MOLECULAR ECOLOGY

Supplemental Information for:

A new subfamily of ionotropic glutamate receptors unique to the echinoderms with putative sensory role

Rubaiyat E Sania, João C.R. Cardoso, Bruno Louro, Nathalie Marquet, Adelino V.M. Canário

Table of Contents:

Legends:

Supplementary Table 1: Descriptive statistics of the de novo assembly transcriptomes from nerve ring (NR), radial nerve (RN) and tentacles (T).

Supplementary Table 2: List and accession numbers of iGluR subunits analysed in this study.

Supplementary Table 3: List of accession numbers, genome location and positions of the neighbouring genes used in the gene synteny analysis.

Supplementary Figure 1: Phylogenetic tree of the *H. arguinesis* and *A. japonicus* and other vertebrate and invertebrate iGluRs. The tree was built using ML method.

Supplementary Figure 2: Schematic linear representation of the predicted structure of the *H. arguinensis* GluH subunits. The consensus structures of the *H. sapiens* GluA, GluK and GluD are represented for comparisons. Only complete sequences are represented with size indicated. The amino-terminal domain is represented in pink, the ligand-binding domain (S1 and S2 domains) are marked with blue boxes, the transmembrane (TM) regions (the three membrane-spanning helices (M1, M3, and M4) and a membrane re-entrant loop (M2)) are represented in yellow and the C-terminal domains in indicated in white. The predicted signal peptide (SP) is also indicated.

Supplementary Figure 3: Schematic linear representation of the predicted structure of the iGluR subunit genes in *A. japonicus*. The consensus structures of the *H. sapiens* GluA, GluK and GluD is represented for comparisons. Only complete sequences are represented, and size (aa) is indicated. The amino-terminal domain is represented in pink, the ligand-binding domain (S1 and S2 domains) are marked with blue boxes, the transmembrane (TM) regions (the three membrane -spanning helices (M1, M3, and M4)

and a membrane re-entrant loop (M2)) are represented in yellow and the C-terminal domains in indicated in white. The predicted signal peptide (SP) is also indicated.

Supplementary Figure 4: Schematic linear representation of the predicted structure of the iGluR subunit genes in *S. purpuratus*. The consensus structures of the *H. sapiens* GluA, GluK and GluD is represented for comparisons. Only complete sequences are represented, and size (aa) is indicated. The amino-terminal domain is represented in pink, the ligand-binding domain (S1 and S2 domains) are marked with blue boxes, the transmembrane (TM) regions (the three membrane-spanning helices (M1, M3, and M4) and a membrane re-entrant loop (M2)) are represented in yellow and the C -terminal domains in indicated in white. The predicted signal peptide (SP) is also indicated.

Supplementary Figure 5: Gene expression levels of *Griha5, Grihb, Grihc1* and *Grihc2* in nerve Ring (NR), radial nerve (RN) and tentacles (T) as determined by qPCR and normalized against *18s*, and represented as the mean ± SEM of three biological replicates (n= 3).

Supplementary Data 1: Aligned sequence alignment used to build the phylogenetic tree.

Supplementary Data 2: A three-way analysis of variance with sex, tissue and receptor as factors to compare differences in expression levels (FPKM), followed by the multicomparison Holm-Sidak a posteriori test when main effects were statistically significant. Statistical analysis was performed using SigmaPlot software (version 14.0, Systat Software, Inc).

Supplementary Table 1: Descriptive statistics of the de novo assembly transcriptomes from nerve ring (NR), radial nerve (RN) and tentacles (T).

	NR	RN	T
Post-QC normalized reads	236 052 610	189 140 018	223 193 422
Total Trinity 'genes'	506 780	331 503	483 550
Total Trinity transcripts	765 497	489 595	719 972
N50 (bp)	1 009	656	1 042
Average length (bp)	688	571	698

Supplementary Table 2

Supplementary Table 2: List and accession numbers of iGluRs analysed in this study

	Scientific Name	Receptor subfamilies	Nomenclature according to Ramos-	Adopted Nomenclature	Protein symbol in the phylogenetic	Accession No (gene or protein)	Gene location (bp)	Database	Observations
CHORDATA									
Mammalia									
Human	*Homo sapiens* (Hsap)	GRIA	GluA1_Hsa	Hsap_GluA1	Hsap_GluA1	ENSG0000001	5: 153,489,615-153,813,869	https://www.ensembl.org/index.html	
			GluA2_Hsa	Hsap_GluA2	Hsap_GluA2	ENSG0000001	4:157,204,182-157,366,075:1	https://www.ensembl.org/index.html	
			GluA3_Hsa	Hsap_GluA3	Hsap_GluA3	ENSG0000001	X:123,184,153-123,490,915:1	https://www.ensembl.org/index.html	
			GluA4_Hsa	Hsap_GluA4	Hsap_GluA4	ENSG0000001	11:105,609,994-105,982,092:1	https://www.ensembl.org/index.html	
		GRID	GluD1_Hsa	Hsap_GluD1	Hsap_GluD1	ENSG0000001	10:85,599,552-86,366,795:-1	https://www.ensembl.org/index.html	
			GluD2_Hsa	Hsap_GluD2	Hsap_GluD2	ENSG0000001	4:92,303,966-93,810,157:1	https://www.ensembl.org/index.html	
		GRIK	GluK1_Hsa	Hsap_GluK1	Hsap_GluK1	ENSG0000001	21:29,536,933-29,940,033:-1	https://www.ensembl.org/index.html	
			GluK2_Hsa	Hsap_GluK2	Hsap_GluK2	ENSG0000001	6:101,181,257-102,070,083:1	https://www.ensembl.org/index.html	
			GluK3_Hsa	Hsap_GluK3	Hsap_GluK3	ENSG0000001	1:36,795,527-37,034,515:-1	https://www.ensembl.org/index.html	
			GluK4_Hsa	Hsap_GluK4	Hsap_GluK4	ENSG0000001	11:120,511,700-120,988,904:1	https://www.ensembl.org/index.html	
			GluK5_Hsa	Hsap_GluK5	Hsap_GluK5	ENSG0000001	19:41,998,321-42,069,498:-1	https://www.ensembl.org/index.html	
		GRIN	GluN1_Hsa	Hsap_GluN1	Hsap_GluN1	ENSG0000001	9:137,139,154-137,168,756:1	https://www.ensembl.org/index.html	
			GluN2A_Hsa	Hsap_GluN2A	Hsap_GluN2A	ENSG0000001	16:9,753,404-10,182,754:-1	https://www.ensembl.org/index.html	
			GluN2B_Hsa	Hsap_GluN2B	Hsap_GluN2B	ENSG0000002	12:13,437,942-13,981,957:-1	https://www.ensembl.org/index.html	
			GluN2C_Hsa	Hsap_GluN2C	Hsap_GluN2C	ENSG0000001	17:74,842,023-74,861,504:-1	https://www.ensembl.org/index.html	
			GluN2D_Hsa	Hsap_GluN2D	Hsap_GluN2D	ENSG0000001	19:48,394,875-48,444,931:1	https://www.ensembl.org/index.html	
			GluN3A_Hsa	Hsap_GluN3A	Hsap_GluN3A	ENSG0000001	9:101,569,352-101,738,647:-1	https://www.ensembl.org/index.html	
			GluN3B_Hsa	Hsap_GluN3B	Hsap_GluN3B	ENSG0000001	19:1,000,419-1,009,732:1	https://www.ensembl.org/index.html	
Actinopteri									
Spotted Gar	*Lepisosteus oculatus* (Loc	GRIA	no	Locu_GluA1	Locu_GluA1	ENSLOCG0	LG6:23,338,043-23,414,928:1	https://www.ensembl.org/index.html	
			no	Locu_GluA2	Locu_GluA2	ENSLOCG0	LG4:20,840,927-20,919,692:-1	https://www.ensembl.org/index.html	
			no	Locu_GluA3	Locu_GluA3	ENSLOCG0	LG7:38,690,001-38,822,115:1)	https://www.ensembl.org/index.html	
			no	Locu_GluA4	Locu_GluA4	ENSLOCG0	LG3:10,345,578-10,431,548:-1	https://www.ensembl.org/index.html	
		GRID	no	Locu_GluD1	Locu_GluD1	ENSLOCG0	LG5:15,093,769-15,449,890:1	https://www.ensembl.org/index.html	
			no	Locu_GluD2	Locu_GluD2	ENSLOCG0	LG2:55,349,903-55,560,392:1	https://www.ensembl.org/index.html	
		GRIK	no	Locu_GluK1	Locu_GluK1	ENSLOCG0	LG3:18,095,786-18,186,967:-1	https://www.ensembl.org/index.html	
			no	Locu_GluK2	Locu_GluK2	ENSLOCG0	LG1:39,330,996-39,572,025:-1	https://www.ensembl.org/index.html	
			no	Locu_GluK3	Locu_GluK3	ENSLOCG0	LG6:5,090,046-5,202,751:-1	https://www.ensembl.org/index.html	
			no	Locu_GluK4	Locu_GluK4	ENSLOCG0	LG26:1,202,411-1,458,215:-1	https://www.ensembl.org/index.html	
			no	Locu_GluK5	Locu_GluK5	ENSLOCG0	LG24:2,031,259-2,041,261:-1	https://www.ensembl.org/index.html	
		GRIN	no	Locu_GluN1	Locu_GluN1	ENSLOCG0	LG21:16,089-44,500:-1	https://www.ensembl.org/index.html	
			no	Locu_GluN2a	Locu_GluN2a	ENSLOCG0	LG13:11,702,883-11,805,831:1	https://www.ensembl.org/index.html	
			no	Locu_GluN2b	Locu_GluN2b	ENSLOCG0	LG12:35,899,227-35,934,905:1	https://www.ensembl.org/index.html	
			no	Locu_GluN2cb	Locu_GluN2cb	ENSLOCG0	LG10:29,847,759-29,940,166:1	https://www.ensembl.org/index.html	
			no	Locu_GluN3a	Locu_GluN3a	ENSLOCG0	LG2:6,805,258-6,827,731:1	https://www.ensembl.org/index.html	
			no	Locu_GluN3b	Locu_GluN3b	ENSLOCG0	LG19:3,399,644-3,456,981:-1	https://www.ensembl.org/index.html	
Holocephali									
Elephant shark	*Callorhinchus milii* (Cmil)	GRIA	no	Cmil_GluA1	Cmil_GluA1	ENSCMIG00(	KI636058.1:127,320-152,235:-1	https://www.ensembl.org/index.html	
			no	Cmil_GluA2	Cmil_GluA2	ENSCMIG00	KI635921.1:3,633,570-3,697,238:-	https://www.ensembl.org/index.html	
			no	Cmil_GluA3	Cmil_GluA3	ENSCMIG00	KI635856.1:14,962,626-15,059,85	https://www.ensembl.org/index.html	
			no	Cmil_GluA4	Cmil_GluA4	ENSCMIG00	KI635977.1:1,689,041-1,804,198:1	https://www.ensembl.org/index.html	
		GRID	no	Cmil_GluD1	Cmil_GluD1	ENSCMIG00	KI635857.1:7,227,869-7,500,265:1	https://www.ensembl.org/index.html	
			no	Cmil_GluD2	Cmil_GluD2	ENSCMIG00	KI636010.1:1,019,865-1,093,765:-	https://www.ensembl.org/index.html	
		GRIK	no	Cmil_GluK1	Cmil_GluK1	ENSCMIG00	KI635858.1: 675,000-760,187	https://www.ensembl.org/index.html	
			no	Cmil_GluK2	Cmil_GluK2	ENSCMIG00	KI635920.1: 3,406,586-3,629,323	https://www.ensembl.org/index.html	
			no	Cmil_GluK3	Cmil_GluK3	ENSCMIG00	KI635890.1:3,887,665-3,950,921:1	https://www.ensembl.org/index.html	
			no	Cmil_GluK4	Cmil_GluK4	ENSCMIG00	KI636507.1:2,381-32,395:1	https://www.ensembl.org/index.html	
		GRIN	no	Cmil_GluN1	Cmil_GluN1	ENSCMIG00	KI635931.1:1,040,664-1,074,668:-	https://www.ensembl.org/index.html	
			no	Cmil_GluN2a	Cmil_GluN2a	ENSCMIG00	KI635985.1:1,390,289-1,492,383:1	https://www.ensembl.org/index.html	
			no	Cmil_GluN2b	Cmil_GluN2b	ENSCMIG00	KI636656.1:16,150-30,681:-1	https://www.ensembl.org/index.html	
			no	Cmil_GluN2cb	Cmil_GluN2cb	ENSCMIG00	KI635864.1:2,506,866-2,533,499:-	https://www.ensembl.org/index.html	
			no	Cmil_GluN3a	Cmil_GluN3a	ENSCMIG00	KI635875.1:8,493,793-8,535,145:1	https://www.ensembl.org/index.html	
			no	Cmil_GluN3b	Cmil_GluN3b	ENSCMIG00	KI636063.1:118,563-130,574:-1	https://www.ensembl.org/index.html	
CEPHALOCHORDATA									
Amphioxus	*Branchiostoma lanceolatu*	GRIA	GluA14alpha_Bla	Blan_GluAalpha	Blan_GluAα	BL13071	Scaffold Sc0000169: 322,003-	https://metazoa.ensembl.org/index.html	
			GluA14beta_Bla	Blan_GluAbeta	Blan_GluAβ	BL03717	Scaffold Sc0000169: 355,728-392	https://metazoa.ensembl.org/index.html	
		GRID	GluD12alpha_Bla	Blan_GluDalpha	Blan_GluDα	BL09067	Scaffold Sc0000013: 1,222,816-1,	https://metazoa.ensembl.org/index.html	
			no	Blan_GluDbeta	Blan_GluDβ	BL22985	Scaffold Sc0000069: 1,283,621-1,	https://metazoa.ensembl.org/index.html	
			no	Blan_GluDgamma	Blan_GluDγ	BL16126	Scaffold Sc0000244: 357,075-388	https://metazoa.ensembl.org/index.html	
			no	Blan_GluDdelta	Blan_GluDδ	BL06770	Scaffold Sc0000076: 1,191,521-1,	https://metazoa.ensembl.org/index.html	
			no	Blan_GluDepsilon	Blan_GluDε	BL11019	Scaffold Sc0000365: 39,035-	https://metazoa.ensembl.org/index.html	
		GRIK	GluK15alpha_Bla	Blan_GluKalpha	Blan_GluKα	BL24523	Scaffold Sc0000446: 62,301-	https://www.ncbi.nlm.nih.gov/	
			GluK15betaB_Bla	Blan_GluKbeta	Blan_GluKβ	BL08733	Scaffold Sc0000446: 75,401-	https://metazoa.ensembl.org/index.html	
		GRIN	no	Blan_GluN1beta	Blan_GluN1β	BL12007	Scaffold Sc0000003: 4,103,935-	https://metazoa.ensembl.org/index.html	
			GluN1_Bla	Blan_GluN1alpha	Blan_GluN1α	BL11108	Scaffold Sc0000003: 4,103,486-4,	https://metazoa.ensembl.org/index.html	
			GluN2ADalpha_B	Blan_GluN2alpha	Blan_GluN2α	BL11102	Scaffold Sc0000241: 278,911-285	https://metazoa.ensembl.org/index.html	
			GluN2ADbeta_Bl	Blan_GluN2beta	Blan_GluN2β	BL08239	Scaffold Sc0000241: 294,676-312	https://metazoa.ensembl.org/index.html	
			no	Blan_GluN2gamma	Blan_GluN2γ	BL96879	Scaffold Sc0000241: 325,945-354	https://metazoa.ensembl.org/index.html	
			no	Blan_GluN3	Blan_GluN3	BL24020	Scaffold Sc0000009: 3,312,962-	https://metazoa.ensembl.org/index.html	
		GRIE	GluE1_Bla	Blan_GluE1	Blan_GluE1	BL10074	Scaffold Sc0000033: 2,060,659-2,	https://metazoa.ensembl.org/index.html	
			no	Blan_GluE2	Blan_GluE2	BL19113	Scaffold Sc0000016: 1,457,174-1,	https://metazoa.ensembl.org/index.html	
			GluE6_Bla	Blan_GluE3	Blan_GluE3	BL95332	Scaffold Sc0000022: 204,505-	https://metazoa.ensembl.org/index.html	
			no	Blan_GluE4	Blan_GluE4	BL24839	Scaffold Sc0000007: 932,665-965	https://metazoa.ensembl.org/index.html	
		GRIF	no	Blan_GluF1	Blan_GluF1	BL06495	Scaffold Sc0000119: 462,353-472	https://metazoa.ensembl.org/index.html	
			GluF2_Bla	Blan_GluF2	Blan_GluF2	BL16016	Scaffold Sc0000038: 1,142,295-1,	https://metazoa.ensembl.org/index.html	
	Branchiostoma floridae (B	GRIF	GluF1_Bfl	Bflo_GluF1	Bflo_GluF1	XP_0356995	NC_049993.1 (4490254..4496483	https://www.ncbi.nlm.nih.gov/	
			GluF2_Bfl	Bflo_GluF2	Bflo_GluF2	XP_0356651	NW_023365777.1	https://www.ncbi.nlm.nih.gov/	
			GluF3_Bfl	Bflo_GluF3	Bflo_GluF3	XP_0356999	NC_049993.1	https://www.ncbi.nlm.nih.gov/	
			GluF4_Bfl	Bflo_GluF4	Bflo_GluF4	XP_0356999	NC_049993.1	https://www.ncbi.nlm.nih.gov/	
TUNICATA									
Sea Vase	*Ciona intestinalis* (Cint)	GRIA	no	Cint_GluA	Cint_GluA	ENSCING00(	Chromosome 2: 3,913,082-3,925,5	https://www.ensembl.org/index.html	
		GRID	no	Cint_GluDalpha	Cint_GluDα	ENSCING00(	Chromosome 12: 254,541-257,893	https://www.ensembl.org/index.html	
			no	Cint_GluDbeta	Cint_GluDβ	ENSCING00(	Chromosome 1: 5,546,365-5,548,7	https://www.ensembl.org/index.html	
		GRIN	no	Cint_GluN1	Cint_GluN1	ENSCING00(	Scaffold HT000019.1: 5,208-5,386	https://www.ensembl.org/index.html	
		GRIE	GluE1_Cin	Cint_GluE1	Cint_GluE1	ENSCING00(	Chromosome 3: 2,229,396-2,230,9	https://www.ensembl.org/index.html	
			GluE2_Cin	Cint_GluE2	Cint_GluE2	ENSCING00(	Scaffold HT000098.1: 114,720-11	https://www.ensembl.org/index.html	
			no	Cint_GluK	Cint_GluK	ENSCING00(	Chromosome 1: 5,546,741-5,547,1	https://www.ensembl.org/index.html	incomplete, not used in the phylogeny
			no	Cint_GluN2	Cint_GluN2	ENSCING00(	Chromosome 9: 4,101,979-4,104,0	https://www.ensembl.org/index.html	incomplete, not used in the phylogeny
HEMICHORDATA									
Acron worm	*Saccoglossus kowalevskii*	GRIA	GluA-14_Sko	Skow_GluA5	Skow_GluA	XP_0068118	NW_003107109.1 (101783..115598)		
		GRID	GluD1-2beta_Sk	Skow_GluDbeta	Skow_GluDβ	XP_0027320	NW_003111970.1		
			GluD1-2alpha_Sk	Skow_GluDalpha	Skow_GluDα	XP_0027342	NW_003122930.1		
			no	Skow_GluDgamma	Skow_GluDγ	XP_0068252	NW_003155759.1 (13522..68870)	https://www.ncbi.nlm.nih.gov/	
		GRIK	GluK1-5_Sko	Skow_GluK6	Skow_GluK	XP_0068229	NW_003147272.1		
		GRIN	GluN1beta_Sko	Skow_GluN1alpha	Skow_GluN1α	XP_0027422	NW_003158233.1		
			GluN1alpha_Sko	Skow_GluN1beta	Skow_GluN1β	XP_0356629	NC_049997.1		
			GluN2ADbeta_Sk	Skow_GluN2alpha	Skow_GluN2α	XP_0027332	NW_003119425.1 (701407..731152, complement)		
			GluN2ADgamma_	Skow_GluN2beta	Skow_GluN2β	XP_0068146	NW_003119425.1		
			GluN2ADdelta_Sk	Skow_GluN2gamma	Skow_GluN2γ	XP_0068229	NW_003146809.1 (9033..24676)		
			GluN2ADalpha_S	Skow_GluN2delta	Skow_GluN2δ	XP_0068146	NW_003146809.1 (9033..24676)	https://www.ncbi.nlm.nih.gov/	
			GluN3ABbeta_Sk	Skow_GluN3alpha	Skow_GluN3α	XP_0027341	NW_003122440.1		
			GluN3ABalpha_S	Skow_GluN3beta	Skow_GluN3β	XP_0027341	NW_003122440.1		
		GRIE	GluE1_Sko	Skow_GluE1	Skow_GluE1	XP_0027377	NW_003137330.1		
			GluE2_Sko	Skow_GluE2	Skow_GluE2	XP_0027303	NW_003105101.1 (129604..150032, complement)		
			Skow_GluF			XP_0027315	NW_003109091.1 (10116..14714)	https://www.ncbi.nlm.nih.gov/	not used in the phylogeny tree
						XP_0068152	NW_003120935.1 (55222..73407)	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0068205	NW_003138337.1 (141954..1683	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0027342	NW_003122930.1 (103446..1201	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0027305	NW_003105604.1 (135976..1594	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0068252	NW_003155759.1 (13522..68870)	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0068157	NW_003158233.1 (144272..18117	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						ADB22420.1	NW_003122908.1 (1285853..131	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0027341	NW_003119425.1 (701407..73115	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0068229	NW_003122440.1 (117255..1959	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0068146	NW_003119425.1 (246711..33954	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
ECHINODERMATA									
Asteroidea									

