPFASYBOY KCGEKGLPFASYBOY ACCEGCLFFASYBOY ACCEGCLFFASYBOY ACCEGCLFFASYBOY ACCEGCLFFASYBOY ACCEGCLFFASYBOY ACCEGCLFFASYBOY ACCEGCLFFASYBOY ACCEGSLFFASYBOY ACCEGSLFFASYBOY ACCEGSLFFASYBOY ACCEGSLFFASYBOY ACCEGSLFFASYBOY CCCEFCLFFASYBOY CCCEFCLFFASYBOY CCCEFCLFFASYBOY CCCEFCLFFASYBOY CCCEFCLFFASYBOY CCCEFCLFFASYBOY	WT HADDIFAMMFALMMEFVXHMUVDLIQLIKNEFDARYKMYLEV WT HACDVSKMKHLRNEFVXHMUVDLIQLIKEFDARYKMYLEV WT HACDVSKMKHLRNEFVXHHEVDLIERLKEFDERYKMYVQI WT HACDVKMSVILREQFIDLHKVDLIERLKEFDERYKMYVQI WT HACDVKMSVILREQFIDLHKVDLIERLKEFDERYKMYVQI WT HADDIKMSVILREQFILHKVDLIQLKKEFDERYKMYVQI WT HADDIKMSLARQFYLHEVDLIQLKEFDERYKMYVQI WT HADDIKMSVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLIERLKKEFDERYKMYQJ WT HASDVDKMSVLREQFIKLHEVDLIERLKKEFDERYKMYQJ WT HACDVDKMSVLREQFIKLHEVDLIERLKKEFDERYKMYQJ WT HADDVKMNVLREQFIKLHEVDLIERLKEFDERYKMYQJ WT HASDVDKMSVLREQFIKLHEVDLIERLKEFDERYKMYQJ WT HASDVDKMSVLREQFIKLHEVDLIERLKEFDERYKMYQJ WT HASDVDKMSVLREQFIKLHEVDLIERLKEFDERYKMYQJ WT HADDIVLSKILRQFVKHESULJQKKEFFRAYKKFLQV WT HADDIVLSKILRQFVKHHSMLINQVRDEFFRAYKKFLQV WT HADDINNSKIRMQFVKHHSMLINQVRDEFFRAYKKFLQV WT HADDINNSKIRMQFVKHHSMLINQVRDEFFRAYKKFLQV WT HADDINNSKIRMQFVKHHSMLINQLKEFFRAYKKFLQV WT HADDINNSTIREQFVKHSMLIQLKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLINQLKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLINZLLKEFFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMJUZILKEFFRAYKKFLQV WT HADNVMSSILRQVKHSTRJKVKHSMLJUZILKEFFRAYKKFLQV WT HADNVKKYKKYKKYKKYKKYKKSYKKSYQI WT HADNVKKYKKYKKYKKYKYKKYKKYKKYKKYKKYKKYKYKKY	1184 1184 1170 1161 1213 1241 1209 1235 1235 1235 1235 1181 1176 1187 1207 1203 1182 1185 1189 1189 1143 1190 1199 1176 1189 1176 1189 1178 1188 1168 1168
ECHKDGLYPASYBOY KCAEGGLPASYBOY QCRANGLEPASYBOY QCRANGLEPASYBOY ACCERCLPPASYBOY ACCERCLPPASYBOY ECGKQGLDPASYBOY ECGKQGLDPASYBOY ECGKQGLDPASYBOY KCCEKCLPPAYBOY KCCEKCLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGECLPPAYBOY ACGESLPAYBOY ACCESSLQPASYBOY SCEESSLQPASYBOF KCTENDLQPAYBOF	WT HADDIFAMMFALMMEFVXHMUVDLIQLIKNEFDARYKMYLEV WT HACDVSKMKHLRNEFVXHMUVDLIQLIKEFDARYKMYLEV WT HACDVSKMKHLRNEFVXHHEVDLIERLKEFDERYKMYVQI WT HACDVKMSVILREQFIDLHKVDLIERLKEFDERYKMYVQI WT HACDVKMSVILREQFIDLHKVDLIERLKEFDERYKMYVQI WT HADDIKMSVILREQFILHKVDLIQLKKEFDERYKMYVQI WT HADDIKMSLARQFYLHEVDLIQLKEFDERYKMYVQI WT HADDIKMSVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLVRLKEFDQAYKMYVXI WT HASDVDKMVVLREQFIKLHEVDLIERLKKEFDERYKMYQJ WT HASDVDKMSVLREQFIKLHEVDLIERLKKEFDERYKMYQJ WT HACDVDKMSVLREQFIKLHEVDLIERLKKEFDERYKMYQJ WT HADDVKMNVLREQFIKLHEVDLIERLKEFDERYKMYQJ WT HASDVDKMSVLREQFIKLHEVDLIERLKEFDERYKMYQJ WT HASDVDKMSVLREQFIKLHEVDLIERLKEFDERYKMYQJ WT HASDVDKMSVLREQFIKLHEVDLIERLKEFDERYKMYQJ WT HADDIVLSKILRQFVKHESULJQKKEFFRAYKKFLQV WT HADDIVLSKILRQFVKHHSMLINQVRDEFFRAYKKFLQV WT HADDINNSKIRMQFVKHHSMLINQVRDEFFRAYKKFLQV WT HADDINNSKIRMQFVKHHSMLINQVRDEFFRAYKKFLQV WT HADDINNSKIRMQFVKHHSMLINQLKEFFRAYKKFLQV WT HADDINNSTIREQFVKHSMLIQLKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLINQLKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLINZLLKEFFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMLJUZILKEFFRAYKKFLQV WT HADNVMSSILRQFVKHSMJUZILKEFFRAYKKFLQV WT HADNVMSSILRQVKHSTRJKVKHSMLJUZILKEFFRAYKKFLQV WT HADNVKKYKKYKKYKKYKKYKKSYKKSYQI WT HADNVKKYKKYKKYKKYKYKKYKKYKKYKKYKKYKKYKYKKY	1184 1184 1170 1161 1213 1241 1209 1236 1235 1235 1235 1281 1171 1197 1207 1203 1192 1195 1195 1198 1199 1199 1199 1176 1180 1179 1188 1168

			1
tr B6K333 B6K333 SCHJY	LTFPEVPERGTFDIRSVL	HSOYFFS	1169
ap 013993 RPOM SCHPO	LEFPFLPARGALDLKKVL	ESKYFFS	1154
t= \$90008 \$90008 SCHOY	LKIPLLPSOGTFDLTKVL	ESKYFFS	1168
tr S9X2W4 S9X2W4 SCHCR	LRIPTLPSQCSFDLTKVL		1167
tr AGA1E303C6 AGA1E303C6 LIPST	LTFPPVPPKGAFDVKTLR		1403
tr A0A167E4J0 A0A167E4J0 9ASCO	LRITKVPAKGDFDVHQLR		1144
tr AGA1E3PUPO AGA1E3PUPO 9ASCO	LKFPEVPPKGEFDVHLLR		1294
tr A0A0H5C7R0 A0A0H5C7R0 CYBJA	LRLPEIPPKGEFDVQELR		1285
tr AGA1E3P5W0 AGA1E3P5W0 WICAO	LRLPEIPPKGOFDVODLR		1299
tr KOKTX3 KOKTX3 WICCF	LRLPDIPPKGDFDVNDLR		1332
tr W6MIL2 W6MIL2 9ASCO	FKLDDIPPRGDFKASEVM		1297
tr AGA1E30PI7 AGA1E30PI7 9ASCO	FALPEVPEKGEFDVNVVK		1274
tr A0A1D2V948 A0A1D2V948 9A9C0	LRLPDVPPKGEFDVREVK		1327
tr A0A1B79ME0 A0A1B79ME0 9A9CO	FDLPPIPLKGEFDVNVVR		965
tr 06CR25 06CR25 KLULA	LRLPEIPPKGEFDVOELL		1263
tr WOTGI8 WOTGI8 KLUMA	LRLPEIPPKCNFDVEELM		1262
tr A0A109UWS1 A0A109UWS1 95ACH	MKFSSVPPKGEYDIKELL		1272
tr G8JM92 G8JM92_ERECY	MKFPDIPPKGEFDVKELV		1298
t= Q75BP7 Q75BP7_ASHGO	LKFSGIPPKGSYDIROLV		1295
tr R9XDF6 R9XDF6 ASHAC	LRFSEIPPKGSYDVRELV		1295
tr H2ASJ8 H2ASJ8 KAZAF	LKLPDIPPKGDFDVENVK		1284
tr J797Y3 J797Y3 KAZNA	LKLPSIPPKDNFDVHEVK		1276
t= GOVDO1 GOVDO1_NAUCC	LELPDIPPKGEFDVETVE		1326
tr GOWE72 GOWE72 NAUDC	LKLPEIPSKGDFDVONVR		1354
tr Q6FLX9 Q6FLX9 CANGA	LILPDIPPKCNFDVEVLR		1326
tr G8BS54 G8BS54 TETPH	LKLPPIPPKGNFDVOETK		1322
tr AOAOLSRKW5 AOAOLSRKW5 SACEU	LRLPEIPPKGDFDVTVLK		1352
tr AOAOLSVRU3 AOAOLSVRU3 95ACH	LRLPEIPPKGDFDVTVLR	NSOYFES	1351
tr J8PP58 J8PP58 SACAR	LRLPEIPPKGDFDVTVLR		1351
tr A0A0C7MY71 A0A0C7MY71 95ACH	LKLPOIPPKGNFDVRELE		1294
tr C5DNP3 C5DNP3 LACTC	LTLPOIPPKCDFDVRELE	KSKYFFS	1289
tr C5DX79 C5DX79 ZYGRC	LRLPOIPPKGNFDVRELK	NSKYFFS	1311
tr G8ZR00 G8ZR00 TORDC	MRLPQIPPKGNFDVQDLR	NSKYFFS	1321
tr AOA1E4ROF7 AOA1E4ROF7 9ASCO	LNFPEIPPKGEFDVAEVK	NSOYFFS	1315
tr AOAOLOP4K6 AOAOLOP4K6 9ASCO	LTFPEIPSKGDLDVSLVK	ESQYFFS	1305
tr AOA1A0HGT7 AOA1A0HGT7 _ 9ASCO	LKFPDIPERGSLDVQVVK	DSPYFFS	1308
tr C4Y8E3 C4Y8E3 CLAL4	LSFPDIPPRGSLDVQVVK	OSPYFFS	1311
tr G3B4C1 G3B4C1_CANTC	ISFPPVPPRCDLDVNVVK	DSTYFFS	1279
tr A3LX46 A3LX46 PICST	LTFPDIPAKGELDVEVVK	ESPYFFS	1251
tr AOA1E49MT6 AOA1E49MT6_9A9CO	LKFPEVPERGDLDVELVK	ESDYFFS	1256
tr A5DN82 A5DN82_PICGU	LTFPSIPPKGELDVKAVM	DSPYFFS	1303
tr B5RTF6 B5RTF6 DEBHA	LKFPEIPKKGDLDVSIVK	DSPYFFS	1312
tr G3AEY0 G3AEY0 SPAPN	LKFPEVPPKGEFDVNRVK	DSLYFFS	1287
tr G8B7X1 G8B7X1_CANPC	IOFPEVPPKGEFDVOKVR	DSHYFFS	1292
tr H8X1L6 H8X1L6_CANO9	IOFPEVPPKGEFDVRKVK	DSHYFFS	1291
tr B9W6L5 B9W6L5_CANDC	LOFPEVPRKGGFDVNLVK	DSQYFFS	1300
tr C4YFJ1 C4YFJ1_CANAW	IOFPEVPSKGEFDVNLVK	DSQYFFS	1280
tr C5ME71 C5ME71_CANTT	IOFPKVPAKGDFDVNLVK	DSQYFFS	1293
tr M3IK19 M3IK19_CANMX	LOFPEIPKKGTFDVNLVK	OSOYFFS	1298
	a a at as a		1

Fig. 5. MSA of various SSU RNA polymerases from various fungal mitochondria

*All the mitochondrial RNA polymerases end in SxYFFS tr|B6K333|B6K333 SCHJY, Schizosaccharomyces japonicus sp[O13993]RPOM SCHPO, Schizosaccharomyces pombe tr|S9Q0Q8|S9Q0Q8 SCHOY, Schizosaccharomyces octosporus tr|S9X2W4|S9X2W4_SCHCR, Schizosaccharomyces cryophilus tr|A0A1E3Q3C6|A0A1E3Q3C6 LIPST, Lipomyces starkeyi tr|A0A167E4J0|A0A167E4J0 9ASCO, Sugiyamaella lignohabitans tr|A0A1E3PUP0|A0A1E3PUP0_9ASCO, Nadsonia fulvescens var. elongata tr|A0A0H5C7R0|A0A0H5C7R0_CYBJA, Cyberlindnera jadinii tr A0A1E3P5W0 A0A1E3P5W0 WICAO, Wickerhamomyces anomalus tr|K0KTX3|K0KTX3_WICCF, Wickerhamomyces ciferrii tr|W6MIL2|W6MIL2_9ASCO, Kuraishia capsulata tr A0A1E3QPI7 A0A1E3QPI7_9ASCO, Babjeviella inositovora tr|A0A1D2V948|A0A1D2V948_9ASCO, Ascoidea rubescens tr|A0A1B7SME0|A0A1B7SME0 9ASCO, Ogataea polymorpha tr|Q6CRZ5|Q6CRZ5 KLULA, Kluyveromyces lactis tr|W0TGI8|W0TGI8 KLUMA, Kluyveromyces marxianus tr|A0A109UWS1|A0A109UWS1 9SACH, Eremothecium sinecaudum tr|G8JMS2|G8JMS2 ERECY, Eremothecium cymbalariae tr|Q75BP7|Q75BP7_ASHGO, Ashbya gossypii tr|R9XDF6|R9XDF6_ASHAC, Ashbya aceri tr|H2ASJ8|H2ASJ8 KAZAF, Kazachstania africana tr|J7S7Y3|J7S7Y3 KAZNA, Schizosaccharomyces octosporus tr|G0VD01|G0VD01 NAUCC, Naumovozyma castellii

tr|G0WE72|G0WE72 NAUDC,Naumovozyma dairenensis tr|Q6FLX9|Q6FLX9 CANGA, Candida glabrata tr|G8BS54|G8BS54 TETPH, Tetrapisispora phaffii tr|A0A0L8RKW5|A0A0L8RKW5 SACEU, Saccharomyces eubayanus tr A0A0L8VRU3 A0A0L8VRU3 9SACH, Saccharomyces sp. 'boulardii' tr|J8PP58|J8PP58 SACAR, Saccharomyces arboricola tr A0A0C7MY71 A0A0C7MY71_9SACH, Lachancea lanzarotensis tr|C5DNP3|C5DNP3 LACTC, Lachancea thermotolerans tr|C5DX79|C5DX79 ZYGRC, Zygosaccharomyces rouxii tr|G8ZR00|G8ZR00 TORDC, Torulaspora delbrueckii tr|A0A1E4RQF7|A0A1E4RQF7 9ASCO, Hyphopichia burtonii tr A0A0L0P4K6 A0A0L0P4K6 9ASCO, Candida auris tr|A0A1A0HGT7|A0A1A0HGT7_9ASCO, Metschnikowia bicuspidata var. bicuspidata tr|C4Y8E3|C4Y8E3_CLAL4, Clavispora lusitaniae tr|G3B4C1|G3B4C1 CANTC, Candida tenuis tr|A3LX46|A3LX46_PICST, Scheffersomyces stipitis tr|A0A1E4SMT6|A0A1E4SMT6 9ASCO, Candida tanzawaensis tr|A5DN82|A5DN82 PICGU, Meyerozyma guilliermondii tr|B5RTF6|B5RTF6 DEBHA, Debaryomyces hansenii tr|G3AEY0|G3AEY0 SPAPN, Spathaspora passalidarum tr|G8B7X1|G8B7X1_CANPC, Candida parapsilosis tr|H8X1L6|H8X1L6_CANO9, Candida orthopsilosis tr|B9W6L5|B9W6L5_CANDC, Candida dubliniensis tr|C4YFJ1|C4YFJ1 CANAW, Candida albicans tr|C5ME71|C5ME71 CANTT, Candida tropicalis tr|M3IK19|M3IK19 CANMX, Candida maltosa

In the viral, chloroplast and mitochondrial RNA polymerases the last 6 amino acids at Nterminal ends are highly conserved, suggesting a possible role for this motif in transcription cycle. Whether it possibly involves in a Rho-dependent or independent termination process to offload the nascent RNA at the termination site is to be elucidated. The consensus motif in viral polymerases is -SDFAFA. Peptide search analysis shows this motif is also found in RNA binding protein of the fungus, Ustilago maydis and primarily involves in RNA transports [6] and in poyA binding protein where it is implicated in both mRNA cleavage and polyadenylation in the nucleus. In chloroplast and mitochondrial polymerases the consensus sequence is -SxYFFS. (The -YPPS tetrad on peptide search analysis is found in ATP-dependent DNA helicase and an ATP-dependent, dual-direction single-stranded exonuclease. This tetrad is also found in plant and human transcriptional activators). Therefore, it is probably involved in termination, i.e., transcript cleavage process.

