

Supplementary Material

Fish lysozyme gene family evolution and divergent function in early development

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Running title: Lysozymes in fish

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Supplementary Tables:

Supplementary Table 1: Accession numbers of the vertebrate and invertebrate lysozyme C-type and lysozyme G-type sequences used in the analysis. (Please see excel spreadsheet).

Supplementary Table 2: Accession number of the invertebrate lysozyme I-type.

Common name	Species name	accession number
Bivalves		
Asiatic hard clam	<i>Meretrix meretrix</i>	ADL27913.1
Mediterranean mussel	<i>Mytilus galloprovincialis</i>	OPL33781.1 AJQ21515.1 BAF63423.1 AAN16210.1
Blue mussel	<i>Mytilus edulis</i>	AAN16207.1 ABB76765.1
Pacific Oyster*	<i>Crassostrea gigas</i>	BAF48045.1 Q6L6Q6.1 NP_001292276.1 BAF48044.2
Cockscomb pearl mussel	<i>Cristaria plicata</i>	AFN66526.1 AFN66527.1
Hydrothermal Vent mussel	<i>Bathymodiolus thermophilus</i>	AAN16209.1
Hydrothermal Vent mussel	<i>Bathymodiolus azoricus</i>	AAN16208.1
Iceland scallop	<i>Chlamys islandica</i>	CAB63451.1
Japanese Scallop	<i>Mizuhopecten yessoensis</i>	XP_021354667.1 XP_021357629.1
Jinjiang oyster	<i>Crassostrea rivularis</i>	ADY38955.1
Manila clam	<i>Ruditapes philippinarum</i>	ACU83237.1
Venus clam	<i>Cyclina sinensis</i>	AET13645.1
Eastern Oyster	<i>Crassostrea virginica</i>	B3A003.1 XP_022306813.1 XP_022343938.1
Farrer's Scallop	<i>Azumapecten farreri</i> <i>Mizuhopecten yessoensis</i>	ANH58186.1 XP_021357629.1
Gastropods		
Disk abalone	<i>Haliotis discus discus</i>	AGQ50334.1 AOX15707.1
Duck clam	<i>Macra quadrangularis</i>	ADM34988.1
Cephalopods		
California two-spot octopus*	<i>Octopus bimaculoides</i>	XP_014768593.1
Annelida		
echiura	<i>Urechis unicinctus</i>	AWA82039.1
medicinal leech	<i>Hirudo medicinalis</i> <i>Capitella teleta</i>	AAA96144.1 R7TR64 R7TIG0
	<i>Eisenia fetida</i> <i>Eisenia andrei</i>	AGJ83864.1 ABC68610.1

Brachiopoda

<i>Adineta vaga</i>	GSADVG00067328001
	GSADVG00026607001
	GSADVG00059746001
	GSADVG00058572001
	GSADVG00066342001

Echinoderm

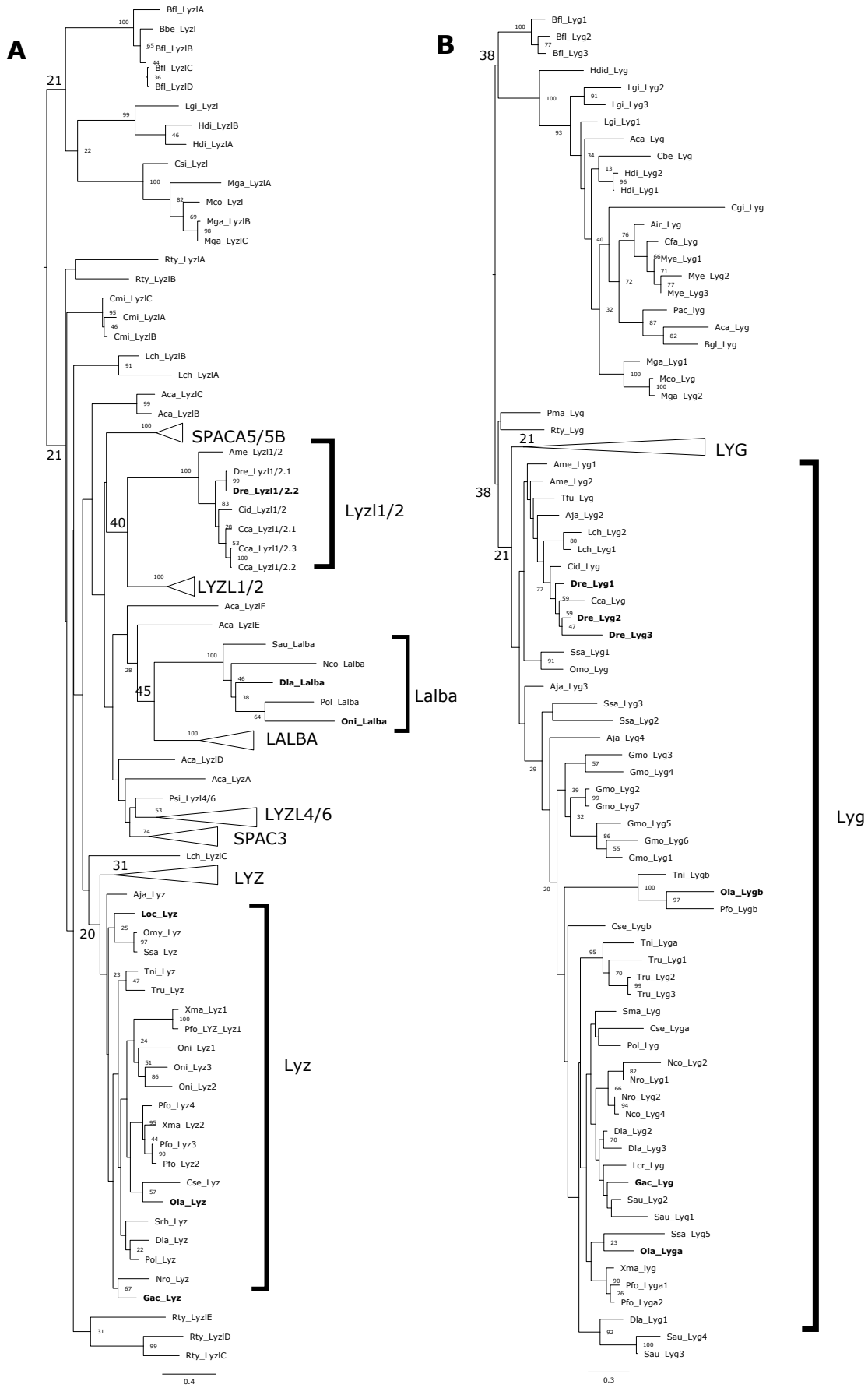
European starfish	<i>Asterias rubens</i>	AAR29291.1
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Cephalochordate

Amphioxus	<i>Branchiostoma floridae</i>	XP_002602594.1
		XP_002593924.1
		XP_002593923.1

Supplementary Figures:

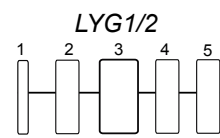
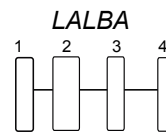
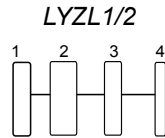
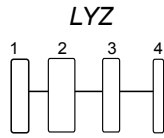
Supplementary Figure 1: Maximum Likelihood phylogenetic tree of the fish lysozyme C-type (A) and G-type (B) with the homologues from other chordates and molluscs. To facilitate interpretation of both trees the teleost clusters are annotated. Both lysozyme C-type and G-type trees were rooted using the invertebrate (cephalochordate and mollusc) sequence cluster. To facilitate interpretation the tetrapod (mammalian, bird, reptile and amphibia) branch was collapsed. A) Teleost lysozyme C-type formed three main clusters with the Human LYZ, LYZL1/2 and LALBA. B) Fish Lyg form a single cluster with the tetrapod Lygs. In both trees species that were used for gene environment characterization (Figure 6, 7 and 8) are highlighted in bold. A similar tree was generated using the BI method and is available as Figure 2. A description of the abbreviations used and the accession numbers are available in Supplementary Table 1. * represent transcript sequences.



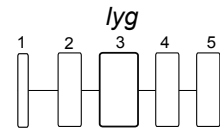
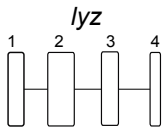
Supplementary Figure 2: Comparison of the gene organization of the teleost *lyz*, *lyz11/2*, *alba* and *lyg* genes with human. The human, stickleback, zebrafish and sea bass gene structures were compared, and the exon and intron positions annotated based on the predicted gene organization available. Exons are numbered and are represented by boxes and introns are represented by lines.



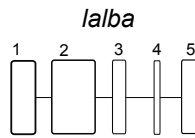
Human



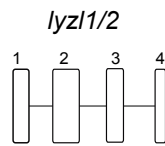
Stickleback



Sea bass



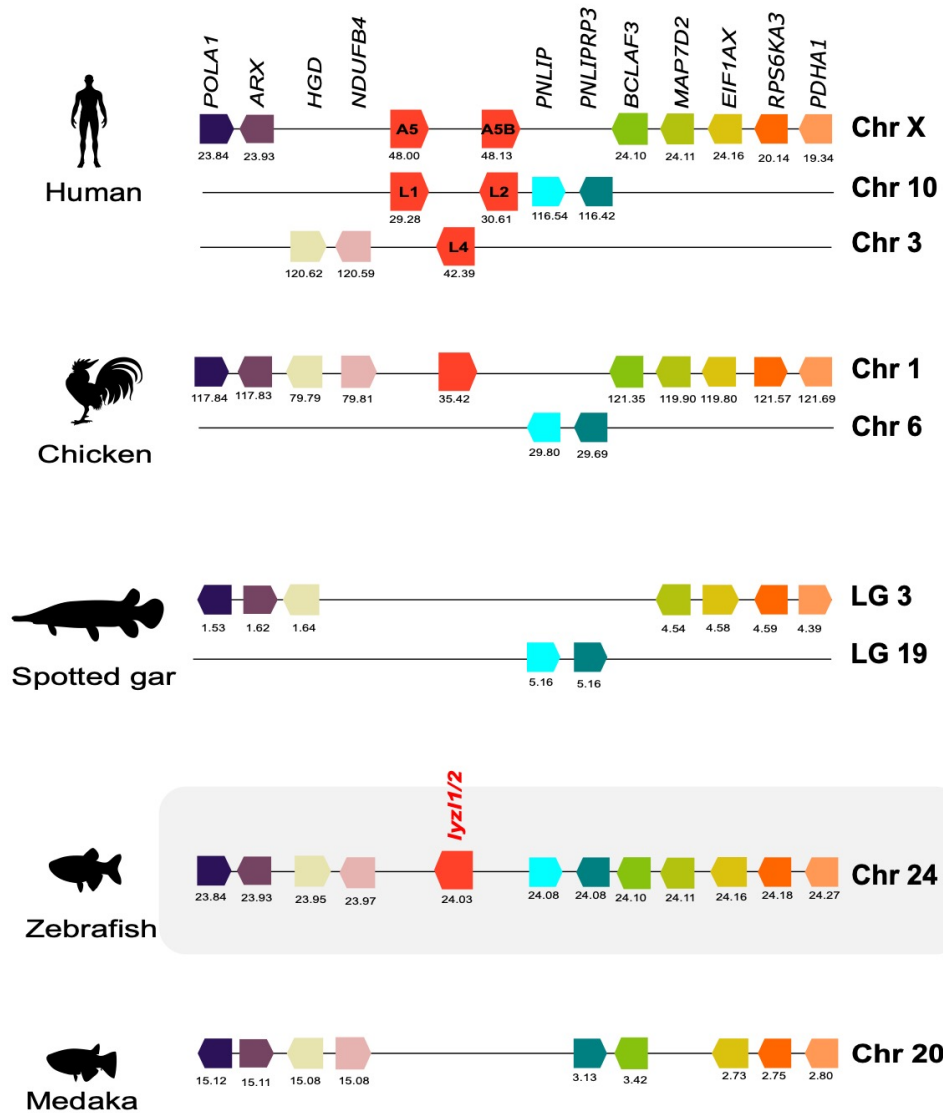
Zebrafish



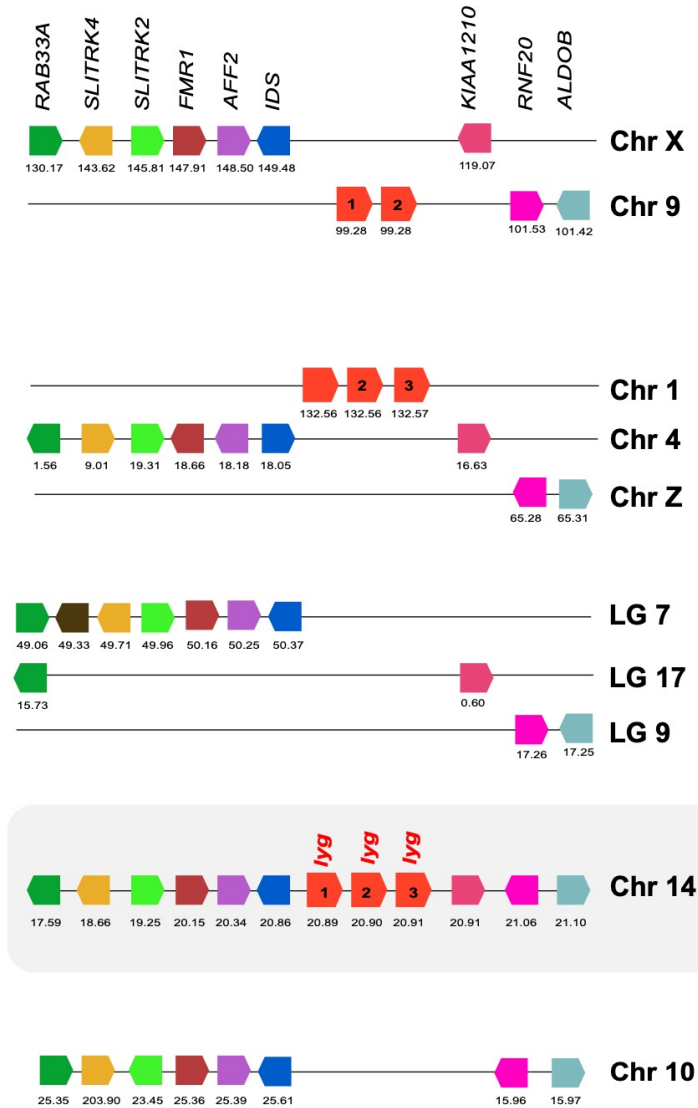
Supplementary Figure 3: Comparison of the zebrafish lysozyme C-type A) and G-type B) gene environment with other vertebrates.