Crown of thorne Star f	*Acanthaster planci* (Aplan)	GRIA	GluA1-4alpha_Ap	Apla_GluAalpha	Apla_GluAα	XP_0220862	NW_019091385.1	https://www.ncbi.nlm.nih.gov/	
			GluA1-4beta_Apl	Apla_GluAbeta	Apla_GluAβ	XP_0220862	NW_019091385.1	https://www.ncbi.nlm.nih.gov/	
		GRID	GluD1-2_Apl	Apla_GluD	Apla_GluD	XP_0220856	NW_019091383.1	https://www.ncbi.nlm.nih.gov/	
		GRIK	GluK15beta_Apl	Apla_GluKalpha	Apla_GluKα	XP_0221035	NW_019091512.1	https://www.ncbi.nlm.nih.gov/	
			GluK15alpha_Apl	Apla_GluKbeta	Apla_GluKβ	XP_0221035	NW_019091512.1	https://www.ncbi.nlm.nih.gov/	
		GRIN	GluN1_Apl	Apla_GluN1	Apla_GluN1	XP_0221119	NW_019091362.1	https://www.ncbi.nlm.nih.gov/	
			GluN3AB_Apl	Apla_GluN3	Apla_GluN3	XP_0221054	NW_019091539.1	https://www.ncbi.nlm.nih.gov/	
		GRIH	GluF_Apl	Apla_GluHA	Apla_GluHA	XP_0221058	NW_019091545.1	https://www.ncbi.nlm.nih.gov/	
			no	Apla_GluHB	Apla_GluHB	XP_0221058	NW_019091545.1 (519395..52814	https://www.ncbi.nlm.nih.gov/	
			no	Apla_GluHC	Apla_GluHC	XP_0221058	NW_019091545.1 (496177..51076	https://www.ncbi.nlm.nih.gov/	
European starfish	*Asterias rubens* (Arub)	GRIA	no	Arub_GluAalpha	Arub_GluAα	XP_0336316	NC_047069.1 (18796746..188409	https://www.ncbi.nlm.nih.gov/	
			no	Arub_GluAbeta	Arub_GluAβ	XP_0336315	NC_047069.1 (18722462..187558	https://www.ncbi.nlm.nih.gov/	
		GRID	no	Arub_GluD	Arub_GluD	XP_0336279	NC_047066.1 (13148097..131927	https://www.ncbi.nlm.nih.gov/	
		GRIK	no	Arub_GluK1	Arub_GluKα	XP_0336351	NC_047072.1 (6699612..6712636	https://www.ncbi.nlm.nih.gov/	
			no	Arub_GluK2	Arub_GluKβ	XP_0336359	NC_047072.1 (6809380..6849825	https://www.ncbi.nlm.nih.gov/	
		GRIN	no	Arub_GluN1	Arub_GluN1	XP_0336293	NC_047067.1 (68809..89316)	https://www.ncbi.nlm.nih.gov/	
			no	Arub_GluN3	Arub_GluN3	XP_0336369	NC_047073.1 (11765967..118033	https://www.ncbi.nlm.nih.gov/	
		GRIH	no	Arub_GluHA	Arub_GluHA	XP_0336342	NC_047071.1 (20143424..201560	https://www.ncbi.nlm.nih.gov/	
			no	Arub_GluHB	Arub_GluHB	XP_0336340	NC_047071.1 (12681745..127024	https://www.ncbi.nlm.nih.gov/	
			no	Arub_GluHC	Arub_GluHC	XP_0336340	NC_047071.1 (20160360..201709	https://www.ncbi.nlm.nih.gov/	
						XP_0336369	NC_047073.1 (11765967..118033	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0308509	NW_022145607.1 (3865542..391	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0308509	NW_003577131.1 (540216..6534	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0308367	NW_022145596.1 (20190359..20	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0308360	NW_022145596.1 (22397414..22	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0308360	NW_022145596.1 (20265519..20	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0308360	NW_022145596.1 (22480884..22	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0308481	NW_022145605.1 (35730642..35	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_782443.3	NW_022145615.1 (7692187..771	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0308321	NW_022145615.1 (7671801..768	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0308323	NW_022145615.1 (7581036..759	https://www.ncbi.nlm.nih.gov/	incomplete, not used in the phylogeny tree
						XP_0037278	NW_022145615.1 (7620241..763	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0336316	NC_047069.1 (18796746..188409	https://www.ncbi.nlm.nih.gov/	incomplete, not used in the phylogeny tree
						XP_0336293	NC_047067.1 (68809..89316, com	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0336279	NC_047066.1 (13148097..131927	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
Bat star	*Patiria miniata* (Pmin)	GRIA	no	Pmin_GluAalpha	Pmin_GluAα	XP_0380556	NW_024037059.1 (18129415..18	https://www.ncbi.nlm.nih.gov/	
			no	Pmin_GluAbeta	Pmin_GluAβ	XP_0380556	NW_024037059.1 (18100099..18	https://www.ncbi.nlm.nih.gov/	
		GRID	no	Pmin_GluD	Pmin_GluD	XP_0380538	NW_024037058.1 (8086450..814	https://www.ncbi.nlm.nih.gov/	
		GRIK	no	Pmin_GluK	Pmin_GluK	XP_0380593	NW_024037061.1 (1310703..139	https://www.ncbi.nlm.nih.gov/	
		GRIN	no	Pmin_GluN1	Pmin_GluN1	XP_0380740	NW_024037072.1 (6425136..644	https://www.ncbi.nlm.nih.gov/	
			no	Pmin_GluN3	Pmin_GluN3	XP_0380559	NW_024037059.1 (22434276..22	https://www.ncbi.nlm.nih.gov/	
		GRIH	no	Pmin_GluHA	Pmin_GluHA	XP_0380680	NW_024037048.1 (10246250..10	https://www.ncbi.nlm.nih.gov/	
			no	Pmin_GluHB	Pmin_GluHB	XP_0380680	NW_024037048.1 (10295979..10	https://www.ncbi.nlm.nih.gov/	
			no	Pmin_GluHC	Pmin_GluHC	XP_0380680	NW_024037048.1 (10267726..10	https://www.ncbi.nlm.nih.gov/	
						XP_0380556	NW_024037059.1 (18100099..18	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0380596	NW_024037061.1 (1467757..150	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0380538	NW_024037058.1 (8086450..814	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0380538	NW_024037058.1 (8086450..814	https://www.ncbi.nlm.nih.gov/	incomplete, not used in the phylogeny tree
						XP_0380538	NW_024037058.1 (8086450..814	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0380538	NW_024037058.1 (8086450..814	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
						XP_0380538	NW_024037058.1 (8086450..814	https://www.ncbi.nlm.nih.gov/	incomplete, not used in the phylogeny tree
						XP_0380680	NW_024037048.1 (10295979..10	https://www.ncbi.nlm.nih.gov/	duplicate isoform, not used in the phylogeny tree
Crinoidea									
Sea lily	*Anneissia japonica* (Ajap)	GRIA	no	Anja_GluA	Anja_GluA	XP_0331129	NW_022727261.1 (121928..1487	https://www.ncbi.nlm.nih.gov/genome	
		GRID	no	Anja_GluD	Anja_GluD	XP_0331115	NW_022724789.1 (680940..7437	https://www.ncbi.nlm.nih.gov/genome	
		GRIK	no	Anja_GluKalpha	Anja_GluKα	XP_0331133	NW_022727891.1 (594063..5979	https://www.ncbi.nlm.nih.gov/genome	
			no	Anja_GluKbeta	Anja_GluKβ	XP_0331133	NW_022727891.1 (539465..5844	https://www.ncbi.nlm.nih.gov/genome	
		GRIH	no	Anja_GluE1	Anja_GluE1	XP_0331076	NW_022715822.1 (1335330..134	https://www.ncbi.nlm.nih.gov/genome	
			no	Anja_GluE2	Anja_GluE2	XP_0330978	NW_022696345.1 (1486621..150	https://www.ncbi.nlm.nih.gov/genome	
		GRIN	no	Anja_GluN1	Anja_GluN1	XP_0331149	NW_022686322.1 (1531297..155	https://www.ncbi.nlm.nih.gov/genome	
			no	Anja_GluN3	Anja_GluN3	XP_0331139	NW_022728604.1 (483880..5137	https://www.ncbi.nlm.nih.gov/genome	
		GRIH	no	Anja_GluHB1	Anja_GluHB1	XP_0331104	NW_022685600.1 (349913..3679	https://www.ncbi.nlm.nih.gov/genome	
			no	Anja_GluHB2	Anja_GluHB2	XP_0331104	NW_022685600.1 (266299..2750	https://www.ncbi.nlm.nih.gov/genome	
Echinoidea									
Purple Sea Urchin	*Strongylocentrotus purpura*	GRIA	GluA1-4alpha_Sp	Spur_GluAalpha	Spur_GluAα	LOC1159221	AAGJ06000011.1:22397727-2241	https://metazoa.ensembl.org/index.html	
			GluA-14beta_Spu	Spur_GluAbeta	Spur_GluAβ	LOC590116	AAGJ06000011.1:22480884-2249	https://metazoa.ensembl.org/index.html	
		GRID	GluD1-2_Spu	Spur_GluD	Spur_GluD	LOC582183	AAGJ06000002.1:35758381-3577	https://metazoa.ensembl.org/index.html	
		GRIK	GluK1-5alpha_Sp	Spur_GluKalpha	Spur_GluKα	LOC579779	AAGJ06000021.1:3867690-39068	https://metazoa.ensembl.org/index.html	
			GluK1-5beta_Spu	Spur_GluKbeta	Spur_GluKβ	LOC584569	AAGJ06000021.1:4053314-40573	https://metazoa.ensembl.org/index.html	
		GRIH	GluF3_Spu	Spur_GluHA1	Spur_GluHA1	LOC577098	AAGJ06000009.1:7696207-77031	https://metazoa.ensembl.org/index.html	
			no	Spur_GluHA2	Spur_GluHA2	LOC591955	AAGJ06000009.1:7672908-76779	https://metazoa.ensembl.org/index.html	
			GluF1_Spu	Spur_GluHB	Spur_GluHB	LOC587837	AAGJ06000009.1:7581266-75974	https://metazoa.ensembl.org/index.html	
			no	Spur_GluHC1	Spur_GluHC1	LOC1008885	AAGJ06000009.1:7620611-76291	https://metazoa.ensembl.org/index.html	
			GluF2_Spu	Spur_GluHC2	Spur_GluHC2	LOC591929	AAGJ06000009.1:7664586-76699	https://metazoa.ensembl.org/index.html	
						LOC590116	AAGJ06000011.1:22480884-2249	https://metazoa.ensembl.org/index.html	incomplete, not used in the phylogeny
						LOC584569	AAGJ06000021.1:4047345-40533	https://metazoa.ensembl.org/index.html	incomplete, not used in the phylogeny
						LOC579779	AAGJ06000021.1:3905593-39068	https://metazoa.ensembl.org/index.html	incomplete, not used in the phylogeny
Green sea urchin	*Lytechinus variegatus* (Lva	GRIA	no	Lvar_GluAalpha1	Lvar_GluAαα	XP_0414529	NC_054740.1 (13404205..134376	https://www.ncbi.nlm.nih.gov/genome	
			no	Lvar_GluAalpha2	Lvar_GluAαβ	XP_0414528	NC_054740.1 (13372822..134000	https://www.ncbi.nlm.nih.gov/genome	
			no	Lvar_GluAbeta	Lvar_GluAβ	XP_0414639	NC_054740.1 (44421088..444508	https://www.ncbi.nlm.nih.gov/genome	
		GRID	no	Lvar_GluD	Lvar_GluD	XP_0414536	NC_054741.1 (47856962..479019	https://www.ncbi.nlm.nih.gov/genome	
		GRIK	no	Lvar_GluKalpha	Lvar_GluKα	XP_0414628	NC_054743.1 (33882748..339206	https://www.ncbi.nlm.nih.gov/genome	
			no	Lvar_GluKbeta	Lvar_GluKβ	XP_0414616	NC_054743.1 (34069994..341429	https://www.ncbi.nlm.nih.gov/genome	
		GRIH	no	Lvar_GluHA1	Lvar_GluHA1	XP_0414648	NC_054744.1 (18534510..185572	https://www.ncbi.nlm.nih.gov/genome	
			no	Lvar_GluHA2	Lvar_GluHA2	XP_0414648	NC_054744.1 (18559749..185749	https://www.ncbi.nlm.nih.gov/genome	
			no	Lvar_GluHB	Lvar_GluHB	XP_0414648	NC_054744.1 (18663422..186826	https://www.ncbi.nlm.nih.gov/genome	
			no	Lvar_GluHC1	Lvar_GluHC1	XP_0414648	NC_054744.1 (18620384..186320	https://www.ncbi.nlm.nih.gov/genome	
			no	Lvar_GluHC2	Lvar_GluHC2	XP_0414648	NC_054744.1 (18580727..185989	https://www.ncbi.nlm.nih.gov/genome	
						XP_0414530	NC_054740.1 (13404205..134376	https://www.ncbi.nlm.nih.gov/genome	
						XP_0414628	NC_054743.1 (33882748..339206	https://www.ncbi.nlm.nih.gov/genome	
Slate pencil urchin	*Eucidaris tribuloides* (Etri)	GRID	no	Etri_GluD	Etri_GluD	JZLH010691	JZLH010691282 (1..11763)	https://www.ncbi.nlm.nih.gov/genome	
		GRIK	no	Etri_GluKalpha1	Etri_GluKαα	JZLH010022	JZLH010022638 (1..13832)	https://www.ncbi.nlm.nih.gov/genome	
			no	Etri_GluKalpha2	Etri_GluKαβ	JZLH010565	JZLH010565238 (1..34221)	https://www.ncbi.nlm.nih.gov/genome	
			no	Etri_GluKbeta1	Etri_GluKβα	JZLH010645	JZLH010645942 (1..17728)	https://www.ncbi.nlm.nih.gov/genome	
			no	Etri_GluK6beta2	Etri_GluKββ	JZLH010008	JZLH010008682 (1..20059)	https://www.ncbi.nlm.nih.gov/genome	
		GRIH	no	Etri_GluHA1	Etri_GluHA1	JZLH010852	JZLH010852176 (1..11688)	https://www.ncbi.nlm.nih.gov/genome	
			no	Etri_GluHA2	Etri_GluHA2	JZLH010262	JZLH010262813 (1..3230)	https://www.ncbi.nlm.nih.gov/genome	
			no	Etri_GluHB1	Etri_GluHB1	JZLH010983	JZLH010983046 (1..3230)	https://www.ncbi.nlm.nih.gov/genome	
			no	Etri_GluHB2	Etri_GluHB2	JZLH010983	JZLH010983041 (1..17568)	https://www.ncbi.nlm.nih.gov/genome	
			no	Etri_GluHB3	Etri_GluHB3	JZLH010933	JZLH010933744 (1..13956)	https://www.ncbi.nlm.nih.gov/genome	
			no	Etri_GluHB4	Etri_GluHB4	JZLH010925	JZLH010925198 (1..14354)	https://www.ncbi.nlm.nih.gov/genome	
			no	Etri_GluHC1	Etri_GluHC1α	JZLH010149	JZLH010149178 (1..19889)	https://www.ncbi.nlm.nih.gov/genome	
			no	Etri_GluHC2	Etri_GluHC1β	JZLH010262	JZLH010262812 (1..6862)	https://www.ncbi.nlm.nih.gov/genome	
Holothuroidea									
Japanese Sea Cucum	*Apostichopus japonicus* (A	GRIA	no	Ajap_GluAalpha1	Ajap_GluAαα	PIK34935.1	MRZV01002035.1:41474..45981	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluAalpha2	Ajap_GluAαβ	PIK47807.1	MRZV01000557.1:199055..20608	https://www.ncbi.nlm.nih.gov/	
		GRID	no	Ajap_GluD	Ajap_GluD	PIK38974.1	MRZV01001294.1:3075..42649	https://www.ncbi.nlm.nih.gov/	
		GRIK	no	Ajap_GluKalpha1	Ajap_GluKαα	PIK52280.1	MRZV01000336.1:753408..76076	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluKalpha2	Ajap_GluKαβ	PIK52281.1	MRZV01000336.1:761677..76454	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluKbeta	Ajap_GluKβ	PIK39976.1	MRZV01001179.1:81722..84891	https://www.ncbi.nlm.nih.gov/	
		GRIH	no	Ajap_GluHA	Ajap_GluHA	PIK48933.1	MRZV01000492.1:265091..27280	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluHB1	Ajap_GluHB1	PIK37299.1	MRZV01001523.1:9101..15901	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluHB2	Ajap_GluHB2	PIK37298.1	MRZV01001523.1:5518..8285	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluHB3	Ajap_GluHB3	PIK48929.1	MRZV01000492.1:195209..20056	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluHC1	Ajap_GluHC1	PIK48931.1	MRZV01000492.1:233381..24372	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluHC2	Ajap_GluHC2	PIK48932.1	MRZV01000492.1:250506..26087	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluHC3	Ajap_GluHC3	PIK48930.1	MRZV01000492.1:211914..22317	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluHC4	Ajap_GluHC4	PIK40199.1	MRZV01001152.1:190046..19076	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluHC5	Ajap_GluHC5	PIK39600.1	MRZV01001222.1:280788..29089	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluHC6	Ajap_GluHC6	PIK40198.1	MRZV01001152.1:170275..17109	https://www.ncbi.nlm.nih.gov/	
			no	Ajap_GluHC7	Ajap_GluHC7	PIK39599.1	MRZV01001222.1:261799..26429	https://www.ncbi.nlm.nih.gov/	
						PIK47807.1	MRZV01000557.1:198490..20608	https://www.ncbi.nlm.nih.gov/	Duplicate, not used in phylogeny
						PIK39977.1	81722-84891	https://www.ncbi.nlm.nih.gov/	Incomplete, not used in the phylogeny
Sea Cucumber	*Holothuria arguinesis* (Har	GRIA	no	Harg_GluAalpha	Harg_GluAα	NR_TRINITY_DN57842_c0_g1_i5		Internal trancriptome database	

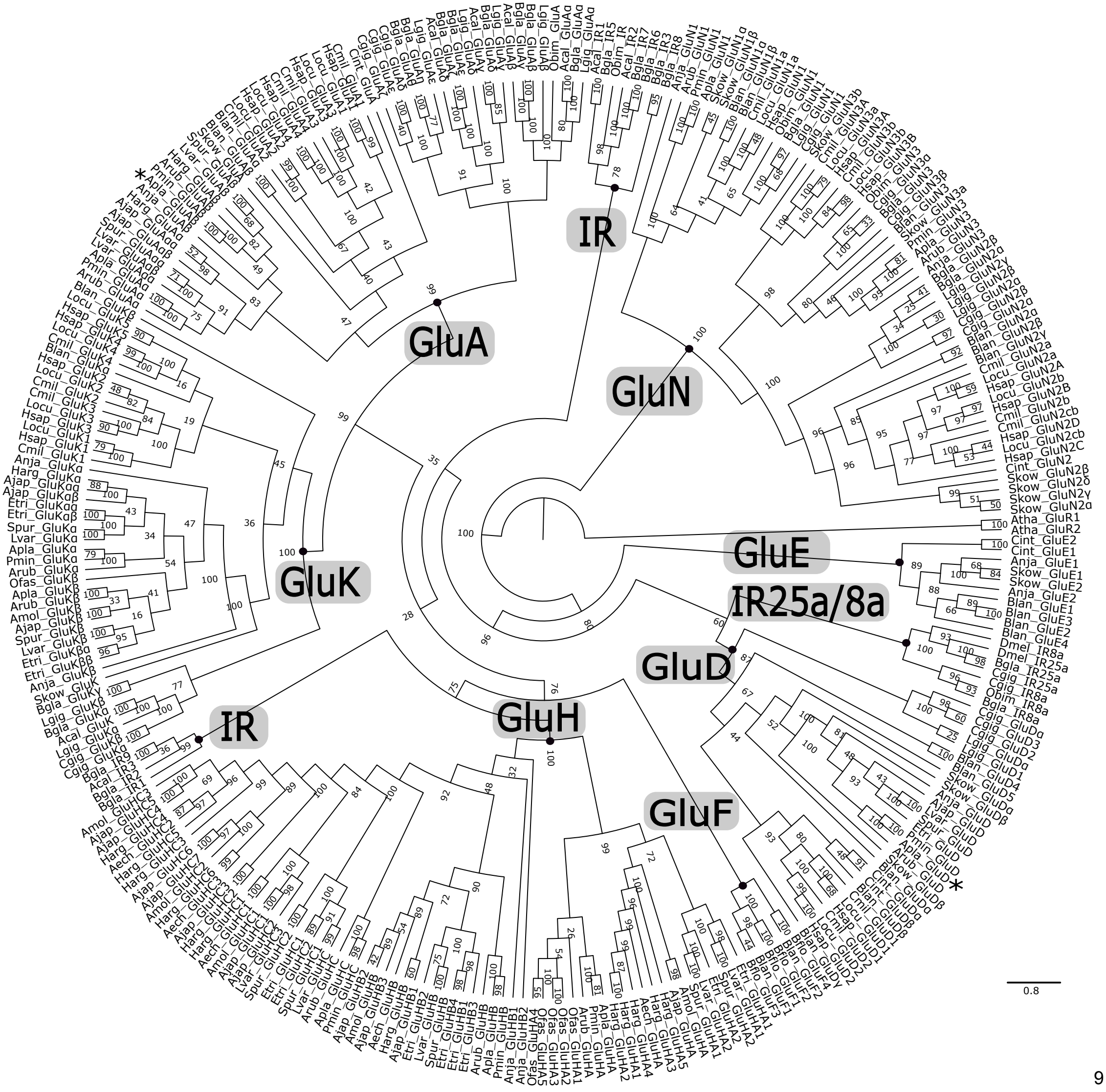
			no	Harg_GluAbeta	Harg_GluAβ	NR_TRINITY_DN44472_c0_g1_i8		Internal trancriptome database	
		GRIK	no	Harg_GluK	Harg_GluK	NR_TRINITY_DN129460_c0_g1_i2		Internal trancriptome database	
		GRIH	no	Harg_GluHA1	Harg_GluHA1	NR_TRINITY_DN7587_c0_g1_i18		Internal trancriptome database	
			no	Harg_GluHA2	Harg_GluHA2	T_TRINITY_DN3736_c0_g1_i12		Internal trancriptome database	
			no	Harg_GluHA3	Harg_GluHA3	RN_TRINITY_DN78_c0_g1_i1		Internal trancriptome database	
			no	Harg_GluHA4	Harg_GluHA4	NR_TRINITY_DN223_c0_g1_i1		Internal trancriptome database	
			no	Harg_GluHA5	Harg_GluHA5	T_TRINITY_DN31_c0_g1_i4		Internal trancriptome database	
			no	Harg_GluHB	Harg_GluHB	NR_TRINITY_DN490_c1_g1_i4		Internal trancriptome database	
			no	Harg_GluHC1	Harg_GluHC1	NR_TRINITY_DN9010_c1_g1_i1		Internal trancriptome database	
			no	Harg_GluHC2	Harg_GluHC2	NR_TRINITY_DN349_c6_g1_i1		Internal trancriptome database	
			no	Harg_GluHC3	Harg_GluHC3	NR_TRINITY_DN26271_c1_g1_i2		Internal trancriptome database	
			no	Harg_GluHC4	Harg_GluHC4	NR_TRINITY_DN3739_c7_g1_i6		Internal trancriptome database	
			no	Harg_GluHC5	Harg_GluHC5	RN_TRINITY_DN26352_c0_g1_i2		Internal trancriptome database	
			no	Harg_GluHC6	Harg_GluHC6	T_TRINITY_DN50453_c0_g1_i8		Internal trancriptome database	
Brownmottled Sea Cu	*Australostichopus mollis* (A	GRIK	no	Amol_GluKbeta	Amol_GluKβ	CZPJ013660	CZPJ013660839 (1..663)	https://www.ncbi.nlm.nih.gov/genome	
		GRIH	no	Amol_GluHA	Amol_GluHA	CZPJ010446	CZPJ010446713 (1..2173)	https://www.ncbi.nlm.nih.gov/genome	
			no	Amol_GluHB	Amol_GluHB	CZPJ010304	CZPJ010304634 (1..2476)	https://www.ncbi.nlm.nih.gov/genome	
			no	Amol_GluHC2	Amol_GluHC2	CZPJ010091	CZPJ010091109 (1..2476)	https://www.ncbi.nlm.nih.gov/genome	
			no	Amol_GluHC3	Amol_GluHC3	CZPJ010556	CZPJ010556346 (1..2351)	https://www.ncbi.nlm.nih.gov/genome	
			no	Amol_GluHC1	Amol_GluHC1	CZPJ013710	CZPJ013710743 (1..2133)	https://www.ncbi.nlm.nih.gov/genome	
						CZPJ013673	CZPJ013673689 (1..742)	https://www.ncbi.nlm.nih.gov/genome	incomplete, not used in the phylogeny
						CZPJ010023	CZPJ010023488 (1..700)	https://www.ncbi.nlm.nih.gov/genome	incomplete, not used in the phylogeny
Brown Sea Cucumber	*Actinopyga echinites* (Aech)		no	Aech_GluHA	Aech_GluHA	JAAAJZ0100	JAAAJZ010029366 (1..4223)	https://www.ncbi.nlm.nih.gov/genome	
			no	Aech_GluHB	Aech_GluHB	JAAAJZ0101	JAAAJZ010112060 (1..2092)	https://www.ncbi.nlm.nih.gov/genome	
			no	Aech_GluHC1	Aech_GluHC1	JAAAJZ0100	JAAAJZ010038813 (1..3744)	https://www.ncbi.nlm.nih.gov/genome	
			no	Aech_GluHC2	Aech_GluHC2	JAAAJZ0100	JAAAJZ010023183 (1..4635)	https://www.ncbi.nlm.nih.gov/genome	
			no	Aech_GluHC3	Aech_GluHC3	JAAAJZ0103	JAAAJZ010302834 (1..869)	https://www.ncbi.nlm.nih.gov/genome	
						JAAAJZ0101	JAAAJZ010197470 (1..1350)	https://www.ncbi.nlm.nih.gov/genome	incomplete, not used in the phylogeny
						JAAAJZ0100	JAAAJZ010029072 (1..4240)	https://www.ncbi.nlm.nih.gov/genome	incomplete, not used in the phylogeny
Ophiuroidea									
The mottled brittle star	*Ophionereis fasciata* (Ofa	GRIK	no	Ofas_GluK	Ofas_GluK	CZLG013965	CZLG013965567 (1…1233)	https://www.ncbi.nlm.nih.gov/genome	
		GRIH	no	Ofas_GluHA1	Ofas_GluHA1	CZLG010785	CZLG010785388 (1..2707)	https://www.ncbi.nlm.nih.gov/genome	
			no	Ofas_GluHA2	Ofas_GluHA2	CZLG010932	CZLG010932769 (1..2448)	https://www.ncbi.nlm.nih.gov/genome	
			no	Ofas_GluHA3	Ofas_GluHA3	CZLG010888	CZLG010888509 (1..2070)	https://www.ncbi.nlm.nih.gov/genome	
			no	Ofas_GluHA4	Ofas_GluHA4	CZLG013961	CZLG013961094 (1..938)	https://www.ncbi.nlm.nih.gov/genome	
			no	Ofas_GluHA5	Ofas_GluHA5	CZLG010035	CZLG010035912 (1..2695)	https://www.ncbi.nlm.nih.gov/genome	
MOLLUSCA									
Bivalvia									
Pacific Oyster	*Crassostrea gigas* (Cgig)	GRIA	Gria1-4δ_Cgi	Cgig_GluAdelta	Cgig_GluAδ	K1PLD5	scaffold42946: 16,674-26,489	https://metazoa.ensembl.org/index.html	
			Gria1-4ε_Cgi	Cgig_GluAepsilon	Cgig_GluAε	K1P308	scaffold43986: 326,358-336,597	https://metazoa.ensembl.org/index.html	
			Gria1-4ζ_Cgi	Cgig_GluAzeta	Cgig_GluAζ	K1P9R4	scaffold43986: 337,997-346,778	https://metazoa.ensembl.org/index.html	
		GRID	GluD12_Cgi	Cgig_GluDalpha	Cgig_GluDα	K1QI71	scaffold471: 442,338-488,954	https://metazoa.ensembl.org/index.html	
			no	Cgig_GluDbeta	Cgig_GluDβ	K1PFG5	scaffold36654: 23,129-30,429	https://metazoa.ensembl.org/index.html	
			no	Cgig_GluDgamma	Cgig_GluDγ	K1P4N0	scaffold43692: 284,177-291,872	https://metazoa.ensembl.org/index.html	
		GRIK	no	Cgig_GluKalpha	Cgig_GluKα	K1PEX2	scaffold42446: 112,794-122,029	https://metazoa.ensembl.org/index.html	
			Grik1-5β_Cgi	Cgig_GluKbeta	Cgig_GluKβ	K1P8R9	scaffold42446: 86,134-106,331	https://metazoa.ensembl.org/index.html	
			Grik1-5γ_Cgi	Cgig_GluKgamma	Cgig_GluKδ	K1P0Y9	C31694: 3,285-9,162	https://metazoa.ensembl.org/index.html	
		GRIN	no	Cgig_GluN1	Cgig_GluN1	K1P6C7	scaffold43272: 3,505-21,132	https://metazoa.ensembl.org/index.html	
			no	Cgig_GluN2alpha	Cgig_GluN2α	K1QZX0	scaffold619: 384,024-405,859	https://metazoa.ensembl.org/index.html	
			no	Cgig_GluN2beta	Cgig_GluN2β	K1Q588	scaffold1227: 9,079-28,834	https://metazoa.ensembl.org/index.html	
			no	Cgig_GluN3alpha	Cgig_GluN3α	K1Q117	scaffold1108: 192,027-208,601	https://metazoa.ensembl.org/index.html	
			no	Cgig_GluN3beta	Cgig_GluN3β	K1Q881	scaffold1108: 210,097-214,282	https://metazoa.ensembl.org/index.html	
		IR	no	Cgig_IR1	Cgig_IR1	K1R0W8	scaffold20: 344,918-350,470	https://metazoa.ensembl.org/index.html	
		IR8a	no	Cgig_IR8a	Cgig_IR8a	K1QAS7	scaffold43692: 277,982-283,141	https://metazoa.ensembl.org/index.html	
		IR25a	no	Cgig_IR25a	Cgig_IR25a	K1RKV0	scaffold77: 1,551,701-1,563,941	https://metazoa.ensembl.org/index.html	
Gastropoda									
Owl Limpet	*Lottia gigantea* (Lgig)	GRIA	GluA1-4alpha_Lg	Lgig_GluAalpha	Lgig_GluAα	LotgiG112937	LOTGlsca_16:2228655-2237064	https://metazoa.ensembl.org/index.html	
			GluA1-4beta_Lgi	Lgig_GluAbeta	Lgig_GluAβ	LotgiG163822	LOTGlsca_42:615631-631669	https://metazoa.ensembl.org/index.html	
			GluA1-4gamma_l	Lgig_GluAgamma	Lgig_GluAγ	LotgiG213266	LOTGlsca_16:2277895-2292980	https://metazoa.ensembl.org/index.html	
			GluA1-4delta_Lgi	Lgig_GluAdelta	Lgig_GluAδ	LotgiG122838	LOTGlsca_42:701198-733348	https://metazoa.ensembl.org/index.html	
			GluA1-4epsilon_L	Lgig_GluAepsilon	Lgig_GluAε	LotgiG123068	LOTGlsca_42:648458-666006	https://metazoa.ensembl.org/index.html	
		GRID	GluD1-2alpha_Lg	Lgig_GluDalpha	Lgig_GluDα	LotgiG110566	LOTGlsca_11:2855774-2858511	https://metazoa.ensembl.org/index.html	
			GluD1-2beta_Lgi	Lgig_GluDbeta	Lgig_GluDβ	LotgiG110473	LOTGlsca_11:2833664-2835064	https://metazoa.ensembl.org/index.html	
		GRIK	GluK1-5alpha_Lg	Lgig_GluKalpha	Lgig_GluKα	LotgiG233226	LOTGlsca_36:1167929-1188128	https://metazoa.ensembl.org/index.html	
			GluK1-5beta_Lgi	Lgig_GluKbeta	Lgig_GluKβ	otgiG121144	LOTGlsca_36:791999-818963	https://metazoa.ensembl.org/index.html	
		GRIN	GluN1_Lgi	Lgig_GluN1	Lgig_GluN1	LotgiG108357	LOTGlsca_8:2996437-3004241	https://metazoa.ensembl.org/index.html	
			GluN2ADalpha_L	Lgig_GluN2alpha	Lgig_GluN2α	LotgiG131225	LOTGlsca_73:201590-219140	https://metazoa.ensembl.org/index.html	
			GluN2ADbeta_Lg	Lgig_GluN2beta	Lgig_GluN2β	LotgiG107328	LOTGlsca_6:2439368-2455077	https://metazoa.ensembl.org/index.html	
			GluN2ADgamma	Lgig_GluN2gamma	Lgig_GluN2γ	LotgiG137890	LOTGlsca_119:129815-150884	https://metazoa.ensembl.org/index.html	
California sea hare	*Aplysia californica* (Acal)	GRIA	no	Acal_GluAalpha	Acal_GluAα	NP_0011915	NW_004797339.1 (1871914..192	https://www.ncbi.nlm.nih.gov/	
			no	Acal_GluAbeta	Acal_GluAβ	NP_0011915	NW_004797327.1	https://www.ncbi.nlm.nih.gov/	
			no	Acal_GluAgamma	Acal_GluAγ	NP_0011913	NW_004797327.1 (1915902..204	https://www.ncbi.nlm.nih.gov/	
			no	Acal_GluAdelta	Acal_GluAδ	AAP41206.1	NW_004797339.1 (1731434..184	https://www.ncbi.nlm.nih.gov/	
		GRIK	no	Acal_GluK	Acal_GluK	NP_0011915	NW_004797717.1 (460947..6566	https://www.ncbi.nlm.nih.gov/	
		IR	no	Acal_IR1	Acal_IR1	ACB05518.1	NW_004797578.1 (719823..7281	https://www.ncbi.nlm.nih.gov/	
			no	Acal_IR2	Acal_IR2	NP_0011915	NW_004797503.1 (478972..6345	https://www.ncbi.nlm.nih.gov/	
			no	Acal_IR3	Acal_IR3	NP_0011916	NW_004797503.1 (372556..3834	https://www.ncbi.nlm.nih.gov/	
Freshwater Snail	*Biomphalaria glabrata* (Bg	GRIA	no	Bgla_GluAalpha	Bgla_GluAα	BGLB00471	Scaffold LGUN_random_Scaffold1264: 14	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluAbeta	Bgla_GluAβ	BGLB00471	Scaffold LGUN_random_Scaffold1264: 14	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluAgamma	Bgla_GluAγ	BGLB00396	Scaffold LGUN_random_Scaffold10516: 1	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluAdelta	Bgla_GluAδ	BGLB03567	Scaffold LGUN_random_Scaffold21456: 7	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluAepsilon	Bgla_GluAε	BGLB00777	Scaffold LGUN_random_Scaffold2528: 9,4	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluAzeta	Bgla_GluAζ	BGLB01786	Scaffold LG74i_random_Scaffold326: 135	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluAeta	Bgla_GluAη	BGLB01119	Scaffold LGUN_random_Scaffold5378: 31	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluAteta	Bgla_GluAθ	BGLB01119	Scaffold LGUN_random_Scaffold5378: 31	https://metazoa.ensembl.org/index.html	
		GRIK	no	Bgla_GluKalpha	Bgla_GluKα	BGLB04024	Scaffold LGUN_random_Scaffold673: 83,4	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluKbeta	Bgla_GluKβ	BGLB01659	Scaffold LGUN_random_Scaffold673: 457	https://metazoa.ensembl.org/index.html	
		GRIN	no	Bgla_GluN1	Bgla_GluN1	BGLB00672	Scaffold LGUN_random_Scaffold192: 178	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluN2alpha	Bgla_GluN2α	BGLB00985	Scaffold LGUN_random_Scaffold4118: 8-;	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluN2beta	Bgla_GluN2β	BGLB00613	Scaffold LGUN_random_Scaffold1714: 39	https://metazoa.ensembl.org/index.html	
			no	Bgla_GluN3	Bgla_GluN3	BGLB00658	Scaffold LGUN_random_Scaffold19: 39,3	https://metazoa.ensembl.org/index.html	
		IR	no	Bgla_IR1	Bgla_IR1	BGLB02371	Scaffold LGUN_random_Scaffold9807: 23	https://metazoa.ensembl.org/index.html	
			no	Bgla_IR2	Bgla_IR2	BGLB02629	Scaffold LGUN_random_Scaffold1846: 54	https://metazoa.ensembl.org/index.html	
			no	Bgla_IR4	Bgla_IR4	BGLB03705	Scaffold LGUN_random_Scaffold2305: 5,;	https://metazoa.ensembl.org/index.html	
			no	Bgla_IR5	Bgla_IR5	BGLB02875	Scaffold LGUN_random_Scaffold17788: 2	https://metazoa.ensembl.org/index.html	
			no	Bgla_IR6	Bgla_IR6	BGLB03561	Scaffold LG68i_random_Scaffold390: 44,3	https://metazoa.ensembl.org/index.html	
			no	Bgla_IR7	Bgla_IR7	BGLB01681	Scaffold LGUN_random_Scaffold543: 6,1	https://metazoa.ensembl.org/index.html	
			no	Bgla_IR8	Bgla_IR8	BGLB01681	Scaffold LGUN_random_Scaffold543: 6,1	https://metazoa.ensembl.org/index.html	
			no	Bgla_IR9	Bgla_IR9	BGLB038737	Scaffold LGUN_random_Scaffold1	https://metazoa.ensembl.org/index.html	
		IR8a	no	Bgla_IR8a	Bgla_IR8a	BGLB008642	Scaffold LGUN_random_Scaffold3	https://metazoa.ensembl.org/index.html	
		IR25a	no	BglaIR25a	BglaIR25a	BGLB00499	Scaffold LGUN_random_Scaffold1	https://metazoa.ensembl.org/index.html	
			no	Bgla_IR3	Bgla_IR3	BGLB02314	Scaffold LGUN_random_Scaffold28211: 4	https://metazoa.ensembl.org/index.html	incomplete, not used in the phylogeny
						BGLB017865	Scaffold LG74i_random_Scaffold3	https://metazoa.ensembl.org/index.html	incomplete, not used in the phylogeny
Cephalopoda									
Octopus	*Octopus bimaculoides* (Ob	GRIA	Gria1-4β_Obi	Obim_GluA	Obim_GluA	XP_0147762	NW_014669279.1	https://www.ncbi.nlm.nih.gov/	
		GRIN	no	Obim_GluN1	Obim_GluN1	XP_0147907	NW_014655921.1	https://www.ncbi.nlm.nih.gov/	
			no	Obim_GluN3	Obim_GluN3	XP_0147861	NW_014709056.1	https://www.ncbi.nlm.nih.gov/	
		IR	no	Obim_IR	Obim_IR	XP_0147687	NW_014658437.1	https://www.ncbi.nlm.nih.gov/	
		IR8a	no	Obim_IR8a	Obim_IR8a	XP_0147684	NW_014658114.1	https://www.ncbi.nlm.nih.gov/	
ARTHROPODA									
Insecta									
Drosophila	*Drosophila melano gaster* (	IR8a	no	Dmel_IR8a	Dmel_IR8a	NP_727328.1	NC_004354.4 (9232726..9236585	https://www.ncbi.nlm.nih.gov/	
		IR25a	no	Dmel_IR25a	Dmel_IR25a	NP_0012600	NT_033779.5 (4830846..4835300	https://www.ncbi.nlm.nih.gov/	
TRACHEOPHYTA									
Magnoliopsida									
Thale cress	*Arabidopsis thaliana* (Atha)		GLR2.7_Ath	Atha_GluR1	Atha_GluR1	NP_180476.3	2; NC_003071.7 (12511246..1251	https://www.ncbi.nlm.nih.gov/	
			GLR5_Ath	Atha_GluR2	Atha_GluR2	NP_565744.1	2; NC_003071.7 (13752263..1375	https://www.ncbi.nlm.nih.gov/	