The metal binding sites are also highly conserved among all these SSU RNA polymerases which are highlighted in yellow. Usually, a D in QD and a D in HDS are found to be involved in binding to Mg²⁺ and in 'NTP charge shielding' and found in all these RNA polymerases.

Fig. 6 shows the MSA of a 'mix and match' analysis and shows the conserved motifs in all the three different categories of SSU RNA polymerases, viz. viruses (4), chloroplasts (2) and mitochondria (2). Such an analysis may narrow down the only motifs common among them that may be essential for substrate binding and catalysis. More conserved regions are seen towards the C-terminal regions. The catalytic, template and substrate binding motifs are highlighted. The C terminal region shows conservation in the catalytic K, YG pair and an invariant R among them as expected. The YG gate keeper motif and the catalytic K is strictly conserved (including distance conservation) in DNA dependent RNA polymerases from all the three different sources. This is in accordance with the DNA polymerases data, reported by Palanivelu [4]. This strongly suggests that the DNA and RNA polymerases might be using the same set of amino acids for template, substrate binding and catalysis.

CLUSTAL O(1.2.4) MSA - 4 viral, 2 Mitochondria RNA polymerases

BAC98394.1 ARATH AAD03373.1 OSATIVA sp P92969 RPOT1_ARATH sp Q93Y94 RPOT1_NIC3Y sp P06221 RPOL_BF8F6 sp P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 AAD03373.1 sp P92969 RPOT1_ARATH	PRPR-LRRLSPPPPMAAVAPPSLSTPVTILPSVSVALPPLPPPATD HTSLVTWIKPPPSSALFRKTLPFPERHSLPISASSSSSSTSLSVHEKPISNSV	2 20 37 60 0 0 0 0 0 0 78 59
<pre>sp Q93Y94 RPOT1_NICSY sp P06221 RPOL_BPSP6 sp P18147 RPOL_BPK11 ACY75835.1 T7 CAC86264.1 T3</pre>	RISRKVRHLEGICEESS-KNPHLGLSQNSLFSSVKG	95 0 0 0
BAC98394.1 AAD03373.1 sp[92969]RPOT1_ARATH sp[093Y94]RPOT1_NIC3Y sp[P06221]RPOL_BPSF6 sp[P18147]RPOL_BPK11 ACY75835.1 CAC86264.1	DFHWLDLFAFLNSFADSYQIPVEDQEVEVEVUEVGVERERERE AGTIKGASLIEELENFVERNGLSGR SSFRHQCYVEGYATAAQAIDSTDPEDESSGSDEVNELITEMEKETERIR DFRVCGKRGSGSLGFIRSYGSAAEAIASTSEEDIDEIQELIEEMNKENEALK 	104 120 110 147 0 11 11 11
BAC98394.1 AAD03373.1 =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NIC3Y =p P06221 RPOL_BP8F6 =p P18147 RPOL_BFK11 ACY75835.1 CAC86264.1	RERERERARKAEHRRIR OP VKAETEAWARAA RRLFMQDPFWISALFLKGLSKMVDQTLKIERKDIDKRKFDSLRROVKEETEAWERMV KKARLA	138 178 151 185 41 69 69 70
BAC98394.1 AAD03373.1 =p 92969 RPOT1_ARATH =p 093Y94 RPOT1_NIC3Y =p P06221 RPOL_BPSP6 =p P18147 RPOL_BPK11 ACY75835.1 CAC86264.1	DEYRELEREMLDRRLAPALPYVKSLFLGWFEPLRDAIARDQEVQRRKRVKHVYAKYLL DEYRDLEKEMCERNLAPNLPYVKHMFLGWFQPLKDVIEREQKLQKNKSKKVRAAYAPHIE RECREILAIMCEQKLAPNLPYMKSLFLGWFEPVRNAIQDDLDFKIKKGKIPYAPFME KEYQELLMIMCEQKLAPNLPYMKSLFLGWFEPLRDAIAAEQKLCDEGKNRGAYAPFFD NRRLLSELIAFMAEGQAYKEEYEGKKGRAPRALAFLQC 	196 238 209 243 80 108 108 108
BAC98394.1 AAD03373.1 =p 92969 RPOT1_ARATH =p 093Y9 RPOT1_NIC3Y =p P06221 RPOL_BPSP6 =p P18147 RPOL_BFK11 ACY75835.1 CAC86264.1	LLPADKVAVIVMHRMMGLLMSSKDGVASVRVVQAAHCIGEA LLPADKMAVIVMHRMMGLVMSGH-EDGCIQVVQAAVSIGIA QLPADKMAVITMHRMMGLLMINAEGVGIVKLVMAATQIGEA QL	237 278 250 283 114 164 144 145
BAC98394.1 AAD03373.1 sp 92969 RPOT1_ARATH sp Q33Y94 RPOT1_NICSY sp P06221 RPOL_BFSP6 sp P18147 RPOL_BFK11 ACY75835.1 CAC86264.1	VEREFKVQTFFQRTRKKSAGENDLALEKEQAKCRKRVKSLVRRRKLTEA- IEQEVRIHNFLKRTRKNNAGDSQEELKEKQLLRKRVNSLIRRKRIIDA- VEQEVRINSFLQKKNKKNATDKT INTEAENVSEEIVAKETEKARKQVTVLMEKNKLRQV- IEHEARIHRFLEKTKKSNALSGDLEDTFGDIMKERERVRKKVKILMKKQKLQQV- IEDQVRFSKLEGHAAKYFEKVKKSLKASR-TKSYRHAHNVAW LEDEARFGRIRDLEAHFKK	286 326 309 337 156 206 186 187

BAC98394.1 ----QKIVQQEIELEEWGTESQVKLGTRLIELLLDSAFVQSPADQTPESSPDIRPAFKH 341 ----LKV-VKSEGTKPWGRATQAKLGSRLLELLIEAAYVQPPLTQSGDSIPEFRPAFRH AAD03373.1 280 -----KALVRKHDSFKPWGGEAQVKVGARLIGLLMENAYIQPPAEQFDDGPPDIRPAFKQ sp|P92969|RPOT1 ARATH 364 -----RKIVKQQDDEKPWGQDNLVKVGCRLIQILMETAYIQPPNDQLDDCPPDIRPAFVH sp |Q93Y94|RPOT1 NICSY 392 sp | P06221 | RPOL_BPSP6 AEKSVAEKDADFDRWEAWPKETOLOIGTTLLEILEGSVFYNGEPVFMR------204 EADMISKGMLGGINWASWKTDEQMHVGTKLLELLIEGTGL---VEMTK----sp|P18147|RPOL_BFK11 251 EADMLSKGLLGGEAWSSWHKEDSIHVGVRCIEMLIESTGM---VSLHR------ACY75835_1 231 CAC86264.1 EADMIGRGLLGGEAWSSWDKETTMHVGIRLIEMLIESTGL---VELQR------232 2 C 🕈 - : : : * BAC98394.1 VLROPIV-ENGRLKKKHWVIECDPLVHEGFESTA---RHVEIPYLPMLVTPKKWKGYDTG 397 AAD02272 1 RFKTVTKYPGSKLVRRYGVIECDSLLLAGLDKSA---KHMLIPYVPMLVPPKRWKGYDKG 437 sp | P92969 | RPOT1 ARATH NFRTVTL-ENTKTSRRYGCIECDPLVLKGLDKSA---RHMVIPYLPMLIPPQNWTGYDQG 420 sp|093Y94|RPOT1_NICSY sp|P06221|RPOL_BPSP6 TLKTV---ETMKGSRRYGVIOCDPLVRKGLDKTA---RHMVI FYMPMLVPPOSWLGYDKG 446 AMRT----YGGKTIYYL---OTSESVGOWISAFKEHVAOLSPAYAPCVIPPRPWRTPFNG 257 NKMA----DGSDDVTSMQMVQLAPAFVELLSKRAGALAGISPMHQPCVVPPKPWVETVGG sp | P18147 | RPOL BPK11 307 QNAG----VVGQD---SETIELAFEYAEAIATRAGALAGISPMFQPCVVPPKPWTGITGG ACY75825 1 284 HNAG----NAGSD---HEALQLAQEYVDVLAKRAGALAGISPMFQPCVVPPKPWVAITGG CAC86264.1 285 2 : . . * .. *. * BAC98394.1 GYLFL---PSYIMRTHGVKDQKEAIKSVPRKQLRKVFEALDTLGSTKWRVNRRVHNAVET 454 GYLFL---PSYIMRTHGSKKQQDALKDISHKTAHRVFEALDTLGNTKWRVNRNILDVVER AAD03373.1 494 sp | P92969 | RPOT1 ARATH AHFFL---PSYVMRTHGAKQQRTVMKRTPKEQLEPVYEALDTLGNTKWKINKKVLSLVDR 477 sp |Q93Y94|RPOT1 NICSY AYLFL---PSYIMRTHGAKQQREAVKRVPKKQLEPVFQALDTLGNTKWRLNRKVLGIVDR 503 sp|P06221|RPOL_BPSP6 sp|P18147|RPOL_BPK11 GENTERVASBIRIVEG----NREHVERLICEGMPRVYKAINALONICSOINEDVLAVIEE 313 GYWSVGRRPLALVRTH----SKKALRRYADVHMPEVYKAVNLAONTFWKVNKKVLAVVNE 363 ACY75825_1 GYWANGRRPLALVRTH----SKKALMRYEDVYMPEVYKAINIAONTAWKINKKVLAVANV 340 CAC86264.1 GYWANGRRPLALVRTH----SKKGLMRYEDVYMPEVYKAVNLAQNTAWKINKKVLAVVNE 341 ****** ÷ . I--WSRGGGIA---GLVDKENIPLPERPET-----EDPDEIQKWKWSLKK L--WADGGNIA---GLVNREDVPIPEKPSS-----EDPEELQSWKWSARK BAC98394.1 494 AAD03373.1 534 sp|P92969|RPOT1 ARATH I--WANGGRIG---GLVDREDVPIPEEPER-----EDQEKFKNWRWESKK 517 I--WASGGRLA---DLVDREDVPLPEEPDA----EDEAQIRKWKWKVKG sp|Q93Y94|RPOT1_NICSY sp|P06221|RPOL_BPSP6 sp|P18147|RPOL_BPK11 543 VIRLDLGYGVPSFKPLIDKENKPANPVFVEFCHLRGRELKEMLSPECWOOFINWKGECAR 272 IVNWKHCP--VGDVPAIEREELPFRPDDIDTN-----EVARKAWRKEAAA 406 ITKWKHCP--VEDIPAIEREELPMKPEDIDMN------PEALTAWKRAAAA ACY75835.1 282 IVNWKNCP--VADIPSLERCELPPKPDDIDTN-----EAALKEWKKAAAG CAC86264.1 384 AKKANRELHAERCDTELKLSVARMREEDGFYYPHNIDERGRAYPMHAHLSHLGSDLCRG ANKINRERHSLRCDVELKLSVARMKDEEGFYYPHNIDERGRAYPMHPHLNHLSSDLCRG AIKQNNERHSQRCDIELKLEVARMKDEEGFYYPHNIDERGRAYPIHPYLNHLGSDLCRG BAC98394.1 554 AAD03373.1 594 50 | P92969 | RPOT1 ARATH 577 sp|Q93Y94|RPOT1 NICSY VKKENCERHSQRCDIELKLAVARFMKDEDGFYYPHNIDFRGRAYPMHPYLNHLGSDLCRG 603 sp | P06221 | RPOL BPSP6 LYTAETKRGSKSAAVVRMVGQARKYSAFESIYFVYAMDSKSRVYVQSSTLSPQSNDLGKA 433 VYRKIKARQSRRCRCEFMVJQANKFANHKAIWFPYNDWBGRVYAV-SMFNPQGNDMTKG VYRKIKARKSRRISLEFMLDQANKFANHKAIWFPYNDWBGRVYAV-SMFNPQGNDMTKG IYRLIKARVSRRISLEFMLEQANKFASKKAIWFPYNDWBGRVYAV-PMFNPQGNDMTKG : : : * * * . . : : * * * . . . * : . 50 | P18147 | RPOL BPK11 465 ACY75835.1 T7 CAC86264.1 T3 442 443 VLEYAEGRPI-GKSGLRWLKIHLANKYGGGIEKLSHEDKVAFVEN--QLPDIFDSATNFV BAC98394.1 611 -GKSGIHWIKIHIANLYAGGVEKISHDARLAFVEN--HIDDIMDSAENPI AAD02272 1 TLEFAEGRE 651 sp|P92969|RPOT1 ARATH ILEFCEGKFL-GKSGLRWLKIHIANLYAGGVDKLAYEDRIAFTES--HLEDIFDSSDRPL 634 sp|Q93Y94|RPOT1 NICSY -GKSGLRWLKIHLANVYGGGVDKLSYEGRVAFSEN--HVEDIFDSAERPL Sp P06221 RPOL BPSP6 ILEFAE GRP 660 LLRFTEGRFVNGVEALKWFCINGANLW--GWDKKTFDVRVSNVLDEEFQDMCRDIAADPL 491 SLTLARGKPI-GLDGFYWLKIHGANCA--GVDKVPFPERIKFIEE--NEGNILASAADPL LLTLARGKPI-GKEGYYWLKIHGANCA--GVDKVPFPERIKFIEE--NHENIMACAKSPL sp|P18147|RPOL BPK11 520 ACY75835.1 497 LITLARGKPI-GEEGFYWLKIHGANCA--GVLKVPFPERIAFIEK--HVDDILACAKDPI * :*:* CAC86264.1 498 DGNCWWMNAEDPFQCLAACMDLSDALKSS---SPQCAVSHLPIHQDGSCNGLQHYAALGR BAC98394.1 668 AAD03373.1 HGKRWWLKAEDPFOCLAACVILTOALKSP---SPYSVISHLPIHODGS NGLOHYAALGR 708 sp | P92969 | RPOT1 ARATH EGKRWWLNAEDPFOCLAACINLSEALRSP---FPEAAISHIPHODGS NGLOHYAALGR 691 sp|Q93Y94|RPOT1_NICSY EGKRWWLGAEDPFQCLATCINIAEALRSP---SPETAISYMPIHQDGS NGLOHYAALGR 717 sp | P06221 | RPOL BPSP6 T-FTOWAKADAPYEFLAWCFEYAOYLDLVDEGRADEFRTHLPVHODGS SGIOHYSAMLR 550 sp | P18147 | RPOL BPK11 N-NTWWTQQDSPFCFLAFCFEYAGVKH----HGLNYNCSLPLAFDG8(SGIOHFSAMLR 574 E-NTWWAEQDSPFCFLAFCFEYAGVQH----HGLSYNCSLPLAFDGSCSGIQHFSAMLR ACY75835.1 **T**7 551 тз N-NTWWAEQDSPFCFLAFCFEYAGVTH----HGLSYNC3LPLAFDGSCSGIQHFSAMLR CAC86264 1 552

.

