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Identification of Major Phylogenetic Branches of Inhibitory Ligand-Gated Channel Receptors

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Abstract. The gene superfamily of ligand-gated ion channel (LGIC) receptors is composed of members of excitatory LGIC receptors (ELGIC) and inhibitory LGIC receptors (ILGIC), all using amino acids as ligands. The ILGICs, including GABAA, Gly, and GluCl receptors, conduct Cl⁻ when the ligand is bound. To evaluate the phylogenetic relationships among ILGIC members, 90 protein sequences were analyzed by both maximumparsimony and distance matrix-based methods. The strength of the resulting phylogenetic trees was evaluated by means of bootstrap. Four major phylogenetic branches are recognized. Branch I, called BZ, for the majority of the members are known to be related to benzodiazepine binding, is subdivided into IA, composed of all GABA_A receptor α subunits, and IB, composed of the γ and ε subunits, which are shown to be tightly linked. Branch II, named NB for non-benzodiazepine binding, and consisting of GABA_A receptor β , δ , π , and ρ subunits, is further subdivided into IIA, containing β subunits; IIB, containing δ , and π subunits; and IIC, containing p subunits. Branch IIIA, composed of vertebrate Gly receptors, is loosely clustered with Branch IIIB, composed of invertebrate GluCl receptors, to form Branch III, which is designated NA for being non-GABA responsive. Branch IV is called UD for being undefined in specificity. The existence of primitive forms of GABA_A receptor non-β subunits in invertebrates is first suggested by the present analysis, and the identities of sequences p25123 from Drosophila melanogaster, s34469 from Lymnaea stagnalis, and u14635

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and p41849 from *C. aenorhabditis elegans* are determined to be different from their previously given annotations. The proposed branching classification of ILGICs provides a phylogenetic map, based on protein sequences, for tracing the evolutionary pathways of ILGIC receptor subunits and determining the identities of newly discovered subunits on the basis of their protein sequences.

Key words: Classification — Evolution — γ -Aminobutyric acid_A — Glutamate — Glycine — Ligand-gated channel — Phylogeny — Receptor

Introduction

Ligand-gated ion channel (LGIC) receptors form a gene superfamily (Betz 1990) composed of excitatory cation channels gated by acetylcholine (nACh) and serotonin (5HT₃) and inhibitory anion channels gated by γ aminobutyric acid (GABA_A), glycine (Gly), and glutamate (GluCl). The members of the superfamily share high degrees of amino acid sequence similarities and are therefore believed to have similar three-dimensional (3-D) structures (Unwin 1993). They are likely to be heteroor homopentamers, with a large N-terminal extracellular domain followed by transmembrane and cytoplasmic domains (Karlin 1993). As members of the LGIC superfamily are often important pharmaceutical targets, their 3-D structural resolution would greatly facilitate the study of drug-receptor interactions. However, the oligomeric and membrane-bound nature of these receptors has so far obstructed all attempts to obtain suitable starting 324

	Subunit	Accession No.							
Receptor		Human	Bovine	Rat	Mouse	Chicken	Goldfish		
GABAA	α1	p14867	p08219	p18504		p19150	_		
A	α2	p47869	p10063	p23576	p26048				
	α3	p34903	p10064	p20236	p26049	_			
	α4	p48169	p20237	p28471	_	_			
	α5	p31644	_	p19969	_	_			
	α6	s81944	_	p30191	p16305	_	x94342		
	γ1	_	_	p23574	_	_			
	γ^2	p18507	p22300	p18508	p22723	p21548	_		
	γ3	_	_	p28473	p27681	_	_		
	$\gamma 4$	_	_	_	_	p34904			
	3	y07637	_	_	_	_	_		
	β1	p18505	p08220	p15431	p50571	_			
	β2	p47870	_	p15432	_	_			
	β3	p28472	_	p15433	_	p19019	_		
	β4	_	_	_	_	p24045			
	δ	_	_	p18506	p22933	_	_		
	π	u95367	_	u95368	_	_			
	ρ1	p24046	_	p50572	_	_			
	ρ2	p28476	_	p47742	_	_			
	ρ3	_	_	p50573	_	_	_		
Gly	α1	p23415	_	p07727	_	_	_		
	α2	p23416	_	p22771	_	_			
	α3	-	_	p24524	_	_			
	β	p48167	—	p20781	p48168	—	—		

materials for 3-D structural studies by either X-ray or nuclear magnetic resonance (NMR). The lack of information about the origin of LGIC receptors has also hampered the application of homology modeling to elucidate the tertiary structure of these receptors.

As a result of the combined power of patch clamping and molecular genetics, new ion channel receptors from various phylogenetic sources are constantly being cloned and characterized (Betz 1990). These advances along with progress in genomic sequencing, including the complete sequencing of four entire genomes from three phylogenetic kingdoms (Garret 1996), have made possible an evolutionary analysis of the LGIC receptor superfamily. The molecular evolution of nACh receptors, an excitatory LGIC (or ELGIC) multigene family, has been the topic of several publications (Novére and Changeux 1995; Ortells and Lunt 1995; Gundelfinger 1995), in contrast to the much less discussed inhibitory LGIC (or ILGIC) receptors. Recently, Ortells and Lunt (1995) analyzed the evolutionary history of the whole superfamily of LGIC receptors, including 47 GABA_A and Gly receptors, but not the GluCl receptors. Their study was based on nucleic acid sequences of the receptor subunits. In contrast, the present study attempts to infer phylogenies from protein sequences, since the greater conservation of amino acid sequences should allow us to bring more information to bear on ancient origins of lineages. Only the phylogeny of ILGICs as a subissue of the phylogeny of the whole LGIC superfamily is addressed. Accordingly, 90 protein sequences of ILGIC members, including GABA_A, Gly, and GluCl receptor subunits, are statistically analyzed for their evolutionary relationships using both cladistic and phenetic methods supported by the use of the resampling method, bootstrap, to test the robustness of resulting tree nodes. Known ELGIC receptor subunits are used as the outgroup, which offers the best basis for placing the root on the phylogenetic trees. The level of sequence density employed has allowed the delineation of four major phylogenetic branches. This branching classification provides a basis for not only tracing the evolutionary history of ILGICs, but also predicting the ligand specificity of newly discovered ILGIC receptor subunits.

Materials and Methods

Sequence Data

Protein sequences were obtained from the SwissProt (release 34.0) or PIR (release 50.0) databases or deduced from DNA sequences in the GenBank (release 97.0) database. We used the tools provided with the Sequence Analysis Software Package, GCG, Version 8.1.0 (Genetic Computer Group 1994), EGCG (Rice 1996), and Entrez available at the National Center of Biotechnology Information for database search and sequence conversion. The sequences employed are listed in Table 1 for vertebrates and Table 2 for invertebrates.

Alignment of Sequences

Multiple sequence alignments were performed by means of the program PILEUP from the GCG package, according to the empirical scor-

Table 2. Thirty-six sequences of ILGICs from invertebrates

Lineage	Species (common name)	Acc. No. ^a	Receptor (alternative name)	Subunit	Suggested identity ^b
Arthropoda	Drosophila melanogaster (fruit fly)	x78349 <u>p25123</u> q08832 m69057 u02042 u58776	LGIC (Grd, Gly-like) GABA (LCCH3, gab_drome) GABA (gab3_drome) GABA (Rdl; cyclodiene resistant) GABA GluCI	β β-like	GA α/γ-like GL/GA GA β GL/GA GL/GA GluCI α
Arthropoda	Aedes aegypti (vellow fever mosquito)	s33744	GABA-like (Rdl; cyclodiene resistant)		GL/GA
Mollusca Nematoda	Lymnaea stagnalis (great pond snail) Caenorhabditis elegans	p26714 <u>s34469</u> u40187	GABA (gab_lymst) GABA-like GABA-like	β ζ	GA β GL GA/GL
		u14525 s50864 u41113	GABA-like GluCl GluCl ILGIC (Cegbr 3)	β α	GA/GL GluCl β GluCl α GluCl α
		u40573 u64840 <u>u14635</u>	ILGIC (Cegbr 2) LGIC-like GABA/Gly-like		GluCl α GluCl α GluCl
		z70270 z74040 <u>p41849</u>	GABA GABA Gly-like (yo99_caeel)	β-like β-like	ILGIC ILGIC ILGIC
		u28929 z68217 u40422	Gly Gly-like GABA-like	α-like	ILGIC ILGIC ILGIC
		z46791 z50027 u64843	GABA GABA-like LGIC-like	β1-like	ILGIC ILGIC ILGIC
		u40948 z49888 u40573 u42836	LGIC-like LGIC-like (Cegbr2)		ILGIC ILGIC
		u42836 u59743 u59744 u64840	GluCl GluCl		
Nematoda	Haemonchus contortus	x73584 y09796	ILGIC-like GluCl	β	— Ga α/γ-like? GluCl β
Nematoda	Onchocerca volvulus	u59745	GluCl		GluCl α

^a Accession No.: underlined, suggested identity is different from previous annotation; boldface, newly suggested identity.

^b GA, GABA_A; GL, GluCl/Gly; ILGIC, undifferentiated ILGIC; —, not included in the present analysis.

ing matrix PAM250 (Dayhoff 1979), with a gap creation weight of 6.0 and a gap length weight of 0.01. Most variable sequences from the N and C termini are excluded from further analysis. The alignments were cross-checked using a more sensitive program, CLUSTAW (Thompson et al. 1994), which made no difference to the final results.

Phylogenetic Analyses

Multiple alignments of amino acid sequences were analyzed using the PHYLIP 3.57c software package (Felsentein 1993). For cladistic analysis, the program PROTPARS based on the maximum-parsimony algorithm (Fitch 1971) was used to construct phylogenetic trees. For phenetic analysis, the program FITCH (Fitch and Margoliash 1967) was employed. Based on sequence alignments corrected distances were calculated according to the PAM250 scoring matrix using PRODIST of the PHYLIP package and scaled in expected historical events per site (Dayhoff 1979). Gaps were treated as missing data and excluded from the calculations. The matrices were then used to construct additional trees by the least-squares method of program FITCH from the PHYLIP package (Fitch and Margoliash 1967). The strength of the tree topology

was tested by bootstrap analysis (Felsenstein 1985) with either 100 or 1000 (as specified in the figure legends) replications employing the program SEQBOOT. Majority-rule consensus trees were obtained with the program CONSENSE.

Results and Discussion

Ninety-four protein sequences (Tables 1 and 2) were retrieved from databases. They all have some highly characteristic sequence motif, for example, a 15-residue cysteine (Cys) loop in the N-terminal domain, and all are annotated as ligand-gated Cl⁻ ion channel receptors regardless of the ligand being GABA, Gly, Glu, or, in some cases, unidentified. Eighty-eight sequences of ninety-five were aligned with PILEUP, five of the remaining seven sequences bearing excessive variations and two others being published recently (Hedblom and



Fig. 1. Bootstrap majority-rule consensus tree obtained from 100 replicates (SEQBOOT, PROTPARS, and CONSENSE programs) of 88 ILGIC sequences using nACh receptor sequence ach9_rat as an outgroup with 80 informative sites. For clarity, bootstrap numbers are omitted. Abbreviations used in Figs. 1–4: GAB, GABA_A receptor;

GLY, Gly receptor; GLU, Glu receptor; a, α subunit; b, β subunit; g, γ subunit; d, δ subunit; e, ε subunit; p, π subunit; r, ρ subunit; chick, chicken; gfish, goldfish; drome, *Drosophila melanogaster*; lymst, *Lymnaea stagnalis;* caeel, *Caenorhabditis elegans;* haeco, *Haemonchus contortus;* oncvo, *Onchocerca volvulus*.

Kirkness 1997). Two most highly conserved regions are revealed by the alignment. The first region covers the 15-residue Cys loop, while the second spans the three tentative transmembrane segments M1–M3. Other regions of the sequences are generally more variable than these two. For example, a LGIC-like sequence (Accession No. x78349 (Harvey et al. 1994) from *Drosophila melanogaster* has a long insertion of about 70 residues

between the two regions. The consensus tree obtained from 100 bootstrap replicates is shown in Fig. 1.

To carry out a thorough search of tree topologies, the 90 sequences were divided into smaller groups and subjected to further extensive analysis. Results from analyzing various combinations of sequences are summarized in Table 3. Only one example of such group analysis is provided graphically (Figs. 2 and 3). This group is a

Table 3. Branch classification of ILGIC receptor subunits

Branch	Name ^a	Members
Ι	ΒZ	GABA _A receptor α and γ subunits plus
TA		GABA receptor a subunits
IA		$GABA_A$ receptor a subunits
ID	ND	$GABA_A$ receptor γ and ε subunits
11	NB	GABA _A receptor β , δ , and ρ subunits plus the new class, π subunit
IIA		GABA _A receptor β subunits
IIB		GABA receptor δ and π subunits
IIC		$GABA_{A}$ receptor ρ subunits
III	NA	Gly and GluCl receptor subunits
IIIA		Gly receptor subunits
IIIB		GluCl receptor subunits
IV	UD	p41849, u28929, u40422, u40948, u64843,
		z46791, z50027, z68217, z70270,
		z74040, z49888
Intermediates		,
I-like		x78349
I/II/III-like		m69057, u02042, s33744, u40187.
		z50016, p25123

^a BZ, relevant to benzodiazepine binding; NB, not involved in benzodiazepine binding; NA, nonresponsive to GABA; UD, specificity undefined.

collection of 30 representative sequences (Figs. 2 and 3). This sample collection included one sequence from each subtype of the GABA, and Gly receptors, along with the nACh receptor subunit ach9_rat as an outgroup. Sequences from rat were chosen from orthologs wherever feasible. For GABA_A receptor $\gamma 4$ and $\beta 4$, for which no rat orthologs were available, chicken sequences were employed. Seven invertebrate sequences were also included due to their being significantly different from the vertebrate sequences. Among them, three were from Drosophila melanogaster, i.e., gab_drome, x78349, and u58776. Two of them, gab_lymst and s34469, were from Lymnaea stagnalis, while the other two, u14525 and y09796, were from Caenorhabditis elegans and Haemonchus contortus, respectively. Other group-analysis results are available on request.

Branches of ILGICs

Four major branches were delineated by both the maximum-parsimony (Figs. 1 and 2) and the distance matrixbased (Fig. 3) methods. Branches I and III each can be further subdivided into two secondary branches, A and B, while Branch II is divided into A, B, and C (Table 3). Alignment with either ach1_caeel or 5ht3_mouse as an outgroup did not change these tree topologies. The ranges of pairwise distances between and within branches are presented in Table 4 to provide a numerical estimation of the relationships among the sequences. While the interbranch distances point to the relative closeness between branches, the intrabranch distances shown on the diagonal in Table 4 are indicative of the relative closeness between members of the same branch. The striking difference in pairwise distance between orthologs (Table 5) suggests an inconstancy in evolutionary rates of ILGICs. Therefore no attempt was made to estimate the divergence times using the molecular clock assumption.