Supplementary Table 3

Supplementary Table 3: List of accession numbers, genome location and positions of the neighbouring genes used in the gene synteny analysis

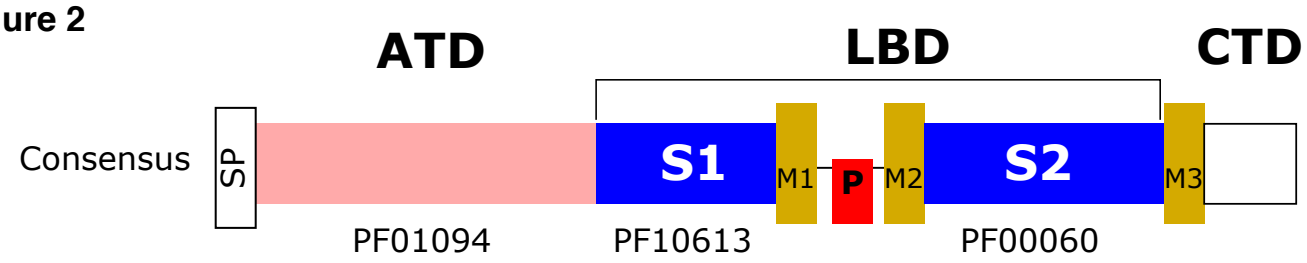
	Japanese sea cucumber (*Apostichopus japonicus*)			Purple sea urchin (*Strongylocentrotus purpuratus*)			Crown of thorne star fish (*Acanthaster planci*)			Spotted gar (*Lepisosteus oculatus*)			Human (*Homo sapiens*)		
Gene	*Genome Location*	Start-End (bp)	Accession number	*Genome Location*	Start-End	Accession number	*Location*	Start-End	Accession number	*Location*	Start-End	Accession number	*Location*	Start-End	Accession number
GRIH neigbouring genes															
TSNAX	*MRZV01001222.1*	125530-136944	PIK39595.1	*AAGJ06000005.1*	36546644-36547011	XP 011675196				*LG16*	4840088-4840411	ENSLOCG00000015831			
TEFA	*MRZV01001222.1*	171328-172074	PIK39596.1	*AAGJ06000005.1*	37497279-37497479	XP 785519.3				*LG12*	34852759-34852941	ENSLOCG00000011595			
MMP16	*MRZV01001152.1*	624-2976	PIK40193.1	*AAGJ06000005.1*	28802940-28812393	XP 030835865.1									
BSL78 22958	*MRZV01001152.1*	14313-17053	PIK40194.1	*AAGJ06000005.1*	26324063-26324263	XP 030854795.1									
BSL78 22959	*MRZV01001152.1*	36611-37180	PIK40195.1	*AAGJ06000005.1*	3864910-3866047	LOC100888199									
SLC3A1	*MRZV01001152.1*	149643-166564	PIK40197.1	*AAGJ06000005.1*	4353297-4361923	LOC586832	*NW 019091545.1*	2367041-2383862	XP 022090707	*LG16*	13349300-13349473	ENSLOCG00000016381			
	MRZV01001222.1	250617-258603	PIK39598.1												
SUB1	*MRZV01000492.1*	5605-10182	PIK48924.1	*AAGJ06000009.1*	26971506-26975199	LOC753210	*NW 019091545.1*	1666-15521	LOC110989948						
GNRHR2	*MRZV01000492.1*	106942-112819	PIK48926.1	*AAGJ06000009.1*	16614014-16614151	LOC100893259									
BCL-2-FAMILY	*MRZV01000492.1*	117043-121492	PIK48927.1	*AAGJ06000009.1*	30964326-30965866	LOC100888576									
TRESLIN-N-FAMILY	*MRZV01000492.1*	133825- 148428	PIK48928.1	*AAGJ06000009.1*	7555836-7557395	LOC587816									
GRIHB3	*MRZV01000492.1*	195209-195451	PIK48929.1												
GRIHC3	*MRZV01000492.1*	211914-211932	PIK48930.1												
GRIHC1	*MRZV01000492.1*	233381-233513	PIK48931.1	*AAGJ06000009.1*	7627396-7630159	LOC100888529									
GRIHC2	*MRZV01000492.1*	250506-250584	PIK48932.1	*AAGJ06000009.1*	7668333-7669407	LOC591929									
GRIHA1	*MRZV01000492.1*	265091-266275	PIK48933.1	*AAGJ06000009.1*	7671801-7689267	LOC591955									
GRIHC6	*MRZV01001152.1*	170275-171090	PIK40198.1												
GRIHC4	*MRZV01001152.1*	190046-190768	PIK40199.1												
GRIHB2	*MRZV01001523.1*	5518-8285	PIK37298.1												
GRIHB1	*MRZV01001523.1*	9101-15901	PIK37299.1	*AAGJ06000009.1*	7581036-7597985	XP 030832310.1									
GRIHC7	*MRZV01001222.1*	261799-264299	PIK39599.1												
GRIHC5	*MRZV01001222.1*	280788-290895	PIK39600.1												
GRIHA2				*AAGJ06000009.1*	7692187-7714828	LOC577098									
GRIHA							*NW 019091545.1*	519395-528141	LOC110987464						
GRIHB							*NW 019091545.1*	519395-528141	LOC110987464						
GRIHC							*NW 019091545.1*	496177-510704	LOC110987463						
grin3b										*LG19*	3399644-3456981	ENSLOCG00000001847			
grin2b										*LG12*	34852759-34852941	ENSLOCG00000011595			
arik2										*LG1*	39330996-39572025	ENSLOCG00000016542			
BSL78 14203	*MRZV01000492.1*	312495-317537	PIK48934.1	*AAGJ06000009.1*	7771928-7773611	LOC105436648	*NW 019091545.1*	537413-563436	LOC110987466						
SORD	*MRZV01000492.1*	322087-330491	PIK48935.1	*AAGJ06000009.1*	17303800-17316767	LOC585570									
FKBP8	*MRZV01000492.1*	344562-358115	PIK48936.1	*AAGJ06000009.1*	19639746-19649703	LOC587884				*LG19*	8070008-8077715	ENSLOCG00000005546			
ABHD17AA	*MRZV01000492.1*	372400-387419	PIK48937.1	*AAGJ06000009.1*	19668169-19675341	LOC578145				*LG19*	9472246-9472776	ENSLOCG00000006487			
SLC35F6	*MRZV01001222.1*	334537-360015	PIK39601.1	*AAGJ06000009.1*	32596228-32601277	LOC764872				*LG1*	31551123-31551632	ENSLOCG00000016385			
GRIK neigbouring genes															
ZUP1	*MRZV01001179.1*	34010-41230	PIK39973.1	*AAGJ06000021.1*	22798225-22811705	LOC100889729							*6*	116651571-116651729	ENSG00000153975
		42186-67938					*NW_019091512.1*						*6*	84155295-84155510	ENSG00000135315
CEP162	*MRZV01001179.1*		PIK39974.1	*AAGJ06000021.1*	4066257-4124716	LOC100891155		389284-409240	LOC110986160	*LG1*	40283291-40328761	ENSLOCG00000016570			
RAI14	*MRZV01000336.1*	481678-496009	PIK52271.1	*AAGJ06000009.1*	18613419-18613601	LOC591988									
CLPX	*MRZV01000336.1*	538918-549409	PIK52273.1	*AAGJ06000009.1*	17809631-17809961	LOC592972				*LG3*	44671596-44682072	ENSLOCG00000014110			
PDCD7	*MRZV01000336.1*	557773-564359	PIK52274.1	*AAGJ06000009.1*	29309645-29309771	LOC576277									
DDB1-CUL4	*MRZV01000336.1*	568781-575283	PIK52275.1	*AAGJ06000009.1*	30036123-30036333	LOC115920568									
ANKRA2	*MRZV01000336.1*	582671-587002	PIK52276.1												
RPS6	*MRZV01000336.1*	590817-595876	PIK52277.1	*AAGJ06000009.1*	28246778-28246991	LOC577989									
GRIK1							*NW 019091512.1*	217585-298061	LOC110986164	*LG3*	18095786-18186967	ENSLOCG00000009083	*21*	29536933-29940033	ENSG00000171189
GRIK2							*NW 019091512.1*	302221-387087	LOC110986162	*LG1*	39330996-39572025	ENSLOCG00000016542	*6*	101181257-102070083	ENSG00000164418
GRIK3										*LG6*	5090046-5202751	ENSLOCG00000003209	*1*	36795527-37034515	ENSG00000163873
GRIK4										*LG26*	1202411-1458215	ENSLOCG00000002001	*11*	120511700-120988904	ENSG00000149403
GRIK5										*LG24*	2031259-2041261	ENSLOCG00000004659	*19*	41998321-42069498	ENSG00000105737
GRIKαα	*MRZV01000336.1*	753408-760765	PIK52280.1												
GRIKαβ	*MRZV01000336.1*	761677-764541	PIK52281.1												
GRIKα				*AAGJ06000021.1*	3867690-3906867	LOC579779									
GRIKB	*MRZV01001179.1*	81722-84891	PIK39976.1	*AAGJ06000021.1*	4053314-4057344	LOC584569									
CE162	*MRZV01000336.1*	909539-912793	PIK52282.1				*NW 019091512.1*	389284-409240	LOC110986160						
ELOA	*MRZV01000336.1*	959541-965621	PIK52285.1	*AAGJ06000021.1*	4066905-4067105	LOC100891155				*LG6*	214038-226379	ENSLOCG00000000997			
	MRZV01001179.1	20018-29363	PIK39972.1												
BHMT	*MRZV01000336.1*	974209-997980	PIK52287.1	*AAGJ06000021.1*	13165885-13166144	LOC580174									
NAALAD2	*MRZV01000336.1*	999684-1018711	PIK52288.1	*AAGJ06000021.1*	18566523-18566703	LOC580576				*LG3*	11081044-11095735	ENSLOCG00000007231			
UPRT	*MRZV01000336.1*	1032931-1037363	PIK52289.1	*AAGJ06000021.1*	34367844-34368015	LOC575128									
RPS4X	*MRZV01000336.1*	1043144-1049783	PIK52290.1	*AAGJ06000021.1*	34377014-34377193	LOC583495							*19*	34092561-34093301	ENSG00000186008
BSL78 23185	*MRZV01001179.1*	231710-232591	PIK39980.1	*AAGJ06000009.1*	10608179-10608844	LOC115920572									
GRIA neigbouring genes															
GABRB3	*MRZV01000557.1*	91426-101624	PIK47806.1	*AAGJ06000011.1*	22517024-22543948	LOC105447122	*NW 019091385.1*	3227763-3262375	LOC110976879	*LG7*	22215052-22215219	ENSLOCG00000013757			
GRIAαα	*MRZV01000557.1*	198490-206081	PIK47807.1												
GRIAαβ	*MRZV01002035.1*	41474-45981	PIK34935.1												
GRIAα				*AAGJ06000011.1*	22397727-22418311	LOC115922114									
GRIAβ				*AAGJ06000011.1*	22417207-22418251	LOC590116									
GRIA2							*NW 019091385.1*	3206238-3227675	LOC110976878						
GRIA1							*NW 019091385.1*	3167439-3197004	LOC110976882						
gria3										*LG7*	38690001-38822115	ENSLOCG00000014528			
GABBR2	*MRZV01000557.1*	296948-314932	PIK47808.1	*AAGJ06000011.1*	28240012-31403455	LOC576813	*NW 019091385.1*	3109034-3159969	LOC110977020	*LG7*	23449687-23449773	ENSLOCG00000013865			
BSL78 15327	*MRZV01000557.1*	344427-350739	PIK47809.1	*AAGJ06000011.1*	31416780-31418200	LOC100890751				*LG7*	23459753-23459917	ENSLOCT00000017132			
PGK1	*MRZV01000557.1*	354590-360605	PIK47810.1	*AAGJ06000011.1*	31408989-31414295	LOC100890751									
GRID neigbouring genes															
FBXO39	*MRZV01001294*	10317-11189	PIK38972.1	*AAGJ06000002.1*	34701079-34702161	LOC105444533									
RDH13	*MRZV01001294*	21004-25403	PIK38973.1												
GRID	*MRZV01001294*	30759-42649	PIK38974.1	*AAGJ06000002.1*	35765352-35767961	LOC582183	*NW 019091383.1*	1596265-1650399	LOC110976589						
GRID1										*LG5*	15093769-15449890	ENSLOCG00000008385			
GRID2										*LG2*	55349903-55560392	ENSLOCG00000012893			
BSL78 24186	*MRZV01001294*	206644-207363	PIK38975.1												
BSL78 24187	*MRZV01001294*	216729-217931	PIK38976.1												
SBSPON	*MRZV01001294*	221280-224865	PIK38977.1	*AAGJ06000002.1*	5516744-5540108	LOC591641				*LG20*	2000147-2000296	ENSLOCG00000002314			
COBO	*MRZV01001294*	265529-267893	PIK38978.1	*AAGJ06000002.1*	5587334-5593382	LOC579282				*LG20*	6026097-6026189	ENSLOCG00000004341			