The zebrafish lysozyme (*lyz11/2* on chromosome 24 and *lyg1/2/3* on chromosome 14) neighbouring genes were used to search for homologues in other vertebrates (human, chicken, spotted gar and medaka). Lysozyme genes are represented by a solid red arrow. The neighbouring gene families are represented by different coloured blocks. The direction of the arrowheads represents the transcript orientation predicted in the genomes analysed. Genes are mapped based on their actual positions predicted in the genome assemblies. Only genes that are conserved across the different homologous genome regions are represented. Only chromosome region that share at least two genes are represented. A) The human lysozyme C-type members represented are: SPACA5 (A5), SPACA5B (A5B), lysozyme like 1 (L1), Lysozyme-like 2 (L2) and lysozyme -like 4 (L4). The neighbouring genes represented are: polymerase (DNA directed), alpha 1 (*POLAI*), aristaless related homeobox (*ARX*), homogentisate 1,2-dioxygenase (*HGD*), NADH:ubiquinone oxidoreductase subunit B4 (*NDUFB4*), Pancreatic triacylglycerol lipase precursor (*PNLIP*), Pancreatic lipase-related protein 3 (*PNLIPRP3*), BCLAF1 And THRAP3 Family Member 3 (*BCLAF3*), MAP7 domain containing 2b (*MAP7D2*), eukaryotic translation initiation factor 1A X-linked (*EIF1AX*), Ribosomal Protein S6 Kinase A3 (*RPS6KA3*) and Pyruvate Dehydrogenase E1 Subunit Alpha 1 (*PDHA1*). B) the duplicate human lysozyme G-type genes LYG1 and LYG2 are represented by 1 and 2 in chromosome 9. The neighbouring genes represented are: RAS oncogene family (*RAB33A*), SLIT and NTRK-like family, member 4 (*SLITRK4*), , SLIT and NTRK-like family, member 2 (*SLITRK2*), fragile X mental retardation 1 (*FMRI*), AF4/FMR2 family, member 2 (*AFF2*), iduronate 2-sulfatase (*IDS*), KIAA1210 (*KIAA1210*), E3 ubiquitin protein ligase (*RNF20*), aldolase b, fructose-bisphosphate (*ALDOB*).

A) Lysozyme C-type

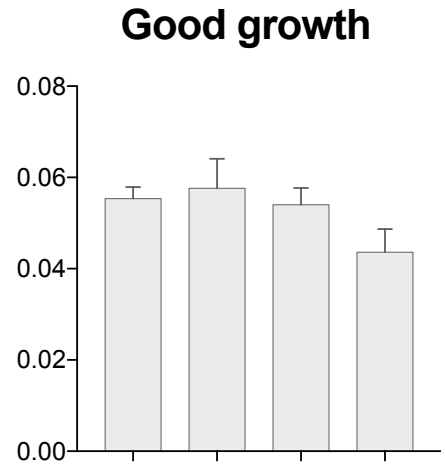
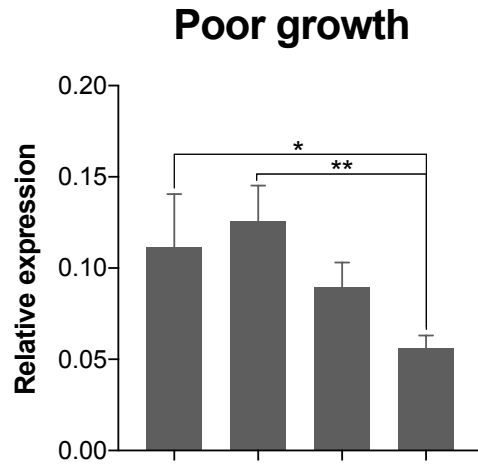


B) Lysozyme G-type

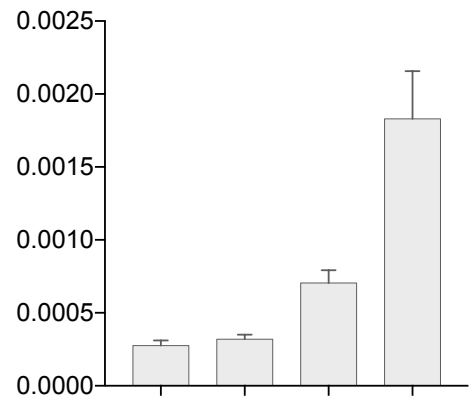
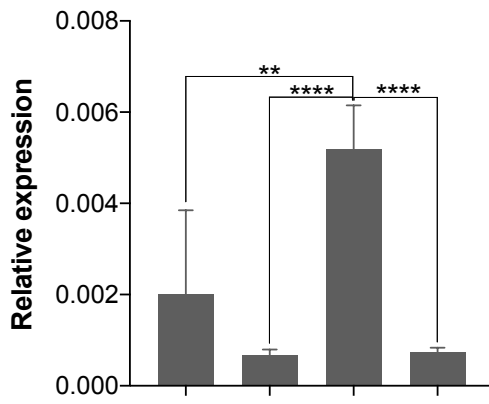


Supplementary Figure 4: Relative expression of the gilthead sea bream *lyg1*, *lyg2* and *lalba* during development. Data correspond to the mean \pm SEM of three to six different samples and gene expression levels were normalized using the geometric mean of two reference genes (*18s* and *ef1a*). Two sample group derived from brood stock that showed a divergent growth performance by mid-metamorphosis when are compared. SPSS 25.0 software was used to assess the significance of differences within each experimental group using Two-way ANOVA. Bars with different letters are significantly different ($p < 0.05$).

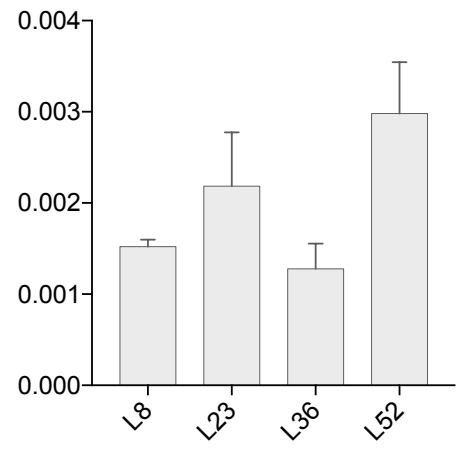
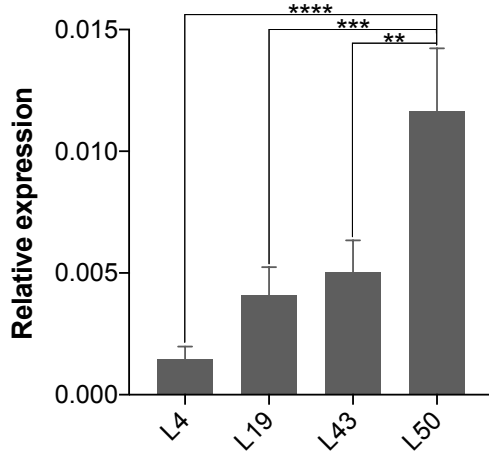
lalba



lyg1



lyg2



Supplementary Data 1: Multiple sequence alignments of the fish and other metazoan

Lysozyme C- type (A) and Lysozyme G-type (B) that used to build the phylogenetic trees.