GABA_A Receptor Subunits

Fifty-three GABA_A receptor sequences (Tables 1 and 2), forty-four from mammals, five from chicken, one from goldfish, two from fruit fly, and one from the great pond snail, were analyzed. Among these are two newly discovered subunit classes, namely, ε (Davies et al. 1997) and π (Hedblom and Kirkness 1997) subunits. All known subtypes of GABA_A receptor subunits can be divided into the two monophyletic Branches I and II (Figs. 2 and 3). Branch I comprises all known GABA_A receptor α and γ subunit sequences, plus the new class, the ε subunit. As the α and γ subunits are known to carry, respectively, the principal and the complementary parts of benzodiazepine sites, Branch I is called BZ. Branch I is further divided into two monophyla, named IA for all α subunits and IB for all γ and ε subunits. Branch II, composed of GABA_A receptor β , δ , and ρ subunits as well as the new class, the π subunit, is designated NB because a majority of the members of this branch are known not to be directly relevant to benzodiazepine binding. Under Branch II, all ß subunits clearly form the monophylum IIA, and all ρ subunits form another monophylum, IIC. Bootstrap did not strongly support the assignment of δ subunits as either IIA or IIC members. They are therefore assigned to a separated secondary branch, IIB. The newly discovered π subunit is assigned to IIB based on our analysis.

Most recently, Davies et al. (1997) suggested the occurrence of a new class of human GABA_A receptor subunits, ε , based on its pharmacological property of conferring insensitivity to the potentiating effects of the intravenous anesthetic agents propofol, pentobarbital, and pregnanolone. The sequence of the ε subunit is nearly identical to that of a putative GABA-gated chloride channel subunit expressed in the human cardiac conduction system (Garret et al. 1997), with the exception that the former has one extravaline (Val) residue at position 261. The latter was not included in our analysis, to avoid redundancy. The ε subunit is shown by our analysis (Figs. 2 and 3) to form a monophyletic group with all the other γ subunits. In this sense, it may be regarded as a type of γ subunit rather than a separate class.

Gly and GluCl Receptor Subunits

Branch III is named NA for being non–GABA responsive; it is essentially a collection of chloride channel receptors gated by either Gly or Glu. The fact that



Fig. 2. Bootstrap majority-rule consensus tree obtained from 1000 replicates (SEQBOOT, PROTPARS, and CONSENSE programs) of 30 ILGIC sequences along with nACh receptor sequence ach9_rat as an outgroup. The reconstruction is based on the alignment shown in Appendix 1 with 267 informative sites. The *numbers beneath the branches* give the bootstrap values of 1000 replications.

 $GABA_A$ and Gly receptors are closely related has long been noted from their high sequence similarity. This close relationship is statistically confirmed by the present analysis. In an evolutionary analysis of the whole LGIC receptor superfamily, including ELGICs and ILGICs, Ortells and Lunt (1995) suggested that Gly receptors were derived from GABA_A receptors. Although the present study does not provide strong support for this hypothesis, the closeness between GABA_A and Gly receptors is evident from the pairwise distance values (Table 4). It has been noted that the sequences of GluCl receptors are related to those of Gly and $GABA_A$ receptors (Cully et al. 1994). Figures 2 and 3 further suggest that GluCl receptors are closer to Gly receptors than they are to $GABA_A$ receptors.

The clustering of Gly and GluCl receptors into Branch III is indicated by both cladistic (Fig. 2) and phenetic (Fig. 3) analyses, but only weakly supported by bootstrap. This looseness in the clustering as shown by the low bootstrapping rate and the relatively large distances (Table 4) between Gly and GluCl suggest that contemporary Gly and GluCl receptors are derived from a rela-



Fig. 3. Bootstrap majority-rule consensus tree obtained from 1000 replicates (SEQBOOT, PROTDIST, FITCH, and CONSENSE programs) of 30 ILGIC sequences along with nACh receptor sequence ach9_rat as an outgroup. The reconstruction is based on the alignment shown in Appendix 1 with 267 informative sites. The *numbers beneath the branches* give the bootstrap values of 1000 replications.

tively remote common ancestor. The internal stabilities of the two secondary branches, IIIA, with all the Gly receptors, and IIIB, with all the GluCl receptors, are strongly established by bootstrapping. This confers substantial confidence in the identification of any potential Gly or GluCl receptors on the basis of protein sequence alone.

So far no GluCl receptor has been discovered in vertebrates, and likewise no Gly receptor could be confirmed in invertebrates (Laughton et al. 1994). Three sequences from *C. elegans*, namely, p41849, u28929, and z68217, were previously annotated as Gly or Glylike receptor subunits (Table 2). Instead, they are found to be members of Branch IV (Table 3). This would suggest that the specialization of Gly and GluCl receptors must have occurred after the divergence of invertebrates and vertebrates. Given the clustering of Branch IIIA with Branch IIIB, Gly and GluCl receptors possibly represent the vertebrate and invertebrate counterparts of one another. This agrees with the suggestion of Vassilatis et al. (1997), based on their gene structure comparisons and phylogenetic analysis, that invertebrate GluCl receptors may be orthologous to the vertebrate Gly receptors, although no outgroup was employed in their analysis.

ILGIC Receptor in Invertebrates

Invertebrate ILGIC sequences are listed in Table 2. The sequences include those obtained by Wilson et al. (1994)

	Branch							
Branch	IA	IB	IIA/B	IIC	IIIA	IIIB	IV	
IA	0.66-61.62	70.45-93.69	96.32-126.38	105.13-135.82	95.89-145.25	95.55-167.90	124.47-177.95	
IB		1.08-40.47	93.44-111.01	110.31-125.35	98.35-130.09	103.54-152.80	117.35-162.44	
IIA			0.21-98.88	93.18-114.42	93.55-121.01	97.98-150.86	119.23-169.79	
IIB				5.44-48.72	109.12-129.29	104.40-154.24	121.70-159.81	
IIIA					0.22-78.30	87.86-156.69	109.05-160.20	
IIIB						17.58-115.59	100.69-195.52	
IV							51.0-178.53	

Table 5. Distances between orthologs

	Dist	ance
Subunit	Human/rat	Rat/mouse
GABA _A receptor		
α1	1.55	
α2	3.16	1.56
α3	3.94	1.85
α4	11.18	
α5	4.89	
α6	9.02	2.98
β1	1.92	0.21
β2	0.21	
β3	2.79	
$\gamma 2$	1.08	1.08
δ	_	0.45
ρ1	5.44	
ρ2	9.49	
Gly receptor		
α1	2.48	0.22
α2	1.11	
β	2.66	0.81

from a 2.2-Mb fragment of C. elegans chromosome III (Wilson et al. 1994), with at least 24 open reading frames encoding proteins bearing sequence similarity to LGIC receptors. All 11 current members of Branch IV (Tables 2 and 3) are from C. elegans. It remains to be seen whether the completion of additional genome sequencing will reveal additional Branch IV members that could shed more light on the nature of this phylogenetic branch. The distances between Branch IV and each of other three branches are of the same order of magnitude (Table 4). In view of the relatively large distances between Branch IV and the other branches, the separations of the three other branches from Branch IV were evidently remote historical events. The large intrabranch distances within Branch IV suggest that the original divergences of the various Branch IV members were likewise ancient occurrences.

The classification scheme developed and illustrated in Figs. 1–3 suggests the nature of many of these invertebrate sequences (Tables 2 and 3) whose specifications were hitherto unknown. These include the assignment of u41113, u40573, and u64840 from *C. elegans* to Branch

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IIIB (Figs. 2 and 3, Tables 2 and 3), thereby implying a GluCl identity, and x78349 from *Drosophila melanogaster* to Branch 1, thereby implying a GABA_A α/γ identity, although the large insertion in its extracellular portion may well have altered its ligand specificity.

Instances where the present branching classification results in a revision of earlier annotations include the placement of s34469 from the great pond snail, previously designated the GABA_A receptor ζ subunit (Hutton et al. 1993), closer to Gly/GluCl than to GABA_A receptors by both the PROTPARS (Fig. 2) and the FITCH (Fig. 3) procedures; also, P41849 from *C. elegans* is grouped with other Branch IV sequences instead of Gly sequences as had been suggested (Swiss-Prot annotation). In yet another example, *C. elegans* u14635 (Wilson et al. 1994), previously annotated as a GABA_A/Gly subunit (Swiss-Prot annotation), is assigned to Branch IIIB (Figs. 2 and 3, Table 3), which implies a potential GluCl identity.

The monophylum consisting of p25123, m69057, and u02042 from *Drosophila melanogaster*, u40187 and z50016 from *C. elegans*, and s33744 from *Aedes aegypti*, represents an intermediate group. All six sequences were previously annotated as GABA or GABA-like, but the present study suggests that they are more likely to be evolutionary intermediates rather than well-differentiated GABA_A receptor subunits. Two of these six sequences, namely, m69057 and s33744, are known to confer cyclodiene resistance (Table 2).

In invertebrates, hitherto only β subunits have been encountered, and there has been no suggestion made of the occurrence of GABA_A non- β subunits in invertebrates. In the present analysis, however, the *Drosophila melanogaster* sequence x78349 is found to cluster with the non- β Branch I sequences (Figs. 2 and 3). The distances between x78349 and Branch I vertebrate sequences are 93.66–120.73, which are smaller than the distances of 123.83–135.79 between x78349 and other *Drosophila melanogaster* ILGICs. Therefore x78349 is closer to Branch I than to other *Drosophila melanogaster* sequences, with the major difference between x78349 and Branch I sequences arising from a single large insertion at its amino-terminal domain (Harvey et al. 1994). In line with this tentative identification of x78349

GABr1_rat	RVTVTAMC NMDFSRF	ΡL	DTQT	CSLEIH	ΞSΥ
GABr2_rat	RITVTAMCNMDFSHF	ΡL	DSQI	CSLELE	ΞSΥ
GABr3_rat	RITVSAMC FMDFSRF	ΡL	D TQN	CSLELE	ΞSΥ
GABb2_rat	RITTTAACMMDLRRY	ΡL	D EQ№	CTLEIS	ΞSΥ
GABb3_rat	RITTTAACMMDLRRY	ΡL	DEQN	CTLEIE	ΞSΥ
GABb1_rat	RITTTAACMMDLRRY	ΡL	DEQN	CTLEIE	ΞSΥ
GABb4_chick	RITTTAACMMDLRRY	PL	DQQN	CTLEIE	ΞSΥ
GABb3_drome	RFTTTLAC MMDLHYY	ΡL	DSQN	CTVEIE	ΞSΥ
GABb_lymst	RFTTTLAC MMDLHNY	ΡL	DHQE	CTVEIE	SΥ
GABp_rat	RITTTVTCNMDLSKY	ΡM	D TQT	CKLQLE	ΞSΥ
GABd_rat	RITSTVAC DMDLAKY	ΡM	DEQE	CMLDLE	ΞSΥ
GABa4_rat	RLTISAEC PMRLVDF	ΡM	DGHA	CPLKFC	SY
GABa6_rat	RLTINADC PMRLVNF	ΡM	DGHA	C PLKFO	SSΥ
GABa1_rat	RLTVRAEC PMHLEDF	ΡM	DAHA	C PLKFC	SΥ
GABa3_rat	RLTIHAEC PMHLEDF	ΡM	DVHA	C PLKFC	SΥ
GABa2_rat	RLTVQAEC PMHLEDF	РM	DAHS	C PLKFC	SΥ
GABa5_rat	RLTISAEC PMQLEDF	ΡM	DAHA	C PLKFC	SY
GABg1_rat	RLTINAEC YLQLHNF	ΡM	DEHS	CPLEFS	SΥ
GABg2_rat	RLTIDAEC QLQLHNF	РM	DEHS	CPLEFS	SΥ
-GABg3_rat	RLTINAEC QLQLHNFI	ΡM	DAHA	C PLTFS	SΥ
GABg4_chick	RLTIEAECLLQLQNF	ΡM	DTHS	C PLVFS	SSY
GABe_human	RMTIDAGC SLHMLRF	ΡM	DSHS	CPLSFS	SF
x78349	RLTIKAGC PMNLADFI	ΡM	DIQK	C PLKFO	SF
x73584	RLTIKTKCLMFLKKF	РM	DVQA	C PIEIC	SL
GLYa1_rat	RITLTLAC PMDLKNF	PM	DVQT	CIMQLE	SF
GLYa3_rat	RLTLTLSC PMDLKNFI	P M	DVQT	CIMQLE	SF
GLYa2_rat	RLTLTLSC PMDLKNFI	P M	DVQT	CTMQLE	SF
GLYb_rat	RLSITLSC PLDLTLFI	P M	DTQR	CKMQLE	SF
GLUb_caeel	RISLTSSC PMRLQLY	ΡL	DYQS	CNFDL	/SY
GLUb_haeco	RISITSSCHMQLQLY	PL	DLQF	CDFDLV	SΥ
GLU_drome	RISLTLAC PMNLKLY	PL	DRQI	C SLRMA	SΥ
ACh9_rat	PAITKSSCVVDVTYFI	PF:	DSQQ	CNLTFG	SW
LGIC common	с	Р	D	С	S
ILGIC specific	R				
Branch I specific			Н	P	

Fig. 4. The neighborhood of the conserved Cys–Cys loop in 31 representative ILGIC subunits aligned with the outgroup ACh9_rat. Residues common to both ILGIC and ELGIC are in *boldface*. They are indicated at the *bottom*, along with residues specific to ILGIC or Branch I members. The Cys–Pro doublet characteristic to Branch I is *boxed*.

as a primitive form of the GABA_A receptor α/γ subunit, sequence x73584 from the nematode *Haemonchus contortus* also displays α/γ -like properties, showing in the C–C loop region the characteristic Cys–proline (Pro) doublet that is unique for Branch I sequences (Fig. 4). Based on x78349 and supported by x73584, the present analysis therefore provides evidence for the first time of the existence of primitive non- β GABA_A receptor subunits among invertebrates.