Supplementary Figure 1



Supplementary Figure 2

Holothuria arguinensis



GluH

GluHA

Harg_GluHA3 — SP — 905 aa

Harg_GluHA4 — SP — 900 aa

Harg_GluHA5 — SP — 904 aa

GluHB

Harg_GluHB — SP — 897 aa

GluHC

Harg_GluHC1 — SP — 895 aa

Harg_GluHC2 — SP — 909 aa

Harg_GluHC3 — SP — 897 aa

Harg_GluHC4 — SP — 904 aa

Harg_GluHC5 — SP — 905 aa

Harg_GluHC6 — SP — 904 aa

GluA

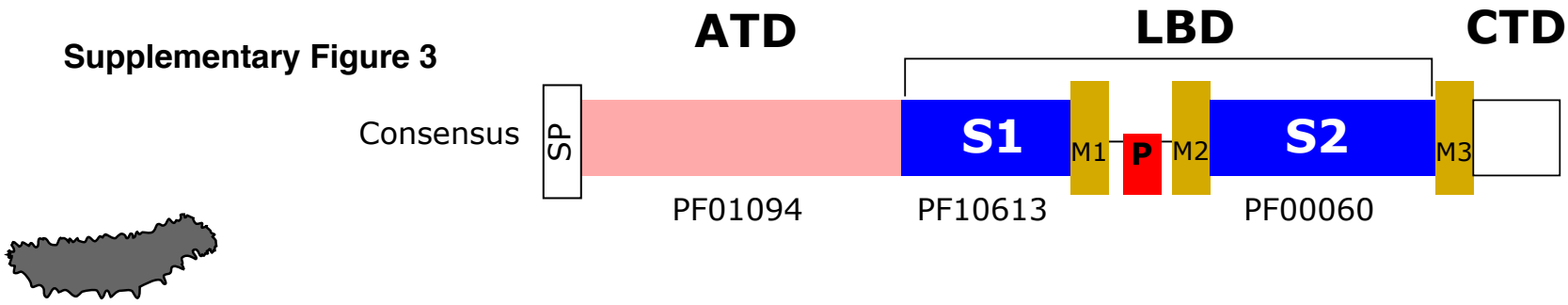
Harg_GluAα — SP — 804 aa

Harg_GluAβ — SP — 923 aa

GluK

Harg_GluK — 617 aa

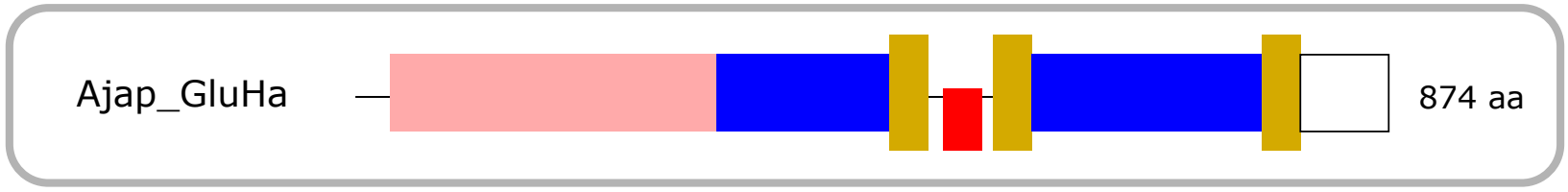
Supplementary Figure 3



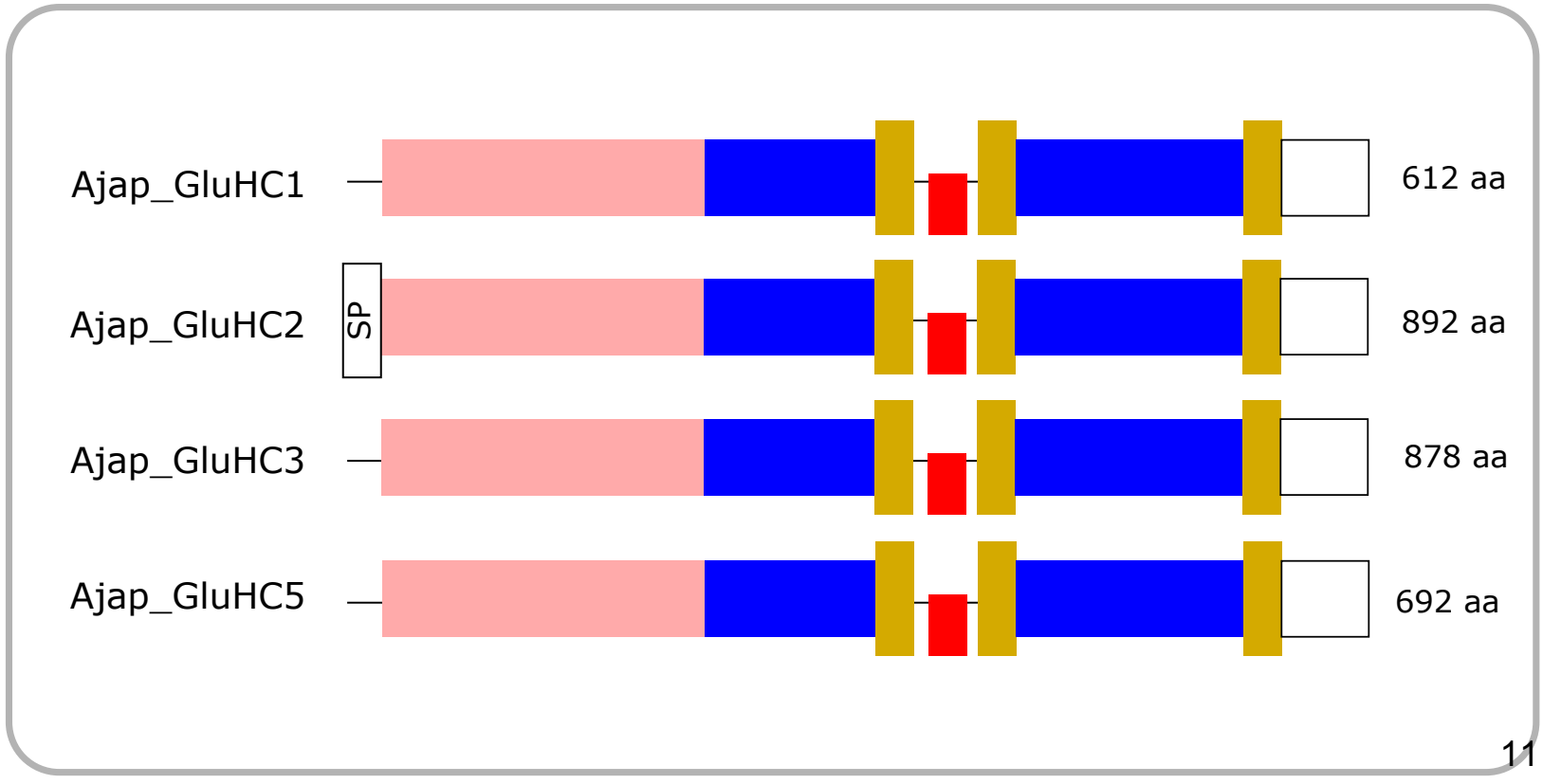
Apostichopus japonicus

GluH

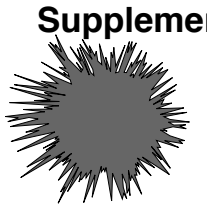
GluHA



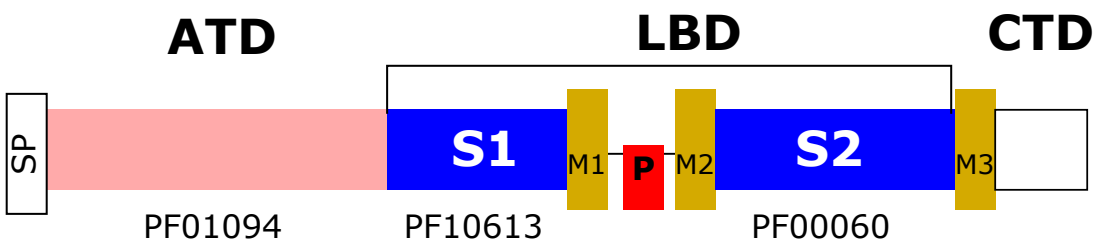
GluHC



Supplementary Figure 4



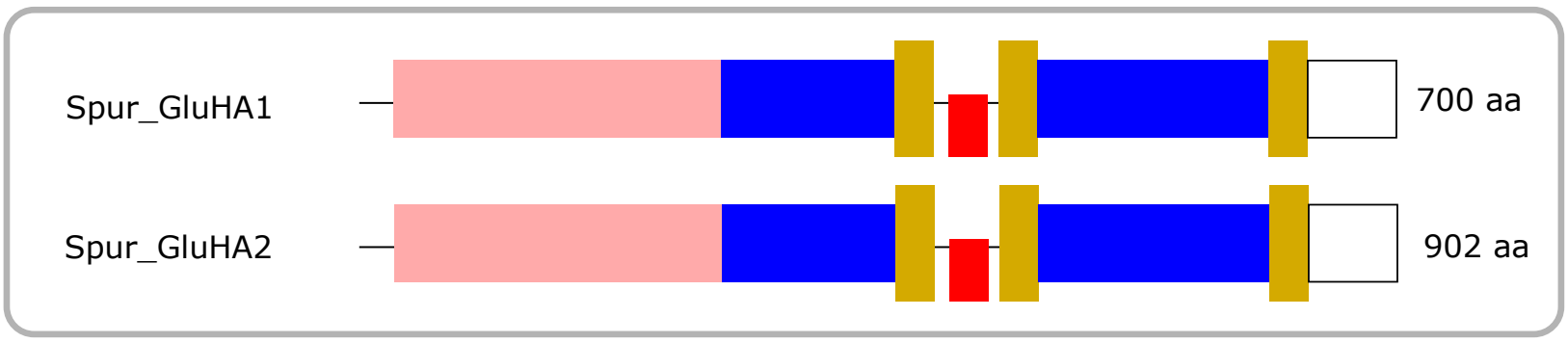
Consensus



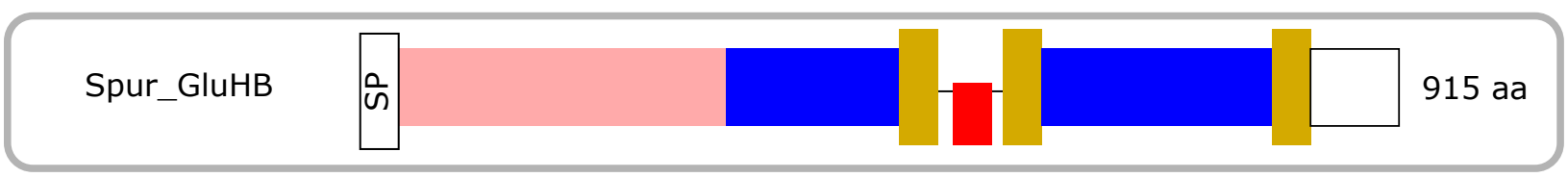
Strongylocentrotus purpuratus

GluH

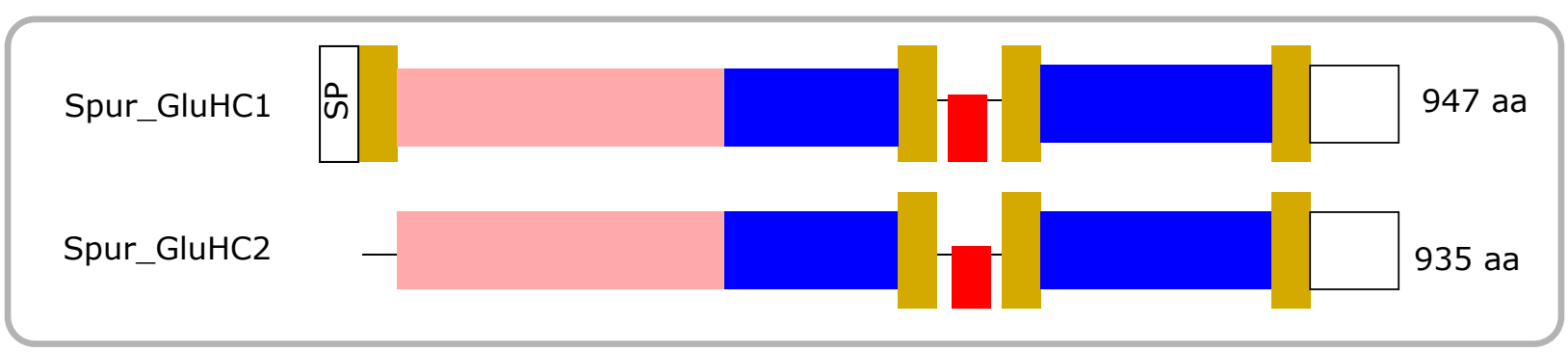
GluHA



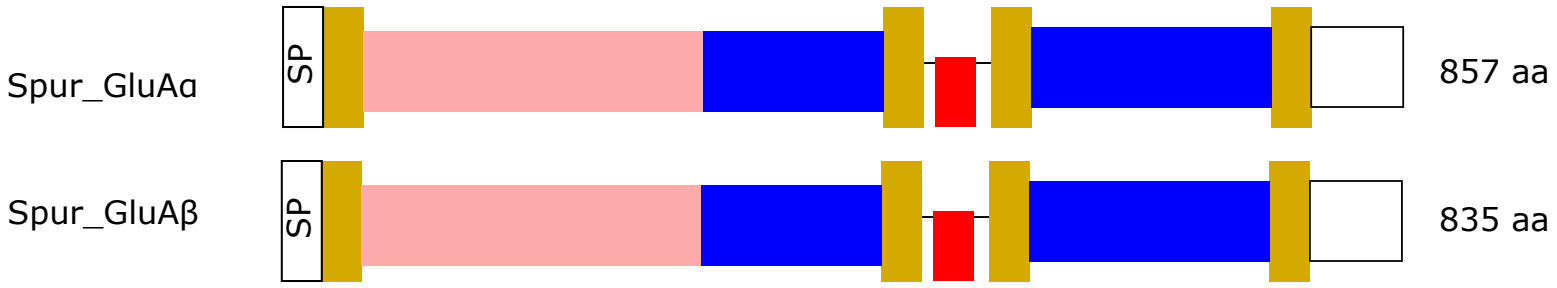
GluHB



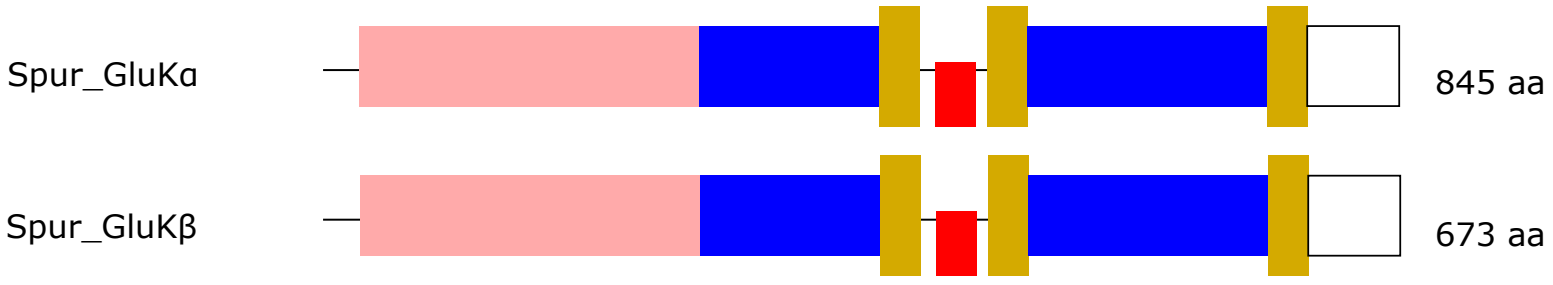
GluHC



GluA

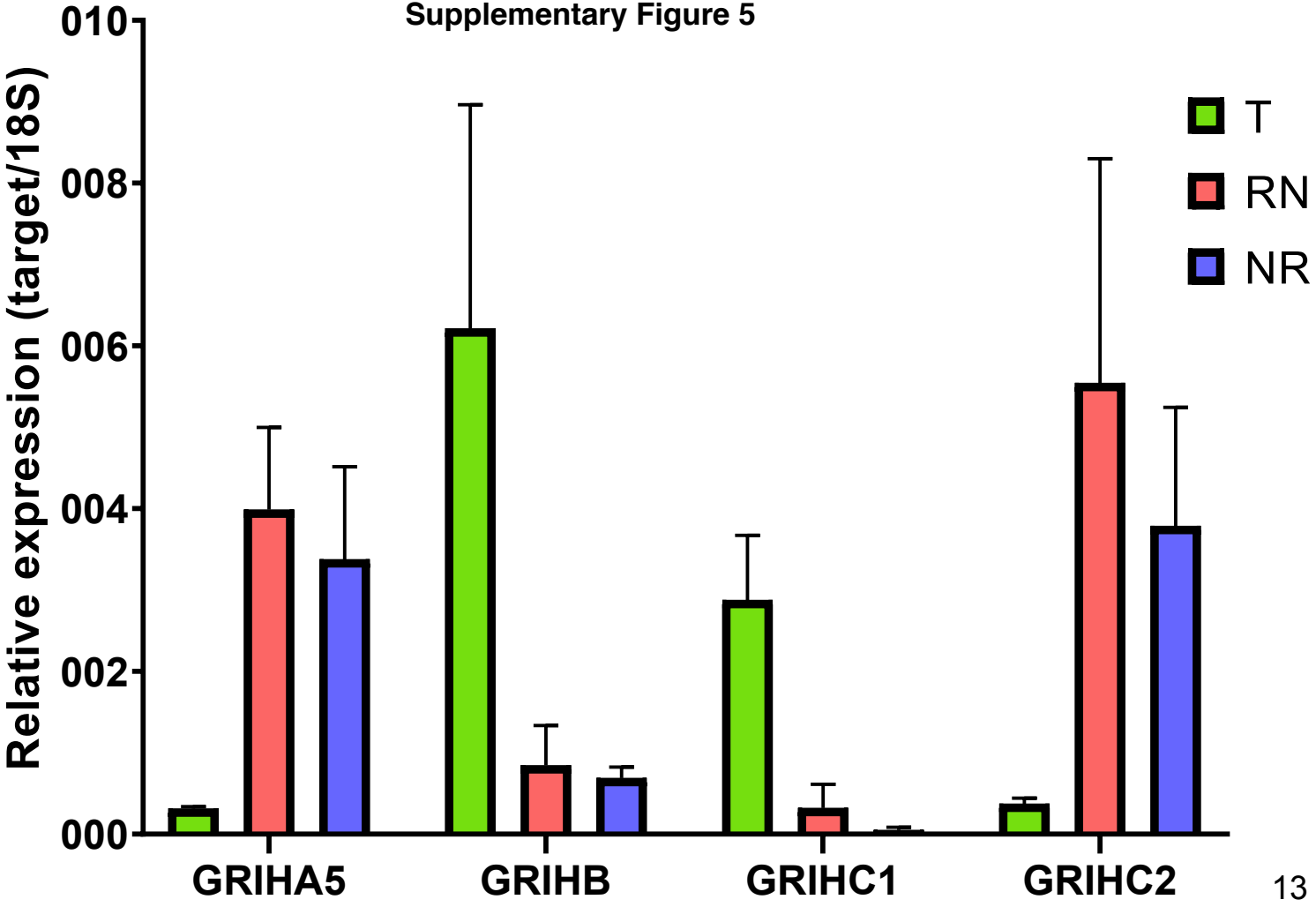


GluK



GluD

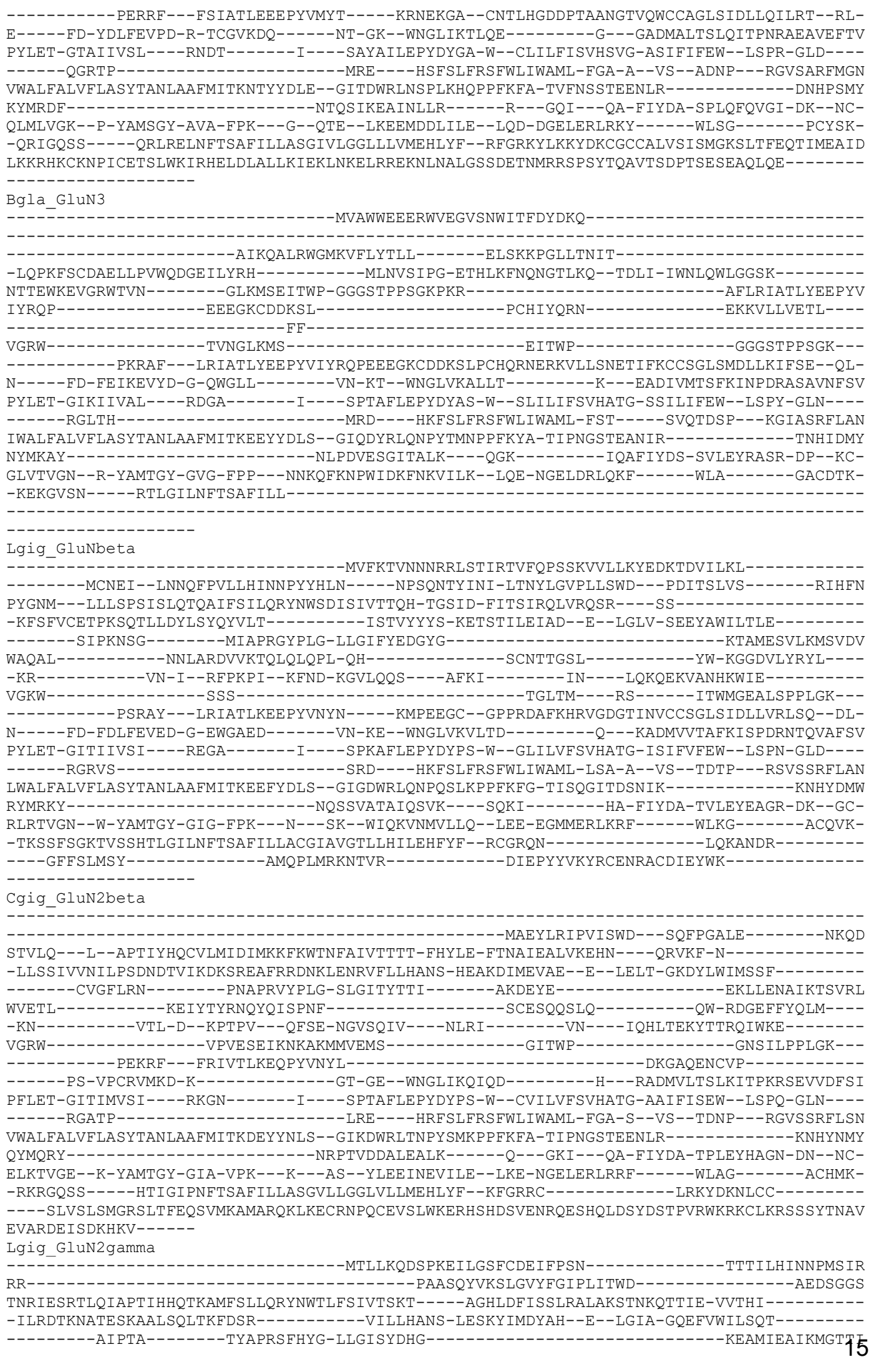
Supplementary Figure 5



```
#NEXUS
```

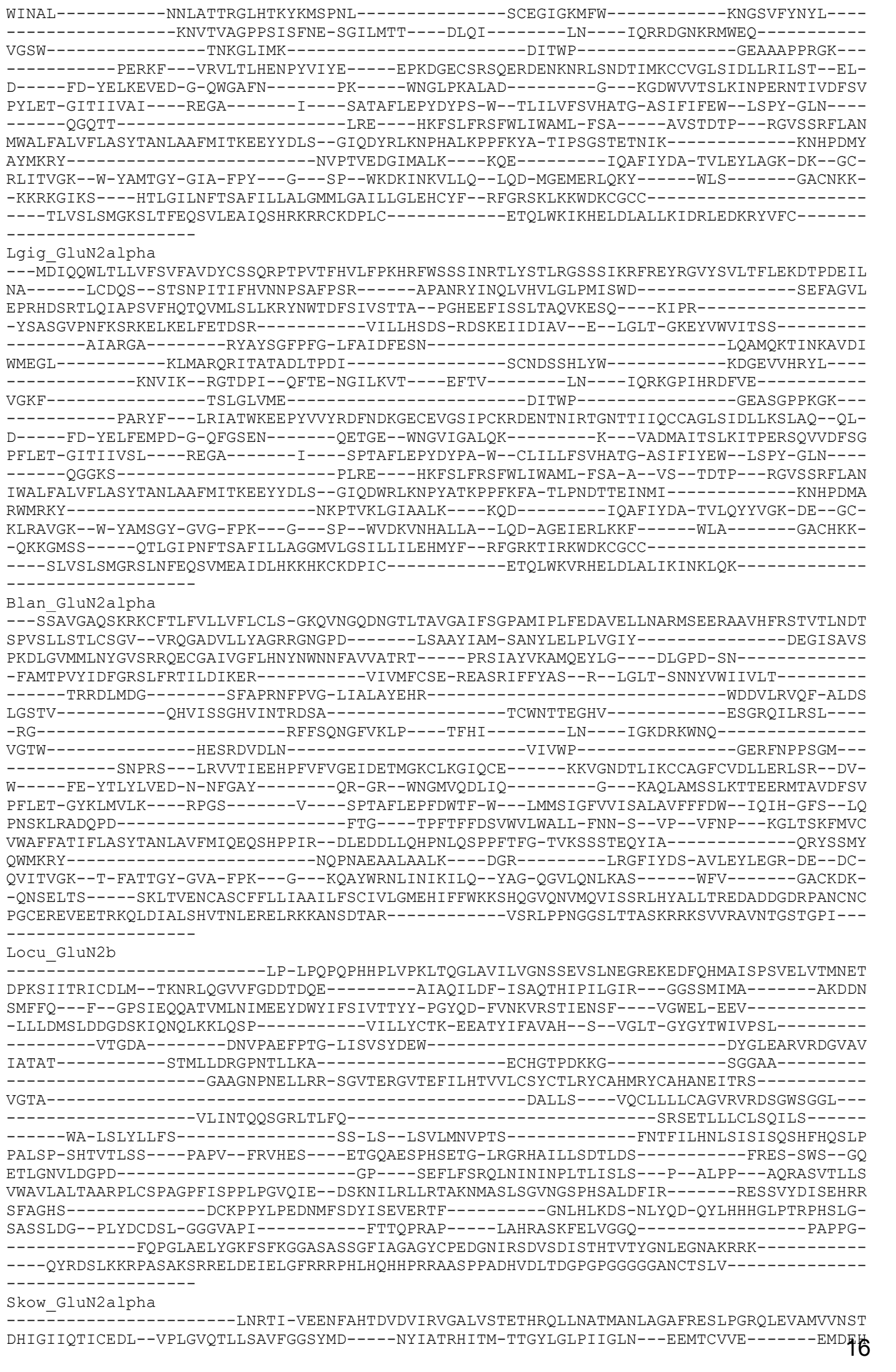
Supplementary Data 1

```
BEGIN DATA;
DIMENSIONS  NTAX=288 NCHAR=1481;
FORMAT DATATYPE=PROTEIN GAP=- MISSING=?;
MATRIX

Skow_GluN2gamma
------MDKNFNITRLVLLCILMDKIGA-HVRIGVIHALTQDTLYVDRRHRRYVVDTD--------KGGIIMHMVPIQLSSGSPYQ
TIQHLKNKICLHN--LSG----LIYSVDEQNTRQWDIGSVFPGSSYIPK-LAESLHIPAVSVT---------------APLVQEKH
GGTDAPGMIYLLPKGRDVCLAILNFLEYFHWYHLTLVPGPN-----H-ASVEFVAEMALAI----QYRDH-WKYN----------
-VYDVLDFEKNISHQVEHIALSSS------------IVIFHMNP-MQTRTVLASAA--E--NGLL-KKGLVWIISGA----ALDEQ
PF--------------------SNNTGVIPIG-LIGVRPGHI-----------------------------SHTSATRTRFAKML
LSEAI-----------ADYVNDGNDLRSLSAG-----------------PCDKNTNR--------------TWDNVLQPYL----
----------------N--RSVIDIADGFDK-DGYLLHP----KLAF--------VN----IDDSYNVKQ--------------
VGTW----------------KKGKIKLK-----------------------SITWI------------GQHSNRQGHQPSPV---
-----------LTQKR---LRIITVEETPFVRAL-----SLDTDGCNNGI-LCKKMNGTYGDFLDRCCGGFAVDLLKELSM--TLD
N----IFE-FDFFVVNS----YGRFL-------ES-GR--WNGAVGELVY---------G---KADMMVGGMKMSSQRTEVLDFSV
PFMTS-GVSVIVME----SKGR--T---------PLHAVYDPFHFLV-W--IMAWIIALAVTA-LAVFFVEW--VSPT-GYA----
------RKLTE-----------------------PRA----SSFTFGDSLWMLWAIN-TNN-S--LP--TRVP---KSVTGKFVTS
IWAFYTLVFVALYTANLTAHMIKVESTLPID--GFMDPKLQNPHQSSPRIKFA-TVQSTNTESLIE-------------DHNPRMH
QYMKQY-----------------------LVKSAAEGIEALN----SGD---------LDVFIYDA-MVSEFLATQAHD---C-
NLVTVDS--A-FAMTGY-AIA-FPK---S---SP--WRGLIDRALLQ--YVD-NGFLNILREK------WIS------LDSCAAK-
-RTRRSEED----NILGSSQVAGAFLFLAGGIAISWFLMFFELFFYKNFRQQEAIALISATFTKIVYPRRDDPGLPTCC-------
----EECENLIDSENWNDSGSSKHQYNGRRDDMAA---------------ATRDRDTNIVSSEVMPDDCRVV--------------
--------------------

Skow_GluN2beta
----VPFWNPETVQALRLTLLAALLVHQASVDSGDAESPTVLLLGAMLTDPKHKHVIEKTIDTLQANMSSLSNVKIEIMDEYINLT
EHLNVIHTICQKM-IPKGITALISAIEGENYVDV-------HIATGFVSMISQYINLPVISIN---------------QATVTKLD
AKTSHSSYLHVGASMKDQAKAMLAFLQYYDWYHFIIVTTMI--PDHDIFISSMENLLFEYA-ESYDQEWE-IC-------------
-DKIEINMEHNLTAQVKLIIESDCT-----------IVLLFSSQ-QEAQLIMDESN--E--HGMM-EHGNVWIGAET---------
------ILRNLNGA--------GEIPDEFPTG-LLAVKYREK-----------------------------SYNVERAIQDSTKI
YLNGL-----------DRYARSMGHRETLKDIEFTK-------------SCWQSNHRPP------------ESLNKFVKYL----
-------------STSPDTDDSDDDY--EFDI-EGNLKNP----KVVI--------MN----VPISRRWDK---------------
VGVW----------------TRHGLVIN-----------------------DITWM---------------GGLHQQPEGL---
-----------TPHRH---ITFTTITEGSYVSVI-----ELNEEECTAGV-RCRLLDDETGEHYYRCCIGFCVDLLLRLSR--DI-
G-----FI-FDLYVVED-L-KFGAN--------EN-GT--WNGMVGDILK---------G---NADAAIASLLDTAARSSVIDTSV
TFMKS-GISVLAKR----EEGM-------V----PSDAFLAPFDYSV-W---LLLTVGIVQVVALAIFVFEC--FSPG-GYD----
------RSLTG-----------------------PRI----TKFTFGSSLWIVWGLL-FNN-T--VP--LKPP---RSYTAKFMTN
MWGCFSLIFIAMYTANLVAHMIREAPTDMVD--GFLDPKLQKPNQYSNPLKFG-TIKSTSVEQYIK-------------KVNTKMQ
EHMDPY-----------------------NLELAEDAVAAVK----HGK---------VDAFIYDE-AALRDLAAK-DQ--DC-
SLKVVGK--T-VGETGY-TIA-LTK---G---SH--WTHKINEKIIK--YTD-SGFLQTLVEK------WLT-------SMCEGK-
-NENSR-------QPLGIEHSSGVFLLLLGGTAVSILVFFGEHLFFKGFTKRFAKKELVAVVSE----------------------
----AMARSMYTPVSKSEQCSCRNKPKVLSNERTNELKSLWIP-------LSQQENDNYTKGHFTSDSDTDSETSERNFC------
--------------------

Bgla_GluN1
--------------------------------MGASPTLKPSARNEIVLSVMERAERLGLTREDYVWIFTLPAMKQAASRDTIKKT
YP-------------VGSFVIGFDSY---------------ASQVKELHNQVSKMWYSALKMM----------------AISKEFE
SVDFQ-----THFSCNVQSQATNQSARSLYWKYGEHLYKKV-----------------------------------------------
-EQSTSKSTDSRGGRFPLKTSPFSS-----------KRDIDFGF-SKSRDIARESR--F--EGFTRKPLFRDRLSGP----------
----------------------LTGPNDLDPD-NPDNPE---------------------------------GTENRDLDLNDDPD
ASSGS-----------SSYKNSSRKYPK-------------------------------------------KIGNSKMKPY----
--------------------GKNDVKRRYAEKHRRPRRQLSDKFSLNI--------LQ--------------------------
KNCW-------------------------------------------------------------------QTVSESNIRN---
---------------------VCEQVKDKYGLYTDLQDMSGNQTLD-----------------VCCTGLSIDLLKRLCT--ML-
N-----FD-VQLTEVAD-G-SYGSP--------INNNESDWTGMVGMLIH---------K---KADMAIGALSITPERSNAVDFSM
PFLQT-GITIIVAI----REGA-------I----SPTAFLEPYDYPS-W--SLILLFSVHATG-ASIFIFEW--LSPY--------
------GLDQG-----------------------------------KTSLRVKT-----C---------ELQIVRFLAN
IWALFAVVFCASYTANLAAFMITKDDYYDLS--GIQDWRLKNPHHRQPPFKYA-TIANSSTDLNIA-------------KNYKAIH
SYMKNY-----------------------PQTSVKDAIRALK----NQE---------IQAFIYDS-TTLEYEFGK-DV--GC-
KLKTVGK--R-IAETGY-GLA-FPK---K---SQ--WVKKVDKALLK--LQE-DGEIERLQKF------WLA-------GACHKK-
-KERGVSS-----HTLGILNFTSAFILLGGGVILGVLLLILEHMYFDYHKHHKCKDPLCETQLWKVKHELDIALLKISQLRRLLAH
SASLEVSREQRAPYKLEMQESTQVNGNAHKRRRQQKSDTELHPAPPTFDEASPSKDSNFTSSPDMRYPQGGVRGIRSMSP------
--------------------

Cgig_GluN2alpha
---------KSPKIVALSWGMFFLAFIA-LISTVCCQRGPKAELDIIVPNIDKVVNAIDKRNFYNIMKPIRRTYSPYARVIELEES
NPDEILGIFCDTI--FQKNVNALVHLSVTKKAEK--------SKDYVLG-LASSLGLPVLSFD---PDYVGALE--------NPQN
RMVLQ---L--APTLYHQAQAMLKFMMTFNWTHFTVVSTTD-DNNFD-FTAALRSLVKQNN----DVNIL-SGQFRYK--------
-IMKEIIFEHDDTESYPNMTKRAVQFLKRETPKDNRIFLLHSS---EAKTLLDAAA--E--AGLT-TYKYLWILTSQ---------
--------SIGIPT--------KRASRSFPVG-TIGVSYLST-----------------------------DSDYVDSVYKKAVE
IGVAT---------WVGALQKLNGRVLQPDF-------------------TCNTSVPAS----------QW-IGGQELYTIM----
-------------RNF-E--DLRGTVPVSFDQ-NGLSRNV----ELNV--------LN----VQ---------------------
IGRW----------------YAEERTLNPKLELK-----------------GITWP---------------GDKKIPPRGR-
```


----------PERRF---FSIATLEEEPYVMYT-----KRNEKGA--CNTLHGDDPTAANGTVQWCCAGLSIDLLQILRT--RL-
E-----FD-YDLFEVPD-R-TCGVKDQ------NT-GK--WNGLIKTLQE---------G---GADMALTSLQITPNRAEAVEFTV
PYLET-GTAIIVSL----RNDT-------I----SAYAILEPYDYGA-W--CLILFISVHSVG-ASIFIFEW--LSPR-GLD----
------QGRTP----------------------MRE----HSFSLFRSFWLIWAML-FGA-A--VS--ADNP---RGVSARFMGN
VWALFALVFLASYTANLAAFMITKNTYYDLE--GITDWRLNSPLKHQPPFKFA-TVFNSSTEENLR------------DNHPSMY
KYMRDF----------------------NTQSIKEAINLLR------R---GQI---QA-FIYDA-SPLQFQVGI-DK--NC-
QLMLVGK--P-YAMSGY-AVA-FPK---G--QTE--LKEEMDDLILE--LQD-DGELERLRKY------WLSG-------PCYSK-
-QRIGQSS-----QRLRELNFTSAFILLASGIVLGGLLLVMEHLYF--RFGRKYLKKYDKCGCCALVSISMGKSLTFEQTIMEAID
LKKRHKCKNPICETSLWKIRHELDLALLKIEKLNKELRREKNLNALGSSDETNMRRSPSYTQAVTSDPTSESEAQLQE--------
----
12 Bgla_GluN3
---------------------------------MVAWWEEERWVEGVSNWITFDYDKQ--------------------------
----
----------------------AIKQALRWGMKVFLYTLL-------ELSKKPGLLTNIT-----------------------
-LQPKFSCDAELLPVWQDGEILYRH----------MLNVSIPG-ETHLKFNQNGTLKQ--TDLI-IWNLQWLGGSK---------
NTTEWKEVGRWTVN--------GLKMSEITWP-GGGSTPPSGKPKR-----------------------AFLRIATLYEEPYV
IYRQP--------------EEEGKCDDKSL-------------------PCHIYQRN-------------EKKVLLVETL----
----------------------------FF--
VGRW----------------TVNGLKMS-----------------------EITWP----------------GGGSTPPSGK---
-----------PKRAF---LRIATLYEEPYVIYRQPEEEGKCDDKSLPCHQRNERKVLLSNETIFKCCSGLSMDLLKIFSE--QL-
N-----FD-FEIKEVYD-G-QWGLL--------VN-KT--WNGLVKALLT---------K---EADIVMTSFKINPDRASAVNFSV
PYLET-GIKIIVAL----RDGA-------I----SPTAFLEPYDYAS-W--SLILIFSVHATG-SSILIFEW--LSPY-GLN----
------RGLTH----------------------MRD----HKFSLFRSFWLIWAML-FST-----SVQTDSP---KGIASRFLAN
IWALFALVFLASYTANLAAFMITKEEYYDLS--GIQDYRLQNPYTMNPPFKYA-TIPNGSTEANIR-------------TNHIDMY
NYMKAY----------------------NLPDVESGITALK----QGK---------IQAFIYDS-SVLEYRASR-DP--KC-
GLVTVGN--R-YAMTGY-GVG-FPP---NNKQFKNPWIDKFNKVILK--LQE-NGELDRLQKF------WLA-------GACDTK-
-KEKGVSN-----RTLGILNFTSAFILL--