A) Lysozyme C-type

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Rty_Lyz1E      MKTLLILSAILTARTKTFERCELARIFKYAGLDGYEGYSLQNWICTAFYESAYNSAALNI
Rty_Lyz1B      MKTFLILSALLTTSPPVYQKCELAQLRRNGLDGYRGSYLANWVCLVQHESNYNTRIVGH
Rty_Lyz1C      MKLILVLSVLLTSSAETLSRCQVVKAIKDSILTKFTHYSVADWVCLAYHESQYNAMEIGH
Rty_Lyz1D      MKLIVLSVLLTSSARVLSRCEFARIKNSILAEFPKYSVADWVCMMAHYESQYNTLAKYD
Rty_Lyz1A      MKTLLLSLLLMIDAKVYEKCEFARILKDKGLDGFHRHRLTDWVCMVEIESGYNTALKRH
Cmi_Lyz1C      KTLFVLSLLFLVASAKIYDRCVLARQLKAAGLDGFRGYSLPNWI CMVQHESYNTRATNE
Cmi_Lyz1B      KTLFVLSLLFLVASAKIYDRCVLARQLKAAGLDGFRGYSLPNWI CMVQHESYNTRATNR
Cmi_Lyz1A      KTLFVLSLLFLVASAKIYDRCVLARQLKAAGLDGFRGYSLPNWI CMVQHESYNTRATNR
Mdo_Lyz2      LILLGLVFLPMLAHGKVEYERCELARVLKRNGLHGFRSNSVADWVCLAKWESDYNTKATNY
Mdo_Lyz3      LILLGLVFLPMLAHGKVEYERCELARVLKQNGMDGFGGNSLADWVCLAKWESDYNTKATNY
Mdo_Lyz1      LILLGLVFLPMLAHGKVEYERCELARILKQNGMDGYRGISLANWVCLAKWESNYNTRVYNY
Mmu_Lyz2      LLTLGLLLSVTAQAKVYNERCELARILKRNMGMDGYRGVKLDADWVCLAQHESYNTRATNY
Mmu_Lyz3      LLTLGLLLSVTAQAKVYERCEFARTLKRNGMAGYGVSLADWVCLAQHESYNTRATNY
Hsa_LYZ      LIVLGLVLLSVTVQGVFERCELARTLKRNGMDGYRGISLANWVCLAKWESYNTRATNY
Mmu_Lyz1      LLTLGLLLSITIQGVYDRCSLARTLQSLGLAGFQGITLANWVCLAKWESNFNTNTTRF
Apl_Lyz1      -----HISARRGDGVCMTSWSFNTQATNR
Apl_Lyz2      -----HISARRGDGVCMTSRSGFNTQATNR
Gga_Lyz      LLILVLCFLPLAALGKVFGRCELAAMKRHGLDNYRGSYSLGNWVCAAKFESNFNTQATNR
Psi_Lyz1      LLILGLVLLPLAAPGKIYEQCELAREFKRHGMDGYHGYSLGDWVCTAKHESNFNTAATNY
Psi_Lyz2      LLILGLFLLPLAAHGKIYERCELARAMKRLGLDGYWGSYSLGNWVCTARFESQFNSTATNY
Xtr_Lyz      VLFWGGIFIFTVTDGKVFERCELAGIMKKMGLDGYRGSYSLPNWVCTAFFESSFYTDRTNF
Oni_Lyz2      MRSLLVLLFLAVANAKIFERCEWARTLKANGMDGYGYSLADWVCLTRWESNYNTMAKNT
Oni_Lyz3      IKSLLFLLLVAVANAKRFQRCCEWAHKLKDSGMDGYRNI SLADWVCLTKWESGYDTMKTHH
Oni_Lyz1      RSVFVFLLLITVASAKVFERCDWARKLKANGMDGYRGSYSLANWVCLTKHESNYNTKATNR
Pfo_Lyz2      TKTLVLLLVAVANAKVFERCAWARTLKASGMDGYRGISLADWVCLTQHESHFNTRATNR
Pfo_Lyz3      MKTLLVLLLVAVANAKVFERCAWARTLKASGMDGYRGISLADWVCLTQHESHFNTRATNR
Pfo_Lyz4      MKTLVLLLVAVANAKRFQRCCEWARTLKASGMDGYRGISLADWVCLTQHESGYDTMKTHH
Xma_Lyz2      TKTLVLLLVAAAANAKVFERCAWARTLKANGMDGYHGISLADWVCLTQHESNFNTNVKYR
Pfo_Lyz1      LVVPAVLLLAADVDRVFERCQWARTMKSNGMDGYRDISLANWVCLTYWESGYNTLAVNH
Xma_Lyz1      LVVLAVLLLAADVDRVFERCQWARTMKNYGMMDGYWGISLANWVCLTYSESSYNTTAVNH
Cse_Lyz      IKGVVLLLVALLSVAVYERCTWAKLLKSQGMDFHGISLPNWWVCLTNWESHFNAINH
Ola_Lyz      MKSLVFLLLVAGASAKVFERCQWARLLKAQGMMDGYRGSYSLANWVCLTQHESRFNAINH
Nro_Lyz      MRSLVFLLLVALLASAKVYERCEWARVLKAHGMMDGYGNSLADWVCLSKWESSWTTSTNH
Gac_Lyz      MRVVVFLLLVAAAGAKVYERCEWARVLKANGMDGYGGYGLADWVCLSYSESGYSTTATNF
Aja_Lyz      MRALVFLLLVAVASAKVFERCELARTLKAAGMDGYRGSVSLGDWVCLARWESSYNTAATNR
Srh_Lyz      MRCLLFLLLVAVAGAKVFERCELARLLKSYGMNNYRGISLADWVCLSQWESSYNTRATNR
Tru_Lyz      YSLFLLVLLVAVANAKVFERCEWARVLKARGMDGYRGISLADWVCLSKWESQYNTNAINH
Tni_Lyz      MRTLVFLLLVAVASAKVYQRCCELARVLKSQGMMDGYRGISLANWVCLSKWESSYNTNAINH
Dla_Lyz      MRSLVFLLVAVANARTYQRCCEWARVLKNNGMMDGYHGYSLANWVCLTQHESNYNTGAINH
Pol_Lyz      MRTLVVLLLVAVANARVYERCEWARLLRNQGMMDGYRGISLANWVCLTEWESHYNTRATNH
Omy_Lyz      MRVVVLLLVAVASAKVYDRCELARALKASGMDGYAGNSLPNWWVCLSKWESSYNTQATNR
Ssa_Lyz      MRVVVLLLVAVASAKVYDRCELARALKAYGMDGYAGNSLPNWWVCLSKWESSYNTQATNR
Loc_Lyz      MKFVVFLCLFALANCKVYDRCELARKLKASGLDGYRGSYSLPNVCLSKWESTYNTTAINH
Aca_Lyz1A     -WSLVLLACLVLGQGEYLSRCEVAQQLQQLGMDGYAGYSLANWVCTAFHESFNTQAMHY
Lch_Lyz1C     --LLIPLLLLVASGMVYSRCELARVLQAGMNGYWGYSLGNWLCMSYYESGYNTQAIDH
Cca_Lyz11_2_2 VTI AVLCLMWLCCESRRLKRCDVVRI FKQEGLDGFEFSGVGNVCTAYWESRPFKTHRVR-
Cca_Lyz11_2_3 VTI AVLCLMWLCCESRRLKRCDVVRI FKQEGLDGFEFSGVGNVCTAYWESRPFKTHRVR-
Cca_Lyz1_2_1  VAI AVLCLMWLCCESRRLGRCDVARI FKQEGLDGFEFSGVGNVCTAYWESRPFKTHKVR-
Dre_Lyz11_2_1 LAVVFLCLAWMSCESKTLGRCDVYKIFKNEGLDGFEGFSGIGNVCTAYWESRPFKTHRVR-
Dre_Lyz11_2_2 LAVVFLCLAWMSCESKTLGRCDVYKIFKNEGLDGFEGFSGIGNVCTAYWESRPFKTHRVR-
Cid_Lyz11_2   VAI AVLCLMWMSCESRTMGRCEVVKIFRAEGLDGFEGFSLGNVCTAYWESRPFKTRQVR-
Ame_Lyz11_2   KLVI VLCVMFLACESRTMSRCEVARAFKAQGLDGFEGFALGNVYVCMFAWESKWKTHKVR-
Hsa_LYZL2     MKAAGILCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAQTV
Hsa_LYZL1     KSVGVFALIIISVAESKIYTRCKLAKIFAKAGLDNYGGFALGNWLCMAYYESHYNTTAEVNV
Mmu_Lyz11_2   LVLLLLISYLLTPIGASILGRCTVAKMLYDGGNLYFEGYSLENWVCLAYFESKFNPSAVYE
Mmu_Lyz14     MKASVVLYLVVPSGAYILGRCTVAKKLDHGGLDYFEGYSLENWVCLAYFESKFNPMAYIE
Hsa_LYZL4     LKALFICVASCVNDGNIHRCSLAKILYEEDLDGFEGYSLPDWLCLAFVSNFNISKVNE
Mmu_Lyz16     LLIYLVSSFLALNQASLISRCDLAQLQLEDLDGFEGYSLSDWLCLAFVSNFNISKVNE
Hsa_LYZL6     LLLQFLLCFASRTGAKVFERCELAKMLKNYGLDGYRGSYLANWVCMMAFYESGFDTKMVRP
Aca_Spaca3    VSLVLLATLASGNMGKIFQRCCELAQVLHHAAGMDGFRGYSLADWVCLAFHESRFDTGTVDH
Psi_Spaca3    ALAYLLSCLLASSKAKVFSRCELAKEMHDFGLDGYRGNLADWVCLAYYTSGFNTNAVDH
Mmu_Spac3     AGIMLLACLPSSEAKLYGRCELARVLHDFGLDGYRGSYSLADWVCLAYFTSGFNAAALDY
Hsa_SPACA3    QTLVLLACFVEATQAKIFDRCQLAHVLDKNGLDAFEGISLADWICMAFFESGFDTEAIDW
Aca_Lyz1D     ALLFLVSLIMANEAKIFSRCELAQVLHHAAGMDGFRGYSLENWVCLAYFESKFNPMAYIEDD
Psi_LyzL4_6   LAFVLLCLFIAVSEAKVYEKCELAKILKISKMDVSSGYSLDNWVCLAYHESRFDKAVGP
Aca_Lyz1B     LAFTFLCFLFIAVNEAKVYERCELARLKNRSLDVSSGYSIADWVCLAYYESRFSRAVGP
Aca_Lyz1C     MKAWGTVLMVVTVDKIIYERCELAARLERAGLNGYKGYGVGDWLCMAHYESGFDTAFVDH
Hsa_SPACA5    MKAWGTVLMVVTVDKIIYERCELAARLERAGLNGYKGYGVGDWLCMAHYESGFDTAFVDH
Hsa_SPACA5B   MKAWGTVLMVVTVDKIIYERCELAARLERAGLNGYKGYGVGDWLCMAHYESGFDTAFVDH
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Mmu_Spaca5 VVVILAVLLIAKLDAKIYERCELAKKLEEAGLDGFKGYTVGDWLCVAHYESGFDTSFVDH
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Lch_Lyz1B -----VCLAYYESTYRTHVTHY
Mmu_Lalba VPLFLVCIILSPPQATELTKCKVSHAIK--DIDGYQGISLLEWACVLFHSTGYDTPQAVVN
Hsa_LALBA VPLFLVGIILFPAILAKQFTKCELSQLLK--DIDGYGGIALPELICTMFHTSGYDTPQAVE
Mdo_Lalba KSLLLLSIIILSATQARELTCELIQDLKNGHMDKYEDFHLNEMICVTFHSSGFNTQIKVS
Aca_Lyz1F FTLALLSSVLVASEAKIIQRCHLAKELNDLGLSQYLGFTLGDWLCTVPHESGFNTDPPVS
Ano_Lyz1E LVLLFLLAIVARNNAIILDKCDLTAIWNVLEGEFEGTTIADWICLVFHSTSGFDTAAYNV
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Hdi_Lyz1B TTLGLVLVAVSVDGKIFYKCELAQELKRLGVN---TELYRWVCMAYAESSFNTAATNT
Lgi_Lyz1 -TLCVLLLTVVVSASAYTFTKCSLSTLVSAGVAR---GDVHKVCMANAESGLRTTAHNV
Bfl_Lyz1C -LAVVLVMGLVCAHAKTIERCELARELVSRLTSTR--SQAGEWICLVQHESFRTGARGG
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Bfl_Lyz1B -LAVVLVMGLVCAHAKTIERCELARELVSRLTSTR--SQAGEWICLVQHESFRTGARGG
Bbe_Lyz1 -LAVLLMGVVCAHAKTIEKCELARELVSRLTSTR--SQAGEWICLVQHESFRTGALGG
Bfl_Lyz1A -LAVLLMGLVCAHAKTIEPCDLANELVKLGLTTR--SGAGDWICLVQHESFRTDARGG
Mga_Lyz1B -VSILLVVLVGSYGATKTKCQVVQALRNQGVV---DSDLRDWLCLKVHESNFHYDAIGT
Mga_Lyz1C -FPILLVLVVGSYGATKTKCQVVQALRNQGVV---DSDLRDWLCLKVHESNFHYDAIGT
Mco_Lyz1 LCPILLVVFALVGSYGATKTKCQVVQALRNQGVV---DSDLRNWCLVKHESNYRYDAVGT
Mga_Lyz1A NSVMVLFALLGCSYAGTISKCDVVKALRAEVSF---DSDLRDWLCLVEHESFRTYELHEV
Csi_Lyz1 VKFLVLLMIIESRAATKTKCQVVQALRAQGVTS--DSELRNWLCLVEKESFRTYDVTS
Sau_Lalba LVVFLLAALGCSAHRDVTRECLRDQLKAAIPDEYEGLVSAHVCHAQFASGFNTSAVQL
Dla_Lalba LVVFLLAALSCSSEGRIVSKCELKDALKQRG--LTVDKLVAKIVCHVEFASGFNTSAVRP
Oni_Lalba HRIFLLVVLGCGAGGRIVPKCELRDQLKDSG--LDKFLVLLSSPVVCFVENVSEFNTSLVSN
Nco_Lalba VCLFVLVSLGCSAEGRVVTKCDLKKKEFLPEGAWGHTMTDLAKLICHVEKASEFNTSAVHL
Pol_Lalba -----SLPSVVVYVELTSGFNTSSVKE