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Appendix

	1			50		101				150
gar1_rat	GGPAIPVGVD VQVESLDSIS	EVDMDFTMTL	YLRHYWKDER	LSFGRLVKKI	garl_rat	RFPLDTQTCS	LEIESYAYTE	DDLMLYWKKG	NDSLKTHTTT	KLAFYSSTGW
gar2_rat	GGPAIPVGVD VQVESLDSIS	EVDMDFTMTL	YLRHYWRDER	LAFGRLVKKI	gar2_rat	HFPLDSQTCS	LELESYAYTD	EDLMLYWKNG	DESLKTHTTS	RLAFYSSTGW
gar3 rat	GGSPVPVGID VOVESIDSIS	EVNMDFTMTF	YLRHYWKDER	LSFRRLIOKI	gar3_rat	REPLDTQNCS	LELESYAYNE	EDLMLYWKHG	NKSLNTSASS	GLAFYSSTGW
gab2 rat	COPPVAVOMN TOTASTOMVS	EVNMDYTLTM	VEOOAWRIJKR	LSYNEVADOL	gab2 rat	RYPLDEONCT	LEIESYGYTT	DDIEFYWRGD	DNAVTGKUTT	KKVVF . STGS
gab3 rat	GGPPVCVGMN TDTASTDMVS	EVINIMITYTT	YFOOYWRDER	LAYNRVADOL	gab3 rat	RYPLDEONCT	LEIESYGYTT	DDIEFYWRGG	DKAVTGRLVS	RNVVF . ATGA
gabj_rut	COPPUDUCMP TOWASTOWNS	FUNDOUTION	VEOOGWEDED	LEVNEVADOL	gabl rat	RVPLDEONCT	LETESVOYTT	DDIEEVWNGG	ROAVTORNUS	KKAEE DAGY
	CONDUMICING INTRODOTO	CUMPLET INTE	VEOOGWIDKK	LAVADUADOL	cab4 chick	BYRIDOONCE	LETERVOYIN	DDTUFFWOON	DENUMORINE	DENNE MACC
gab4_chick	CORPUTIONS INTESTIONS	EVINAL/IIIIM	11 VOLUMEDRE	LAINAVALQU	gab4_chick	VVDI DCONOT	VELECYCVE	CDIRAGRA V	DONVIGROUD	NEVVE . 1100
gabs_drome	GGEPLHVGMD DFIASFDAIS	EVINIDITIT	ILNQIWRDER	LAFGDFAERI	yabs_drome	TIPLDSQNCT	VELESIGITV	SDVVHIWK	PTPVRGETND	KKERLLAIGV
gab_iymst	GGAPLEIGIE VILASFDSIS	EVOMDYTITM	YLNQYWRDER	LOFGAFAEKI	gab_1ymst	NYPLDHQECT	VELESIGITM	DDIVLYWLND	RGAVIGATIN	KIEEL.STGD
gad_rat	GGPPVNVALA LEVASIDHIS	EANMEYTMTV	FLHQSWRDSR	LSISREVDEL	gad_rat	KIPMDEQECM	LDLESIGISS	EDIVIIWSEN	QEQINGRETT	ELMNFRSAGQ
gaa4_rat	GGPVTEVKTD IYVTSFGPVS	DVEMETTMDV	FFROTWIDER	LKYNMMVTKV	gaa4_rat	DFPMLGHACP	LKFGSYAYPK	SEMIYTWIKG	PERSVEQTVS	SETIKSITGE
gaab_rat	GGAVTEVETD 19VTSFGPVS	DVEMEYTMDV	FFROTWIDER	LKFNLMVSKI	gaat_rat	NFPMDGHACP	LKFGSYAYPK	SELLYTWKKG	PLYSVEQTVS	SETIKSNIGE
gaal_rat	GERVTEVETD IFVTSFGPVS	DHDMEYTIDV	FFROSWKDER	LKFNLMASKI	gaal_rat	DFPMDAHACP	LKFGSYAYTR	AEVVYEWTRE	PARSVVQTVD	SGIVQSSTGE
gaa3_rat	GDAVTEVETD IYVTSFGPVS	DTDMEYTIDV	FFRQTWHDER	LKFNLLASKI	gaa3_rat	DFPMDVHACP	LKFGSYAYTK	AEVIYSWTLG	KNKSVEHVVG	TEIIRSSTGE
gaa2_rat	GDSITEVFTN IYVTSFGPVS	DTDMEYTIDV	FFRQKWKDER	LKFNSMASKI	gaa2_rat	DFPMDAHSCP	LKFGSYAYTT	SEVTYIWTYN	PSDSVQQSIG	KETIKSSTGE
gaa5_rat	GERITQVRTD IYVTSFGPVS	DTEMEYTIDV	FFROSWKDER	LRFNLLASKI	gaa5_rat	DFPMDAHACP	LKFGSYAYPN	SEVVYVWTNG	STKSVVQTVG	TENISTSTGE
gac1_rat	GVRPTVIETD VYVNSIGPVD	PINMEYTIDI	IFAQTWFDSR	LKFSNMVGKI	gac1_rat	NFPMDEHSCP	LEFSSYGYPK	NEIEYKWKKP	SVEVADLRNS	TEISHTISGD
gac2_rat	GVKPTLIHTD MYVNSIGPVN	AINMEYTIDI	FFAQTWYDRR	LKFSNMVGKI	gac2_rat	NFPMDEHSCP	LEFSSYGYPR	EEIVYQWKRS	SVEVGDLRNT	TEVVKTTSGD
gac3_rat	GIKPTVIDVD IYVNSIGPVS	SINMEYQIDI	FFAQTWTDSR	LRFSNMVGLI	gac3_rat	NFPMDAHACP	LTFSSYGYPK	EEMIYRWRKN	SVEAADLRNT	TEIVTTSAGD
gac4_chick	GIKPTFIDVD IYVNSIGPVS	VIQMEYTIDI	FFAQTWYDRR	LRFTNMVSRI	gac4_chick	NFPMDTHSCP	LVFSSYGYPR	EEIVYRWRRY	SIEVSDLRNT	SEVLRTGAGE
gac5_human	GEKPTVVTVE IAVNSLGPLS	ILDMEYTIDI	IFSQTWYDER	LCYGNVVSQL	gac5_human	RFPMDSHSCP	LSFSSFSYPE	NEMIYKWENF	KLEINEVSNK	TEII.TTPGD
x78349	GGPPATIEVD IMVRSMGPIS	EVDMTYSMDC	YFRQSWVDKR	LAFVSMLARI	x78349	DFPMDIQKCP	LKFGSFGYTT	SDVIYRWNKE	RPPVAILSGT	ITLETNHPSE
gra1_rat	KGPPVNVSCN IFINSFGSIA	ETTMDYRVNI	FLRQQWNDPR	LAYPSMLDSI	gra1_rat	NFPMDVQTCI	MQLESFGYTM	NDLIFEWQEQ	GAVQVARYCT	KH Y. NTGK
gra3_rat	KGPPVNVTCN IFINSFGSIA	ETTMDYRVNI	FLRQKWNDPR	LAYPSMLDSI	gra3_rat	NFPMDVQTCI	MQLESFGYTM	NDLIFEWQDE	APVQVARYCT	KHY.NTGK
gra2_rat	KGPPVNVTCN IFINSFGSVT	ETTMDYRVNI	FLROOWNDSR	LAYPSMLDSI	gra2_rat	NFPMDVQTCT	MQLESFEYTM	NDLIFEWLSD	GPVQVAGYCT	KH Y. NTGK
grb rat	KGIFVDVVVN IFINSFGSIC	ETTMDYRVNI	FLROKWNDPR	LKLPTMYKCL	grb_rat	LFPMDTQRCK	MQLESFGYTT	DDLRFIWQSG	DPVQLEGNCT	KYYKGTGY
114525	TEGAVNVRVN IMTRMLSKID	VVNMEYSTOL.	TEREOWIDPR	LAVPHVKKSI.	u14525	LYPLDYOSCN	FDLVSYAHTM	NDIMYEWDPS	TPVOLKADCT	SHTNTGS
v09796	PMCPUTURUN TMTRMLSKIT	WWWWWWWW	TEREOWLOSE	LAVDHTKSNI.	v09796	LYPLDLOFCD	FDLVSYAHTM	KDTVYEWDPL	APVOLKDDCT	SH TNTGS
1158776	TIXPATURIN LEVESTMITS	DIKMEYSVOL	TEREOWTOER	LKELTEANEV	1158776	LYPLDROTCS	LEMASYGWTT	NDLVFLWKEG	DPVOVVDYCN	SK TNTGE
e34469	KLEPARTOVI, LYVSSTDAVN	EASMDRTVGT	LUHURWTUTR	TARGENTRKY	s34469	NYPEDKOTCH	ILIMSEGYSD	ODIVLOWMNL	TTADDLFCNR	RY. HOKAGN
ach9 rat	TOAVLANTIO VTLSOIKAN	ERNOTL/TAVI.	WIROTWHDAY	LTWRTPSDIA	ach9 rat	VEPEDSOOCN	LTEGSWTYNG	NOVDIENALD	SGDLSDAVKN	VISYGCCSEP
	51			100		151				200
gar1_rat	51 WVPDMFFVHS KRSFIHDTTI	DNVMLRVQPD	GKVLYSLRVT	100 VTAMCNMDFS	gar1_rat	151 YNRLYINFTL	RRHIFFFLLQ	TYFPATLMVM	LSWVSFWIDR	200 RAVPARVPLG
gar1_rat gar2_rat	51 WVPDMFFVHS KRSFIHDTTI WVPDVFFVHS KRSFTHDTTI	DNVMLRVQPD DNIMLRVFPD	GKVLYSLRVT GHVLYSMRIT	100 VTAMCNMDFS VTAMCNMDFS	gar1_rat gar2_rat	151 YNRLYINFTL YNRLYINFTL	RRHIFFFLLQ	TYFPATLMVM TYFPATLMVM	LSWVSFWIDR LSWVSFWIDH	200 RAVPARVPLG RAVPARVSLG
gar1_rat gar2_rat gar3_rat	51 WVPDMFFVHS KRSFIHDTTI WVPDVFFVHS KRSFIHDTTI WVPDIFFVHS KRSFIHDTTV	DNVMLRVQPD DNIMLRVFPD ENIMLRVHPD	GKVLYSLRVT GHVLYSMRIT GNVLFSLRIT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS	gar1_rat gar2_rat gar3_rat	151 YNRLYINFTL YNRLYINFTL YYRLFINFVL	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFVLQ	TYFPATLMVM TYFPATLMVM TYFPAMLMVM	LSWVSFWIDR LSWVSFWIDH LSWVSFWIDR	200 RAVPARVPLG RAVPARVSLG RAVPARVSLG
gar1_rat gar2_rat gar3_rat gab2_rat	51 WVPDMFFVHS KRSFIHDTTT WVPDUFFVHS KRSFIHDTTV WVPDIFFVHS KRSFIHDTTV WVPDIYFLMD KKSFVHGVTV	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD	GKVLYSLRVT GHVLYSMRIT GNVLFSLRIT GTVLYGLRIT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS TTAACMMDLR	gar1_rat gar2_rat gar3_rat gab2_rat	151 YNRLYINFTL YNRLYINFTL YYRLFINFVL YPRLSLSFKL	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFVLQ KRNIGYFILQ	TYFPATLMVM TYFPATLMVM TYFPAMLMVM TYMPSILITI	LSWVSFWIDR LSWVSFWIDH LSWVSFWIDR LSWVSFWINY	200 RAVPARVPLG RAVPARVSLG RAVPARVSLG DASAARVALG
gar1_rat gar2_rat gar3_rat gab2_rat gab3_rat	51 WVPDMFFVHS KRSFIHDTTI WVPDVFFVHS KRSFIHDTTI WVPDIFFVHS KRSFIHDTTV WVPDTFLND KKSFVHGVTV WVPDTFLND KKSFVHGVTV	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD KNRMIRLHPD	GKVLYSLRVT GHVLYSMRIT GNVLFSLRIT GTVLYGLRIT GTVLYGLRIT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR	gar1_rat gar2_rat gar3_rat gab2_rat gab3_rat	151 YNRLYINFTL YNRLYINFTL YYRLFINFVL YPRLSLSFKL YPRLSLSFRL	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFVLQ KRNIGYFILQ KRNIGYFILQ	TYFPATLMVM TYFPATLMVM TYFPAMLMVM TYMPSILITI TYMPSILITI	LSWVSFWIDR LSWVSFWIDH LSWVSFWIDR LSWVSFWINY LSWVSFWINY	200 RAVPARVPLG RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG
gar1_rat gar2_rat gar3_rat gab2_rat gab3_rat gab1_rat	51 WVPDMFFVHS KRSFIHDTTI WVPDIFVUS KRSFIHDTTI WVPDIFVHS KRSFIHDTTV WVPDTYFLND KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WVPDTYFLND KKSFVHGVTV	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD KNRMIRLHPD	GKVLYSLRVT GHVLYSMRIT GNVLFSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR	garl_rat gar2_rat gar3_rat gab3_rat gab3_rat gab1_rat	151 YNRLYINFTL YYRLYINFTL YYRLSLSFKL YPRLSLSFRL YPRLSLSFRL	RRHIFFFLLQ RRHIFFFLQ RRHIFFFVLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ	TYFPATLMVM TYFPATLMVM TYFPAILMVM TYMPSILITI TYMPSILITI	LSWVSFWIDR LSWVSFWIDH LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY	200 RAVPARVPLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG
gar1_rat gar2_rat gar3_rat gab2_rat gab1_rat gab4_chick	51 WVPDMFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDTYELND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD	GKVLYSLRVT GHVLYSMRIT GNVLFSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR	gar1_rat gar2_rat gar3_rat gab3_rat gab3_rat gab4_chick	151 YNRLYINFTL YNRLYINFTL YYRLSINFVL YPRLSLSFRL YPRLSLSFRL YLRLSLSFRI	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFVLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ	TYFPATLMVM TYFPATLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYMPSILITI	LSWVSFWIDR LSWVSFWIDH LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY	200 RAVPARVPLG RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG DASAARVALG
gar1_rat gar2_rat gar3_rat gab2_rat gab1_rat gab4_chick gab3_drome	51 WVPDMFFVHS KRSFIHDTTI WVPDJFFVHS KRSFHDTTI WVPDJFFVHS KRSFHDTTI WVPDTFLND KKSFHGVTV WVPDTFLND KKSFVHGVTV WLPDTYFLND KKSFLHGVT WLPDTFFND KKSFLHGVT	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD RNKURLGGD	GKVLYSLRVT GHVLYSMRIT GNVLFSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMRFT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLR	gar1_rat gar2_rat gar3_rat gab2_rat gab3_rat gab4_chick gab3_drome	151 YNRLYINFTL YYRLFINFVL YPRLSLSFKL YPRLSLSFRL YLRLSLSFRI YQRLSLSFKL	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFVLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ QRNIGYFVFQ	TYFPATLMVM TYFPATLMVM TYFPAMLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM	LSWVSFWIDR LSWVSFWIDH LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINH	200 RAVPARVPLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG DASAARVALG EATSARVALG
<pre>gar1_rat gar2_rat gar3_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst</pre>	51 WVPDMFFVHS KRSFIHDTT WVPDIFVUS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDTYFLND KKSFVHGVT WVPDTYFLND KKSFVHGVT WLPDTYFLND KKSFLHGVT WVPDTFAND KNSFLHDVT WVPDTFAND KNSFLHDTT	DNVMLRVQPD DNIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD RNKLVRLGGD KNKMVRLYGN	GKVLYSLRVT GRVLFSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMRFT GSLVYGMRFT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTLACMMDLH TTLACMMDLH	garl_rat gar2_rat gar3_rat gab2_rat gab1_rat gab4_chick gab3_drome gab1_ymst	151 YNRLYINFTL YNRLYINFTL YPRLSLSFKL YPRLSLSFRL YLRLSLSFRL YQRLSLSFKL YQRLSLSFKL	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFLQ KRNIGYFLQ KRNIGYFILQ KRNIGYFILQ QRNIGYFIFQ QRNIGYFIFQ	TYFPATLMVM TYFPATLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM TYLPSILIVM	LSWVSFWIDR LSWVSFWIDH LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINH LSWVSFWINH LSWVSFWINH	200 RAVPARVPLG RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG
gar1_rat gar2_rat gab2_rat gab2_rat gab4_chick gab4_chick gab3_drome gab_lymst gad_rat	51 WVPDMFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDIFFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTFFAND KNSFLHCVTV WVPDTFFAND KNSFLHCVTV WVPDTFLAND KNSFLHCVTV	DNVMLRVQPD DNIMLRVPPD ENIMLRVHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNKMVRLYGN ENKLIKLQPD	GKVLYSLRVT GHVLYSMRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMRFT GSLVYGMRFT GVLYSIRIT	100 VTAMCNMDFS VTAMCNMDFS VTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLH TTLACMMDLH TTLACMMDLH	gar1_rat gar2_rat gab3_rat gab3_rat gab4_rat gab4_chick gab3_drome gab_1ymst gad rat	151 YNRLYINFTL YNRLYINFTL YYRLFINFVL YPRLSLSFRL YLRLSLSFRL YLRLSLSFRI YQRLSLSFRL YQRLSLFRL FPRLSLHFQL	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFVLQ KRNIGYFLQ KRNIGYFLQ KRNIGYFLQ QRNIGYFVPQ QRNIGYFVPQ QRNIGYFVPQ	TYFPATLMVM TYFPATLMVM TYFPAMLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM TYLPSILIVM SYMPSVLIVA	LSWVSFWIDR LSWVSFWIDH LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINH LSWVSFWINH LSWVSFWINH	200 RAVPARVPLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG AAVPARVSLG
gar1_rat gar2_rat gar3_rat gab3_rat gab1_rat gab4_chick gab5_drome gab_lymst gad_rat	51 WVPDMFFVHS KRSFIHDTTI WVPDJFFVHS KRSFHHDTTI WVPDJFFVHS KRSFHHDTTI WVPDTYFLND KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WVPDTFFAND KNSFLHGVTI WVPDTFFAND KNSFLHDTT WLPDTFINN KSSHHDTT WLPDTFINN KSAWHDVTV	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRVIRLGD KNKLWRLGGD ENKLIRLQPD PNKLFRIMRN	GKVLYSLRVT GHVLYSMRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GXVIYGMRFT GVLYSIRIT GTLYYMRLT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLH TTLACMMDLH STVACDMDLH STVACDMDLA	gar1_rat gar2_rat gab2_rat gab3_rat gab4_chick gab3_drome gab_lymst gad_rat gad_rat	151 YNRLYINFTL YNRLYINFTL YPRLSLSFRL YPRLSLSFRL YLRLSLSFRI YQRLSLSFRI YQRLSLSFRI YQRLSLFFQL FPRLSLHFQL FIVMYVYFHL	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFLLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ QRNIGYFIPQ QRNIGYFIPQ RRNRGVFIIQ RRNRGVFIIQ	TYFPATLMVM TYFPALMVM TYFPALMINT TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM TYLPSILIVM SYMPSVLIVA SYMPSVLIVA	LSWVSFWIDR LSWVSFWIDH LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINH LSWVSFWINH LSWVSFWINH MSWVSFWINH	200 RAVPARVPLG RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG AAVPARVSLG ASVPARVSLG
gar1_rat gar2_rat gar3_rat gab2_rat gab1_rat gab4_chick gab1_drome gab_lymst gad_rat gaa4_rat gaa6_rat	51 WVPDMFFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDTYFLND KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WLPDTFLND KKSFLHGVTV WVPDTFAND KNSFLHDITE WLPDTFINNA KSAWFHDVTV WTPDTFFNNG KKSVSHMTA	DNVMLRVQPD DNIMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNKMRLVSN ENKLFRIMS PNKLFRIMS	GKVLYSLRVT GHVLYSMRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMRT GXLYYGMRT GVLYSIRIT GTILYTMRLT	100 VTAMCNMDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTIACMMDLH STVACDMDLA ISABCPMRLV	garl_rat gar2_rat gar3_rat gab3_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat	151 YNRLYINFTL YNRLFINFVL YPRLSLSFKL YPRLSLSFKL YLRLSLSFRI YQRLSLSFKI YQRLSLSFKI FPRLSLFFQL YIVMTVYFHL	RRHIFFFLLQ RRHIFFFVLQ KRNIGYFLLQ KRNIGYFLLQ KRNIGYFLLQ KRNIGYFLQ QRNIGYFVPQ QRNIGYFVPQ RRNRGVYIIQ RRKMGYFMIQ	TYFPATLMVM TYFPATLMVM TYFPATLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM SYMPSVLLVA TYIPCIMTVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY MSWVSFWINY LSWVSFWINS LSWVSFWINK	200 RAVPARV5LG RAVPARV5LG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG AAVPARV5LG ESVPARTVFG