----
13 Lgig_GluNbeta
---------------------------------MVFKTVNNNRRLSTIRTVFQPSSKVVLLKYEDKTDVILKL------------
--------MCNEI--LNNQFPVLLHINNPYYHLN-----NPSQNTYINI-LTNYLGVPLLSWD---PDITSLVS-------RIHFN
PYGNM---LLLSPSISLQTQAIFSILQRYNWSDISIVTTQH-TGSID-FITSIRQLVRQSR----SS--------------------
-KFSFVCETPKSQTLLDYLSYQYVLT----------ISTVYYYS-KETSTILEIAD--E--LGLV-SEEYAWILTLE---------
-------SIPKNSG--------MIAPRGYPLG-LLGIFYEDGYG---------------------------KTAMESVLKMSVDV
WAQAL-----------NNLARDVVKTQLQLQPL-QH--------------SCNTTGSL-----------YW-KGGDVLYRYL----
-KR-----------VN-I--RFPKPI--KFND-KGVLQQS----AFKI--------IN----LQKQEKVANHKWIE----------
VGKW----------------SSS-----------------------------TGLTM----RS------ITWMGEALSPPLGK---
-----------PSRAY---LRIATLKEEPYVNYN-----KMPEEGC--GPPRDAFKHRVGDGTINVCCSGLSIDLLVRLSQ--DL-
N-----FD-FDLFEVED-G-EWGAED-------VN-KE--WNGLVKVLTD---------Q---KADMVVTAFKISPDRNTQVAFSV
PYLET-GITIIVSI----REGA-------I----SPKAFLEPYDYPS-W--GLILVFSVHATG-ISIFVFEW--LSPN-GLD----
------RGRVS----------------------SRD----HKFSLFRSFWLIWAML-LSA-A--VS--TDTP---RSVSSRFLAN
LWALFALVFLASYTANLAAFMITKEEFYDLS--GIGDWRLQNPQSLKPPFKFG-TISQGITDSNIK-------------KNHYDMW
RYMRKY----------------------NQSSVATAIQSVK----SQKI--------HA-FIYDA-TVLEYEAGR-DK--GC-
RLRTVGN--W-YAMTGY-GIG-FPK---N---SK--WIQKVNMVLLQ--LEE-EGMMERLKRF------WLKG-------ACQVK-
-TKSSFSGKTVSSHTLGILNFTSAFILLACGIAVGTLLHILEHFYF--RCGRQN----------------LQKANDR---------
----GFFSLMSY--------------AMQPLMRKNTVR------------DIEPYYVKYRCENRACDIEYWK--------------
----
14 Cgig_GluN2beta

---MAEYLRIPVISWD---SQFPGALE--------NKQD
STVLQ---L--APTIYHQCVLMIDIMKKFKWTNFAIVTTTT-FHYLE-FTNAIEALVKEHN----QRVKF-N--------------
-LLSSIVVNILPSDNDTVIKDKSREAFRRDNKLENRVFLLHANS-HEAKDIMEVAE--E--LELT-GKDYLWIMSSF---------
-------CVGFLRN--------PNAPRVYPLG-SLGITYTTI-------AKDEYE----------------EKLLENAIKTSVRL
WVETL-----------KEIYTYRNQYQISPNF------------------SCESQQSLQ----------QW-RDGEFFYQLM----
-KN----------VTL-D--KPTPV---QFSE-NGVSQIV----NLRI--------VN----IQHLTEKYTTRQIWKE--------
VGRW----------------VPVESEIKNKAKMMVEMS--------------GITWP----------------GNSILPPLGK---
-----------PEKRF---FRIVTLKEQPYVNYL-----------------------------DKGAQENCVP------------
------PS-VPCRVMKD-K--------------GT-GE--WNGLIKQIQD---------H---RADMVLTSLKITPKRSEVVDFSI
PFLET-GITIMVSI----RKGN-------I----SPTAFLEPYDYPS-W--CVILVFSVHATG-AAIFISEW--LSPQ-GLN----
------RGATP----------------------LRE----HRFSLFRSFWLIWAML-FGA-S--VS--TDNP---RGVSSRFLSN
VWALFALVFLASYTANLAAFMITKDEYYNLS--GIKDWRLTNPYSMKPPFKFA-TIPNGSTEENLR-------------KNHYNMY
QYMQRY----------------------NRPTVDDALEALK------Q---GKI---QA-FIYDA-TPLEYHAGN-DN--NC-
ELKTVGE--K-YAMTGY-GIA-VPK---K---AS--YLEEINEVILE--LKE-NGELERLRRF------WLAG-------ACHMK-
-RKRGQSS-----HTIGIPNFTSAFILLASGVLLGGLVLLMEHLYF--KFGRRC-------------LRKYDKNLCC---------
----SLVSLSMGRSLTFEQSVMKAMARQKLKECRNPQCEVSLWKERHSHDSVENRQESHQLDSYDSTPVRWKRKCLKRSSSYTNAV
EVARDEISDKHKV------
15 Lgig_GluN2gamma
---------------------------------MTLLKQDSPKEILGSFCDEIFPSN--------------TTTILHINNPMSIR
RR-------------------------------------PAASQYVKSLGVYFGIPLITWD----------------AEDSGGS
TNRIESRTLQIAPTIHHQTKAMFSLLQRYNWTLFSIVTSKT-----AGHLDFISSLRALAKSTNKQTTIE-VVTHI----------
-ILRDTKNATESKAALSQLTKFDSR----------VILLHANS-LESKYIMDYAH--E--LGIA-GQEFVWILSQT---------
---------AIPTA--------TYAPRSFHYG-LLGISYDHG-----------------------------KEAMIEAIKMGTTI

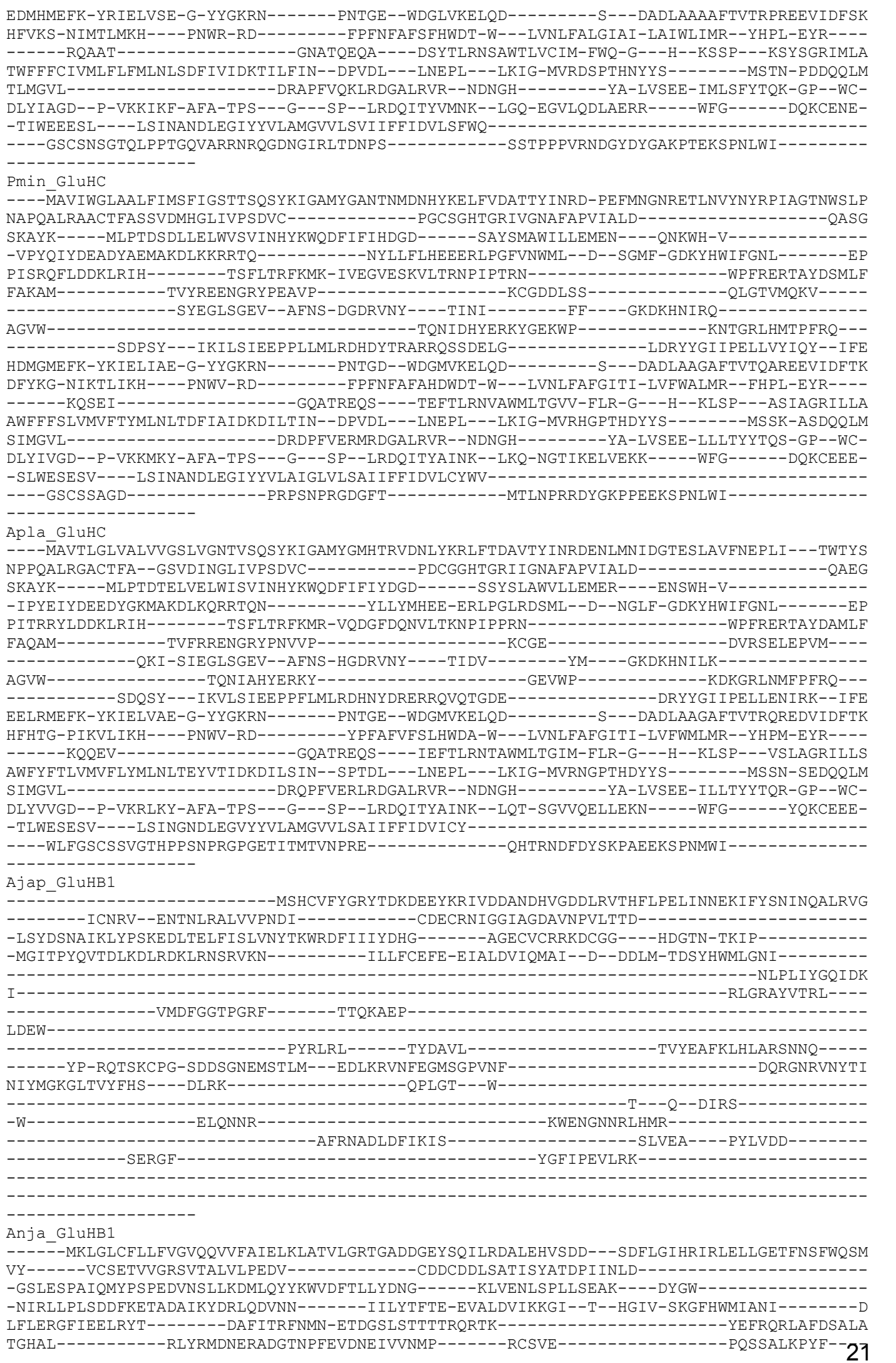

WINAL----------NNLATTRGLHTKYKMSPNL--------------SCEGIGKMFW----------KNGSVFYNYL----
----------KNVTVAGPPSISFNE-SGILMTT----DLQI--------LN----IQRRDGNKRMWEQ----------
VGSW---------------TNKGLIMK----------------------DITWP---------------GEAAAPPRGK---
----------PERKF---VRVLTLHENPYVIYE-----EPKDGECSRSQERDENKNRLSNDTIMKCCVGLSIDLLRILST--EL-
D-----FD-YELKEVED-G-QWGAFN-------PK-----WNGLPKALAD---------G---KGDWVVTSLKINPERNTIVDFSV
PYLET-GITIIVAI----REGA-------I----SATAFLEPYDYPS-W--TLILVFSVHATG-ASIFIFEW--LSPY-GLN----
------QGQTT----------------------LRE----HKFSLFRSFWLIWAML-FSA-----AVSTDTP---RGVSSRFLAN
MWALFALVFLASYTANLAAFMITKEEYYDLS--GIQDYRLKNPHALKPPFKYA-TIPSGSTETNIK----------KNHPDMY
AYMKRY----------------------NVPTVEDGIMALK----KQE---------IQAFIYDA-TVLEYLAGK-DK--GC-
RLITVGK--W-YAMTGY-GIA-FPY---G---SP--WKDKINKVLLQ--LQD-MGEMERLQKY------WLS-------GACNKK-
-KKRKGIKS----HTLGILNFTSAFILLALGMMLGAILLGLEHCYF--RFGRSKLKKWDKCGCC----------------------
----TLVSLSMGKSLTFEQSVLEAIQSHRKRRCKDPLC----------ETQLWKIKHELDLALLKIDRLEDKRYVFC-------
----
16 Lgig_GluN2alpha
---MDIQQWLTLLVFSVFAVDYCSSQRPTPVTFHVLFPKHRFWSSSINRTLYSTLRGSSSIKRFREYRGVYSVLTFLEKDTPDEIL
NA------LCDQS--STSNPITIFHVNNPSAFPSR------APANRYINQLVHVLGLPMISWD----------SEFAGVL
EPRHDSRTLQIAPSVFHQTQVMLSLLKRYNWTDFSIVSTTA--PGHEEFISSLTAQVKESQ----KIPR----------
-YSASGVPNFKSRKELKELFETDSR----------VILLHSDS-RDSKEIIDIAV--E--LGLT-GKEYVWVITSS---------
--------AIARGA--------RYAYSGFPFG-LFAIDFESN----------------------------LQAMQKTINKAVDI
WMEGL----------KLMARQRITATADLTPDI----------SCNDSSHLYW----------KDGEVVHRYL----
----------KNVIK--RGTDPI--QFTE-NGILKVT----EFTV--------LN----IQRKGPIHRDFVE----------
VGKF----------TSLGLVME----------DITWP----------GEASGPPKGK---
----------PARYF---LRIATWKEEPYVVYRDFNDKGECEVGSIPCKRDENTNIRTGNTTIIQCCAGLSIDLLKSLAQ--QL-
D-----FD-YELFEMPD-G-QFGSEN-------QETGE--WNGVIGALQK---------K---VADMAITSLKITPERSQVVDFSG
PFLET-GITIIVSL----REGA-------I----SPTAFLEPYDYPA-W--CLILLFSVHATG-ASIFIYEW--LSPY-GLN----
------QGGKS----------------------PLRE----HKFSLFRSFWLIWAML-FSA-A--VS--TDTP---RGVSSRFLAN
IWALFALVFLASYTANLAAFMITKEEYYDLS--GIQDWRLKNPYATKPPFKFA-TLPNDTTEINMI----------KNHPDMA
RWMRKY----------------------NKPTVKLGIAALK----KQD---------IQAFIYDA-TVLQYYVGK-DE--GC-
KLRAVGK--W-YAMSGY-GVG-FPK---G---SP--WVDKVNHALLA--LQD-AGEIERLKKF------WLA-------GACHKK-
-QKKGMSS-----QTLGIPNFTSAFILLAGGMVLGSILLILEHMYF--RFGRKTIRKWDKCGCC----------------------
----SLVSLSMGRSLNFEQSVMEAIDLHKKHKCKDPIC----------ETQLWKVRHELDLALIKINKLQK----------
----
17 Blan_GluN2alpha
---SSAVGAQSKRKCFTLFVLLVFLCLS-GKQVNGQDNGTLTAVGAIFSGPAMIPLFEDAVELLNARMSEERAAVHFRSTVTLNDT
SPVSLLSTLCSGV--VRQGADVLLYAGRRGNGPD-------LSAAYIAM-SANYLELPLVGIY----------DEGISAVS
PKDLGVMMLNYGVSRRQECGAIVGFLHNYNWNNFAVVATRT-----PRSIAYVKAMQEYLG----DLGPD-SN----------
-FAMTPVYIDFGRSLFRTILDIKER----------VIVMFCSE-REASRIFFYAS--R--LGLT-SNNYVWIIVLT---------
------TRRDLMDG--------SFAPRNFPVG-LIALAYEHR----------------------------WDDVLRVQF-ALDS
LGSTV----------QHVISSGHVINTRDSA----------TCWNTTEGHV----------ESGRQILRSL----
-RG----------RFFSQNGFVKLP----TFHI--------LN----IGKDRKWNQ----------
VGTW----------HESRDVDLN----------VIVWP----------GERFNPPSGM---
----------SNPRS---LRVVTIEEHPFVFVGEIDETMGKCLKGIQCE------KKVGNDTLIKCCAGFCVDLLERLSR--DV-
W-----FE-YTLYLVED-N-NFGAY--------QR-GR--WNGMVQDLIQ---------G---KAQLAMSSLKTTEERMTAVDFSV
PFLET-GYKLMVLK----RPGS-------V----SPTAFLEPFDWTF-W---LMMSIGFVVISALAVFFFDW--IQIH-GFS--LQ
PNSKLRADQPD----------FTG----TPFTFFDSVWVLWALL-FNN-S--VP--VFNP---KGLTSKFMVC
VWAFFATIFLASYTANLAVFMIQEQSHPPIR--DLEDDLLQHPNLQSPPFTFG-TVKSSSTEQYIA----------QRYSSMY
QWMKRY----------NQPNAEAALAALK----DGR---------LRGFIYDS-AVLEYLEGR-DE--DC-
QVITVGK--T-FATTGY-GVA-FPK---G---KQAYWRNLINIKILQ--YAG-QGVLQNLKAS------WFV-------GACKDK-
-QNSELTS-----SKLTVENCASCFFLLIAAILFSCIVLGMEHIFFWKKSHQGVQNVMQVISSRLHYALLTREDADDGDRPANCNC
PGCEREVEETRKQLDIALSHVTNLERELRKKANSDTAR----------VSRLPPNGGSLTTASKRRKSVVRAVNTGSTGPI---
----
18 Locu_GluN2b
----------LP-LPQPQPHHPLVPKLTQGLAVILVGNSSEVSLNEGREKEDFQHMAISPSVELVTMNET
DPKSIITRICDLM--TKNRLQGVVFGDDTDQE---------AIAQILDF-ISAQTHIPILGIR---GGSSMIMA-------AKDDN
SMFFQ---F--GPSIEQQATVMLNIMEEYDWYIFSIVTTYY-PGYQD-FVNKVRSTIENSF----VGWEL-EEV----------
-LLLDMSLDDGDSKIQNQLKKLQSP----------VILLYCTK-EEATYIFAVAH--S--VGLT-GYGYTWIVPSL---------
---------VTGDA--------DNVPAEFPTG-LISVSYDEW----------DYGLEARVRDGVAV
IATAT----------STMLLDRGPNTLLKA----------ECHGTPDKKG----------SGGAA---------
----------GAAGNPNELLRR-SGVTERGVTEFILHTVVLCSYCTLRYCAHMRYCAHANEITRS----------
VGTA----------DALLS----VQCLLLLCAGVRVRDSGWSGGL---
----------VLINTQQSGRLTLFQ----------SRSETLLLCLSQILS------
------WA-LSLYLLFS----------SS-LS--LSVLMNVPTS----------FNTFILHNLSISISQSHFHQSLP
PALSP-SHTVTLSS----PAPV--FRVHES----ETGQAESPHSETG-LRGRHAILLSDTLDS----------FRES-SWS--GQ
ETLGNVLDGPD----------GP----SEFLFSRQLNININPLTLISLS---P--ALPP---AQRASVTLLS
VWAVLALTAARPLCSPAGPFISPPLPGVQIE--DSKNILRLLRTAKNMASLSGVNGSPHSALDFIR-------RESSVYDISEHRR
SFAGHS----------DCKPPYLPEDNMFSDYISEVERTF----------GNLHLKDS-NLYQD-QYLHHHGLPTRPHSLG-
SASSLDG--PLYDCDSL-GGGVAPI----------FTTQPRAP-----LAHRASKFELVGGQ----------PAPPG-
----------FQPGLAELYGKFSFKGGASASSGFIAGAGYCPEDGNIRSDVSDISTHTVTYGNLEGNAKRRK----------
----QYRDSLKKRPASAKSRRELDEIELGFRRRPHLHQHHPRRAASPPADHVDLTDGPGPGGGGGANCTSLV----------
----
19 Skow_GluN2alpha
----------LNRTI-VEENFAHTDVDVIRVGALVSTETHRQLLNATMANLAGAFRESLPGRQLEVAMVVNST
DHIGIIQTICEDL--VPLGVQTLLSAVFGGSYMD-----NYIATRHITM-TTGYLGLPIIGLN---EEMTCVVE-------EMDEH

```
EVFLQ---I--GSSISQQVGALLAFLEYHHWYHFAIITSQLPGRVEF-LSELQHRTIGEGS----DHDSS-WE----------
-ICETFAMGIGENDTITSTLSKLTKGECT-------IIILFADA-GEAREVFKVAE--E--LDLL-TYGYIWLVLEL---------
------SLGGHEGI--------LKPPPEFPVG-LVAVKFEGI-----------------------------DYTIDDAIVDAATT
YTTRL-----------TGYLADGYQIELGNNA-----------------GCKAQGGHSY------------HGSKYFYDYL----
-------------TRD-E--IPYKNF--VFDK-HGVVKNP----KLSI--------LN----LDSSRTWKE---------------
VGYW----------------QDNNMTMA-----------------------TVLWI----------------GGTHEAPKGL---
-----------SPHRH---MRFTTIVEEPFVLTI----PLEKNEVV--CK--------------KCCLGFCISLLEKLKE--DI-
G-----FT-YELRLVDD-G-NYGAKV---EADGKE-DE--WNGMIGAIVK---------H---RADAAIGAVRITEERSEVVDFST
PFIST-GISVLVKK----KDGE-------I----PNSAFLGSFHLSV-W--IFLLVIAVNVTA-VVVFIFEW--FSPG-GYD----
------RNFDN-----------------------GRA----SKFTIGSSIWMTYGIL-FNN-T--VH--LNVP---RSYTAKFVTN
MWACFALVFVAMYTADLVTHMIQEDSHRIIT--GFNDPKLQYPLSSRKPLRFA-TVASSSVENLIK-------------KSNKEMH
TYMQKF------------------------VKRNTTEAVNALK------R---GEL---DA-FIYDS-EVLNSFAKKDDH---C-
DLMLVGD--V-YASTGY-AVA-FEK---D---SH--WKERFDSNILH--YNH-NGFLQKISDT------WME-------STCDTV-
-GGNTASR-----QRLGIENLAGVFYLLSAGILASLAVFVVEHFCRCCRKKQSLSVLVQVVAQNLSTPHRVAKDPVC---------
----HNIGCLRQTTELRRTRSRIAELEKALAKRMSSTSEMYSNLVPLKLSFLQKYNSSFLEEEEHSEEKRKRCLV-----------
--------------------
20 Skow_GluN2delta
EKTCGEGFCELDCEYYSLALFAAFLMCK-CGEMRGNINIVGLGAFVSTRTQRDMLTNLTAKAFGQLDKNITGKVPEFDTSNYFEIA
RV------ICEEL--LPHNAQGLLVANDEDSFAD-----NYMMSRYVVT-AAVTVGLPVISLN---PGLPLETL-------FTETP
PTLLQ---L--AASIHQQCAAILDFLAYHEWFHFNVITSNA-PGHVD-FLHELELQIKQLK----SYYYQ-WQ-------------
-IAKSVVVDVSANVYLPMQELSYSNTS---------VHILYSTR-EEARTLFKYAK--S--FNYL-DKGYVWIAAEL---------
------AMGSMESL--------RRAPSEFPPG-LIAVKFQSL-----------------------------AYNFEERTVDAVSL
YKETF-----------VKFSKSRSFSYDSKKR-----------------NCNNPN----------------VSDTDFYDIL----
-KN----------ISV-P--GRSSF---AFTD-SGFVQNP----RIIF--------AS----LNENHIWKK---------------
VGMW----------------KNGTVDVG-----------------------EIEWM----------------GNPELSPTGF---
-----------THRKH---LRIVTIVEEPFVTIV------PYEQVN--VT---------------ECCSGYCMDLLKMISR--DL-
G-----FT-YDIYIVED-N-LYGVVF-------DN-GS--WNGIVKDLIE---------G---KADAAVAAVKMSTERYKVIDFSV
PFMDV-GVAVLVPK----SSGV-------V----LPHAFLAPFDIAI-W--VIVLVVTLNVAA-VSVFVFEF--VSPT-GYN----
------RKIAG-----------------------LKE----SNFTLGRAVWMTWGIL-FNN-SVP----AKVP---RSYTGKFMTN
MWASFALVFVAMYTGNLAAHMIHEERHEKIT--GINDTKIQHPDLIDPPFKFG-TVQHTSVERLIM-------------KTYPEMY
KYMKDY------------------------VQPSAVDAAAALE------A---GII---DA-FVYDS-AVLENLEDK-DP--SC-
NLVMVGK--V-YGSTGF-AVA-FSR---G---SP--WKAQFDKTLLL--YDD---------------------------------
-------------------------------LGMRLFVQYDD-----------------------------------------
----------------------------------------------------------------------------------
--------------------
21 Blan_GluN2beta
-----MEMMSRKGANFAAFFLVVWTFLARAQDNGTLWMERTLTLAAILESEEEITAFLEGVRTQGPIRGNDVAVVSMVANNSNPMG
TMVW----ACDEAVPRGPDAILFAGGHDTS-----------LLSARYVMMVAKYLDIPVISAY----------RGMSGVVARQEEL
PNFVH-----LGVSVDQEYSALMSILKYFFLTRFSIITTLH--TGHKAFIRYFQEQTEKEG-----DAWG-VEG------------
-VLTLDLDSMEMMDLYMSLARDITSS----------IILLYCTK-QEATVLLPAAE--F--VGKF-MENSVWIVPEI---------
------VIGDLDSA--------LSAPYEYPVG-LLGIKYESP-----------------------------SYSTRKMTLDGLSV
YRTAM-----------EKYLAKGDVLDTFMSD-----------------TCWNYTTRTK------------SDSLSFKDFL----
----------------QNASIPERDI--QFGA-DGFVDSP----NFAI--------LN----LASTGTWQR---------------
VGSI----------------IMNRISLN-----------------------GIIWP----------------GNSYLPPRPV---
------------VQRH---LKVVTIEEEPFVIVTDLHPVTGDCIKAALPC----TKFDSHGQEEDKCCTGFCMDMLEQLKD--DA-
W-----FT-VEIYVVAD-G-RHGT---------VQSGH--WNGVIGDLIN---------G---TADMAVGSLTITEERLEAVEFSV
PFIET-GLKVLVAK----KKGV-------V----SPSAFLEPYDATL-W---IIIAVLIINVITCALWLFEK--SRPG--------
-----QAEHPQ----------------------KDPS----KRFAPFHALWLLWTLL-FNN-T---MPLIRVP---KGLASKFMVC
VWAMFSTIFIASYTANLAAFMIQEQVSEKIT--GLTDPRFQRPEEFQPSFKFG-SVVGTSMEMKIR-------------DNYPRMY
SYMQKF------------------------NTRSAKEAVEALK----KRE---------LDSFIYDA-VVLEYLAGK-DD--GC-
NLVTVGN--V-FASTGY-GVA-FPK---G---SQ--WKSTIDLLILS--YND-NGYLDMFKSQ------WVE-------GLCSRK-
-QELEKNT-----HRLAIENCSGVFILLLAAIALSLVIFCLEHIVYGKPPSPVYENVQGTGSLRINGAERVVVTEHKVVAHVGDVF
DDECPGCQVAQEQIHALSSQVRHGNEQLRKDVTARVPEQPGAPIS-----LHDVVQQLTGGDGAEDEGSSHEYENSSQADSSGNVS
--------------------
22 Cint_GluN1
----MKGILVLALFMCYLGLVLGKMRLENCACNSTSLKQQFLIYGAIVSTAKQKAVFEHYLSMFNHNERAMNTYNQNTWIVVVNET
DPSELLQTICEEIVSQCVLYIMWIPNTFADPLMSWLLPTLSRKVKLLTFTTDHLKLTPSFLPT---------------------KK
RYLYQ-----FTPSVDDTTNTMLSMVGKYDWKQVTLLVTEA------PGYDTFLTSWNSKKDQINCKTDI-IGP------------
-MDVWTTPNDKIIQLLDGIQSM--------------IVVVYASL-DELGILFQNLG-----KTNKKTVSRSWLVHEI---------
---------GLMKRLYNEEQKLAYSLQSHPDA-TFVTELPDYFPKPLSILVHFPT-----------------SNRGTQSILQAILP
ITKAL---------AEKELQKNFGAFHYYMKN-----------------NLWKHPYFIN------------QVAQGISSYL----
--------------------KVGDPP--KFNE-NGYLFDP----SFTL--------------LSTNSDNMLIESPPSLIAAIKLNN
VTLW------------------------------------------------------------------RQLHTDPSFA---
---------YLSKDRH---IRVVTLGEASIVTVDNSSSICSSISVQCYVTAGDHNDSSFMNVWKPSCCKGFCIDLLQQLKK--EI-
G-----FT-YNIFVVRH-G-RHGKFT-------KD-GE--WEGAVGDVVN---------G---KADVAVGSITINKQREYVVDFSV
PFMET-GIGIMVNK----FNGT-------V----PPFAFLGPYDCLS-W---ACMLVVAMLASSIAVLTFEY--FSPS-GYN----
------GDITI-----------------------NKNA----SRFTLGKSIWLHYGIM-VNN-S--VP--IENP---HSPSSRYMVS
VWAFFCVIFLAMYTANLAAFMIQEESEDVIT--GLTDKRFTNPTATNPPFRFG-TVPNGSTELNMR-------------TYYPLYH
RYMEGY------------------------NMESLNDAVEALK----TRK---------LDAFLYDY-AVLKYAAGK-DK--DC-
EMNVIRK--P-SFTSGY-GVV-FTK---H---SP--WKEKFDIVLLN--LMQ-NGYIERISNV------WLT-------GLCGLP-
-TKSRDFTS----SRLDISNMAGLFIMLGGALALSILVFLFEHIFSRYFKKMKARRIAVKCSQPVIWQDGRISTHSLLPRIFECEN
STELVITSTIPRSTTCSHTSPVHHNRQKRPKEIVSETEKERTTPTCSRNSSACSRHNNKKLKSKTPSPCRRLLTIPLSRSFGSLRD
SL----------------
```