* *

Rty_Lyz1E EWRGSMDCGLFQINSFWWCLDNTPSLRNCGMNCSDFLDDDLTDDIVCVKSIKVLPGMSA
Rty_Lyz1B NRAGSSDYGIFQINSVKWCEGDGTPKRKGCRRKCSDFINDNIIDDIQCAKRIVTOG--MNA
Rty_Lyz1C ETNGASEYGIFQISSKWWCDDGRTTPSNGCGIACN-----
Rty_Lyz1D ERNNSGDYGIFQISSKWWCSDVMPFPGNCGNMNCFHLNNDIEPDINCAAIIVNQOGMEA
Rty_Lyz1A YRLGSTNYGIFQINNKWECDDG--TPSYNLCQIKCSLLDDDDITNDIQCVKSVVVTLEMDI
Cmi_Lyz1C NRQGSTDYGLFQINSRYWCDDGRTPTSTNTCNIKCSAFLNDDITDDIRCVKRVVSDNGMGA
Cmi_Lyz1B NRLGSTDYGLFQINSRYWCDDGQTRTSNTCNIKCSAFLNDDITDDIRCVKRVVSDNGMGA
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Mdo_Lyz3 NPDQSTDYGIFQINSHYWCNDGKTPAKNVCGISCRDLTDNISKAITCAKRVVRDSGIRA
Mdo_Lyz1 NSDRSTDYGIFQINSRYWCNDGKTPAVNACGISCRDLTDNISKAITCAKRVVRDSGIRA
Mmu_Lyz2 NRDRSTDYGIFQINSRYWCNDGKTPSKNACGINSALLQDDITAAIQCAKRVVRDQGIRA
Mmu_Lyz3 NRQSTDYGIFQINSRYWCNDGKTPAVNACGINSALLQDDITAAIQCAKRVVRDQGIRA
Hsa_LYZ NADRSTDYGIFQINSRYWCNDGKTPAVNACHLSCSALLQDDNADAVACAKRVVRDQGIRA
Mmu_Lyz1 NPDQSTDYGIFQINSRWCNDGKTPSRNFCRISCKALLKSNISAVVCAKRVKDGQIYS
Apl_Lyz1 NTDGSTDYGILQINSRWCCDDGKTPSKNACGIPCSGLLRKPASAVINCPDPLPSR-----
Apl_Lyz2 NTDGSTDYGILQINSRWCCDDGKTPSKNACGIPCSGLLRKPASAVINCPDPLPSR-----
Gga_Lyz NTDGSTDYGILQINSRWCCDDGRTTPSRNLCNIPCSALLSSDITASVNCAKRIVSDNMGMA
Psi_Lyz1 NRQSTDYGILQINSRWCCNDGKTPAKNACGIECSELLKADITAAVNCAKRIVRDNGMGA
Psi_Lyz2 NRQSTDYGILQINSRWCCNDGKTPAKNACGQCSDLLTADITNSVNCAKRIVRDNGMAA
Xtr_Lyz NRDNSTDYGILQINSRWCCNDKTPSHNACNINCRAALLSDITQSVICAKRVVRDQGMMA
Oni_Lyz2 NNDGSTDFGIFQINSYWCNDYIINSNGCNMDCSALSDNVSAAITCAKRVVSDQGISA
Oni_Lyz3 NNDGSTDFGIFQINNRRWCNDKIMSFRNGCQINCKDLSDDDVTVAINKAKRVVVKDQGI
Oni_Lyz1 NTDGSTDFGIFQINSRWCCNDRRINSANGCNI DCSVLLTDDVTSAINCAKRVREQGITTA
Pfo_Lyz2 NTDGSTDYGIFQINSKYWCDDGRTGVSRSNGCGINCSQLQTDVVTTAITCAKRVVRDNGIRA
Pfo_Lyz3 NRDGSTDYGIFQINSKYWCDDGRTGVSRSNGCGINCSQLQTDVVTTAITCAKRVVRDNGIRA
Pfo_Lyz4 NRDGSTDYGIFQINSRWCCDDGRTGVSRSNGCGINCSQLQTDVVRTAITCAKRVVRDNGIRA
Xma_Lyz2 NTDGSTDYGIFQINSRWCCDDGRTGVSRSNGCGINCSQLQTDVVRKAITCAKRVVRDNGVGA
Pfo_Lyz1 NRDKSTDYGIFQINSRWCCNDTQIRTANGCHIMCELLSDDVGVAISCAKRVVRDQGI
Xma_Lyz1 NRDKSTDYGIFQINSRWCCNDTQIRTANGCHIMCELLSDDVGVAISCAKRVVRDQGI
Cse_Lyz NRDGSTDYGIFQINSRWCCDDRTTTTSNACNVACETLR--SSVSASIRCAKRVVRDQGLSA
Ola_Lyz NRDGSTDYGIFQINSYWCDDGRTGVRNGCKIPCSALLSDSVGTAIAKAKRVVRDQSGIAA
Nro_Lyz NTDGSTDYGIFQINSRWCCDDGLTPSRNACNINCSDLLTNDVGVVAITCAKRVVRDNGIRA
Gac_Lyz NTDGSTDYGIFQINSRWCCDDGRTGTPSKNACNISCSALLSDSVVAITCAKRVVRDNGMRA
Aja_Lyz NTDGSTDYGIFQINSRWCCNNGVTPSKNACNINCSALLSDSITAITCAKRVVRDNGIRA
Srh_Lyz NTDGSTDYGIFQINSRWCCNNGQTPTSNACGISCALLTDDVIAIAKAKRVVRVSDNGIRA
Tru_Lyz NTDGSTDYGIFQINSRWCCNDRIPTRNACNIKCSALQTDVVTTVAINKAKRVVRDQGI
Tni_Lyz NTDGSTDYGIFQINSRWCCNDVTPTSNACNICKRALLTDDISVAIAKAKRVVRDQGI
Dla_Lyz NTDGSTDYGIFQINSRWCCNGLTPTSNACGQCSELLTNDVVAIKAKRVVRDNGIGA
Pol_Lyz NTDGSTDYGIFQINSRWCCNSQTPTSNACNIRCSELLTDDVIVAIKAKRVVRDNGIGA
Omy_Lyz NTDGSTDYGIFQINSRYWCDDGRTGTPAKNVCGRCSQLLTDVVAIKAKRVVRDNGIGA
Ssa_Lyz NTDGSTDYGIFQINSRYWCDDGRTGTPAKNVCGRCSQLLTDVIVAVSACAKRVVRDNGIGA
Loc_Lyz NSDGSTDYGIFQINSRWCCDDGRTGTPSKNACGISC-----
Aca_Lyz1A DSDGSDYGIFQINSRYWCYQYNEKSNACGQCSELLTNNLAVDAACAKIVVSNNGMGA
Lch_Lyz1C DSDGSDYGIFQINSYWCYDGT--TPGKNACNIRCSERGLDSVHAVRCVIAKIAAT--VLS
Cca_Lyz11_2_2 --SDTGKDYGIFQINSFKWCDDGTP--GKNKCKIPCSDLLKDDLKASVECAKLVKTEGLKS
Cca_Lyz11_2_3 --SDTGKDYGIFQINSFKWCDDGTP--GKNKCKIPCSDLLKDDLKASVECAKLVKTEGLKS
Cca_Lyz1_2_1 --SDTGKDYGIFQINSFKWCDDGTP--GKNLCKMPCSDLLQDDLKASVECAKLVKTEGLKS
Dre_Lyz11_2_1 --SDTGKDYGIFQINSFKWCDDGTP--GKNLCKVACSDLLNDDLKASVECAKLVKMDGLKS

Dre_Lyz11_2_2 -SDTGKDYGIFQINSFKWCDDGTP-GKNLCKVACSDLLNDDLKASVECAKLI VKMDGLKS
 Cid_Lyz11_2 -TDVGKDYGIFQINSFKWCDDGTP-GKNLCLNLPDSDLLKDDLKPSVECAKLI VKTGLKLS
 Ame_Lyz11_2 SDDSGKDYGIFQINSFKWCDDGTANGQNLRCRVPCGDLLNDNLQASVECAKLI VKREGLKA
 Hsa_LYZL2 LDDGSIDYGIFQINSFAWCRRGKLENNHCHVACSALVTDDLTDAL ICAKKIVETQGMNY
 Hsa_LYZL1 LDDGSIDYGIFQINSFAWCRRGKLENNHCHVACSALITDDLTDAL ICAKKIVETQGMNY
 Mmu_Lyz11_2 LEDGSTDYGIFQINSFTWCRNARKKHQKNHCHVACSALITDDLTDAL ICAKKIVKET----
 Mmu_Lyz14 DDPDGTGFGLFQIRDNNEWCGHGK----NLCVSVCTALLNPNLKDTIQCAKKIVKGGMGMA
 Hsa_LYZL4 NREGYTGFGFLQMRGSDWCGDGR----NRCHMCSALLNPNLEKTIKCAKTI VVKEGGMGA
 Mmu_Lyz16 NVDGSDYDYGIFQINSRYWCNDYQSHSENFCHVDCQELLSPLNLI STIHC AKKIVVSG-----
 Hsa_LYZL6 NADGSFDYGLFQINSHYWCNDYKSYSENLCVHVCQDILLNPNLAGIHC AKKIVGARGMNN
 Aca_Spaca3 QDNGSTSNIGFQINSYLWCEDYKHYTPNICQMHCSDDLTSYIRDDVACAMRIVQGGKGLGA
 Psi_Spaca3 EADGSTDNGIFQINSRLWCEDYKSSARNLCHMHCSDDLTSNINDDIVCAMQIVQQRGLGA
 Mmu_Spac3 EADGSTNNGIFQISSRRWCRTLASNGPNLCRIYCTDLLNNDLKDSIVCAMKIVQELGLGY
 Hsa_SPACA3 EADGSTNNGIFQINSRRWCSNLTTP-VPNVCRMYCSDDLNPNLKDTVICAMKITEPQGLGY
 Aca_Lyz1D HNDGTDYDYGIFHINSGWCKDLDSSENLCMNCCKLSDDDITDDINCAKRI VQDQSMGA
 Psi_Lyz14_6 NADGSTDYGMFQINSRVWCNNYRSPTEENLCHIPCTDLLSNDIADDIACA KRI VQDQMDA
 Aca_Lyz1B PNDGSRDYGIFQINSRWCSNGEGTTANGCKTSCSAFTTDDITDDITCAKRI VQDNGIRA
 Aca_Lyz1C PNDGSRDYGIFQINSRWCSNGEGTTANGCRSSCSAFTDDDITDDIACA KRI VQDNGIRA
 Hsa_SPACA5 NPDGSSEYGFQINSAAWCDNGITPTKNLCHMDCHDLLNRHILDDIRCAKQIVSQNGLSA
 Hsa_SPACA5B NPDGSSEYGFQINSAAWCDNGITPTKNLCHMDCHDLLNRHILDDIRCAKQIVSQNGLSA
 Mmu_Spaca5 NPDGSSEYGFQINSAAWCCNGITPTQNLNCIDCNLLNRHILDDI ICAKRVASSKSKMKA
 Lch_Lyz1A NHDSSDYGILQINSRWCEDEG-TPSRNICGIDCNLLNDNIDDDIACA KRI VQDQMDA
 Lch_Lyz1B NHDSSDYGILQINSRWCEDEG-TPSKNLCRIDCNKFTDEDITDDLQCAKRI VQDQMDA
 Mmu_Lalba -DNGSTEYGLFQISDRFWCKSSEFPSENICGISC DKLLDDELDDIACA KRI IAIKGLDY
 Hsa_LALBA -NNESTEYGLFQISNKLWCKSSQVPSRNICDI SCDKFLDDDI TDDIMCAKRI IAIKGLDY
 Mdo_Lalba -NNGNTEYGFQISNNGWCAEKQEDAKSTCGILCSKLLDDDI TDDIACA KRI IAIKGLDY
 Aca_Lyz1F -PTRRKAYGLFRINNSDWCSGQVQPSKNLNCI SCSKLI DDDI KDDILCAKRI IAIKGLKA
 Ano_Lyz1E -GPRATNHGIFLLSSRWCCNDKTPPRNYCNISCEALQDSDIADDITCAKRI VQKGFKA
 Hdi_Lyz1A NSGGSSDYGIFQINSYWCNDGGRKT-KNGCGHPCSDYLNSNIGDDVTCVKQLLREGGWGF
 Hdi_Lyz1B NSGGSSDYGIFQINSYWCNDGGRKT-KNGCGHPCSDYLNTYLGDDIQCI RQLLREGGWGF
 Lgi_Lyz1 NRDGSADHGIFQINDYWCNDGGRKT-KNGCKHPCTDFENSSLDVRCMKTLG---WQH
 Bfl_Lyz1C PNDGSDYDYGIFQINDHYWCNDGPP--HNDCGVSCSNLRDNNIADDVRC AKLI YQRHGFA
 Bfl_Lyz1D PNDGSDYDYGIFQINDHYWCNDGPP--HNDCGVSCSNLRDNNIADDVRC AKLI YQRHGFA
 Bfl_Lyz1B PNDGSDYDYGIFQINDHYWCNDGPP--HNDCGVSCSNLRDNNIADDVRC AKLI YQRHGFA
 Bbe_Lyz1 PNDGSDYDYGIFQINDHYWCNDGPP--HNDCGVSCSNLRDNNIADDVRC AKLI YQRHGFA
 Bfl_Lyz1A PNDGSDYDYGIFQINDHYWCNDGPP--HNDCGVSCSNLRDNNIADDVRC AKLI YQRHGFA
 Mga_Lyz1B NSG-SKDYGIFQINSKFNCGSSTIRNTYGCADSCSLTNSDI SNDAYCAVRI KKGCGFSK
 Mga_Lyz1C NSG-SKDYGIFQINSKFNCGSSTIRNTYGCADSCSLTNSDI SNDAYCAVRI KKGCGFSK
 Mco_Lyz1 NSG-SKDYGIFQINSKFNCGSSTIRNTYGCADSCSLTNSDI SNDAYCAVRI KKGCGFSK
 Mga_Lyz1A NSDKSIDYGFQLNKYNWCDTTSKNTCGCTDCTSLIDSDI SNDAYCAVRI KKGCGFSK
 Csi_Lyz1 NSNGSKDYGIFQINDGFWCGSGTIRRTNGCQDSCSSFLNSDI SNDAYCAVRI KKGCGFSK
 Sau_Lalba DPSNHVDYGLFQLSNHLVCSGDESPPH-LSG-----
 Dla_Lalba SSDGCTLYGLFQLSHLVCSGDESPPH-ICGMDCSELTDNNI QDDISCVLKI FTDNGFGA
 Oni_Lalba GLDDDTLYGIFQLDWQLVCGNGTNPPI-I-----
 Nco_Lalba RRRGSVDYGLFQLSHLCSDGATPPDRICNVTC SALVDDDI EDDIGCVLNI ISNGGFAM
 Pol_Lalba KKENSIFYGIFQLSHLCSDGATPPDRICNVTC SALVDDDI EDDIGCVLNI ISNGGFAM