BAC98394.1		
DAC 908 94.1	DYMGAAAVNLVPGDKPADIYSEIAARVLDVVREDSMEDPAT	709
AAD03373.1	DSFEARAVNLVAGEK PADVYSE I SRRVHE IMKKDSSKDFE S	749
sp P92969 RPOT1 ARATH	DKLGADAVN.VTGEKPADVYTEIAARVLKIMQQDAEEDPET	732
sp Q93Y94 RPOT1 NICSY	DILGAAAVN,VAGDKPADVYSGIAARVLDIMKRDAAKDPAN	758
sp P06221 RPOL BPSP6	DEVGARAVNLKPSDAPQDIYGAVAQVVIKKNALYMDADDATTFTSGSVTL	600
5p P18147 RPOL BPK11	DSIGGRAVNLLPSDTVODIYKIVADKVNEVLHOHAVNGSOTVVEQIADKETGEFHEKVT-	633
ACY75835.1 T7	DEVGGRAVNLLPSETVODIYGIVAKKVNEILOADA INGTDNEVVTVTDENTGEISEKVK-	610
CAC86264.1 T3	DEVGGRAVNLLPSETVODIVGIVACKVNEILKODAINGTPNEMITVTDKDTGEISEKKK	611
P3 000004 4 00377		
BAC98394.1 OSATI	NPTASIARVLVDQVDEKLVKQTVMTSVYQVTYIGARQQITKRLQE	754
AAD03373.1 ARATH	NPTAALAKILITQVDEKLVKQTVMTSVYQVTYVGAREQIKRRLEE	794
sp P92969 RPOT1_ARATH	FFNATYAKLMLDQVDEKLVKQTVMTSVYQVTYSGARDQIKKRLKE	777
sp Q93Y94 RPOT1_NICSY	DFNVMRARLLINQV <mark>DF</mark> KLV <mark>KQ</mark> TVMTSVYQVTYIGARDQIKRRLKE	803
sp P06221 RPOL_BPSP6	SGTELRAMASAWDSIGI <mark>TE</mark> SL <mark>TKE</mark> PVMTL <mark>PYG</mark> STRLTCRESVIDYIVDLEEKEAQKAVAE LGESVLAAQWLQYGV <mark>TE</mark> KVT <mark>KE</mark> SVMTLA <mark>YG</mark> SKESLVRQQVLEDTIQPAIDN	660
sp P18147 RPOL_BPK11	LGESVLAAQWLQYGV <mark>TH</mark> KV <mark>IKH</mark> SVMTL <mark>AY¢</mark> SKESLVRQQVLEDTIQPAIDN	684
ACY75835.1 T7	LGTKALAGOWLAYGVTR SVTKRSVMTLAYGSKEFGFRQQVLEDTIQPAIDS	661
CAC86264.1 T3	LGTSTLAQOWLAYGVTR SVTKRSVMTLAYGSKEFGFRQQVLDDTIQPAIDS	662
	بالتبع ومالعه وماريقا بالتار	
BAC98394.1	KGLITDDKLLYEVSCYATRVTLDALGOMFOSARGIMAWLGDCAKMIAS	802
AAD03373.1	KGVITDERMLFAAACYSAKVTLAALGEIFEAARAIMSWLGDCAKIIAS	842
sp P92969 RPOT1 ARATH	RGTFEDDSLTFHASCYAAKITLKALEEMFEAARAIKSWFGDCAKIIAS	825
sp Q93Y94 RPOT1 NICSY	RGVIEDINELFAACYAAKTTLTALGEMFEAARSIMSWLGDCAKIIAM	851
sp P06221 RPOL BPSP6	GRTANKVHFFEDDRQDYLTPGAAYNYMTALIWPSISEVVKAPIVAMMIRQLARFAAK	718
		733
sp P18147 RPOL_BPK11	GEGLMFTHENQAAGYMAKLIWDAVTVTVVAAVEAMMWLKSAAKLLAAEV	
ACY75835.1 T7	GKGLMFTQPNQAAGYMAKLIWESVSVTVVAAVEAMNWLKSAAKLLAAEV	710
CAC86264.1 T3	GKGLMFTQFNQAAGYMAKLIWDAVSVTVVAAVEAMNWLKSAAKLLAAEV	711
	: . * : . : . : . : . *: *	
BAC98394.1	ENHPVKWTSPVGLFVVQPYKKYKNYMIRTSLQCLALRREGDAIA	846
AAD03373.1	DNHPVFWITPLGLFVVQFYCRSERHLIRTSLQVLALQREGNTVD	886
sp P92969 RPOT1 ARATH	ENNAVCWTTPLGLFVVQFYRKPGRHLVKTTLQVLTLSRETDKVM	869
sp Q93Y94 RPOT1 NICSY	ENHPVFWTTPLGLFVVQFYRKLGRHLIKTSLQILTLQRETDKVM	895
SD PO6221 RPOL BPSP6	RNEGLMYTLPTGFILEOKIMATEMLRVRTCLMGDIKMSLOVETDIVD	765
sp P06221 RPOL_BPSP6 sp P18147 RPOL_BPK11		
sp P18147 RPOL_BFK11	KDKKTKEVLRKRCAIHWVT PDGFFVWOEYRKONOARLKLVFLGOANVKMTYNTGKDSE ID	765 793
5p P18147 RPOL BPK11 ACY75835.1 T7	KDKKTKEVIRKRCAIHWYT PDGFFVWOEYRKONOARLKIVFLGOANVKMT YNTGKDBE ID KDKKTGE IIRKRCAVHWYT PDGFFVWOEYKKPIOTRLNIMFLGOFRLOFT INTNKDBE ID	765 793 770
sp P18147 RPOL_BFK11	KDKKTKEVIRKRCAIHWYT PDGFFVWOEYRKONOARLKIVFLGOANVKMT YNTGKDBE ID KDKKTGEIIRKRCAVHWYT PDGFFVWOEYKKPIOTRLNIMFLGOFRLOFT DNTNKDBE ID KDKKTKEIIRHRCAVHWTT PDGFFVWOEYRKPLOKRLDMIFLGOFRLOFT DNTLKDBG ID	765 793
5p P18147 RPOL BPK11 ACY75835.1 T7	KDKKTKEVIRKRCAIHWYT PDGFFVWOEYRKONOARLKIVFLGOANVKMT YNTGKDBE ID KDKKTGE IIRKRCAVHWYT PDGFFVWOEYKKPIOTRLNIMFLGOFRLOFT INTNKDBE ID	765 793 770
=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3	KDKKTKEVIRKRCAIHWVT PDGFFVWQEYRKQNQARLKIVFLGQANVKMTYNTGKDBE ID KDKKTGE IIRKRCAVHWVT PDGFFVWQEYKKPIQTRLNIMFLGQFRLQFT INTNKDBE ID KDKKTKE IIRHRCAVHWTT PDGFFVWQEYRKPLQKRLDMIFLGQFRLQFT INTLKDSGID . : : * *: : * : : : : : : : : : : : : :	765 793 770 771
5p P18147 RPOL BPK11 ACY75835.1 T7	KDKKTKEVLRKRCAIHWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE ILRKRCAVHWVT PDGF FVW OEYRK PIQTRLNIMFLOOFRLOPT INTIKD SE ID KDKKTKE ILRHRCAVHWTT PDGF FVW OEYRK PLQKRLDMI FLGOFRLOPT INTIKD SG ID 	765 793 770
=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3	KDKKTKEVLRKRCA I HWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE I LRKRCAVHWYT PDGF FVW OEYRKPI QTRLNIMFLGQFRLQFT INTNKD SE ID KDKKTKE I LRHRCAVHWTT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTLKD SG ID . : : * * : : : : : : : : : : : : : : :	765 793 770 771
BAC98394.1 OSATI	KDKKTKEVLRKRCAIHWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE ILRKRCAVHWVT PDGF FVW OEYRK PIQTRLNIMFLOOFRLOPT INTIKD SE ID KDKKTKE ILRHRCAVHWTT PDGF FVW OEYRK PLQKRLDMI FLGOFRLOPT INTIKD SG ID 	765 793 770 771 904
BAC98394.1 OSATI AAD03373.1 ATHALI	KDKKTKEVIRKRCAIHWVT PDGFFVWQEYRKONQARLKIVFLGQANVKMT YNTGKDSE ID KDKKTGE IIRKRCAVHWVT PDGFFVWQEYRKPIQTRINIMFLGQFRLQFT INTNOSE ID KDKKTKE IIRHRCAVHWTT PDGFFVWQEYRKPIQTRINIFLGQFRLQFT INTIKDSE ID 	765 793 770 771 904 944
<pre>=p P18147 RPOL_BEK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH</pre>	KDKKTKEVIRKRCAIHWVT PDGFFVWOEYRKONQARLKIVFLGQANVKMT YNTGKDSE ID KDKKTGE IIRKRCAVHWVT PDGFFVWOEYRKPIQTRINIMFLGQFRLQFT INTNKDSE ID KDKKTKE IIRHRCAVHWTT PDGFFVWOEYRKPLQKRLDMI FLGQFRLQFT INTIKDSG ID 	765 793 770 771 904 944 927
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p P93Y94 RPOT1_NICSY =p P06221 RPOL_BF8P6</pre>	KDKKTKEVLRKRCA I HWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE I LRKRCAVHWVT PDGF FVW OEYRKPIQTRLNIMFLOG FRLOFT INTNKD SE ID KDKKTKE I LRHRCAVHWTT PDGF FVW OEYRKPLQKRLDMI FLGO FRLOFT INTNKD SE ID KDKKTKE I LRHRCAVHWTT PDGF FVW OEYRKPLQKRLDMI FLGO FRLOFT INTLKD SG ID 	765 793 770 771 904 944 927 953 824
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_MIC3Y =p P06221 RPOT1_BFSF6 =p P18147 RPOL_BFS11</pre>	KDKKTKEVLRKRCA I HWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE I LRKRCAVHWVT PDGF FVW OEYRKPI QTRLNIIMFLGQFRLQFT INTNKD SE ID KDKKTKE I LRHRCAVHWYT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTNKD SE ID KDKKTKE I LRHRCAVHWTT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTNKD SE ID LQRQKAAF FPNTVHSLD S SHOMMTA IACKKAGLHFAG HD SEWVHACDVDKMON I LRE VRKORT AF FPNTVH SLDG SHOMMTA IACKKAGLHFAG HD SEWVHACDVDTMOR I LRE ARROMT AF APNT HISLDG SHOMMTA IACKRAGLSFAG HD SEWTHACDVDVMNT I LRE VRKORT AF FPNTVH SLDG SHOMMTA IACKRAGLSFAG HD SEWTHACDVDVMNT I LRE VRKORT AF FPNTVH SLDG SHOMMTA IACKRAGLSFAG HD SEWTHACDVDVMNT I LRE EAAMGAAAPNTYHGHD SHI LITVCEL-VDRGVT SI AVLHD SFOTHADNILL ILRVALKS AHKOESG I APNTVHSDG SHLRMTVVHANEVYG ID SFATHADNILT LRVALKS	765 793 770 771 904 944 927 953 824 853
<pre>=p P18147 RPOL_BEK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NIC3Y =p P06221 RPOL_BE8P6 =p P18147 RPOL_BE811 ACY75835.1 T7</pre>	KDKKTKEVLRKRCA I HWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNT GKD SE ID KDKKTGE I LRKRCAVHWYT PDGF FVW OEYRKPIQTRINIMFLGQFRLQFT INTINGDSE ID KDKKTKE I LRHRCAVHWYT PDGF FVW OEYRKPIQKRLDMI FLGQFRLQFT INTIKDSE ID 	765 793 770 771 904 944 927 953 824 853 830
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_MIC3Y =p P06221 RPOT1_BFSF6 =p P18147 RPOL_BFS11</pre>	KDKKTKEVLRKRCA I HWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE I LRKRCA VHWVT FDGF FVW OEYRK PI QTRLNIMFLOO FRLOPT INTING SE ID KDKKTKE I LRKRCA VHWTT FDGF FVW OEYRKPLQKRLDMFLGO FRLOPT INTIKD SE ID KDKKTKE I LRHRCA VHWTT FDGF FVW OEYRKPLQKRLDMFLGO FRLOPT INTIKD SE ID KDKKTKE I LRHRCA VHWTT FDGF FVW OEYRKPLQKRLDMFLGO FRLOPT INTIKD SE ID KDKKTKE I LRHRCA VHWTT FDGF FVW OEYRKPLQKRLDMFLGO FRLOPT INTIKD SE ID KDKKTKE I LRHRCA VHWTT FDGF FVW OEYRKPLQKRLDMFLGO FRLOPT INTIKD SE ID KDKKTKE I LRHRCA VHWT FDGF FVW OEYRKPLQKRLDMFLGO FRLOPT INTIKD SE ID VRK ORTA FFPNT VHSLDG SHM MATA IACK KAGLHF AG THD SYWTHA CDVDTMMR I LRE ARROMTA FFPNT VHSLDG SHM MATA IACK ESGL SFAG THD SYWTHA CDVDTVM I LRE VKR ORTA FFPNT VHSLDG SHM MATA IACK ESGL SFAG THD SYWTHA SDVDQ MKK I LRE EAAMMGAAAPNT VHGHDA SHL I LTVCEL-VDRGVT SI AV HD SFGTHAD DNTLT LRVALKG AHK OESGI APNT VHSODG SHLRMTVVHANEVYGI DSFALL HD SFGT IPADAGNL FKAVRE AHK OESGI APNT VHSODG SHLRMTVVHANEVYGI ESFALL HD SFGT IPADAGNL FKAVRE AHK OESGI APNT VHSODG SHLRMTVVYAHEKYGI ESFALL HD SFGT IPADAGNL FKAVRE	765 793 770 771 904 944 927 953 824 853
<pre>=p P18147 RPOL_BEK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NIC3Y =p P06221 RPOL_BE8P6 =p P18147 RPOL_BE811 ACY75835.1 T7</pre>	KDKKTKEVLRKRCA I HWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNT GKD SE ID KDKKTGE I LRKRCAVHWYT PDGF FVW OEYRKPIQTRINIMFLGQFRLQFT INTINGDSE ID KDKKTKE I LRHRCAVHWYT PDGF FVW OEYRKPIQKRLDMI FLGQFRLQFT INTIKDSE ID 	765 793 770 771 904 944 927 953 824 853 830
<pre>sp[P18147]RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI sp[P92969]RPOT1_ARATH sp[P92949]RPOT1_ARATH sp[P96221]RPOL_BF8F6 sp[P18147]RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3</pre>	KDKKTKEVLRKRCA I HWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE I LRKRCAVHWVT PDGF FVW OEYRKPIQTRLNIMFLGQFRLQFT INTNKD SE ID KDKKTKE I LRHRCAVHWVT PDGF FVW OEYRKPIQTRLNIMFLGQFRLQFT INTNKD SE ID KDKKTKE I LRHRCAVHWTT PDGF FVW OEYRKPIQTRLNIMFLGQFRLQFT INTNKD SE ID KDKKTKE I LRHRCAVHWTT PDGF FVW OEYRKPIQKRLDMI FLGOFRLQFT INTNKD SE ID KDKKTKE I LRHRCAVHWTT PDGF FVW OEYRKPIQKRLDMI FLGOFRLQFT INTNKD SE ID KDKKTKE I LRHRCAVHWTT PDGF FVW OEYRKPIQKRLDMI FLGOFRLQFT INTNKD SE ID KDKKTKE I LRHRCAVHWTAVACHKAGLHFAGTHD SFWTHACDVDKMODI LRE VRKORTAFFPNT UHSLDGSHMMTAVACHRAGLSFAGTHD SFWTHACDVDVMTI LRE VRRORTAFFPNT UHSLDGSHMMTAVACHESGLSFAGTHD SFWTHACDVDVMTI LRE VRRORTAFFPNT UHSLDGSHMMTAVACHESGLSFAGTHD SFWTHACDVDVMTI LRE VRRORTAFFPNT UHSLDGSHMMTAVACHESGLSFAGTHD SFWTHACDVDVMMTI LRE ARKOESGLAPNT UHSLDGSHLRMTVVHANEVYGI DSFALHD SFGTHADNTLTLKVALKS AHKOESGLAPNT VHSODGSHLRKTVVWAHEKYGI ESFALHD SFGT IPADAANLFKAVRE AHKOESGLAPNT VHSODGSHLRKTVVWAHEKYGI ESFALHD SFGT IPADAAKLFKAVRE AHKOESGLAPNT VHSODGSHLRKTVVVAHEKYGI ESFALHD SFGT IPADAAKLFKAVRE AHKOESGLAPNT VHSODGSHLRKTVVVAHEKYGI ESFALHD SFGT IPADAAKLFKAVRE	765 793 770 771 904 944 927 953 824 853 830
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NIC3Y =p P08147 RPOL_BF876 =p P18147 RPOL_BF811 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1</pre>	KDKKTKEVIRKRCA HWVT PDGF FVW OEYRKONQARLKIVFLGQANVKMT YNTGKD SE ID KDKKTGE I LRKRCAVHWVT PDGF FVW OEYRKONQARLKIVFLGQFRLQFT INTIKD SE ID KDKKTKE I LRKRCAVHWVT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTIKD SE ID KDKKTKE I LRKRCAVHWVT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTIKD SE ID KDKKTKE I LRKRCAVHWVT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTIKD SE ID KDKKTKE I LRKRCAVHWVT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTIKD SE ID KDKKTKE I LRKRCAVHWVT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTIKD SE ID KDKKTKE I LRKRCAVHWVT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTIKD SE ID VRKORTAFFPNT VHSLDGTHMMMTAVACREAGLNFAG'HD SYWTHACDVDTMNTILRE ARROMTAFAPNT UHSLDGSHMMMTAVACNRAGLSFAG'HD SYWTHACDVDTMNTILRE VRKORTAFFPNT VHSLDGSHMMMTAVACNRAGLSFAG'HD SYWTHACDVDTMNTILRE ARROMTAFAPNT UHSLDGSHMMMTAVACNRAGLSFAG'HD SYWTHACDVDTMNTILRE ARROMTAFAPNT VHSLDGSHLMMTVVANLAKESGLSFAG'HD SYMTHACDVDVMNTILRE EAAMMGAAAPNT VHSUDGSHLRMTVVVANLEKYGIESFALHD SGT IPADAGNLFKAVKE AHKOESGIAPNT VHSODGSHLRMTVVVANLEKYGIESFALHD SGT IPADAGNLFKAVKE AHKOESGIAPNT VHSODGSHLRMTVVYANLEKYGIESFALHD SGT IPADAGNLFKAVKE AHKOESGIAPNT VHSODGSHLRMTVVYANLEKYGIESFALHD SGT IPADAGNLFKAVKE AHKOESGIAPNT VHSODGSHLRMTVVYANLEKYGIESFALHD SGT IPADAGNLFKAVKE AHKOESGIAPNT VHSODGSHLRMTVYANLEKYGIESFALHD SGT IPADAGNLFKAVKE AHKOESGIAPNT VHSODGSHLRMTVYANLEKYGIESFALHD SGT IPADAGNLFKAVKE AHKOESGIAPNT HSODGSHLRMTVYANLEKYGIESFALHD SGT IPADAGNLFKAVKE AHKOESGIAPNT HSONGSHLKAVKE AHKOESGIAPNT HSONG AHKOK	765 793 770 771 904 944 927 953 824 853 830
<pre>=p P18147 RPOL_BEK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NIC3Y =p P06221 RPOL_BE8P6 =p P18147 RPOL_BE8C1 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 AAD03373.1</pre>	KDKKTKEVLRKRCA IHWVT PDGF FVWOEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE ILKRRCA HHWVT PDGF FVWOEYRKPIQTRLNIMFLOOFRLOPT INTINGSE ID KDKKTKE ILRRRCA HHWVT FDGF FVWOEYRKPIQKRLDMFLGOFRLOPT INTINGSE ID KDKKTKE ILRRRCA HHWVT FDGF FVWOEYRKPIQKRLDMFLOOFRLOPT INTINGSE ID KDKKTKE ILRRRCA HHWVT FDGF FVWOEYRKPIQKRLDH FLOOFRLOPT INTINGSE ID VRRQFTA FFPNT VHSLDG SHMMMTA IACK KAGLHFAG HHD SFWTHA CDVDVMMT ILRE ARROMTA FFPNT VHSLDG SHMMMTA VACN RAGLSFAG HHD SFWTHA CDVDVMMT ILRE VRRQFTA FFPNT VHSLDG SHMMMTA VACN RAGLSFAG HHD SFWTHA CDVDVMMT ILRE ARROMTA FFPNT VHSLDG SHMMMTA VACN RAGLSFAG HHD SFWTHA CDVDVMMT ILRE ARROMTA FFPNT VHSLDG SHMMMTA VACN RAGLSFAG HHD SFWTHA CDVDVMMT ILRE ARROMTA FFPNT VHSLDG SHMMMTA VACN RAGLSFAG HHD SFWTHA CDVDVMMT ILRE ARROMTA FFPNT VHSLDG SHMMMTA VACN RAGLSFAG HHD SFWTHA CDVDVMMT ILRE ARROMTA FFPNT VHSLDG SHMMMTA VACN RAGLSFAG HHD SFWTHA CDVDVMMT ILRE ARROMTA FFPNT VHSLDG SHMMTA VACN RAGLSFAG HHD SFWTHA CDVDVMMT ILRE ARROMTA FFPNT VHSLDG SHMMTA VACN RAGLSFAG HHD SFWTHA CDVDVMMT ILRE ARROMTA FFPNT VHSLDG SHMMTA VACN RAGLSFAG HHD SFGT IPADAGNL FKAVRE ARROMTA FFPNT VHSLDG SHLRMTVVHARE VIG ID SFALL HD SFGT IPADAGNL FKAVRE ARROES GIAPNT VHSLOG SHLRMTVVYAHE KYG ID SFALL HD SFGT IPADAGNL FKAVRE ARROES GIAPNT VHSLOG SHLRMTVVYAHE KYG ID SFALL HD SFGT IPADAGNL FKAVRE ARROES AF MUNSCOG SHLRMTVVYAHE KYG ID SFALL HD SFGT IPADAGNL FKAVRE ARROES GIAPNT VHSLOG SHLRMTVVYAHE KYG ID SFALL HD SFGT IPADAGNL FKAVRE ARROES AF MUNSCOG SHLRMTVVYAHE KYG ID SFALL HD SFGT IPADAGNL FKAVRE ARROES AF MUNSCOG SHLRMTVVYAHE KYG ID SFALL HD SFGT IPADAGNL FKAVRE ARROES AF MUNSCOG SHLRMTVYAHE YG ID SFALL HD SFGT IPADAGNL FKAVRE ARROES AF MUNSCOG SHLRMTVYAHE YG ID SFALL HD SFGT IPADAGNL FKAVRE ARROES AF MUNSCOG SHLRMTVYAHE YG ID SFALL HD SFGT IPADAGNL FKAVRE ARROES AF MUNSCOG SHLRMTVYAHE YG ID SFALL HD SFG	765 793 770 771 904 944 927 953 824 853 830
