# Exposition of a family of RNA m<sup>5</sup>C methyltransferases from searching genomic and proteomic sequences

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## ABSTRACT

The Escherichia coli fmu gene product has recently been determined to be the 16S rRNA m<sup>5</sup>C 967 methyltransferase. As such, Fmu represents the first protein identified as an S-adenosyl-L-methionine (AdoMet)dependent RNA m<sup>5</sup>C methyltransferase whose amino acid sequence is known. Using the amino acid sequence of Fmu as an initial probe in an iterative search of completed DNA sequence databases, 27 homologous ORF products were identified as probable RNA m<sup>5</sup>C methyltransferases. Further analysis of sequences in undeposited genomic sequencing data and EST databases yielded more than 30 additional homologs. These putative RNA m<sup>5</sup>C methyltransferases are grouped into eight subfamilies, some of which are predicted to consist of direct genetic counterparts, or orthologs. The enzymes proposed to be RNA m<sup>5</sup>C methyltransferases have sequence motifs closely related to signature sequences found in the well-studied DNA m<sup>5</sup>C methyltransferases and other AdoMet-dependent methyltransferases. Structure-function correlates in the known AdoMet methyltransferases support the assignment of this family as RNA m<sup>5</sup>C methyltransferases.

## INTRODUCTION

RNA modifications have been well characterized (1), but relatively little is known about the enzymes that catalyze such modifications or about the functions of the modified residues. We have undertaken a program directed at identifying the enzymes responsible for formation of the modified nucleotides in RNAs. Recently, the *fmu* gene product (Fmu) was reported to catalyze formation of m<sup>5</sup>C at position 967 of *Escherichia coli* 16S rRNA (2,3), and this represents the first RNA m<sup>5</sup>C MTase whose amino acid sequence is known. [Fmu was renamed rrmB (2) and rsmB (3). To avoid confusion we have returned to the older designation.] Tscherne and co-workers (3) also reported searching GenBank and finding proteins similar to Fmu in 13 organisms. They suggested that three of these proteins might be RNA m<sup>5</sup>C MTases.

In the present work, we have used the Fmu sequence as an initial probe in an iterative search of all available sequence databases, and we have identified more than 55 open reading frames (ORFs) that encode proteins that are homologous to Fmu. These homologs have sequence motifs which are closely related to signature sequences found in the well-studied DNA m<sup>5</sup>C MTases, and these motifs allow us to identify the Fmu homologs as putative RNA m<sup>5</sup>C MTases and to assign some structure–function relationships. Further, from homology comparisons within the family, we are able to classify these m<sup>5</sup>C RNA MTases into eight subfamilies, of which at least five are likely to represent orthologs.

## MATERIALS AND METHODS

This study used databases of deposited and undeposited sequences reported up to February 22, 1999. Using Fmu as a starting probe, Blast 2.0 and PSI-Blast (4) were used in iterative searches through NCBI databases of deposited protein sequences translated from DNA. Usual search parameters included an EXPECT value of 1000 and a minimum word length of 2 to pick up weak similarities. Filtering was usually turned off. Various similarity matrices were used of both PAM and BLOSUM types. Gap penalties were also varied, with low penalties chosen to enhance detection of homologs with insertions or deletions relative to the probes. We collected a large set of deposited protein sequences which were homologous to Fmu, and these sequences were used as probes in further iterative searches which were widened to include other databases available through NCBI. Preliminary sequence data were obtained from The Institute for Genomic Research website at http://www.tigr.org . These data come from many different sequencing projects and are made available through TIGR (http://www.tigr.org/tdb/mdb/mdb.html).

In certain eukaryotic cases, sequences from EST databases were collected by BLAST searches of type tblastn, and assembled into partial ORFs using the putative m<sup>5</sup>C MTase sequences as guides. This procedure was done iteratively to produce substantial approximates of theoretical ORFs.

In the eubacterial and archaebacterial cases, undeposited genomic sequencing data available for Blast searches were used to collect homologous patches of translated sequence which were assembled into larger putative protein fragments. As in the eukaryotic case, these patches were added to our set of homologs, and the procedure was iterated.

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Organism	I (Fmu)	<u>П</u> (Р120)	III (Yebu)	IV	V	VI	VII (Ncl1)	VIII
I.Eubacteria		···· · · · · · · · · · · · · · · · · ·					()	
Proteobacteria								
Actinobacillus actinomyces <sup>a</sup>	$U^b$	-	-	-	-	-	-	-
Haemophilus influenzae <sup>c</sup>	P44788 <sup>d</sup>	-	-	-	-	-	-	-
Pseudomonas aeruginosa <sup>a</sup>	U	-	-	-	-	-	-	-
E. coli <sup>c</sup>	P23866	-	2829645	-	-	-	-	-
Yersinia pestis <sup>a</sup>	U	-	-	-	-	-	-	-
Coxiella burnetii ª	P45679	-	-	-	-	-	-	-
Vibrio alginolyticus	Fmu/v <sup>e</sup>	-	-	-	-	-	-	-
Neisseria gonorrhoeae <sup>a</sup>	U	-	-	U	-	-	-	-
Neisseria meningitidis <sup>a</sup>	U	-	-	U	-	-	-	-
Campylobacter jejuni *	-	-	-	-	U	-	-	-
Gram Positives								
B.subtilis <sup>c</sup>	3915867	-	-	-	-	-	-	-
Staphylococcus aureus <sup>a</sup>	U	-	-	-	-	-	-	-
Streptococcus pneumoniae <sup>a</sup>	U	-	U	-	-	-	-	-
Streptococcus pyogenes a	U	-	U	-	-	-	-	-
Lactococcus lactis <sup>a</sup>	P72943	-	-	-	-	-	-	-
Enterococcus faecalis <sup>a</sup>	U	-	-	-	-	-	-	-
Clostridium acetobutylicum <sup>a</sup>	U	-	-	-	-	-	-	-
Mycobacterium tuberculosis <sup>c</sup>	2829532	-	-	-	-	-	-	-
Other phyla								
Synechocystis <sup>c</sup>	P72943	-	-	-	-	-	-	-
Deinococcus radiodurans <sup>a</sup>	U	-	-	-	-	-	-	-
Porphyromonas gingivalis <sup>a</sup>	-	-	U	-	-	-	-	-
Thermotoga maritima <sup>a</sup>	U	-	-	-	-	-	-	-
II.Eukaryotes								
human	_	P46087	_	_	_		$\mathbf{E}^{\mathbf{b}}$	Е
mouse	_	A48998			-	-	Ē	Ē
D. melanogaster		E			-	-	4185892	E
C. elegans <sup>c</sup>	_	3886025		_	_	_	4105092	Е
S. cerevisiae <sup>c</sup>	_	P40991	, _	_	_	_	586408	1730712
S. pombe	_	3810844	-	_	_			2414617
III Archaebacteria		5010044				-	2403139	2414017
Methanococcus jannaschii	-	-	-	-	2500953	-	-	
Archaeoglobus fulgidus°	-	-	-	2648195	2649749	-	-	-
D					2648496			
Pyrococcus horikoshii°	-	-	-	3131344	3131814	3130211	-	-
Bungagagag Gunianun 8				3131110	2696448			
Pyrococcus furiosus <sup>a</sup>	-	-	-	2 U	2 U	U	-	-

Table 1. Putative RNA m5C MTase ORFs

<sup>a</sup>Undeposited genomic sequences from http://www.tigr.org . Funding sources and institutes supplying sequence are listed in http://www.tigr.org/tdb/mdb/mdb.html

<sup>b</sup>U, ORFs compiled from undeposited genomic sequencing data (2 U indicates there are two ORFs). E, ORFs compiled from the EST division of GenBank/EMBL/DDBJ. Most of these ORFs are incomplete.

<sup>c</sup>Complete genomic sequence is available.

<sup>d</sup>All numbers in cells are accession numbers for GenBank/EMBL/DDBJ databases.

<sup>e</sup>BAA31227 and BAA31226 are accession numbers are for fmu and fmv which have been combined to yield a single ORF as found in *E.coli*.

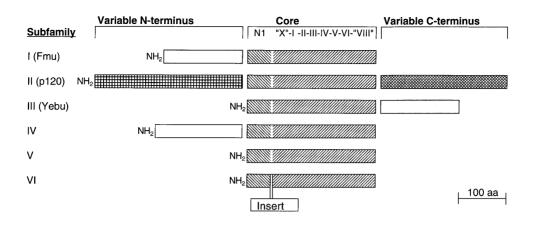
The collection of homologs was used to create a database that was used as the object of Blast searches using individual homologs as probes. Analysis of this set of protein sequences allowed division into subfamilies of closer relatives. The extended homologies within these subfamilies were used to further expand fragmentary individual sequences within our database in continued iterations of the procedure described above.

Alignment of each subfamily was initiated using the Pileup program inside GCG v.9.1 (5) and was then further adjusted. Alignments between subfamilies were initiated using conserved sequence patches in each subfamily and then adjusted.

RNA sequence data were obtained from the rRNA WWW server at the University of Antwerp, Belgium (http:// rrna.uia.ac.be). The phylogenetic assignments and terminology used (e.g. 'epsilon division of Proteobacteria') are those available on the NCBI web site (http://www.ncbi.nlm.nih.gov/ Taxonomy).

## **RESULTS AND DISCUSSION**

We used the sequence of Fmu as an initial probe in an iterative search of the available sequence databases. In the databases of finished sequences (GenBank/EMBL/DDBJ), we found a family of 27 ORFs with deduced proteins homologous to Fmu, and in the undeposited genomic sequencing data and EST sequences we found more than 30 additional Fmu homologs (Table 1). To obtain the latter, sequences were identified as putative m<sup>5</sup>C MTase fragments and assembled into larger ORFs for incorporation into the analysis of the family of Fmu homologs. The translated sequences of the complete and incomplete ORFs are available at http://www.sacs.ucsf.edu/home/SantiLab/m5c.html . As this work progressed, we performed comparisons of the Fmu homologs with the more extensively studied DNA m<sup>5</sup>C MTases and other nucleic acid MTases. This analysis revealed that the Fmu homologs possess a



**Figure 1.** Arrangement of conserved regions in subfamilies of the putative RNA m<sup>5</sup>C MTase family. A core region of about 270 amino acids is conserved throughout subfamilies I–VI of this family of putative AdoMet-dependent MTases, with extensive, but lower, homology in subfamilies VII and VIII (not shown). The core is divided into a small N-terminal region of about 40–50 amino acids and a larger C-terminal region of about 220–230 amino acids. The larger region contains conserved motifs which appear to be homologous to those seen in a wide range of AdoMet-dependent MTases.

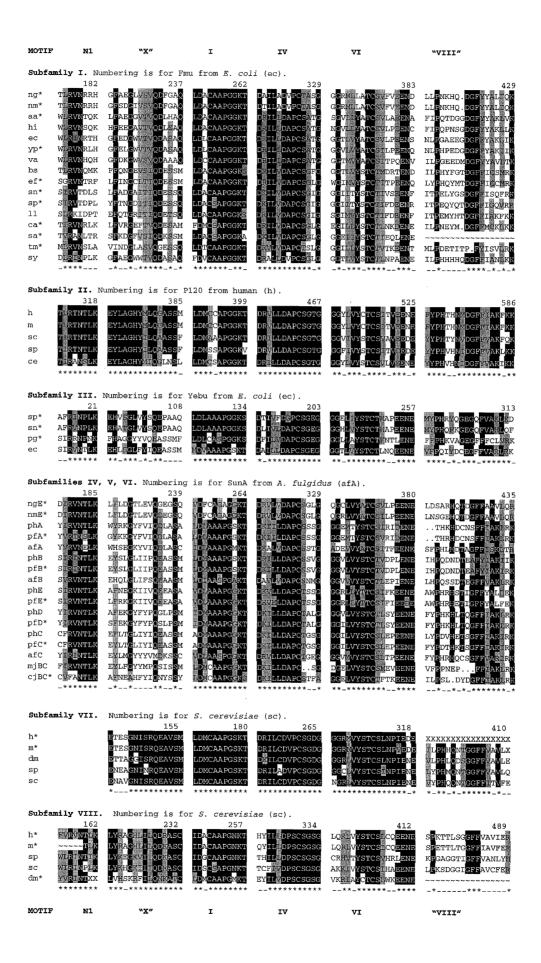
conserved core with sequence motifs that have homology to conserved signature motifs described in DNA MTases and other *S*-adenosyl-L-methionine (AdoMet)-dependent MTases (6–12). The established structure–function correlates of these motifs in the DNA MTases enabled provisional assignment of  $m^5C$  MTase function to this family of RNA modifying enzymes. In the following, we first describe the overall family of putative RNA  $m^5C$  MTases obtained by homology searches using Fmu as an initial probe, followed by a comparison of conserved sequence motifs to the signature sequences of other AdoMet MTases.

## Subfamilies of RNA m<sup>5</sup>C MTases

Based on the linear arrangement of conserved motifs and sequence homology levels, the family of RNA m<sup>5</sup>C MTases was subdivided into eight subfamilies (I–VIII). Figure 1 shows the arrangement of conserved regions in subfamilies I–VI. All subfamilies have a conserved core region consisting of a small N-terminal region of ~40–50 amino acids and a larger C-terminal region of about 220–230 amino acids which contains signature sequence motifs (Fig. 2). The subfamilies are distinguished by N- or C-terminal extensions or, in the case of subfamily VI, an insertion into the core sequence. These extensions of the core sequence have regions of homology within a subfamily, but vary between subfamilies (Fig. 3). The RNA substrate recognition domains may exist in these non-core extensions, or they may exist in thus far unrecognized proteins that serve as RNA-binding subunits for these putative RNA m<sup>5</sup>C MTases. We propose that members of subfamilies I, II, VII, VIII and probably III, are made up of direct genetic counterparts or orthologs.

Subfamily I, which includes Fmu and putative orthologs, has 20 eubacterial members. Members of this family contain an Nterminal extension of ~220 amino acids (Fig. 3A). In addition to homology, strong evidence that members of subfamily I are orthologs is derived from a correlation between the presence of the gene and a C residue at the target site of small subunit RNA. The target of Fmu, C967 of E.coli 16S rRNA, is the fourth base from the 5' end of the loop of a conserved 4 bp stem-8 base loop found in all small subunit RNAs (helix 31 in Escherichia coli 16S rRNA) (13). All ORFs of subfamily I belong to species of Eubacteria that contain a C residue at the analogous site of their small subunit RNAs. In five other complete and two nearly complete eubacterial genomes we did not find putative Fmu orthologs, and in each case the nucleotide in the small subunit RNAs corresponding to position 967 of E.coli 16S rRNA was not a C (G in Mycoplasma genitalium and Mycoplasma pneumoniae, and A in Helicobacter pylori, Treponema pallidum, Borrelia burgdorferi, Campylobacter jejuni and Porphyromonas gingivalis). Together with certain sequence homologies, this correlation suggests that all members of subfamily I are Fmu orthologs that methylate the 5 carbon of a C residue at the fourth base of the loop of the

**Figure 2.** (Opposite) Signature motifs of the putative RNA m<sup>5</sup>C MTases. Motifs assignments are as described (8). Identical residues are black with white lettering, gray shading indicates similar residues. Organisms are designated by the first initials of the genus and species name in lower case, except for *S.pneumoniae* and *Synechocystis*, which are sn and sy, respectively. \* following the organism designation indicates that the amino acid sequence is a translation of an incomplete ORF. ~ indicates N- or C-terminus of the available sequence. X indicates incomplete internal sequence. Motifs shown are from 16 members from subfamily I, five members from subfamily II, and all members of the other subfamilies listed in Table 1. Subfamilies IV–VI are combined. In the databases, Sun is a common designation for Fmu homologs, SunA–SunE refers to the Fmu homologs in families IV–VI. In the organism designations for these families, A or E, subfamily IV; B, C or BC, subfamily V; D, subfamily VI.