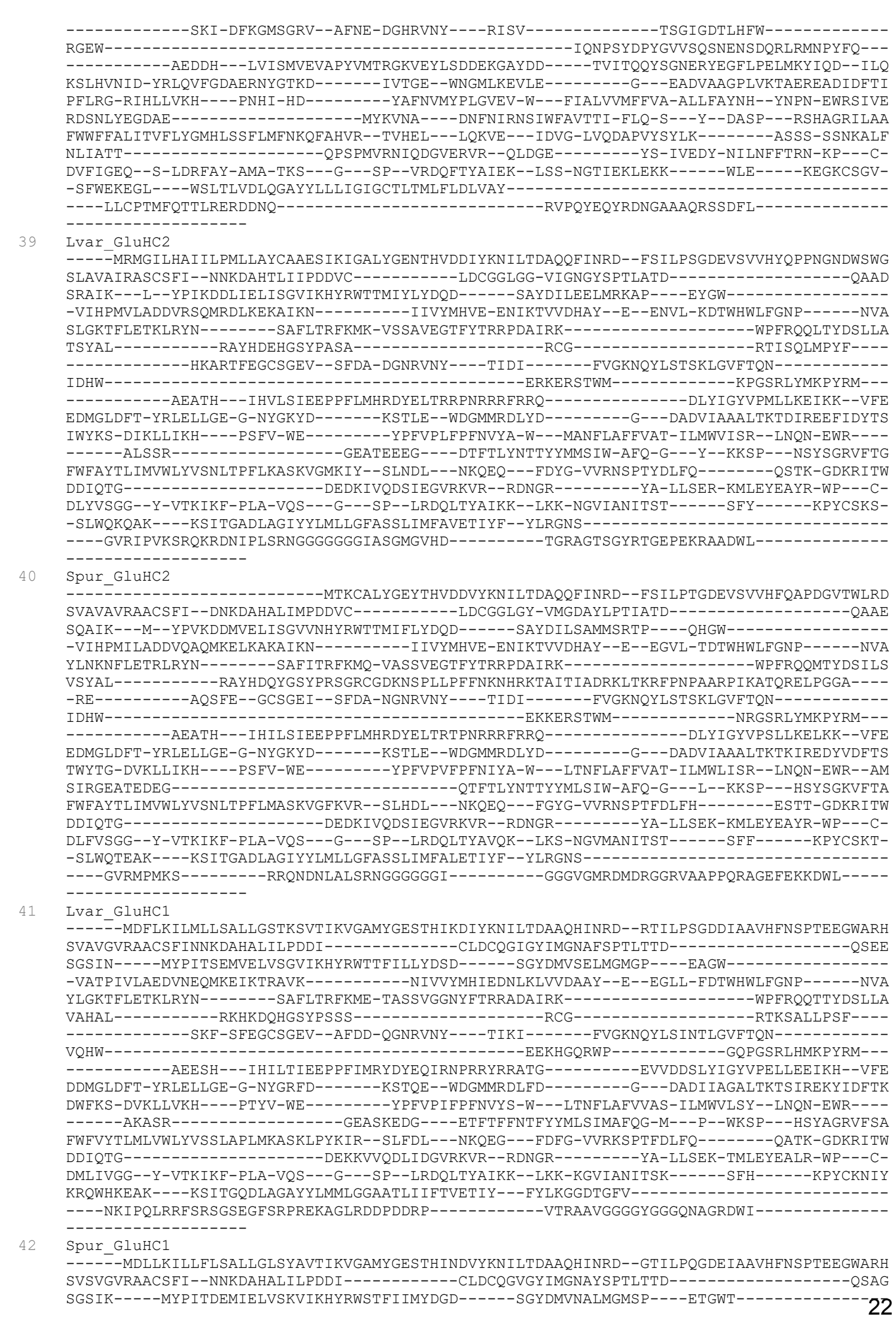
```
23  Blan_GluN2gamma
    ---------LLFFARSGDRAATMKVLVGLYSRRICGSDRAAPEIKLGGMFVEQGMVQPYRDAVIEANYRSGQSLEIKPLDKVLKNV
    SPENIVRSMCEDLVKKVVNAVIYGGDEDN------------VKSTLYVKQIAGELGMPILMAG------------GGSSEILHSQD
    NPFYP---LLLRSSIAQQAEVMVAVLKLQRWYRFSVVTSEM--PGHRLFQKTLRDMVINFKENEEKGVWS-IYRT-----------
    -FTLNVHPTSTVQDVKSQLAGRNMSQ----------VILLYCSK-REAKTIFQAAG--A--LGYT-SEDYVWIAAES---------
    ------VIGDFTKL--------REAPPQYPVG-LLSLVSQSQ-----------------------------KYNKEATIRTGVLL
    YMEAL-----------RQYIQDGNSVSDLQTY-----------------NCKSIRGSRSS-----------NATKLLYRYL----
    ------------------TSTTIEDLDIKFNE-DGTTTIS----TFDI--------MN----VDGMKLWER---------------
    VGSW----------------NKDSLYME-----------------------GVTWP----------------GNKASPPDGI---
    -----------SKDKH---IRIVAVLEHPFITAT-----EPDITGECHNTVECKKINRTARGGIKMCCTGFCIDLLKELAR--DV-
    M-----FS-YDLYLVPD-N-KHGKY--------EK-GK--WTGCIGELVK---------G---HAQMALGSITITKERATAVDFSM
    PFVET-GISVMTRR----RKGV-------V----PATAFLEPFDVFA-W---MAMFAVCLSCVAFTVMAFEF--FSPE-GYA----
    -----GNLHPS----------------DDAPPRASEA----GRFTVGKAFWLLWALI-FNN-S--VP--VENP---RGATSKYMIT
    FWAFFAVIFLATYTANLAAFMIQEEYTDSIT--GLTDEKFSNPFAHS--FRFG-TKPNGSTEAFIS-------------KNFRRMH
    EYMMRY-----------------------NQPSVNAAIQALK----GGT---------LDAFIYDA-AVLNYEAGK-DE--GC-
    QLRTIGHGSV-FATTGY-GIG-FPK---N---SE--WVDDIDLALLS--YFA-NGKLEELHEL------WLT-------GSCNQA-
    -SSDLDT------HPLGIENTAGVFYLLLAAIVLSIVILILEHFFYLKKRKKRKRSEVEADVIMATRAFAYSSVKHSKPYMSELYA
    EDNENEAGNAKGKDAIEKAFVNHLVSAVSNKRQMNPKPRPRNVHTVVGVSHVNANHQANYLRQDNPPRPRSAVEFPFKELEPNGIV
    ------------------
24  Hsap_GluN2A
    ---------MGRVGYWTLLVLPALLVWRGPAPSAAAEKGPPALNIAVMLGHSHDVTERELRTLWGPEQAAGLPLDVNVVALLMNRT
    DPKSLITHVCDLMSGARIHGLVFGDDTDQ------------EAVAQMLDFISSHTFVPILGIH----------GGASMIMADKDPT
    STFFQ-----FGASIQQQATVMLKIMQDYDWHVFSLVTTIF------PGYREFISFVKTTV-DNSFVGWD-MQ-------------
    -NVITLDTSFEDAKTQVQLKKIHSS-----------VILLYCSK-DEAVLILSEAR--S--LGLT-GYDFFWIVPSL---------
    ---------VSGNT--------ELIPKEFPSG-LISVSYDDW-----------------------------DYSLEARVRDGIGI
    LTTAA-----------SSMLEKFSYIPEAKA-------------------SCYGQMERPE------------VPMHTLHPFM----
    -------------VNV-TWDGKDL----SFTE-EGYQVHP----RLVV--------IV----LNKDREWEK---------------
    VGKW----------------ENHTLSLR-----------------------HAVWP-----------------RYKSFSDCE---
    -----------PDDNH---LSIVTLEEAPFVIVEDIDPLTETCVRNTVPCFVKINNSTNEGMNVKKCCKGFCIDILKKLSR--TV-
    K-----FT-YDLYLVTN-G-KHGKK--------VN-NV--WNGMIGEVVY---------Q---RAVMAVGSLTINEERSEVVDFSV
    PFVET-GISVMVSR----SNGT-----------VSPSAFLEPFSASV-W---VMMFVMLLIVSAIAVFVFEY--FSPV-GYN----
    ------RNLAK--------------------GKAPHG----PSFTIGKAIWLLWGLV-FNN-----SVPVQNP---KGTTSKIMVS
    VWAFFAVIFLASYTANLAAFMIQEEFVDQVT--GLSDKKFQRPHDYSPPFRFG-TVPNGSTERNIR-------------NNYPYMH
    QYMTKF-----------------------NQKGVEDALVSLK----TGK---------LDAFIYDA-AVLNYKAGR-DE--GC-
    KLVTIGSGYI-FATTGY-GIA-LQK---G---SP--WKRQIDLALLQ--FVG-DGEMEELETL------WLT-------GICHNE-
    -KNEVMS------SQLDIDNMAGVFYMLAAAMALSLITFIWEHLFYWKEKKKSPDFNLTGSQSNMLKLLRSAKNISSMSNMNSSRM
    DSPKRAADFIQRGSLIMDMVSDKGNLMYSDNRSDIDEDQMLQETGNPATGSLKDRERLLEGNFYGSLFSVPSSKLSGKKSSLFPQG
    LEDSKRSKSLLPDHTSDNP
25  Cmil_GluN2
    -------MEGRKMGHLGFLTAVFFHVFALRLDVSAVQKDYPTLNIAVILGRTTYLADIRDTWSKELPIDVNVVMIEVNHTDPKSII
    TH------VCDLMSGTKIHGVVFADDTDQ------------EAIAQILDFISSHTFIPILGIH---------------GGSSMIMA
    DKDLKSTFFQFGASIQQQVMVMLNIMEEYDWHIFSIVTSTF------PGYGEFISILKNTV-ENSFVGWE-LV-------------
    -NTITVDATEGDSKAQIQLKKIQSS-----------VILLYCAK-DEAVFILEEAR--S--LGLT-DYGFVWIVPSL---------
    ---------VTGNT--------EIIPSEFPAG-IISVSYDEW-----------------------------DYLLQERVRDGLGI
    ITTAA-----------SAMMDEYGYIPEAKT-------------------SCYGQLETNV------------LPFNSIHRFM----
    -------------MNI-SWDGRDL----SFTR-DGYQANP----KLVV--------IV----LNKERTWEK---------------
    VGKW----------------ENSSLNLK-----------------------YPVWP-----------------RFSSFADSE---
    -----------VDDNH---LTIVTLEEAPFVIVENVDALTGTCVRNNVPCIKTSNATNHKGTYVKKCCKGFCIDILKKLSR--TV-
    K-----FT-YDLYLVTN-G-KHGKKIH---------GV--WNGMVGDVVY---------E---RAHMAVGSLTINEERSEVIDFSV
    PFVET-GISVMVSR----SNGT-----------VSPSAFLEPFSAAV-W---VMMFVTLLMVSAVAVFLFEY--FSPL-GYN----
    ------RNLAQ--------------------GKNPHG----PSFTIGKAIWLLWGLV-FNN-----SVPVQNP---KGTTSKIIVS
    VWAFFAVIFLASYTANLAAFMIQEEFVDQVT--GLSDNKFQRPYDYSPPFRFG-TVPNGSTERNIR-------------NNYPDMH
    AYLSKY-----------------------NLKGVQDALMNLK----AGK---------LDAFIYDA-AVLNYMAGR-DE--GC-
    KLVTIGSGYV-FSTTGY-GIA-LQK---G---SP--WKRQIDLALLQ--FVG-DGEMEELEAL------WLT-------GICHNE-
    -KNEVMS------SQLDVDNMAGVFYMLAAAMALSLITFVWEHWFYWNNRPYQPKETVFADNTSEMLTFSANRHKDNRNNYMLQAQ
    HPLTLNDAISEDYMLQEPVSPMQPEESFAHHWAASEACNMQKVNRLRISRSLKEKDRFQDDNPYAHVFNIKPDKLYSAKVSVFDHN
    LEESKRSKSLYPDHVSENP
26  Locu_GluN2a
    ----DAGMKMTNMGNMGWLLLTLPALLCHSGSVWGAEKVPILNIAVILGQTRYVSDRD-----IRALWSKDDPIDVNVVTLLVNET
    DPKSIITHVCDLMSGTKIHGVVFGDGTDQ------------EAIAQILDFISSQTFIPIFGIH----------GGSSMIMADKDQK
    STFFQ-----FGASIQQEALLMLNIMEEYDWHVFSIVTSKF--PGYQDFISILKSTVDNSF-----VGWD-LQ-------------
    -NTITLDAVDGDTKTQIQLKKIQSS-----------VILLYCSK-DEAVYILEEAR--S--LGLT-GYGFIWIVPSL---------
    ---------TTGNT--------EVTPNEFPSG-MISVSYDEW-----------------------------DYPLEARVRDGLGI
    ITTAA-----------SSMLEEFGDIPEAKT-------------------SCYGQMEKTK------------LPPSALHKYM----
    -------------MNV-TWDGRDL----SFTE-DGYQANP----KLVV--------IV----LNKDREWEK---------------
    MGKW----------------ENKSLTLK-----------------------YPVWP-----------------RFNSFGDSE---
    -----------SDDNH---LSIVTLEEAPFVIVENVERLTGTCMRNSVPCKHIKDNTTVEGTYIKKCCKGFCIDILKKIAR--NV-
    K-----FT-YDLYLVTN-G-KHGKK--------IN-NV--WNGMVGEVVY---------K---KAVMAVGSLTINEERSEVIDFSV
    PFVET-GISVMVSR----SNGT-------V----SPSAFLEPFSASV-W---VMMFVMLLIVTAMAVFIFEY--VSPL-GFN----
    ------RNLAQ--------------------GRDPHG----PSFTIGKAVWLLWGLV-FNN-S--VP--VQNP---KGTTSKIMVS
    VWAFFAVIFLASYTANLAAFMIQEEFVDQVT--GLSDKKFQSPYSYSPPFRFG-TVPNGSTERNIR-------------NNYPDMH
    QYMVKY-----------------------NQKGVQDALVSLK----SGK---------LDAFIYDA-AVLNYMAGR-DE--GC-
    KLVTIGSGYI-FATTGY-GIA-LQK---G---SS--WKRQVDLAILA--IIG-DGEMEELEAQ------WLT-------GICHNE
```

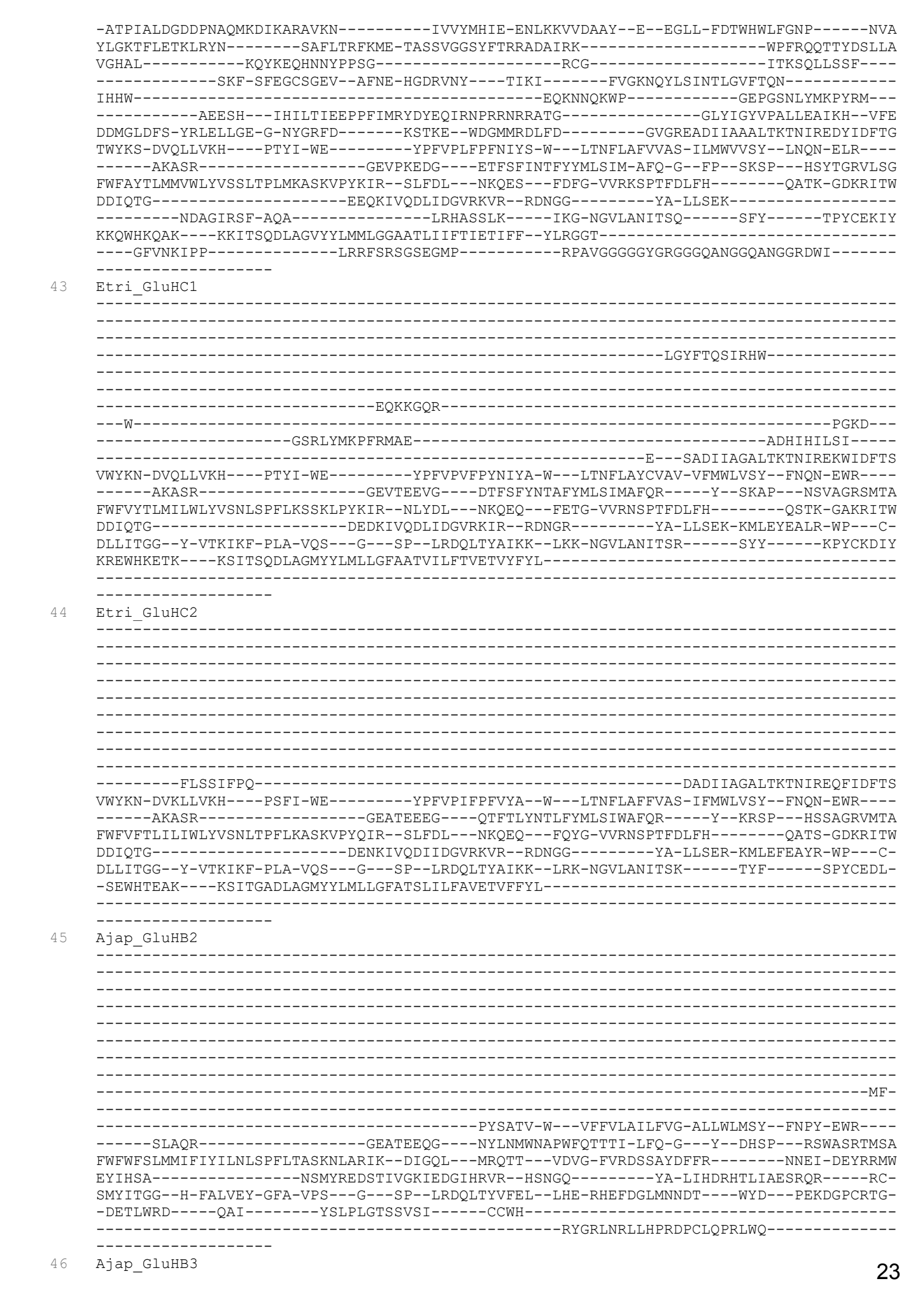
```
-KNEVMS------SQLDIDNMAGVFYMLAAAMALSLITFIWEHLFYWREKKKSSDLDFSSPQANMLKLIKSAKNMTTMSNLNASRI
NSPKRATDYMHGGPMMMDMVVDKGNFLYADNRSISEDQMLQEAISPLNQDSLKEKDRFLEDSPYANMFSMKPDKLFSSKSMLFNHN
LEESKRSKSLYPDHTSENP
27  Hsap_GluN2B
-------MKPRAECCSPKFWLVLAVLAVSGSRARSQKSPPSIGIAVILVGTSDEVAIK---DAHEKDDFHHLSVVPRVELVAMNET
DPKSIITRICDLMSDRKIQGVVFADDTDQ------------EAIAQILDFISAQTLTPILGIH----------GGSSMIMADKDES
SMFFQ-----FGPSIEQQASVMLNIMEEYDWYIFSIVTTYF--PGYQDFVNKIRSTIENSF-----VGWE-LEEV----------
-LLLDMSLDDGDSKIQNQLKKLQSP-----------IILLYCTK-EEATYIFEVAN--S--VGLT-GYGYTWIVPSL---------
---------VAGDT--------DTVPAEFPTG-LISVSYDEW-----------------------------DYGLPARVRDGIAI
ITTAA-----------SDMLSEHSFIPEPKS-------------------SCYNTHEKRI------------YQSNMLNRYL----
-------------INV-TFEGRNL----SFSE-DGYQMHP----KLVI--------IL----LNKERKWER---------------
VGKW----------------KDKSLQMK-----------------------YYVWP-------------------RMCPETEE---
-----------QEDDH---LSIVTLEEAPFVIVESVDPLSGTCMRNTVPCIVTENKTDEEPGYIKKCCKGFCIDILKKISK--SV-
K-----FT-YDLYLVTN-G-KHGKK--------IN-GT--WNGMIGEVVM---------K---RAYMAVGSLTINEERSEVVDFSV
PFIET-GISVMVSR----SNGT-----------VSPSAFLEPFSADV-W---VMMFVMLLIVSAVAVFVFEY--FSPV-GYN----
------RCLAD--------------------GREPGG----PSFTIGKAIWLLWGLV-FNN-----SVPVQNP---KGTTSKIMVS
VWAFFAVIFLASYTANLAAFMIQEEYVDQVS--GLSDKKFQRPNDFSPPFRFG-TVPNGSTERNIR-------------NNYAEMH
AYMGKF------------------------NQRGVDDALLSLK----TGK---------LDAFIYDA-AVLNYMAGR-DE--GC-
KLVTIGSGKV-FASTGY-GIA-IQK---D---SG--WKRQVDLAILQ--LFG-DGEMEELEAL------WLT-------GICHNE-
-KNEVMS------SQLDIDNMAGVFYMLGAAMALSLITFICEFYWQSRRLLRTAKNMANLSGVNGSPQSALDFIRRESSVYDISEH
RRSFTHSDCKSYSTTKYPQSPTNSKAQKKNRNKLRRQHSYDTFVDLQKEESKSLYPDRVTQNPFIPTFGDDQCLLH----------
--------------------
28  Cmil_GluN2b
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
-------------------------------------------------------TQPS-----------------------------
-----------------------------------LAAFFCPQ-NTQ-----------------------------------------
----------------------SLHCAAYPV-------------------------------------------------------
-------------------------------------------------------------------KPAVMIYLCL----------
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
--------------------APSNQTEGGIYIK-------------------------------RCCKGFCIDILKKIAK--YV-
K-----FT-YDLYLVTN-G-KHGKK--------IN-GT--WNGLVGEVVR---------K---KAHMAVGSLTINEERSEVVDFSV
PFIET-GISVMVSR----SNGT-------V----SPSAFLEPFSADV-W---VMMFVMLLIVSAVAVFVFEY--FSPV-GYN----
------RCLAD--------------------GREPGG----PSFTIGKAIWLLWGLV-FNN-S--VP--VQNP---KGTTSKIMVS
VWAFFAVIFLASYTANLAAFMIQEEYVDQAQ----------SPP----------FPTPRSTKRNIR-------------NNYPEMH
SYMTKF------------------------NQKSVLDALVSLK----AGK---------LDAFIYDA-AVLNYMAGR-DE--GC-
KLVTIGSGKV-FATTGY-GIA-IQK---V---SG--WKRPVDLAILQ--LFG-DGDMEELEAL------WLT-------GICHNE-
-KNEVMS------SQLDLDNMAGVFYMLGAAMALSLITFICEHLFYWQESHKYPFKGDRYAHDDLIRSDVSDISTHTVTYGNIGSA
KRRKQYKDSLRKRPPGGVTVGVAANVKHHQSPAGSAKLQRRDRGKLRRQHSKSLYPDRVTHNPFIPTFGDDQCLLH----------
--------------------
29  Hsap_GluN2D
GPRGPRGPAKMLLLLALACASPFPEEAPGPGGAGGLGGARPLNVALVFSGPAYAAEAA----------RLGPAVAAAVRALVLNGS
DPRSLVLQLCDLL--SGLRVHGVVFEDDSRA----------PAVAPILDFLSAQTSLPIVAVH----------GGAALVLTPKEKG
STFLQ-----LGSSTEQQLQVIFEVLEEYDWTSFVAVTTRA--PGHRAFLSYIEVLTDGSL-----VGWE-HR-------------
-GALTLDPGAGEAVLSAQLRSVSAQ-----------IRLLFCAR-EEAEPVFRAAE--E--AGLT-GSGYVWFMVGP---------
--------QLAGGG--------GSGAPGEPPL-LPGGAPLPAGLFAVRSAGW--------------------RDDLARRVAAGVAV
VARGA-----------QALLRDYGFLPELGH-------------------DCRAQNRT--------------HRGESLHRYF----
-------------MNI-TWDNRDY----SFNE-DGFLVNP----SLVV--------IS----LTRDRTWEV---------------
VGSW----------------EQQTLRLK-----------------------YPLWS----------------RYGRFLQPVDD---
-------------TQH---LTVATLEERPFVIVEPADPISGTCIRDSVPCNRTHSPPPDAPRPEKRCCKGFCIDILKRLAH--TI-
G-----FS-YDLYLVTN-G-KHGKK--------ID-GV--WNGMIGEVFY---------Q---RADMAIGSLTINEERSEIVDFSV
PFVET-GISVMVAR----SNGT-------V----SPSAFLEPYSPAV-W---VMMFVMCLTVVAVTVFIFEY--LSPV-GYN----
------RSLAT--------------------GKRPGG----STFTIGKSIWLLWALV-FNN-----SVPVENP---RGTTSKIMVL
VWAFFAVIFLASYTANLAAFMIQEEYVDTVS--GLSDRKFQRPQEQYPPLKFG-TVPNGSTEKNIR-------------SNYPDMH
SYMVRY------------------------NQPRVEEALTQLK----AGK---------LDAFIYDA-AVLNYMARK-DE--GC-
KLVTIGSGKV-FATTGY-GIA-LHK---G---SR--WKRPIDLALLQ--FLG-DDEIEMLERL------WLS-------GICHND-
-KIEVMS------SKLDIDNMAGVFYMLLVAMGLSLLVFAWEHLVYWRRWRRTKGAGPPGGAGLADGFHRYYGPIEPQGLGLGLGE
ARAAPRGAAGRPLSPPAAQPPQGAPAAPPPCRAAPPPCPYLDLEPSPSDSPPRSGPAAWHCRHCASLELLPPPRHLSCSHDGLDGG
WW-----------------
30  Hsap_GluN2C
--------------MGGALGPALLLTSLFGAWAGLGPGQGEQGMTVAVVFSSSGPPQAQFRARLTPQSFLDLPLEIQPLTVGVNTT
NPSSLLTQICGLLGAAHVHGIVFEDNVDT------------EAVAQILDFISSQTHVPILSIS----------GGSAVVLTPKEPG
SAFLQ-----LGVSLEQQLQVLFKVLEEYDWSAFAVITSLH--PGHALFLEGVRAVADASH-----VSWR-LLDV----------
-VTLELGPGGPRARTQRLLRQLDAP-----------VFVAYCSR-EEAEVLFAEAA--Q--AGLV-GPGHVWLVPNL---------
---------ALGST--------DAPPATFPVG-LISVVTESW-----------------------------RLSLRQKVRDGVAI
LALGA-----------HSYWRQHGTLPAPAG-------------------DCRVHPGPVS------------PAREAFYRHL----
-------------LNV-TWEGRDF----SFSP-GGYLVQP----TMVV--------IA----LNRHRLWEM---------------
VGRW----------------EHGVLYMK-----------------------YPVWP----------------RYSASLQPVVD---
-------------SRH---LTVATLEERPFVIVESPDPGTGGCVPNTVPCSNHTFSSGDVAPYTKLCCKGFCIDILKKLAR--VV-
K-----FS-YDLYLVTN-G-KHGKRVR---------GV--WNGMIGEVYY---------K---RADMAIGSLTINEERSEIVDFSV
PFVET-GISVMVAR----SNGT-------V----SPSAFLEPYSPAV-W---VMMFVMCLTVVAITVFMFEY--FSPV-SYN----
------QNLTR--------------------GKKSGG----PAFTIGKSVWLLWALV-FNN-----SVPIENP---RGTTSKIMVL
```

```
    VWAFFAVIFLASYTANLAAFMIQEQYIDTVS--GLSDKKFQRPQDQYPPFRFG-TVPNGSTERNIR-------------SNYRDMH
    THMVKF-----------------------NQRSVEDALTSLK----MGK---------LDAFIYDA-AVLNYMAGK-DE--GC-
    KLVTIGSGKV-FATTGY-GIA-MQK---D---SH--WKRAIDLALLQ--FLG-DGETQKLETV------WLS-------GICQNE-
    -KNEVMS------SKLDIDNMAGVFYMLLVAMGLALLVFAWEHLVYWKPPRQASPDLTASSAQASVLKMLQAARDMVTTAGVSSSL
    DRATRTIENWGGGRRAPPPSPCPTPHYSSFPRADRSGRPFLPLFPELEDLAEAFARPSSLPAGCTGPACARPDGHSACRRLAQAQS
    MCLPIYREACQEGEQAGAP
31  Cmil_GluN2cb
    ----SWYSTGNRLQLFQMFGACAFSRDPSRPAISVAVVLGGSWYSLEIKGQFSRDVFQ------GLPLQINPIIEVVNNTNPSSLL
    TQ------ICGVLSSSSIHGVIFEDNIES------------DAVAQILDFISAQTLIPIIGIS---------------GGSAAVLA
    PKEQRSAFLQLGASIEQQISVIFKVLEEYDWNSFAIITSLF------PGYQEFIDYIKLFT-GTSYFGWE-IEQT-----------
    -LTFEMTRDENNSKTQRLLKQIDAQ-----------VLLLYCSR-EEAEYLFEEAE--E--AGLV-GPGYIWIVPSV---------
    ---------TVGNT--------EQVAKSFPVG-LIGIMTDRW------------------------------NTNLRQRVRDGVAI
    VAKGV-----------DSFFSEHGYIPDLSS--------------------DCRSLGG---------------LYNNAFYRYM----
    -------------LNV-SWEGKDF----SFNE-DGYLVRP----IMVV--------MT----LNRGRYWEM---------------
    VGKW---------------ENSLIRMK-----------------------YPVWP--------------RYGTSLQPVSD-----
    -------------SHH---LTVATLEERPFVIVEAVEPMTGGCVRNTVPCKQANHSESIVDPYTKLCCKGFCIDILKKLSK--TV-
    K-----FS-YDLYLVTN-G-KHGKKVR---------GI--WNGMIGEVFY---------K---RADMAIGSLTINEERSEIVDFSV
    PFVET-GISVMVAR----SNGT-------V----SPSAFLEPYSPAV-W---VMMFVMCLTVVAITVFIFEY--FSPV-GYN-----
    ------RNLND--------------------GKNPGG----PTFTIGKSVWLLWALV-FNN-----SVPIENP---KGTTSKIMVL
    IWAFFAVIFLASYTANLAAFMIQEQFIDTVS--GLSDNKFQKPQEHYPPFRFG-TVPNGSTERNIK-------------NNYPDMH
    SHMTKY-----------------------NQRSVEDALNSLK----SGK---------LDAFIYDA-AVLNYMAGK-DE--GC-
    KLVTIGSGKV-FATTGY-GIA-MQK---E---SK--WKRPIDLGLLQ--FLG-DGETQKLQTV------WLT-------GICENE-
    -KNEVMS------SKLDIDNMAGVFYMLLVAMGLSLLVFAWEHLFYWKRTSQPMEDACGIASKHHFVPCISNSNHIHCIPRTINTA
    PTLLQNRGPGRQFMEPQRITADHPIITYKSHSPREQRGKPRLQDVCGSIEHIHLDADCRHAGPQHRLKHSQSAKLPSYSEACLQSS
    AALRRSSTVVHRHYSWL--
32  Locu_GluN2cb
    ----------MGMPLGWLSASLWLLLWGARSSLGRPFGPPTVNVAVVFSGSTYQTEIK---GRLSRENFADLPIEVNPITVLVNDT
    NPRALLTRICDTL--DTNRVHGVVFEDNVGS----------EAVAQILDFISTQTSMPIIGVS----------GGSAVVIPHKGDG
    STFLQ-----LGSSIEQQINAMFKVMEEYDWGNFAVITSLY--PGYEHFVDYIRSFTDTSY-----FLWE-LQEV----------
    -VTFEMSEGANDIRSRRLLQQVDAQ-----------VLMVYCSH-EEAQYLFSMAS--E--VGLI-SPGYIWLVPSL---------
    --------VVGNLD--------IPPPENFPVG-LISITTDRW------------------------------KMSLRQRVRDGVAI
    VVKGV-----------QSFRRHHGYIPEGHT-------------------DCHNPIGP--------------TTNNTLFRHM----
    -------------LNV-TWEHKDF----SFNS-NGYLVNP----ALVI--------IT----LDREHQWDR---------------
    VGNY----------------EMGILQAR-----------------------YPVWP--------------RYGSLMEPVSD-----
    -------------NRH---LTVATLEERPFVIVE-----SVDPLTGTCVRNKTDLFVGHTEPYTKLCCKGFCIDILKKLSR--TI-
    K-----FS-YDLYLVTN-G-KHGKK--------VR-GI--WNGMIGEVFY---------K---RADMAIGSLTINEERSEIIDFSV
    PFVET-GISVMVAR----SNGT-------V----SPSAFLEPYSPAV-W---VMMFVMCLTVVAITVFVFEY--FSPV-GYN-----
    ------RSLVS--------------------AKEPGG----PTFTIGKSVWLLWGIV-FNN-S--VP--IENP---KGTTSKIMVL
    VWAFFAVIFLASYTANLAAFMIQEQYIDTVS--GLSDKKFQKPQEQYPPFRFG-TVPNGSTERNIR-------------SNYPDMH
    THMIKY-----------------------NQRGVEDALNSLK----TGK---------LDAFIYDA-AVLNYMAGK-DE--GC-
    KLVTIGSGKV-FATTGY-GIA-LQK---D---SR--WKRPIDLALLQ--FLG-DGDTQRLETV------WLS-------GICQNE-
    -KNEVMS------SKLDIDNMAGVFYMLLVAMGLSLLVFAWEHLLYWKRRSEHIKGGIPTRVPQVATSDTSVGIGRHPYISSITDN
    HSPFSQRALTPTLTVHYAENASQPLLEKQRGMARPTPVRPEPEDLPLLGKINPYKAQKLKYSQSTRLPSYREAVLQNAAALRRSST
    VV-----------------
33  Cint_GluE2
    TAESASRYVRTGFCSFLLFFVLLPFCMCEEATIAEIAVIYPAPRNLTFESSMQCVTQY-------INANILQNVTLRLQTNTLEYD
    HTGVNAFKAGLALNKRSGVMGLLGPIH--------------TNDVTVLHSQIAAMNIPQIVPI----------------SRVTTKS
    YMSHFPMLVKMTKGYMNQVSAMVDLILEMQWKTVGILIENS-----EYYRDISRNFYPSVRAANITVKFF-IS-------------
    -FNEVGIGVADTKEEMQTIKKSGQR-----------VILLLTSD-RLVNSVLDEAK--N--CGLT-NSEWVWLLWAD-------IV
    NTMKGMQSLEVQSG--------FALVQTFPST-NLSETLKTCEIP---------------------------HNFVFRKYMDSLFA
    FAYGL-----------KSLFSENRTSVKAPTAGIRW-----------------------------------ENGRLFLEHI-----
    -------------LSNHQYNEGIASHKIEFDVKTAEVLSTP---TFDV--------VH----LHNSSCQT----------------
    VGNW-------------------------------------------------SMTSR----LSMNNQSKLTALKNNSFNLNNM---
    -----------LKNSK---IRVITMNAPPFVMQE------DENVAN-------------------NTYTGYSFELFRKLQE--DI-
    G-----FT-YEVLTMPS-G-VFGARD-------PLSGQ--WNGLIGQIVD---------G---LADIAVGPFTLTAERSKAVDFTE
    VFYKT-NLKYIIDI----QAAG------GMMSGYDRYGFLRPFTWTL-W---LVIAICVLVVG-IFFTLVSH--LSPY-GHYFQSD
    EAEAAIKKEESRDRSVDRQIASKPNVTDDDESDEESRSKAQRQMSLSNALYFACAGL-LWQ-S---P--ESVP---RAPSARIVAA
    IWYMVGVIIVASYTANMVTFVSIKIEASHLL--NVREL---VAQTH---VPPG-TISSSSVETLLK--------TSQY-PIAEKLY
    DAILLD---------------PRMPGYKYHTLQPNQEKALEQVR----IGK----------LA-FVWEG-ALLDHAALE----SDC-
    HLKTVKL--G-FGPTSY-AFV-LKQ---G---SP--YREELSKHIKI--LAK-NGYLDELNKK------YFS-------QTCSHG-
    -LAEDDSNSV---TAISWLSLIGVLDLLLLSAALSVIVLLFEWIV---ASISDIDKTNPR-------------------------
    ----APATFSRAFAARWRRMVQDAKRMGKKEVPVVNAI------------EPDQWKRYTTSTDAINLKPGQSISNPELF-------
    ------------------
34  Arub_GluHC
    ----MAVHGWIAVQLVLALIGYATSFEYKIGAMYGANTHEKDLYKNLFTDASVFINRD-RELSNDGRDRISIYNYAPVGGIEWALP
    NTPQALRAACTFA--SSVDLHGLIIPSDMC-----------PNCGGHTGRIVGDAFSPVIALD-------------------QAEG
    SNAYK-----MLMTDSDLMDLWISVINHYKWQDFIFIYDGD------SAYSVALMLMAMEE----DNDW----------------
    -HIVPYEISEDWDVMAKDLKKRRIQN----------YLLYVHEE-ELLPDLRDWML--D--SGMF-GDKYHWIFGNM-------EP
    PISRNFLDDKLRIH--------TSFLTRFKME-TVFGVDQDVHTRNPIPPRK--------------------WPFRQRTAYDSMVF
    MAKAV-----------MAYHAEWNRWPEAVP-------------------KCGE-----------------DIVCDLDPTM----
    -------------QKI-SHEGLSGEV--AFNE-NRDRVNY----TINI--------FM----GKDKHNILQ---------------
    AGRW-----------------------------------TQNIDHYERKKGVKWP-------------EGKGRLDMFPFRQ---
    -----------SDQGY---IKILSIEEPPFMMLKDRDYTRETRQVEENDG-------------LDRYIGYIPELLQHVKR--VEE
```