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NICSY =p P06221 RPOL_BF8P6 =p P18147 RPOL_BF811 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 AAD03373.1 =p P92969 RPOT1_ARATH</pre>	KDKKTKEVLRKRCA I HWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE I I LRRRCAVHWYT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I I LRRRCAVHWYT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I LRRRCAVHWTT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I LRRRCAVHWTT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I LRRCAVHWTT PDGF FVW OEYRKPI QKRLOMI FLGOFRLOPT INTINGD SE ID KDKKTKE I LRRCAVHWTT PDGF FVW OEYRKPI QKRLOMI FLGOFRLOPT INTINGD SE ID VRRQRTAFFPNT VHSLDG SHOMMTAIACKKAGLHFAGHD SYWTHACDVDKMNDI LRE VRRQRTAFFPNT VHSLDG SHOMMTAIACKEAGLAFAGHD SYWTHACDVDVDVMT I LRE VRRQRTAFFPNT VHSLDG SHOMMTAIACKEAGLAFAGHD SYWTHACDVDVMT I LRE VRRQRTAFFPNT VHSLDG SHOMMTAIACKEAGLAFAGHD SYWTHACDVDVMT I LRE AAK 0ESGIAPNT VHSLDG SHOMMTAIACKEAGLAFAGHD SYWTHACDVDVMT I LRE AHKOESGIAPNT VHSLDG SHLMTVVHANE VIGI DSFALLHD SGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDG SHLRMTVVHANE VIGI DSFALL HD SGT IPADAGNLFKAVRE AHKOESGIAPNT VHSQDG SHLRMTVVYAHEKYGI ESFALL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSQDG SHLRMTVYAHEYGI SFFNL YMST ST S	765 793 770 771 904 944 927 953 824 853 830
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT_BF8F6 =p P18147 RPOL_BF811 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 AAD03373.1 =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NICSY</pre>	KDKKTKEVLRKRCA HWVT PDGF FVWOEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE ILRKRCAVHWVT PDGF FVWOEYRKPLQTRLNIMFLGQFRLQFT INTINGSE ID KDKKTKE ILRKRCAVHWVT PDGF FVWOEYRKPLQKRLDMI FLGQFRLQFT INTINGSE ID KDKKTKE ILRKRCAVHWTT PDGF FVWOEYRKPLQKRLDMI FLGQFRLQFT INTINGSE ID KDKKTKE ILRKRCAVHWTT PDGF FVWOEYRKPLQKRLDMI FLGQFRLQFT INTINGSE ID LQROKAAFFPNT VHSLDS SHMMMTAIACKKAGLHFAGHD SFWTHACDVDKMONILRE VRKORTAFFPNT VHSLDG SHMMMTAIACKRAGLSFAGHD SFWTHACDVDVMMTILRE ARROMTAFFPNT VHSLDG SHMMMTAVACHRAGLSFAGHD SFWTHACDVDVMMTILRE VRRORTAFFPNT VHSLDG SHMMMTAIACKESGLSFAGHD SFWTHACDVDVMMTILRE ARROMTAFFPNT VHSLDG SHMMMTAIACKESGLSFAGHD SFWTHACDVDVMMTILRE VRRORTAFFPNT VHSLDG SHLMMTAVACHRAGLSFAGHD SFWTHACDVDVMMTILRE ARROMTAFFPNT VHSLDG SHLMMTAVACHRAGLSFAGHD SFWTHACDVDVMMTILRE ARROESGIAPNT VHSLDG SHLMMTAVACHRAGLSFAGHD SFWTHACDVDVMMTILRE ARROESGIAPNT VHSLDG SHLRMTVVHANEVYGID SFALHD SFGT IPADAGNLFKAVRE ARROESGIAPNT VHSODG SHLRMTVVHANEKYGIE SFALHD SFGT IPADAGNLFKAVRE ARROESGIAPNT VHSODG SHLRMTVVHANEKYGIE SFALHD SFGT IPADAGKLFKAVRE ARROESGIAPNT VHSODG SHLRMTVVH SHOFT SFF SFF STF SFF SFF SFF SFF SFF SFF SFF SFF	765 793 770 771 904 944 927 953 824 853 830
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_MIC3Y =p P06221 RPOL_BF8F6 =p P18147 RPOL_BF8F6 =p P18147 RPOL_BF8F1 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 AAD03373.1 =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_MIC3Y =p P06221 RPOL_BF8F6</pre>	KDKKTKEVLRKRCA HWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE ILRKRCAVHWVT PDGF FVW OEYRKONQARLKLVFLGQFRLQFT INTINGD SE ID KDKKTKE ILRKRCAVHWVT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTINGD SE ID KDKKTKE ILRKRCAVHWTT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTINGD SE ID KDKKTKE ILRKRCAVHWTT PDGF FVW OEYRKPLQKRLDMI FLGQFRLQFT INTINGD SE ID KDKKTKE ILRKRCAVHWT PDGF FVW OEYRKPLGFT FLGGFRLGFT INTINGD SE ID VRORTAFFPNT VHSLDGSHMMTATACKKAGLHFAGTHD SYWTHACDVDTMNTILRE ARROMTAFAPNT HISLDGSHMMTATACKRAGLSFAGTHD SYWTHACDVDTMNTILRE EAAMGAAAPNT VHSLDGSHMMTATACKRAGLSFAGTHD SYWTHASDVDOMMKILRE EAAMGAAAPNT VHSLDGSHLRMTVVHANEVYGIDSFALHD SFOTHADNTLTLKVALKA AHKOESGIAPNT VHSLDGSHLRMTVVHANEVYGIDSFALHD SFOTHADNTLTLKVALKE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFALHD SFOTIPADAANLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFALHD SFOTIPADAGKLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFALHD SFOTIPADAGKLFKAVRE AHKOESGIAPNT VHSLDGSFCNLVFPPVPKRGDEDLKEVLASTYFFN 953 KFVELYM-PILENLLKEFOTSFPTLEFPPCP3QGDFDVREVLASTYFFN 953 KFVELYM-PILENLLKSFCKSFPDISFPPLPERGDFDLREVLESTYFFN 976 KFVELYDA-PILENLLESFCKSFPDISFPPLPERGDFDLREVLESTYFFN 905 KFVELYDA-PILENLLESFCKSFPDISFPPLPERGDFDLREVLESTYFFN 905 KFVELYDA-PILENLLESFCKSFPDISFPPLPERGDFDLREVLESTYFFN 905 KFVELYDA-PILENLLESFCKSFPDISFPLPERGDFDLREVLESTYFFN 905	765 793 770 771 904 944 927 953 824 853 830
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NICSY =p P18147 RPOL_BF811 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 AAD03373.1 =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_ARATH =p Q93Y94 RPOT1_ARATH =p Q93Y94 RPOT1_NICSY =p P06221 RPOL_BF876 =p P18147 RPOL_BF811</pre>	KDKKTKEVLRKRCA HWVT PDGF FVWOEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE I IKRRCA HWVT FDGF FVWOEYRKPI QTRLNIMFLGQFRLQFT INTINGSE ID KDKKTKE I IRRRCA HWVT FDGF FVWOEYRKPI QTRLNIMFLGQFRLQFT INTINGSE ID KDKKTKE I IRRRCA HWVT FDGF FVWOEYRKPI QTRLNIMFLGQFRLQFT INTINGSE ID KDKKTKE I IRRRCA HWVT FDGF FVWOEYRKPI QKRLDMFLGQFRLQFT INTINGSE ID KDKKTKE I IRRRCA HWVT FDGF FVWOEYRKPI QKRLDMFLGQFRLQFT INTINGSE ID KDKKTKE I IRRRCA HWVT FDGF FVWOEYRKPI QKRLDMFLGQFRLQFT INTINGSE ID KDKKTKE I IRRRCA HWVT FDGF FVWOEYRKPI QKRLDMFLGGFRLQFT INTINGSE ID VRQRTAFF FPNT VHSLDGSHMMMTA IACKKAGLHFAG FHD SFWTHACDVDTMMR I LRE ARROMTAFF PNT VHSLDGSHMMMTATACARAGLSFAG FHD SFWTHACDVDTMMK I LRE VRRQRTAFF PNT VHSLDGSHMMMTATACARAGLSFAG FHD SFWTHACDVDTMMK I LRE EAAMMGAAADNF VHGHDA SHL I LTVCEL-VDKGVT SI AV HHD SFGTHADANTLT LRVALKG AHKQESGIAPNT VHSQDGSHLRMTVVHANEVYGI DSFAL HHD SFGTI PADAGNL FKAVKE AHKQESGIAPNT VHSQDGSHLRMTVVHANEVYGI DSFAL HHD SFGTI PADAGNL FKAVKE AHKQESGIAPNT VHSQDGSHLRMTVVYAHEKYGI ESFAL HHD SFGTI PADAGNL FKAVKE AHKQESGIAPNT VHSQDGSHLRMTVVYAHEKYGI ESFAL HHD SFGTI PADAGNL FKAVKE AHKQESGIAPNT VHSQDGSHLRMTVVYAHEKYGI ESFAL HHD SFGTI PADAGNL FKAVKE AHKQESGIAPNT VHSQDGSHLRMTVVTAHEKYGI ESFAL HHD SFGTI PADAGNL FKAVKE AHKQESGIAPNT VHSQDGSHLRMTVVTAHEKYGI ESFAL HD SFGTI PADAGNL FKAVKE AHKQESGIAPNT VHSQDGSHLRMTVYAHEKYGI ESFAL HD SFGTI PADAGNL FKAVKE AHKQESGIAPNT VHSQDGSHLRMTVYAHEKYGI ESFAL HD SFGTI PADAGNL FKAVKE AHKQESGIAPNT HENDI HEFGT SFPDISFPPLPERGDFDL FKULSGYFFN 953 KFVELYM-PILENLLESFQGSFPDISFPPLPERGDFDL FKULSGYFFN 976 KFVELYDAPILENLESFQGSFPDISFPPLPERGDFDL FKULSGYFFN 97	765 793 770 771 904 944 927 953 824 853 830
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NICSY =p P18147 RPOL_BFR11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 AAD03373.1 =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NICSY =p P06221 RPOL_BF8P6 =p P18147 RPOL_BF8P6</pre>	KDKKTKEVLRKRCA IHWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE I IRRRCAVHWVT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I IRRRCAVHWTT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I IRRCAVHWTT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I IRRCAVHWTT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I IRRCAVHWTT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I IRRCAVHWTT PDGF FVW OEYRKPI QKRLOMFI GFG FRADTINTIKD SE ID KDKKTKE I IRRCAVHWTT PDGF FVW OEYRKPI QKRLOMF I IRE VRRQRT AFFDNT VHSLDGSHMMATAIACKKAGLHFAG HD SWTHACDVDVMNTILRE VRRQRT AFFDNT VHSLDGSHMMATAIACKEAGLMFAG HD SWTHACDVDVMNTILRE VRRQRT AFFDNT VHSLDGSHMMATAIACKEAGLMFAG HD SWTHACDVDVMNTILRE VRRQRT AFFDNT VHSLDGSHMMATAIACKEAGLMFAG HD SWTHACDVDVMNTILRE VRRQRT AFFDNT VHSLDGSHMMATAIACKEAGLMFAG HD SWTHACDVDVMNTILRE ARKOESGIAPNT VHSLDGSHLRMTVVHANE VIGIDFAL HD SGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANE VIGIDFAL HD SGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANE VIGIDFAL HD SGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVYHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVYANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVYANTG SEVENG STYFN 953 KFVELYND-PILEDLLLESFOSFPDISFPPLPERGDFDLREVLASTYFN 966 KVVELYND PILENLLESFOSFPDISFPPLPERGDFDLREVLSSVYFN 1002 OVAMY JONALCKLIEEHEVRWWDTGIEVPDQFFDLREVLSSVFN 1002 MVAMY JONALKLIEHEVRWWDTGIEVPARGDLNLRDILESDFAFA 966 MVDTYESCDVLADFYDOFADQLHE	765 793 770 771 904 944 927 953 824 853 830
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NICSY =p P18147 RPOL_BF811 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 AAD03373.1 =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_ARATH =p Q93Y94 RPOT1_ARATH =p Q93Y94 RPOT1_NICSY =p P06221 RPOL_BF876 =p P18147 RPOL_BF811</pre>	KDKKTKEVLRKRCA HWVT PDGF FVWOEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE ILRKRCAVHWVT PDGF FVWOEYRKPLQTRLNIMFLGQFRLQFT INTINGSE ID KDKKTKE ILRKRCAVHWTT PDGF FVWOEYRKPLQKRLDMI FLGQFRLQFT INTINGSE ID KDKKTKE ILRKRCAVHWT FDGF FVWOEYRKPLQKRLDMI FLGQFRLQFT INTINGSE ID KDKKTKE ILRKRCAVHWT FDGF FVWOEYRKPLQKRLDMI FLGDFT INTINGSE ID VRORTAFFPNT VHSLDGTHMMMTAVACHRAGLSFAGHD SYWTHACDVDVMMT ILRE VRORTAFFPNT VHSLDGSHMMTAVACHRAGLSFAGHD SYWTHACDVDVMMT ILRE VRORTAFFPNT VHSLDGSHMMTAVACHESGLSFAGHD SYWTHASDVDQMMKILRE EAAMGAAAPNT VHGHDASHLI LTVCEL-VDRGVTSIAVHD SFGTHADNTLTLKVALKS AHKOESGIAPNT VHSCDGSHLRMTVVHANEVYGIDSFALHD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSCDGSHLRMTVVHANEKYGIESFALHD SFGT IPADAGKLFKAVRE AHKOESGIAPNT VHSCDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGKLFKAVRE AHKOESGIAPNT VHSCDGSHLRMTVVANEKYGIESFAL HD SFGT IPADAGKLFKAVRE AHKOESGIAPNT VHSCDGSHLRMTVVANEKYGIESFAL HD SFGT IPADAGKLFKAVRE AHKOESGIAPNT VHSCDGSHLRMTVVANEKYGIESFAL HD SFGT IPADAGKLFKAVRE AHKOESGIAPNT VHSCDGSFGSFFDISFPPLPERGDFDLREVLSSTYFFN 953 KFVELYSH-PILEDLLSSFGSFFDISFPPLPERGDFDLREVLSSTYFFN 976 KFVELYSH-PILEDLLSSFGSFFDISFPPLPERGDFDLREVLSSTYFFN 976 KFVELYSH-PILEDLLSSFGSFFDISFPPLPERGDFDLREVLSSTYFFN 976 KFVELYSH-PILEDLLSFGGSFFRWWDTGIEVPPQGEFDLNE IMSEVVFA 874 DWVKTYEDDVLADFYDOFADOLHSGUDKMPALPA	765 793 770 771 904 944 927 953 824 853 830
<pre>=p P18147 RPOL_BFK11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 OSATI AAD03373.1 ATHALI =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NICSY =p P18147 RPOL_BFR11 ACY75835.1 T7 CAC86264.1 T3 BAC98394.1 AAD03373.1 =p P92969 RPOT1_ARATH =p Q93Y94 RPOT1_NICSY =p P06221 RPOL_BF8P6 =p P18147 RPOL_BF8P6</pre>	KDKKTKEVLRKRCA IHWVT PDGF FVW OEYRKONQARLKLVFLGQANVKMT YNTGKD SE ID KDKKTGE I IRRRCAVHWVT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I IRRRCAVHWTT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I IRRCAVHWTT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I IRRCAVHWTT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I IRRCAVHWTT PDGF FVW OEYRKPI QTRLNIMFLOOFRLOPT INTINGD SE ID KDKKTKE I IRRCAVHWTT PDGF FVW OEYRKPI QKRLOMFI GFG FRADTINTIKD SE ID KDKKTKE I IRRCAVHWTT PDGF FVW OEYRKPI QKRLOMF I IRE VRRQRT AFFDNT VHSLDGSHMMATAIACKKAGLHFAG HD SWTHACDVDVMNTILRE VRRQRT AFFDNT VHSLDGSHMMATAIACKEAGLMFAG HD SWTHACDVDVMNTILRE VRRQRT AFFDNT VHSLDGSHMMATAIACKEAGLMFAG HD SWTHACDVDVMNTILRE VRRQRT AFFDNT VHSLDGSHMMATAIACKEAGLMFAG HD SWTHACDVDVMNTILRE VRRQRT AFFDNT VHSLDGSHMMATAIACKEAGLMFAG HD SWTHACDVDVMNTILRE ARKOESGIAPNT VHSLDGSHLRMTVVHANE VIGIDFAL HD SGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANE VIGIDFAL HD SGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANE VIGIDFAL HD SGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVYHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVHANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVYANEKYGIESFAL HD SFGT IPADAGNLFKAVRE AHKOESGIAPNT VHSLDGSHLRMTVVYANTG SEVENG STYFN 953 KFVELYND-PILEDLLLESFOSFPDISFPPLPERGDFDLREVLASTYFN 966 KVVELYND PILENLLESFOSFPDISFPPLPERGDFDLREVLSSVYFN 1002 OVAMY JONALCKLIEEHEVRWWDTGIEVPDQFFDLREVLSSVFN 1002 MVAMY JONALKLIEHEVRWWDTGIEVPARGDLNLRDILESDFAFA 966 MVDTYESCDVLADFYDOFADQLHE	765 793 770 771 904 944 927 953 824 853 830