Subfamily I (Fmu) N-terminal extension

<ul> <li>58: LLCETCF SVCRVLPREBOITKRLVDKPLKGKTRIVHCELLVGLKOTLAM. KVFAHAADDE:</li> <li>43: LLCBCCF VCRVLPREBOITKRLVDKPLKGKCRTVHVLTMVGLKOTLAT. H: SPHALAGE:</li> <li>43: LLCBCCF TERVLPCGUART STARTGKGRTVHVLTMVGLKOTLAT. H: SPHALAGE:</li> <li>44: LLTBGVYFTLORKIA DYMLKPFIN. KPGKVDYHVLTMVGLKOTLAT. H: SPHALAGE:</li> <li>44: LLTBGVYFTLORKIA DYMLKPFIN. KPGKVDYHVLTMVGLKOTLAT. H: SPHALAGE:</li> <li>44: LLTBGVYFTLORKIA DYMLKPFIN. KPGKVDNWKRMITLSLGCVDELLGCKTODHATHE:</li> <li>44: LLTBGVYFTLORKLA DYMLKPFIN. KPGKVDNWKRMITLSLGCVDELLGCKTODHATHE:</li> <li>44: LLTBGVYFTLORKLA DYMLKPFIN. KPGKVDNWKRMITLSLGCVDELLGCNGDHAVTHE:</li> <li>44: LLTBGVYFTVARKLLEWYSHTPFWK. KPGKVDNWKRMITLSLGCTGLGLKGARATHE:</li> <li>44: LLTBGVYFTVARKLLEWYSHTPFWK. KPGKVDNWKRMITLSLGCTGLGLKGARATHE:</li> <li>44: LLTBGVYFTVARKLLEWYSHTPLKK. REPKLARMSTLOTTOVDLKMKVTSLGARATHE:</li> <li>44: LLTBGVYTVARKKELDWYSHTPLKK. REPKLARMSTLOTTOVDLKMKVTSLGARATHE:</li> <li>44: LLTBGVYTVARKKELDWYSHDYLKKYKINKI KIKKYNWKRSTLOTVULDKVARASKALLEWNSED</li> <li>44: LLTBGVYSTVRUKRKYTDOYLKKKK JNURQHWNSTLOTVULDKVORMHTITME:</li> <li>45: FPHELWREVKSELDWYSTDOLLFRULGERDKLAASCK KDDVAKHNLELWWAYLKNH:</li> <li>42: FCTGLVYSVVRQRTDCLEDQLGRPIGKQPPDERTVQLGTUDRHLDWYALKKNH:</li> <li>44: STAKIGRGQ, YRSFARATHRFLEEDESSMLAKVDKH. WOTLHGDWYAKLKKV:</li> <li>44: STAKIGRGQ, YRSFARATHRFLEEDESSMLAKVDKH. WOTLHGDWYAKLKKV:</li> <li>44: STAKIGRGQ, YRSFARATHRFLEEDESSMLAKVDKH. WOTLHGDWYAKLKKV:</li> <li>44: STAGTAKLKRP, LKGLLGGUSOFOG QOELLARVNNDS. HYLHSSCLARIKQA:</li> <li>45: TYGGTALKRP, LKGLLGGUSOFOG QOELLARVNNDS. HYLHSSCLARIKQA:</li> <li>46: TYGGTAELKGPR, LGGLNGAFTRRFLEEDESSMLAKVDKH. WOTLHGDWYAKLKKV:</li> <li>47: VINATKSLKSDS. FRGLWAATHRFLEGOSSMLAKVDKH. WOTLHGDFWKKKKX:</li> <li>48: TYGGTAELKGPR, LGGLNGAFTRRFLEGOSSMLAKVDKH. WOTLHGDFWKKKKKV:</li> <li>49: TYGGTAELKGPR, LGGLNGAFTRRFLEGOSSMLAKVDKH. WOTLHGDFWKKKKKV:</li> <li>49: TYGGTAELKGPR, LGGLNGAFTRGNGYGNGAPSLAAISDPVDRATESSMARKUTEKLLQQ:</li> <li>40: ALELAR, KKGSEKLVAAITRRFLEGOSSMLAKVDKHLWYSLVSLVVLUKKEDQ:</li> <li>40: ALELAR, KKGSEKLVA</li></ul>	1:		Subfamily I (Fmu) N-terminal extension
<ul> <li>1:</li></ul>	1:		
1 MKKFSSKTIKAKNSVKMTALSTRAT ANLTLQVLDEGKSLSALTPEVQLSVAQCLP: 1	1 : MKKPSSKTIKAKNSVKMTALSTRAT ANL LUQUDEGKSLSALI PEVQLSVGAQ LP: 1 :		1:~~~~~~~QKLAADSIAAVAE.GRNLQDVLAQIRTAHPDLTAQENG:
<ul> <li>MKKQRNLRSMAQAVEQVVEQGQSLSVTLPPLQKVSDKXA:</li> <li>MKNTYNLRSTAAATSQVLDQQSLSAVLPPLQKVSDKXA:</li> <li>MKNTYNLRSTAAATSQVLDQQSLSAVLPPLQKVSDKXA:</li> <li>MKNTYNLRSTAAATSQVLDQQSLSAVLPPLQKVSDKXA:</li> <li>MKNTYNLRSTAAATSQVLDQQSLSAVLPPLQQKVSDKXA:</li> <li>MKKTSVRDT2LEALIKDEQVCSAVTSLLKSVKSNELSDQNRG:</li> <li>MKTSVRDT2LEALIKDEQVCSAVTSLLKSVKSNELSDQNRG:</li> <li>MKTSVRDT2LEALIKDEQVCSAVTSLLKSVKSNELSDQNRG:</li> <li>MKTSVRDT2LAVLEDVEVVO, AYSNLLLNEMMYKSELSENGRG:</li> <li>MKKNSNRCTLDVLDTTRQD, AYSNLLLNEMMYKSELSENGRG:</li> <li>MKKNSNRCTLDVLDVTNKUSHD, GFSNTVLNKALKGEETSKKG;</li> <li>MKKNSNRCTLDVLDVTNKUSHD, GFSNTVLNKALKGEETSKKG;</li> <li>MKKNSNRCTLDVLDVTNKUSHD, GYDTVLNKALKGEETSKKG;</li> <li>MKKNSNRCTLDVLDVTNKUSHD, GYDTVLNKALKGEETSKKG;</li> <li>MKSRCVERSKKINGAQMKKPIDNQ, LESSTLAALVGDHYT, RNAPHFVNN;</li> <li>ALODIAK GQRYLGS KHMLAQMIKKPIGNQ, LESSTLAALVGDHYT, RNAPHFVNN;</li> <li>ALODIAK GQRYLGS KHMLAQMIKKPIGNPQ, LESSTLAALVGDHYT, RNAPHFVNN;</li> <li>LLOBICFVCNUPREDTIAQUADRELGKRRTUHGISVENNILLT, REPYNANDG;</li> <li>LLOBICFVCNUPREDTIAQUADRELGKRRTUHGISVENNILLT, REPYNANDG;</li> <li>LLOBICFVCNUPREDTIAQUADRELGKRRTUHGISVENNILLT, REPYNANDG;</li> <li>LLOBICFVCNUPREDTIAQUADRELGKRRTUHGISVENNILLT, REPHNALAG;</li> <li>LLOBICFVCNUPREDTIAQUADRELGKRRTUHGISVENNILLT, REPHNALAG;</li> <li>LLOBICFVCNUPREDTIAQUADRELGKRRTUHGISVENNILLT, REPHNALAG;</li> <li>LLOBICFVCNUPREDTIAQUADRELKGKRVPHVINGCLGUILT, KKEANAVG;</li> <li>LLOBICFVCNUPREPTISKLLBYYTPFVK, NPQKVKPWUIQURELSLCONSRLEKSGRNATHG;</li> <li>LLOBICFTSKLLBYYTPFVK, RPQKVKPWUIQURELSLCONSRLEKSGRNATHG;</li> <li>LUTSUYTTSKKISSYTLAHYK, RPKUKPWUIQURELSLCONSRLEKSGRNATHG;</li> <li>LUTSUYTTSKKISSYTLAHYK, RPKUKPWUIQURELSLCONSRLEKSGRNATHG;</li> <li>LUTSUYTTSKKISSYTLAHYK, RPKUKPWUIQURELSLCONSRLEKANAVGLEANSTVOTNALSLAW;</li> <li>LUTSUYTTSKKISSYTLAHYK, RPKUKPWUIQURELSLCONSRLEKANAVGLEANSTVOTNKKKK;</li> <li>LUTSUYTTSKKISSYTLAHYK, RPKUKPKKWWUIQURELSLCONSRLEKANAVGLEANSTVOTNKKKKWX;</li></ul>	1:MKKQRNLRSMAQAVGQUVEQQQLSNTLPPLQKVDKKA: 1:MKKQRNLRSMAAAVGQUVEQQQLSNTLPPLQKVDKKA: 1:MKKTSVRDJLEATEQUIDQGSLSAULPELQKNSDKRA: 1:MKKTSVRDJLEATEQUIDGGSLSAULPELQKNSDKRA: 1:		
<ol> <li>MINTRADANULGSI AKAISOVLDQQQISLSAVLPELQKNISDK RA:</li> <li></li></ol>	1:MKNTYNLESTÄÄKÄSSULDQGQSLÄÄVLPELOKN ISDKORA: 1:		1:MKKFSSKTIKAKNSVKMTALSTRAINANLILQVLDEGKSLSALIPEVQLSVKAQLP:
1:MVRTANAANUIYUVDKGHSLSALPELQKNTSDK RA: 1:MVRTANAANUIYUVDKGHSLSALPELQKNTSDK RA: 1:MKTSYKRI LEALIKEOQO.AYSMLLLNEMMTKSELSEKGGR: 1:VVLLETIERVDKGG.AYSMLLLNEMMTKSELSEKGGR: 1:NKTSYKRI LEALIKEOQO.AYSMLLLNEMMTKSELSEKGGR: 1:NKTSYKRI LEALIKEOQO.AYSMLLLNEMMTKSELSEKGGR: 1:NKTSYKRI LEALIKEOQO.AYSMLLUNQLISKASAKRA: 1:NKTSYKRI LEALIKEOQO.AYSMLLUNQLISKASAKRA: 1:NKTSYKRI LEALIKEOQO.AYSMLLUNQLISKASAKRA: 1:NKTSYKRI LIJIAISED GENTYLNKALKEGEISSIKKG: 1:NKTSIL TULDVINDIFGND.AYANISLDRNLRDESISTVKG: 1:NKTSIL TULDVINNUSED GENTYLNKALKEGEISSIKKG: 1:NKTSIL TULDVINNUSED GENTYLNKALKEGEISSIKKG: 1:NKTSIL TULDVINNUSED GENTYLNKALKEGEISSIKKG: 1:NKTSIL TULDVINNUSED GENTYLNKALKEGEISSIKKG: 1:NKTSIL TULDVINNUSED GENTYLNKALKEGEISSIKKG: 1:NKTSIL TULDVINNUSED GINTVINKALKEGEISSIKKG: 1:NKTSIL TULDVINNUSED GINTVINKALKEGEISSIKKG: 1:NKTSIL TULDVINNUSED GINTVINKALKEGEISSIKKG: 1:NKTSIL TULDVINNUSED GINTVINNIS; 2: ALODIAKECQRYLGSIKHMIAQMIKKPIDNPQ.LESHILAALKCHMPT.RNAPHYVINS; 2: ALODIAKECQRYLGSIKHMIAQMIKKPIDNPQ.LESHILAALKCHMPT.RNAPHYVINS; 2: LLOEICKFVCRVLPREDOIIKKLIVKPLCGKKRIVHCUSVGNDM.KWTSIANDEN; 2: LLOEICKFVCRVLPREDOIIKKLIVKPLCGKKRIVHCUSVGNDM.KWTSIANDEN; 2: LLOEICKFVCRVLPREDOIIKKLIVKPLKGKKRIVHCUSVGNDM.KWTSIANDEN; 2: LLOEICKFTRULPOITSCICOLMARPMTGKQRVFHY IMVCIGUIT: HEPMALAG; 2: LUTEUVYTYAKKLITEWYLFPTVK.KPCKVDNVKNMI ILSKCILLADKVDRHPATNG; 2: LUTEUVYTYAKKLITEWYLFPTVK.KPCKVDNVKNMI ILSKCILLADKVDRHPATNG; 2: LUTEUVYTYAKKLITEWYLFPTVK.KPCKVDNVKNMI ILSKCILLADKVDRHPATNG; 3: LITEUVYTYKKKITESENYLANYK.KPKLIKKNACHMPSTCITALDKISTOPANNG; 3: LITEUVYTYKKKITESENYLANYK.KPKLIKKVMUKMSTGITALDKISTOPANNG; 3: LITEUVYTYKKKYTTPFVK.KPCKVDNVKNMI ILSKCILLADKVDRHPATNG; 3: LITEUVYTYKKKYTTPFVK.KPCKVDNVKNMI ILSKCILLADKVDRHPATNG; 3: LITEUVYTYKKKKYTYTPFVK.K.DKKVLNVGRMSTGITALDKISTOPANNG; 3: LITEUVYTYKKKYTYTPFVK,KPCKARGHMSTKVDYKNKKSTALLADKVLKKK; 2: TYEGATUKKYTYKYTTPFVK,KPCKYKNKKILLASKYKYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	1:MKNTYNLESTÄÄKÄSSULDQGQSLÄÄVLPELOKN ISDKORA: 1:		1:~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1 :	1:		1:AKNTYNLRSIMAKATSOVLDOGOSLSAVLPELOKNISDKORA:
1 :	1:		1: MNVRAAMANVLYLVVDKGHSLSSALPAAQQTVRPRCHA:
1:	1:		1:MKKTSVRDILEALIKLEONO.AYSNILLKSVIKSNELSDONRG:
1 :	1:		1:~~~~~~~~~~~~YVLETLERVDKGG.AYSNLLLNEMMTKSELSEKEGR:
<ul> <li>1</li></ul>	1 :RCK_LLVTEATEDG. AYINTALNQQLSNKALGAKERA: 1 :		1:VETARSLALAVIEDVFVNQ.AYSNTALNKHLKGSOLLAARKG:
1:RNENMENTER I VLDVTINKVLSHD. GFSHTVLINKALKGEETSSK KG: 1:	1:		1:~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1:	1:		1:SURVERSENSIVERSE
1:DDR.BRR: 1:MISARQLEFLIENDINGRD.SYTDVATDRALQKNPLSPPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPERR: 1:MISARQLEFLIENDING.SYTDVATDRALQKNPLSPERR: 1:VISARQLEFLIENDING.SYTDVATDRALQKNPLSPERR: 1:VISARQLEFLIENDING.SYTDVATDRALQKSTVATDRALQKSTVATS 1:VISARQLEFNISSERVISHING.SYTDVATDRALQKSTVATS 1:VISARQLEFNISSERVISHING.SYTDVATDRALQKSTVATS 1:VISARQLEFNISSERVISHING.SYTDVATDRALGKSTVATS 1:VISARQLEFNISSERVISHING.SYTDVATDRALGKSTVATS 1:VISARQLEFNISSERVISHING.SYTDVATS 1:VISARQLEFNISSERVISHING.SYTDVATS 1:VISARQLEFNISSERVISHING.SYTDVATS 1:VISARQLEFNISSERVISHING.SYTDVATS 1:VISARQLEFNISSERVISHING.SYTDVATS 1:VISARQLEFNISSERVISHING.SYTDVATS 1:VISARQLEFNISSERVISHING.SYTDVATS 1:VISARQLEFNISSERVISHING.SYTDVATS 1:VISARQLEFNISSERVISHING.SYTDVATS 1:VISARQLEFNISSERVISH 1:VISARQLEFNISSERVISH 1:VISARQLEFNISSERVISH 1:JISARQLEFNISSERVISH 1:JISARQLEFNISSERVISH 1:JISARQLEFNISSERVISH 1:	1:		
1:	1:		1:~~~~~~~~~~~~NVRSLAFDTIQDILNEG.AYSNLRINEVLSENELNAMEKA:
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<ul> <li>38 : ALODIAN SCORYLGSUKIMLAQMIKKPIDNPQ LESULAALVOHAT. KNAPHRVUNS</li> <li>38 : ALODIAN SCORYLGSUKIMLAQMIKKPIDNPQ LESULAALVOHAT. KNAPHRVUNS</li> <li>49 : LLOSIC SVCRULPRESOLTAQLUDKPLCGKKRIVHCULSURMISTLUT. RIPVIANDE</li> <li>51 : LLOSIC SVCRULPRESOLTARLUDKPLCGKRIVHCULSURMISTLUT. RIPVIANDE</li> <li>43 : LLOSIC SVCRULPRESOLTARLUDKPLCGKRIVHCULSURMISTLUT. RIPVIANDE</li> <li>43 : LLOSIC SVCRULPRESOLTARLUDKPLCGKRIVHCULSURMISTLUT. RIPVIANDE</li> <li>44 : LLOSIC SVLRULPOESKI KINDORPLKGKORVYHV IMVGLVOLINT. SUPPHALAS</li> <li>57 : LPTEVYSTESKI LESUTENCE DENKELVORPLKGKORVYHV IMVGLVOLINT. SUPPHALAS</li> <li>58 : LLTELVYSTESKI LESUTENPEKI. NPOKVKPVULUKLSLVORSULEKGORVALINT.</li> <li>44 : LLTELVYSTESKI LESUTENPEKI. NPOKVKPVULUKLSLVORSULEKGORVALINT.</li> <li>45 : LUTELVYSTESKI LESUTENPEKI. NPOKVKPVULUKLSLVORSULEKGORVALINT.</li> <li>46 : LUTELVYSTESKI LESUTENPEKI. NPOKVKPVULUKLSLVORSULEKGORVALINT.</li> <li>47 : LPTELVYSTESKI LESUTENVENTERVK. NEOKVPNVULUKLSLVORSULEKGORVALINT.</li> <li>48 : LITELVYSTESKI LESUTENVENTERVK. NEOKVPNVULUKLSLVORSULEKGORALINT.</li> <li>49 : LTELVYSTESKI LESUTENVENTERVK. NEOKVPNVULUKSLVORSUKUTESKOTTELKSTORALINT.</li> <li>40 : LPTELVYSTESKI LESUTENVENTELK. KEPK. JPARMULLINT.</li> <li>41 : LTELVYSTESKALLESUTENVENTELK. KEPK. JPARMULLINT.</li> <li>42 : FUTELVYSTESKI LESUTENVENTELK. KEPK. JPARMULLINT.</li> <li>43 : FFKLUVNEVKRKELLOMYINOLLKKK. DIPPAVAVALERKAGACILENNSKEYVALSKASALT.</li> <li>44 : LTELVYSTEKKRYSTED LI ISSEVYKKKI. AWVROLLWASIKVILENNSKEYVAVKKKY.</li> <li>45 : AGESTAKIGRGO. YRSFARATIGRE FEBEREKLAASCK KDDVAKHNILLEWAYLKNH:</li> <li>46 : LITELVYSTERKELLOMYINOLLKKK. DIPPAVAVALERKAGACILENNSKEYVAVKASALT.</li> <li>47 : VERAVKRYRORTEDCLEGUGDRIGKOPPDERRIVOLUKKKKV.</li> <li>48 : INTAKNLOLOS. FOGLVAATIGRE HEBEDSILAASCK KDDVAKHNLELWAYLKNH:</li> <li>49 : TEGSTAKIGRGO. YRSFARATIGRE HEBEDSILAASCK KDDVAKHNLELWAYLKNH:</li> <li>40 : LESTAKIGRGO. YRSFARATIGRE HEBEDSILAASCK KDDVAKHNLELWAYLKNH:</li> <li>41 : LITTKKILGK, SGASTASIASKA, KUKKKKKKKKK, SAVKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK</li></ul>	<ul> <li>38 : ALODIAYRCQRYLGSUKHMIAQMLKKPIDNPQESULAALVOHNT.RNAPHRVUNS</li> <li>38 : ALODIAYRCQRYLGSUKHMIAQMLKKPIDNPQESULAALVOHNT.RNAPHRVUNS</li> <li>38 : ALODIAYRCQRYLGSUKHMIAQMLKKPIDNPQESULAALVOHNT.RNAPHRVUNS</li> <li>38 : LLODICYCRVLPRDQII AQLVDKPLCGKKRIVHCLLSURMNEILHT.RIPVTANTDS</li> <li>38 : LLODICYCRVLPRDQII KKLVDKPLKKKRIVHCLLSURMNEILHT.RIPVTANTDS</li> <li>38 : LLODICYCRVLPRDQII KKLVDKPLKKKRIVHCLLSURMNEILHT.RIPVTANTDS</li> <li>38 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>39 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>39 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>39 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>31 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>31 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>31 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTYLSIS KORAATHS</li> <li>31 : LUTSUVYTISTIKKI JOHNYK KALVENYK KARVARAVGULURSI KORAATHS</li> <li>32 : LUTSUVYTVSKI SUSAYLAHYK. DRDKLDKWYYULLKSSCOUTYLDKYGVANATHS</li> <li>33 : FUTSUVYTVSKI SUSAYLAHYK. NDRKLKVVULLKSSCOUTYLDKYGVANATHS</li> <li>34 : LUTSUVYTVSKI SUSAYLAHYK. NDRKLKVNURSI KOVULDKANAV I SAAPOS</li> <li>35 : LUTSUVYTVKKYTDPYKKYNDLKKKK. DRDKLKMVNURSI KOVULDKVYTANNI SAAPOS</li> <li>42 : FFGLUVYTVKKYTDPYKKPVKTKI KL INKUNKYNNURSI KOVULDKVANAYLKNH:</li> <li>55 : ANESIAKIGRQ, YRSFAKAUERFLEBERKLAASCKKDDVAKHNLEU WAYLKNH:</li> <li>56 : MESIAKIGRQ, YRSFAKAUERFLEBERKLAASCKKDDVAKHNLEU WAYLKNH:</li> <li>57 : SAESIAKIGRQ, YRSFAKAUERFLEBERKLAASCKKDDVAKHNLEU WAYLKNH:</li> <li>58 : INTAKNLOLOS, FOGUNAVUSRUERFLEBEVKLAASCKKDDVAKHNLEU WAYLKNH:</li> <li>59 : AGEIAKIGRQ, YRSFAKAUERFLEBERKLAASCKKDDVAKHNLEU WAYLKNH:</li> <li>50 : INTAKNLOLOS, FOGUNAVUSRUERFLEBEVKLAASCKKDDVAKHNLEU WA</li></ul>		1:SYTDVAIDRALOKHPLSPPERR:
<ul> <li>38: ALODIAY CORVLGS KHMLAOMLKKPIONPO. LESS LAALKOHMT. KNAPHRVINS</li> <li>38: ALODIAY CORVLGS KHMLAOMLKKPIONPO. LESS LAALKOHMT. KNAPHRVINS</li> <li>49: LLODICE VCRULER BOI TAQUUKKPIONPO. LESS LAALKOHMT. KNAPHRVINS</li> <li>43: LLODICE VCRULER BOI TAQUUKKPIONPO. LESS LAALKOHMT. KNAPHRVINS</li> <li>43: LLODICE VCRULER BOI TAQUUK KURKPIONPO. LESS LAALKOHMT. KNAPHRVINS</li> <li>44: LLODICE VCRULER BOI TAQUUK KURKPIONPO. LESS LAALKOHMT. KNAPHRVINS</li> <li>43: LLODICE VCRULER BOI TAQUUK KURKPINSKI KURGUKULET. KIEPHALAG</li> <li>44: LLODICE VLSULPOUKLOULMARPHTGKORVERH LILVCIVOLSKI. K. ESEPHALAG</li> <li>51: LLODICE VLSULPOUKLOULMARPHTGKORVERH LILVCIVOLSKI. K. ESEPHALAG</li> <li>51: LLODICE VLSULPOUKLOULMARPHTGKORVERH LILVCIVOLSKI. K. ESEPHALAG</li> <li>51: LLODICE VLSULPOUKLA DYMLKPETN. KPOKVERVULUKLSKOKDEN KIESL KURDAATHS</li> <li>51: LLODIVTYTARKLITENYISHTE. DROLDSKILVUL HSACKIERALVGE</li> <li>44: LLTDEVYTYSKEL DRYLAHVK, DROLLKKK PAAKMELLITTIOULSKEK KERKAVKNIST</li> <li>45: LFTELVYSTVSKKALLENYITIPLIK. KERK PAAKMELLITTIOULSKEK KERLANST</li> <li>46: LVTDIVYTYKKKSEL DYMINOLKKK DIPPA KNARKALDT KUNKPANNE STAVEN SAVEN AVKS</li> <li>41: SFFRELWEV KURKSEL DYMINOLKKK DIPPA KNARKALGLENNSKEY AVS VIS</li> <li>42: FCTELVYTVRVRORT DICLEBOLGDRPIGKOPPDERRIVOLUK KUNKILLEW VAYLKNH:</li> <li>51: ALESIAKIGRGO, YRSFANALLER FLEEREKLAASCK KDDVAKHNL LLWWAYLKNH:</li> <li>95: ALESIAKIGRGO, YRSFANALLER FLEEREKLAASCK KDDVAKHNL LLWWAYLKNH:</li> <li>96: THESIAKIGRGO, YRSFANALLER FLEEREKLAASCK KDDVAKHNL LLWWAYLKNH:</li> <li>97: ALESIAKIGRGO, YRSFANALLER FLEEREKLAASCK KDVAKHNL LLWWAYLKNH:</li> <li>98: TYESIKKLOGPR, LROLMANLER FLEEREKLAASCK KDDVAKHNL LLWWAYLKNH:</li> <li>99: THESIAKIGRGO, YRSFANALLER FLEEREKLAASCK KDDVAKHNL LLWWAYLKNH:</li> <li>99: THESIAKIGRGO, YRSFANALLER FLEEREKLAASCK KDVAKHNL LLWWAYLKNH:</li> <li>91: TYESIKLKOPR, LROLMANDAR KELESONDIASIKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK</li></ul>	<ul> <li>38 : ALODIAYRCQRYLGSUKHMIAQMLKKPIDNPQESULAALVOHNT.RNAPHRVUNS</li> <li>38 : ALODIAYRCQRYLGSUKHMIAQMLKKPIDNPQESULAALVOHNT.RNAPHRVUNS</li> <li>38 : ALODIAYRCQRYLGSUKHMIAQMLKKPIDNPQESULAALVOHNT.RNAPHRVUNS</li> <li>38 : LLODICYCRVLPRDQII AQLVDKPLCGKKRIVHCLLSURMNEILHT.RIPVTANTDS</li> <li>38 : LLODICYCRVLPRDQII KKLVDKPLKKKRIVHCLLSURMNEILHT.RIPVTANTDS</li> <li>38 : LLODICYCRVLPRDQII KKLVDKPLKKKRIVHCLLSURMNEILHT.RIPVTANTDS</li> <li>38 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>39 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>39 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>39 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>31 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>31 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTY.RIPHRALAS</li> <li>31 : LLODICYVLRILSOUMLINK MARPMTGKQRVFHY INVGI KOLTYLSIS KORAATHS</li> <li>31 : LUTSUVYTISTIKKI JOHNYK KALVENYK KARVARAVGULURSI KORAATHS</li> <li>32 : LUTSUVYTVSKI SUSAYLAHYK. DRDKLDKWYYULLKSSCOUTYLDKYGVANATHS</li> <li>33 : FUTSUVYTVSKI SUSAYLAHYK. NDRKLKVVULLKSSCOUTYLDKYGVANATHS</li> <li>34 : LUTSUVYTVSKI SUSAYLAHYK. NDRKLKVNURSI KOVULDKANAV I SAAPOS</li> <li>35 : LUTSUVYTVKKYTDPYKKYNDLKKKK. DRDKLKMVNURSI KOVULDKVYTANNI SAAPOS</li> <li>42 : FFGLUVYTVKKYTDPYKKPVKTKI KL INKUNKYNNURSI KOVULDKVANAYLKNH:</li> <li>55 : ANESIAKIGRQ, YRSFAKAUERFLEBERKLAASCKKDDVAKHNLEU WAYLKNH:</li> <li>56 : MESIAKIGRQ, YRSFAKAUERFLEBERKLAASCKKDDVAKHNLEU WAYLKNH:</li> <li>57 : SAESIAKIGRQ, YRSFAKAUERFLEBERKLAASCKKDDVAKHNLEU WAYLKNH:</li> <li>58 : INTAKNLOLOS, FOGUNAVUSRUERFLEBEVKLAASCKKDDVAKHNLEU WAYLKNH:</li> <li>59 : AGEIAKIGRQ, YRSFAKAUERFLEBERKLAASCKKDDVAKHNLEU WAYLKNH:</li> <li>50 : INTAKNLOLOS, FOGUNAVUSRUERFLEBEVKLAASCKKDDVAKHNLEU WA</li></ul>		·····································
<ul> <li>38. ALCOLAX CORYLGS KHMLAQMIKKPIGNPO. LESE LAALMCINET. SNAPHRVDRS :</li> <li>49. LLOBICRVCRUPREDITALOLADINELOGKKRIUHEN SURMNILLET. STOYMANDE :</li> <li>43. LLOBICRVCRUPREDITRLOODINARPHORKGRUPHY LINNGLUDILET. STOYMANDE :</li> <li>43. LLOBICRVUPREDITRLOODINARPHORKGRUPHY LINNGLUDILET. STOYMANDE :</li> <li>44. LLOBICRVLPOLEMCIQOLMARPHORKGRUPHY LINNGLUDILET. STOPMANDE :</li> <li>45. LLOBICRVLPOLEMCIQOLMARPHORKGRUPHY LINNGLUDILET. STOPMANDE :</li> <li>46. LUDENUY TLONKIADOYMIKPITN. KPOKVRPWILOURSLCKORDLEKZ CORALESE CONSLEXE CORALESE :</li> <li>47. LLOBICRY TLONKIADOYMIKPITN. KPOKVRPWILOURSLCKORDLEKZ CORALESE :</li> <li>48. LLDBIVY TLONKIADOYMIKPITN. KPOKVRPWILOUR RESLECTING ALCONG DAVING :</li> <li>49. LUDIVY TJESKLLEYY TYPFKK. K. POKVNPMVIL MASACLENICKYCHVING :</li> <li>40. LUTDUVY TVSKKLUEWY TYPFKK. K. POKVRPWILOUR RESLECTINGLKLEADHYDR :</li> <li>41. LUTDUVY TVSKKLUEWY TYPFKK. K. POKVRPWILOUR MASACLENICKYCHWING :</li> <li>42. LVTDUVY TVSKKLUEWY TYPLK, KERK . PNANNE :</li> <li>44. LUTDUVY TVSKKLUEWY TYPLK, KERK . PNANNE :</li> <li>45. LDTTVV TVSKKYT DYY LKPVKKYKIKI DYNANNE :</li> <li>46. LVTTVV VSKKALLEWY TYPLK, KERK DYNANNE :</li> <li>47. FTELVYE VVRRORT DOLI FOLGOR PEDRRIVOLOUR MAST OTHULKED STAPANS :</li> <li>48. FFRELWEWY WREELDWY INOLKKK DIPPAURA MAST OTHULKED STAPANS :</li> <li>49. FFRELWEWY WRORT DOLI FOLGOR PEDRRIVOLOUR MAST OTHULKENS :</li> <li>41. ETTELYY TVRRORT DOLI FOLGOR PEDRRIVOLOUR MAST OTHULKKENS :</li> <li>42. FOTELWY WRORT DOLI FOLGOR PEDRRIVOLOUR MAST OTHULKKKY :</li> <li>43. FFRELWEWY WRORT DOLI FOLGOR PEDRRIVOLOUR MAST OTHULKKKY :</li> <li>44. ETTELWY WRORT DOLI FOLGOR PEDRRIVOLOUR MAST OTHULKKKY :</li> <li>45. AVESTAKIGRO, YRSFAALTRRUE EQUEDLATID KNUCH MAST ONKKKYK :</li> <li>44. ETTELWY WRORT DOLI FOLGO OSELLAREST KDDVAKINI LLAWWAYLKKH :</li> <li>45. AVESTAKIGRO, SIGKUMANDER EDEDILATID WOTHED SUMKKLOKA :</li> <li>46. ANDTAKKLOKAS KERVONDING EDEVORALAREST SUMKKLOKA :</li> <li>47. FORKEKROR, PEGRKUMANDEN ONGERDELDOWAY NNAKKYOL SUMKKLOKA :</li> <li>46</li></ul>	38 : ALODIA: SCORYLGSE KHMLAQMLKKPIGNPO DESHLAAL COMPT. RNAPHAVNE : 99 : LLOGICK YCRVLPREGITAQUINKPLCKKRIVACULSURAPLIYE. BITYYMATDS : 99 : LLOGICK YCRVLPREGITAQUINKPLCKKRIVACULSURAPLIYE. BITYYMATDS : 91 : LLOGICK YCRVLPREGITAQUINKPLCKKRIVACULSURAPCIENT, BITYMATDS : 93 : LLOGICK YCRVLPREGITAQUINKPLCKKRIVACULSURAPCIENT, BITYMATDS : 93 : LLOGICK TLRULQUEWCIQOLMAR PMTGKQRTVHYDIAVGCTOILT. BITYMAALAS : 94 : LLTBGVY TTGALVLPOHWCIQOLMAR PMTGKQRVFHYDIAVGCTOILT. BITYMAALAS : 95 : LLTGTVY TY SKLI LWYN BITYPIK. KPGKVDMWKNULLBS & CHELDKITGRAALHS : 97 : LFTBTVY TT SKLI LWYN BITYPIK. KPGKVDMWKNULL BISTACIL LDKYS DHAVTMS : 98 : LLTGTVY TY ARKLD BYYT BYFK. KPGKVDMWKNULL BISTACIL LDKYS DHAVTMS : 94 : LUTGTVY TY ARKLD BYYT BYFK. KPGKVDMWKYNULLMS & CHELDKIT DHAVANS : 94 : LUTGTVY TY ARKLD BYYT BYFK. KPKKT INKI DKWINY LLMS & CHELDKIT DHAVANS : 94 : LUTGTVY TY ARKLD BYYT BYFKK KNIK I DKWINY BUMS STOTATILDKI BAHT TYN : 95 : LWESTVY TY KYKYS JDI I SKY KYKT INKI DKWI MY BUMS STOTATILDKI BAHT TYN : 95 : FRESIAKIGRGO, YR SFAATILFRUEREKLAASCK KDDVAKHNLELWWAYLKNH : 95 : ADESIAKIGRGO, YR SFAATILFRUEREKLAASCK KDDVAKHNLELWWAYLKNH : 96 : TUTTAKNLQLOS : FOGUNAVLERELBEQESMLAKVD . KH. WOTLHED MAVKLYKKKY 97 : TYEGATVLKRPO, LKGLINGVLG ROOQOELLARAYNNDS . HYLHSS LUTAR(XA) 98 : TUTTAKNLQLOS : FOGUNAVLERELBEQOSMLAKVD . KH. WOTLHED MAVKLYKKY 94 : TYEGATVLKRPO, LKGLINGVLG ROOQOELLARAYNNDS . HYLHSS LUTAR(XA) 95 : ADESIAKIGRGO, YR SFAATILFRUEREVLBERVDAAYLS KDTYLHSS LUTAR(XA) 95 : ADESIAKIGRGO, LKGLINGVLG ROOQOELLARAYNNDS . HYLHSS LUTAR(XA) 95 : ADESIAKIGRGO, LKGLINGVLG ROOQOELLARAYNNDS . HYLHSS LUTAR(XA) 95 : ADESIAKIGRGO, LKGLINGVLG ROOQOELLARAYNNDS . HYLHSS LUTAR(XA) 95 : ADESIAKIGRGO, LKGLINGVLG ROOGOELDAAY WOTLHED MYKLLQAS 95 : ADESIAKI		708090 100 110 120
<ul> <li>38 ALODIAX SCORYLGS KHMLAQMIKKPIGNPO. LESKILAALKUINKT. SNAPHRVINS :</li> <li>49 LLOBICRVCRUPREOITAQUADRPLOGKKRIUHGISCHAMITUT. STUYANDEJ:</li> <li>51 LLOBICRVCRUPREOITAQUADRPLOGKKRIUHGISCHAMITUT. STUYANDEJ:</li> <li>43 LLOBICRVCRUPREOITAQUADRPLOGKKRIUHGISCHAMITUT. STUYANDEJ:</li> <li>43 LLOBICRVCRUPREOITAQUADRPLOGKRIUHYIMMGLUDILIT. STUPHALAB :</li> <li>44 LLOBICRVTRLSOLDWLINKLMARPMTGKQRTHYIMMGLUDILIT. STUPHALAB :</li> <li>45 LLOBICRVCRUPREMIANCIAL SUCCEMARYDGKQRYHYIMMGLUDILIT. STUPHALAB :</li> <li>46 LLOBICRVTRLDONGLINKLMARPTGKQRYHYIMMGLUDILIT. STUPHALAB :</li> <li>47 LLOBICRVTRLPORTINKLMARPTGKQRYHYIMMGLUDILIT. STUPHALAB :</li> <li>48 LLDBIVYTTIONKIA DYMLKPFIN. KPOKVKPWIIOURESLCONSLEKSCORALHE :</li> <li>49 LLOBICYTALSKILLEYYTTPFVK. KPOKVNEWIIOURESLCONSLEKSCORALHE :</li> <li>40 LTDBIVYTTVARKLTEWYTSHFIE. DRODLDSWIYUILMSSLEWIDYDLKBCHAPTNN :</li> <li>41 LUBIVYTVSKRIJ SEWYILAHYK. DROKLDSWIYUILMSSLEWITYDLKDAHTNN :</li> <li>42 LVTBIVYTVSKRIJ SEWYILAHYK. DROKLDSWIYUILMSSLEWITYDLKDEAHTTNN :</li> <li>43 FUTALWYTVSKRIJ SEWYILAHYK. DROKLDSWIYUILMSSLEWITYDLKDEAHTTNN :</li> <li>44 FUTBIVYTVSKRIJ SEWYILAHYK. DROKLDSWIYUILMSSLEWITYDLKDEAHTTNN :</li> <li>45 FUTBIVYTVSKRIJ SEWYILAHYK. DROKLDSWIYUILMSSLEWITYDLCHAPHTNN :</li> <li>46 LUTBIVYTVSKRIJ SEWYILAHYK. NAURCHWNYILMTN :</li> <li>41 FUTBIVYTVKRYTDYLKPYKKKK JIPPAVRVARMACHILTNNSVDYNJUS :</li> <li>42 FUTBIVYTVRRYTDPLKPYKKKK DIPPAVRVARMACHILTNNSVDYNJUS :</li> <li>43 FUTSIKKKKSELDWYINOLIKKK DIPPAVRVARMACHILTNNSVDYNJUS :</li> <li>44 SETAKIGGQ, YRSFAALMERFLEEDESLALASCK KDDVAKINILLAWWAYLKNH :</li> <li>54 KESIAKIGRGO, YRSFAALMERFLEEDESLALASCK KDDVAKINILLEWWAYLKNH :</li> <li>54 KESIAKIGRG, YRSFAALMERFLEEDESLALID KN. WOTLHEDFLWKKKKX :</li> <li>102 TWGATKRDLKGLESCOOCOELLERAN. ASDA . KHLMAYKKKKKVAKKKXKXXXXXXXXXXXXXXXXXXXXXXXXXX</li></ul>	38 : ALODIA: SCORYLGSE KHMLAQMLKKPIGNPO DESHLAAL COMPT. RNAPHAVNE : 99 : LLOGICK YCRVLPREGITAQUINKPLCKKRIVACULSURAPLIYE. BITYYMATDS : 99 : LLOGICK YCRVLPREGITAQUINKPLCKKRIVACULSURAPLIYE. BITYYMATDS : 91 : LLOGICK YCRVLPREGITAQUINKPLCKKRIVACULSURAPCIENT, BITYMATDS : 93 : LLOGICK YCRVLPREGITAQUINKPLCKKRIVACULSURAPCIENT, BITYMATDS : 93 : LLOGICK TLRULQUEWCIQOLMAR PMTGKQRTVHYDIAVGCTOILT. BITYMAALAS : 94 : LLTBGVY TTGALVLPOHWCIQOLMAR PMTGKQRVFHYDIAVGCTOILT. BITYMAALAS : 95 : LLTGTVY TY SKLI LWYN BITYPIK. KPGKVDMWKNULLBS & CHELDKITGRAALHS : 97 : LFTBTVY TT SKLI LWYN BITYPIK. KPGKVDMWKNULL BISTACIL LDKYS DHAVTMS : 98 : LLTGTVY TY ARKLD BYYT BYFK. KPGKVDMWKNULL BISTACIL LDKYS DHAVTMS : 94 : LUTGTVY TY ARKLD BYYT BYFK. KPGKVDMWKYNULLMS & CHELDKIT DHAVANS : 94 : LUTGTVY TY ARKLD BYYT BYFK. KPKKT INKI DKWINY LLMS & CHELDKIT DHAVANS : 94 : LUTGTVY TY ARKLD BYYT BYFKK KNIK I DKWINY BUMS STOTATILDKI BAHT TYN : 95 : LWESTVY TY KYKYS JDI I SKY KYKT INKI DKWI MY BUMS STOTATILDKI BAHT TYN : 95 : FRESIAKIGRGO, YR SFAATILFRUEREKLAASCK KDDVAKHNLELWWAYLKNH : 95 : ADESIAKIGRGO, YR SFAATILFRUEREKLAASCK KDDVAKHNLELWWAYLKNH : 96 : TUTTAKNLQLOS : FOGUNAVLERELBEQESMLAKVD . KH. WOTLHED MAVKLYKKKY 97 : TYEGATVLKRPO, LKGLINGVLG ROOQOELLARAYNNDS . HYLHSS LUTAR(XA) 98 : TUTTAKNLQLOS : FOGUNAVLERELBEQOSMLAKVD . KH. WOTLHED MAVKLYKKY 94 : TYEGATVLKRPO, LKGLINGVLG ROOQOELLARAYNNDS . HYLHSS LUTAR(XA) 95 : ADESIAKIGRGO, YR SFAATILFRUEREVLBERVDAAYLS KDTYLHSS LUTAR(XA) 95 : ADESIAKIGRGO, LKGLINGVLG ROOQOELLARAYNNDS . HYLHSS LUTAR(XA) 95 : ADESIAKIGRGO, LKGLINGVLG ROOQOELLARAYNNDS . HYLHSS LUTAR(XA) 95 : ADESIAKIGRGO, LKGLINGVLG ROOQOELLARAYNNDS . HYLHSS LUTAR(XA) 95 : ADESIAKIGRGO, LKGLINGVLG ROOGOELDAAY WOTLHED MYKLLQAS 95 : ADESIAKI		38: ALODIAYSCORYLGSIKHMLAOMIKKPIDNPOLESILLAALYSLHYT. RNAPHEVVNE:
58 : LIGORICE VCRVLPR DO LIKELUDKPLKGKTRIJHCHLLUGZKORLAM. KVGAHAADDS : 43 : LIGORICE VCRVLPR DO LIKELUDKPLKGKTRIJHCHLLUGZKORLAM. KVGAHAADDS : 43 : LIGORICE VGRTLSGUDMLINKIMARPMTGKGRTVHY LINVCLTORLAM. KI SPHALAG : 39 : LIGORICE TIERVLDOI BWCTOGLIANAPMTGKGRTVHY LINVCLTORLAM. KI SPHALAG : 39 : LIGORICE TIERVLDOI BWCTOGLIANAPMTGKGRTVHY LINVCLTORLAM. KI SPHALAG : 30 : LIGORICE TIERVLDOI BWCTORLAMPMTGKGRTVHY LINVCLTORLAM. RUPHALAG : 44 : LITDEUVYTTORINIA DYMLKPFTN. KPGKVDRWKNUT LINSE VGENLIGDTOD HAVTNS : 21 : LITDEUVYTTORINIA DYMLKPFTN. KPGKVDRWKNUT LINSE VGENLIGDTOD HAVTNS : 24 : LITDEUVYTTORINIA DYMLKPFTN. KPGKVDRWKNIG LINSE VGENAVING : 38 : LITDEUVYTTORINIA DYMLKPFTN. KPGKVDRWKNIG LINSE VGENAVING : 40 : LITDEUVYTTORINI DE DYMLHYKK. DRIKLDKWYYULLMSE VGENTELDKIE DFANDS 20 : LITDEUVYTTKKKYST DI LI SKYVKYKTINKI DKENVUNDKRSTNO YVILDKVDRWHTI INS 21 : FFREIDVYDVRVRKKELLDWYTNDLIKKK DIPPA URVA BWGARGLE HNSVEDYNAVSE 22 : FCTBLVVTVRVRVRKKELLDWYTNDLIKKK JAVRQLUWASTNO YVILDKVDRWHTI NS 23 : FFREIDVRVVRVRRKELLDWYTNDLIKKK DIPPA URVA BWGARGLE HNSVEDYNAVSE 24 : FCTBLVTVVRVRVRRKELLDWYTNDLIKKK MOTORDUNG LIWWAYLKNH: 55 : ADESTAKIGRGO, YRSFARATURR FLEEDERLAASCK KDDVAKHNL LLWWAYLKNH: 108 : INTAKNLOLOS. FOGLMAATURR FLEEDERLAASCK KDDVAKHNL LLWWAYLKNH: 102 : TVEGATAKRPO, LKGLINGULG FOGOQUELLERAV NNDS. HYLHS SCHARKKKVE 102 : TVEGATAKRPO, LKGLINGULG FOGOQUELLERAV NNDS. HYLHS SCHARKLOKA 102 : TVEGATAKRPO, LKGLINGULG FOGOQUELLERAV NNDS. HYLHS SCHARKLAGA 96 : ADEGKRGN, PGIGKFUNGULAR DO GOGQUELLERAV NNDS. HYLHS SCHARKLAGA 101 : ADEGKRER, PGIGKFUNGULAR OF MORAPSLAAISDPUDRLATEISMRCHTKSMSKLLLQER 102 : ADEGAKRGN, PGIGKFUNGULAR DO SOORDEDDMAY SNNAGKYGHS STIEKLLQEA 103 : AWELAK, KKSSEKLWAATUR INEDGEWORDDISI KRINKRNSTAYSL WYD VAKLLEE 104 : AMELKKR, KKSSEKLWAATUR INEDGEWORDDISI KRINKRDSTAYSL WYD VAKLLEE 17	58 : LIGETCREVCRVLPROSQIEKRLÜKKPLKGKTRIVHCHLUGEKGILM. RVSAHAADD : 33 : LLOGETCRURTLSGIGMLINKLMARPMTGKGRYFHUIDVGLYGILM. RUSPHALAS : 33 : LLOGETCRURTLSGIGMLINKLMARPMTGKGRYFHUIDVGLYGILM. RUSPHALAS : 39 : LIGETCRURTLSGIGMLINKLMARPMTGKGRYFHUIDVGLYGILM. RUSPHALAS : 39 : LIGETCRURTLSGIGMLINKLMARPMTGKGRYFHUIDVGLYGILM. RUSPHALAS : 30 : LIGETCRURTLSGIGMLINKLMARPMTGKGRYFHUIDVGLYGILM. RUSPHALAS : 30 : LIGETCRURTLSGIGMLINKLMARPMTGKGRYFHUIDVGLYGILM. RUSPHALAS : 30 : LIGETCRURTLSGIGMLINKLMARPTGKGRYFHUIDVGLYGILM. RUSPHALAS : 30 : LIGETCRURTLSGIGMLINKLMARPTGKGRYFHUIDVGLYGILM. RUSPHALAS : 31 : LUTELVYTLSGIGMLINKLLGAYMERPTN. NEOKVNEWYTOLURSSY GULDKSSYGALHDYTOPHYNNS : 32 : LUTELVYTTVARKLIGSYTIATPYK K PQKVDNWKNULI SSYGALHDYTOPHYNNS : 33 : LUTETVYTTVKRKISELDSYTIATPUK K KEPK . PWARMELLDTTOPILMEN HISAGOR : 40 : LYTETYY GTVKRKYTEDFILSK. KEPK . PWARMELLDTTOPILMEN HISAGOR : 40 : LYTETYY GTVKRKYTEDFILSK. KEPK . PWARMELLDTTOPILMENSTOPYN LDKYTANDE : 41 : GYDETYY GTVKRKYTEDFILSK. KEPK . PWARMELLDTTOPILMENSTOPYN LDKYTANDE : 42 : FCTELVYGTVKRKYTEDFILKRLERELSERKLASCK KDDVAKHNLELWWAYLKNH : 53 : AMESIAKIGRGQ . YRSFARAULERELSEREKLASCK KDDVAKHNLELWWAYLKNH : 54 : FCTELVYGTVKRKTDDFILKRUERELSEGELGANDA WOTLHEDLINKLKKV : 54 : FUETXKLSSS . FRGUNAVLERELSEGESMLAKVD WOTLHEDLINKLKKV : 54 : TUEGATVLKRPQ . LKGLINAULERELSEGESMLAKVD WOTLHEDLINKLKKV : 54 : TUEGATVLKRPQ . LKGLINAULERELSEGESMLAKVD		