gar1_rat gar2_rat gab2_rat gab2_rat gab4_rat gab4_chick gab3_drome gab_lyms: gad_rat gaa4_rat gaa6_rat gaa6_rat	51 WVPDMFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDIFFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTFFLND KKSFLHCVTT WVPDTFFAND KNSFLHCVTT WVPDTFFAND KNSFLHCVTT WTPDTFFRNG KKSVSHNMTA WTPDTFFRNG KKSVSHNMTA	DNVMLRVQPD DNIMLRVPPD ENIMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNKLVRLGGD ENKLIFLQPD ENKLFRIMEN PNKLFRIMEN PNKLFRIMEN	GKVLYSLRVT GHVLYSMRIT GNVLFSLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMRFT GSLYVYGMRFT GTLLYTMRLT GTLLYTMRLT	100 VTAMCNNDFS VTAMCNNDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLH TTAACMMDLH TTAACMMDLA ISABCPMRLV INADCPMRLV VRABCPMHLE	garl_rat gar2_rat gab2_rat gab3_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa4_rat	151 YNRLYINFTL YNRLYINFTL YPRLSISFRL YPRLSLSFRL YPRLSLSFRL YORLSLSFRL YORLSLSFRL YORLSLFOL YINTVYFHL YVIMTVYFHL YVIMTVYFHL	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ QRNIGYFILQ QRNIGYFILQ QRNIGYFILQ QRNIGYFILQ RRNRGVYFLQ QRKMGYFMIQ QRKMGYFMIQ	TYFPATLMVM TYFPAMLMVM TYFPAMLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM TYLPSILIVM TYLPCIMTVI IYTPCIMTVI IYTPCIMTVI	LSWVSFWIDR LSWVSFWIDH LSWVSFWIDH LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINH LSWVSFWINH LSWVSFWINK LSQVSFWINK LSQVSFWINK	200 RAVPARVPLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG ESVPARTVFG ESVPARTVFG ESVPARTVFG
gar1_rat gar2_rat gar3_rat gab2_rat gab3_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa6_rat gaa1_rat gaa1_rat	51 WVPDMFFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDTYFLND KKSFVHGVT WVPDTYFLND KKSFVHGVT WVPDTYFLND KKSFVHGVT WVPDTFLAND KKSFLHDTT WLPDTFINA KSSHLHDTT WLPDTFFRNG KKSSHNTT WTPDTFFRNG KKSJAHNTT WTPDTFFRNG KKSJAHNTT	DNVMLRVQPD DNIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNKLFRLHPD ENKLFRIMEN PNKLFRIMEN PNKLFRIMEN PNKLRITED PNKLRIKLN	GKVLYSLRVT GHVLYSMRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GVILYGLRIT GVILYSIRIT GTILYTMRLT GTLLYTMRLT GTLLYTMRLT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLH TTLACMMDLH STVACDMDLA STVACDMDLA STVACDMDLA STVACDMDLA INADCPMRLV VRAECFMILE	gar1_rat gar2_rat gab2_rat gab2_rat gab4_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa4_rat gaa4_rat	151 YNRLYINFTL YNRLFINFVL YPRLSISFKL YPRLSLSFKL YDRLSLSFRL YQRLSLSFRL YQRLSLSFRL YQRLSLFQL FPRLSLHFQL YUMTVYFLL YVWMTVFHL YVWMTHFFL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFLLQ KRNIGYFLLQ KRNIGYFLQ QRNIGYFLQ QRNIGYFLQ QRNIGYFLQ RRKMGYFLQ RRKMGYFLQ KRKIGYFNLQ KRKIGYFVLQ	TYFPATLMVM TYFPATLMVM TYFPATLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM SYMPSULUX TYLPSILIVM TYIPCIMTVI TYLPCIMTVI TYLPCIMTVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINN LSWVSFWINN LSQVSFWINN LSQVSFWINN LSQVSFWINN	200 RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG EATSARVALG ESVPARTVFG ESVPARTVFG ESVPARTVFG
gar1_rat gar2_rat gab2_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa6_rat gaa1_rat gaa2_rat	51 WVPDMFFVHS KRSFIHDTTI WVPDVFFVHS KRSFIHDTTU WVPDIFFUND KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WVPDTFLND KKSFLHDVTT WVPDTFLND KKSFLHDITE WLPDTFINN KSAWFHDVTV WTPDTFFNNG KKSVSHNMTM WTPDTFFHNG KKSVAHNMTW	DNVMLRVQPD DNIMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNKLPRIMN PNKLFRIMN PNKLFRIMN PNKLFRIMN PNKLRITED PNKLRIODD	GKVLYSLRVT GHVLYSMRIT GNVLFSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GXLYYGMRFT GXLVYGMRFT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT	100 VTAMCNNDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLH TTLACMMDLH TTLACMMDLH STACCMMDLA ISAECPMILU VRAECPMILE INADCPMILE INADCPMILE	<pre>gar1_rat gar2_rat gar3_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa5_rat gaa1_rat gaa2_rat gaa2_rat</pre>	151 YNRLYINFTL YNRLFINFVL YPRLSLSFRL YPRLSLSFRL YLRLSLSFRI YQRLSLSFRI YQRLSLSFRI YQRLSLIFQL FPRLSLHFQL YVLMTVYFHL YVLMTVYFHL YVVMTHFHL YVVMTHFHL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ QRNIGYFILQ QRNIGYFILQ QRNIGYFILQ QRNIGYFILQ RRKRGYFILQ KRKIGYFVLQ KRKIGYFVLQ KRKIGYFVLQ	TYFPATLWVM TYFPATLWVM TYFPATLWVM TYFPATLWVM TYMPSILITI TYMPSILITI TYLPSILIVM SYMPSULUVA TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY MSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK	200 RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG EATSARVALG ESVPARTVFG ESVPARTVFG ESVPARTVFG ESVPARTVFG
<pre>gar1_rat gar2_rat gab2_rat gab3_rat gab4_rat gab4_chick gab3_drome gab_lymst gaa4_rat gaa4_rat gaa6_rat gaa3_rat gaa2_rat gaa2_rat</pre>	51 WVPDMFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDTYELND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTFFAND KNSFLHOVT WVPDTFFAND KNSFLHOVT WVPDTFFAND KNSFLHOVT WTPDTFFNG KKSVSHNMTA WTPDTFFNG KKSVAHNMTA WTPDTFFNG KKSVAHNMTA WTPDTFFNG KKSVAHNMTA	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD RNKLVRLGGD NKLFRIMRN PNKLFRIMRN PNKLFRIMRN PNKLFRIMRN PNKLLRIVDN PNKLLRIVDN PNKLLRIVDN	GKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMRFT GSLYYGMRFT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT	100 VTAMCNNDFS VTAMCNNDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLH TTAACMMDLH TTAACMMDLH ISAACPMRLW INADCPMRLW INADCPMRLW INADCPMRLW INADCPMRLW INADCPMRLW ISABCPMOLE ISABCPMOLE	<pre>gar1_rat gar2_rat gab2_rat gab3_rat gab3_rat gab3_rat gab4_chick gab_lymst gad_rat gaa4_rat gaa4_rat gaa3_rat gaa5_rat gaa5_rat gaa5_rat</pre>	151 YNRLYINFTL YNRLYINFTL YPRLSISFRL YPRLSLSFRL YPRLSLSFRL YORLSLSFRL YORLSLSFRL YORLSLFRL YUMTVYFHL YVWMTVFHL YVWMTHFHL YVWMTHFHL YTVMTAHFHL	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ QRNIGYFILQ QRNIGYFILQ QRNIGYFILQ QRNKGYFILQ RRKMGYFMIQ QRKKGYFVIQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ	TYFPATLMVM TYFPANLMVM TYFPANLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM TYLPSILIVM TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI	LSWVSFWIDR LSWVSFWIDH LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINH LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINR LSQVSFWINR LSQVSFWINR	200 RAVPARVPLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG ESVPARTVFG ESVPARTVFG ESVPARTVFG ESVPARTVFG ESVPARTVFG
gar1_rat gar2_rat gar3_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst gad4_rat gaa6_rat gaa6_rat gaa2_rat gaa2_rat gaa5_rat	51 WVPDMFFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDIFVHD KKSFVHGVT WVPDTYFLND KKSFVHGVT WVPDTYFLND KKSFVHGVT WVPDTFLND KKSFLHGVTT WVPDTFFNNG KKSFLHDIT MLPDTFFVNG KKSVHNTA WTPDTFFNNG KKSVHNTA WTPDTFFNNG KKSVHNTA WTPDTFFHNG KKSVHNTA WTPDTFFHNG KKSVHNTA	DNVMLRVQPD DNIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD RNKLVRLGD RNKLVRLGD PNKLFRIMRN PNKLFRIMRN PNKLFRIMRN PNKLRILMIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD	GKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GXUYYGNRFT GXLYYMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT	100 VTAMCNMDFS VTAMCNMDFS TTAACMMDFS TTAACMMDFS TTAACMMDFS TTAACMMDFS TTAACMMDFS TTAACMMDFS TTAACMMDFS STVACCMMDFS STVACCMMDFS INADCPMRLFS INADCPMRLFS INADCPMRLFS INADCPMILE INABCCPMILE INABCCPMILE INABCCYNOLH	<pre>garl_rat gar2_rat gar2_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst gad4_rat gaa4_rat gaa4_rat gaa3_rat gaa2_rat ga</pre>	151 YNRLYINFTL YNRLJINFTL YPRLSLSFRL YPRLSLSFRL YPRLSLSFRL YRLSLSFRI YQRLSLSFRI YQRLSLSFRI YQRLSLFQL YIVMTYFHL YVVMTYFHL YVVMTYFHL YVVMTHFHL YTVMTAHHL YTVMTAHHL YTIMTFFDL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFLQ KRNIGYFLQ KRNIGYFLQ GRNIGYFLQ GRNIGYFLQ GRNIGYFLQ RRKMGYFNIQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ	TYFPATLMVM TYFPATLMVM TYFPATLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM TYLPSILIVM TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWIDY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK	200 RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG ESVPARTVFG ESVPARTVFG ESVPARTVFG ESVPARTVFG ESVPARTVFG
gar1_rat gar2_rat gab3_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa6_rat gaa1_rat gaa2_rat gaa5_rat ga2_rat ga2_rat	51 WVPDMFFVHS KRSFIHDTT WVPDFFVHS KRSFIHDTT WVPDIFFUNG KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WVPDTFLND KKSFUHGVTV WVPDTFLND KKSFLHDTT WVPDTFLND KSSVHGVTV WTPDTFFNG KKSVSHNMTN WTPDTFFHNG KKSVAHNMTN WTPDTFFHNG KKSVAHNMTN WTPDTFFHNG KKSVAHNMTN WTPDTFFHNG KKSVAHNMTN WTPDTFFNG KKSVAHNMTN WTPDTFFNG KKSVAHNMTN WTPDTFFNG KKSVAHNMTN WTPDTFFNG KKSVAHNMTN WTPDTFFNG KKSVAHNMTN	DNVMLRVQPD DNIMLRVPPD ENIMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD NKLFRIMM PNKLFRIMM PNKLFRIMM PNKLRICD PNKLLRLVD PNKLLRLDD PNKLLRIDD PNKLLRIDD PNKLLRIDD	GKVLYSLRVT GHVLYSMRIT GNVLFSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GXLYYGMRFT GSLVYGMRFT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GRVLYTLRIT	100 VTAMCNNDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLH TTLACMMDLH TTLACMMDLH TTLACMMDLH ISAECPMRLV VRAECPMILE INADCFMRLV VRAECPMILE ISAECPMULE ISAECPMULE INAECYLQLH	<pre>gar1_rat gar2_rat gar3_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst gaa4_rat gaa4_rat gaa5_rat gaa5_rat gac1_rat gac2_rat ga</pre>	151 YNRLYINFTL YNRLFINFVL YPRLSINFVL YPRLSLSFRL YLRLSLSFRL YLRLSLSFRI YQRLSLSFRL YQRLSLIFQL FPRLSLHFQL YVLMTVYFHL YVLMTVYFHL YVLMTVFHL YTVMTAHFHL YTIMTAHFHL YILMTIFFDL YVLMYVFIL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ QRNIGYFILQ QRNIGYFILQ QRNIGYFILQ QRNIGYFILQ QRXMGYFILQ KRKIGYFVLQ KRKIGYFVLQ KRKIGYFVLQ KRKIGYFVLQ SRRMGYFTLO SRRMGYFTLO	TYPPATLMVM TYPPATLMVM TYPPATLMVM TYPPATLMVM TYMPSILITI TYMPSILITI TYLPSILIVM SYMPSULUX TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY MSWVSFWINY LSQVSFWINR LSQVSFWINR LSQVSFWINR LSQVSFWINR LSQVSFWINR LSQVSFWINR	200 RAVPARV5LG RAVPARV5LG DASAARVALG DASAARVALG DASAARVALG EXTSARVALG EXTSARVALG EXTSARVALG EXTPARV5LG ESVPARTVFG ESVPARTVFG ESVPARTVFG DAVPART5LG
<pre>gar1_rat gar2_rat gab2_rat gab3_rat gab4_chick gab3_drome gab_lymst gad4_rat gaa4_rat gaa4_rat gaa3_rat gaa3_rat gaa5_rat gac1_rat gac2_rat gac2_rat</pre>	51 WVPDMFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDTYLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTFFAND KKSFVHCVTV WVPDTFFAND KNSFLHCVTV WVPDTFFAND KNSFLHCVTV WTPDTFFNG KKSVAHNMTM WTPDTFFNG KKSVAHNMTM WTPDTFFNG KKSVAHNMTM WTPDTFFNG KKSVAHNMTM WTPDTFFNNG KKSVAHNMTM WTPDTFFNNG KKSVAHNMTM WTPDTFFNNG KKSVAHNMTM WTPDTFFNNG KKSVAHNMTM WTPDTFFNNG KKSVAHNMTM WTPDTFFNNG KKSVAHNMTM	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD RNKLVRLGGD NKLLRLQPD PNKLFRIMRN PNKLFRIMRN PNKLLRIVDN PNKLLRIVDN PNKLLRIVDN PNKLLRIVDN PNKLLRIDD PNRLLRIWSD PNRLLRIWSD	GKVLYSLRVT GHVLYSLRIT GNVLFSLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMRFT GSLVYGMRFT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GRVLYTLRLT GRVLYTLRLT	100 VTAMCINDFS VTAMCINDFS VSANCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLA TTAACMMDLA ISACCPMRLV INADCPMRLV VRAECPMILE INAECPIQLH INAECYIQLH INAECYIQLH INAECYIQLH INAECYIQLH	<pre>gar1_rat gar2_rat gar3_rat gab2_rat gab3_rat gab3_rat gab3_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa2_rat gaa2_rat gaa2_rat gac1_rat gac2_rat gac3_rat gac3_rat</pre>	151 YNRLYINFTL YNRLYINFTL YPRLSISFRL YPRLSLSFRL YPRLSLSFRL YORLSLSFRL YORLSLSFRL YORLSLSFRL YUMTVYFHL YUMTVYFHL YUMTVYFHL YUMTVFHH YIMTAHFHL YIIMTAHFHL YIIMTIFFDL YUMMTVFRL	RRHIFFFLLQ RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ ORNIGYFILQ ORNIGYFILQ ORNIGYFILQ ORNIGYFILQ RRKMGYFHLQ RRKMGYFHLQ KRKIGYFVLQ KRKIGYFVLQ SRRMGYFTLQ SRRMGYFTLQ SRRMGYFTLQ	TYFPATLMVM TYFPATLMVM TYFPAMLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM TYLPSILIVM TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTVV TYIPCILTVV	LSWVSFWIDR LSWVSFWIDH LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWINK	200 RAVPARVPLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG ESVPARTVFG ESVPARTVFG ESVPARTVFG ESVPARTVFG DAVPARTSLG DAVPARTSLG DATPARTTLG
<pre>gar1_rat gar2_rat gar3_rat gab2_rat gab3_rat gab4_chick gab1_rat gab4_chick gab1_drome gab_lymst gac4_rat gac4_rat gac4_rat gac3_rat gac3_rat gac2_rat gac2_rat gac2_rat gac2_rat</pre>	51 WVPDMFFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDTYFLND KKSFVHOTV WVPDTYFLND KKSFVHOTV WVPDTFLND KKSFUHOTT WVPDTFLND KKSFLHDTT WLPDTFFNN KSAWHDT WTPDTFFNNG KKSIAHMTT WTPDTFFHNG KKSVAHMTM WTPDTFFHNG KKSVAHMTM WTPDTFFHNG KKSVAHMTM WTPDTFFHNG KKSVAHMTM WTPDTFFHNG KKSVAHMTM WTPDTFFHNG KKSVAHMTM WTPDTFFHNG KKSVAHMTM WTPDTFFHNG KKSVAHMTM WIPDTFFRNS KKADAHMTT WIPDTFFRNS KKADAHMTT	DNVMLRVQPD DNIMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNKLFRIMN PNKLFRIMN PNKLFRIMN PNKLRIND PNKLRIDD PNKLLRIVD PNKLLRIDD PNRLLRIWD PNRLLRIWD PNRLLRIWD PNRLLRIWD	CKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMFT GVLYGLRIT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GRVLYTLRLT GKULYTLRLT GKULYTLRLT	100 VTAMCNNDFS VTAMCNNDFS VTAMCNNDFS TTAACMDJR TTAACMDJR TTAACMDJR TTAACMDJR TTAACMDJR STCACMDJL STCACMDJL STCACMDJL ISAECPMILE INADCPMILE INADCPMILE INABCPMILE INABCPMILE INABCPUQLE INABCYLQLH INABCQLQLH INABCQLQLH INABCQLQLH	<pre>garl_rat gar2_rat gar3_rat gab2_rat gab1_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa3_rat gaa3_rat gaa2_rat gaa2_rat gac3_rat gac3_rat gac3_rat gac3_rat</pre>	151 YNRLYINFTL YNRLYINFTL YPRLSINFVL YPRLSLSFKL YLRLSLSFRI YLRLSLSFRI YQRLSLSFRI YQRLSLIFQL YVRLSLFPQL YVVRTYFHL YVVMTYFHL YVVMTHFHL YIVMTHFHL YIVMTHFHL YIIMTHFHL YIIMTHFHL YVVMSYFDL YVVMIYFPL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ CRNIGYFILQ CRNIGYFILQ CRNIGYFILQ CRNIGYFILQ CRNIGYFILQ CRKMGYFNIQ KRKIGYFVIQ KRKIGYFVIQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ	TYFPATLWVM TYFPATLWVM TYFPATLWVM TYFPATLWVM TYMPSILITI TYMPSILITI TYLPSILIVM TYLPSILIVM TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTVV TYIPCILIVV	LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK	200 RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EXTSARVALG EXTSARVALG EXTPARVSLG ESVPARTVFG ESVPARTVFG ESVPARTVFG DAVPARTSLG DAVPARTSLG DAVPARTSLG DAVPARTSLG