Fig. 6. MSA of T3, T7, K11, SP6 with SSU mitochondrial and chloroplast RNA polymerases

BAC98394.1, *Oryza sativa*, Japonica group (Chloroplast) AAD03373.1, *Arabidopsis thaliana* (Chloroplast) sp|P92969|RPOT1_ARATH, *Arabidopsis thaliana* (Mitochondria) sp|Q93Y94|RPOT1_NICSY, *Nicotiana sylvestris* (Mitochondria) sp|P06221|RPOL_BPSP6, Enterobacteria phage SP6 sp|P18147|RPOL_BPK11, Enterobacteria phage K11 ACY75835.1 T7, Enterobacteria phage T7 CAC86264.1 T3, Enterobacteria phage T3

Fig. 7 shows the results of MSA of a 'mix and match' analysis between DNA and RNA polymerases, viz. the *E. coli* DNA polymerase I

and the RNA polymerases. In this analysis, the *E. coli* DNA polymerase I and the 4 viral RNA polymerases are mixed and aligned to identify

the conserved motifs common to both of them. Such an analysis may narrow down the motifs common among DNA and RNA polymerases that may be essential for catalysis and substrate binding as both belong to the same class of enzymes. The DNA repair (5'-3' exonuclease) and proof-reading (3'-5' exonuclease) functions did not show any super imposable regions. However, interestingly the C terminal region (polymerase domain) shows few super imposable regions including the catalytic K, YG pair and the invariant R (marked 1-9). Additionally, a GT, YM diad and an LPL/V triad are also observed, in addition to few single amino acid conservations. The catalytic, template and substrate binding motifs are highlighted. The YG gate keeper motif and the catalytic K are strictly conserved (including distance conservation) in both DNA dependent DNA polymerases and DNA dependent RNA polymerases. This suggests that the polymerase reaction is accomplished using the same set of amino acids in DNA and RNA polymerases.

CLUSTAL O(1.2.4) MSA of E. coli DNA polymerases I, T7, T3, SP6 and K11 RNA polymerases

sp P00582 DP01_ECOLI		30 31
sp P06221 RPOL_BPS P6 sp P18147 RPOL_BPK11	MQDLHA IQLQLEE EMFNGGI RRFEADQQRQI -MNALN IGRNDFSEIELAAI PYNILSEH YGDQAAR EQLALEHEAYELGRQRFLKMLE RQV	31 59
ACY75835.1 T7	-MATIN IAKNDFS DIELAAI PENTLADH YGERLAR EQLALEHESYEMGE ARFRWIFE ROL	59
CAC86264.1 73	MNIIEN IEKNDFSEIELAAI PFNTLADH YGSALAKEOLALEHESYELGE RRFLKMLE ROA	60
	· · · · ·	
sp P00582 DP01_ECOLI	SAGEPT GAMYGVLIMLESLI MQYKPTHA AVVFDAK GKTFEDE LFEHYKS HEPPMPDD LEA	90
sp P06221 RPOL_BP3P6	AAGSESDTAWNRRLLSELIAPMAEGIQAYKEEYEGKKGRAPRALA-	76
sp P18147 RPOL_BPK11	KAGEFA DNAAAKPLVLTLHPQLTKRIDDWKEEQAN ARGKKPRA YY-	104
ACY75835.1 T7	KAGEVA DNAAAKPLI TTLLPKMIARINDWFEEVKA KRGKRPTA FQ-	104
CAC86264.1 T3	KAGEIADNAAAKPLLATLLPKLTTRIVEWLEEYASKKGRKPSAYA- **.:. : *:	105
sp P00582 DP01_ECOLI	QIEPLHAM/KAMG LPLLAVS GVEADDVI GTLAREA EKAGRPVLISTGDKDMAQLVTPNIT	150
sp P06221 RPOL BP3P6	FLQCV	81
sp P18147 RPOL_BPK11	PIKHG	109
ACY75835.1 T7	FLQEI	109
CAC86264.1 T3	PLQLL	110
sp P00582 DP01 ECOLI	LINTMINTILGPE EVVNKYG VPPELIID FLALMGDS SDNIPGV PG-VGERT - AQ	202
sp P06221 RPOL_BP3P6	DATLQAI AMSVAERIEDQ	118
sp P18147 RPOL_BPK11	-VASELAVSMGAEVLKEKRGVSSEAIALLTIKVVLGNAHRPLKGHNPAVSSQLGKALEDE	168
ACY75835.1 T7	APEAVAY ITIKTTLACLTSADNTTVQAVASAIGRAIEDE	148
CAC86264.1 T3		149
	* :.: . : :	
sp P00582 DP01_ECOLI	ALLQGL GGLDTLY AEPEKIAGL SFRGART MAAKLEQ	238
sp P06221 RPOL_BPSP6	VRFSKLEGHAAKY FEKVKKSLKASR-TKSYRHAHNVAVVAEKSVAEKDADFDRWEAW PKE	177
sp P18147 RPOL_BPK11	ARFGRIREQEAAY FKKNVADQLDKRVGHVYKKA-FMQVVEADMISKGMLGGDNWASWKTD	227
ACY75835.1 T7	ARFGRIRDLEAKH FKKNVEE QLNKRVGHVYKKA-FMQVVEADMLSKGLLGGEAWSSWHKE	207
CAC86264.1 T3	ARFGRIRDLEAKHFKKHVEEQLNKRHGQVYKKA-FMQVVEADMIGRGLLGGEAWSSWDKE	208
sp P00582 DP01_ECOLI		275
sp P06221 RPOL_BP3P6	TQLQIGTTLLEILEGSVFYNGEFVFMRAMRTYGGKTIYYLQTSESVGQWISAFKEHV	234
sp P18147 RPOL_BPK11	EQMHVGTKLLELL IEGTGLVEMTKNIKMADGSD DVTSMQMVQLAPAFVELLSKRAGAL	284
ACY75835.1 T7	DSIHVGVRCIEMLIESTOM VSLHRQNAGVVGQDSETIELAPEYAEAIATRAGAL	261 262
CAC86264.1 T3	TTMHVG IRLIEML IESTGLVELORHNAGNAGS DHEALQLAGEYVDVLAKRAGAL : : : : :	202
sp P00582 DP01 ECOLI	LGLFMKYE FWRWTAD VEAGHWLQAKGAKPA AKPQETSVA DEAPEVTAT] (VI	325
sp P06221 RPOL_BP3 P6	AQLSPA YAPCVIP PRPWRTP FNGGFHTE KVASRIR LVKGNRE HVRKLTQKQMPKVYKAIN	294
sp P18147 RPOL_BPK11	AGISPMHQPCVVP PKPWVET VGGGYWSV GRRPLAL VRTHSKKALRRYAD VHMPEVYKAVN	344
ACY75835.1 T7	AGISPM FOPCVVP PKPWTGI TGGGYWAN GRRPLAL VRTHSKKALMRYED VYMPEVYKAIN	321
CAC86264.1 T3	AGISEM FOPCVVP PKPWVAI TGGGYWAN GRRPLAL VRTHSKKGLMRYED VYMPEVYKAVN : * * *	322
sp P00582 DP01 ECOLI	SYDNYVTILDEET LKAWIAKLEKAP VFA FD TETDS LDNISAN LVGLSPA IEPGVAAY IPV	385
sp P06221 RPOL BP3P6	AEEVIRLDLGYGVPSFKPL	329
sp P18147 RPOL_BPK11	LNEIVNWKHCPVGDVPA	377
ACY75835.1 T7	INVITKWKHCPVED IPA	354
CAC86264.1 T3	LNEIVNWKNCPVADIPS	355
	· * : . *:*. *	
sp P00582 DP01_ECOLI	AHDY <mark>LD</mark> APDQI SRERA-LELLKPLLEDEKA	414
sp P06221 RPOL_BPSP6	IDKENK PANFVF <mark>VE</mark> FOHLRGRELKEMLS PEOWOOF INWKGEC ARLYTAE TKRGSKSA AVV	389
sp P18147 RPOL_BPK11	IEREEL PPRPDD <mark>ID</mark> TNEVAR KAWRKEA AAVYRKD KAR <u>O</u> SRRC RCE	422
ACY75835.1 T7	IER <mark>EEL PMKPED<mark>I D</mark>MNPEAL TAWKRAA AAVYRKDKARKSRRI SLE</mark>	399
CAC86264.1 T3	<mark>ler</mark> gel ppkpdd <mark>id</mark> tneaal kewkkaa agiyrldkarvsrri sle	400
	* 1. I	