<ul> <li>43:LLOBECREVERTLSOEDMETNKELMARPMTGKQRTYHYEDMVGENCHLFT. ELEPHALLAG:</li> <li>43:LLOBECREVERTLSOEDMETNKELMARPMTGKQRTYHYEDMVGENCHLFT. ELEPHALLAG:</li> <li>44:LLODECRETERULPOLTANCIQOLMARPMTGKQRVFHYEDMVGENCHLFT. ELEPHALLAG:</li> <li>51:LLOBECRETERULPOLTANCIDOQUMARPMTGKQRVFHYEDMVGENCHLFT. ELEPHALLAG:</li> <li>44:LLTBUVENTGALRULPARTHADUMEKPEIN. KPOKVKPWI LOURESLYONDHLEKEGRAATHG:</li> <li>37:LLTBUVENTGALRULPARTHADUMEKPEIN. KPOKVKPWI LOURESLYONDHLEKEGRAATHG:</li> <li>37:LLTBUVENTGALRULPARTHADUMEKPEIN. KPOKVDNWUNUL ILSEVOLDELDKEGRAATHG:</li> <li>37:LLTBUVENTGALRULPARTHADVKI DRVKLKPVI LUDLSKEYUHLMASCHLFREDHAVTNG:</li> <li>38:LLTBUVENTSKKALLEMYTTPPLK. K.POKVKWYY LUMESLYOTAULDKEBAPHAVING:</li> <li>38:LLTBUVENTSKKALLEMYTTPLEK. KEPK. PMARMELLITTYOVTEMEKMETSATOR</li> <li>40:LLTTUVETVKRYKSTDI LISKFYKTKINKIKKRVLNWURMSTVOTRULDKIBOPANTNS:</li> <li>40:LLTUVETVKRYKSTDI LISKFYKTKINKIKKVL. ADVARMEMASTVOTRULDKIBOPANTNS:</li> <li>40:LLTUVETVKRYKSTDI LISKFYKTKINKIKK. DIPPAVRVARMAACOLLENNSVEDVANUS;</li> <li>41:ENTUVETVKRQRTHDELLENGULGRPIGKOPPDERRIVOLOURALDOHAANNSVEDVANUS;</li> <li>42:FFEBUVEVVRVQRREELDOWINOLLEKK. DIPPAVRVARMAACOLLENNSVEDVANUS;</li> <li>42:FFEBUVEVVRVQRTMOLLERELBEREKLAASCK. KDDVAKHNLELMWAYLKNH:</li> <li>51:AVESIAKIGRGO, YRSFANATURFELGEREKLAASCK. KDDVAKHNLELMWAYLKNH:</li> <li>52:AVESIAKIGRGO, YRSFANATURFELGEDSILAIDD. KN. WOTLHEDEVNKLKKV:</li> <li>17:VMATKSLKSDS, FROLMAVLERELBEQESMLAKVD. KH. WOTLHEDEVNKLKKV:</li> <li>12:TYEGATVLKRPO, LKGLINGULSOFOOGOGELLERAN. ASDA RVHESLEMAXAAA</li> <li>21:TWEGATVLKRPO, LKGLINGULSOFOOSOOUELLERAV. NNDS. HYLHSSCHARTKOA:</li> <li>21:TWEGATVLKRPO, LKGLINGULSOFOSOOUELLERAV. NNDS. HYLHSSCHARTKOA:</li> <li>33:AVEIAKHGH.KGIASFMOSULBISOFOSIDAIDPVDIATESINGRVDIAKKLAASS</li> <li>34:AVEIAKINGH.KGIASFMOSULBISOFOSIDAIDPVDIATESINGRVDIAKKLAASS</li> <li>34:AVEIAKINGH.KGIASFMOSULBISOFOSIDAIDPVDIATTESINGRUKKASSLKDAV</li> <li>34:AVEIAKINGH.KGIASFMOSULBISOFOSIDAIDPVDIATTESINGRVDIAKKLAASS</li> <li>34:AVEIAKINGH.KGIASFMOSULBISOFOSIDAIDPVDIATTESINGRVDIAKKLAASS</li> <li>34:AVENGRIKKGAEKPUNGUNGTAROOPTASIKRINK</li></ul>	43 : LICEECE VIETLSOLUMLINKIMARPHTGKORTYHYLINVGINGILGT. KISPHALAS: 43 : LICEECE VIETLSOLUMLINKIMARPHTGKORTYHYLINVGINGILGT. KISPHALAS: 43 : LICEECE ALRYLER KUTANOLDKYLKGROVFHYLINGGINGILGT. KISPHALAS: 53 : LICEEN ALRYLER KUTANOLDKYLKGROVFHYLINGGINGILGT. KISPHALAS: 44 : LITEEVYTTONKIALGYYLKPFIN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 57 : LPTEUYTTISKLIPYYTTPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 42 : LUTEEVYTTYSKLIPYTTISPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 43 : LUTEIVYTTYSKLIPYTTISPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 44 : LITEIVYTTYSKLIPYTTISPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 45 : LUTEIVYTTYSKLIPYTTISPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 46 : LUTEIVYTTYSKLIPYTTISPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 47 : LUTEIVYTTYKKNISTISPYLK. KEPK. PWARMULLMITTOVI LMKSTOTTADKYSDHATAS: 40 : LUTEIVYTYKKNISTISPYLK, KEPK. PWARMULMITTOVI LMKSTOTTADKYSDHATAS: 40 : LUTEIVYTYYKKKITDSYLKPYNTKIK AWKOLLMASIYOTRYLDKYSDYAVSS: 42 : FOELVYGYVKKELLOWYINOLLKK. DIPPAVRVALMASYOTAVLS: 42 : FOELVYGYVKKELLOWYINOLLKK. DIPPAVRVALMASYNUTYLDKWAYLKNI: 53 : ADESIAKIGRGO, YRSFANAUERFLIEREKLAASCK KDDVAKHNLELWWAYLKNI: 54 : INTAKNLOLOS. FOGUNAVLRRFLIEREKLAASCK KDDVAKHNLELWWAYLKNI: 52 : INTAKNLOLOS. FOGUNAVLRRFLIEREKLAASCK KDDVAKHNLELWWAYLKNI: 53 : INTAKNLOLOS. FOGUNAVLRRFLIEREKLAASCK KDDVAKHNLELWWAYLKNI: 54 : INTAKNLOLOS. FOGUNAVLRRFLIEREKLAASCK KDDVAKHNLELWWAYLKNI: 55 : ADESIAKIGRGO, YRSFANTORRHUEROLELAIDO KN. WOTLHED LUNKLKKV: 57 : WGGATVLKRPO, LKGLINOVLG OFOOQUELLERAV. NNDS. HYLHES LUARKAOA: 58 : INTAKNLOLOS. FOGUNAVLRRFLIEREVANAVCAV. SNNAGKYGHSS IUKLOKA: 59 : NEGTKELKOR, LGGINAVLG RUGOGOGOLDAY SNNAGKYGHSS IUKLOKA: 50 : AWEIGKRGN, PGIGKYMAVLFRIIEREVPTASISKKUTTESHED LYKEWAADA: 50 : AWEIGKRGNKKAEKFWANJER INGORAPSIAASISSINKLATEISHE LUKEWAADA: 50 : AWEIGKRGNKKAEKFWANJER INGONAPSIAASISSINKULATEISHE LUKEWAADA: 50 : AWEIGKRGNKKAEKFWANJER INGONAPSIAASISSINKLATEISHE LUKEWAADA: 50 : AWEIKK, RIGSSKUNAVLFRIERIEREFTIEREVPTISTKRNKKYSINKULOKAKLEDO; 50 : AWEIKK, RIGSSKUNAVLFRIERIEREFTIEREVPTISTKRNKYSINKUSINYSENSELLOKAYSISO		49: LLOBICFEVCRVLPRHEOILAOLVDKPLCGKKRIVHCHLSVRMNEILWT, RTPVYMAVDD:1
<ul> <li>43:LLCBCCCVVLRTLSQEDMLTNKLMARPMTGKQRTYHYLDMVGLWCLLGT. ELEPHALAG:</li> <li>43:LLCBLCEVTEVLPOURCEQOLMARPMTGKQRTYHYLDMVGLWCLLGT. ELEPHALAG:</li> <li>44:LLCBLCEVTEVLPOURCEQOLMARPMTGKQRVFHYLDMVGLWCLLGTHT. ELEPHALAG:</li> <li>44:LLTBLVYGTWSRLLEVLANDLMDKPLKGRQVFHYLDMVGLWGLWCLEKLESTGRAATHG:</li> <li>37:LLTBLVYGTWSRLLEVLANDLMDKPLKGRQVFHYLDWLGLWGLWGLWGLWGDHAVTNG:</li> <li>44:LLTBLVYGTWSRLLEVLYDFPVK, KPQKVDNWKNNLLESLWOHDLEKTGDRAATHG:</li> <li>37:LLTBLVYGTWSRLLEVYJTPPVK, KPQKVDNWKNNLLESLWOHDLEKTGDRAATHG:</li> <li>37:LLTBLVYGTWSRLLEVYJTPPVK, KPQKVDNWKNNLLESLWOHDLDKLEKTGDRAATHG:</li> <li>38:LLTBLVYGTWSRLLEVYJTPPVK, KPQKVDNWKNNLLESLWOHDLDKLEDHAVTNG:</li> <li>38:LLTBLVYGTWSRLLEVYJTPPLK, KPQKVDNWKNNLLESLWOHDLDKGBAHTINN:</li> <li>40:LLTBLVYGTWSRKISDEWYLAHVWK, DRDKLDKWYYULMSSLWOHNLDKKBOFANTNG:</li> <li>40:LLTBLVYGTWSRKISDEWYLAHVWK, DRDKLDKWYYULMSSLWOHNLDKKBOFANTNG:</li> <li>40:LLTBLVYGTWSRKISDEWYLAHVWK, DRDKLDKWYYULMSSLWOHNLDKWHSTSATPANTNG:</li> <li>40:LLTBLVYGTWSRKISDEWYLAHVWK, DRDKLDKWYYULMSSLWOHNLDKWHSTSATPANTNG:</li> <li>40:LLTBLVYGTWRRYGTUDCLEWYTNOLEKKK DIPPARRAFGLWGSTWCTWLDKWMAYLKNH:</li> <li>8:FFRELWRVVRRQRTDCLEGUGDRPIGKOPPDERRTVQGLWOHRASKOLLENNSVDYANUSG:</li> <li>42:FCTBLVYGTWRRQRTDCLEGUGDRPIGKOPPDERRTVQGLWOHRASKOLLENNSVDYANUSG:</li> <li>42:FCTBLVKTVKRQRTDCLESKLUGARFLUEGESMLAKVDKHWQTLHEDEVWKLKKV:</li> <li>17:VMARKSLKSDS, FRELMAVLERRFLEEQDSLIAIIDKNWQTLHEDEFWKLKKA:</li> <li>21:TWEGKKLKGR, KGLSFWSGUGSEDFRELDGANZSNNAGKYGHSSLUKLLQA:</li> <li>21:TWEGKKLKGR, EGLSFWSGUGSEVDSFDAIEDPVRLATETSHGEJUMWAALAGA</li> <li>34:ALLKRGH, KGLSFWSGUGSEVDSFDAIEDPVRLATTSHGEJUMWAALAGA</li> <li>34:EGKRRGN, GGLSFWSGUGSEVDSFDAIEDPVRLATTSHGEJUMWAALAG</li> <li>34:AELKKLR, KKSSEKLWAAULRINGESTANFDISTKRNKRDSTASISUTWLUKKKUAAULAKKUSSE</li> <li>34:AELKK, KKSSEKLWAAULRINGENDENSSELDEMTAXSISKURVELUKWSSLAWVYKSES</li> <li>34:AELKK, KRSSEKLWAAULRINGENSENDENTASSEKLUKANSELLDAWVYSLAWYNYKSE</li> <li>34:AELKK, KRSSEKLWAAULRINGENSENDENTASSEKLUKANSELLDAWVSLUKKEDS</li> <li>34:AELKK, KRSSEKLWAAULRINGENSENDENTASSEKLUKNKNSTANSELCHVYSLESSENTWSSEKLUKANVK</li></ul>	43 : LICEECE VIETLSOLUMLINKIMARPHTGKORTYHYLINVGINGILGT. KISPHALAS: 43 : LICEECE VIETLSOLUMLINKIMARPHTGKORTYHYLINVGINGILGT. KISPHALAS: 43 : LICEECE ALRYLER KUTANOLDKYLKGROVFHYLINGGINGILGT. KISPHALAS: 53 : LICEEN ALRYLER KUTANOLDKYLKGROVFHYLINGGINGILGT. KISPHALAS: 44 : LITEEVYTTONKIALGYYLKPFIN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 57 : LPTEUYTTISKLIPYYTTPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 42 : LUTEEVYTTYSKLIPYTTISPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 43 : LUTEIVYTTYSKLIPYTTISPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 44 : LITEIVYTTYSKLIPYTTISPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 45 : LUTEIVYTTYSKLIPYTTISPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 46 : LUTEIVYTTYSKLIPYTTISPYN. KPOKVDWVRNUTISISOLI LDKYSDHATAS: 47 : LUTEIVYTTYKKNISTISPYLK. KEPK. PWARMULLMITTOVI LMKSTOTTADKYSDHATAS: 48 : FFKELVNGVVRKELLDWYTNOLLKK. DIPPAVRVLRMSTOTTAULKSNSDOTAUSS: 40 : LUTEIVYTYVRRKTTDPTLKPYNTKKWARGULMSTOTTAULKSNSDOTAUSS: 42 : FCELVYTVRVRRTDOTLKPYNTKKWARGULMSTOTTAULKNNSDOTAUSS: 42 : FCELVYTVRVRRTDOTLKPYNTKKWARGULMSTOTTAULKNNSDOTAUSS: 42 : FCELVYTVRVRRTDOLLEQUGDPIGOPPDIRRTOGING WUNDKMSTOTAUSS: 42 : FCELVYTVRVRRTDOLLEQUGDPIGOPPDIRRTOGING WUNDKMSTOTAUSS: 42 : FCELVYTVRVRRTDOLLEQUGDRIGOPPDIRRTOGING WUNDKMSTOTAUSS: 42 : FCELVYTVRVRRTDOLLEQUGDRIGOPPDIRRTOGING WUNDKMSTOTAUSS: 42 : FCELVYTVRVRRTDOLLEQUGDRIGOPPDIRRTNOSICA SALANT: 53 : ADESIAKIGRGO, YRSFARATGRRHEREDKLAASCKKDDVAKHNLELWVAYLKNH: 54 : INTAKNLQLOS. FOGUNAVLRRFLEEQESMLAKVDKH. WQTLHEDTUNKLKKV: 57 : MGGTKLKNOG, LKGLINOVLG OFOQOELLATIDKN. WQTLHEDTUNKLKKV: 52 : TVEGATVLKRPO, LKGLINOVLG OFOQOELLARVNNDS. HYLHES LUARKAQA: 54 : MEETKELKOPR, LGLINOVLG OFOQOELLARVNNDS. HYLHES LUARKAQA: 54 : MEETKELKOPR, LGLINOVLG OFOQOENLARSSIN .SNAGKYGHSS ILKLOPA: 54 : MEETKELKOPR, LGLINOVLG OFOQOENLARSSIN .SNAGKYGHSSI LUKLOPA: 55 : AMEETKLKOP, LGLINOVLG OFOQOENLARSSIN SNAGKYGHSS LUKLOPA: 54 : AMEETKELKOPR, LGLINOVLG OFOQOENLARSSIN SNAGKYGHSSI LUKLOPA: 55 : AMEETKLKOP, LGLINOVLG OFOQOENLARSSIN SNAGKYGHSSI LUKLOPA: 56 : MELKKR, RKKSSKLUNAVLERTIESOPPTALSKRWRDISSI		
43:Licobock Tirkulpolewciaodian Rewigkowy Hybrid Moot Noi Hybrid Rewight 33:Licobock Tirkulpolewciaodian Korkawy Hybrid Host Korsen, Russharades 34:Licobock Tirkulpolemciaodian Korkawy Hybrid Host Korsen, Russharades 37:LFTBUVYTI SRKLLDHYIDTPFVK, KPOKVDNVKNULI LSUVOLHLDKVSDHVINS 42:LVTBUVYTI SRKLLDHYIDTPFVK, KPOKVDNVKNULI LSUVOLHLDKVSDHVINS 37:LFTBUVYTI SRKLLDHYIDTPFVK, KPOKVDNVKNULI LSUVOLHLDKVSDHVINS 42:LVTBUVYTI SRKLLDHYIDTPFVK, KPOKVDNVKNULI LSUVOLHLDKVSDHVINS 34:LTTBUVYTI SRKLLDHYIDTPFVK, KPOKVDNVKNULI LSUVOLHLDKVSDHVINS 43:LVTBUVYTI SRKLLDHYIDTPLK, KEPK, PWAKMULLDT VOLJMDKVH SANDA 44:LVTBUVYTVKNYIDTPILK, KEPK, PWAKMULLDT VOLJMDKVH SANDA 45:LVTBUVYTVKNYIDTPILK, KEPK, PWAKMULLDT VOLJMDKVH SANDA 40:LVTBUVYTVKNYIDTPILK, KEPK, PWAKMULLDT VOLJMDKVH SANDA 40:LVTBUVYTVKNYIDTPILK, KEPK, DRKLLKVWRGHWSIVUTRULDKASANDA 40:LVTBUVYTVKRYIDTPILK, KEPK, DRKLLKVYVULMSSIVUTRULDKISS 40:LTTBUVYTVKRYIDTPILKPUKKKK, DIPPAVRVA RMGAKGULZANSVEDY AUSS 42:FFCBUVYTVKRYRIDPILKPUKKKK, DIPPAVRVA RMGAKGULZANSVEDY AUSS 42:FFCBUVYTVKRYRIDSCLEQUGDRIGKOPPDERRITVGIOLWERLDOVEASANDT: 5:AMESIAKIGRGO, YRSFANAUGRITUSECENAKKD, KH. WOTHHDEYWKLKKKK 17:VMANKSLKSDS, FROLMANIERFUSECENLAASCK, KDDVAKHNIELWWAYLKNH; 6:TDNTAKNLOLOS, FOOLWAUHRRFUSECENLAASCK, KDDVAKHNIELWWAYLKNH; 6:TDNTAKNLOLOS, FOOLWAUHRRFUSECENLAASCK, SANDAVKKKV 2:TVEGAIAIKRPQ, LKGLINGUNGFOOQOUSLLERAV, NND, HVLHSSLUKKKVQAA 2:TVEGAIVKRPQ, LKGLINGUNGFOOQOUSLLERAV, NND, HVLHSSLUKRLOKAA 2:TVEGAIVKRPQ, LKGLINGUNGFOOQOUSLLERAV, NND, HVLHSSLUKRLOKAA 2:TVEGAIVKRPQ, LKGLINGUNGFOOQOUSLLERAV, NND, HVLHSSLUKRLOKAA 2:TVEGAIVKRPQ, LKGLINGUNGFOOQOUSLLERAV, NND, HVLHSSLUKRLOKAA 2:TVEGAIVKRP, LKGLINGUNGFOOQOUSLLERAV, NND, HVLHSSLURAKLAQAA 2:TVEGAIVLKPQ, LKGLINGUNGFOOQOUSLLERAV, NNDAKYGHSSLUKLLOKAA 2:TVEGAIVLKPQ, LKGLINGUNGFOOQOUSLLERAV, NNDAKYGHSSLUKLLDKAA 2:TVEGAIVLKPQ, LKGLINGUNGFOOQOUSLLERAV, NNDAKYGHSSLUKLLOKAA 2:TVEGAIVLKPQ, LKGLINGUNGFOOQOUSLLERAV, NNDAKYGHSSLUKLLOKAA 2:TVEGAIVLKPQ, LKGLINGUNGFOOQOUSTAAISTASLUVYVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	43 : LUCGINCTERTERVLPQERWCIQQLMARPMTGKQRVFHYDIAVGLYQLIINT. KIPPHALAF. 39 : LUCGINCTERTERVLPQERWCIQQLMARPMTGKQRVFHH DIJOSTYCISKA. STBAHAAVGS 39 : LUCGINCTERTERVLPQERMIANQLMAKPLKGKQRVFHH DIJOSTYCISKA. STBAHAAVGS 41 : LUTGINY GTLQKKLDIYTTPFK. KPQKVENVGLURSLYGH BELKSGORAL 37 : LPTGINY GTLQKKLDIYTTPFK. KPQKVENVGLURSLYGH BELKSGORAL 37 : LPTGINY GTLQKKLDIYTTPFK. KPQKVENVGLUSSKA. GRED FISHAVAG 38 : LPTGINY GTUGKKLDIYTTPLK. KPQKVENVGLUSSKA. GRED FISHAVAG 39 : LPTGINY GTUGKKLDIYTTPLK. KPK. PWAKMLLIGISYGLUGKGEND 30 : LPTGINY GTUGKKYKSTGDII SKYVKTKINKIDKVLNVGKSSTQTRI LDKTSDPAAVAG 40 : LVTGINY GTUGKKYKSTGDII SKYVKTKINKIDKVLNVGKSSTQTRI LDKTSDPAAVAG 41 : LVTGINY GTUGKKYKSTGDII SKYVKTKINKIDKVLNVGKSSTQTRI LDKTSDPAAVAG 42 : CTTGINY GTUGKYKYSTGDII SKYVKTKINKIDKVLNVGKSSTQTRI LDKTSDPAAVAG 43 : FFKSLVMCVVREELDWYINOLLKKK. JIPPAVRAJENGAGAGLEANSVDYAAVGS 42 : CTTGINY GTUKRYKRTICLIEQLGGRPIGROPPDERFUQGING RULDOVESSAUTT : 55 : AMESIAKIGGQ, YRSFAASIGERFUGESKLAASCK. KDDVAKHNIELWWAYLKNH: 39 : DNTAKNLGQS, YRSFAASIGERFUGESKLAASCK. KDDVAKHNIELWWAYLKNH: 30 : DNTAKNLGQS, YRSFAASIGERFUGESKLAASCK. KDDVAKHNIELWWAYLKNH: 30 : DNTAKNLGQS, FOGUNAUGERFUGESKLAASCK. KDDVAKHNIELWWAYLKNH: 30 : DNTAKNLGQS, FOGUNAUGERFUGESKLAASCK . NDDVAKHNIELWWAYLKNH: 30 : DNTAKNLGQS, FOGUNAUGERFUGESKLAASCK . NDDVAKHNIELWWAYLKNH: 30 : DNTAKNLGGS, FOGUNAUGERFUGESKLAASCK . NDDVAKHNIELWWAYLKNH: 31 : DNTAKNLGGS, FOGUNAUGERFUGESKLAASCK . NDDVAKHNIELWWAYLKNH: 32 : TUGGAIAIKRPO, LKGLINAUGERFUGESGUSAASCH . NNI. WOTLHESFUMKKKVS 32 : TUGGAIAIKRPO, LKGLINAUGERFUGESGUSAASCH . SNIAGKYGHS SUKLLQKA: 33 : AMELAKLR, KKOSEKUNAUGERFUGESGOPTGAIEDPWRLATETSHES DIKKLLQAA: 34 : AMEGIAKNGN, GGIKKVMAUGR SIGESOPSTAIEDPWRTYSKKSSI SUKLLQKAA: 35 : AMEGIAKNGN, KGGAKFUNAUGERSI SUGESOPSTAIEDPWRTALATETSHES DIKKENLAGA: 36 : AMEGIKKNGN, SUKKLLDAVGSR SIGNAPSIAAISTYSLVSI VLUVAKLKES; 37 : AGGIAKNGNKGAEKUNAUGERSI PORTASCH . SHNEEPKWETYSSE SUKLLDAA: 36 : AMEGIKKNGNKGAEKUNAUGERSI PORTASCH . SHNEEPKWETYSSE SUKLLDAA: 37 : AGGIAKNRGNKGAEKUNAUGERSI PORTASCH . SHNEEPKWETYSSE SUKLLDAA: 36 : AM		43: LEORECFEVERTLSOLEWLENKLMARPMTGKORTVHYLEMVGEVOLLAT, REPHEALAR 1
<ul> <li>39: LEGETCH ALRYLPRIERITANOLMDRPLKGNORVEHHEILWCT KORSEM, REGAMANGE 44: LEGETCH ALRYLPRIERITANOLMDRPLKGNORVEHHEILWCT KORSEM, REGAMANGE 43: LEGETCH ALRYLPRIERITANOLMDRPLKGNORVEHHEILWCT KORSEM, REGAMANGE 42: LÜTEUVNETT SKRLIDSNYIDTPIN, KPOKUNAWANILIISLUKULDRVGHANTME 42: LÜTEUVNETT SKRLIDSNYIDTPILK, KEPK, PMARMULINT KOVLPMDR LESTONAUVNE 33: FUTALVSVUSKALLESNYIDTPILK, KEPK, PMARMULINT KOVLPMDR LESTONAUVNE 43: FUTALVSVUSKALLESNYIDTPILK, KEPK, PMARMULINT KOVLPMDR LESTANDE 44: LÜTEUVNETVSKIS LESNYIDTPILK, KEPK, PMARMULINT KOVLPMDR LESTANDE 45: FUTALVSVUSKALLESNYIDTPILK, KEPK, PMARMULINT KOVLPMDR LESTANDE 46: LÜTEUVNETVKRYKISTIDI II SKEVKYKINKI DKAVLMVRHSIKOTVALDKNONDALTINE 54: FUTALVSVUSKALLESNYIDTPILKER LESKALK, DIPPA KVALRMARKOLLENNSGEVYMLANSE 42: FCTEIVNETVKRYKTOPYLKPFUKTKIK, LIPPA KVALRMARKOLLENNSGEVYMLANSE 42: FCTEIVNETVKRYKTOPYLKPFUKTKIK, LIPPA KVALRMARKOLLENNSGEVYMLANSE 42: FCTEIVNETVKRYKTOPYLKPFUKTKIK, LIPPA KVALRMARKOLLENNSGEVYMLSE 43: INTAKNLOLOS, FOGLMANDERFUESEKELLASCK, KDDVAKHNILL MVAYLKNH: 55: AUESIAKIGRGO, YRSFANDURFUESEKELLASCK, KDDVAKHNILL MVAYLKNH: 71: VMARKSLKSDS, FROLMANDERFUESEDELLARD, K.K., WOTLHEDEVMKLKKX 72: TUEGATULKRPO, LKGLINGUNG FOGOODELLAEFN, ASDA, RYLHSS LÜRKLKKA 73: TUEGATULKRPO, LKGLINGUNG FOGOODELLAEFN, SNAGKYGHSSEMKLLOEA 74: ELGKIRGH, KGIASTWOSTIASIOS FOGISFDAISEDILATID, SNAGKYGHSSEMKLLOEA 74: AUEIAKIRGH, KGIASTWOSTIASIOS FOGISFDAISEDILATIS VANKRDSISTASILVLDAAKKESE 75: AUEIAKIRGH, KGIASTWOSTIASIOSEDISTASIDEVDILATETSMENUTESISTEVLLAGA 71: AUEIAKIRGH, KGIASTWOSTIASIOSESPALEDPURKIKRDSISTASILVLDAAKKESE 77: AUGIAKIRGH, KGIASTWOSTIASIOSESPALEDPURSTANKENSISTASILVDVAKKLESE 77: AUGIAKIRGH, KGIASTWOSTIASIOSESPALEDPURTIATETSMENUTESISTEVLIAGA 77: AUGIAKIRGH, KGIASTWOSTASIOSTIASIONTIASIONDASIASIKYNYSVENUTENNINTKKIST 77: TUEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</li></ul>	39 : LIGETCY SARVLERE MITANOLHOK PLKGROVPHHETUOTTOS SM. ALBAHAVGE 44 : LIGETCY SARVLERE MITANOLHOK PLKGROVPHI TOUR SLOOTED SM. ALBAHAVGE 44 : LIGEUVY TI SAKLLERY TÜTPFVK. KPQKVRWVINULTI SLOOTED LEKTEDRAATHE 37 : PTBUVY TUSAKLLERY TÜTPFVK. KPQKVRWVINULTI SLOOTED LEKTEDRAATHE 38 : LIGETVY TUSAKLERY TÜTPFVK. KPQKVRWVINULTI SLOOTED LEKTEDRAATHE 38 : LIGETVY TUSAKLERY TÜTPFVK. KPQKVRWVINULTI SLOOTED LEKTEDRAATHE 38 : LIGETVY TUSAKLERY TÜTPFVK. KPQKVRWVINULTI SLOOTED LEKTEDRAVINE 38 : LIGETVY TUSAKLERY TITPLK. KEPK. PWARMLLET TOUTEDRATS AND 40 : LITETVY TUSAKLERY TITPLKK. KPK. PWARMLLET TOUTEDRATS FANDE 40 : LITETVY TUKAKY TIDPVIK PFVKKI.K AW ROLLMEST OF VLDKVORHTITNE 51 : FVRLUWS VVR SKALLERY TINDLEKK DIPPA KVALRKAAKGLERNS UPVILDKVORHTITNE 52 : FVRLUWS VVR ROLLKK DIPPA KVALRKAAKGLERNS UPVILDKVORHTITNE 53 : FVRLUWS VVR ROLLKK DIPPA KVALRKAAKGLERNS UPVILDKVORHTITNE 54 : SURSTAKLIGEQ, YRSPANATLERE HEEREKLAASCK KDDVAKHNILL WVAYLKNI: 55 : AVESIAKLIGEQ, YRSPANATLERE HEEREKLAASCK KDDVAKHNILL WVAYLKNI: 56 : SURSTAKLIGEQ, YRSPANATLERE HEEREKLAASCK KDDVAKHNILL WVAYLKNI: 57 : SURSTAKLIGEQ, YRSPANATLERE HEEREKLAASCK KDDVAKHNILL WVAYLKNI: 50 : INNAKKLKSD, ERGUNAVES REUE BOESHLAKVD . KH. WOTLHED FUNKLKKV 51 : WNATKSLKSD, FRGUNAVES REUE BOESHLAKVD . KH. WOTLHED FUNKLKKV 52 : TUEGALAIKRPQ, LKGLIN VLG PKO QOQUSLLATID KN. WOTLHED FUNKLKKX 53 : TUEGALAIKRPQ, LKGLIN VLG PKO QOQUSLLATU NNJ KYLHES LIKLLQAS 54 : AVESTKELKOPR, LGGLIN VLG PKO QOQUSLLATEV NNJ KYLHES LIKLLQAS 54 : AVESTKELKOPR, LGGLIN VLG PKO QOQUSLLATED NNJ KYLHES LIKLLQAS 54 : AVESTKELKOPR, LGGLIN VLG PKO QOS QOVELLER NDJ RYLHES LIKLLQAS 54 : AVESTKELKOPR, LGGLIN VLG FRO QOS QOVELLER NDJ RYLHES LIKLLQAS 54 : AVESTKELKOPR, LGGLIN VLG FRO AVEST SDEVORLATETSING UVKENDA 54 : AVESTKELKOPR, LGGLIN VLG FRO AVEST SDEVORLATETSING UVKENDAS 55 : AVESTKELKOPR, LGGLIN VLG SG OND SFDA IED PVRLISTES MAR LITELS AVE 56 : AVESTKELKOPR, LGGLIN VLG SG OND SFDA IED PVRLIST SMAR LITELS AVE 56 : AVESTKELKOPR, LGGLIN VLG SG OND SFDA IED PVRLIS		43: LLOPECFETERVLPOLEWCTOOLMARPMTGKORVFHYLLMVGLWOTIWT, EXTEPHNALAE: 1