<pre>gar1_rat gar2_rat gab2_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa6_rat gaa3_rat gaa5_rat gaa2_rat gac2_rat gac2_rat gac3_rat gac4_chick</pre>	51 WVPDMFFVHS KRSFIHDTTI WVPDIFFVHS KRSFIHDTTI WVPDIFFVHS KRSFIHDTTI WVPDTYFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTFFLND KKSFUHCVTV WVPDTFFAND KNSFLHVTT WTPDTFFNNG KKSVAHMTM WTPDTFFNNG KKSVAHMTM WTPDTFFNNG KKSVAHMTM WTPDTFFNNG KKSVAHMTM WTPDTFFNNG KKSVAHMTM WTPDTFFNNG KKSVAHMTM WTPDTFFNNG KKSVAHMTM WTPDTFFNNG KKSVAHMTM WIPDTFFNNG KKSDAHMITT WIPDTFFNNG KKDAHMITM	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNKLVRLGQD KNKLVRLGQD ENKLFRIMEN PNKLFRIMEN PNKLFRIMEN PNKLLRIQDD PNKLLRIQDD PNKLLRIQDD PNKLLRIQDD PNKLLRIQDD PNKLLRIMSD PNQLLRIMND PNQLLRIMND	CKVLYSLRVT GHVLYSLRIT GNVLFSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GSLVYGMRFT GSLVYGMRFT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GRVLYTLRLT GRVLYTLRLT GKVLYTLRLT GKVLYTLRLT	100 VTAMCNINDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLH TTLACMMDLH TTLACMMDLH STACCDMLS ISAECPMRLV INACCPMRLV VARECPMILE INACCPLLL INACCYLQLH IDAECLQLH INAECLQLH IDAECLQLH	<pre>gar1_rat gar2_rat gab2_rat gab3_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa3_rat gaa2_rat gaa2_rat gac1_rat gac2_rat gac3_rat gac6_chick gac6_chick</pre>	151 YNRLYINFTL YNRLFINFVL YPRLSISFRL YPRLSLSFRL YLRLSLSFRL YQRLSLSFRL YQRLSLSFRL YQRLSLFRL YVMTVYFIL YVWMTVFHL YVWMTVFHL YTIMTAHFHL YTIMTAHFHL YITIMTAHFHL YVWMYYFDL YVVMTVFEL YVWMTVFFL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ QRNIGYFIQ QRKMGYFIQ QRKMGYFMIQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ	TYPPATLWVM TYPPATLWVM TYPPATLWVM TYPPATLWVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM SYMPSVLLVA TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILIVV TYIPCILIVV TYIPCILIVV	LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWIKK LSWVSFWIKK	200 RAVPARVSLG DASARVALG DASARVALG DASARVALG DASARVALG EATSARVALG EATSARVALG EXTSARVALG ESVPARTVG ESVPARTVFG ESVPARTVFG ESVPARTVFG DAVPARTSLG DATPARTLG DSTPARTSLG
<pre>gar1_rat gar2_rat gab2_rat gab3_rat gab4_chick gab3_drome gab_lymst gad4_rat gaa4_rat gaa4_rat gaa3_rat gaa3_rat gaa5_rat gac1_rat gac2_rat gac4_rat gac3_rat gac3_rat</pre>	51 WVPDMFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDTYELND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTFFLND KKSFVHCVTV WVPDTFFAND KNSFLHDVTE WVPDTFFAND KNSFLHDVTE WVPDTFFANG KKSVAHNATM WTPDTFFNG KKSVAHNATM WTPDTFFNG KKSVAHNATM WTPDTFFNG KKSVAHNATM WTPDTFFNG KKSVAHNATM WTPDTFFNG KKSVAHNATM WTPDTFFNS KKADAHWITT WIPDTFFRNS KKADAHWITT WIPDTFFRNS KKADAHWITT WIPDTFFRNS KKADAHWITT WIPDTFFRNS KKADAHWITT WIPDTFFRNS KRADAHWITT WIPDTFFRNS KRADAHWITT	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD RNKLVRLGGD NKKLRLPD PNKLFRIMRN PNKLFRIMRN PNKLLRIVDN PNKLLRIVDN PNKLLRIVDN PNKLLRIVDN PNRLLRIWSD PNRULRIWSD PNQLLRIWND PNQLLRIWND PNQLLRIWND PNQLLRIWND	GKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMRFT GSLVYGMRFT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GRVLYTLRLT GRVLYTLRLT GRVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT	100 VTAMCINDFS VTAMCINDFS VSANCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDL TTAACMMDL ISACCPMRLV INADCPMRLV VRACCMILE INAECYIQLH INAECYIQLH INAECYIQLH INAECYIQLH INAECYIQLH INAECYIQLH INAECYIQLH INAECYIQLH INAECYIQLH	<pre>gar1_rat gar2_rat gar3_rat gab2_rat gab3_rat gab3_rat gab3_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa2_rat gaa2_rat gac1_rat gac2_rat gac3_rat gac4_chick gac5_human y78240</pre>	151 YNRLYINFTL YNRLFINFUL YPRLSISFKL YPRLSLSFKL YPRLSLSFKL YQRLSLSFKL YQRLSLSFKL YQRLSLSFKL YQRLSLFRU YUMTVYFHL YVVMTTHFL YTVMTHFFL YTVMTHFFL YTVMTHFFL YVVMTTHFFL YVVMTYFPL YVVMTYFPL YVVMTYFPL YVVMTYFPL YVVMTYFPL YVVMTYFPL YVVMTYFPL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFLQ KRNIGYFLQ KRNIGYFLQ QRNIGYFLQ QRNIGYFVQ QRNIGYFVQ QRKMGYFMQ QRKMGYFMQ QRKMGYFMQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ SRRMGYFTQ SRRMGYFTQ SRRMGYFTQ QRRMGYFIQ QRFMGNFTQ	TYPPATLMVM TYPPATLMVM TYPPATLMVM TYPPATLMVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM SYMPSULUX TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTVV TYIPCILITVV TYIPCILITVV TYIPCILITVV	LSWVSFWIDR LSWVSFWIDH LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK	200 RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG DASAARVALG EXTSARVALG EXTSARVALG EXTSARVALG EXTPARVSLG EXTPARTYFG EXTPARTYFG EXTPARTYFG DAVPARTSLG DAVPARTSLG DATARTTLG DSTPARTSLG ESAPARTSLG
gar1_rat gar2_rat gar3_rat gab3_rat gab1_rat gab1_rat gab1_chick gab1_drome gab_lymst gaa4_rat gaa4_rat gaa4_rat gaa3_rat gaa3_rat gaa2_rat gaa2_rat gaa2_rat gac2_rat gac2_rat gac3_rat	51 WVPDMFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDIFFUNS KRSFIHDTT WVPDIFFLND KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WLPDTYFLND KKSFVHGVTV WLPDTFFLND KKSFLHGVT WUPDTFFAND KNSFLHDTT WLPDTFFNNG KKSLHNTT WTPDTFFNNG KKSLAINMTT WTPDTFFHNG KKSVAINMTW WTPDTFFHNG KKSVAINMTW WTPDTFFHNG KKSVAINMTW WTPDTFFHNG KKSVAINMTW WTPDTFFHNG KKSVAINMTW WTPDTFFNG KKSVAINMTW WIPDTFFNS KKSDAWITT WIPDTFFNS KKSDAWITT WIPDTFFNS KKSDAWITT WIPDTFFNS KKSDAWITT WIPDTFFNS KKSDAWITT WIPDTFFNS KKSDAWITT WIPDTFFNS KKSDAWITT WIPDTFFNS KKSDAWITT WIPDTFFNS KKSDAWITT WIPDTFFNS KKSDAWITT	DNVMLRVQPD DNIMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNKLFRIMN PNKLFRIMN PNKLFRIMN PNKLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD PNRMIRINN PNQLRIND PNQLRIND PNQLRIND	GKVLYSLRVT GHVLYSMRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GXUYYGMRFT GVLYSIRIT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYSLRLT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLH STVACDMDLA ISAECPMILA ISAECPMILA ISAECPMILE INABCYLQLH INABCYLQLH INABCYLQLH IDAECQLQLH IDAECQLQLH IEAECLLQLQ IDACCSLHAL IKACCPMILA	<pre>garl_rat gar2_rat gar3_rat gab3_rat gab1_rat gab1_rat gab1_rat gab1_rat gad_rat gaa4_rat gaa6_rat gaa5_rat gaa5_rat gac3_rat gac3_rat gac3_rat gac4_rat</pre>	151 YNRLYINFTL YNRLFINFVL YPRLSLSFRL YPRLSLSFRL YLRLSLSFRI YQRLSLSFRI YQRLSLSFRI YQRLSLFRQL FPRLSLFPQL FPRLSLFPQL YVWTVYFHL YVVMTVFHL YIVMTHFHL YIVMTHFHL YIIMTHFPL YVVMTYFPL YVVMTYFPL YVVMTYFPL YVVMTYFPL YVVMTYFPL YVVMTYFPL YVVMTYFPL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ RRKKGYFILQ RRKKGYFILQ KRKIGYFVIQ KRKIGYFVIQ SRRMGYFILQ SRRMGYFTIQ SRRMGYFTIQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ SRRMGYFLD	TYFPATLWVM TYFPATLWVM TYFPATLWVM TYFPATLWVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM SYMPSULUVA TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTVV TYIPCILIVV TYIPCILIVV TYIPCILIVV	LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK	200 RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EXTSARVALG EXTSARVALG EXTSARVALG EXTPARTVEG ESVPARTVFG ESVPARTVFG DAVPARTSLG DATPARTSLG DATPARTSLG DATPARTSLG DATPARTSLG DATPARTSLG DATPARTSLG
<pre>gar1_rat gar2_rat gab2_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa3_rat gaa5_rat gaa5_rat gac1_rat gac3_rat gac4_chick gac3_rat gac4_chick</pre>	51 WVPDMFFVHS KRSFIHDTTI WVPDIFFVHS KRSFIHDTTI WVPDIFFVHS KRSFIHDTTU WVPDTYFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTFFLND KKSFUHCVTV WVPDTFFAND KNSFLHCVTV WVPDTFFAND KKSVHNTM WTPDTFFHKS KKSVHNTM WTPDTFFHKS KKSVHNTM WTPDTFFHKS KKSVHNTM WTPDTFFHKS KKSVHNTM WTPDTFFHKS KKSVHNTM WTPDTFFHKS KKSVHNTM WTPDTFFHKS KKSVHNTT WIPDTFFRKS KKSDHWITT WIPDTFFRKS KKSDHWITT	DNVMLRVQPD DNIMLRVPPD ENIMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNKLVRLGQD ENKLIRLOPD PNKLPRIMN PNKLPRIMN PNKLPRIMN PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIND PNQLLRIND PNQLLRIND PNQLLRIND PNQLLRIND PNQLLRIND PNQLLRIND PNQLLRIND PNQLLRIND PNQLLRIND PNQLLRIND PNQLLRIND PNQLLRIND	GKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GXVLYGLRIT GXLYYGMRFT GSLVYGMRFT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GNVLYSIRLT GNVLYSIRLT	100 VTAMCNINDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTLACMMDLH TTLACMMDLH TTLACMMDLH STACCDMLS ISACCPMCLU INACCPMCLU INACCPMCLU INACCPMCLU INACCQUCH INAECQUCH INAECQUCH INAECQUCH INAECQUCH INAECQUCH INAECQUCH INAECQUCH INAECQUCH	<pre>gar1_rat gar2_rat gar3_rat gab3_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa3_rat gaa2_rat gaa2_rat gac1_rat gac2_rat gac2_rat gac6_chick gac5_human x78349 gra1_rat gra3_rat</pre>	151 YNRLYINFTL YNRLFINFVL YPRLSISFKL YPRLSLSFKL YLRLSLSFRL YCRLSLSFRL YQRLSLSFRL YQRLSLFQL TVVKTYPHL YVVMTYPHL YVVMTYPHL YTVMTHPHL YTVMTHPHL YTVMTHPHL YTVMTHPHL YVVMTYPEL YVVMTYPEL YVVMTYPEL YVVMTYPEL YVVMTYPEL YVVMTYPEL YVVMTYPEL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ QRNIGYFIQ QRNIGYFIQ QRKMGYFIQ QRKMGYFIQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ QRHGYFIQ QRHGYFIQ QRHGYFIQ ERQMGYFLQ	TYPPATLWVM TYPPATLWVM TYPPATLWVM TYPPATLWVM TYPPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTVV TYIPCILIVV TYIPCILIVV NVVPSVTVM NVVPSVLVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWIKK LSWVSFWIKK LSWVSFWIKK LSWVSFWIKN LSWVSFWINK	200 RAVPARVSLG DASARVALG DASARVALG DASARVALG DASARVALG EATSARVALG EATSARVALG EXPARTVAG ESVPARTVFG ESVPARTVFG ESVPARTVFG DAVPARTSLG DATPARTSLG ESAPARTSLG ESAPARVSLG DAPARVSLG DAPARVSLG
<pre>gar1_rat gar2_rat gar2_rat gab2_rat gab1_rat gab4_chick gab4_chick gab4_chick gab_lymst gad_rat gaa6_rat gaa6_rat gaa2_rat gaa2_rat gac3_rat gac2_rat gac3_rat gac4_chick gac5_human x78349 gra1_rat gra3_rat</pre>	51 WVPDMFFVHS KRSFIHDTTJ WVPDIFVHS KRSFIHDTTJ WVPDIFVHS KRSFIHDTTJ WVPDIFVHDI KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WVPDTFLAND KKSFLHDTT WVPDTFLAND KKSFLHDTT WIPDTFFNNG KKSVHNTA WTPDTFFNNG KKSVHNTA WTPDTFFNNG KKSVHNTTJ WTPDTFFNNG KKSVHNTTJ WTPDTFFNNS KKADAHWITTJ WIPDTFFNNS KRABHWITTJ WIPDTFFNS KRABHWITTJ WIPDTFFNNS KRABHWITTJ WKPDLFFANE KGAMFHEITTJ WKPDLFFANE KGAMFHEITJ	DNVMLRVQPD DNIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNKLFRLHPD RNKLFRIMEN PNKLFRIMEN PNKLFRIMEN PNKLLRIVDN PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIMEN PNRLLRIMEN PNQLLRIMND PNQLLRIMND PNQLLRIMND PNQLLRIMND DNKLLRISEN DNKLLRISEN	GKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMRFT GSLVYGMRFT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GRVLYTLRLT GRVLYTLRLT GRVLYTLRLT GRVLYTLRLT GRVLYTLRLT GRVLYTLRLT GRVLYSLRLT GRVLYSLRIT GNVLYSLRIT GNVLYSLRIT	100 VTAMCNMDFS VTAMCNMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLH TTAACMMDLH TTAACMMDLH ISACCPMRLV INADCPMRLV INADCPMRLV INADCPMRLV INACCPMRLV INACCPMRLE INAECYLQLH INAECYL	<pre>garl_rat gar2_rat gar2_rat gab2_rat gab1_rat gab1_rat gab1_rat gab1_rat gad_rat gaa4_rat gaa4_rat gaa2_rat gaa2_rat gaa2_rat gac2_rat gac2_rat gac3_rat</pre>	151 YNRLYINFTL YNRLYINFTL YYRLFINFVL YPRLSLSFKL YPRLSLSFKL YQRLSLSFKL YQRLSLSFKL YQRLSLSFKL YQRLSLFQL FPRLSLHFQL YUMTVYFHL YUVMTVYFHL YTVMTHFFL YTVMTHFFL YTVMTHFFL YTVMTHFFL YTVMTYFPL YVVMTIFFDL YVVMTIFFDL FCIEARFHL FTCIEARFHL FTCIEARFHL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFLQ KRNIGYFLQ QRNIGYFLQ QRNIGYFLQ QRNIGYFLQ QRNIGYFIQ RRKMGYFMIQ RRKMGYFMIQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ SRRMGYFTQ SRRMGYFTQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ	TYPPATLMVM TYPPATLMVM TYPPATLMVM TYPPATLMVM TYMPSILITI TYMPSILITI TYLPSILIVM TYLPSILIVM TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTVV TYIPCILTVV TYIPCILTVV TYIPCILTVV TYIPCILTVV MYIPSLLVI MYIPSLLVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK	200 RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG DASAARVALG EXTSARVALG EXTSARVALG EXTSARVALG EXVPARTVFG ESVPARTVFG ESVPARTVFG ESVPARTVFG DAVPARTSLG DAVPARTSLG DATPARTSLG EATADRVSLG DAPPARVALG DAPPARVALG DAPPARVALG
<pre>gar1_rat gar2_rat gar3_rat gab3_rat gab1_rat gab1_rat gab1_chick gab1_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa2_rat gaa2_rat gaa2_rat gac2_rat gac3_rat gac3_rat gac4_chick gac5_human x78349 gra1_rat gra2_rat gra2_rat</pre>	51 WVPDMFFVHS KRSFIHDTT WVPDJFFVHS KRSFIHDTT WVPDJFFUNS KRSFIHDTT WVPDJFFLND KKSFVHGVTV WVPDTYFLND KKSFVHGVTV WVPDTFFLND KKSFVHGVTV WVPDTFFLND KKSFLHGVT WVPDTFFAND KNSFLHDTT WLPDTFFNNS KKSLHDITT WTPDTFFNNS KKSJAHNTT WTPDTFFNNS KKSJAHNTT WTPDTFFNNS KKSJAHNTT WIPDTFFNNS KKSJAHNTT WIPDTFFNNS KKSJAHNTT WIPDTFFNNS KKSJAHNTT WIPDTFFNNS KKSJAHNTT WIPDTFFNNS KKSJAHNTT WIPDTFFNNS KKSJAHNTT WIPDTFFNS KKSJAHNTT WIPDTFFNS KKSJAHNTT WIPDTFFNS KKSJAHNTT WIPDTFFNS KKSJAHNTT WIPDTFFNS KKSJAHNTT WIPDTFFNS KKSJAHNTT WIPDTFFNS KKSJAHNTT WIPDTFFNS KKSJAHNTT WIPDTFFNS KRALHTT WKPDLFFANE KGANFHEVTT WKPDLFFANE KGANFHEVTT	DNVMLRVQPD DNIMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNLFRIMN ENKLFRIMN PNKLFRIMN PNKLFRIMN PNKLLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIDD PNKLLRIND PNQLLRIND PNQLRIND PND	GKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GXUYYGMFT GVLYSIRIT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GRVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYSLRLT GKVLYSIRLT GNVLYSIRLT GKVLYSIRLT GKVLYSIRLT GKVLYSIRLT	100 VTAMCNMDFS VSAMCFMDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLH STVACDMDLA ISAECPMILE INADCPMLLE INADCPMLLE INADCPMLLE INADCPMLLE INADCPMLLE INABCPMQLE INABCPMQLE INABCPMQLE INABCPMQLE INABCPMQLE INACCPMLLA LTLACPMDLK	<pre>garl_rat gar2_rat gar2_rat gar3_rat gab2_rat gab1_rat gab1_rat gab1_rat gab1_rat gad_rat gaa4_rat gaa6_rat gaa5_rat gac2_rat gac3_rat gac2_rat gac3_rat gac4_rat gac4_rat gac5_human x78349 gra1_rat gra2_rat gra2_rat gra2_rat gra2_rat gac5_human x78349 gra1_rat gra2_rat gra2_rat</pre>	151 YNRLYINFTL YNRLYINFTL YPRLSLSFRL YPRLSLSFRL YLRLSLSFRI YQRLSLSFRI YQRLSLSFRI YQRLSLSFRI YQRLSLFRQL FPRLSLFPQL FPRLSLFPQL YVWTYFHL YVWMTYFHL YIWTYFHL YIWMTHFHL YIIMTAFFLL YWWMTYFPL YWWMTYFPL YWWMTYFPL YWWTYFPL YWWTYFPL FNCIEXRFHL FTCIEXRFHL FTCIEXRFHL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ RRNRGVYILQ RRNRGVYILQ KRKIGYFVLQ KRKIGYFVLQ KRKIGYFVLQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ	TYFPATLWVM TYFPATLWVM TYFPATLWVM TYFPATLWVM TYMPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM SYMPSULUVA TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTVV TYIPCILTVV TYIPCILTVV TYIPCILTVV MYIPSLLIVI MYIPSLLIVI MYIPSLLIVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK	200 RAVPARV9LG RAVPARV9LG DASAARVALG DASAARVALG DASAARVALG DASAARVALG EXTSARVALG EXTSARVALG EXTSARVALG EXVPARTVFG ESVPARTVFG DAVPARTSLG DAPPARTSLG DATPARTSLG DAPPARTSLG DAPPARTSLG DAPPARTSLG DAPPARTSLG DAPPARVALG DAPPARVALG DAPPARVALG DAPPARVALG DASABRUPC