sp P00582 DP01_EC0LI sp P06221 RP01_BP3P6 sp P18147 RP01_BP811 ACT75835.1 T7 CAC86264.1 T3	LKAGONLKYDRGILANYG TELRGIAFDTMLE	463 449 480 457 458
sp[P00582]DP01_EC0LI sp[P06221]RP01_BPSP6 sp[P18147]RP01_BPSP6 AC75835.1 T7 CAC86264.1 T3	FWLKHKTITFEELAGKGFONQLTFNQIALEEAGRYAAEDADVTLQLHLMAM PDL KWFCINGANLGWODHGTEDVRVSNVLDEEFQDMCFDIAADELTFNQWAFA YWLKIHGANCGWIDKVPFPERIKFIEENEGNILASAADELNNTWWTQQ YWLKIHGANCAGVDKVPFPERIKFIEENHENDMACAKSPLENTWWAEQ YWLKIHGANCAGVDKVPFPERIAFIEKHVDDILACAKDFINNTWWAEQ *:: * * :: *	516 499 528 505 506
<pre>>p P00582 DP01_ECOLI >p P06221 RP0L_BPSP6 >p P18147 RP0L_BPK11 ACY75835.1 T7 CAC86264.1 T3</pre>	Q] KHK [GPLNVFE NIEMPLV PVLSRIER NGVKIDP KVLHNHS EELTLRL AELEKKAH EIAGE D D D	576 1 500 529 506 507
sp P00582 DP01_ECOLI sp P06221 RP01_BE9P6 sp P18147 RP01_BBPK11 ACY75825.1 T7 CAC86264.1 T3	EFNLSS TKQLQT I LFEKQGI KPLKKTPGGAPSTSE EVLEELA LDYPLFKVILE YRGL AK- APYEFLA WCFEYAQY LDL SPFCFLA FCFEYAGVKH- SPFCFLA FCFEYAGVQH- SPFCFLA FCFEYAGVTH- : : :**	635 518 546 523 524
<pre>>p P00582 DP01_EC0LI >p P06221 RP0L_BPSP6 >p P18147 RP0L_BPK11 ACY75835.1 T7 CAC86264.1 T3</pre>	LKSTYTDKLDLMINEKTGRV-HTSYHQAVTATGRLSSTDPNLQNI FVRMEEGRRIR VDEGRADEFRTHLFVHQDGSCSGIQHYSAMIRDEVGAKAV HGLMYNCSLFLAFDGSCSGIQHYSAMIRDEVGGRAV HGLSYNCSLFLAFDGSCSGIQHYSAMIRDEVGGRAV HGLSYNCSLFLAFDGSCSGIQHYSA	690 558 582 559 560
<pre>>p P00582 DP01_ECOLI >p P06221 RP0L_BPSP6 >p P18147 RP0L_BPK11 ACY75835.1 T7 CAC86264.1 T3</pre>	QAFIAPEDVVIVSADYSQIELRIMAHLSRDKGLLTAFAEGKDIHRATAAEVFGLP NLKPSDAPODIYGAVAQVVIKKNALYMDADDATTFTSGSVTLSGTE NLLPSDTVQDIYKUVNEV-LHQ-HAVNGSQTVVEQIADKETGEFHEKVTLG NLLPSETVQDIYGIVAKKVNEI-LQA-DAINGTDNEVVTVTDENTGEISEKKKLG NLLPSETVQDIYGIVAKKVNEI-LKQ-DAINGTPNEMITVTDKNTGEISEKLKLG : : * . * * : : : ::	745 x 604 635 612 613
sp P00582 DP01_ECOLI sp P06221 RP01_BP3P6 sp P18147 RP01_BPK11 ACY75825.1 T7 CAC86264.1 T3	LETVTSE CRESH INFGL WSMSAFGLARQINIPRKE LRAMAS ANDSIG: TESLIKK FWMILEYS STRITCRESVIDYI VDLEEKE AQKAVAEGRTA ESVIAQ QULQYGVIEKVIKS SVMILAYS SKESUK QQULEDI IQPAIDSGK TKAIAQ QULAYGVIESVIKS SVMILAYS SKESFER QQULEDI IQPAIDSGK .::	782 664 686 663 664
sp[P00582]DP01_ECOLI sp[P06221]RP0L_BPSP6 sp[P18147]RP0L_BPSP1 ACY75835.1 T7 CAC86264.1 T3	NKVHEFEDERODYLTEGANYN YN TALIW FSISEVVKAPIVAMMIROLARFAAK NKVHEFEDERODYLTEGANYN YN TALIW FSISEVVKAPIVAMMIROLARFAAK GLMFTHEN AR GYNAKLIW BSVSVTVVAAVEAMMWIRSAAKLLAAEVKDRK GLMFTQENCAR GYNAKLIW BAVSVTVVAAVEAMMWIRSAAKLLAAEVKDRK GLMFTQENCAR GYNAKLIW DAVSVTVVAAVEAMMWIRSAAKLLAAEVRDRK 	792 718 737 714 715
sp P00582 P001_COLI sp P06221 RP0L_BPSP6 sp P18147 RP0L_BPK11 ACY75835.1 T7 CAC86264.1 T3	RNEGIMYTLFYGER TR RNEGIMYTLFYGEI LEGKIMAT EMIKURT CLMSDIKMSLQVET DTVDE AAM TKEVLR KRCALHWVTPDGFP VWQEYRKQ NQARLKLVFLGQAN VMMTYNT GKDSE IDAHKQ TGEILR KRCAVHWVTPDGFP VWQEYRKQ LQKRLIM IFLGQFR LQFTINT IKDSE IDAHKQ TKEILR HRCAVHWTPDGFP VWQEYRKQ LQKRLIM IFLGQFR LQFTINT IKDSE IDAHKQ :	806 769 797 774 775
sp P00582 DP01_EC0LI sp P06221 RP01_BP3P6 sp P18147 RP01_BPK11 ACY75835.1 T7 CAC56264.1 T3	AGAKEQ GYVETLD GRRLYLP DIKSSNGARRAAA ERAAINA FMG ^E TAA DIIKRAMI AVD MGAAAPNFVHGHDASHLILT VCEL-VDKGVTSIAVIHD-SHGTHA DNTL ESGIAPNFVHSQD SSHLRMT VVHANEVY GIDSFALIHD-SHGTIP ADAG ESGIAPNFVHSQD SSHLRMT VVHAHEKY GIESFALIHD-SHGTIP ADAA ESGIAPNFVHSQD SSHLRMT VVHAHEKY GIESFALIHD-SHGTIP ADAA L.:*.*	864 816 845 822 × 823
<pre>sp P00582 DP01_ECOLI sp P06221 RP0L_BPSP6 sp P18147 RP0L_BPK11 ACY75835.1 CAC86264.1</pre>	AWLQAE QPRVFMLMQVHDEIU FEVHKUD VDAVARQ IHQIMEN CTRLUVP LIVEVGSGENW TLRVALKGMUAMYIDGNALQKL LEEHEVRWMVD TGIEVPEQGEF NLFYAVRETMUKTYEDINUVLAP YDQFADQ LHESQL DAVPALPARGDL NLFYAVRETMUTYESCUVLAP YDQFADQ LHESQL DAVPALPARGNL KLFYAVRETMUTYENIVLAP YSQFADQ LHETQLDKMPPLPKKGNL : :: : :	924 × 861 893 870 871
sp P00582 DP01_EC0LI sp P06221 RP0L_BP5P6 sp P18147 RP0L_BPK11 ACY75835.1 CAC86264.1	DQAH928 DLNEIMDSEYVFA 874 NIRDILESDFAFA 906 NIRDILESDFAFA 883 NLQDILKSDFAFA 884	

Fig. 7. Multiple sequence alignment *E. coli* **DNA pol I, T3, T7, K11 and SP6 RNA polymerases** sp|P00582|DPO1_ECOLI, adjust spacing *Escherichia coli* sp|P06221|RPOL_BPSP6, Enterobacteria phage SP6 sp|P18147|RPOL_BPK11, Enterobacteria phage K11 ACY75835.1, Enterobacteria phage T7 CAC86264.1, Enterobacteria phage T3 *(E. coli* DNA polymerase I is made up of three domains, viz. amino acids 1-323 constitute the 5'-3' exonuclease domain or DNA repair domain (323 amino acids length); amino acids 324-517 constitute the 5'-3' exonuclease domain or proof-reading domain (194 amino acids length); and amino acids 521-928 constitute the polymerase domain (408 amino acids length). The proof-reading and the polymerase domain from 324 to 928 amino acids (605 amino acids length) is known as Klenow polymerase. All three domains are shown in different colours).

3.2 Dissection of DNA and RNA Polymerases

Different domains of the E. coli DNA polymerase I are shown in Fig. 8 [4]. E. coli DNA polymerase I is made up of three domains, viz. amino acids 1-323 constitute the 5'-3' exonuclease domain or DNA repair domain (323 amino acids length); amino acids 324-517 constitute the 5'-3' exonuclease domain or proof reading domain (194 amino acids in length); and amino acids 521-928 constitute the polymerase domain (408 amino acids in length). The proof reading and the polymerase domain from 324 to 928 amino acids (605 amino acids in length) is also known as Klenow polymerase. In T7 RNA polymerase also the polymerase domain is found in the C terminal region starting from 507-883 (376 amino acids length (Fig. 8). In T7 RNA polymerase, the amino-terminal region is reported to be involved in promoter recognition and DNA melting functions [7].

3.3 Analysis of Polymerase Active Site in the RNA and DNA Polymerases

Both the RNA and DNA polymerases belong to the same Main class (Transferases) and come under the sub class nucleotidyl transferases (EC 2.7.7.6 and EC 2.7.7.7). Therefore, both the enzymes might be of similar structure and use similar mechanism of action. It is well established by biochemical, genetic and site-directed mutagenesis that the polymerase I active is at the carboxy terminal domain (CTD) of the enzyme (Fig. 8). The CTD contains KA, a YG pair and an invariant R at -4 where the KA pair involves in catalysis and the YG pair and R act as steric gate allowing only the dNTPs for polymerization. It is interesting to note that the polymerase active is in CTD of T7 RNA polymerase [8] and similar conserved amino acids are also found in all the SSU DNA dependent RNA polymerases studied (Figs. 2-7). Another interesting finding is that in the viral polymerases an additional YG is found in the downstream exactly at the same distance but downstream.

3.4 Distance Conservation between Catalytic K and YG Pair in DNA and RNA Polymerases

3.4.1 Catalytic K and YG pair in DNA polymerases

It is interesting to note that the catalytic amino acid K and the gate keeper pair YG are completely conserved in different polymerases from a diverse group of organisms (Table1). The mismatched regions in some of the polymerases were aligned as suggested by Palanivelu [9]. (In this analysis only the amino acids around the active site regions of different DNA polymerases from different sources ranging from virus to plant and animals were selected and analyzed by T-COFFEE advanced version). Table summarizes the above findings. It is interesting to note that irrespective of the type of polymerases and their origin, all of them showed a completely conserved K at the catalytic site and YG pair at the steric gate position. A distance conservation is also observed in all these polymerases, (i.e.), the YG pair is 8/9 amino acids downstream of the catalytic K. The invariant G is found in all these DNA and RNA polymerases, probably as it is the only amino acid, achiral and fit into both hydrophilic and hydrophobic environments.

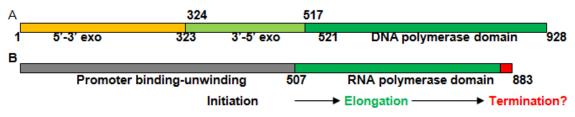


Fig. 8. Dissection of *E. coli* DNA polymerase I (A) and T7 RNA polymerase (B)

3.4.2 Catalytic K and YG pair in RNA polymerases

The distance between the catalytic K and YG pair is remarkably conserved among both the SSU RNA polymerases from viruses, mitochondria and chloroplasts and the DNA polymerases [4]. From the catalytic amino acid K, the YG pair is exactly the 8th amino acid upstream in all the SSU RNA polymerases from viruses, mitochondria and chloroplasts (Table 2). It is interesting to note that in the viral polymerases, an additional YG pair is placed exactly at the same distance but towards downstream (-8) of the catalytic K. Thus, the viral polymerases show two YG pairs placed exactly at the same distances from the catalytic amino acid on both the sides. Such additional YG pair is not found in the mitochondrial and chloroplast RNA polymerases and also in the *E. coli* DNA polymerase I. This suggests that the YG pair may bind on both the strands and placing the catalytic K in the middle and all three moving downstream incorporating the NTPs. In fact. Kotsyuk et al. [5] have shown that the T7 polymerase requires both the strands for activity and there was no activity when single-stranded DNA was used as the substrate.

It is interesting to note that the YG pair appears to be specific for polymerases using DNA as the template (including the prokaryotic and eukaryotic multi-subunit RNA polymerases, data not shown) as it is not reported in RNA dependent polymerases where they use RNA as the template [2].

Table 1. The catalytic amino acid (K) and gate keeper pair (YG) in different polymerases from
diverse sources

T4 DNA pol	546 ATLANTNQLNRK1ILINSLY®GALGNIH
Human HSV 1	800 AVLLDKQQAAIK ¹ VVCNSVY ⁸ GFTGVQH
E. coli DNA pol I	748 TVTSEQRRSAK1AINFGLIY ⁹ GMSAFGLAR
E. coli DNA pol II	482 RQGNKPLSQALK1IIMNAFY8GVLGTTA
E. coli DNA pol III (alpha subunit)	663 YPDVQWQHESLK1PVLEPTY ⁸ GIILYQE
P. furiosus DNA pol	477 KILLDYRQKAIK ¹ LLANSFY ⁸ GYYGYAK
Yeast alpha DNA pol	933 RVQCDIRQQAL <mark>K1LTAN SMY8G</mark> CLGYVN
Human alpha DNA pol	939 ILQYDIRQKALK ¹ LTANSMY ⁸ GCLGFSY
Human Gamma DNA pol	917 TTVGISREHAK1IFNYGRIY ⁹ GAGQPFAER
Human Delta DNA pol (Catalytic subunit)	683 RQVLDGRQLALK ¹ VSANSVY ⁸ GFTGAQV
Human epsilon DNA pol	798 EVLYDSLQLAHK1CILNSFY8GYVMRKGAR
A. thaliana Delta DNA pol (Catalytic subunit)	679 KAVLDGRQLALK ¹ ISANSVY ⁸ GFTGATV

N.B: Some of the above polymerases did not align in T COFFEE advanced version. So the conserved regions were selected and aligned as suggested by Palanivelu [9]. Table 1 from Palanivelu [4]).

Table 2. The catalytic amino acid (K) and gate keeper pair (YG) in different SSU RNApolymerases from diverse sources

Viral RNA po	lymerases						
E. coli DNA pol	I -LETVT	-SEQRRSAK AIN	IFGL <mark>IY^sG</mark> MSAH	GLARQLNI	PRKE	783	
Virus	T3 -TSTLAQQWLA	^{7*} GVTRSVT <mark>K[*]R</mark> SV	MTL <mark>AY[®]G</mark> SKEF	GFRQQVLDDTIQ	PAID	SGK664	
Virus	T7 -TKALAGQWLA	<mark>(°G</mark> VTRSVT <mark>K'R</mark> SV	MTL <mark>AY^sG</mark> SKEF	GFRQQVLEDTIQ	PAID	SGK663	
Virus	K11-ESVLAAQWLQ	^{(*} GVTRKVT <mark>K*R</mark> SV	MTL <mark>AY[®]G</mark> SKES	LVRQQVLEDTIQ	PAID	NGE686	
Virus	SP6-LRAMASAWDS	t ^e gitrslt <mark>k*</mark> kpv	MTL <mark>PY[®]G</mark> STRL	TCRESVIDYIVDL	EEKEAQKAVA	EGRTA664	
Mitochondrial RNA polymerases							
BAC98394.1 AAVN	LVPGDKPADIYSEIAA	ARVLDVVREDSMEI	DPATNPTASLA	RVLVDQV <mark>DR</mark> KL <mark>VK</mark>	DTVMT SVY [®] C	VTYIGARQ	746
AAD03373.1 AAVN	LVAGEKPADVYSEISF	RRVHE IMKKDSSK	DPESNPTAALA	KILITQV <mark>DR</mark> KL <mark>VK</mark>	OTVMT SVY [®] C	VTYLGARE	786
BAF01496.1 AVN	LVAGEKPADVYSEISF	RRVHE IMKKDSSK	DPESNPTAALA	KILITQV <mark>DH</mark> KL <mark>VK</mark>	OTVMT SVY [®] G	VTYLGARE	786
BAE98468.1 AVN	LVAGEKPADVYSEISP	RRVHE IMKKDSSKI	DPESNPTAALA	KILITQV <mark>DE</mark> KL <mark>VK</mark>	°QTVMT S <mark>VY®</mark> G	VTYLGARE	786