EDMHMEFK-YRIELVSE-G-YYGKRN-------PNTGE--WDGLVKELQD---------S---DADLAAAAFTVTRPREEVIDFSK
HFVKS-NIMTLMKH----PNWR-RD---------FPFNFAFSFHWDT-W---LVNLFALGIAI-LAIWLIMR--YHPL-EYR----
------RQAAT-----------------GNATQEQA----DSYTLRNSAWTLVCIM-FWQ-G---H--KSSP---KSYSGRIMLA
TWFFFCIVMLFLFMLNLSDFIVIDKTILFIN--DPVDL---LNEPL---LKIG-MVRDSPTHNYYS--------MSTN-PDDQQLM
TLMGVL---------------------DRAPFVQKLRDGALRVR--NDNGH---------YA-LVSEE-IMLSFYTQK-GP--WC-
DLYIAGD--P-VKKIKF-AFA-TPS---G---SP--LRDQITYVMNK--LGQ-EGVLQDLAERR-----WFG------DQKCENE-
-TIWEEESL----LSINANDLEGIYYVLAMGVVLSVIIFFIDVLSFWQ-----------------------------------
----GSCSNSGTQLPPTGQVARRNRQGDNGIRLTDNPS-----------SSTPPPVRNDGYDYGAKPTEKSPNLWI---------
----
35 Pmin_GluHC
----MAVIWGLAALFIMSFIGSTTSQSYKIGAMYGANTNMDNHYKELFVDATTYINRD-PEFMNGNRETLNVYNYRPIAGTNWSLP
NAPQALRAACTFASSVDMHGLIVPSDVC-------------PGCSGHTGRIVGNAFAPVIALD-------------------QASG
SKAYK-----MLPTDSDLLELWVSVINHYKWQDFIFIHDGD------SAYSMAWILLEMEN----QNKWH-V--------------
-VPYQIYDEADYAEMAKDLKKRRTQ-----------NYLLFLHEEERLPGFVNWML--D--SGMF-GDKYHWIFGNL-------EP
PISRQFLDDKLRIH--------TSFLTRFKMK-IVEGVESKVLTRNPIPTRN-------------------WPFRERTAYDSMLF
FAKAM-----------TVYREENGRYPEAVP-------------------KCGDDLSS--------------QLGTVMQKV-----
----------------SYEGLSGEV--AFNS-DGDRVNY----TINI--------FF----GKDKHNIRQ---------------
AGVW-----------------------------------TQNIDHYERKYGEKWP-------------KNTGRLHMTPFRQ---
-----------SDPSY---IKILSIEEPPLLMLRDHDYTRARRQSSDELG--------------LDRYYGIIPELLVYIQY--IFE
HDMGMEFK-YKIELIAE-G-YYGKRN-------PNTGD--WDGMVKELQD---------S---DADLAAGAFTVTQAREEVIDFTK
DFYKG-NIKTLIKH----PNWV-RD---------FPFNFAFAHDWDT-W---LVNLFAFGITI-LVFWALMR--FHPL-EYR----
------KQSEI------------------GQATREQS----TEFTLRNVAWMLTGVV-FLR-G---H--KLSP---ASIAGRILLA
AWFFFSLVMVFTYMLNLTDFIAIDKDILTIN--DPVDL---LNEPL---LKIG-MVRHGPTHDYYS--------MSSK-ASDQQLM
SIMGVL---------------------DRDPFVERMRDGALRVR--NDNGH---------YA-LVSEE-LLLTYYTQS-GP--WC-
DLYIVGD--P-VKKMKY-AFA-TPS---G---SP--LRDQITYAINK--LKQ-NGTIKELVEKK-----WFG------DQKCEEE-
-SLWESESV----LSINANDLEGIYYVLAIGLVLSAIIFFIDVLCYWV-----------------------------------
----GSCSSAGD--------------PRPSNPRGDGFT-----------MTLNPRRDYGKPPEEKSPNLWI--------------
----
36 Apla_GluHC
----MAVTLGLVALVVGSLVGNTVSQSYKIGAMYGMHTRVDNLYKRLFTDAVTYINRDENLMNIDGTESLAVFNEPLI---TWTYS
NPPQALRGACTFA--GSVDINGLIVPSDVC-----------PDCGGHTGRIIGNAFAPVIALD-------------------QAEG
SKAYK-----MLPTDTELVELWISVINHYKWQDFIFIYDGD------SSYSLAWVLLEMER----ENSWH-V--------------
-IPYEIYDEEDYGKMAKDLKQRRTQN----------YLLYMHEE-ERLPGLRDSML--D--NGLF-GDKYHWIFGNL-------EP
PITRRYLDDKLRIH--------TSFLTRFKMR-VQDGFDQNVLTKNPIPPRN-------------------WPFRERTAYDAMLF
FAQAM-----------TVFRRENGRYPNVVP-------------------KCGE-----------------DVRSELEPVM----
-------------QKI-SIEGLSGEV--AFNS-HGDRVNY----TIDV--------YM----GKDKHNILK---------------
AGVW----------------TQNIAHYERKY---------------------GEVWP-------------KDKGRLNMFPFRQ---
-----------SDQSY---IKVLSIEEPPFLMLRDHNYDRERRQVQTGDE--------------DRYYGIIPELLENIRK--IFE
EELRMEFK-YKIELVAE-G-YYGKRN-------PNTGE--WDGMVKELQD---------S---DADLAAGAFTVTRQREDVIDFTK
HFHTG-PIKVLIKH----PNWV-RD---------YPFAFVFSLHWDA-W---LVNLFAFGITI-LVFWMLMR--YHPM-EYR----
------KQQEV------------------GQATREQS----IEFTLRNTAWMLTGIM-FLR-G---H--KLSP---VSLAGRILLS
AWFYFTLVMVFLYMLNLTEYVTIDKDILSIN--SPTDL---LNEPL---LKIG-MVRNGPTHDYYS--------MSSN-SEDQQLM
SIMGVL---------------------DRQPFVERLRDGALRVR--NDNGH---------YA-LVSEE-ILLTYYTQR-GP--WC-
DLYVVGD--P-VKRLKY-AFA-TPS---G---SP--LRDQITYAINK--LQT-SGVVQELLEKN-----WFG------YQKCEEE-
-TLWESESV----LSINGNDLEGVYYVLAMGVVLSAIIFFIDVICY-----------------------------------
----WLFGSCSSVGTHPPSNPRGPGETITMTVNPRE-------------QHTRNDFDYSKPAEEKSPNMWI--------------
----
37 Ajap_GluHB1
---------------------------MSHCVFYGRYTDKDEEYKRIVDDANDHVGDDLRVTHFLPELINNEKIFYSNINQALRVG
--------ICNRV--ENTNLRALVVPNDI------------CDECRNIGGIAGDAVNPVLTTD----------------------
-LSYDSNAIKLYPSKEDLTELFISLVNYTKWRDFIIIYDHG-------AGECVCRRKDCGG----HDGTN-TKIP----------
-MGITPYQVTDLKDLRDKLRNSRVKN----------ILLFCEFE-EIALDVIQMAI--D--DDLM-TDSYHWMLGNI---------
---NLPLIYGQIDK
I---RLGRAYVTRL----
---------------VMDFGGTPGRF-------TTQKAEP---
LDEW---
----------------------------PYRLRL------TYDAVL-------------------TVYEAFKLHLARSNNQ-----
------YP-RQTSKCPG-SDDSGNEMSTLM---EDLKRVNFEGMSGPVNF-----------------------DQRGNRVNYTI
NIYMGKGLTVYFHS----DLRK-----------------QPLGT---W---------------------------------------
---T---Q--DIRS-------------
-W-----------------ELQNNR-----------------------------KWENGNNRLHMR-----------------
-------------------------------AFRNADLDFIKIS-------------------SLVEA----PYLVDD--------
------------SERGF-----------------------------------YGFIPEVLRK----------------------
----

----
38 Anja_GluHB1
------MKLGLCFLLFVGVQQVVFAIELKLATVLGRTGADDGEYSQILRDALEHVSDD---SDFLGIHRIRLELLGETFNSFWQSM
VY------VCSETVVGRSVTALVLPEDV-------------CDDCDDLSATISYATDPIINLD----------------------
-GSLESPAIQMYPSPEDVNSLLKDMLQYYKWVDFTLLYDNG------KLVENLSPLLSEAK----DYGW-----------------
-NIRLLPLSDDFKETADAIKYDRLQDVNN-------IILYTFTE-EVALDVIKKGI--T--HGIV-SKGFHWMIANI--------D
LFLERGFIEELRYT--------DAFITRFNMN-ETDGSLSTTTTRQRTK----------------------YEFRQRLAFDSALA
TGHAL-----------RLYRMDNERADGTNPFEVDNEIVVNMP-------RCSVE----------------PQSSALKPYF--


39 Lvar_GluHC2
40 Spur_GluHC2
41 Lvar_GluHC1
42 Spur_GluHC1


-ATPIALDGDDPNAQMKDIKARAVKN----------IVVYMHIE-ENLKKVVDAAY--E--EGLL-FDTWHWLFGNP------NVA
YLGKTFLETKLRYN--------SAFLTRFKME-TASSVGGSYFTRRADAIRK-------------------WPFRQQTTYDSLLA
VGHAL----------KQYKEQHNNYPPSG--------------------RCG-------------------ITKSQLLSSF----
-------------SKF-SFEGCSGEV--AFNE-HGDRVNY----TIKI-------FVGKNQYLSINTLGVFTQN------------
IHHW---EQKNNQKWP-----------GEPGSNLYMKPYRM---
----------AEESH---IHILTIEEPPFIMRYDYEQIRNPRRNRRATG--------------GLYIGYVPALLEAIKH--VFE
DDMGLDFS-YRLELLGE-G-NYGRFD-------KSTKE--WDGMMRDLFD---------GVGREADIIAAALTKTNIREDYIDFTG
TWYKS-DVQLLVKH----PTYI-WE---------YPFVPLFPFNIYS-W---LTNFLAFVVAS-ILMWVVSY--LNQN-ELR----
------AKASR-----------------GEVPKEDG----ETFSFINTFYYMLSIM-AFQ-G--FP--SKSP---HSYTGRVLSG
FWFAYTLMMVWLYVSSLTPLMKASKVPYKIR--SLFDL---NKQES---FDFG-VVRKSPTFDLFH--------QATK-GDKRITW
DDIQTG--------------------EEQKIVQDLIDGVRKVR--RDNGG---------YA-LLSEK------------------
---------NDAGIRSF-AQA---------------LRHASSLK-----IKG-NGVLANITSQ------SFY------TPYCEKIY
KKQWHKQAK----KKITSQDLAGVYYLMMLGGAATLIIFTIETIFF--YLRGGT---------------------------------
----GFVNKIPP-------------LRRFSRSGSEGMP-----------RPAVGGGGGYGRGGGQANGGQANGGRDWI-------
----
Etri_GluHC1

---LGYFTQSIRHW--------------

----------------------------EQKKGQR---
---W---PGKD---
--------------------GSRLYMKPFRMAE---ADHIHILSI-----
---E---SADIIAGALTKTNIREKWIDFTS
VWYKN-DVQLLVKH----PTYI-WE---------YPFVPVFPYNIYA-W---LTNFLAYCVAV-VFMWLVSY--FNQN-EWR----
------AKASR-----------------GEVTEEVG----DTFSFYNTAFYMLSIMAFQR-----Y--SKAP---NSVAGRSMTA
FWFVYTLMILWLYVSNLSPFLKSSKLPYKIR--NLYDL---NKQEQ---FETG-VVRNSPTFDLFH--------QSTK-GAKRITW
DDIQTG--------------------DEDKIVQDLIDGVRKIR--RDNGR---------YA-LLSEK-KMLEYEALR-WP---C-
DLLITGG--Y-VTKIKF-PLA-VQS---G---SP--LRDQLTYAIKK--LKK-NGVLANITSR------SYY------KPYCKDIY
KREWHKETK----KSITSQDLAGMYYLMLLGFAATVILFTVETVYFYL-----------------------------------
----

Etri_GluHC2

---------FLSSIFPQ---DADIIAGALTKTNIREQFIDFTS
VWYKN-DVKLLVKH----PSFI-WE---------YPFVPIFPFVYA--W---LTNFLAFFVAS-IFMWLVSY--FNQN-EWR----
------AKASR-----------------GEATEEEG----QTFTLYNTLFYMLSIWAFQR-----Y--KRSP---HSSAGRVMTA
FWFVFTLILIWLYVSNLTPFLKASKVPYQIR--SLFDL---NKQEQ---FQYG-VVRNSPTFDLFH--------QATS-GDKRITW
DDIQTG--------------------DENKIVQDIIDGVRKVR--RDNGG---------YA-LLSER-KMLEFEAYR-WP---C-
DLLITGG--Y-VTKIKF-PLA-VQS---G---SP--LRDQLTYAIKK--LRK-NGVLANITSK------TYF------SPYCEDL-
-SEWHTEAK----KSITGADLAGMYYLMLLGFATSLILFAVETVFFYL-----------------------------------
----

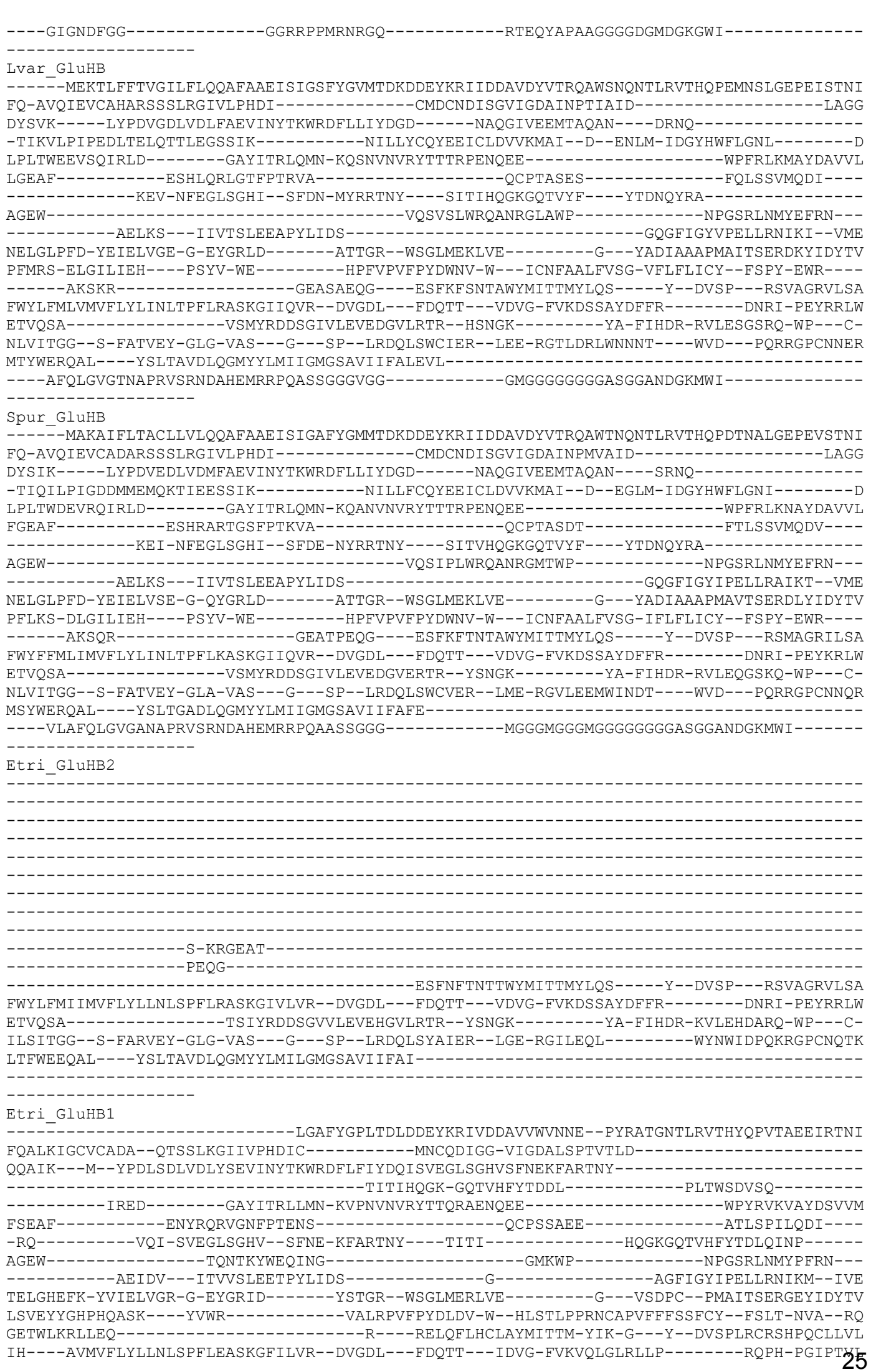
Ajap_GluHB2

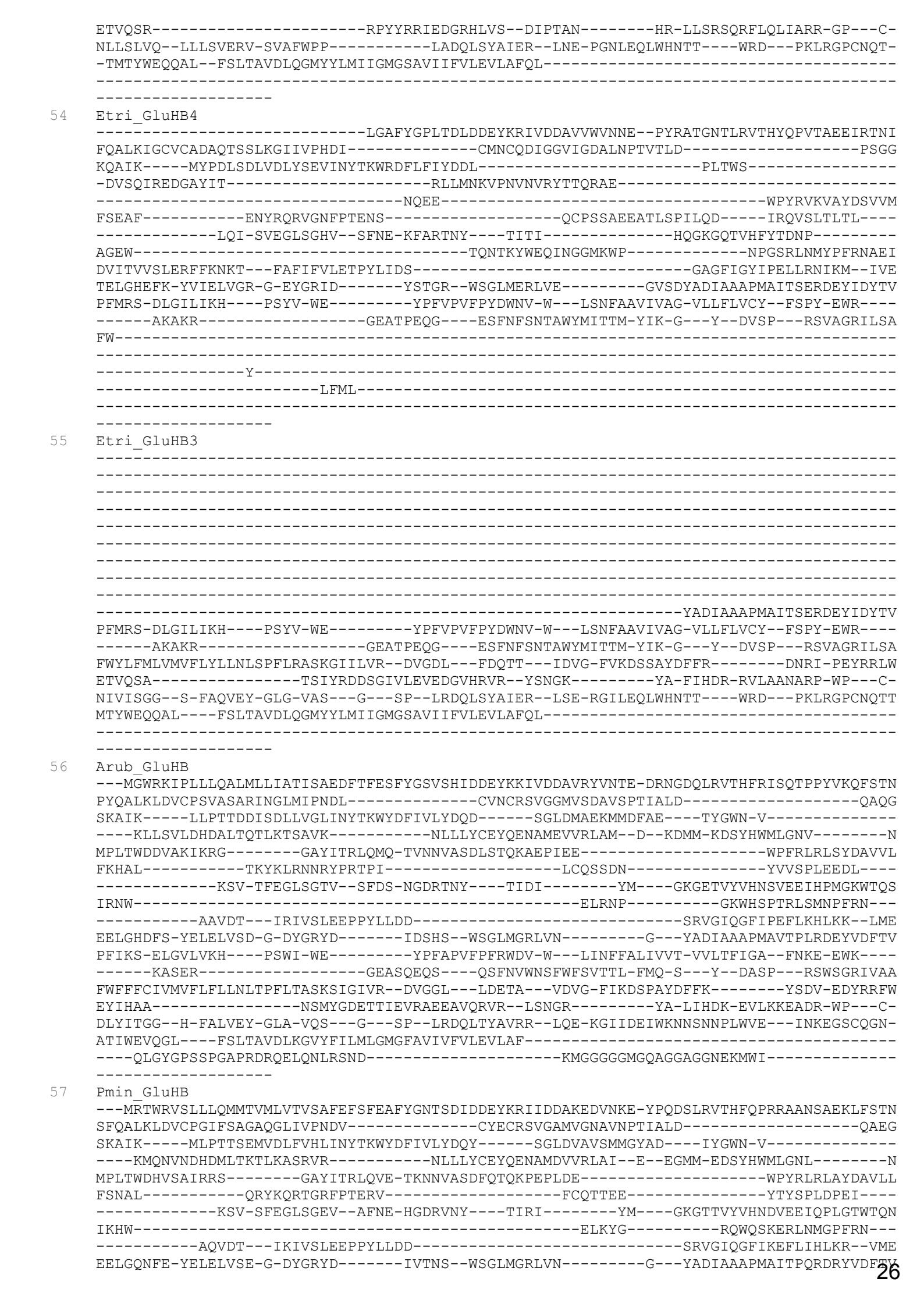
---MF-

---PYSATV-W---VFFVLAILFVG-ALLWLMSY--FNPY-EWR----
------SLAQR-----------------GEATEEQG----NYLNMWNAPWFQTTTI-LFQ-G---Y--DHSP---RSWASRTMSA
FWFWFSLMMIFIYILNLSPFLTASKNLARIK--DIGQL---MRQTT---VDVG-FVRDSSAYDFFR--------NNEI-DEYRRMW
EYIHSA----------------NSMYREDSTIVGKIEDGIHRVR--HSNGQ---------YA-LIHDRHTLIAESRQR-----RC-
SMYITGG--H-FALVEY-GFA-VPS---G---SP--LRDQLTYVFEL--LHE-RHEFDGLMNNDT----WYD---PEKDGPCRTG-
-DETLWRD-----QAI--------YSLPLGTSSVSI------CCWH---
---RYGRLNRLLHPRDPCLQPRLWQ--------------