<pre>gar1_rat gar2_rat gab2_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa3_rat gaa5_rat gaa5_rat gac1_rat gac2_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gra1_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat</pre>	51 WVPDMFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDTYFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTYFLND KKSFVHCVTV WVPDTFFLND KKSFVHCVTV WVPDTFFNN KKSFLHCVTV WVPDTFFNN KKSVHNTM WTPDTFFHNS KKSVHNTM WTPDTFFHNS KKSVHNTM WTPDTFFHNS KKSVHNTM WTPDTFFHNS KKSVHNTM WTPDTFFHNS KKSVHNTM WTPDTFFNS KKSAHWIT WIPDTFFNS KASHWIT WIPDTFFNS KSANFHVTI WKDLFFANE KGANFHEVTI WKPDLFFANE KGANFHEVTI WKPDLFFANE KGANFHEVTI	DNVMLRVQPD DNTMLRVPPD ENTMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD RNKLFRIMRN ENKLFRIMRN PNKLFRIMRN PNKLFRIMRN PNKLFRIMRD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNQLLRIND PNQLLRIND PNQLLRIND PNQLLRIND DNKLLRISN DNKLLRISN DNKLLRISN	GKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GXUYYGLRIT GSLVYGMRFT GSLVYGMRFT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYSLRLT GNVLYSIRLT GNVLYSIRLT GVVLYSIRLT GVVLYSIRLT	100 VTAMCNNDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTLACMMDLH TTLACMMDLH TTLACMMDLH STACCDULS ISACCPMRLV INADCPMRLV VARECPMILE INADCYLQLH IDAECQLQLH IDAECQLQLH IDAECQLQLH IDAECQLQLH IDAECQLQLH IDAECQLQLH IDAECQLQLH IDAECQLQLH IDAECQLQLH IDAECQLQLH IDAECQLQLH IDAECSLMIL ITLSCPMDLX ITLSCPMDLX ITLSCPMDLX	<pre>gar1_rat gar2_rat gar3_rat gab3_rat gab1_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa3_rat gaa2_rat gac1_rat gac2_rat gac2_rat gac3_rat gac4_chick gac5_human x78349 gra1_rat gra2_rat gra2_rat</pre>	151 YNRLYINFTL YNRLYINFTL YRLSINFVL YPRLSLSFKL YLRLSLSFRL YLRLSLSFRL YQRLSLSFKL YQRLSLSFL YURYVYFIL YVWTYPHL YVWMTYPHL YVWMTHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YTIMTAHPHL YCULSUFFL FTCIEVRHL	RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ QRNIGYFIQ QRNIGYFIQ QRNIGYFIQ QRKMGYFIQ QRKMGYFMIQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ RRMGYFIQ RRMGYLIQ ERQMGYLLQ ERQMGYLLQ RQUGYMMG	TYPPATLWVM TYPPATLWVM TYPPATLWVM TYPPATLWVM TYPPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTVV TYIPCILIVV TYIPCILIVV TYIPCILIVV TYIPCILIVV MYIPSLLVI MYIPSLLVI MYIPSLLVI WYPSLLVI WYPSLLVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINM LSWVSFWINM	200 RAVPARVSLG DASARVALG DASARVALG DASARVALG DASARVALG DASARVALG EATSARVALG EXTARVALG EXTARVALG EXPARTVFG ESVPARTVFG ESVPARTVFG DAVPARTSLG DATPARTSLG DATPARTSLG DATPARTSLG DAPARVSLG DAPARVALG DAPARVALG DAPARVALG DAPARVALG DAPARVALG DAPARVALG DAPARVALG DAPARVALG DAPARVALG DAPARVALG DAPARVALG DAPARVALG DAPARVALG DAPARVALG
<pre>gar1_rat gar2_rat gar3_rat gab3_rat gab1_rat gab4_chick gab4_chick gab4_chick gab4_rat gaa4_rat gaa6_rat gaa3_rat gaa2_rat gac3_rat gac2_rat gac4_chick gac5_human x78349 gra1_rat gra3_rat gra3_rat gra3_rat gra2_rat gra3_rat gra2_rat</pre>	51 WVPDMFFVHS KRSFIHDTTI WVPDIFFVHS KRSFIHDTTY WVPDIFFVHS KRSFIHDTTY WVPDIFYLND KKSFVHOTV WVPDTYFLND KKSFVHOTV WVPDTYFLND KKSFVHOTV WVPDTFAND KKSFLHOTT WVPDTFFNNG KKSFLHDIT WIPDTFFNNG KKSVHNTA WTPDTFFNNG KKSVHNTA WTPDTFFNNG KKSVHNTA WTPDTFFNNG KKSVHNTT WTPDTFFNNG KKSVHNTT WIPDTFFNNG KKSVHNTT WIPDTFFNNG KKSVHNTT WIPDTFFNNG KKSVHNTT WIPDTFFNNG KKSVHNTT WIPDTFFNNG KKSVHNTT WIPDTFFNNG KKSVHNTT WIPDTFFNNG KKSVHNTT WIPDTFFNKS KKADAHWITT WIPDTFFNKS KKADAHWITT WIPDTFFNKS KKADAHWITT WIPDTFFNKS KKADAHWITT WIPDTFFNKS KKADAHWITT WIPDTFFNKS KKADAHWITT WIPDTFFNKS KKADAHWITT WIPDTFFNKS KKADHWITT WKPDLFFANE KGANFHEVTT WKPDLFFANE KGANFHEVTT WKPDLFFANE KGANFHEVTT	DNVMLRVQPD DNIMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD RNKLVRLGD RNKLVRLGD RNKLVRLGD PNKLFRIMRN PNKLFRIMRN PNKLFRIMRN PNKLLRIVDN PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIFN DNKLLRIFN DNKLLRIFN DNKLLRIFN DNKLLRIFN	CKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GTULYGLRIT GTLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYSLRLT GKVLYSLRLT GKVLYSLRLT GKVLYSLRLT GVVLYSLRLT GVVLYSLRLT GVVLYSLRLT GVVLYSLRLT GVVLYSLRLT GVVLYSLRLT GVVLYSRLS	100 VTAMCNMDFS VTAMCNMDFS TTAACMMDFS TTAACMMDFS TTAACMMDFS TTAACMMDFR TTTAACMMDFS TTAACMMDFS TTAACMMDFS STVACMMDFS STVACMMDFS STVACMMDFS ISABCPMILE ISABCPMILE ISABCPMILE ISABCPMILE INABCYLQLH INABCY	<pre>garl_rat gar2_rat gar2_rat gab2_rat gab2_rat gab1_rat gab1_rat gab1_rat gaa4_rat gaa4_rat gaa5_rat gaa2_rat gac2_rat gac2_rat gac2_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gac3_rat gac4_chick</pre>	151 YNRLYINFTL YNRLYINFTL YRLSINFVL YPRLSLSFKL YPRLSLSFKL YRLSLSFKL YQRLSLSFKL YQRLSLSFKL YQRLSLSFKL YQRLSLFQL FPRLSLHFQL YUVMTVFHL YUVMTVFHL YUVMTHFHL YTVMTHFHL YTVMTHFHL YUVMTYFDL YVVT	RRHIFFFLLQ RRHIFFFLQ KRNIGYFLQ KRNIGYFLQ KRNIGYFLQ QRNIGYFLQ QRNIGYFLQ QRNIGYFLQ QRNIGYFLQ QRNIGYFLQ RRKMGYFLQ RRKMGYFNQ KRKIGYFVLQ KRKIGYFVLQ KRKIGYFVLQ SRRMGYFLQ SRRMGYFLQ SRRMGYFLQ SRRMGYFLQ SRRMGYFLQ RRMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ	TYFPATLWW TYFPATLWW TYFPATLWW TYFPATLWW TYMPSILTI TYMPSILTI TYMPSILTI TYLPSILIVM TYLPSILIVM TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTWV TYIPCILTWV TYIPCILTWV MYIPSLLVI MYIPSLLVI MYIPSLLVI MYIPSLLVI MYIPSLLVI UYAPTTMIVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWIDY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINM LSWVSFWINM	200 RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EATSARVALG EXTPARVSLG ESVPARTVFG ESVPARTVFG ESVPARTVFG ESVPARTVFG DAVPARTSLG DAVPARTSLG DAVPARTSLG DATPARTSLG DATPARTSLG DATATSLG DATATSLG
gar1_rat gar2_rat gar3_rat gab3_rat gab1_rat gab1_rat gab1_chick gab1_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa2_rat gaa2_rat gaa2_rat gac3_rat gac3_rat gac3_rat gac4_chick gac5_human x78349 gra1_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat gra2_rat	51 WVPDMFFVHS KRSFIHDTT WVPDDFFVHS KRSFIHDTT WVPDIFFLNB KRSFIHDTT WVPDTYFLND KKSFVHGVT WVPDTYFLND KKSFVHGVT WVPDTYFLND KKSFVHGVT WVPDTFAND KNSFLHDVT WVPDTFAND KNSFLHDTT WLPDTFFNNG KKSVHMTM WTPDTFFNNG KKSVHMTM WTPDTFFNNG KKSVHMTM WTPDTFFNNG KKSVHMTM WTPDTFFNNG KKSVHMTT WTPDTFFNNG KKSVHMTT WTPDTFFNNG KKSVHMTT WTPDTFFNNG KKSVHMTT WIPDTFFNNG KKSVHMTT WIPDTFFNNG KKSVHMTT WIPDTFFNNG KKSVHMTT WIPDTFFNNG KKSVHMTT WIPDTFFNNG KKSVHMTT WIPDTFFNG KKSVHMTT WIPDTFFNG KKSVHMTT WIPDTFFNG KASHNTT WIPDTFFNG KASHNTT WIPDTFFNG KGSHFHTT WKPDLFFANE KGANFHEVTT WKPDLFFANE KGANFHEVTT WKPDLFFANE KGANFHEVTT WKPDLFFANE KGANFHEVTT WKPDLFFANE KAARHLIDB WIPDTFFPTE KAARHLIDB	DNVMLRVQPD DNIMLRVPPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNLFRIMM PNKLFRIMM PNKLFRIMM PNKLFRIMM PNKLLRICD PNKLLRICD PNKLLRUDD PNKLLRUDD PNKLLRUDD PNKLLRUDD PNKLLRUDD PNKLLRUDD PNKLLRUDD PNKLRICO DNKLRIFN DNKLLRISN DNKLLRISN ENNFRIPD NKLLRISN DNKLLRISN	GKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GAVTYGMRT GSLVYGMRT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GRVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYSLRLT GNVLYSIRLT GNVLYSIRLT GVVLYSIRLT GVVLYSRLS GVVLYSRLS	100 VTAMCNNDFS VSAMCFMDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLR STVACDMDLA ISAECPMILA ISAECPMILA ISAECPMILA ISAECPMILA ISAECPMILA ISAECPMILA INABCQLQLH INABCQLQLH INABCQLQLH ISAECPMILA ITLACPMDLX ITLSCFMDLX ITLSCFMDLX ITLSCFMDLX ITLSCFMDLX ITLSCFMDLX ITSSCFMQLQ	<pre>gar1_rat gar2_rat gar3_rat gab3_rat gab3_rat gab1_rat gab1_rat gab1_rat gab1_rat gad_rat gaa4_rat gaa5_rat gaa5_rat gac3_rat gac2_rat gac3_rat gac5_human x78349 gra1_rat gra2_rat gra2_rat gra2_rat gra2_rat gac3_hick gra5_human x78349 gra1_rat gra2_rat gra2_ra</pre>	151 YNRLYINFTL YNRLYINFTL YYRLSINFVL YPRLSLSFRL YLRLSLSFRL YLRLSLSFRI YQRLSLSFRL YQRLSLSFRL YQRLSLFPQL FPRLSLHFQL FVRLSLFPQL YVWMYYFHL YVWMYTHFHL YTVMTAHFHL YTVMTAHFHL YTVMTAHFHL YTVMTAHFHL YTVMTAHFHL YTVMTYFDL FWVMTIFFNV SSMLMWNFHL FTCIEXFHL FTCIEXFHL TCIEXFHL YCVEVIFTL YCCLENQLF YACLENQLTF	RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ RRNRGYFILQ RRNRGYFILQ KRKIGYFVLQ KRKIGYFVLQ KRKIGYFVLQ SRRMGYFILQ SRRMGYFILQ SRRMGYFILQ ERQMGYFLQ ERQMGYLLQ RRQCFYMKQ KRQFSYLLQ RRQCFYMKQ	TYFPATLWVM TYFPATLWVM TYFPATLWVM TYFPATLWVM TYMPSILITI TYMPSILITI TYLPSILITI TYLPSILIVM SYMPSULUVA TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYIPCILTVV TYIPCILTVV TYIPCILTVV TYIPCILTVV MYIPSLLIVI MYIPSLLIVI UYAPTLLIVV LYAPTTMIVI LYAPTTMIVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINM LSWVSFWINM	200 RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EXTSARVALG EXTSARVALG EXTSARVALG EXTSARVALG ESVPARTVFG ESVPARTVFG DAVPARTSLG DAVPARTSLG DAPPARTSLG DAPPARTSLG DAPPARTSLG DAPPARTSLG DAPPARTSLG DAPPARTSLG DAPPARTSLG DAPPARTSLG DAPPARVALG DAPPARVALG DASARVALG HSTAGRVALG BSTAGRVALG
<pre>gar1_rat gar2_rat gab2_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa3_rat gaa5_rat gaa5_rat gac4_chick gac3_rat gac4_chick gac3_rat gac4_chick gac3_rat gra1_rat gra2_rat gra2_rat gac4_rat gac3_rat gac3_rat gac3_rat gra3_rat gra3_rat gra3_rat gra3_rat gra2_rat gra3_rat gr3_</pre>	51 WVPDMFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDIFFVHS KRSFIHDTT WVPDIFFLND KKSFVHCVT WVPDTYFLND KKSFVHCVT WVPDTYFLND KKSFVHCVT WVPDTFFLND KKSFVHCVT WVPDTFFNN KKSFHCVT WVPDTFFNN KKSVHNTM WTPDTFFNN KADHWIT WIPDTFFNN KADHWIT WIPDTFFNN KADHWIT WIPDTFFNN KADHWIT WIPDTFFNN KADHWIT WIPDTFFNN KADHWIT WIPDTFFNN KANDHWIT WIPDTFFNN KANHHUT WKPDLFFANE KGANFHEVTI WKPDLFFANE KGANFHEVTI	DNVMLRVQPD DNIMLRVFPD ENIMLRVFPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD RNKLFRIMR ENKLIRLOPD ENKLIRLOPD PNKLFRIMR PNKLFRIMR PNKLFRIMR PNKLRITED PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD PNKLLRIVD DNKLLRISN DNKLLRIFN DNKLLRIFN DNKLLRIFN DNKLLRIFN DNKLLRIFN DNKLLRIFN DNKLLRIFN DNKLLRIFN DNKLLRIFN DNKLLRIFN	CKVLYSLRVT GHVLYSLRIT GNVLFSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GXUYYGLRIT GXUYYGMRFT GXLYYMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GKULYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYSLRIT GNVLYSIRLT GNVLYSIRLT GNVLYSIRLT GVVLYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT GXULYSIRLT	100 VTAMCNINDFS VSAMCFMDFS VSAMCFMDFS TTAACMMDLR TTAACMMDLR TTAACMMDLR TTAACMMDLH TTLACMMDLH TTLACMMDLH STACCDMLS ISACCPMRLV INACCPMRLV INACCPMILE INACCJULH IDAECJULH IDAECJULH IDAECJULH IDAECJULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH IDAECSULH ITLSCPMDLK ITLSCPMLK ITLSCPMLK ITSSCHQUL ITSSCHQUL	<pre>gar1_rat gar2_rat gar3_rat gab2_rat gab3_rat gab1_rat gab4_chick gab3_drome gab_lymst gad_rat gaa4_rat gaa4_rat gaa3_rat gaa2_rat gac1_rat gac2_rat gac2_rat gac3_rat gac4_chick gac5_human x78349 gra1_rat gra2_rat gra2_rat gra2_rat gac3_rat gra2_rat</pre>	151 YNRLYINFTL YNRLFINFUL YRLFINFUL YPRLSLSFKL YPRLSLSFRL YRLSLSFRL YQRLSLSFRL YQRLSLSFRL YQRLSLFQL TYUNTYFHL YVWMTYFHL YVWMTYFHL YTWMTHFHL YTWMTHFHL YTWMTHFHL YTWMTHFHL YTWMTYFEL YWWMTYFFL FNVMTIFFNV YSMLWNVFHL FTCIENFFHL FTCIENFFHL FTCIENFFHL FTCIENFFHL SCLAWQLIFL YACLRMQLT YSCLKWDLT YSCLKWDLT YSCLKWDLT YSCLKWDLT	RRHIFFFLLQ RRHIFFFLQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ KRNIGYFILQ QRNIGYFIQ QRNIGYFIQ QRNIGYFIQ QRKMGYFIQ QRKMGYFIQ QRKMGYFIQ KRKIGYFVIQ KRKIGYFVIQ KRKIGYFVIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ RRMGYFIQ RRMGYFIQ RRMGYFIQ RRMGYLIQ ERQMGYLLQ RQVGYMMG KRQFSYLLQ RRQFSYLLQ RRPSYLLQ RRMGFYLD	TYPPATLWVM TYPPATLWVM TYPPATLWVM TYPPATLWVM TYPPSILITI TYMPSILITI TYMPSILITI TYLPSILIVM TYLPCIMTVI IYTPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTVV TYIPCILTVV NYVPSSVTTW MYIPSLLVI MYIPSLLVI MYIPSLLVI MYIPSLLVI UYAPTTMIVI LYAPTTMIVI LYAPTTMIVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWIDY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINK LSWVSFWINM LSWVSFWINM LSWVSFWINM LSWVSFWINM	200 RAVPARVSLG DASARVALG DASARVALG DASARVALG DASARVALG EATSARVALG EATSARVALG EXPARTVAG ESVPARTVFG ESVPARTVFG ESVPARTVFG DAVPARTSLG DATPARTSLG DATPARTSLG DATPARTSLG DAPARVSLG DAPARVALG DAFARVALG HSTAGRVALG GAVPARVSLG GAVPARVSLG STAGRVALG STAGRVALG
<pre>gar1_rat gar2_rat gar2_rat gab3_rat gab1_rat gab4_chick gab4_chick gab4_chick gab4_trat gaa4_rat gaa4_rat gaa6_rat gaa2_rat gaa2_rat gac3_rat gac2_rat gac4_chick gac5_human x78349 gra1_rat gra2_rat gra2_rat gac4_chick gac5_human x78349 gra1_rat gra2_rat gra2_rat gra2_rat gra2_rat gra3_rat gra2_rat gra3_</pre>	51 WVPDMFFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTT WVPDIFVHS KRSFIHDTY WVPDTYFLND KKSFVHOYT WVPDTYFLND KKSFVHOYT WVPDTFLND KKSFUHOTT WVPDTFLND KKSVHOTT WTPDTFFNNG KKSVHNTA WTPDTFFNNG KKSVHNTA WTPDTFFNNG KKSVHNTA WTPDTFFHNG KKSVHNTA WTPDTFFHNG KKSVHNTA WTPDTFFHNG KKSVHNTA WTPDTFFHNG KKSVHNTA WTPDTFFNG KKSVHNTA	DNVMLRVQPD DNIMLRVPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD KNRMIRLHPD NKLFRIMN PNKLFRIMN PNKLFRIMN PNKLRIND PNKLRIQD PNKLLRIVDN PNKLRIQD PNKLRIND PNKLRIND PNKLRIND PNKLRIND PNKLRIND PNKLRIND PNKLRIND PNKLRIND PNKLRIND PNKLRISN DNKLLRISN DNKLLRISN DNKLLRISN DNKLLRISN DNKLLRISN DNKLLRISN DNKLLRISN DNKLLRISN DNKLLRISN DNKLLRISN DNKLLRISN DNKLLRISN	CKVLYSLRVT GHVLYSLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GTVLYGLRIT GXUYYGMFT GYLLYSIRIT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GTLLYTMRLT GKULYTLRLT GKVLYTLRLT GKVLYTLRLT GKVLYSLRIT GNVLYSIRIT GNVLYSIRIT GNVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT GKVLYSIRIT	100 VTAMCNNDFS VTAMCNNDFS TTAACMDJR TTAACMDJR TTAACMDJR TTAACMDJR TTAACMDJR TTAACMDJR STOCOM ISAECMGJU ISAECMGJU ISAECMGJU INADCPMHLE ISAECPMHLE ISAECPMJLE INAECYLQLH INAECYLQLH INAECYLQLH INAECYLQLH INAECYLQLH INAECYLQLH INAECYLQLH INAECYLQLH INAECYLQLH INAECYLQLH ITACCPMDLK LTLSCPMDLK LTLSCPMDLK LTLSCPMDLK LTLSCPMDLK LTLSCPMDLK LTLSCPMDLK LTLSCPMDLK	<pre>garl_rat gar2_rat gar2_rat gar2_rat gab2_rat gab2_rat gab1_rat gab4_chick gab3_drome gab_ymst gaa4_rat gaa4_rat gaa4_rat gaa5_rat gaa2_rat gac2_rat gac2_rat gac2_rat gac5_human x78349 gra1_rat gra3_rat gra3_rat gra5_rat gra</pre>	151 YNRLYINFTL YNRLYINFTL YYRLSINFVL YPRLSLSFKL YPRLSLSFKL YRLSLSFKL YQRLSLSFKL YQRLSLSFKI YQRLSLSFKI YQRLSLFYCL YUNTYFHL YUVMTYFHL YTVMTHFHL YTVMTHFHL YTVMTHFHL YTVMTHFHL YTVMTHFHL YTVMTHFHL YTVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YVVMTYFDL YCVEVFHL FTCIEVKFHL TCIEVKFHL TCIEVKFHL TCIEVKFHL TCIEVKFHL YCCLEVKHLF YACLRMQLTF YSCLKVDLFF	RRHIFFFLLQ RRHIFFFLQ KRNIGYFLQ KRNIGYFLQ KRNIGYFLQ CRNIGYFLQ CRNIGYFLQ CRNIGYFLQ CRNIGYFLQ CRNIGYFLQ CRNIGYFLQ RRKMGYFNQ KRKIGYFVQ KRKIGYFVQ SRRMGYFNQ SRRMGYFTQ SRRMGYFTQ SRRMGYFTQ SRRMGYFIQ SRRMGYFIQ SRRMGYFIQ SRRMGYFLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ ERQMGYLLQ CRHFSYLLQ KRQFSYLLQ ARNIGFYLQ	TYFPATLWW TYFPATLWW TYFPATLWW TYFPATLWW TYMPSILTI TYMPSILTI TYMPSILTI TYLPSILIVM TYLPSILIVM TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCIMTVI TYLPCILTWV TYIPCILTWV TYIPCILTWV MYIPSLLVI MYIPSLLVI MYIPSLLVI MYIPSLLVI LYAPTTMIVI LYAPTTMIVI	LSWVSFWIDR LSWVSFWIDR LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINY LSWVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSQVSFWINK LSWSFWINK LSWVSFWINK L	200 RAVPARVSLG RAVPARVSLG DASAARVALG DASAARVALG DASAARVALG EATSARVALG EXTSARVALG EXTSARVALG EXTPARVSLG EXPARTVFG ESVPARTVFG ESVPARTVFG DAVPARTSLG DAVPARTSLG DAVPARTSLG DAPARTSLG DAPARTSLG DAPARTSLG DAPARTSLG DAPARVALG DAPARVALG DASARVVGL HSTAGRVALG HSTAGRVALG SNPORVSLG NSVPORVSLG