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Rty_Lyz1E WYKVPFFVFL-----
 Rty_Lyz1B WYSWKKQCQRNLGDFLDDCKI
 Rty_Lyz1C -----
 Rty_Lyz1D WQGWAAACKGKWI DYTFFCFW
 Rty_Lyz1A WPGWEEVHGERPQSIG----
 Cmi_Lyz1C WYGWRDHCRGRNLQRYVQGCNV
 Cmi_Lyz1B WYGWRDHCRGRNLQRYVQGCNV
 Cmi_Lyz1A WYGWRDHCRGRNLQRYVQGCNV
 Mdo_Lyz2 WVAWRNHCEGRDVSSYIRGC SL
 Mdo_Lyz3 WVAWRNHCEGRDVSSYIRGC GL
 Mdo_Lyz1 WVAWRNRCQGNLSSYIQGCRL
 Mmu_Lyz2 WVAWRNRCQGNLSSYIRNCGV
 Mmu_Lyz3 WVAWRNRCQGNLSSYIRNCGV
 Hsa_LYZ WVAWRNRCQNRDVRQYVQGC GV
 Mmu_Lyz1 WAGWIKHKCNKLNKEYIRGC HL
 Apl_Lyz1 -VAWRNRCRGTDVSKWIRGC RL
 Apl_Lyz2 -VAWRNRCRGTDVSKWIRGC RL
 Gga_Lyz WVAWRNRCRGTDVQAWIRGC RL
 Psi_Lyz1 WVAWTKYCKGKDV SQWIKGC KL
 Psi_Lyz2 WVAWTRNCKGRDVSQWIRGC GV
 Xtr_Lyz WVGWRNHCKGRDLSQWIKDC KL
 Oni_Lyz2 WYGWRSNCDGRDLSYVSGCG V
 Oni_Lyz3 WYGWRSHCQGRDLAPYLDGC GL
 Oni_Lyz1 WSRLGSHCRGSYLT SF LRGA-
 Pfo_Lyz2 WVAWTTHCQNRDLSYLRGC RL
 Pfo_Lyz3 WVAWRKYCQNRDLSYLRGC RL
 Pfo_Lyz4 WVAWRNRCQNRDLSYLRGC RL
 Xma_Lyz2 WVAWRRHQNRDLSYLRGC RL
 Pfo_Lyz1 WVGWRMHCKNQDVS KYLQGC GL

Xma_Lyz1	WVGWRTHCKNQDVSKYLDGCGL
Cse_Lyz	WVAWRVHCQGRDLSEYIRGCVL
Ola_Lyz	WVAWRDHCRGRDVSSYIQGCGF
Nro_Lyz	FTSEPVDCTLRKQPSSAASCRP
Gac_Lyz	WVGWRNHCEHRDVSSYLAGCRL
Aja_Lyz	WVAWRAHCEGQDVSQYIAGCGV
Srh_Lyz	WVAWKSHCEGRDLSPYLAGCGV
Tru_Lyz	WVAWNRHCQNRDLSAYIAGCGL
Tni_Lyz	WVAWNRNCQGRDLSGYVAGCGL
Dla_Lyz	WVAWRRYCQNRDLSSYVAGCGL
Pol_Lyz	WVAWRQHCQGDLSYLAGCGL
Omy_Lyz	WVAWRLHCQNQDLRSYVAGCGV
Ssa_Lyz	WVAWRLHCQNQDLRPYVDGCGV
Loc_Lyz	-VAWNRNCQGRDLSQYTAGCGV
Aca_Lyz1A	WVAWRLHCQGDLSYVEGCVL
Lch_Lyz1C	WLSYNMRQRNGGLSNYIVGCEA
Cca_Lyz11_2_2	WDTWGSYCKGRKMSRWVKGCEE
Cca_Lyz11_2_3	WDTWENYCKGRKMSRWVKGCEE
Cca_Lyz1_2_1	WDTWDSYCKGRKMSRWVKGCEE
Dre_Lyz11_2_1	WETWDSYCNCRKMSRWVKGCEQ
Dre_Lyz11_2_2	WETWDSYCNCRKMSRWVKGCEQ
Cid_Lyz11_2	WETWDSYCNCRKMKRWTKGES
Ame_Lyz11_2	WDTWDKYCNGRKLRSRWKSCDV
Hsa_LYZL2	WQGWKKHCEGRDLSWKKDCVF
Hsa_LYZL1	WQGWKKHCEGRDLSWKKGCEV
Mmu_Lyz11_2	-----
Mmu_Lyz14	WPIWSKNCQLSDVLRWLDGCCL
Hsa_LYZL4	WPTWSRYCQYSDLARWLDGCCL
Mmu_Lyz16	-----
Hsa_LYZL6	WVEWRLHCSGRPLFYWLTGCRL
Aca_Spaca3	WKMWKKNCEGEDVDIWLKGCCL
Psi_Spaca3	WLAWRKHCEGRDLSQWVEGCNV
Mmu_Spac3	WEAWRHHCQGRDLSWVDGCGF
Hsa_SPACA3	WEAWRHHCQGDLTEWVDGCGF
Aca_Lyz1D	WNQWKMHCQDQDLFRWVKGCCL
Psi_LyzL4_6	WEDWTMHCKGRDLSWVDGCDL
Aca_Lyz1B	WVAWVNHCCEGRDLSWTKDCSL
Aca_Lyz1C	WVAWVKYCQGNLTRWTQGCRL
Hsa_SPACA5	WTSWRLHCSGHDLSEWLKGCCL
Hsa_SPACA5B	WTSWRLHCSGHDLSEWLKGCCL
Mmu_Spaca5	WDSWTQHCAHDLSEWLKGCCL
Lch_Lyz1A	WLVYGTIKKHHLQERLDGSG-
Lch_Lyz1B	WNGWKDNCKGKDVSEFVEGCGV
Mmu_Lalba	WKAYKPMCSEKLEQWRCEK---
Hsa_LALBA	WLAHKALCTEKLEQWLCEK---
Mdo_Lalba	WKAHKTFCLENLDQWRCLN---
Aca_Lyz1F	WPRWAKRCRGKDLVYVKSCNF
Ano_Lyz1E	WRRAWERNCKGQDLTQYIAGCEF
Hdi_Lyz1A	SYGHGAQCSS-VTSSYLSGCTY
Hdi_Lyz1B	SYGYADKAS-VTSSYLSECSL
Lgi_Lyz1	SYGYAARCKG-VTASYLSGCSY
Bfl_Lyz1C	WYGWQNNCQG-STSSYVSGCF-
Bfl_Lyz1D	WYGWQNNCQG-STSSYVSGCW-
Bfl_Lyz1B	-----
Bbe_Lyz1	WYGWINHCQG-HNNANLVTSCW
Bfl_Lyz1A	WYGWVNKCGG-DTTSYVKDCW-
Mga_Lyz1B	WNGWKDYCSNVQSEYYSTC--
Mga_Lyz1C	WNGWKDYCSNVQSEYYSTC--
Mco_Lyz1	WYGWKDHCNPNVQSEYYSSTC--
Mga_Lyz1A	WYGWRDHCANVQSSEYFSDC--
Csi_Lyz1	WEGWKNCKGKLNKPPSGC--
Sau_Lalba	-----
Dla_Lalba	FKAYQEEDRDVKASDYFTDCTL
Oni_Lalba	-----
Nco_Lalba	KPKFQPECDNETAVHYFAECKD
Pol_Lalba	WEEFLPECIEKKPSEYFSDCR-