tr B6K333 B6K333_SCHJY		EDIP-KDLLRDASAFLAKRVFQ 944
ap 013993 RPOM_SCHPO		DGME-KLKVADYANYLTKKVFE 937 GDIF-KDMLNNYSSYLTKMVFR 951
t= \$90008 \$90008_\$CHOY		
tr S9X2W4 S9X2W4_SCHCR		GDIP-KDMLNNYSSYLTKMVFR 950
tr A0A1E3Q3C6 A0A1E3Q3C6_LIPST		KOID-ERDLWRCAAYLTTLVFK 103 GLE-OEHLYSTAGYLAKTVLG 801
t= A0A167E4J0 A0A167E4J0_9ASCO t= A0A1E3PUP0 A0A1E3PUP0_9ASCO		-GLE-QEHLYSTAGYLAKTVLG 801 PHIG-PENIFIVASYLTINVFA 100
		PRIG-PENIFIVASILTINVFA 100 PFGE-DTYKYSLYLTKHVFA 974
t= A0A0H5C7R0 A0A0H5C7R0_CYBJA t= A0A1E3P5W0 A0A1E3P5W0 WICA0		FDDT-ESYKLSTYLAKHVFA 982
tr KOKTX3 KOKTX3_WICCF tr W6MIL2 W6MIL2 9ASCO		FSED-QSYKLSVYLTKVVFA 100 GFSKDDAKLHSRYLARRVFD 101
tr A0AlE30PI7 A0AlE30PI7 9ASCO		IFDDK-EAYALSRFLATHTFA 992
tr A0A1D2V948 A0A1D2V948 9ASCO		FGKD-TAYFLSKYLAVHVFA 103
		EFDEKYMSMSSKYLTOKVFK 683
t= A0A1B75ME0 A0A1B75ME0_9A5C0 t= Q6CRZ5 Q6CRZ5_KLULA		FDERINSMSSRILTORVFR 683
tr WOTGI8 WOTGI8 KLUMA		PDNPEESNELSRILAKHVFA 973
tr A0A109UWS1 A0A109UWS1 9SACH		LPEDADCYALSRYLARHVFA 984
tr G8JM92 G8JM92 ERECY		AFPDKNESYDMARYLTRHVFA 101
tr 075BP7 075BP7 ASHG0		AFPDNSYDMARYLTKHVFN 100
tr R9XDF6 R9XDF6 ASHAC		AFPDNSYDMARYLTKHVFD 100
tr H2ASJ8 H2ASJ8 KAZAF		FDDSSDSMKYSKYLARHVFA 995
tr J797Y3 J797Y3 KAZNA		FSDHRESLKYSKYLAKHVFA 986
tr GOVD01 GOVD01 NAUCC		PFDRKECFDLSKYLTSHVFA 103
t= COWE72 COWE72 NAUDC		PDRRECT-DLSKILISHVFA 105
triO6FLX9106FLX9 CANGA		FDDRAYSLELSKYLAKHVFA 103
tr G8BS54 G8BS54 TETPH		FENRNOSLELSKILARHVFM 103
triA0A0L8RKW5 A0A0L8RKW5 SACEU		FDDRKESLDFSKYLTKHVFG 105
tr A0A0L8VRU3 A0A0L8VRU3 9SACH		FDDRKESLDFSKILIKHVFS 100
tr J8PP58 J8PP58 SACAR		FDDRKESLDFSKYLTKHVFG 106
tr A0A0C7MY71 A0A0C7MY71 9SACH		FDDYRRSYEMSKYLTKHVFA 100
tr C5DNP3 C5DNP3 LACTC		FNDHKRSYELSKYLTKHVFA 100
tr C5DX79 C5DX79 ZYGRC		FEDRKYSLELSKYLTKHVFG 102
tr G82R00 G82R00_TORDC		FDDRTYSLELSKYLTKHVFA 103
tr A0AlE4ROF7 A0AlE4ROF7 SASCO		FGKDEDEKAKKFTKYLTSLVFD 102
tr A0A0L0P4K6 A0A0L0P4K6 9ASCO		FKGEPSDKLSIYSRYLTTHVFA 101
tr A0A1A0HGT7 A0A1A0HGT7 9ASCO		FGKDDYATVOKHSRYLTSLVFA 102
tr C4Y8E3 C4Y8E3 CLAL4		FEKDDYDSVTLYARYLTSLVFA 102
tr[G3B4C1[G3B4C1 CANTC		FDSDSEENSGEYAOYLTOHVFA 995
tr A3LX46 A3LX46 PICST		FSGEEDVADYARYLTMHVFN 967
tr A0A1E49MT6 A0A1E49MT6 9A9CO		IFTKDMEEDVVDYARYLTLHVFA 970
tr A5DN82 A5DN82 PICGU		FSKEDODKVADYSRYLTMLVFA 101
tr B5RTF6 B5RTF6 DEBHA		FDENDTENVDEYARYLTAHVFA 102
tr G3AEY0 G3AEY0 SPAPN		FPDNQRDSLQEHARYLTTHVFA 100
tr G8B7X1 G8B7X1 CANPC		FGDEHDAHIYTKYLTKOVFA 100
tr H8X1L6 H8X1L6 CANO9		IFGEDODAHIYTKYLTKOVFA 100
tr B9W6L5 B9W6L5 CANDC		YPRDADHNMPARYLAROVFA 101
tr CAYFJ1 CAYFJ1 CANAW		FPKDADHHAAARYLAVOVFA 996
tr C5ME71 C5ME71 CANTT		VPEDNSAHLYARYLANOVFI 101
tr M3IK19 M3IK19 CANKK		IFGDNDNEHLYAKYLASOVFA 101
an increase a language a Terration	1 + 1 + +++ ++++ +. +: .:	i i*i .i

3.4.3 Three critical pairs of amino acids in <u>DNA and RNA polymerases and their</u> <u>possible function(s)</u>

These analyses have revealed three critical pairs of amino acids in all these polymerases belonging to different types and origins. Table 3 shows these three critical pairs from different representative DNA and RNA polymerases.

The pair 1 involves in polymerization, (the Lys functions as proton abstractor); and the Arg with its guanidinium group make multiple hydrogen bonds to the NTP/dNTP.

The pair 2 (YG pair) acts as "*steric gate*" and involves in template binding and allows only NTPs in RNA polymerases (dNTPs in DNA polymerases) at polymerization site possibly with other conserved amino acids and

The pair 3 involves as "charge shielder" of NTPs/dNTPs through a Mg ion (Table 3) and

orients the α -phosphates of NTPs/dNTPs for polymerization.

3.4.4 Similarities in the active sites of DNA and RNA polymerases

3.4.4.1 The invariant K and its role in E. coli DNA polymerase I and T7 RNA polymerase

The DNA and RNA polymerase active sites were probed by a variety of techniques:

In the *E. coli* DNA polymerases I, DNase footprinting assay using DNase I and methidiumpropyl EDTA-Fe²⁺ indicated that the enzyme binds to the primer terminus and covers 8 base pairs [10].

Photo affinity labeling of the enzyme with dNTP analogue, 8-azido-dATP, and sequencing of the labeled peptide, identified Tyr^{766} at the active site of the enzyme [11]. Thus, the foot printing and photo cross-linking experiment has suggested the Tyr^{766} in the active site.

Enzyme	Arg/Lys	Tyr//Gly	Asp//Asp
DNA polymerase	S		
T ₇ pol	Arg518/Lys522	Tyr530/Gly531	Asp475/Asp654
E. coli pol I	Arg754/Lys758	Tyr766/Gly 767	Asp705/Asp882
E. coli pol II	Leu*523/Arg527	Phe533/Gly534	Asp452/ Asp545
E. coli pol III	^/Lys758	Tyr764/^Ala765	Asp405/Asp733
Human α	Lys947/Lys950	Tyr957/Gly958	Asp860/Asp1004
Human β	Leu*163/Lys168	Tyr 173/Leu*174	Asp192/Asp256
Human γ	Arg943/Lys947	Tyr955/Gly956	Asp890/Asp935
Human δ	Arg689/Lys694	Tyr701/Gly702	Asp602/Asp757
Yeast ɛ	Leu*819/Lys824	Tyr831/Gly832	Asp669/ Asp2118
Viral RNA polyme	erases		
T7	Arg627/Lys631	Tyr639/Gly640	Asp537/Asp812
Т3	Arg628/Lys632	Tyr640/Gly641	Asp538/Asp813
Chloroplast RNA			
A Thaliana	Arg725/Lys729	Tyr737/Gly738	Asp654/Asp886
O. Sativa	Arg765/Lys769	Tyr777/Gly778	Asp694/Asp926
Mitochondrial RN	IA polymerases [#]		
A Thaliana	Arg748/Lys752	Tyr760/Gly761	Asp677/Asp909
N. sylvestris	Arg774/Lys778	Tyr786/Gly787	Asp703/Asp935

Table 3. Critical pairs of amino acids found in DNA polymerases and RNA polymerases

Based on multiple sequence analysis

* Instead of Arg, a Leu is found at the corresponding position in the repair polymerases, viz., pol II and pol β . ^ No Arg or Leu is found near vicinity of the probable catalytic K. A good number of prokaryotic replicative polymerases (pol III) had an Ala adjacent to the Tyr)

In almost all the pol IV polymerases, only a G (PXG) is seen at the 11th position from the catalytic K; no regular gate keeper Y is found which possibly explains the error-prone nature of these polymerases

The ε polymerases also maintain a Leu near the catalytic K, as it is also involved in DNA repair. Pol ε 's main function is to extend the leading strand during replication while Pol δ is involved in the lagging strand synthesis. The most striking difference between the two DNA polymerases is that processive DNA synthesis by DNA polymerase delta is dependent on proliferating cell nuclear antigen (PCNA), a replication factor, while DNA polymerase epsilon is inherently processive.

[#] RNA polymerase data based on MSA delete single bracket

However, Basu and Modak [12], who have probed the polymerase active site with pyridoxal phosphate, found Lys⁷⁵⁸ at the active site (pyridoxal phosphate binds competitively to the dNTP site through Schiff's base formation and covalently links the amino acid involved possibly in polymerization reaction). These results suggest that the polymerase active site is in the bigger domain remote from the 3'→5' exonuclease activity and totally not connected to the dNMP site. Similar observations were made with an adenovirus DNA polymerase, e.g., the phosphate modification of an pvridoxal adenovirus DNA polymerase resulted in the loss of DNA polymerase activity, whereas the 3'- 5' exonuclease activity was unaffected. Inhibition of adenovirus DNA polymerase by pyridoxal phosphate was time-dependent and displayed saturation kinetics [13]. It is interesting to note that Zaldivar et al. [14] have shown that not only in DNA polymerases but also in RNA polymerases I and II of rat liver and RNA polymerase I of yeast, were also inactivated by

pyridoxal phosphate and hence suggested a possible involvement of a Lys residue in the catalytic site of RNA polymerases too.

Thus, both the Lys and Tyr are completely conserved in DNA polymerases analyzed by Palanivelu [4] and RNA polymerases (this communication). The phi 29 viral DNA polymerase shares several regions of amino acid similarity with other alpha-like DNA polymerases. Among them, the conserved region characterized by the amino acid motif "Kx3NSxYG" has been proposed to form part of the polymerization active site of alpha-like DNA polymerases [15]. However, by MSA analysis, these polymerases have shown a completely conserved R exactly at the 4th position downstream from the catalytic K and hence should be also included the template binding and catalysis and thus active site motif in both DNA and RNA polymerases is "R ⁴xxx**K**¹xxxxxX**Y**⁺⁸**G**^{*}. By using a library with totally random nucleotides at five different codons (R659, R660, K663, F667, and G668), Suzuki et

al. [16] confirmed that R^{659} and K^{663} were immutable in the DNA polymerase from *T. aquaticus* (R^{754} and K^{758} in *E. coli* DNA polymerase I, respectively),

The following observations also support As the Lys is completely conserved in both the types of polymerases [4 and this communication]) *it is proposed that the catalytic amino acid could be the completely conserved K in both the RNA and DNA polymerases*

Furthermore, Lys is the active site amino acid in NAD- and ATP dependent ligases, and also GTP dependent mRNA capping enzymes, which are all involved in making a phosphodiester bond as in polymerases [17].

Like DNA polymerases the DNA ligases are also inhibited by pyridoxal 5'-phosphate indicating the presence of a K at the catalytic domain of the enzyme [18]. Both the types of ligases (ATPdependent and NAD-dependent DNA ligases) from various organisms showed a highly conserved motif KY/I/VDGXR with the reactive K residue, followed by a Y or a hydrophobic amino acid [17].

Interestingly, not only in DNA ligases, but also in RNA ligases the catalytic K is conserved [18].

In *E. coli* DNA polymerase I Y⁷⁶⁶ and Y⁷⁵⁸ are found to be in close proximity to the 3'-OH of the primer and interestingly, such proximity is completely conserved in both the types of polymerases. Further analysis by site-directed mutagenesis, Doublie and Ellenberger [19] and Astatke et al. [20] have shown that the critical Y may possibly be involved in template recognition and dNTP selection in DNA polymerases [21] and the same function is proposed for RNA polymerases as well in this communication. It is interesting to note that a highly conserved Tyr residue in reverse transcriptase controls substrate selection. It is interesting to note that the highly conserve Y^{955} residue is critical for nucleotide recognition among Family A DNA polymerases, i.e., γ polymerases from eukaryotes. Furthermore, Y955 is a highly conserved residue among a wide variety of DNA polymerases (Table 1). Further proof of Y766 involvement in nucleotide selection was obtained Y⁷⁶⁶; from site-directed mutagenesis of substitution of an equivalent amino acid as in $Y^{766} \rightarrow F$ substitution in the Klenow polymerase did not show an appreciable increase in nucleotide misinsertion; however, substitution with Ala or Ser generated an error-prone DNA

polymerase attributable to decreased stringency for selection of dNTPs [19]. Interestingly the YG doublet is highly conserved and found to be a common pair in different types of DNA and RNA polymerases (Table 4).

Further proof is provided by crystallographic analysis of T7 DNA polymerase. The T7 DNA replication complex at 2.2 Å resolution have shown that the invariant K^{522} ($\equiv K^{758}$ in *E. coli* DNA pol I) actually makes contact with the α phosphate of dNTP [22].

mechanism of Since. the action for polymerization reactions of RNA polymerases, proposed in this article, is based on a proton abstraction at the catalytic site amino acid, K is placed as the catalytic amino acid. The other active site amino acids, viz. the YG pair and possibly with other conserved amino acid(s), holds the complementary base inserted by the finger domain onto the catalytic site, the catalytic K adds the NTP to the 3'-OH. The reaction essentially occurs through proton abstraction by K followed by an electrophilic-nucleophilic attack at the growing 3" end (Figs. 9.1-9.4).

3.4.4.2 T7 polymerase used as the model enzyme for studying transcription

Perhaps the most widely studied single-subunit RNA polymerase is bacteriophage similar to the E. coli DNA polymerase I for polymerase family. The common feature of all these SSU RNA polymerases from T7, T3, SP6, and K11, mitochondrial and chloroplast, is their simpler structure compared to prokaryotic and eukaryotic multi-subunit RNA polymerases which are more complex. Interestingly, even though they are single-subunit RNA polymerases, they are able to perform the complete transcriptional cycle in the absence of additional protein factors. The single-subunit composition, relatively low molecular weight, makes the T7 RNA polymerases the most convenient model for investigating the physicochemical aspects of transcription and its catalytic mechanism. Furthermore, the enzyme can be produced in large amounts for structural analysis.

3.4.4.3 Properties of T7 RNA polymerase

T7 RNA polymerase was first isolated from T7infected *E. coli* cells in 1970 [23]. It has 883 amino acids with a molecular mass of 98,092 Daltons, optimally active in the pH range 8.0-9.0 and the elongation rate is 100-200 nucleotides/sec. The T7 polymerase requires a double-stranded DNA template and 5- 10 mM Mg²⁺ as a cofactor for the optimal synthesis of RNA [2]. It is an extremely promoter-specific enzyme and transcribes only DNA downstream of a T7 promoter (TAATACGACTCACTATAG) and the transcription begins with the 3' G. It has a very low error rate. Interestingly, the 3D structures of polymerization domains are very similar in DNA and RNA polymerases, including the T7 RNA polymerase [8]; they all resemble a right hand and the sub domains are referred to as "palm", "thumb", and "fingers". However, the T7 family of RNA polymerases is structurally and evolutionarily distinct from the multi-subunit family of RNA polymerases of bacterial and eukaryotic families and is not inhibited by the antibiotic, rifampicin. In biotechnology applications, T7 RNA polymerase is used to transcribe DNA in many modern-day vectors that have been cloned into such vectors.