	201				250	
gar1_rat	ITTVLTMSTI	ITGVNASMPR	VSYIKAVDIY	LWVSFVFVFL	SV.LEYAAVN	gar1
gar2_rat	IMTVLTMSTI	ITGVNASMPR	VSYIRAVDIY	LWVSFVFVFL	SV.LEYAAVN	gar2
gar3_rat	ITTVLTMSTI	VTGVSASMPQ	VSYVKAVDVY	MWVSSLFVFL	SV. IEYAAVN	gar3
gab2_rat	ITTVLTMTTI	NTHLRETLPK	IPYVKAIDMY	LMGCFVFVFM	AL.LEYALVN	gab2
gab3_rat	ITTVLTMTTI	NTHLRETLPK	IPYVKAIDMY	LMGCFVFVFL	AL.LEYAFVN	gab3
gab1_rat	ITTVLTMTTI	STHLRETLPK	IPYVKAIDIY	LMGCFVFVFL	AL.LEYAFVN	gab1
gab4_chick	VTTVLTMTTI	NTHLRETLPK	IPYVKAIDVY	LMGCFVFVFL	AL.LEYAFVN	gab4_c
gab3_drome	ITTVLTMTTI	STGVRSSLPR	ISYVKAIDIY	LVMCFVFVFA	AL.LEYAAVN	gab3_d
gab_1ymst	ITTVLTMTTI	SNGVRSSLPR	ISYVKAIDIY	LVMCFVFVFA	AL.LEYAAVN	gab_1
gad_rat	ITTVLTMTTL	MVSARSSLPR	ASAIKALDVY	FWICYVFVFA	AL.VEYAFAH	gad
gaa4_rat	ITTVLTMTTL	SISARHSLPK	VSYATAMDWF	IAVCFAFVFS	AL.IEFAAVN	gaa4
gaa6_rat	ITTVLTMTTL	SISARHSLPK	VSYATAMDWF	IAVCFAFVFS	AL.IEFAAVN	gaa6
gaa1_rat	VTTVLTMTTL	SISARNSLPK	VAYATAMDWF	IAVCYAFVFS	AL.IEFATVN	gaa1
gaa3_rat	VTTVLTMTTL	SISARNSLPK	VAYATAMDWF	MAVCYAFVFS	AL.IEFATVN	gaa3
gaa2_rat	VTTVLTMTTL	SISARNSLPK	VAYATAMDWF	IAVCYAFVFS	AL.IEFATVN	gaa2
gaa5_rat	VTTVLTMTTL	SISARNSLPK	VAYATAMDWF	IAVCYAFVFS	AL.IEFATVN	gaa5
gac1_rat	ITTVLTMTTL	STIARKSLPK	VSYVTAMDLF	VSVCFIFVFA	AL.MEYGTLH	gac1
gac2_rat	ITTVLTMTTL	STIARKSLPK	VSYVTAMDLF	VSVCFIFVFS	AL.VEYGTLH	gac2
gac3_rat	ITTVLTMTTL	STIARKSLPR	VSYVTAMDLF	VTVCFLFVFA	AL.MEYATLN	gac3
gac4_chick	ITTVLTMTTL	STISRKHLPR	VSYITAMDLF	VSVCFIFVFA	AL.MEYATLN	gac4_c
gac5_human	ITSVLTMTTL	GTFSRKNFPR	VSYITALDFY	IAICFVFCFC	AL.LEFAVLN	gac5_h
x78349	ITTVLTMTFL	GLEARTDLPK	VSYPTALDFF	VFLSFGFIFA	TI.LQFAVVH	x 7
gra1_rat	ITTVLTMTTQ	SSGSRASLPK	VSYVKAIDIW	MAVCLLFVFS	AL.LEYAAVN	gra1
gra3_rat	ITTVLTMTTQ	SSGSRASLPK	VSYVKAIDIW	MAVCLLFVFS	AL.LEYAAVN	gra3
gra2_rat	ITTVLTMTTQ	SSGSRASLPK	VSYVKAIDIW	MAVCLLFVFA	AL.LEYAAVN	gra2
grb_rat	IFSVLSLASE	CTTLAAELPK	VSYVKALDVW	LIACLLFGFA	SL.VEYAVVQ	grb
u14525	VTTLLTMTTM	QSAINAKLPP	VSYVKVVDVW	LGACQTFVFG	AL.LEYAFVS	ul
y09796	VTTLLTMTTM	QAAINAKLPP	VSYVKVVDVW	LGACQTFVFG	AL.LEYAFVS	у0
u58776	VTTLLTMATQ	TSGINASLPP	VSYTKAIDVW	TGVCLTFVFG	AL.LEFALVN	u5
s34469	LLTVLTMTTQ	SSSVNAALPR	VSYTKAIDVW	MSTCLVFVFA	AL.LEFAVVN	s3
ach9_rat	VTILLAMTVF	OLMVAEIMPA	SENVPLICKY	YIATMALITA	STALTIMVMN	ach9