B) Lysozyme G-type

Apl_Lyg1 CYGDINALQAPTISCAGIAAVRRRTADADIIRLRKYEIPIKRVARNLCLDPALIAAIIISQE
Gga_Lyg3 CWPTERRCASSGLSGAGLALRRRTVEADVIRLRRYEVPIKRVARRLCLDPALIAAIIISQE
Mdo_Lyg1 CYGNIRNIDTPGASCCGVRASERLAEMDLPYVQRYQPTLRLVGRKYCLDPAVIAGILSRE
Mmu_Lyg1 TYGNIRTLDTPGASCCGVRASERLAEDRYPYLLRHQPTMRLVGGQKYMCDPAVIAGVLSRE
Hsa_LYG1 CYGNIQSLDTPGASCCGVRASERLAEDMPYLLKYQPMMQTIGQKYCMDPAVIAGVLSRK
Hsa_LYG2 CYGDIIMTKTSGATCCGIRGSEMFAEMDLRAIKPYQTLIKEVQQRHCVDPAVIAAIIISRE
Mmu_Lyg2 CYGDIIMTMEFTGAPCCGIHSGSEMFAEMDLKAIKPYRILIKEVQQRHCIDPALIAAIIISRE
Mdo_Lyg2 CYGDVMRMDTPGASCCGIRGSELFAEMDLALMMKYQTMIKTVGQKQCVDPALIAAIIISRE
Ola_Lygb EYRNLEEMRTTGVSALGVEGSEILAKKDLKPMKSKYRNQIMNVGRKRLRHPALIAAMISKQ
Pfo_Lygb EYRNLSQMTTGTGASKTGVEVSKMLAQDLELMSKYKDKIKSVGKALRRLHPALIAAIIISKQ
Tni_Lygb EYGHHTTCLETSERGTEASNILAAKDLKMKKFKDDITSVGQRLGVPEPALIAAIIISRQ
Sau_Lyg3 TYGDIIMRVETSGASLSGVRASNAERDLNEINKYKSTINNVAEKRVHPALIAALISRS
Sau_Lyg4 TYGDIIMRVETSGASLSGVRASNAERDLNEINKYKSTINNVAEKRVHPALIAALISRS
Dla_Lyg1 SYGNIMKVETTGASESGVRASSAMAETDLEKMKDYKSIKKNVARQKIDPALIAAIIISRS
Ssa_Lyg3 RYGNIMDVETSGADLEGPASHRMAEHDLAAMNKYKGLIMKVAERNAVDPAVICGIIISRE
Ssa_Lyg5 TYGDIIMKVETTGASKSGVSASERMAEDDEDDVKYIDIIKEVKGKENEIAPALICGIIISRE
Gmo_Lyg3 TFGDILKVETTGASEKGVTAASEIMAKEDLDSMKKYKTIKKNVAERRHVNPAIAGIIISRE
Tru_Lyg3 SYGNIMSIETSGASAPGIQGSREMARIDLERMKYKSIIRQAGQKQCVDPALIAAIIISRE
Tru_Lyg2 SYGNIMSIETSGASAP---GHEMARIDLERMKYKSIIRQAGRECDVDPALIAAIIISRE
Tru_Lyg1 SYGKIEDIKETSGASDGGWKSASHRMAEIDSNRMENYRTIINEAGKQCVDPALIAAIIISRE
Tni_Lyga AYGNIMKISTTGASAVGVAASEKMAQIDVERMRYTGIISRAAQKQCVDPALIAAIIISRE
Pfo_Lyg1 SYGDIITRVSASGASESGVEASEKMAQMDSGRMNKYKSKINSVGSQCGIDPALIAAIIISRE
Pfo_Lyg2 SYGDIITRVSASGASESGVEASEKMAQTDGSRMKNYKSKINSVGSQCGIDPALIAAIIISRE
Xma_Lyg SYGDIINRVEASGASEFGVRASETMAQTDGSRMKNYKSKITRVSQSGIDPALIAAIIISRE
Pol_Lyg SYGQIRLVETSGASGSGVKASHKMAEIDSGRMSKYKSKINKVGGQSYGIEPALIAAIIISRE
Sma_Lyg GYANIKDVQTTGASWSGVEASHTMAETDGRMSRYKSKIFNVGQKCGIDPALIAAIIISRE
Nro_Lyg2 GYASVMRVETSGASWSGVAASHTMAQTDGSRMANYRSKINSVGGQGTGIEPALIAAIIISRE
Nco_Lyg4 GYASVMRVETSGASWSGVAASHTMAQTDGSRMANYRSKINSVGGQGTGIEPALIAAIIISRE
Nro_Lyg1 -----GGRSVSRDMAQTDADRMMKYRSKINKVAKQHNIDPALIAAIIISRE
Gac_Lyg RYGDIMKVPTTGASLAGEKASHTLAQTDKNRMEKYRSKINTVGAQYIDPALIAAIIISRE
Dla_Lyg2 AYGNIMRVETTGASWSGKASHTMAQTDAGRMEKYRSKINKVGGSCGIDPALIAAIIISRE
Dla_Lyg3 DFGDIMKVETTGASQSGVKASHTMAQTDADRMEKYRSKINKVGGSCGIDPALIAAIIISRE
Sau_Lyg2 GYGNIMRVETTGASESGVKASHRMAEIDADRMEKYRSNINRVGGYKIDPAIAAIIISRE
Lcr_Lyg GYGNIMRVQTTGASESGVKASQAMAELDAGRMEKYRSKINSVGRYDIDPALIAAIIISRE
Ola_Lyga VFDIRNVSTTGASASGVSASHAMAQTDAGRMMRYKDKITAVGHRLGVDPALIAAIIISRE
Sau_Lyg1 SYGNIMDVETTGASATGVKASHKMAETDADRMEKYKSKINSVGVKYGIDPAIAAIIISRE
Nco_Lyg2 NNGDIMRVETDGASRGGRSVSRDMAQTDADRMMKYRSKINRVAKHNIDPALIAAIIISRE
Cse_Lyga SFGNINRIPTSGASWKGAKASQTLAETDSRMMKYRDKIIRVANETGIQPLIAAIIISRE
Xtr_Lyg1 QYGDINKVPTSGASCCGVQASERMAQTDLTRMNRYSIIESVSRKMGMDAALIAAIIISRE
Cse_Lygb GYGSVLDVETSGASAAGVEASHTMAKTDLQRMERYKAIIEVGRKYGVEPALIAAIIISRE
Gmo_Lyg6 GYGDIMRVETSGASNGGVQASEKMANHDLACMRTYKTIIGKVASKRVDVDPALIAAIIISRE
Gmo_Lyg1 GYGDIMRVETSGASNGGVQASREMANHDLACMRTYKTIIGNVARRRNVDPALIAAIIISRA
Gmo_Lyg5 EYGNIMNVETSGASSGGVQASEKMASDDLDRMESYKTIIGNVARKHDVDPALIAAVASRE
Gmo_Lyg4 GYGDIMTVITEGASDAGVPASQKMAKDDLGNMETYKTIIEENVAKRHVDVDPALIAAIIISRE
Gmo_Lyg2 GYGDITQVETSGASSDGVRASTMAQTDAGRMEKYKSFINNVAKHVVDPAVIAAIIISRE
Gmo_Lyg7 GYGDIMQVEMSGASSDGVRASTMAQTDARRMEKYKSFINNVAEKHDVDPAVIAAIIISRA
Ssa_Lyg2 RYGDIMGVDTTGASWSGVSASHEMAKDRPYVDKYKGRITSAGQKYGVDPAVLGGIIISRE
Aja_Lyg4 IYGDVNRIDTTGASQQGVSASHELARTDLSRVNQYKDAIQRAAQDQHDPAVVAIIISRE
Psi_Lyg1 CYGDINKVDTTGASCCGINASAKMAEKDLPTMNNYKAIKKNASRAICMDPAVITGIIISRE
Psi_Lyg2 CYGDIITKVDTTGASCCGVQASEKIAEKDLNMMNKYKAIKGTGLKTCVDPALIAAIIISRE
Psi_Lyg4 -----MTFPLTTGVRASAEIARKDLSRMNRKTIKSAKKYCVDPVSVVAGIIISRE
Psi_Lyg3 CNGNINDVDTTGASSSGVRASAEIARKDLDRMKYKPMIISAARKHNMDPAVIAGIIISRE
Gga_Lyg1 CYGSVSRIDTTGASCCGVRASRTIAERDLGSMNKYKVLIKRVGEALCIEPAVIAGIIISRE
Apl_Lyg2 CYGSVNRIDTTGASCCGVPASKIAERDLKAMDYKTLIKKVGKLCIEPAVIAGIIISRE
Gga_Lyg2 FYGNIANVETTGASQAGVAASEKIAERDLKNMDKYKETITKVANSKICPPSLVAAVIISRE
Bfl_Lyg1 SYGNIMAVDTTGASAGGVSASNQMASTDLHRLNNTYKSKIIDAAAKSMDPAVIAAIIISRE
Bfl_Lyg2 NYGNIMAVDTTGASAGGTSASQQMARTDLNRLNTYKSKIIYNAASAKNMDPAVIAAIIISRE
Bfl_Lyg3 -YGNILVVDTTGASATGVAASHQMASTDLRSLNNTYKSKIIQAAAKNMDPAVIAAIIISRE
Lch_Lyg1 IYGNVNMIDTTGASQTPASHKMAENDSGRMCKYKTRILEVGRKQMDPAVIAAIIISRE
Lch_Lyg2 NYGNVNMIDTTGASKGGKLASRMAETDSARMEKYKDIIVKVGKAKNIDPAVIAAIIISRE
Pma_Lyg CYGDIMNIDTTGASIRGVAASKLVNADLMLKNTYKTIIVATANAKCNDPAVIAAIIISRE
Rty_Lyg VYGDITKVDTTGASERGVAAASHKMMSTDLERVNKYKTLIEKAACANQIDLAIISAIICRE
Ssa_Lyg1 CFGDITKVDTSGASEQGVDAESHKLAEHDLVRMKNYKELITRVGQKHGLDPAIIAGIIISRE
Omo_Lyg LFGDIMKVETSGASEKGVASHKMAEHDMKRMTQYKSMVQTVGHSKGLDPAIIAGIMSRE
Ame_Lyg1 TYGDIITKVPTTGASEKGVASHKMAEHDLKMKDQYKSIITKVGHAQKMDPAVIAAIIISRE
Ame_Lyg2 IFGDVMKIDTTGASEKGVASHKMAEHDLKRMQYKSIITRVGAQKQMDPEVIAAIIISRE
Tfu_Lyg IYGDVMKIDTTGASDKGVEASYKLAEHDFSRMKTYYRDIIVKVGRAQKMDPAVISAIIISRE
Aja_Lyg2 IYGDITKVETTGASQQGVEASHKLAESDLTRMKNYKDVITKVAKAHKIEPAVIAGIIISRE
Aja_Lyg3 IYGDITKVETTGASQQGVEASHKLAESDLTRMKNYKDVITKVAKAHKIEPAVIAGIIISRE
Cid_Lyg IYGDVMKIDTTGASDKGVEASRKLAEHDLARMEKYKSIIVKVGRAKQMDPAVIAAIIISRE
Dre_Lyg2 IYGDIMKIDTTGASEKGVASHKLAEHDLARMEKYKSKILKVARAKQMDPAVIAAIIISRE

Dre_Lyg1 IYGDIMKVGTGASKTGEVASKKLAEHDLARMEKYKTKIINVGRAKQMDPAVIAAIIISRE
Cca_Lyg SGIDIMKIDTTGASEKGEVAPKLAEHDLARGEKYKNMITKVGAKKMDPAVIAAMISRE
Dre_Lyg3 SGIDIMDITKASPKGEVASKKLAADDFVRMEKYKCKIFKVAKEKDVPALIAAIIISRE
Bgl_Lyg2 CYGDINNLSPTGRKVGVPKSNSEVQTDLTYLNRYSYQTAADKLCIQASVIAAVASRE
Pac_Lyg CHGDIDQLHPTGKHTGGVAGSNAEVQHDLPALNNHRSCYQASADTNCIQASVIAALASRE
Aca_Lyg1 CHGNVMDLSPTGQKSGGVSASNSDAQADITLNLKYKTCFQKVAVSQCIQASLIAALASRE
Myc_Lyg3 CHGDVRRLLHPTGEHNGGVAASNHVDYDLHDLNKKSCYASGAHAIQPSVIAALASRE
Myc_Lyg1 CHGDVRRLLHPTGEHNGGVAASNHVDYDLHDLNKKSCYASGAHAIQPSVIAALASRE
Afa_Lyg CHGDVTRLHPHGQHNNG-VAASNRGVDYDYLHDLAKKSCYASGARHC IQPSVIAALASRE
Myc_Lyg2 CHGDVRRLLHPTGRANGGVTTSKNEVEHDYRDLNKKSCYASGAHAIQPSVIAALASRE
Air_Lyg CHGDVRRLLHPTGEHNGGVAASNHVDYDYLHDLNKKSCYDQAGATYCIQPSVIAALASRE
Mga_Lyg2 CHGNVTVLHPRGMAPGGMAASHLAIDQDITTEIDKRKSCYLKAAANNCIHPAVIAGIASRE
Mco_Lyg CHGNVTVLHPRGMAPGGMAASHLAIDQDITTEIDKRKSCYLKAAANNCIHPAVIAGIASRE
Mga_Lyg1 CHGDVTRLHPTGMG--GMAGSHQADIDQDIAEINKRSCYVQAGAANC IHPAVIAGIASRE
Hdi_Lyg1 CYGDVMMKLRPTGASSSGVQASNHMVDQDYAELNKRKSCYVRAGANNCIHPAVVAGVASRE
Hdi_Lyg2 CYGDVMMKLRPTGASSSGVQASNHMVDQDYAELNKRKSCYVRAGANNCIHPAVVAGVASRE
Lgi_Lyg1 CHGDVMMKLRPTGASSSGVQASNHMVDQDYAELNKRKSCYVRAGANNCIHPAVVAGVASRE
Aca_Lyg CHGNVTVLHPRGMAPGGMAASHLAIDQDITTEIDKRKSCYLKAAANNCIHPAVIAGIASRE
Lgi_Lyg2 CYGDFMMLNPTGAGKTGVRASNKMLDIDLAEELNKRKQCYIRAGRNSCIHPAVIAAIIASRE
Lgi_Lyg3 CHGDFMMLNPTGAGKTGVRASNKMLDIDLAEELNKRKQCYIRAGRNSCIHPAVIAAIIASRE
Cbe_Lyg CHGNFMMLRPTGASAGGVSASQTMVANDINELNKRKSCYIRAGNNNCVHPAVIAGIASRE
Cgi_Lyg CFGDITLLHPTGKSNNGGVSSQLDVSKTYNLAHSYKACFEQIGFTFCIHPAVIAAIIASRE
Hdid_Lyg LYGDITKISPKGASASGVAASQALVDADIAELDKLDIFVRVGESLNIHPALIGAIASRE