44:LUTGLVYETLONKIALDYYLEPPIN. KPOKVDRAVIQLIRELEKTEDRALTHE 37:LETDLVYETTSEKLLDEYYLEPPIN. KPOKVDRAVKNUILSEVOLKLERTERLEKTEDRALTHE 32:LUTGLVYETYARKLLDEYYLEPPIN. KPOKVDRAVKNUILSEVOLTHELKTEDAVDE 33:LUTEIVYETYARKLLDEYYLEPPIN. KPOKVDRAVKNUILSEVOLTHELKTEDAVDE 43:FUTAIVXEVYSKALLEWYITPLLK. KEPK. PARMELLTTTOVLSHEKTEANTE 40:LUTEIVYETYKRKIILDEYYLEPPIK. KEPK. PARMELLTTTOVLSHEKTEANTE 40:LUTEIVYETYKRKIIDIISEVYLEYKKIKL. AWUROLUMASIKYVULDKUSHOFTALDKIEPANNE 3:FUTAIVXEVYSKALLEWYITPLLK. KEPK. PARMELLTTTOVLSHEKTEANTE 40:LUTEIVYETYKRKITDPLKREKKINICHEKTUNVERSIKYVULDKVDENHILINE 3:FUTAIVXEVYSKALLEWYITPLLK. KEPK. AWUROLUMASIKYVULDKVDENHILINE 3:FUTAIVXEVYKRKYTTDPLKRELEDVYINOLLKK. DIPPARVALKAGAYOLENNSVEDYSAVSE 4:LUTEIVYETYKRKYTTDPLERDYLTRELEEREKLAASCK. KDDVAKHNLELWVAYLKNH: 5:AGESIAKIGRO, YRSFARAJUREREEGESENLAKVD. KH. WOTLHEDEVNKLKKV: 7:VNATKSLKSDS. FOGLWAATUREREEGESENLAKVD. KH. WOTLHEDEVNKLKKV: 17:VNATKSLKSDS. FOGLWAATUREREEGESENLAKVD. KH. WOTLHEDEVNKLKKV: 2:TVEGATIVKRPQ.LKGLAGULGEFOGOOELLAIDD. KN. WOTLHEDEVNKLKKV: 2:TVEGATIVLRPQ.LKGLAGULGEFOGOOELLAIDD. KN. WOTLHEDEVNKLKKV: 3:AGEIAKIGH.KGIASPUNSUUS GEOGOELDIAIID. SNNAGKYGHSSILELLQEA 3:AGEIAKIGH.KGIASPUNSUUS GEOGOESELDAN SNNAGKYGHSSILTKLLQEA 3:AGEIAKIGH.KGIASPUNSUUS GEOGOESELDAISDVORLATEISHEDEVNELAKEADA 9:AGEIGKRGN. PGIGKFUNSUUS GEOGOESEDIAISDVORLATEISHEDEVNELAKUAALLED 1:AGEIAKUR, KKOSEKLWAATUR HEGONAPSIAISKENKENSIAYSILVYNINKKEND 1:AGEIAKUR, KKOSEKLWAATUR HEGONAPSIAISKENKENSIAYSILVYNINKKEND 1:AGEIAKUR, KKOSEKLWAATUR HEGONAPSIAISKENKENSIAYSILVYNINKKEND 1:AGEIAKUR, KKOSEKLWAATUR HEGONAPSIAISKENKENSKYSILVUNKKEND 1:AGEIAKUR, KKOSEKLWAATUR HEGONAPSIAISKENKENSKYSILVUNKKEND 1:AGEIAKUR, KKOSEKLWAATUR HEGONAPSIAISKENKENSKYSILVUNKKEND 1:AGEIAKUR, KINSKIKKALENYNENSENCHTYSEKLEPYNSEKLEDANTYKSENSKILLENKYRG 1:AGEIAKURGIKKGAEKFWAATUR FILEGEWPIASIKKENKENSKYSILVUNKKEND 1:AGEIAKURGIKKGAEKTWAATUR FILEGEWPIASIKKENKENSKYSILVUNKKEND 1:AGEIAKURGIKKGAEKTWAATUR FILEGEWPIASIKKENKENSKYSILVUNKKEND 1:AGEIAKURGIKKGAEKTWAATUR FILEGEWPIASIKKINKENSKYSILVUNKKEND 1:AGEIAKUR, KINSKIKKINKINKINSKYX	44 :LUTBLVY FTLONKIAL SYMEKPFIN. KPOKVDRWATCULRESS COMPACE CONVENTION 1 37 :LFTBUYFTISKLLDSYMEKPFIN. KPOKVDRWAKNILLESS COMPACE ADDRIGHT 37 :LFTBUYFTISKLLDSYMEKPFIN. KPOKVDRWAKNILLESS COMPACE ADDRIGHT 38 :LITETYYSTVSKILDSWTAHYVK. DRDKLDKWYYLLMSSKOGTYLDKISAN 40 :LTTBIYYSTVSKILDSWTAHYVK. DRDKLDKWYYLLMSSKOGTYLDKISAN 40 :LFTBIYYSTVSKILDSWTAHYVK. NRDKILNIVERSIKOGTYLDKISAN 40 :LFTBIYYSTVSKILDSWTAHYVK. NRDKILNIVERSIKOGTYLDKISAN 40 :LFTBIYYSTVKKKYTDDFYLKYKKK. DIPPAVRAL SKOGTYLDKISAN 40 :LFTBIYYSTVKRKYTDDFYLKYKKK. DIPPAVRAL SKOGTYLDKYSTVYNDKYTKK 42 :FCTBIYYSTVKRKYTDDFYLKYKKK. DIPPAVRAL SKOGTYLDKYSTVYNDKYTKK 42 :FCTBIYYSTVKRKYTDDFYLKYKKK. DIPPAVRAL SKOGTYLDKYKKAKOL SKOGTYLDK 42 :FCTBIYYSTVKRKYTDDFYLKYKKK. DIPPAVRAL SKOGTYLDKYKKAKOL SKOGTYLDK 42 :FCTBIYYSTVKRKYTDDFYLKYKKK. DIPPAVRAL SKOGTYLDK 42 :FCTBIYSTVKRKYTDDFYLKFKKK. DIPPAVRAL SKOGTYLDK 42 :FCTBIYYSTVKRKYTDDFYLKFKKK. DIPPAVRAL SKOGTYLDK 42 :FCTBIYSTVKRKYTDDFYLKFKKK. DIPPAVRAL SKOGTYLDK 42 :FCTBIYSTVKRKYTDDFYLKFKKK. DIPPAVRAL SKOGTYLDK 42 :FCTBIYSTVKRKYTDDFYLKFKKK. DIPPAVRAL SKOGTYLDK 42 :FCTBIYSTVKRKYTDDFYLKFKLDSK 55 :AMESIAKIGRG, YRSFANDLERFLDSCHGRUNG 50 : TMTSKNLDLOS. FOGUNALUS SKOGTYLDSK 51 : SKOGTYLKRKLDK 52 :TUEGATYLKRPQ. LKGLINGUE SKOGTYLDSK 52 :TUEGATYLKRPQ. LKGLINGUE SKOGTYLDSK 53 : AMESIAKIGH, KGLSTNGVLGFNG SKOGTYLDSK 54 : SKOGTKLKGH, KGLSTNGVLGFNG SKOGTYLDSK 56 : AMESIGKRGN, PGIGKTVNGVLGFNG SKOGTYLDSK 56 : AMESIGKRGN, PGIGKTVNGVLGFNG SKOGTYLDSK 56 : AMESIGKRGN, SGIGKTVNGVLGFNG SKOGTYLDSK 57 : AGEIAKURGNKKAGEKTVNG SLUS OFTSHPDIASIKKKNKKDSIAYSIG VLGVKKLEDQ 50 : AKKIAK. RINGSKKAGEKTVNG SLUS OFTSHPDIASIKKKNKNEDSTAYSIG VLGVKKLEDQ 57 : TWEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		39: LLOETCYCALRYLPREEMIANOLMDKPLKGKORVFHHLTLVGIVOESFM, RTEAHAAVGE:
<ul> <li>37: LFTBEVYETT SRKLLERYTTOPFVK. KPQKVDNVKNMLTIGELVELALDKVEDHAVTNE:</li> <li>42: LVTBUVKTVARVARLITENYISHTIE. DROLDSWLYVLLUKSAROIDREDET DEHAVUNG:</li> <li>43: FUTBUVKTVARVARLITENYISHTIE. DROLDSWLYVLLUKSAROIDREDET DEHAVUNG:</li> <li>43: FVTALVNETVSKKSLEENVITHYLLK. KEPK. PWARMULLETTVOILSMLAVHARITVNE:</li> <li>44: LVTETVVGTVKRYTTPLLK, KEPK. PWARMULLETTVOILSMLAVELSARDE:</li> <li>45: LVTETVVGTVKRYTTPLLK, KEPK. PWARMULLETTVOILSMLAVELSARDE:</li> <li>46: LVTETVVGTVKRYTTPLLK, KEPK. PWARMULLETTVOILSMLAVELSARDE:</li> <li>47: FVTALVNETVKRYTTPLLK, KEPK. PWARMULLETTVOILSMLAVELSARDE:</li> <li>48: FFKELVNETVKRYSTDLIISKYVKTKIK. ALPPAVRALMENSIKOILSANSVEDYANDS:</li> <li>42: FVTELVNETVKRYTTPLCE.EQUGDRFICKOPPDIRTTOICLEVERALDOFLASSARDT:</li> <li>5: AVESIAKIGRO, YRSFANAURRELEREKLAASCK. KDDVAKHNELLEWAAVLKNH:</li> <li>95: AVESIAKIGRO, YRSFANAURRELEREKLAASCK. KDDVAKHNELEWAAXLKKV:</li> <li>97: AVESIAKIGRO, YRSFANAURRELEREKLAASCK. KDDVAKHNELEWAAXLKKV:</li> <li>97: AVESIAKIGRO, YRSFANAURRELEREKLAASCK. KDVAKKNESIAVLUKKKVOANAURANIKASIASULOVAVLAKKVSIAVLUKKKVOANAURANIKERSIAVSULOVAVKKVSIAVLUKKKVOANAURANIKASIAVSULOVAVLAKKVSIAVLUKKKVOANAURANIKERSIAVSULOVAVLAKKVSIAVLUKKKVOANAURANIKASIAVSULOVAVLAKKVSIAVLUKKKVOANAURANIKASIAVSULOVAVLAKKVSIAVLUKKKVSIAVLUKKKVSIAVLUKKKVSIAVLUKKKVSIAVLUKKKVSIAVLUKKKVSIAVLUKKKVKSIAVLUKKKVSIAVLUKKKVSIAVLUKKKVS</li></ul>	37: LFTEVYETTSRKLLGTYYTTPFVK. KPQKVDNWKNHLISSYGLALDDK BOHWYTNE 22: LUTBUYYTVARKLTEWYTSHFTE. DRDCLDSWIYVLLHSANCERHDDTTCHWAVNE 23: LHTETVYFYSKT 15 EWYTSHFTE. DRDCLDSWIYVLLHSANCERHDDTTCHWAVNE 33: FUTALVXSVJSKALLSWYTTPLLK. KEPK. PWARMULLTTVOLEMDXVHISANCE 4: LWTETVYFVSKT 15 LIISKYVTTPLLK. KEPK. PWARMULLTTVOLEMDXVHISANCE 4: LWTETVYFVSKT 15 LIISKYVTTPLLK. KEPK. PWARMULLTTVOLEMDXVHISANCE 4: LWTETVYFVSKT 15 DIISKYVTTPLLK. KEPK. PWARMULLTTVOLEMDXVHISANCE 4: LWTETVYFVSKT 15 DIISKYVTTPLLK. KEPK. PWARMULLTTVOLEMDXVHISANCE 4: LWTETVYFVKKYSTDIISKYVTTPLLK. AMVGLMSTVC 10: LFTETVYFVFVKYTDPTVFVFVKTKI. AMVGLMSTVC 10: LFTETVYFVKVTRORTLCLEQLGORPTGROPPDEREVQCLCCFCLDOVFASANUT: 5: AMESIAKIGRQ, YRSFANJUGEREUSEREKLASCK. KDDVAKHNLELWWAYLKNH: 5: AMESIAKIGRQ, YRSFANJUGEREUSEREKLASCK. KDDVAKHNLELWWAYLKNH: 03: INTAKNLOLOS. FOGLVGAUGEREUSEREKLASCK. KDDVAKHNLELWWAYLKNH: 03: INTAKNLOLOS. FOGLVGAUGEREUSEREWERDXIAASCK. KDDVAKHNLELWWAYLKNH: 03: INTAKNLOLOS. FOGLVGAUGEREUSERGENAASCK. KDDVAKHNLELWWAYLKNH: 03: AMEIAKIRGQ, KSGAUNAUGEREUSERGAUAASCK. KDDVAKHNLELWWAYLKNH: 04: TVEGAIAIKRPQ. LKGLINGUE BEORGOOQVELLERAV. NND. HYLHES DIGKRLQAA: 02: TVEGAIAIKRPQ. LKGLINGUE BIO BEORGOOQVELLERAV. NND. SHYLHES DIGKRLQAA: 03: AMEIAKIR, KRGSKLUNAUGERIS GEGORSPEDAAISDPURLATETSHPB LVKEWADA: 04: AMEIGKREN, PGIGKVOULS SIGEOVESTAI SDPURLATETSHPB LVKEWADA: 04: AMEIGKREN, RGIGKVOULS SIGEOVESTAI SDPURLATETSHPB LVKEWADA: 04: AMEIGKREN, RGIGKVOULS SIGNASSIAAISDPUNGUENTYS SUKLLOPKUAKKES: 04: AMEIGKREN, RGISKVOULS SIGEOVESTAI SUKVENKEDIAYLUPKUAKKES: 04: AMEIGKREN, RGISKVOULS SIGENSSIAAISDPUNGUENTYS SWELLOPKUAKKES: 04: AMEIGKREN, RGISKVOULS SIGENSSIAAISDPUNKTYS SWELLDENVYLVAKKES: 04: AMEIGKREN, RGISKVOULS RIEGERENTASSUKKEDIAAISDVUUNKESSIAAISDPUNG 05: AMUTKKYSISK, SSKVONAUSERINGERENTYSKKENDEVSISKKILDENVYLVESSIG 05: AMUTKKYSISK, SSKV		44: LETELVYCTLONKIALDYMLKPFIN. KPOKVKPWVIOL RLSLYCMEWLEKIPDRAATHT: 1
42:LVTBUVXTVARKLTENYLSHFIE.DRDQLDSWLYVULLMSANCLRHLDKICHNUNG: 33:LUTBUVXTVARKLTENYLSHFIE.DRDQLDSWLYVULLMSANCLRHLDKICHTHUDK: 44:LVTBUVXTVSKKLUENYTPUKK.KEN.PVKNMHUDTKOUTHUDKIEDSWLTBAND; 46:LVTBUVYTVKRKYTDPYLKYKYSIDIISKYKKINKIDKVLNMURMSINOTMUDKIEDSWLTBAND; 40:LTTBUVYTVKRKYTDPYLKYKYK,LEN.ANVROLMMSINOTMUDKIEDSWLDDNAS; 8:FFKBUVMSVVKEELDWYINULLKKK.DIPPAVRVARMSINOTMUDKIEDSWLDDNAS; 2:FCTBUVYTVKRKYTDPYLKPFVKYK,L.DIPPAVRVARMSINOTMUDKIEDSWLDDNAS; 9:FKBUVMSVVKEELDWYINULLKKK.DIPPAVRVARMSINOTMUDKIEDSWLDDNAS; 4:FCTBUVYTVKRRTDCLEFGUGDRIGOPDIGKTVGLGVUERULDCKASANJUR; 5:AVESIAKIGRGQ.YRSFANAULRFUEREKLAASCKKDDVAKHNULLWVAYLKNH; 9:AVESIAKIGRGQ.YRSFANAULRFUEREKLAASCKKDDVAKHNULLWVAYLKNH; 10:LTTALKSSS,FGLMAAULRFUERESSLAKVDKH.WOTHHDDLWKKKKX; 10:TVEGAIAIKRPQ.KKGLINGUERGPOQOEELLAEN.ASSA.RVLHSSILKKLKKA; 10:TVEGAIAIKRPQ.KKGLINGUERGPOQOEELLAEN.ASSA.RVLHSSILKKLKA; 10:TVEGAIAIKRPQ.KKGLINGUERGPOQOEELDAENSNAGKYGHSSILKKLQKA; 10:AVEGAIAIKRPL.KKGLINGUERGPOQOEELDAN.SNAGKYGHSSILKKLQKA; 10:AVEGARRGN.FGIGKFUNGULRAFONGAPSLAAISDPVDRLATEISHBRUTEKLAQ; 9:AVEGKRGN.PGIGKFUNGULRAFONGAPSLAAISDPVDRLATEISHBRUTEKLAQ; 9:AVEGKRGN.PGIGKFUNGULRAFONGAPSLAAISDPVDRLATEISHBRUTEKLAQ; 9:AVEGKRGN.PGIGKFUNGULRAFONGAPSLAAISDPVDRLATEISHBUVYNVKSEC 10:AVEIAKR,KKSSEKLWAAULRFUEGOBSLAKVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	<pre>42 : LVTELVYSTVARKLTDEWYTSHFIE. DRDQLDSW1YWLLMSAYCHRALDKTCDHWWNE : 38 : LUTELVYSTVARKLTDEWYTSHFIE. DRDQLDSW1YWLLMSAYCHRALDKTCDHWWNE : 38 : FUTALVYSTVARKLTDEWYTSHLK. KEPKWARMILLDT YOU FADKYNT : SAVDE : 46 : LVTETVYSTVIKYKLTDI I SKFVKTKINKIDKRVLNVLRMST YOTRILDKTSDFADWE : 47 : LVTETVYSTVIKYKLTDI I SKFVKTKINKIDKRVLNVLRMST YOTRILDKTSDFADWE : 48 : FFKDLVMSVVYRKQRTDCLEGOLGORPIGKOPDDERKTVQGLCUCTANSVDDYAVSE : 42 : CTTELVYSTVRQRTLCLEGOLGORPIGKOPDDERKTVQGLCUCTANSVDDYAVSE : 53 AMESIAKIGRQO, YRSFANATLERRELERCHARCK KDDVAKHNLELAWAYLKNH: 54 : DMTAKNLCLOS : FGGLVNAVLERRELEGOESLAKVD KH WOTLHED LVMKLKKX : 52 : TMEGATULKRPO KGLINGVEG ØCOQCEELLAREN ANDS RYLHES LUARIKLKKA : 52 : TMEGATULKRPO KGLINGVEG ØCOQCEELLAREN SNDAGKGHNES TUKLLQRA : 54 : MEGTKELKGPR RGLINGVEG ØCOQCEELLAREN SNDAGKGHNES TUKLLQRA : 56 : AMEIGKRGN GLINGVEG ØCOQCEELLAREN SNNAGKGHNEST INKLLQRA : 57 : MEGTKELKGPR RGLINGVEG ØCOQCEELLAREN SNNAGKGHNEST INKLLQRA : 56 : AMEIGKRGN GLINGVEG ØCOQCEELLAREN SNNAGKGHNEST INKLLQRA : 57 : MEGTKELKGPR RGLINGVEG ØCOQCEELLAREN SNNAGKGHNEST INKLLOGA 56 : AMEIGKRGN GLINGVEG ØCOQCEELLAREN SNNAGKGHNEST INKLLORA : 57 : AGIAKNENKAKKYN LEG OF STELPOVRLATETSMEN UTEKLLAQ : 51 : AMEIAKI RCH KGSSKLVN VLG RT I HEGWPDIASIKRNIKNEDSINYS LVY LVKLLEDQ : 51 : AMEIAKIR KKSSKLVN VLG RT I HEGWPDIASIKRNIKNEDSINYS LVY LVKKLEDQ : 51 : AMEIAKIR KKSSKLVN VLG RENTHENDENTY SNEKLLDENVYS VLG VLVKKLEDQ : 51 : AMEIAKIR, RHDGATANFTNOV LFNPINGS EHNEEPKDWETY SNEKLLDKVKSKK TIDHWATH : 56 : TAKLVKN ENFKKLVKAKIN SNEKLYN VLG SNEKLLDYNYSEF MAKKFFLKDC : 51 : AMEIAKIN ENFKKLVKAKIN SNEKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</pre>		37: LFTELVYCTISRKLLLEYYLTPFVK.KPOKVDNWVKNUJILSLYOFLULDKWCDHEVINE;