3.4.4.4 Analysis of active site and metal binding site(s) of T7 RNA polymerase

Table 4 shows the summary of site-directed mutagenesis of the T7 RNA polymerase active site [24]. The catalytic K^{631} when modified with either G or L or R, only partially inactivated the T7 RNA polymerase whereas in DNA polymerase I, it was completely inactivated. However, in another site-directed mutagenesis experiment, Osumi-Davis et al. [25] have shown when the K^{631} is modified to M, T7 RNA polymerase has lost almost all the activity.

Interestingly, the Y⁶³⁹ of the YG pair is also essential for its activity as the modification of this critical Y⁶³⁹ yielded no activity as expected. Sitedirected mutagenesis experiments have also shown other amino acids like P⁵⁶³, Y⁵⁷¹, T⁶³⁶, F⁶⁴⁶ are also important for the activity of the enzyme (Table 4). By electron paramagnetic resonance spectroscopy, flow-dialysis and transcription analysis, the D537 and D812 in bacteriophage T7 RNA polymerase are found to be as metal ion-binding sites and are essential in the catalytic mechanism [26, 27].

<u>3.4.5 Mechanism of NTP and dNTP</u> <u>discrimination in SSU RNA</u> polymerases

Though the RNA polymerases, DNA polymerases or reverse transcriptases are divergent, the overall 3 D structures are found to be very similar and follow right handed palm. and thump shape. finaers The RNA polymerases, DNA polymerases use the same catalytic amino acid and gate keeper pair and an invariant R in their catalytic motif. Then the most intriguing guestion is how the RNA polymerases discriminate NTPs from dNTPs and allow only NTPs to the polymerization site. This problem was solved by an interesting mutagenesis experiment by Kotsyuk et al. [5]. They observed that the YG pair in viral RNA polymerases is characterized by a unique distribution of invariant hydroxyl-containing amino acids like S and T, whereas no such

Amino acid position and modification	Result	Reference
K ¹⁷² → L	No change in activity	[28]
P ⁵⁶³ → A	Inactivated	[24]
Y ⁵⁷ S	Inactivated	ibid
K ⁶³¹ — → G/L/R	Partially inactivated	ibid
T ⁶³⁶ —▶P	Inactivated	ibid
Y ⁶³⁹ →D	Inactivated	ibid
F ⁶⁴⁶ → C	Inactivated	ibid
D ⁵³⁷ → N	Inactivated (Total)	[25]
D ⁸¹² → N	Inactivated (Total)	ibid
K ⁶³¹ → M	Inactivated (1% activity)	[29]
Y ⁶³⁹ → F	Fully active*	ibid
S ⁶⁴¹ → A	No RNAP but shows DNAP	[5]

*kinetic parameters are somewhat different

RNAP/DNAP = RNA polymerases/ DNA polymerase activity

regularity is seen in DNA polymerases [4]. In order to find out whether this unique Ser⁶⁴¹ in T7 RNA polymerase $(Y^{639}GS^{641})$ play any role in the discrimination between NTPs and dNTPs, they made a single amino acid substitution and the S⁶⁴¹ was modified to Ala. The mutant enzyme was purified to homogeneity and found to their surprise that the mutant enzyme allowed dNTPs also and the T7RNA polymerase lost RNA polymerase activity and exhibited DNA polymerase activity. The Ser hydroxyl likely recognizes the 2'-OH in the NTPs and possibly makes a hydrogen bond and discriminate dNTPs, where they lack a 2'-OH. If you have close look at the other SSU RNA polymerase from mitochondria and chloroplasts a functionally equivalent T is placed in the vicinity of the YG pair as YGxT. A similar observation was made by Cermakian et al. [3] The invariant T in these polymerases possibly involves in the NTP and dNTP discrimination as in the case of T7 RNA polymerases.

3.4.6 Mechanism of action of T7 RNA polymerase

The mechanism of action of T7 RNA polymerase is proposed based on the data obtained by MSA and data already available by biochemical, sitedirected mutagenesis and X-ray crystallographic analysis. X-ray crystallographic analysis of T7 polymerase have shown that the B motif is located in the 'finger' subdomain, close to motifs A and C with both these motifs likely to form the active site. The side chain radicals of the three invariant amino acids (R⁶²⁷, K⁶³¹ and Y⁶³⁹) are found to be directed towards the substrate binding cleft [30]. Temiakov et al. [31] have also shown that $Y^{\rm 639}$ is mainly involved in discrimination of ribose versus deoxyribose substrates and the substrate selection occurs prior to the isomerization to the catalytically active conformation. However, an invariant Y is also found in DNA polymerases as well, at the same distance from the catalytic K [4]. Therefore, the presence of an invariant S or T adjacent to YG pair in these RNA polymerases was found to be playing an important role in substrate selection [5,3]. Whitney Yin and Steitz [32] have observed two divalent metal ions in the active site of T7 RNA polymerase; metal ion A is associated exclusively with the 3' end of RNA in the product complex while metal ion B remains bound to the product pyrophosphate as well as the catalytic carboxylate.

The proof-reading mechanism is well established in DNA polymerases [4]. However, it is poorly understood in RNA polymerases. Maintaining high fidelity during transcription is essential for the accurate transfer of genetic information from DNA to RNA. (RNA polymerases generally misincorporate only one wrong nucleotide/~100000 bases). As RNA polymerases are also Zn metalloenzymes (possibly the metal ion A, which is associated exclusively with the 3' end of RNA as discussed elsewhere) the Zn-mediated deletion [4] of the misincorporated NTP could be a possible mechanism, as the enzyme stalls at every misincorporation like DNA polymerases. Zn mediated hydrolysis could be also the possible mechanism for RNA cleavage followed by dissociation at transcription termination, where the RNA polymerase again stalls at the termination site.

Fig. 9.1. Watson-Crick base pairing of the incoming nucleotide with the template and nucleotide discrimination by steric gate amino acids Tyr, Gly and Ser

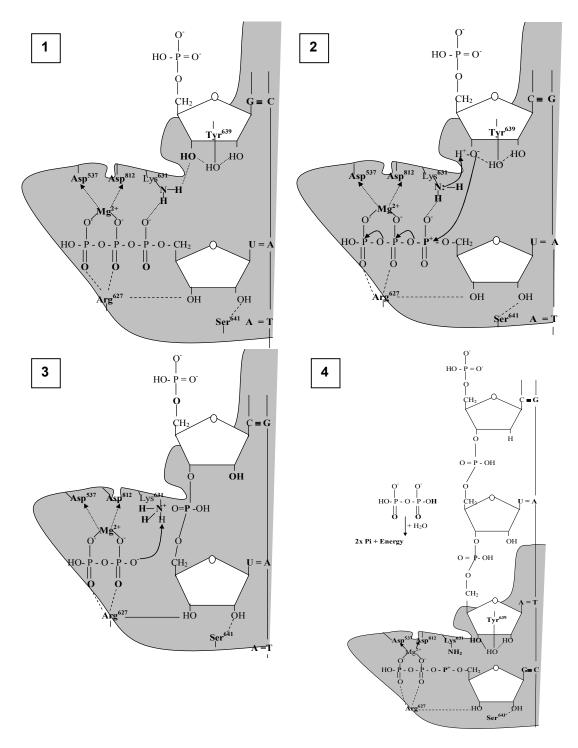
Fig. 9.2. Electronic transition at the active site for proton abstraction and an electrophilic and nucleophilic attack

Fig.9.3. Proton abstraction by the active site amino acid Lys with simultaneous formation of $3' \rightarrow 5'$ phosphodiester bond with the incoming NTPs

Fig. 9.4. Transfer of the proton from Lys to pyrophosphate and formation of inorganic pyrophosphate and the translocation of the enzyme to next complementary nucleotide inposition that is to be polymerized.

<u>3.4.7 Other conserved amino acids and</u> regions in these polymerases

It should also be noted that the above discussed conserved motifs and amino acids form only the substrate binding and catalytic cores. Apart from these, there are a large number of single amino acid invariants (Ys, Ws, Cs, Ps and Gs,) diads, triads and long conserved stretches of amino acids in all these polymerases (Figs. 2–7). A good number of highly conserved Ps in these polymerases is implicated in making the necessary bents on the enzyme's structure during substrate binding, polymerization and translocation processes. The long conserved stretches of amino acids might be required to



Figs. 9.1-9.4. Steps proposed in the polymerization reaction of T7 RNA polymerase

make the correct, unique 3D structures. The highly conserved Cs might be useful for making the disulphide bridges which make the enzyme more compact and stable.

4. CONCLUSION

MSA have shown that a basic amino acid K, a YG pair and an invariant R and S/T are highly conserved in all SSU RNA polymerases.

Distance conservation is also found among the conserved motifs and amino acids among these RNA polymerases. Site-directed mutagenesis, biochemical and X-ray crystallographic analyses of T7 RNA polymerase have also suggested their involvement in substrate binding and catalysis. Based on these results, a plausible mechanism of action is proposed for the polymerization reactions for T7 RNA polymerase as the model enzyme.

ACKNOWLEDGEMENTS

The author wishes to thank Dr. S. Krishnaswamy, Centre of Excellence in Bioinformatics (Retd.) and Dr. R. Usha, Department of Plant Biotechnology (Retd.), School of Biotechnology, Madurai Kamaraj University, Madurai, for their useful suggestions on the manuscript.

COMPETING INTERESTS

Author has declared that no competing interests exist.

REFERENCES

- 1. Hurwitz J. The discovery of RNA polymerase. J Biol Chem. 2005;280: 42477–85.
- Tunitskaya VL, Kochetkov SN. Structural and functional analysis of bacteriophage T7 RNA polymerase. Biochemistry (Moscow). 2002;67:1124–1135.
- Cermakian N, Ikeda TM, Miramontes P, Lang BF, Gray MW, Cedergren R. On the evolution of the single-subunit RNA polymerases. J Mol Evol. 1997;45:671– 681.
- Palanivelu P. DNA polymerases An insight into their active sites and mechanism of action, Int. J. Biochem. Res. & Rev. 2013;3:205-247.
- Kostyuk SM, Dragan DL, Lyakhov VO, Rechinsky VL, Tunitskaya BK. Chernov SN. Kochetkov E. Mutants ofT7 RNA polymerase that are able to synthesize both RNA and DNA. FEBS Letters. 1995;369:165-168.
- Konig J, Baumann S, Koepke J, Pohlmann T, Zarnack K, Feldbrugge M. The fungal RNA-binding protein Rrm4 mediates longdistance transport of ubi1 and rho3 mRNAs. EMBO J. 2009;28:1855-1866.
- 7. Cheetham GM, Jeruzalmi D, Steitz TA, Structural basis for initiation of

transcription from an RNA polymerasepromoter complex. Nature. 1999;399:80-83.

- Sousa R, Je Chung Y, Rose JP, Wang BC. Crystal structure of bacteriophage T7 RNA polymerase at 3.3 Å resolution. Nature. 1993;364:593-599.
- 9. Palanivelu P. Multiple sequence analysis of polygalacturonases and invertases and phase shift in conserved motifs. Indian J Biotechnol. 2007;6:24-30.
- Brenowitz M, Senear DF, Shea MA Ackers GK. Quantitative DNase footprint titration: A method for studying protein-DNA interactions. Methods Enzymol. 1986;130: 132-181.
- 11. Rush J, Konisberg W H. Photoaffinity labeling of the Klenow fragment with 8-azido-dATP. J Biol Chem. 1990;265:4821-27.
- Basu A, Modak MJ. Affinity labeling of *E. coli* DNA polymerase I by pyridoxal 5'-phosphate. Biochemistry. 1987;26:704-1709.
- Monaghan N, Hay RT. Pyridoxal 5'phosphate inhibition of adenovirus DNA polymerase. J Biol Chem. 1996;271: 24242-8.
- 14. Zaldivar MJ, Bull P, Venegas A, Valenzuela P Inactivation of rat liver RNA polymerases I and II and yeast RNA polymerase I by pyrodixal 5'-phosphate. Evidence for the participation of lysyl residues at the active site. Biochemistry. 1975;14:4907-11.
- Blasco MA, Lázaro JM, Blanco L, Salas M. Phi 29 DNA polymerase active site. The conserved amino acid motif "Kx3NSxYG" is involved in template-primer binding and dNTP selection, Proc Natl Acad Sci. (USA). 1997;94:1619–1622.
- Suzuki M, Baskint D, Hoodt L, Loeb, LA. Random mutagenesis of *Thermus* aquaticus DNA polymerase I: Concordance of immutable sites in vivo with the crystal structure. Proc Natl Acad Sci. (USA). 1996;93:9670-9675.
- Doublie S, Tabor S, Long AM, Richardson, CC, Ellengerger T. Crystal structure of a bacteriophage T7 DNA replication complex at 2.2 Å resolution. Nature. 1998;391: 251-258.
- Sriskanda V, Schwer B, Ho K, Shuman S. Mutational analysis of *Escherichia coli* DNA ligase identities amino acids required for nick-ligation *in vitro* and for *in vivo* complementation of their growth of yeast

cells for CDC9 and LIG4, Nucleic acids Res. 1999;27:3953-3963.

- Tomkinson AE, Totty NF, Ginsburg M, Lindahl T. Location of the active site for enzyme-adenylate formation in DNA ligases, Pro Natl Acad Sci. (USA). 1991;88:400-404.
- 20. Astatke M, Grindley N D, Joyce C M. How *E. coli* DNA polymerase I (Klenow fragment) distinguishes between deoxyand dideoxynucleotides, J Mol Biol. 1998;278:147-165.
- Kaushik N, Pandey VN, Modak MJ. Significance of the O-helix residues of Escherichia coli DNA polymerase I in DNA synthesis; dynamics of the dNTP binding pocket. Biochemistry. 1996;35:7256-66.
- Derbyshire V, Freemont PS, Sanderson MR, Beese L, Friedman JM, Joyce CM, Steitz TA. Genetic and crystallographic studies of the 3,5'-exonucleolyitc site of DNA polymerase I, Science. 1988;240: 199-201.
- Chamberline M, McGrath J, Wakshell L. New RNA polymerase from *Escherichia coli* infected with Bacteriophage T7. Nature. 1970;228:227-231.
- Rechinsky VO, Kostyuk DA, Lyakhov DL, Chernov BK, Kochetkov SN. Random mntagenesis of the gene for bacteriophage T7 RNA polymerase. Mol Gen Gen. 1993;238:455–458.
- Osumi-Davis P de Aguilera MC, Woody RW, Woody AY. Asp537, Asp812 are essential and Lys631, His811 are catalytically significant in bacteriophage T7 RNA polymerase activity. J Mol Biol. 1992;226:37-45.
- Osumi-Davis P, Sreerama N, Volkin DB, Middaugh CR, Woody RW, Woody AYM.

Bacteriophage T7 RNA polymerase and its active-site mutants. Kinetic, spectroscopic and calorimetric characterization. J Mol Biol. 1994;237:5-19.

- Woody AY, Eaton SS, Osumi-Davis PA, Woody RW, Asp537 and Asp812 in bacteriophage T7 RNA polymerase as metal ion-binding sites studied by EPR, flow-dialysis, and transcription. Biochemistry. 1996;35:144-52.
- Lyakhov DL, Ilgenfrtiz H, Chernov BK, Dragan SM, Rechinsky VO, Pokholok DK, Tunitskaya VL, Kochetkov SN. Sitespecific mutagenesis of residue Lys-172 of phage T7 RNA polymerase: Characterization of transcription properties of mutant proteins. Mol Biol. (Moscow). 1992;26:1022-1035.
- Maksimova TG, Mustayev AA, Zaychikov EF, Lyakhov DL, Tunitskaya VL, Akbarov AK, Luchin SV, Rechinsky VO, Chernov BK, Kochetkov SN. Lys631 residue in the active site of the bacteriophage T7 RNA polymerase. Affinity labeling and sitedirected mutagenesis, Eur J Biochem. 1991;195:841-847.
- Doublie S, Ellenberger T. The mechanism of action of T7 DNA polymerase. Curr Opin Struct Biol. 1998;8:704-712.
- Temiakov D, Patlan V, Anikin M, McAllister WT, Yokoyama S, Vassylyev DG. Structural basis for substrate selection by T7 RNA polymerase. Cell. 2004;116:381-391.
- 32. Whitney Yin Y, Steitz TA. The Structural Mechanism of Translocation and Helicase Activity in T7 RNA Polymerase. Cell. 2004;116: 393-404.

© 2017 P. Palanivelu; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history: The peer review history for this paper can be accessed here: http://www.sciencedomain.org/review-history/22801