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Apl_Lyg1 SRAGLLDNGWDQGRQRFLMQIDRRQPYGTWDSSEHINQCSTMLVLGINEMRVRHPTWTW
Gga_Lyg3 SRAGLLDNGWDQGRQRFLMQIDRRQPYGTWDSSEHINQCSTMLVLGINEMRVRHPTWTW
Mdo_Lyg1 SQGGNLSV--GGNVASGIGLVQPGGIQOPTYWTSETRASQVSENLMRIKEIRRYPTISA
Mmu_Lyg1 SPGNNVVD--LGNIGSGLGMVKETKFYPPATAWKSETWVSQKTQTLTSSIKEIKTRFPWTWA
Hsa_Lyg1 SPGDKLVN--MGDRS---MVQDPSQATSWISESQVSQTTEVLTRIKEIQRRFPWTWP
Hsa_Lyg2 SHGSLQDQGDWHRGLKFLGMLQDLKQHPVGAWDSKEHLSQATGILTERIKAIQKFPWTSV
Mmu_Lyg2 SHGGALQNGWDHKGQRFLMQDLKHPVGAWDSKEHLSQATGILTERIKAMKRPWTWNT
Mdo_Lyg2 THAGSLQDQGDWHRGLKFLGMLQDLKHPVGAWDSKEHLSQATGILTERIKAIQKFPWTSV
Ola_Lygb SNAGQLKDGHGMDNSYGLMQINRKFVAVGEPFSEHDHIDEGSTYLIHLIKTVNWRPDWSR
Pfo_Lygb SRAGLNDKGYGKLDVCFGLMQIDKRIKDYELGTAFSREHIDQGSTCLHLIKDMKIQKPDWSE
Tni_Lygb SQAGTSSGYSVNDNCFGLMQINKHYAVGNAYSSEHIDQGVTFILQIKTRMRTRPDWSK
Sau_Lyg3 SRAGLNDKGYGKLDVCFGLMQIDKRIKDYELGTAFSREHIDQGSTCLHLIKDMKIQKPDWSE
Dla_Lyg1 SRAGLNDKGYGKLDVCFGLMQIDKRIKDYELGTAFSREHIDQGSTCLHLIKDMKIQKPDWSE
Ssa_Lyg3 CRAGLKRGR--YDNSYGLMQINGDTTKVPFDFSEHLLLEGTNILYFILIRKNAFPDWSK
Ssa_Lyg5 SRAGTLDHGRGDNGKAFGLMQISGGTPKGEWNSSEHLQATEILVGFILIKQKFLHLWTK
Gmo_Lyg3 TRGGRIKNGWGDYKGFGLMQVNGGNKRGWDSKEHLEQATGILVHFIKRIKQKFPKCTK
Tru_Lyg3 TEAGFINKGWGDGNAFGLMQIDKRIKDYELGTAFSREHIDQGSTCLHLIKDMKIQKPDWSE
Tru_Lyg2 SRAGNLVNGRGRDHGRAFLMQISG--TPVGSWDSVEHLIQATKILLSFIDVIRKKNFPWNA
Tru_Lyg1 SRAGNLVNGRGRDHGRAFLMQISG--TPVGSWDSVEHLIQATKILLSFIDVIRKKNFPWNA
Tni_Lyga SRAGNLINGWGDHGNKAWGLMQVNGGTPVGNWDSLEHLVQATNIVYFIRGRDKFPWDA
Pfo_Lyg1 SRAGNLDDGWDHGNKAWGLMQVSNIQKEGDWSEHLLRQATGILVHFIRKIQKFPNWSR
Pfo_Lyg2 SRAGNLNRNGWGDHGNKAWGLMQVDIRKEGDWSEHLLRQATGILVHFIRKIQKFPNWSR
Xma_Lyg SRAGNLHDGWDHGNKAWGLMQVDIRKEGDWSEHLLRQATGILVHFIRKIQKFPNWSR
Pol_Lyg SRAGNLKDGWGDGNAWGLMQVNGGTPVGNWDSLEHLVQATNIVYFIRGRDKFPWDA
Sma_Lyg SRAGNLHDGWDHGNKAWGLMQVSGGTAEGAWDSEVHLCQATGILVGFIRGRIRKKNFPWWSG
Nro_Lyg2 SRAGNLKNGWGDGNAWGLMQVNGGTPVGNWDSVEHLSQATGILVNFIDRISKFPWSWS
Nco_Lyg4 SRAGNLQNGWGDGNAWGLMQVNGGTPVGNWDSVEHLSQATGILVNFIDRISKFPWSWS
Nro_Lyg1 SRAGALTDGWDHGNKAWGLMQVNGGTPVGNWDSVEHLSQATGILVNFIDRISKFPWSWS
Gac_Lyg TRAGNLQGGWGDGNAWGLMQVNGGTPVGNWDSVEHLSQAEILVHFIRGRIRKKNFPWSA
Dla_Lyg2 SRAGNLKNGWGDGNAWGLMQVNGGTPVGNWDSVEHLSQATGILVNFIDRISKFPWSWS
Dla_Lyg3 SRAGNLKNGWGDGNAWGLMQVNGGTPVGNWDSVEHLSQATGILVNFIDRISKFPWSWS
Sau_Lyg2 SRAGNLNNGWGDGNAWGLMQVNGGTPVGNWDSVEHLSQATEILVYFIRGRIRKKNFPWNT
Lcr_Lyg SRAGNLKNGWGDYSNWGLMQVQGGTAKGAWDSEHLLRQATGILVHFIRKIRKKNFPWST
Ola_Lyga SRAGNLQNGWGDHGNKAWGLMQVRRGGAEGAWDSEHLSQATGILVHFIHRMEKFPNCSK
Sau_Lyg1 SRAGNLKDGWGDGNAWGLMQVQGGTAKGAWDSEHLLRQATEILVDFIKIQVTKKLPWSTK
Nco_Lyg2 SRAGALTDGWDHGNKAWGLMQVDDGPEGDWSEHLSQATEILVDFIKIQKFPNWSR
Cse_Lyga SRAGLKNNGWGDGNAWGLMQVGGTAPRGAWDSEHLLRQATEILVDFIKIQKFPNWSR
Xtr_Lyg1 SRAGNLINGWGDGNAWGLMQVDRKRFHKGAWNSSEHVTQATEILIGMFASIRKKNFPQWST
Cse_Lygb SRAGLSSGYSVNDNCFGLMQVNGGTPVGNWDSVEHLSQATEILVDFIKIQKFPNWSR
Gmo_Lyg6 SRGGAISGGWCPRRIGFGLMQVDKTPVIGAWNSVEHVDQATGILVDIIVEVQRDFPDWSR
Gmo_Lyg1 TRGGAISGGWGDGNGFGLMQVDKTPVIGAWNSVEHVDQATGILVDIIVEVQRDFPDWSR
Gmo_Lyg5 SRGGAISGGWGDGNGFGLMQVDKTPVIGAWNSVEHVDQATGILVDIIVEVQRDFPDWSR
Gmo_Lyg4 SEAGHINKGWGDYNAFGLMQVDRKRFHKGAWNSSEHVTQATEILVDFIKIQKFPNWSR
Gmo_Lyg2 SRAGNIFNGWGDYNAFGLMQVDRKRFHKGAWNSSEHVTQATEILVDFIKIQKFPNWSR
Gmo_Lyg7 SRAGNIFNGWGDYNAFGLMQVDRKRFHKGAWNSSEHVTQATEILVDFIKIQKFPNWSR
Ssa_Lyg2 SRGGTFLVNGSGDNGNAHGLMQVDRKRFHKGAWNSSEHVTQATEILVDFIKIQKFPNWSR
Aja_Lyg4 TRGGMSDGDGHDGYAFGLMQVDRKRFHKGAWNSSEHVTQATEILVDFIKIQKFPNWSR
Psi_Lyg1 SNAGTLKDGWDELGNKFLGMLQIDKHQLFGPWNSKVHLIQGTGILADNLIKIQKFPNWSR
Psi_Lyg2 SHAGALKNGWGDGNAWGLMQVDRKRFHKGAWNSSEHVTQATEILVDFIKIQKFPNWSR
Psi_Lyg4 SHAGALKNGWGDGNGFGLMQVDRKRFHKGAWNSSEHVTQATEILVDFIKIQKFPNWSR
Psi_Lyg3 SHAGHLENGWGDHGNKAWGLMQVDRKRFHKGAWNSSEHVTQATEILVDFIKIQKFPNWSR

Gga_Lyg1 SHAGKLNKNGWDRNGFGLMQVDRKRIEGTWNGEAHIRQGTTRILIDMVKKIQKFPWRTR
Apl_Lyg2 SHAGTLKGGWGDNGNGFGLMQVDRKRLQGTWNGEAHTQGTILINFIKRIQKFPNWT
Gga_Lyg2 SHAGTLKGGWGDHGNFGLMQVDRKRLPHGAWDSEEHIKQGTIDILCQSITDIQKFPWTSK
Bfl_Lyg1 SRAGALADGTGDHNGYGLMQVDIRTPGGPYSTAHMRQGTQILIDTINCVRNHPGWTO
Bfl_Lyg2 SRAGALADGTGDNGNGYGLMQVDIRTPQGGPYTTTHIKQGTQILIDTINCVRNHPGWST
Bfl_Lyg3 TRAGALADGTGDNGNGFGLMQVDYRTPQGGPYSTEHEMMQGTQILIDTINCVRKHFGWTA
Lch_Lyg1 SRAGALHDGWDHGNFGLMQVDRKTPVGAWDSEEHISQGTQILIDMITSIQKFPGWTL
Lch_Lyg2 TRAGGLTKGWDHGNFGLMQVDRKTPVGAWDSEEHISQGTQILIDMITSIRKNFPRWTL
Pma_Lyg SRAGALVKGFGDNGNGFGLMQQDKRNIVGTWDEHLKQGTGILIDMISAIKPKFPNWTQ
Rty_Lyg SRGGNLKNGWGDHGNFGLMQVGSKTKIGTWTSEHLQGTQILIDMITSIQKFPGWTL
Ssa_Lyg1 SRAGSLDHGWDHGNFGLMQVDRKRVGAWDSEKHISQGTQILIEFIRRIQAKFPAPWK
Omo_Lyg SRAGALVNGWGDHGNFGLMQVDRKRLVGEWDSKEHVNQATGILVDFINTIQKFPKPKPK
Ame_Lyg1 SRAGALVNLGDKNGFGLMQVDRKTPRGAWNSEEHIVQGTGILIKAITDIQKFPSPWK
Ame_Lyg2 SRAGALVDGWDHGNFGLMQVDRKTPKGAWNSEEHVQGTQILIDLIQIKQKFPSPWL
Tfu_Lyg SRAGALVNGWGDHGNFGLMQVDRKPRGTWDEEHIRQGTQILINSIKQIQKFPKPKPK
Aja_Lyg2 SRAGALKDGDHGNFGLMQVDRKTPRGAWDSEEHVQGTQILIDFIKIKQSKFPDWPK
Aja_Lyg3 SRAGALVNGWGDHGNFGLMQVDRKSPKGEWNSEHQVTQGTQILIDSIKQIQKFPSPWSK
Cid_Lyg SRAGALIDGWDHGNFGLMQVDRKTPKGAWNSEEHVQGTQILIDFIKIKAKFPQWTO
Dre_Lyg2 SRAGALKDGDHGNFGLMQVDRKRLVGEWDSSEHLTQGTQILIDFIKIKAKFPWTK
Dre_Lyg1 SRAGALKDGDHGNFGLMQVDRKTPVGAWDSEHLTQATEILIDFIKIKAKFPWTK
Cca_Lyg SRAGALKNGWEPAGNGFGLMQVDRKTPVGAWDSEHQVTQATEILIDFIKIKVNFKWTQ
Dre_Lyg3 SRAGLLKNGWGDHGNFGLMQVDRKTPVGAWDSEHLTQATEILIDFIKIKAKFPWTK
Bgl_Lyg2 SRGGSLNLYGDDGKAYGIMQCDIKNPCVSWNSCAHIEMMTGALIAKINEVKKKFPNWP
Pac_Lyg SRGGSLNLYGDDGKAYGIMQCDIKNCCGWDSCHEVMMVRLVPIINQVAKKHPDWSQ
Aca_Lyg1 SRGGSLNLYGDDGKAYGIMQCDIKNCCGWDSCHEVMMVRLVPIINQVAKKHPDWSQ
Mye_Lyg3 SRGGRLNLYGDDHHAAYGILQCDIRYSCYAWDSCHEIEQMVSVLVPYVNVQVAKKHPWTSR
Mye_Lyg1 SRGGRLNLYGDDHHAAYGILQCDIRYSCYAWDSCHEIEQMVSVLVPYVNVQVAKKHPWTSR
Afa_Lyg SRGGRLNLYGDDHHAAYGILQCDIRYSCYAWNSCEHIEQMVSVLVPYVNVQVAKKHPWTSR
Mye_Lyg2 SRGGRLNLYGDDHHAAYGILQCDIRYSCYAWNSCEHIEQMVSVLVPYVNVQVAKKHPWTSR
Air_Lyg SRGGRLNLYGDDHHAAYGILQCDIRYSCYAWNSCAHISQMVQVLPYINQVAKKHPWTSK
Mga_Lyg2 SRAGKMLNLYGDDHHAAYGIMQCDVVRNCFWYSCDHINAMTKVLPYIEAVKQKLPWSQ
Mco_Lyg SRAGKMLNLYGDDHHAAYGIMQCDVVRNCFWYSCDHINAMTKVLPYIEAVKQKLPWSQ
Mga_Lyg1 SRAGKMLNLYGDDHHAAYGIMQCDINATCYHWDSCAHINAMTAVLVPNIQGVKRRKHSWSD
Hdi_Lyg1 TRGGKLLGWDHHAAYGIMQCDVYATCYAWNSCDHIDQMTTRILVPIKQVAKKHPWTSR
Hdi_Lyg2 TRGGKLLGWDHHAAYGIMQCDVYATCYAWNSCDHIDQMTTRILVPIKQVAKKHPWTSR
Lgi_Lyg1 TRGGKLLGWDHHAAYGIMQCDLHAQCYGWDSCAHIDMMTRILVPIKQVAKKHPWTSR
Aca_Lyg TRGGKLLGWDHHAAYGIMQCDGGAQCYAWNSCAHIDFVVKLPYINQVAKKHPWTSR
Lgi_Lyg2 SRGGRLNLYGDDGKAYGIMQCDLHKDCYKWDSCDHINMTQVLLPFVKTIRKNHPSWAA
Lgi_Lyg3 TRGGKLLNLYGDDGGRAYGIMQCKY-----WDSCEHINQLTDILLNLYVNMKTKHPSWPA
Cbe_Lyg SRGGALVIGWGDHHAAYGIMQCDGALCYPWSCEHINMMVELLVRDIRTSKHPSWAP
Cgi_Lyg TNVGAUSRGWNAHFYEGMLPCDTRSTCYPWNTCDHALMMAQVLLPFVKSITQKFPWSLS
Hdid_Lyg SRAGTLNLYGDDGNGYGIMQCDIHTTEHAWNSEGHIRQATEVLIPIKIRGVQNKHPAWTK