<ul> <li>38 LETTERVNETVSERISERVTLAHYVK, DROKLDKWYYLMLSENGTTLDKERAHETYNE</li> <li>43 FYTALVENUSKKALLENYTPLLK, KEPK, PWARMELLTTTOOLENDKUFTSERAVDE</li> <li>44 FYTALVENUSKKALLENYTPLLK, KEPK, PWARMELLTTTOOLENDKUFTSERAVDE</li> <li>46 LUTETVVTVKRVTTDYLKKELDVYTNOLTKKK, DROKNALMYRNETKYVULDKVDENHETINE</li> <li>8 FFRELVNETVKRKYTDOYLKPFVKTKK, AWUROLAWSTKYVULDKVDENHETINE</li> <li>8 FFRELVNETVKRKELDDVYTNOLTKKK, DIPPAVRVARWAGAGGLENNSVEDYAVSE</li> <li>42 FCTEVNETVKRKELDDVYTNOLTKKK, DLIPPAVRVARWAGAGGLENNSVEDYAVSE</li> <li>42 FCTEVNETVKRKYTDOYLKPFVKTKK, AWUROLAWSTKYVULDKVDENHETINE</li> <li>8 FFRELVNEVVRRQRTDCLEEQLGDRPIGKOPPDERRTVQLOTUGRALDVBASADINT;</li> <li>42 FCTEVNETVVRQRTDCLEEQLGDRPIGKOPPDERRTVQLOTUGRALDVWASLKNH;</li> <li>95 AMESIAKIGRO, YRSFARATUGRELEEREKLAASCK, KDDVAKHNLELWWAYLKNH;</li> <li>95 AMESIAKIGRO, YRSFARATUGRELEEOSLAKVD, KH, WOTLHEDDLYNKLKKV;</li> <li>17 YVNATKSLKSDS, FGGLVNAJURGEDEODEILAITD, NN, WOTLHEDDLYNKLKKV;</li> <li>17 YVNATKSLKSDS, FGGLVNAJURGEOGQUELLERAV, NNDS, HYLHSSCHARIVGA;</li> <li>18 THGETKELKOPR, LRGLINGULGOFOSQUVELERAV, NNDS, HYLHSSCHARIKQA;</li> <li>198 THGETKELKOPR, LRGLINGULGOFOSQUVELERAV, NNDS, HYLHSSCHARIVGA;</li> <li>198 AMEIGKRGN, PGIGKFUNGULAROSONAPSLAAISDPVDRLATETSHRBLVKEWADA;</li> <li>96 AMEIGKRGN, PGIGKFUNGULAROSONAPSLAAISDPVDRLATETSHRBLVKEWADA;</li> <li>97 AMEIAKR, KKOSEKLWAAUR RIEGEWDEDIASIKRNKRDSTAYSLWDVDVAKLEDQ;</li> <li>10 AMELAKLR, KKOSEKLWAAUR RIEGEWDEDIASIKRNKRDSTAYSLWDVDVAKLEDQ;</li> <li>11 AMELAKLR, KKOSEKLWAAUR RIEGEWDEDIASIKRNKRDSTAYSLWDVDVAKLEDQ;</li> <li>12 AMEIAKR, KHOQATANFDAVLINNYDENS, HRNNEPSKWERLCHVYSLVDVVKKEDQ</li> <li>14 AMEIAKR, KHOQATANFDAVLINNYDENS, HRNNEPSKERLEPAVKRYSKYSLVDVKKEDQ;</li> <li>15 AMEIAKR, HOQATANFDAVLINNYDENS, HRNNEPSKERVERVSKYSLVDVKKEDQ;</li> <li>16 AMITKKYJSLK, SSKFWAAUR FILEGWPIASIKRNKRDSTAYSLWDVKKEDQ;</li> <li>16 AMITKKYSLKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</li></ul>	38: LITETVYETYSKISPERNYTAHYVK. DRDKLDKWYYTLMISTYGETYLDK:CAHTYND: 31: FUTALVYETYSKISPERNYTAHYVK. DRDKLDKWYYTLMISTYGETYLDK:CAHTYND: 31: FUTALVYETYKKSTIDI ISKY WYTLMIN DIRKYNDYRSTYGYNLDKYSTYGANANG: 40: LFTETVYETYKRKYTDDFYLKPFUKTKIKAWRONLMISTYGYNLDKWENSTYGYNLDKYENNYTY 51: FUTETVYETYKRKYTDDFYLKPFUKTKIKAWRONLMISTYGYNLDKWENSTYGYNLDKYENNYTY 22: FCTELVYETYKRKYTDDFYLKPFUKTKIKAWRONLMISTYGYNLDKWENSTYGYNLDKYENNYTY 22: FCTELVYETYKRKYTDDFYLKPFUKTKIKAWRONLMISTYGYNLDKWENSTYGYNLDKWENNYTY 22: FCTELVYETYKRKYTDDFYLKPFUKTKIKAWRONLMISTYGYNLDKWENYTYTY 22: FCTELVYETYKRKYTDDFYLKPFUKTKIKAWRONLMISTYGYNLDKWENYTY 22: FCTELVYETYKRKYTDDFYLKPFUKTKIKAWRONLMISTYGYNLDKWENYTY 22: FCTELVYETYKRKYTDDFYLKPFUKTKIKAWRONLMISTYGYNLDKWENYTYKRY 23: FCTELVYETYKRKYTDDFYLLFRELEEREKLAASCKKDDVAKHNLELWWAYLKNH: 25: AMESIAKIGRG, YRSFANTLERFLEEREKLAASCKKDDVAKHNLELWWAYLKNH: 23: TUGTAKISCS, FGLUNAVLERFLEERESLAKVDKHWQTLHEDFYNKLKKV: 21: TUGTAKISKSS, FRGUNAVLERFLEERESLAKVDKHWQTLHEDFYNKLKKX: 22: TUGGATVLKRPQ, LKGLINAVLERFLEERESLEDWRLATENSSSA.RYLHSSDLIARIKQA: 33: AWEIAKIRCH, KGLSTNAVGERGUEGUEGUEGUEGTANSNNAGKYGHSSILKLQEA: 34: AWEIAKH, KGSSKLUNAVLERFLEEREVELDEWNLATETSHEDFYNLATENSHEDLWENADA: 26: AWEIGKRGN, PGIGKFUNAVLERFLEEREVELDEWTIX FRNKKVSISJENKLUAG: 21: AWEIAKKEN, KGSSKLUNAVLERTLEEREVEDIASISPURLATEISHER LUTEKLLAQ: 21: AWEIAKKKGSSKLUNAVLERTLEENEPTISTREDVERLATEISHER LUTEKLLAQ: 21: AWEIAKKKGSSKLUNAVLERTLEENEPTISTREDVERLATEISHER LUTEKLLAQ: 21: AWEIAKKINGSKKAGEKFUNAVLERTLEENEPTISTREDINGKLUTEKLLDAWING 22: AWEIAKKINGSSKLUNAVLERTUENETYNDENETYSTENENETYSTENENEUPYNKYSISJENEN 23: AWEIAKKSSKFUNAVLERTUENENTYSNEKLLDEWTYSSKKLUDAVSKELD 24: AWEIAKKINGSKKAGEKFUNAVLERTUENENTYSNEKLLDDKWTYSSKKLUDAWING; 26: AWEIAKENEFUNAVLENENTYSNEKLLDDKWYREFTYSTER TUDHWATH: 26: TYKUNNENFKKUNAVLENENTYSKKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		42: LVTELVYSTVARKLTHEWYLSHFIE, DROOLDSWLYVIJLMSANOLRNLDKTEDHAVVNE: 1
<ul> <li>43: FÜTALVXZVVSKKALLENVITPPLIK. KEPK. PVARMELLTT KOVILENDKVILSAVDI.</li> <li>44: LÜTALVXZVVSKKALLENVITPPLIK. KEPK. PVARMELLTT KOVILENDKVILSAVDI.</li> <li>46: LUTETVYTIKYKYSTD I I ISKFVKTKINKIDKVLNVURMENSTOTRILDKNEDFADNS.</li> <li>40: LETETVYTVKRKYTD OPVILKPVKRKIK ADVRAME MEGAVOLLENNSVIDYSAVS.</li> <li>42: FERELVNEVVRORTDOLLENVITOLEKKK DIPPAVRVA EMGAVOLLENNSVIDYSAVS.</li> <li>42: FOTBINATION, VRSFANATIORFLEEREKLASCK KDDVAKINL LLENVAYLKNI:</li> <li>51: AMESIAKIGRO, VRSFANATIORFLEEREKLASCK KDDVAKINL LLENVAYLKNI:</li> <li>10: AMESIAKIGRO, VRSFANATIORFLEEREKLASCK KDDVAKINL LLENVAYLKNI:</li> <li>10: AMESIAKIGRO, VRSFANATIORFLEEREKLASCK KDDVAKINL LLENVAYLKNI:</li> <li>10: INTAKNLOLOS. FOGLINATURARTISEOESMLAKVD KH. WOTLHEDFLANKLKKV:</li> <li>10: INTAKNLOLOS. FOGLINATURARTISEOESMLAKVD KH. WOTLHEDFLANKLKKV:</li> <li>10: INTAKNLOLOS. FOGLINGTISCOCOLELERAV NND. NYLHSSDIKRLOKA:</li> <li>10: TYEGATVLKRPQ. LKGLINGTIS ORGOVELLERAV NND. NYLHSSDIKRLOKA:</li> <li>10: AMELAKIRGH. KGIASTMOOTURSI ORGOVELLERAV NNDS. NYLHSSDIKRLOKAA:</li> <li>10: AMELAKIRGH. KGIASTMOOTURSI ORGOVELDOMAV SNNAKVOHSSDIKLLOPAANA</li> <li>14: AMELAKIRGH. KGIASTMOOTURSI ORGOVENDIASI KRINKRDSI AVSI VADVAKLLED;</li> <li>16: AMELAKIRGH. KGIASTMOOTURSI ORGOVENDIASI KRINKRDSI AVSI VADVAKLED;</li> <li>17: AMELAKIR, KKSSEKLUNATURATIST PTALINNYSS</li></ul>	<ul> <li>13 : FUTALVY SVÝ SKALLSNY I TPLLK. KEPK PAARMALLIT I COLEMBANG I SAVEJ</li> <li>14 : LVTE TVY STVERKALLSNY I TPLLK. KEPK PAARMALLIT I COLEMBAT (V VLDKY CHARAN)</li> <li>14 : LVTE TVY STVERKY I DY LKPY VKTKIK AV ROLAMST (V VLDKY CHARAN)</li> <li>14 : FFKELVNS VVRKEELDOWY INQLEKK DI PPAVRALRMANCHLENNSVEDY DAVS</li> <li>24 : FCTELVY STVERKY I DY LKPY VKTKIK AV ROLAMST (V VLDKY CHARAN)</li> <li>25 : AVESIAKI GRO, YRSPANDUELKK DI PPAVRALRMANCHLENNSVEDY DAVS</li> <li>25 : AVESIAKI GRO, YRSPANDUERFLEEDRY GOVEPDERRY (GOLGORALDOVENSBAUNT :</li></ul>		38: LETEIVYETVSRKISLEWYLAHYVK, DRDKLDKWYYLLMLSIWOTTWLDKLEAHEIVND:
46:LVTDIVY TIXYKYSTDIIISKFVKTKINKIDKPUNDERSITOTRIDERSPANNS: 40:LTTDIVYTVKRYTDYILSKFVKTKIKAVVRCHWISTKYVYLDKYCHNATINS: 41:FFDIVYTVKRYTDYILSKKKDIPAVRVARMAKKISTKYVYLDKYCHNATINS: 42:FCTBIVYTVKRQRTDDLIFQLGDRPIGKQPPDDRTVQGLGVGRHLDKHSSNDYDYAVSG 42:FCTBIVYTVKRQRTDDLIFQLGDRPIGKQPPDDRTVQGLGVGRHLDKHSSNDYTY 55:AVESIAKIGRGQ.YRSFANAVLRFLGEREKLAASCKKDDVAKHNLLLWVAYLKNH: 95:AVESIAKIGRGQ.YRSFANAVLRFLGEREKLAASCKKDDVAKHNLLLWVAYLKNH: 100:IDNTAKNLQLOS.FOGLWAAVLRFLGEREKLAASCKKDDVAKHNLLWVAYLKNH: 101:TUTGAIAIKEKLSS.FCGLWAAVLRFLGEOSENLAKUDKHWOTLHGDLWKKKKX 102:TUEGAIAIKRPQ.LKGLINGVLGFGOQOELLAFENASDA.RVLHSSDIARKLQAA: 102:TUEGAIAIKRPQ.LKGLINGVLGFGOQOELLAFENASDA.RVLHSSDIARKLQAA: 98:TUEGTKELKGPR.LRGLINGVLGFGOQOELLAFENASDA.RVLHSSDIARKLQAA: 91:ABEAKIRGH.KGIASFWSQLBSIGGEVPSFDAIEDPVRLATETSHGELVKENADA: 96:AVEIGKRRGN.FGIGKFWSQLBSIGGEVPSFDAIEDPVRLATETSHGELVKENADA: 97:AGIAKIRGH.KGIASFWSQLBSIGGEVPSFDAIEDPVRLATETSHGELVKENADA: 96:AVEIGKRRGN.FGIGKFWSQLBSIGGEVPSFDAIEDPVRLATETSHGELVKENADA: 97:AGIAKIRGH.KGIASFWYSLBYCSBISIGEVPSFDAIEDPVRLATETSHGELVKENADA: 96:AVEIGKRRGN.FGIGKFWSQLBSIGSEVPSFDAIEDPVRLATETSHGELVKENADA: 97:AGIAKIRGH.KGIASFWYSLBYCSBISIGEVPSFDAIEDPVRLATETSHGELVKENADA: 96:AVEIGKRRGN.FGIGKFWSQLBSIGSEVPSFDAIEDPVRLATETSHGELVKENADA: 97:AGIAKIRGH.KGIASFWYSLBYCSBISIGEVPSFDAIEDPVRLATETSHGELVKELAQ: 97:AGIAKIRGH.KGIASFWYSLBYCSBISIGEVPSFDAIEDPVRLATETSHGELVKELAQ: 97:AGIAKIRGH.KGIASFWYSLBYCFBSLMAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	<pre>16 : LVTETVX BTIKYKYSTDIIISKPVKTKINKIDKRVINVERMSTKOTRYLDKTBOFAANNE : 10 : LFTETVYGTVIKKKYTEPPTKTPVKTKIKAWROLLMASTKYVYLDKVGANATINE : 10 : LFTETVYGTVIKKKYTEPPTKTPVKTKIKAWROLLMASTKYVYLDKVGANATINE : 8 : FFKELVKGVVREQRTLECLEQLGORFIGKOPPDERRTVOJGJACGERLDOVEASALVINIS : 12 : FCTELVKGVVRCQRTLECLEQLGORFIGKOPPDERRTVOJGJACGERLDOVEASALVIT : 5 : AVESIAKIGRGO, YRSFANATLERELBEREKLAASCKKDDVAKHNLELMVAYLKNH: 95 : AVESIAKIGRGO, YRSFANATLERELBEREKLAASCKKDDVAKHNLELMVAYLKNH: 95 : AVESIAKIGRGO, YRSFANATLERELBEREKLAASCKKDDVAKHNLELMVAYLKNH: 95 : AVESIAKIGRGO, YRSFANATLERELBEREKLAASCKKDDVAKHNLELMVAYLKNH: 96 : TVEGATALKSDS.FRGLUNAUERFULEQOSILAITDKNWOTLHEDELVNKLKKA: 92 : TVEGATVLKRPO, LKGLUNAVLERFULEQOSILAITDKNWOTLHEDELVKKLKKA: 93 : TVEGATVLKRPO, LKGLUNAVLERFULEQOSULAEFNNNDS.HYLHESSLUARIKLKAA: 94 : TVEGTKELKGPR.LRGLUNAVLERFULEQOSOLLERAVNNDS.HYLHESSLUARIKLKAA: 95 : AVESTKELKGPR.LRGLUNAVLERFULEQOSOLLERAVNNDS.HYLHESSLUARIKLKAA: 96 : AVESTKELKGPR.LRGLUNAVLERMONQEELDQMAVSNNAGKYGHES ULKLLQAA: 97 : AVGIAKINGKKAASKYNALEGISTICEOVESPDATEDPVRLLATETSHED UVNIVAKKLEDO: 91 : AVGIAKINGKKKASKYNALEGIER ILBEGWEDIASIKKNIKKDSIAYSI VNIVAKKLEDO: 91 : AVGIAKINGKKKASKYNALEDRINGERILBEGVESIAAISDPVDRLATETSHED UVNIVAKKLEDO: 91 : AVGIAKINGKKKASKYNALEDRINGERILBEGWESIAKINGKYSSKILLDKAVQO: 91 : AVGIAKINGKKKASKYNALEDO'S SIDEROVESPDIASIKKNIKKDSIAYSI VSIJVUKKLEDO: 91 : AVGIAKINGKKKASKYNALEDO'S SIDEROVESPDIASIKKKINKDSIAYSI VSIJVUKKLEDO: 91 : AVGIAKINGKKKASKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</pre>		43: FVTALVYEVVSKKALLEWYTTPLEK, KEPK, PWAKMELDTTYOVLEMDXVEISEAVD
40:LFTBTVYGTVKRKYTDDYUKPFVKTKIKAWURQHWMSTKYTVULDKVDNHTITM: 8:FFREGVWGVVRKSELDWYTNODJKKKDIPPAURVARKGARGILFNSVEDYAVSG 42:FCTBVYGVRORTHDCLIEQLGDRPIGKOPPDERTVQLGTVGLPRILOOVASADVSI 95:AVESIAKIGRQ,YRSFAROULRFLGEREKLAASCKKDDVAKHNLGLWVAYLKNH: 95:AVESIAKIGRQ,YRSFAROULRFLGEREKLAASCKKDDVAKHNLGLWVAYLKNH: 108:INTAKNLQLOS.FQGLWAATLRFLGEREKLAASCKKDDVAKHNLGLWVAYLKNH: 102:TVEGATXKRQ,LKGLUGVLGFCGQCELLAFNASDA.RYLHSDLUKKKVX 117:VUNATKSLKSDS.FRGLWAATLRFLGEREKLAASCKKDVAKHNLGLWVAYLKNH: 102:TVEGATXKRQ,LKGLUGVLGFCGQCELLAFNASDA.RYLHSDLUKKLQKA: 102:TVEGATVLKRPQ.LKGLUGVLGFCGQCELLERAVNNDS.HYLHSDLUAKLLQKA 98:TVEGTKELKCPR.LKGLUGVLGFCGQCELLERAVNNDS.HYLHSDLUAKLAKA: 96:AVEIGKRGN.PGIGKFWGVLGFCGCGCVEFLDAVSNNAGKYGHSSILKLLQEA: 97:AVEIGKRGN.FGIGKFWGVLGFCGCGCVEFLDAVSSNNAGKYGHSSILTEKLLQEA: 96:AVEIGKRGN.PGIGKFWGVLGFCGCGCVEFLDAVSSNNAGKYGHSSILTEKLLQEA: 97:AVEIAKRH.KGLASFWGVLGFCGCGCVEFLDAVSSNNAGKYGHSSILTEKLLQEA: 96:AVEIGKRGN.PGIGKFWGVLGFCGCGCVEFLDAVSSNNAGKYGHSSILTEKLLQEA: 96:AVEIGKRGN.FGIGKFWGVLGFCGCGCVFFLDAVSLLTEISMGRLTTEKLLAQ: 91:AVELAKLR.KKSSEKLWGATURFILGEWFDIASIKRNKRDSTAYSILVDVDVKLEDQ: 100:AVELAK.SSKFVGATURFILGEWFDIASIKRNKRDSTAYSILVDVDVKKLEDQ: 100:AVELKKSSKSKVGATURFILGEWFDIASIKRNKRDSTAYSILVDVDVKKLEDQ: 100:AVELKKLS.SKFVGATURFILGEWFDIASIKRNKRDSTAYSILVDVDVKKLEDQ: 100:AVELKKLS.SKFVGATURFILGEWFDIASIKRNKRDSTAYSILVDVVKKLEDQ: 100:AVELKX.KXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	40: LFTETVYETVERKYTIDFYLKPFVEKTKIKAWURONLMESTKYTVILDEMVENHATINE 8: FFKBUWREVEREELDWYTNOLLEKKDIPPATEVALERGARGLEANSUGYATES 42: FCTELVYETVERGTUCLEGULGDPIGKOPPDERTVOUGLEGULDAULDOWEASAANNT: 		
8: FFKBUWGWVRKEELDWYINQLEKKK., DIPPAURVARKAAWAILEMNSVEDYBAYSG: 42: FCTBUWYEVURRQRTDCLEQLGDRPICKOPPDERFYGICLWERLOOMASBAUNT: 95: ANESIAKIGRGO, YRSFABAUGRFLGEREKLAASCKKDDVAKHNELLWWAYLKNH: 109: INTAKNLQLOS.FOGLWAVLRFLGEREKLAASCKKDDVAKHNELLWWAYLKNH: 109: INTAKNLQLOS.FOGLWAVLRFLGEOESMLAKVDKHWOTLHEDEVNKLKKV: 109: INTAKNLQLOS.FOGLWAVLRFLGEOESMLAKVDKHWOTLHEDEVNKLKKV: 102: TVEGATVLKRPQ.LKGLINC/LGFOGOQOEELLAEFNASDA.RYLHSSLUKRLQKA: 102: TVEGATVLKRPQ.LKGLINC/LGFOGOQOEELLAEFNSNDA.RYLHSSLUKRLQKA: 103: AVEIAKIRGH.KGIASVMOVLRGIGEOSPOJELAIDSNNAGKYGHSSLUKRLQKA: 103: AVEIAKIRGH.KGIASVMOVLRGIGEOSPOJELAAISDVDRLATETSMGRLUTEKLLAO: 98: TMSGTKELKOPR.LRGLINC/LGFOGOQVELLERAVNNDS.HYLHSSLUKRLQKA: 103: AVEIAKIRGH.KGIASVMOVLRGIGEOSPSTDAIEDPVRLATETSMGRLUTEKLAO: 97: ANGIAKNRGNKKGAEKIVAAULRFLGEOEVDSFDAIEDPVRLATETSMGRLUTEKLAO: 97: ANGIAKNRGNKKGAEKIVAAULRFLGEOMPDIASIKRNKRDSIAYSLVNUVAKLEDO: 101: AVIAKA.R.KKGSEKLWAAULRFLGEOMPDIASIKRNKRDSVSLVDVDVAKLEDO: 101: AVIAK.S.SKFVAAULRFLGEOMPDIASIKRNKRDSVSLUCNVSEDUIVKKUEDO: 101: AVIAKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	8 : FFKELVNGVURKEELLUWY INOLLKKK, DI PPAVRVALRINGA VGLEMNSVEDY DAVS 22 : FCUELVY AVVRQUTLYCLEGOLGORPTGKOPPDERRIVG GUTCER LOOP AS BAUNT : 25 : AMESIAKIGRGO, YRSFANATLER LEREKLAASCKKDDVAKHNLELWWAYLKNH: 26 : AMESIAKIGRGO, YRSFANATLER LEREKLAASCKKDVAKHNLELWWAYLKNH: 27 : IONTAKNLOLOS, FOGLWAYLER LEREKLAASCKKDVAKHNLELWWAYLKNH: 28 : IONTAKNLOLOS, FOGLWAYLER LEREKLASCKKDVAKHNLELWWAYLKNH: 20 : IONTAKNLOLOS, FOGLWAYLER LEREKLASCKKDVAKHNLELWWAYLKNH: 20 : IONTAKNLOLOS, FOGLWAYLER LEREKLASCKKDVAKHNLELWWAYLKNH: 20 : IONTAKNLOLOS, FOGLWAYLER LEREVLEROKLASCKKDVAKHNLELWWAYLKNH: 20 : TUGGAT KRPO, LKGLINGYLER OF SOLOOLELAFT DKN. WOTLHED LYNKLKKY: 21 : TUGGAT KRPO, LKGLINGYLER OF SOLOOLELAFT DNNG KYCHS SULKLUQA: 22 : TUGGAT KRPO, LKGLINGYLER OF SOLOOLOS SOLOKLUGASSNNAGKYCHS SULKLUGA: 23 : AMEIAKIRG, KGLASTWOYLER I LEGWPSTAI EDVIRLATETSHE LYKEWADA: 36 : AMEGTKREN, FGLAKYMAYLER I LEGWPTALATETSHE LYKEWADA: 36 : AMEGTKREN, RGLASTWOYLER I LEGWPTALATETSHE LYKEWADA: 37 : AGIAKNRGNKKGAEKFWANTLER OF SOLDEDIASTEHNNEPKWETYYSKYLLDKWLWQ: 20 : AMELAKLRKROSEKLUNAYLER I LEGWPTALSTKRINKENSIAYSLW LWAKLEDO; 20 : AMELAKLR.KINGSKKUNAYLER I LEGWPTALSTKRINKENSTAYSLW LWAKLEDO; 20 : AMELAKLR.KINGSKKUNAYLER OF SOLDEDIAST EHNNEPKWETYSKEKLLDAKWVQ; 20 : AMELAKLR.KINGSKKUNAYLER OF SOLDEN S EHNNEPKWETYSKEKLTD, MYKFELOP 21 : AMELAKLR.XINGSKKUNAYLER I LEGWPTAST FUNDISVEKLCPNYSEF SVYKFELOP 21 : AMELAKLN.SSKYWANJER TI DONYMS EHNNEPKWETYSKEK TIDHWATH; 21 : TUELAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		
42:FCTBUVKYVWRQRTBOLLEQLGDRPIGKQPPDERRTVQLCLKORRHLDOWASBADNT: 95:AMESIAKIGRGQ,YRSFANAULSRFLBEREKLAASCKKDDVAKHNLELEWWAYLKNH: 95:AMESIAKIGRGQ,YRSFANAULSRFLBEREKLAASCKKDDVAKHNLELEWWAYLKNH: 108:IQNTAKNLQLQS.FOGLWAAVLSRFLBEQESMLAKVDKHWQTLHEBFUKKLKKA: 102:TYEGATALKRPQ.LKGLING'LEOFOGQOEELLAEFNASDA.RYLHESDLWKLKKA: 102:TYEGATALKRPQ.LKGLING'LEOFOGQOEELLAEFNNSDS.HYLHESDLWKLKKA: 103:AMELAKIRGH.KGLASULWAYLSRFLBEQDSILLA.NSNAGKYGHSSTLKLLQAA: 98:TYEGTKELKGPR.LRGLING'LEOFOGQOEELLAEFNNSDS.HYLHESDLWKLKKA: 91:AMELAKIRGH.KGLASULWAYLSRFLBEQDSILLAYNNDS.HYLHESDLWKLKAA: 92:TYEGTKELKGPR.LRGLING'LEOFOGQOEELLAEFNNSDS.HYLHESDLWKLKAA: 93:AMELAKIRGH.KGLASULWAYLSRFLBEQDSILAISDPURLATETSHPELUKKENADA: 94:TYEGTKELKGPR.LRGLING'LENGYDSNGEEDQMAVSNAGKYGHSSTLKLLQAA: 95:AMELGKRRGN.PGIGKFUNSYLSRFCBNGAPSLAAISDPURLATETSHPELUKKENADA: 96:AMELGKRRGN.PGIGKFUNSYLSRFCBNGAPSLAAISDPURLATETSHPELVKENADA: 97:AGIAKNEGNKKGBEKFUNSYLSRFCBNGAPSLAAISDPURLATETSHPELVKKLEDQ: 100:AMKIAK.RHDGQATANFUNSYLSNYLENNTAFYNKDNSVELCPNYSFPEP MYKFLKGD; 97:TYELAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	42 : FCTELVYNVURRQRTLOCL EQLGDRPIGKQPPDERREVOLGLWGRWLDOVHASHALAT: 53 : AMESIAKIGRGQ, YRSFARAULERUHERELHEREKLAASCKKDDVAKHNLELWWAYLKNH: 54 : SANESIAKIGRGQ, YRSFARAULEREUHEREKLAASCKKDDVAKHNLELWWAYLKNH: 58 : TUNTAKNLQLQS, FQGUVAUURRWLBRQESMLAKVDKHWOTLHEDFLWKKLKKA: 50 : TUNTAKNLQLQS, FQGUVAUURRWLBRQESMLAKVDKHWOTLHEDFLWKKLKKA: 52 : TVEGAIAIKRPQ, LKGLINGUERGROOQEELLAEFNASDA.RYLHESDIHKRLQKA: 53 : TVEGAIAIKRPQ, LKGLINGUERGROOQEELLAEFNASDA.RYLHESDIHKRLQKA: 54 : TVEGAIAIKRPQ, LKGLINGUERGOOQOULLERAVNNDS.HYLHESSIIIKRLQKA: 53 : TVEGKELKGPR, LRGLINGUERGROOQOELLAEFNNNDS.HYLHESSIIIKRLQKA: 54 : TVEGKELKGPR, LRGLINGUERGROOQOELLAEFNNNDS.HYLHESSIIIKRLQKA: 55 : AMELGKRGR, PGIGKFUNGUERGROOQOELLAFTNNDS.HYLHESSIIIKRLQAA 56 : AMELGKRGR, PGIGKFUNGUERGROORAPSLAAISDPURLATETSHESLIKKENDAA 56 : AMELGKRGN, PGIGKFUNGUERTINGONGAPSLAAISDPURLATETSHESLIKKELDQ: 51 : AMELAKIRKKGSEKUNGAUERTINGONGAPSLAAISDPURLATETSHESLIKKELDQ: 51 : AMELAKIRKKGSEKUNGAUERTINGONGAPSLAAISDPURLATETSHESLIKKELDQ: 51 : AMELAKIR.KKKKKKLEDQ: 52 : AMELAKIR, RHDGQATANFINGUERRIGHS,EHRNEEPKDWETKYSMEKLLDKHVRQ: 53 : AMITKKYISLK, SSKFUNGAUENTURNYNTAFYNKDNSVEKLCPYNSPER MYKPFLKG: 54 : TVEJAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		