250		251		280
YAAVN	gar1_rat	YNTHAIDKYS	RIIFPAAYIL	FNLIYWSIFS
YAAVN	gar2_rat	YNTHAIDKYS	RLIFPAFYIV	FNLIYWSVFS
YAAVN	gar3_rat	YNNHVIDTYS	RIVFPVVYII	FNLFYWGIYV
YALVN	gab2_rat	YDVNAIDRWS	RIFFPVVFSF	FNIVYWLYYV
IYAFVN	gab3_rat	YDVNAIDRWS	RIVFPFTFSL	FNLVYWLYYV
YAFVN	gab1_rat	YDVNSIDKWS	RMFFPITFSL	FNVVYWLYYV
YAFVN	gab4_chick	YDVSTIDKWS	RIIFPITFGF	FNLVYWLYYV
YAAVN	gab3_drome	YDVNIIDKYS	RMIFPISFLA	FNLGYWLFYI
YAAVN	gab_lymst	YDVNTIDKYA	RLMFPLLFII	FNTSYWSVYL
YAFAH	gad_rat	FDADTIDIYA	RAVFPAAFAA	VNIIYWAAYT
FAAVN	gaa4_rat	YGTSKIDKYA	RILFPVTFGA	FNMVYWVVYL
FAAVN	gaa6_rat	YGTSKIDQYS	RILFPVAFAG	FNLVYWIVYL
FATVN	gaa1_rat	YSVSKIDRLS	RIAFPLLFGI	FNLVYWATYL
FATVN	gaa3_rat	YSVSKVDKIS	RIIFPVLFAI	FNLVYWATYV
FATVN	gaa2_rat	YSVSKIDRMS	RIVFPVLFGT	FNLVYWATYL
FATVN	gaa5_rat	YSISKIDKMS	RIVFPILFGT	FNLVYWATYL
YGTLH	gac1_rat	YRIAKIDSYS	RIFFPTAFAL	FNLVYWVGYL
YGTLH	gac2_rat	YRIAKMDSYA	RIFFPTAFCL	FNLVYWVSYL
YATLN	gac3_rat	YDVSELDSYS	RVFFPTSFLL	FNLVYWVGYL
YATLN	gac4_chick	YHISRLDSYS	RVFFPTAFLL	FNIVYWIAYL
FAVLN	gac5_human	FHVYRLDNYS	RVVFPVTFFF	FNVLYWLVCL
FAVVH	x78349	YSVSKIDRAS	RIVFPLLFIL	INVFYWYGYL
YAAVN	gra1_rat	FRAKKIDKIS	RIGFPMAFLI	FNMFYWIIYK
YAAVN	gra3_rat	FRAKKIDTIS	RACFPLAFLI	FNIFYWVIYK
IYAAVN	gra2_rat	FRAKRIDTIS	RAAFPLAFLI	FNIFYWITYK
<u>Q</u> VVAY2	grb_rat	VAAKRIDLYA	RALFPFCFLF	FNVIYWSIYL
YAFVS	u14525	YLPAKIDFYA	RFVVPLAFLA	FNVIYWVSCL
YAFVS	y09796	YLPAKIDYYA	RFCVPLGFLA	FNAIYWTSCL
FALVN	u58776	YRSKRIDVIS	RITFPLVFAL	FNLVYWSTYL
FAVVN	s34469	VYAIYVDMTA	RVVFPICFII	FIMSYWLYYV
IMVMN	ach9_rat	IKGSEWKKVA	KVIDRFFMWI	FFAMVFVMTV