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Apl_Lyg1 DQQLRGGICAYRARIGNI-QVYDEDPCCGRDNSYVNSVIGRAQYFKRHGF
Gga_Lyg3 DQQLRGG-ICTYHARAGNL-QIYDEDPCCSRDNNYVNSVIRRAQYLRKNGF
Mdo_Lyg1 DQYLRRGGLCAYSEGPG-----YVRSNQDFSCDFCNDVRLARARYKGGHGF
Mmu_Lyg1 DQHLRGGGLCAYSKGPN-----FVRSNQDLNCFDNDVRLARAKYFKDHGF
Hsa_Lyg1 DQYLRRGGLCAYSGGAG-----YVRSNQDLSCDFCNDVRLARAKYLRKHGF
Hsa_Lyg2 AQHLKGGLSAFKSGIE-----AIATPSDIDNDFVNDIARAKFYKRQSF
Mmu_Lyg2 AQQLKGGLTAFKSGME-----TIVTPADIDGDLVDDVRLARAKFYKRHGF
Mdo_Lyg2 SQHLKGGLYAYRSGID-----ALVTPDVENYDNTDILARCKFYRRHGF
Ola_Lygb EQHLKGGALVCMVGLLEKEKLYDELQDPTPRDFANDVIARAQFYAENGF
Pfo_Lygb EMQLKGGALVAYMTGLDRVLDPDHLDSETRTKDFSNDIARAQFFEQKGY
Tni_Lygb EQQLKGGALACYVAGEERVALYEDLDSVTPSKDFSSDVVARAHWFAQNGF
Sau_Lyg3 EQQLKGGIAAYHAGPLAHSYEEVDAKTYGGDYSNDVVARAQWYKSEGF
Sau_Lyg4 EQQLKGVFYLTNCLHTVLCVTHLYLSFQE-----
Dla_Lyg1 EQQLKGGIAAYNAGDGNHHSYEEVDAKTTGCDYSNDVIARAQWYKRNFG
Ssa_Lyg3 EQQLKGGIAAYNKGQDCVSEYKVDAAHTTGMDYSNDVVARAQWYRHGY
Ssa_Lyg5 EQQLKGGIAAYNQDGAIDSCEEVDENTTGKDYSDNVVARAQWYHTNLV
Gmo_Lyg3 EEQLKGGALAAYNKGDGVVHSYKNDVENTTGKDYSDNVVARAQWYWDNLF
Tru_Lyg3 NQHLKGGIAAYNMGDQNVRSYETVDAATTRDYSNDVVARAQWYKRY--
Tru_Lyg2 NQHLKGGIAAYNMGDQNVRSYETVDAATTRDYSNDVVARAQWYKRY--
Tru_Lyg1 DQHLKGGALAAYNKGEKNVESYASVDAKTTGKDYSDNVVRAQWYKSNFG
Tni_Lyga NQHLKGGIAAYNMGDGNVEPGKVDANTTGGDYSNDVVARAKWYKRNSF
Pfo_Lyg1 EQQLKGGIATYNMGDGNVHSYENVDAITTGKDYSNYVVARAKWYKRNGY
Pfo_Lyg2 EQQLKGGIAAYNTGDGKVHSYENVQHTTGKDYSDNVVARAKWYKRNGF
Xma_Lyg EQQLKGGIAAYNTGDGKVHSYENVDEKTTGKDYSDNVVARAKWYKRNGF
Pol_Lyg EKQLKGGIAAYNMGDKNVHSYEGVDENTTGKDYSDNVVARAQWYRDNGY
Sma_Lyg EQHLKGGIAAYNMGDGNVHSYAEVDANTTGGDYSNDVVARAQWYKRNGF
Nro_Lyg2 EQQLKGGIAAYNMGDGNVHSYSDVDANTTGGDYSNDVVARAQWYKNNGF
Nco_Lyg4 EQQLKGGIAAYNMGDGNVHSYSDVDANTTGGDYSNDVVARAQWYKNNGF
Nro_Lyg1 EQQLKGGIAAYNMGDGNVHSYSDVDANTTGGDYSNDVVARAQWYKNNGF
Gac_Lyg EQQLKGGIAAYNMGDGNVHSYDQVDANTTGRDYSNDVVARAQWYKNNGF
Dla_Lyg2 EQQLKGGIAAYNMGDGNVHSYERVDGTTGGDYSNDVVARAQWYKTNGF
Dla_Lyg3 EQQLKGGIAAYNMGDKNVRTVENVDGGSTGGDYSNDVVARSSVQVQ---
Sau_Lyg2 EQQLKGGIAAYNMGDGNVHSYENVDGSTTGRDYSNDVVARAQWYKNNGF

Lcr_Lyg EEQLKGGIAAYNMGDGSVEDRD-VDKNTTGS DYSDVVARAQWYKNNNY
 Ola_Lyga EQQLKGGIAAYNTGDGRVHSCDDVDAHTTGKDYANDVVARAQWYKNGY
 Sau_Lyg1 EQQLKGGIAAYNFVKNVQTVAGVDVGTNHGDYSDVVARAQWYKNGY
 Nco_Lyg2 EQQLKGGIVAYNVGDGKVKNYKAVDYTTTHGDYSDVVARAKHWYKEKDY
 Cse_Lyga EHQLKGAIAAYNQDGGKVSFENVDETTGKDYSDVVISRALWYQRNGY
 Xtr_Lyg1 EQHLKGAIAAYNAGPGNVI SND-VDVRTTGKDYANDVVARAKFYKGRGY
 Cse_Lygb EQQLKGGIAAYNAGDQRVSTN-VDEYTTGGDYSDVVARAQWYKNGY
 Gmo_Lyg6 EKQLKGAIAAYNMGRNVLSCPHGVDHLTTGKDYSDVVARAQFYKRNFG
 Gmo_Lyg1 EQHLKGAIAAYNMGERVLEYAD-VDHLLTTGNDYSDVVARAQFYKQNGF
 Gmo_Lyg5 EQQLKGGIAAYNMGEGVLDNAD-VDRITTTGNDYSDVVARAQFYKRNFG
 Gmo_Lyg4 NWQLKGAIAAYNKGYKVLDPHNDQITTTGGDYSDVVARAQWYKENLF
 Gmo_Lyg2 EQQLKGAIAAYNTGDGRVSEYESVDSRTTGKDYSDVVARAQWYKNGF-
 Gmo_Lyg7 EQQLKGAIAAYNTGDSRVSEYESVDSRTTGKDYSDVVARAQWYKNGF
 Ssa_Lyg2 EKQLKGGIAAYNMGAGSISSEYEQVDAKTTGEDYSDVVARAQFYKNGY
 Aja_Lyg4 EQQLKGGIAAYNCGDQRVCSYEGIDSSTTGRDYSDVVARAQFYKRNFG
 Psi_Lyg1 EQQLKGGISVYNAGLENVQSYDKTDIGTTNNDYANDIVARAKFYKNGY
 Psi_Lyg2 EQQLKGAISAYNGGIGNVRSYDNMDIGTPGNDYASDARAKFFKQGY
 Psi_Lyg4 EQQLKGGISAYNAGVGNVRTYAGMDIGTTHNDYANDVVARAKFYKNGY
 Psi_Lyg3 EQQLKGGISAYNTGPGNVHNYPGVDNGTTHQDYANDVVARAKFYKNGY
 Gga_Lyg1 DQQLKGGISAYNAGVGNVRSYERMDIGTLHDDYSDVVARAQFYKQHG
 Apl_Lyg2 DQQLKGGISAYNAGDGNVRTYERMDIGTTHDDYANDVVARAQFYKQHG
 Gga_Lyg2 EQQLKGGISAYNAGTRNVRTYEGMDVGTTHDDYANDVVARAKFFQRNGY
 Bfl_Lyg1 EMALKGGISGYNAGCGNVQTYAGMDGTTGDDYANDVVARAQWLKNGY
 Bfl_Lyg2 EMALKGGISGYNAGCGNVQTYNGMDIGTTGDDYANDVVARAQWLKNGY
 Bfl_Lyg3 EMALKGGISGYNAGCGNVQTYAGMDVDTTGGDYANDVVARAQWLKNGY
 Lch_Lyg1 DQQLKGGISAYNAGVGNVRTYKMDVGTTHGGDYANDVVARAQWYKNGY
 Lch_Lyg2 DQQLKGGISAYNAGVGNVRTYKMDVGTTHGGDYANDVVARAQWYKNGY
 Pma_Lyg DQQLKGGISAYNAGTRNVGSYANMDIGTTGDDYANDVVARAQMLRDNH
 Rty_Lyg ---FTGGISAYNAGTKNVQTYARMDIGTTHGHDYANDVVARAQWLKNGY
 Ssa_Lyg1 EHQLKGGISAYNAGDKNVRTYERMDVGTTHGGDYSDVVARAQWFKSQGY
 Omo_Lyg EHQLKGGISAYNAGAKNVQTYERMDVGTTHGGDYSDVVARAQWFKQGF
 Ame_Lyg1 EHQFKGGIAAYNFVGNVRTYERMDIGTTHGGDYSDVVARAQWFKRHGY
 Ame_Lyg2 EHQFKGGIAAYNAGVGNVRTYERMDIGTTHDDYSDVVARAQWFKRNGY
 Tfu_Lyg EHQFKGGISAYNAGVGNVRTYEGMDIGTTHGNDYSDVVARAQWFKCKGY
 Aja_Lyg2 EHQFKGGISAYNAGDKNVRTYEHMDVGTTHGGDYSDVVARAQWFKRNGY
 Aja_Lyg3 EQQLKGGISAYNAGVGNVRTYERMDMGTTHGGDYSDVVARAQWFKRNGY
 Cid_Lyg EQCFKGGISAYNAGPGNVRTYERMDVGTAGDYSDVVARAQWYKSKGY
 Dre_Lyg2 EQCFKGGISAYNAGVKNVQTYERMDVGTTHGGDYANDVVARAQWFKSKGY
 Dre_Lyg1 EQCFKGGISAYNAGVKNVQTYEHVDDHTTGHGNDYSDVVARAQWFKSKGY
 Cca_Lyg EQCFKGGIAAYNKGVSRVTSYENIDVKTGLDYSDVVARAQWFRSKGY
 Dre_Lyg3 EQCVKGGIAAYNAGVKNVKSIEDVDEGTTGRDYANDVVARAQWFKTDGY
 Bgl_Lyg2 ERQLQGGVAAAYNFVSNVQSWGGLDVGTTNNDYSDVVARAKYLYSIGW
 Pac_Lyg HQALQGGVAAAYNFVSNVQSWGGLDVGTTGNDYSDVVARAKWLGANGW
 Aca_Lyg1 AQAALQGGVAAAYNFNLDNVRTWSKLDVGTTHDDYSDVVARAQYHLHGQGW
 Mye_Lyg3 DQQLQGGIAAYNSGVSNVQVWAHLVGTTHGNDYSDVVARAKHLIASNW
 Mye_Lyg1 DQQLQGGIAAYNFVGNVQSWANLDGTTQNDYSDVVARAKRLIANNW
 Afa_Lyg DQQLQGGIAAYNSGVGNVQVWAHLVGTTHGNDYSDVVARAKHLISSGW
 Mye_Lyg2 DQQLQGGIAAYNFVGNVQSWANLDGTTQNDYSDVVARAKRLIANNW
 Air_Lyg EQQLLGGIAAYNSGVGNVQVWSGLDVGTTGNDYSDVVARAQYLI SHGW
 Mga_Lyg2 AQAALQGGVAAAYNFVGNVQVWDLKLDIGTTHNDYSDVVARAQWLIHRNW
 Mco_Lyg AQAALQGGVAAAYNFVGNVQVWDLKLDIGTTHNDYSDVVARAQWLIHRNW
 Mga_Lyg1 AQAALQGGVAAAYNFVGNVQVWSGGLDVGTTGNDYSDVVARAQWLIHRNW
 Hdi_Lyg1 EQQMGGVSAYNAGVGNVATWVSHLDVGTTHGNDYSDVVARAQHLINQGW
 Hdi_Lyg2 EQQMGGVSAYNAGVGNVATWVSHLDVGTTHGNDYSDVVARAQHLIKQGW
 Lgi_Lyg1 ENQLKGGVSAYNAGVGNVATVARMMDIGTTGNDYSDVVARAQRLITSGW
 Aca_Lyg DQALKGGISAYNAGVGNVQTYAGMDLGTTHGNDYANDVVARAQRLISHHW
 Lgi_Lyg2 KYQLKGGVAAAYNFVGNVQVTPGMDDKTTGDDYSDVVARAQRLVKAGW
 Lgi_Lyg3 HYQLKGGVSAYNAGVGNVQVTPGMDDKTTGDDYSDVVARAQRLVNRAGW
 Cbe_Lyg EQQLQGGVAAAYNAGTGNVRSFRRMDVGTTHGNDYSDVVARAQYLVNRGW
 Cgi_Lyg EQHILQGGVAAAYNAGIDHVDSWSNVQHTTHGNDYSDVVARAQYLVSHSW
 Hdid_Lyg EQQLQGGIAAYNFVKNVQTVAGTVDVGTTHGNDYSDVVARAQRLIDKGW

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