<ul> <li>95. AMESIAKIGRGO, YRSFANAYLARFIGEREKLAASCKKDDVAKHNLELMWAYLKNH:</li> <li>95. AMESIAKIGRGO, YRSFANAYLARFIGEREKLAASCKKDDVAKHNLELMWAYLKNH:</li> <li>95. AMESIAKIGRGO, YRSFANAYLARFIGEGESKLAKVDKHWOTLHGDLYNKLKKY.</li> <li>108. I JUNTAKNLOLOS. FOGLMAAYLARFIGEGESKLAKVDKHWOTLHGDLYNKLKKY.</li> <li>102. TMEGATAIKRPO, LKGLINSYLLOFFOGOQUELLAETNASDA. RYLHSSLIKKLOKA:</li> <li>102. TMEGATAIKRPO, LKGLINSYLLOFFOGOQUELLERAVNNDS. HYLHSSLIARIKOA:</li> <li>98. TMEGTKELKOPR. LRGLINSYLLOFFOGOQUELLERAVNNDS. HYLHSSLIARIKOA:</li> <li>98. TMEGTKELKOPR. LRGLINSYLLOFFOGOQUELLERAVNNDS. HYLHSSLIARIKOA:</li> <li>99. TMEGTKELKOPR. LRGLINSYLLOFFOGOQUELLERAVNNDS. HYLHSSLIARIKOA:</li> <li>99. AMEIGKRGN, PGIGKFMOVLRAFOGNGAPSLAAISDPVDRLATEISMERLTEKLLORA:</li> <li>96. AMEIGKRGN, PGIGKFMOVLRAFOGNGAPSLAAISDPVDRLATEISMERLTEKLLAQ:</li> <li>97. AGIAKNRGNKKGAEKFYNAILSOFTSHPLDMETIKRINKYSVKYSLVDLYKKLEDO;</li> <li>100. AMKIAK. RHGQATANFDAYLINYLENPNIAFYNKDNSVELCENYSEPP MYKPFLKOJ</li> <li>97. TYELAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</li></ul>	95 : ANESIAKIGRGQ, YRSFANAYLER IS EREKLAASCKKDDVAKHNLEL WWAYLKNH: 95 : ANESIAKIGRGQ, YRSFANAYLER PLSERKLAASCKKDDVAKHNLEL WWAYLKNH: 95 : ANESIAKIGRGQ, YRSFANAYLER PLSENLAKVDKHWQTLHEDDLYNKLKKY: 93 : DUNTAKNLLQLQS. FOGLYNAYLER PLSEQDSILAIIDKNWQTLHEDDLYNKLKKY: 17 : VUNAKSLKSDS. FFGLYNAYLER PLSEQDSILAIIDKNWQTLHEDDLYNKLKKA: 22 : DUEGAITVLKRPQ.LKGLID YLE QEGOQOUELLERAVNNDS.HYLHESDLARIKQA: 94 : DUEGAUTVLKRPQ.LKGLID YLE QEGOQOUELLERAVNNDS.HYLHESDLARIKQA: 95 : DUEGAUTVLKRPQ.LKGLID YLE QEGOQOUELLERAVNNDS.HYLHESDLARIKQA: 96 : ANEGTKELKOPA.LRGLID YLE QEGOQOUELLERAVNNDS.HYLHESDLARIKQA: 96 : ANEGTKELKOPA.LRGLID YLE DEGVESPDATEDPVRLATETSHPB LYKENADA: 97 : AGITAKNENKKALEK FUNALE QENSPENDIASIKENKINKDSIAYSI YN DYAKLKED Q: 91 : AMELAKLRKKSSEKUNAVLER ILE GEWEDIASIKENKINKDSIAYSI YN DYAKLKED Q: 91 : AGITAKNENKKALEKFUNALE QENSPENDEDIASIKENKINKDSIAYSI YN DYAKLEDQ: 91 : AGITAKNENKKALEKFUNALE QENSPENDEDIASIKENKINKDSIAYSI YN DYAKKKED 92 : AGITAKNENKKALEKSENYL YN DYN DYN SI YN DYAKKED YN SEFD YN DYAKKED 93 : AGITAKNYSIKYN XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		
95:AVESTAKIGRGQ.YRSFAKATURRFILERDKLAASCKKDDVAKHNLILAWVAYLKNH: 108:IMNTAKNLQLQS.FQGLMAAYLRRFILEGESMLAKVDKHWQTLHGDLVNKLKKV: 117:VMNATKSLKSDS.FQGLMAAYLRRFILEGESMLAKVDKHWQTLHGDLVNKLKKA: 102:TDEGAINIKRPQ.LKGLINGULOFOGQQESLLAEFNASDA.RYLHSSLIKKRLQKA: 102:TDEGAINIKRPQ.LKGLINGULOFOGQQESLLAEFNASDA.RYLHSSLIKKRLQKA: 98:TDEGTKELKGPR.LGLINAVLANVGPNQEELDQNAVSNNAGKYGHSSTIKKLQGA: 90:AEGKRGN.PGIGKFMAGULSGIGEGVPSFDAIEDPVRLATETSHBELVKENADA: 96:AVEIGKRGN.PGIGKFMAGULSGIGEGVPSFDAIEDPVRLATETSHBELVKENADA: 97:AGIAKNGNKKGAEKFFNASILOFTSHDELMMETIKKNENSTAYSIVATVAKKLEDQ: 97:AGIAKNGNKKGAEKFFNASILOFTSHDELMMETIKKNENSTAYSIVATVAKKLEDQ: 100:AKIAK.RHKGIKKAGKFFNASILOFTSHDELMMETIKKNENSTAYSIVATVAKKLEDQ: 100:AKIAK.RHGQATANFTAVLENPENSEHRNEEPKDWETKYSMELLDKAVKLEDQ: 97:TPEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	95: AUESIAKIGRGQ. YRSFADATLERELHERDKLAASCKKDDVAKHNLELWWAYLKNH: 28: TUNTAKNLOLOS. FOGUVAYUGRRUE ROESMLAKVDKH WOTLHED LYNKLKKY: 21: VUNAKKSLKSDS. FRGLUNAVLERELE RODSILAIIDKN WOTLHED FYNKLKKY: 22: TVEGATVLKRPO.LKGLINGVLG OF OGOCELLAEPNSDA.RYLHES DUARIKOA: 23: TVEGATVLKRPO.LKGLINGVLG OF OGOCELLAEPNNNDS.HYLHES DUARIKOA: 38: TVEGTKELKGPR.LRGLINGVLG OF OGOCELLERAVNNDS.HYLHES DUARIKOA: 39: TVEGTKELKGPR.LRGLINGVLG OF OGOCELLERAVNNDS.HYLHES DUARIKOA: 31: AGELAKIRGH.KGIASYNGVLG SIG BEOVESFDAIEDPVRLLATETSHED LIVKLUQEA: 51: AGELAKIRGH.KGIASYNGVLG RILBEGWEDIASIKRNIKRDSIAYSI VADVAKKLED O: 51: AGELAKIRKKSSEKUVAVLG RILBEGWEDIASIKRNIKRDSIAYSI VADVAKKLED O: 51: AGELAKIRKKSSEKUVAVLG RILBEGWEDIASIKRNIKRDSIAYSI VADVAKKLED O: 51: AGELAKIR.SKKASKENNALEO OF SHEPLDMETI KRNIKYSYSISJULUKKLED O: 50: AJKIAK.RHDGATANFIDAVLENDISEHRNEEPKDWETKYSMEKLLDKAVRQ: 52: ANITKKYISLK.SSKFVLAVLENDINGENTIFYNNDNSVELCPNYSEELDKAVYSKEKILDKAVRQ: 54: TVEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		
95: ADESTAKIGRGQ. YRSPA KATURRELEERDKLAASCKKDDVAKHNLELEWVAYLKNH: 108: I'NATAKNLQLOS. FOGLYKAYTRRELEEOESMLAKUDKHWQTLHEDDLYNKLKKY: 117: VWAATKSLKSDS. FRGLYNAVLBRELEEOESMLAKUDKHWQTLHEDDLYNKLKKY: 102: TVEGATVLKRPQ. LKGLINGVLGFOGQOEELLAEFMASDA.RYLHESDLIKKLQKA: 102: TVEGATVLKRPQ. LKGLINGVLSOFOGQOEELLAEFMASDA.RYLHESDLIKKLQKA: 103: AVELAKIRGN.LKGLINGVLSOFOGQOEELLAEFMNNDS.HYLHESSULARIKQA: 98: TVEGATVLKRPQ.LKGLINGVLSOFOGQOEELLAFMNNDS.HYLHESSULARIKQA: 103: AVELAKIRGH.KGLSFYNGVLSFGCQOEELLAFMNNDS.HYLHESSULARIKQA: 96: AVEIGKREGN.PGIGKFYNGVLSFGCQUSFDAIEDDVRLATETSHERDYKENADA: 96: AVEIGKREGN.PGIGKFYNGVLRAFOGNGAPSLAAISDPVDRLATETSHERDYKELAKUKKLEDQ: 101: AVELAKLRKKGSEKLVKAJLERILEGWPSFDAIEDDVRLATETSHERDYKVLEVQL 97: AVGIAKNERNKKGAEKFYNAIGOSTHENDEDMETIKRENKYSVSYSLVDIVAKLEDQ: 102: AVKIAK.RHKGQATANFIGAVLENFESSEHRNEEPKDWETKYSMSLLIDDAWYRQ: 106: ANITKKYISLK.SSKFYGAUENYLENFESSEHRNEEPKDWETKYSMSLLIDDAWYRQ: 106: ANITKKYISLK.SSKFYGAUENYLENFELSYNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	95: AUESIAKIGRGQ. YRSFADATLERELHERDKLAASCKKDDVAKHNLELWWAYLKNH: 28: TUNTAKNLOLOS. FOGUVAYUGRRUE ROESMLAKVDKH WOTLHED LYNKLKKY: 21: VUNAKKSLKSDS. FRGLUNAVLERELE RODSILAIIDKN WOTLHED FYNKLKKY: 22: TVEGATVLKRPO.LKGLINGVLG OF OGOCELLAEPNSDA.RYLHES DUARIKOA: 23: TVEGATVLKRPO.LKGLINGVLG OF OGOCELLAEPNNNDS.HYLHES DUARIKOA: 38: TVEGTKELKGPR.LRGLINGVLG OF OGOCELLERAVNNDS.HYLHES DUARIKOA: 39: TVEGTKELKGPR.LRGLINGVLG OF OGOCELLERAVNNDS.HYLHES DUARIKOA: 31: AGELAKIRGH.KGIASYNGVLG SIG BEOVESFDAIEDPVRLLATETSHED LIVKLUQEA: 51: AGELAKIRGH.KGIASYNGVLG RILBEGWEDIASIKRNIKRDSIAYSI VADVAKKLED O: 51: AGELAKIRKKSSEKUVAVLG RILBEGWEDIASIKRNIKRDSIAYSI VADVAKKLED O: 51: AGELAKIRKKSSEKUVAVLG RILBEGWEDIASIKRNIKRDSIAYSI VADVAKKLED O: 51: AGELAKIR.SKKASKENNALEO OF SHEPLDMETI KRNIKYSYSISJULUKKLED O: 50: AJKIAK.RHDGATANFIDAVLENDISEHRNEEPKDWETKYSMEKLLDKAVRQ: 52: ANITKKYISLK.SSKFVLAVLENDINGENTIFYNNDNSVELCPNYSEELDKAVYSKEKILDKAVRQ: 54: TVEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		95: AMESIAKIGRGO, YRSFAMAWIRRELSEREKLAASCK KDDVAKHNI BIAWWAYIKNH - 1
<ul> <li>108: IUNTAKNLQLOS. FOGLYNAALLERFUSEOESMLAKVDKHWOTLHEDELYNKLKKV:</li> <li>117: VUNATKSLKSDS. FRGLWNAVLERFUSEOEILATIDKNWOTLHEDEFYNKLKKS:</li> <li>102: TVEGATATKRPO.LKGLINGVLOFOGQOEELLAFENASDA.RYLHESDLUARIKQA:</li> <li>102: TVEGATVLKRPQ.LKGLINGVLOFOGQOEELLERAVNNDS.HYLHESDLUARIKQA:</li> <li>98: TVEGTKELKOPR.LRGLINGVLOFOGQOVELLERAVNNDS.HYLHESDLUARIKQA:</li> <li>98: TVEGTKELKOPR.LRGLINGVLOFOGQOVELLERAVNNDS.HYLHESDLUARIKQA:</li> <li>98: TVEGTKELKOPR.LRGLINGVLOFOGQOVELLERAVNNDS.HYLHESDLUARIKQA:</li> <li>96: AVEIGKRRGN.PGIGKFWOVLRAFORNAPSLAAISDPVDRLATETSHEDUKKMADA:</li> <li>96: AVEIGKRRGN.PGIGKFWOVLRAFORNAPSLAAISDPVDRLATETSHEDUKKKADAA:</li> <li>97: AVGIAKNRONKKGAEKFWAATLRFILEGWMPDIASIKRNKRDSTAYSILWIDVKLEDQ:</li> <li>100: AQKIAR.RHDQATANFTAATINPARSEHRNEEFKDWETKYSMELLDKWVRQ:</li> <li>100: AQKIAR.RHDQATANFTAATINPARSEHRNEEFKDWETKYSMELLDKWVRQ:</li> <li>100: AQKIAR.RHDQATANFTAATINPARSEHRNEEFKDWETKYSMELLDKWVRQ:</li> <li>97: TVEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</li></ul>	38 : IMPTAKNLOLOS. FOGLAMSAUERRUS EQESMLAKUDKHWOTLHEDELMAKLKKV: 17 : VUNATKSLKSDS. FOGLAMSAUERRUS EQESTLAITDKNWOTLHEDELMAKLKKV: 17 : VUNATKSLKSDS. FRGLUNAVLERRUS EQEDLAITDKNWOTLHEDEFVAKLEKKS 20 : TUEGATVLKRPQ.LKGLINAVLERUS EQOSOQUVELLERAVNNDS.HYLHESDLIARIKQA: 38 : TUEGATVLKRPQ.LKGLINAVLERUS EQOSOQUVELLERAVNNDS.HYLHESDLIARIKQA: 39 : TUEGATVLKRPQ.LKGLINAVLERUS EQOSOQUVELLERAVNNDS.HYLHESDLIARIKQA: 39 : TUEGATVLKRPQ.LKGLINAVLERUS EQOSOQUVELLERAVNNDS.HYLHESDLIARIKQA: 39 : TUEGATVLKRPQ.LKGLINAVLERUS EQOSOQUVELLERAVNNDS.HYLHESDLIARIKQA: 30 : AMELAKLGH.KGIASYNGAVESIG EGOVESFDALIEDVRNLAFETSHED LAVKENADA: 30 : AMELAKLRKKOSEKLUNAVLERILBEGVEDIASIKRKNKRDSIAYSILVEDVENLARLEDQ: 11 : AMELAKLRKKOSEKLUNAVLERILBEGVEDIASIKRKNKRDSIAYSILVEDVENLEDQ: 30 : AMELAKLRKKOSEKLUNAVLERILBEGVEDIASIKRKNKRDSIAYSILVEDUVKKLEDQ: 30 : AMELAKLR. KKOSEKLUNAVLERILBEGVEDIASIKRKNKRDSIAYSILVEDUVKKLEDQ: 30 : AMELAK.R.RIDGOATANFINAVLENTARISEHNNEEPKUWETXYSKELLDKAVRQ: 30 : AMELAK.RINGOKKAGAEKFUNAVLENTARISEHNNEEPKUWETXYSKELDDAVKNEDQ: 30 : AMELAK.RINGOATANFINAVLENTARFINGENCELCONVSEELOPMSETER MAKKENTA 30 : TUEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		95: AVESIAKIGRGO, YRSFANATINERFLEERDKLAASCK KDDVAKHNI EL AMAAVI.KNH - 1
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102: TyeGAIAIKRPQ, LKGLINGUTOFOGQOESLLAEFN ASDA. RYLHESSLEKRLQKA: 102: TyeGAIVLKRPQ, LKGLINGVINOFOGQOESLLAEFN ASDA. RYLHESSLEKRLQKA: 98: TyeGATVLKRPQ, LKGLINGVINOFOGQOESLLOMAV SNNAGKYGH SYLLKLUQEA: 103: AVEIAKIRGH. KGIASFMOULHSIOEGUVPSFDAIEDPVRLATETSHPDINKEWADA: 96: AVEIAKIRGH. FGIGKFMNGULHSIOEGUVPSFDAIEDPVRLATETSHPDINKEWADA: 97: AVEIAKIRGH. FGIGKFMNGULHSIOEGUVPSFDAIEDPVRLATETSHPDINKEWADA: 101: AVELAKLRKKGSEKIMAAULHSIDEGWPDIASIKKNNKRDSIAYSLIVALVKKLEDO: 102: AVELAKLRKKGSEKIMAAULHSIDEGWPDIASIKKNNKRDSIAYSLIVALVKKLEDO: 103: AVELAKLRKKGSEKIMAAULHSIDEGWPDIASIKKNNKRDSIAYSLIVALVKKLEDO: 104: AVELAKLRKKGSEKIMAAULHSIDEGWPDIASIKKNNKRDSIAYSLIVALVKKLEDO: 106: ANNITKKYISLKSSKFVMAULHNIPMES EHRNEEPKDWETKYSM KLLDKMVRQ: 106: ANNITKKYISLKSSKFVMAULHNIPMES EHRNEEPKDWETKYSM KLLDKMVRQ: 107: TYEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	22 : DIEGAIAIKRPO, LKGLHGVERORGOQUELLAEFNASDA.RYLHESDIDKRLQKA: 22 : TUEGAIVLKRPO, LKGLHGVERORGOQUELLAEFNNDS.HYLHESDIDKRLQKA: 23 : TUEGKLKOFR, LKGLHGVERORGORGEELOMAVNNAGKYGHSSIDLKLQEA: 33 : AKEIAKIRGH.KGIASTVOOVLESIGEGVPSFDAIEDPVRLATETSHFEILVKEWADA: 54 : AMELGKRGN. PGIGKYVGVLFARGGNGAPSLAAISDPVDRLATETSMFRITTKLLAG: 31 : AMELGKRGN. PGIGKYVGVLFARGGNGAPSLAAISDPVDRLATETSMFRITTKLLAG: 31 : AMELGKRGN. PGIGKYVGVLFARGGNGAPSLAAISDPVDRLATETSMFRITTKLLAG: 31 : AMELGKRGN. PGIGKYVGVLFARGGNGAPSLAAISDPVDRLATETSMFRITTKLLAG: 31 : AMELAKLRKKGSEKLVGAULERILBEGWPDIASIKKNKRDSIAYSLVVLVKLEDD: 32 : AMELAKLRKKGSEKLVGAULERILBEGWPDIASIKKNKRDSIAYSLVVLVKLEDD: 30 : AMKIAK.RHDGQATANFIGAVLENDYNGSEHRNEEPKDWETKYSMFKLLLDKMVRQ: 36 : AMKITKKYISLK.SSKFVGAULENDYNGSEHRNEEPKDWETKYSMFKLLLDKMVRQ: 37 : TUEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	L	17: VWNATKSLKSDS, FRGLMANDERELEODEILAIIDKN. WOTLHERAFWNKLKKA-1
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103 : AVEIAKIRGH. KGIASFMOULRSICHEGUPSFDAIEDPVRRLATETSH DILVKEWADA : 96 : AVEIAKIRGH. POIGKFUNG UTARCONCAPSLAISDPUDRLATETSM RRUTEKLLAD: 101 : AVELAKLR. KKGSEKLWAAULRIUEGGWPDIASIKKNNKRDSIAVSLVVHDVAKLKED : 97 : AVGLAKNRGNKKGGEKFUNGTOOFTSHELPDMETIKRNNKYSVKVSLVULVKKLED : 100 : AVKIAK. RHDGQATANFIGAULHNEMES EHRNEEPKDWETKYSM KLLUXMVRQ : 106 : ANNITKKJISLK. SSKFUNGUENVILUNVILGYNKNDSVEKLCPNVSFEP AVKFELKD : 97 : TVELAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	03: AVEIAKIRGH. KGIASFUNGULESIGREGVPSFDAIEDPVRRLATETSHEB DYKEWADA: 56: AVEIGKRRON. PGIGKY VNOVDRAR GONGAPSLAAISDPUNRLATEISMER UTEKLLAQ: 01: AVELAKLR. KKGSEKLUNAVLERI HEGWPDIASIKKNKRDSIAYSLVVDVAKLKED: 7: AVGIANNRONKKGAEKFUNATLEGTSHPLDDMETIKRNKYYSVXSLVDVDVAKLKED: 00: AVKIAK. RHDGQATANFIDAVLENINGS EHRNEEPKDWETKYSMEKLLDKMVRQ: 56: AVKITKKYISLK. SSKFUNAVLENINGS EHRNEEPKDWETKYSMEKLLDKMVRQ: 7: TVEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKRPIEYSMEKITDHWATH: 56: TVKLVKN ENFKLVMAVLERENTVEPE KELLVYSHEB ITVNMSF:		98 : TWEGTKELKGPR, LRGLTNAW GNOEELDOMAV SNNAGKYCH STREKLLOFA . 1
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101 A BELAKLR. KKOSEKLUMADUR ILEGOWPDIASIKRINKRDSTAYSLUVDVAKLKED 97 ANGLAKNRONKKGAEKFUNATUR OFTSHPLPDMETIKRINKVISVSLVVLVKKLEDD: 000 ANKLAK. RHDGQATANFTAATISNEMES BHRNEEPKOWETKYSMIKLLKNVRQ: 100 ANNITKKVISLK. SSKFUNATURING HINTAFYNKDNSVELCENVSFEP MYNFFLKQ: 97 TYELAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKMPIEYSMIK TIDHWATH: 66 TYKLVKN ENFKLMANTERLETVEPKELHUVSHEPETMYNFRSF.	D1:ABELAKLRKROSEKLUMAVLERILEBONPDIASIKRKINKRDSIAYSLUVEVAKLKEE. 97:AUGIAKNRGNKKGAEKPUNAILEOETSHPLPDMETIKRNKVYSUVYUVVSUVDLUVKKLED. 05:AUKIAK.RIDGOATANFIAYULPNYMSEHRNEEPKUWETYYSMEXLUDAVUVO. 05:AUKIAK.RIDGOATANFIAYULPNYLENPYILFYNKDNSVEKLCPNYSPEP MYKPFLKO. 97:TVEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKMPIEYSMEK IIDHWATH: 6:TVKUVMENFKKUVMAVLERKLTYPEPKELULVYSHEBIINVRSF:		96 : AWEIGKERGN, PGIGKEVAGWABAKOBNGAPSLAAISDPUDRLATETSMEDDIVERTAA
97: ANGIAKNRGNKKGAEKFYNATER OFTSHPLPDMETIKRRNKYYSVKYSLEVELVKLEDQ: 100: ANKIAK.RHDCQATANFTYALLENEMSEHRNEEPKDWETKYSMEKLLDKMVRQ: 106: ANNITKKYISLK.SSKFYNAULENVLENENIAFYNKDNSVEKLCFNYSFEP MYKFFLKQ: 97: THEIAXXXXXX,XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	97: AVGIAKNRGNKKGAEKFUNATLE OFTSHPLPDMETIKRRNKYYSVKYSLEVDUVKKLEDQ: 00: AUKIAK.RHDGQATANFIRATIENTESBHRNEEPKUWETYYSMSKLULDKUVRQ: 06: AUKITKKYSKIKS.SSKFURIENTLENTENPNIAFYNKDNSVEKLCFNYSTEP MUKFFLKQ: 9: TWEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKMPIEYSMEKITDHWATH: 66: TVKLVKNENFKKUVMAVLERETVPEPKELLLYYSHEBITMYWRSF:	1	.01: AWELAKLR. KKGSEKLUNAWARTI ZEGWPDIASIKRKNKRDSIAVSIAVSIAVARTI PRO . 1
00: Aukiak.rhdgqatanftgatlineresehrneepkdwetkysmelilldkmyrg: 06: Aunitkyisk.sskfygatlinnienen lefnnknnsveklepnyspep rykfflkg: 97: Tyflaxxxxxxx.xxxxxxxxxxxxxxxxxxxxxxxxxxxxmpieysmek tidhwath: 65: Tyklinkenfklingatlerleftepkelhuvshepethynyrbsf:	00: AUKIAK.RHDGQATANFTISALLENEVESEHRNEEPKDWETKYSMEKLLLDKMVRQ: 06: ANNITKKYISLK.SSKFVIAULENVILNYNIAFYNKDNSVEKLCFNYSPEP MYKFFLKQ: 97: TVEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKMPIEYSMEK IIDHWATH: 56: TVKLVKNENFKLVMAN GRLETVPEPKELLLVYSHEBIINYNESF:		
.06:AMNITKXYISLK.SSKF <mark>UAALIST</mark> YLENNILAFYNKDNSVERLCFNYSFEP AVVFFLKQ: 97:TVEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKMPIEYSMEK TIDHWATH: 66:TVKLVKNENFKKL <mark>WAATL</mark> SLRTVFEPKELHLVYSHEPE LYNNYRSF:	06:ADNITKKYISLK.SSKFVEAUEDAYLENAYLENAPENIAFYNKDNSVERLCPNYSTEP ATVRFFLKQ: 97:TVEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		00: AWKIAK, RHDGOATANFINAWI ENFMAS. EHRNEEPKDWETKYSMERI III. DVM/DO. 1
97:TVEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	97:TYEIAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		
66: TWKLVKNENFKKLVMAVLRRLRTVPEPKELHLVYSHEETIVNYWRSF:	66:TWKLVKNENFKKLVNAVLRRLRTVPEPKELHLVYSHPEYIVNYWRSF:		
in the second se	02: GUDLAKANG. LKGLSKVVNG4LERYCHAEEQGKNILDQEKISLGEQYSFDD114ELFEQT:		
02 CONDLAKANG LKGLSKVON MERKONAFFOCKNTLDOFKTCLCFOVCFONT	-********************************	1	02 CODLAKANG LKGLSKVANGALERYODAEEOCKNTLDOEKTSI CEOVODERTATIN WSF 1

#### B. Subfamily III (Yebu) C-terminal extension

sp*	EGQSTKLAPKSNLIKDQLRLWKMFEKDHANITL:300
sn*	NNPAPHPRASKSNLSREQVALWQEFAQNHEKVNL:315 .PERESVRHQQPKSKEKKNAEKHIPHGIK.CFVHa:324
pg* ec	.PERSSVEREQPERSSVEREQPERSKEREKKAAEKHIPHGIK.CFVHA:324 IPALPAP <mark>KYK</mark> VGNFPFSPVKDREAGQIRQAATGYGINW:353
ec	IPALPAPE WEVGNPPFEPVKDREAGQIRQAATG COMMUNICASS
sp*	301: SGTLQTFEL.YLYLLEDEEPAL.DGLKIANNELELEVFKKEREPSYALGLALKPDEV: 356
sn*	316: PGILOIFGD.OLYLLEELEPDU.WELKIAFNSLHLGTFKKERFEPSFALGLAUKPSOV: 371
pg*	325: PEKYEWRWMCEEYWWEFPVSTEALIGWVRFSELSTKLAETHNNGYRWOHEAVTALASPIN: 384
ec	354: DENLR. LWORDKELWLFEVEIEALIGWYRFSRLCIKLAETHNWGWRWQHEAVIALASPIN: 412
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	<b>•</b> *
sp*	357:RSSIBUREBO~~~~
sn*	372: EQSVEIGQEAFVKYAAGETVQLAESLPNGWYQVLVKGNGLGFEKVTGNVLKNYF: 425
pg*	385: MNAPE HALTPNVL EMVECLKANGIRLHTAGITVGMQKGKDLVPAPALALSTEMDDHSFE: 444
ec	413:MNAFELTPQBAEEWYRGRDVYPQAAPVADDVLVTFQHQPI.GLAKRIGSRLKNSY:466
	_*****_**
c.	Sufamily IV Archaebacteria N-terminal extension
•••	sarding it homosacorra a communicate excension
pfE	1: MEAEKEKKLSIPPRGURE. IITEAVRLGEVIKPSOYEKREAEKEHDIKEAWLMEVITMIF.: 58
phE	1: MEAEK.KKLSIPPKGURE.IIEAIRLGEIIKPSOYEKREAEKKHDVEEAWLNEVITMIF.: 57
pfA	1:~~~~MELFYRVTIHEIVEDALMLVEEKEL.SSKHALEKIEKKVEGKOKEKARGIAHAVV: 54
phA	1:~~~~MELFYRVTLHEIIEDALTLIEEREL.SEKHALERVERRVEGKIKETASGIAHAVV: 54
afA	1:MSARSDGSNVIPTQEIAAKVLAEVERSRISVKSDVQKLAGGFD.YKVEGSVHAYS: 54
	*
pfE	59: YDIMRKQGLIIKAIKDVVGVTPLI. DEMIRAALRVAFDVVLGHDENQNILKNIKWKA: 115
phE	58:YDIMKKOGLIDKVIKEIVGVIPLI.LDPWIRAALRVAVDIALEHDESSONIKNIKWKA:114
pfA	55: FEIEWWRAKIIFIINSVLRGSKVEDLDEYHANLLRICVFENKSKKINEAIAIDSIWEVVK:114
phA	55: FETERWRAKTEFILNSVIKGSRVEDGETYLANLEFIGTFEMKSKGVNBAIAIDSVVRVVK:114
afA	55: VETLERLNALFYFLKSTLKKFDGLDFFTRNLLEFTAVYEMKYKGVHEALADSAVEIAR:112
	***_***********************
pfE	116:SDTISSETHPYVGMYYWTIFERILEYKPNPKTELERIEMEXLABAALKERWRKING.:171
phE	115: SDTISSETHPYVGMYFWDLDKTFTYKPNPKNPLERIDA KYLAPSTARRWKGTC 170
pfA	115:SD ISSRTHPYVGNYFWDLLDKIF PYKPNPKNPLEELEMKYLASSALTEROKGIGS.:170 115:EK DLTRA.KFANAILREVEKFNVEKALKRLKEKDRIEMLAVRESHTRIVYPYVIDLCY:173
phA	115: EKEDLTRA. KFANAVLREVEKFNVBRALKRLKBRDRIEGLSVRFSHPROVVDYVKLLCY: 173
afA	113: ER GKA. SLVNAVLRKVEKLDTO. AEGRLKE LSLTYFHEEAFVKYAIEM CE: 161
	*****************
	<b>—</b> • •
pfE	172: DETKAFFEAV <mark>N</mark> RKHEW
phE	171: DETEDFFRSVNKRHEW
pfA	174: DEAVRLLLS. NLKPOR
phA	174:DETVRLLLS.NLRPQR
afA	162: GALKLMKA.NLENPP
	***-*

Figure 3. Conserved extensions of three subfamilies of the putative RNA m<sup>5</sup>C MTases. Numbering is shown for each amino acid sequence.  $\sim$  and X as in Figure 2. (A) N-terminal extension of selected members of subfamily I. (B) Conserved region of the C-terminal extension of members of subfamily III. (C) N-terminal extension of members of subfamily IV.

conserved 4 bp stem–8 base loop of small subunit RNAs. Although some Eukaryotes and Archaebacteria have a C in the corresponding position, the known modification patterns in this region are very different from those found in Eubacteria (14,15), and no putative orthologs of Fmu were found in these phyla.

Subfamily II possesses several putative orthologs in eukaryotes; six ORFs are listed in Table 1. Members of this family have a C-terminal extension in addition to a large N-terminal extension which has been shown to contain nuclear and nucleolar localization motifs (16). The proteins from human, mouse and yeast have been studied without knowledge that they might be RNA m<sup>5</sup>C MTases. Previously, the AdoMet-binding motifs and the nucleolar localization of these proteins led workers to propose that they may be RNA methylating enzymes (17), possibly nucleotide 2'-O-MTases (18). Because of the signature motifs described below, we now propose that these ORFs encode RNA m<sup>5</sup>C MTases rather than 2'-O-MTases. The human protein in this subfamily, P120, has attracted interest as a tumor marker (19–22).

Subfamily III, including YebU from *E.coli*, contains four eubacterial members that we predict to be orthologs. These ORFs encode the core plus a conserved C-terminal extension (Fig. 3B). Since rRNA of *E.coli* contains only three m<sup>5</sup>C residues, and Fmu methylates C967 of 16S rRNA, YebU from *E.coli* may be responsible for producing one or both of the remaining m<sup>5</sup>C residues of rRNA: C1407 of 16S rRNA or C1962 in 23S rRNA.

Subfamily IV contains five members from Archaebacteria which have in common a conserved set of N-terminal extensions different from the set found in the Fmu subfamily (Fig. 3C). Two Archaebacteria, *Pyrococcus horikoshii* and *Pyrococcus*  *furiosus*, each contain two putative RNA m<sup>5</sup>C MTases in this subfamily. The two eubacterial homologs listed in Table 1 are represented by incomplete sequences; provisional assignment to subfamily IV is based primarily on homology in the core region.

Subfamily V contains seven archaebacterial members of unknown function. This subfamily contains only the core sequence. Three Archaebacteria, *Archaeoglobus fulgidus*, *P.horikoshii* and *P.furiosus*, each contain two putative RNA m<sup>5</sup>C MTases in this subfamily. There is also one eubacterial RNA m<sup>5</sup>C MTase homolog that appears to possess only the core sequence. It is provisionally assigned to this subfamily.

Subfamily VI contains two archaebacterial members of unknown function that are uniquely characterized by an internal insert between two portions of the conserved core sequence.

The proteins encoded by the eukaryotic ORFs in subfamilies VII and VIII are more diverged from Fmu than the members of groups I-VI. A yeast ORF (NCL1) from subfamily VII has recently been identified as encoding a non-essential nuclear protein (23). Disruption of NCL1 leads to increased sensitivity to paramomycin, an aminoglycoside antibiotic that affects translational fidelity. The core sequences of subfamily VII contain the sequence motifs (discussed below) which clearly identify them as members of the family of probable m<sup>5</sup>C MTases. Motif N1, whose function is unknown, is more diverged or absent. Members of the family have N- and C-terminal extensions with conserved regions whose lengths are uncertain due to incomplete sequence data. Subfamily VIII possesses a variation in one of the prime signature motifs for RNA m<sup>5</sup>C MTases (motif IV discussed below; ProSerCys rather than ProCys) and assignment of the 5 position of C as the target of methyl transfer is therefore less certain for this subfamily. Members of subfamily VIII have at most a minimal C-terminal extension; there is an N-terminal extension with a conserved region whose length is uncertain.

The phylogenetic distribution of the Fmu subfamily (subfamily I) (Table 1) suggests that this enzyme originated in a common ancestor of many eubacterial phyla, in particular the Firmicutes (the Gram-positives) and the Proteobacteria phylum (which includes E.coli). Also the wide distribution suggests continuing and strong selection pressure to retain this enzyme. Analysis of small subunit rRNA sequences suggests that secondary loss of the activity is correlated with loss of the substrate C in specialized genera such as Mycoplasma (in the Gram-positives), in divisions such as the epsilon division of the Proteobacteria (which includes H.pylori and C.jejuni), and perhaps in entire secondarily reduced phyla such as the Spirochaetes (T.pallidum, B.burgdorferi). Representatives of subfamilies II, VII and VIII show a distribution suggestive of an ancient origin in a common ancestor of Fungi and Animalia, with secondary loss of VII and VIII in the nematode Caenorhabditis elegans. The eubacterial homologs in subfamilies III-V show widely scattered phylogenetic distributions more consistent with lateral transmission (Table 1).

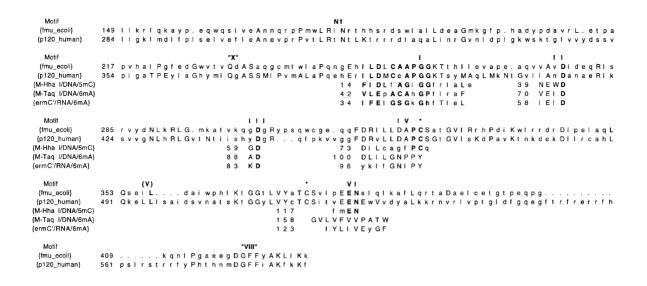
## Sequence motifs and structural homologies in the AdoMetdependent DNA and RNA MTases

Alignments of known DNA and RNA AdoMet MTases exhibit an ordered set of up to 10 motifs, designated I–X (9,10) for which functions have been assigned from structural studies (24–27). Motifs I–V contain binding elements for AdoMet. Motifs IV and VI contain signature sequences that target specific bases. Motif IV contains a ProCys consensus for the DNA m<sup>5</sup>C MTases or a Pro(Tyr/Phe) consensus for the exocyclic amino m<sup>6</sup>A and m<sup>4</sup>C MTases. Motif VI contains an acidic residue for recognition of the target C of m5C MTases or hydrophobic residues in exocyclic amino MTases (6,7,11). Two other motifs found in AdoMet-dependent MTases, VIII and X, are well conserved within but not between separate families of DNA MTases. The linear arrangements of motifs I-X are found as circular permutations characteristic of different AdoMet-dependent MTase families (8). Most DNA m5C MTases have the arrangement, I-VI...VIII....X; one unusual DNA m<sup>5</sup>C MTase is circularly permuted to have motif X at the N-terminus (28), a pattern also seen in the DNA exocyclicamino MTase family gamma (29). Regardless of their linear arrangement, motifs VIII and X occupy similar positions in the three-dimensional structures, and hence probably serve similar functions. Recent work suggests that for polynucleotide substrates, a likely function for motif VIII is to help stabilize the target base in a position flipped out from its normal position in the secondary structure (30).

Crystal structures show that the DNA m<sup>5</sup>C MTases are folded into two domains. The larger 'catalytic' domain is composed of the N-terminal region and usually has a small contribution from the C-terminus. This domain consists of a typical MTase fold containing the motifs that provide the AdoMet binding and catalytic sites. The core region (excluding motif N1) of the RNA m<sup>5</sup>C MTase family corresponds to this domain of the DNA m<sup>5</sup>C MTases. The smaller variable domain provides sequence-specific recognition of DNA substrates. The RNA super-family does not contain this smaller domain, but either the extensions and inserts that characterize the subfamilies or separate subunits may serve as RNA binding domains.

The crystal structure of the RNA MTase ErmC' and the solution structure of the related ErmAM have recently been determined (31,32). These enzymes are members of a family of enzymes which confer erythromycin resistance to microbes by methylating N6 of a highly conserved A residue in large subunit rRNAs (A2058 in *E.coli*) (33). The *erm*-related gene products show conserved core sequence motifs homologous to the AdoMet binding motifs and base-specific motifs of the exocyclic amino DNA m<sup>6</sup>A and m<sup>4</sup>C MTase families. Analysis of these motifs and their location in the structures shows them to be organized in the same fold found in the DNA m<sup>5</sup>C and m<sup>6</sup>A/m<sup>4</sup>C MTase families. The sequence and structural homologies of these proteins strongly suggest evolutionary relation-ships connecting AdoMet-dependent MTases, including the RNA and DNA m<sup>5</sup>C and m<sup>6</sup>A/m<sup>4</sup>C MTases.

The larger region of the conserved core of the putative RNA m<sup>5</sup>C MTases contains eight conserved motifs ('X'-I-II-III-IV-V-VI-'VIII') that as a group have strong homologies to the signature motifs described above. Figure 4 shows the core region of two representatives of the putative RNA m<sup>5</sup>C MTase superfamily aligned with conserved motifs from representatives of three other nucleic acid MTase families. Alignments of motif regions, N1, 'X' I, IV, VI and 'VIII', for all eight subfamilies of the putative RNA m<sup>5</sup>C MTases are shown in Figure 2. 'X' and 'VIII' are two conserved motifs that flank motifs I–VI and thus are in the positions of motifs X and VIII, respectively, in the unusual DNA m<sup>5</sup>C MTase described above. The conserved motifs provide evidence that all of the



**Figure 4.** RNA m<sup>5</sup>C MTases aligned with the signature motifs of representatives of other AdoMet-dependent MTases. Two RNA m<sup>5</sup>C MTases, Fmu and P120, are shown. Capital letters indicate residues that are moderately to highly conserved in subfamilies I–VI. The two Cys residues that are totally conserved throughout the superfamily are indicated with \*. R M-*Hha* I, M-*Taq* I and ErmC' are representatives of different superfamilies of AdoMet MTases. The alignment of the conserved regions shown is based on published crystal structures (31). Analogous conserved regions from different families have been given standardized motif names (I–VIII and X) (8). Bold letters in motifs I–VI indicate residues likely to be involved in substrate and AdoMet binding.

Fmu homologs are MTases that specifically target the 5 position of C.

## Relationship of the Fmu homologs to the DNA m<sup>5</sup>C MTases

Conserved motifs I–VI of the putative RNA m<sup>5</sup>C MTases bear a striking resemblance to the six AdoMet and cytosine-binding motifs (I–VI) of the large catalytic domain of DNA-m<sup>5</sup>C MTases. Following is a comparison of conserved motifs of the putative RNA m<sup>5</sup>C MTases to the motifs of DNA m<sup>5</sup>C MTases using Fmu and M-*Hha*I as examples of the two families (Fig. 4).

Motif I is one of the most conserved motifs in the DNA m<sup>5</sup>C MTases (residues 18–22, FAGLGG, in M-*Hha*I). It is rich in Gly and other small side-chain amino acids that allow a tight turn that interacts with AdoMet. In Fmu the analog of motif I appears at residues 254–259 (CAAPGG), and it is also one of the most conserved motifs in the RNA m<sup>5</sup>C MTase family alignment.

Motifs II and III are among the least conserved motifs in the DNA-m<sup>5</sup>C MT family. Each contains an acidic residue which provides part of the AdoMet binding site (E40 and D60 in M-*Hha* I). Motif II is usually spaced 10–20 residues after motif I, and motif III occurs about 20 residues thereafter. In Fmu, the candidates for motifs II and III are those which contain D267 and D303.

In the DNA m<sup>5</sup>C MTase family, conserved motif IV provides binding residues for both AdoMet and cytosine and includes the active site Cys that forms a covalent adduct with the 6 carbon of the cytosine ring during catalysis (34). The catalytic Cys follows about 20 residues after the acidic residue of motif III, and it is invariably preceded by a Pro, the side-chain of which interacts with AdoMet (Pro80Cys81 in M-*Hha* I). As expected, the ProCys of motif IV is not found in the MTases that methylate the exocyclic amino groups of A or C, since covalent adduct formation with the target base is not an essential feature of these reactions. In Fmu, motif IV contains Pro324Cys325 and is one of the three most highly conserved motifs of the RNA m<sup>5</sup>C MTase family. Although there is a second completely conserved Cys in the RNA m<sup>5</sup>C MTase family, Cys325 is likely to be the nucleophilic catalyst. A recent report of a mutagenic analysis of the yeast subfamily II (p120) homolog shows that the Cys residue in the ProCys motif is essential for function, while the second conserved Cys is not (35).

Motif V is not always clearly identifiable in members of the DNA m<sup>5</sup>C MTase family (Leu100 in M-*Hha* I). The suggested function is to provide a hydrophobic residue, usually Leu, as part of the AdoMet binding site. In Fmu, the candidate for motif V is that which contains the highly conserved L357.

Motif VI, a third highly conserved motif of the DNA m<sup>5</sup>C MTase family, provides a glutamate in the sequence GluAsn as an important contributor to cytosine-binding (E119 in M-*Hha*I). The Glu side chain carboxyl forms H-bonds to N3 and N4 of the target cytosine, serving a role in determining cytosine specificity. In Fmu, motif VI contains E381N382 and is highly conserved throughout the RNA m<sup>5</sup>C MTase family. This motif region also contains the second Cys residue which is totally conserved in this family.

### Summary

Using Fmu as a probe to search the available sequence databases, we uncovered more than 50 proteins that are likely to be RNA m<sup>5</sup>C methyltransferases. Only one Fmu homolog, YebU, was found in the *E.coli* genome database, and we propose that this enzyme is responsible for producing one or both of the remaining m<sup>5</sup>C residues in rRNA (C1407 of 16S RNA or C1962 of 23S RNA). Of significance is the finding that human P120, a proliferation-associated nucleolar antigen and important tumor marker, is also likely to be an RNA m<sup>5</sup>C MTase. Comparison of sequences of the putative RNA m<sup>5</sup>C MTases to those of DNA m<sup>5</sup>C MTases revealed that at least six conserved signature motifs in the DNA MTases were also found in the RNA m<sup>5</sup>C MTases. From this comparison, we identified Cys325 of Fmu, and the corresponding Cys residue in each of the Fmu homologs, as the probable candidate for the catalytic nucleophile in the enzymatic reaction.

## ACKNOWLEDGEMENT

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