Ajap_GluHB3


47 Amol_GluHB
48 Aech_GluHB
49 Harg_GluHB


50 Lvar_GluHB
51 Spur_GluHB
52 Etri_GluHB2
53 Etri_GluHB1

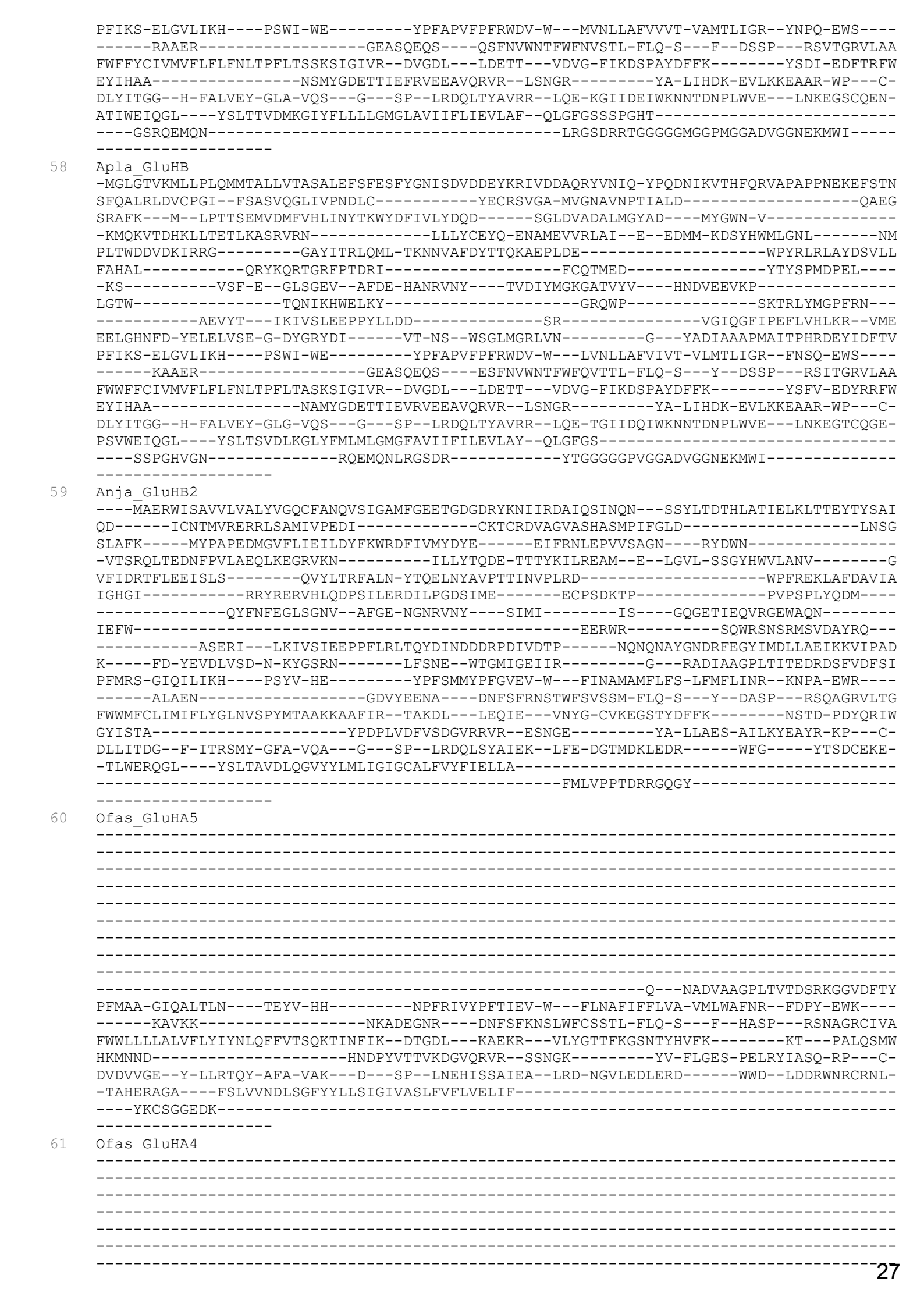

ETVQSR----------RPYYRRIEDGRHLVS--DIPTAN--------HR-LLSRSQRFLQLIARR-GP---C-
NLLSLVQ--LLLSVERV-SVAFWPP----------LADQLSYAIER--LNE-PGNLEQLWHNTT----WRD---PKLRGPCNQT-
-TMTYWEQQAL--FSLTAVDLQGMYYLMIIGMGSAVIIFVLEVLAFQL----------
----
54 Etri_GluHB4
----------LGAFYGPLTDLDDEYKRIVDDAVVWVNNE--PYRATGNTLRVTHYQPVTAEEIRTNI
FQALKIGCVCADAQTSSLKGIIVPHDI----------CMNCQDIGGVIGDALNPTVTLD----------PSGG
KQAIK-----MYPDLSDLVDLYSEVINYTKWRDFLFIYDDL----------PLTWS----------
-DVSQIREDGAYIT----------RLLMNKVPNVNVRYTTQRAE----------
----------NQEE----------WPYRVKVAYDSVVM
FSEAF----------ENYRQRVGNFPTENS----------QCPSSAEEATLSPILQD-----IRQVSLTLTL----
----------LQI-SVEGLSGHV--SFNE-KFARTNY----TITI----------HQGKGQTVHFYTDNP----------
AGEW----------TQNTKYWEQINGGMKWP----------NPGSRLNMYPFRNAEI
DVITVVSLERFFKNKT---FAFIFVLETPYLIDS----------GAGFIGYIPELLRNIKM--IVE
TELGHEFK-YVIELVGR-G-EYGRID-------YSTGR--WSGLMERLVE---------GVSDYADIAAAPMAITSERDEYIDYTV
PFMRS-DLGILIKH----PSYV-WE---------YPFVPVFPYDWNV-W---LSNFAAVIVAG-VLLFLVCY--FSPY-EWR----
------AKAKR----------GEATPEQG----ESFNFSNTAWYMITTM-YIK-G---Y--DVSP---RSVAGRILSA
FW----------

----------Y----------
----------LFML----------

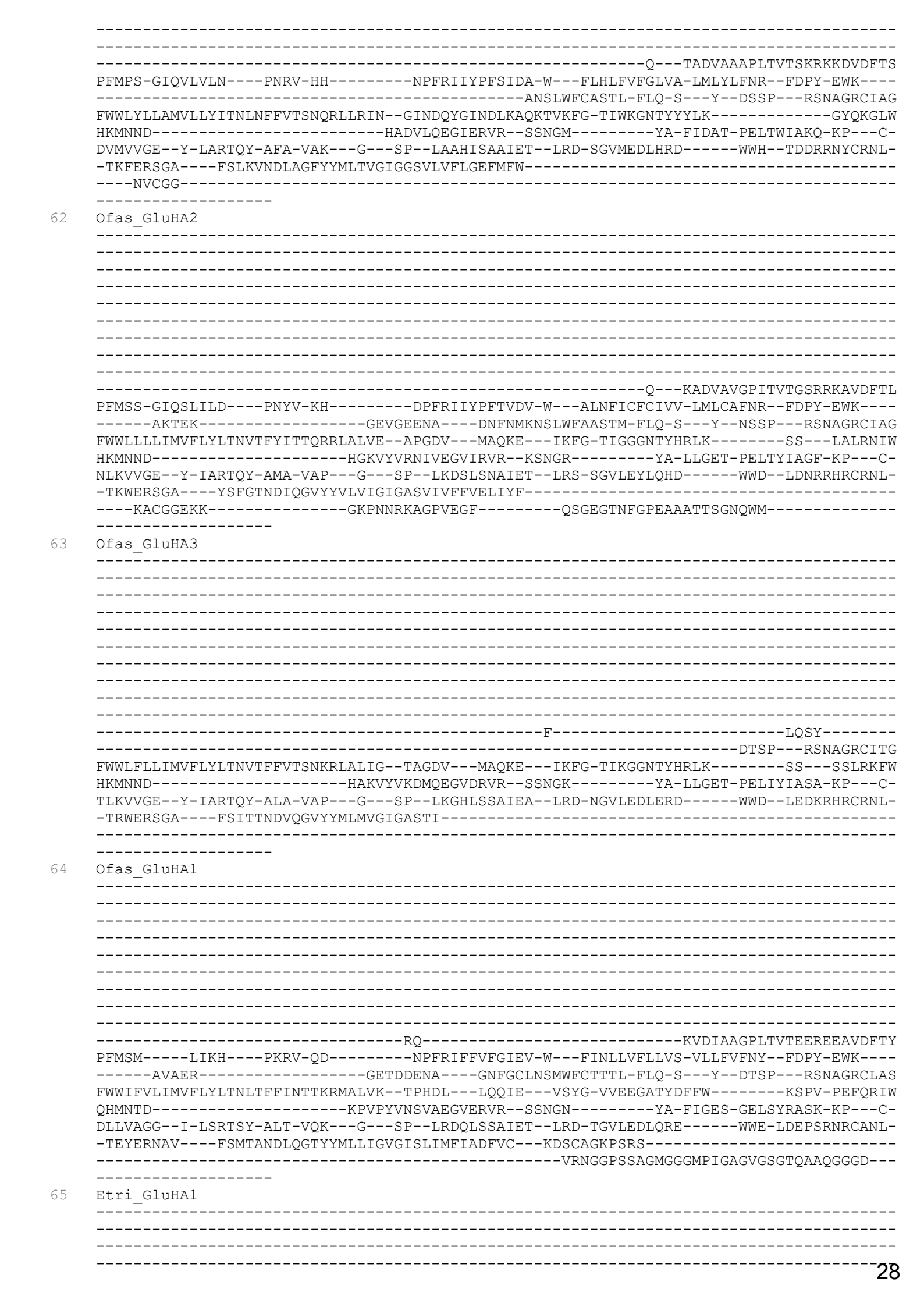
----
55 Etri_GluHB3

----------YADIAAAPMAITSERDEYIDYTV
PFMRS-DLGILIKH----PSYV-WE---------YPFVPVFPYDWNV-W---LSNFAAVIVAG-VLLFLVCY--FSPY-EWR----
------AKAKR----------GEATPEQG----ESFNFSNTAWYMITTM-YIK-G---Y--DVSP---RSVAGRILSA
FWYLFMLVMVFLYLLNLSPFLRASKGIILVR--DVGDL---FDQTT---IDVG-FVKDSSAYDFFR--------DNRI-PEYRRLW
ETVQSA----------TSIYRDDSGIVLEVEDGVHRVR--YSNGK---------YA-FIHDR-RVLAANARP-WP---C-
NIVISGG--S-FAQVEY-GLG-VAS---G---SP--LRDQLSYAIER--LSE-RGILEQLWHNTT----WRD---PKLRGPCNQTT
MTYWEQQAL----FSLTAVDLQGMYYLMIIGMGSAVIIFVLEVLAFQL----------

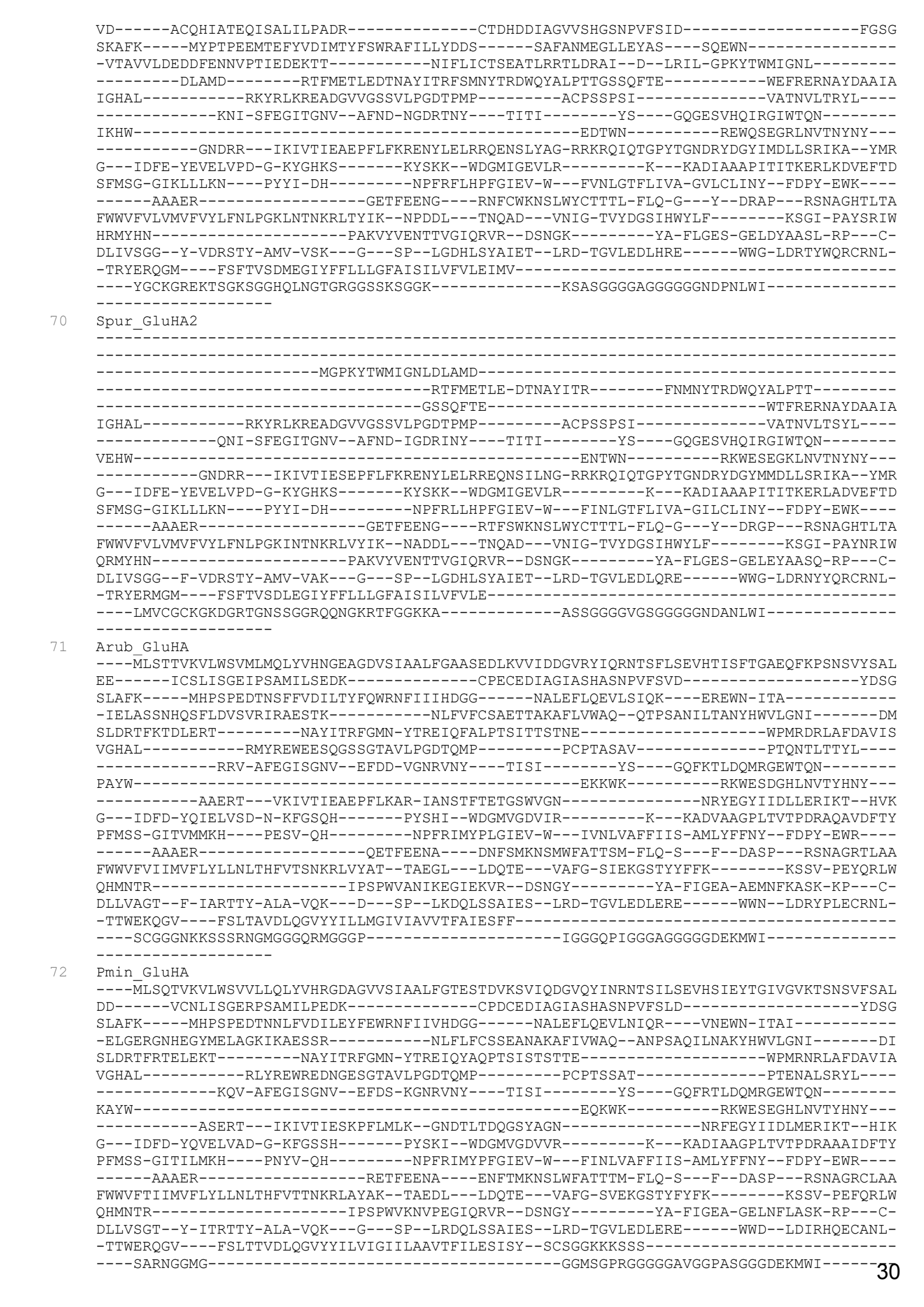
----
56 Arub_GluHB
---MGWRKIPLLLQALMLLIATISAEDFTFESFYGSVSHIDDEYKKIVDDAVRYVNTE-DRNGDQLRVTHFRISQTPPYVKQFSTN
PYQALKLDVCPSVASARINGLMIPNDL----------CVNCRSVGGMVSDAVSPTIALD----------QAQG
SKAIK-----LLPTTDDISDLLVGLINYTKWYDFIVLYDQD------SGLDMAEKMMDFAE----TYGWN-V----------
----KLLSVLDHDALTQTLKTSAVK----------NLLLYCEYQENAMEVVRLAM--D--KDMM-KDSYHWMLGNV--------N
MPLTWDDVAKIKRG--------GAYITRLQMQ-TVNNVASDLSTQKAEPIEE----------WPFRLRLSYDAVVL
FKHAL----------TKYKLRNNRYPRTPI----------LCQSSDN----------YVVSPLEEDL----
----------KSV-TFEGLSGTV--SFDS-NGDRTNY----TIDI--------YM----GKGETVYVHNSVEEIHPMGKWTQS
IRNW----------ELRNP----------GKWHSPTRLSMNPFRN---
----------AAVDT---IRIVSLEEPPYLLDD----------SRVGIQGFIPEFLKHLKK--LME
EELGHDFS-YELELVSD-G-DYGRYD-------IDSHS--WSGLMGRLVN---------G---YADIAAAPMAVTPLRDEYVDFTV
PFIKS-ELGVLVKH----PSWI-WE---------YPFAPVFPFRWDV-W---LINFFALIVVT-VVLTFIGA--FNKE-EWK----
------KASER----------GEASQEQS----QSFNVWNSFWFSVTTL-FMQ-S---Y--DASP---RSWSGRIVAA
FWFFFCIVMVFLFLLNLTPFLTASKSIGIVR--DVGGL---LDETA---VDVG-FIKDSPAYDFFK--------YSDV-EDYRRFW
EYIHAA----------NSMYGDETTIEVRAEEAVQRVR--LSNGR---------YA-LIHDK-EVLKKEADR-WP---C-
DLYITGG--H-FALVEY-GLA-VQS---G---SP--LRDQLTYAVRR--LQE-KGIIDEIWKNNSNNPLWVE---INKEGSCQGN-
ATIWEVQGL----FSLTAVDLKGVYFILMLGMGFAVIVFVLEVLAF----------
----QLGYGPSSPGAPRDRQELQNLRSND----------KMGGGGGMGQAGGAGGNEKMWI----------
----
57 Pmin_GluHB
---MRTWRVSLLLQMMTVMLVTVSAFEFSFEAFYGNTSDIDDEYKRIIDDAKEDVNKE-YPQDSLRVTHFQPRRAANSAEKLFSTN
SFQALKLDVCPGIFSAGAQGLIVPNDV----------CYECRSVGAMVGNAVNPTIALD----------QAEG
SKAIK-----MLPTTSEMVDLFVHLINYTKWYDFIVLYDQY------SGLDVAVSMMGYAD----IYGWN-V----------
----KMQNVNDHDMLTKTLKASRVR----------NLLLYCEYQENAMDVVRLAI--E--EGMM-EDSYHWMLGNL--------N
MPLTWDHVSAIRRS--------GAYITRLQVE-TKNNVASDFQTQKPEPLDE----------WPYRLRLAYDAVLL
FSNAL----------QRYKQRTGRFPTERV----------FCQTTEE----------YTYSPLDPEI----
----------KSV-SFEGLSGEV--AFNE-HGDRVNY----TIRI--------YM----GKGTTVYVHNDVEEIQPLGTWTQN
IKHW----------ELKYG----------RQWQSKERLNMGPFRN---
----------AQVDT---IKIVSLEEPPYLLDD----------SRVGIQGFIKEFLIHLKR--VME
EELGQNFE-YELELVSE-G-DYGRYD-------IVTNS--WSGLMGRLVN---------G---YADIAAAPMAITPQRDRYVDFTV


PFIKS-ELGVLIKH----PSWI-WE---------YPFAPVFPFRWDV-W---MVNLLAFVVVT-VAMTLIGR--YNPQ-EWS----
------RAAER-----------------GEASQEQS----QSFNVWNTFWFNVSTL-FLQ-S---F--DSSP---RSVTGRVLAA
FWFFYCIVMVFLFLFNLTPFLTSSKSIGIVR--DVGDL---LDETT---VDVG-FIKDSPAYDFFK--------YSDI-EDFTRFW
EYIHAA---------------NSMYGDETTIEFRVEEAVQRVR--LSNGR---------YA-LIHDK-EVLKKEAAR-WP---C-
DLYITGG--H-FALVEY-GLA-VQS---G---SP--LRDQLTYAVRR--LQE-KGIIDEIWKNNTDNPLWVE---LNKEGSCQEN-
ATIWEIQGL----YSLTTVDMKGIYFLLLLGMGLAVIIFLIEVLAF--QLGFGSSSPGHT-----------------------
----GSRQEMQN-----------------------------------LRGSDRRTGGGGGMGGPMGGADVGGNEKMWI-----
----
58 Apla_GluHB
-MGLGTVKMLLPLQMMTALLVTASALEFSFESFYGNISDVDDEYKRIVDDAQRYVNIQ-YPQDNIKVTHFQRVAPAPPNEKEFSTN
SFQALRLDVCPGI--FSASVQGLIVPNDLC-----------YECRSVGA-MVGNAVNPTIALD-------------------QAEG
SRAFK---M--LPTTSEMVDMFVHLINYTKWYDFIVLYDQD------SGLDVADALMGYAD----MYGWN-V--------------
-KMQKVTDHKLLTETLKASRVRN-------------LLLYCEYQ-ENAMEVVRLAI--E--EDMM-KDSYHWMLGNL-------NM
PLTWDDVDKIRRG---------GAYITRLQML-TKNNVAFDYTTQKAEPLDE-------------------WPYRLRLAYDSVLL
FAHAL-----------QRYKQRTGRFPTDRI------------------FCQTMED--------------YTYSPMDPEL-----
-KS----------VSF-E--GLSGEV--AFDE-HANRVNY----TVDIYMGKGATVYV----HNDVEEVKP---------------
LGTW----------------TQNIKHWELKY--------------------GRQWP--------------SKTRLYMGPFRN---
-----------AEVYT---IKIVSLEEPPYLLDD--------------SR---------------VGIQGFIPEFLVHLKR--VME
EELGHNFD-YELELVSE-G-DYGRYDI------VT-NS--WSGLMGRLVN---------G---YADIAAAPMAITPHRDEYIDFTV
PFIKS-ELGVLIKH----PSWI-WE---------YPFAPVFPFRWDV-W---LVNLLAFVIVT-VLMTLIGR--FNSQ-EWS----
------KAAER-----------------GEASQEQS----ESFNVWNTFWFQVTTL-FLQ-S---Y--DSSP---RSITGRVLAA
FWWFFCIVMVFLFLFNLTPFLTASKSIGIVR--DVGDL---LDETT---VDVG-FIKDSPAYDFFK--------YSFV-EDYRRFW
EYIHAA---------------NAMYGDETTIEVRVEEAVQRVR--LSNGR---------YA-LIHDK-EVLKKEAAR-WP---C-
DLYITGG--H-FALVEY-GLG-VQS---G---SP--LRDQLTYAVRR--LQE-TGIIDQIWKNNTDNPLWVE---LNKEGTCQGE-
PSVWEIQGL----YSLTSVDLKGLYFMLMLGMGFAVIIFILEVLAY--QLGFGS--------------------------------
----SSPGHVGN--------------RQEMQNLRGSDR------------YTGGGGGPVGGADVGGNEKMWI--------------
----
59 Anja_GluHB2
----MAERWISAVVLVALYVGQCFANQVSIGAMFGEETGDGDRYKNIIRDAIQSINQN---SSYLTDTHLATIELKLTTEYTYSAI
QD------ICNTMVRERRLSAMIVPEDI-------------CKTCRDVAGVASHASMPIFGLD-------------------LNSG
SLAFK-----MYPAPEDMGVFLIEILDYFKWRDFIVMYDYE------EIFRNLEPVVSAGN----RYDWN----------------
-VTSRQLTEDNFPVLAEQLKEGRVKN----------ILLYTQDE-TTTYKILREAM--E--LGVL-SSGYHWVLANV--------G
VFIDRTFLEEISLS--------QVYLTRFALN-YTQELNYAVPTTINVPLRD--------------------WPFREKLAFDAVIA
IGHGI-----------RRYRERVHLQDPSILERDILPGDSIME-------ECPSDKTP--------------PVPSPLYQDM----
--------------QYFNFEGLSGNV--AFGE-NGNRVNY----SIMI--------IS----GQGETIEQVRGEWAQN--------
IEFW---EERWR----------SQWRSNSRMSVDAYRQ---
-----------ASERI---LKIVSIEEPPFLRLTQYDINDDDRPDIVDTP------NQNQNAYGNDRFEGYIMDLLAEIKKVIPAD
K-----FD-YEVDLVSD-N-KYGSRN-------LFSNE--WTGMIGEIIR---------G---RADIAAGPLTITEDRDSFVDFSI
PFMRS-GIQILIKH----PSYV-HE---------YPFSMMYPFGVEV-W---FINAMAMFLFS-LFMFLINR--KNPA-EWR----
------ALAEN-----------------GDVYEENA----DNFSFRNSTWFSVSSM-FLQ-S---Y--DASP---RSQAGRVLTG
FWWMFCLIMIFLYGLNVSPYMTAAKKAAFIR--TAKDL---LEQIE---VNYG-CVKEGSTYDFFK--------NSTD-PDYQRIW
GYISTA---------------------YPDPLVDFVSDGVRRVR--ESNGE---------YA-LLAES-AILKYEAYR-KP---C-
DLLITDG--F-ITRSMY-GFA-VQA---G---SP--LRDQLSYAIEK--LFE-DGTMDKLEDR------WFG-----YTSDCEKE-
-TLWERQGL----YSLTAVDLQGVYYLMLIGIGCALFVYFIELLA---
---FMLVPPTDRRGQGY---------------------
----
60 Ofas_GluHA5

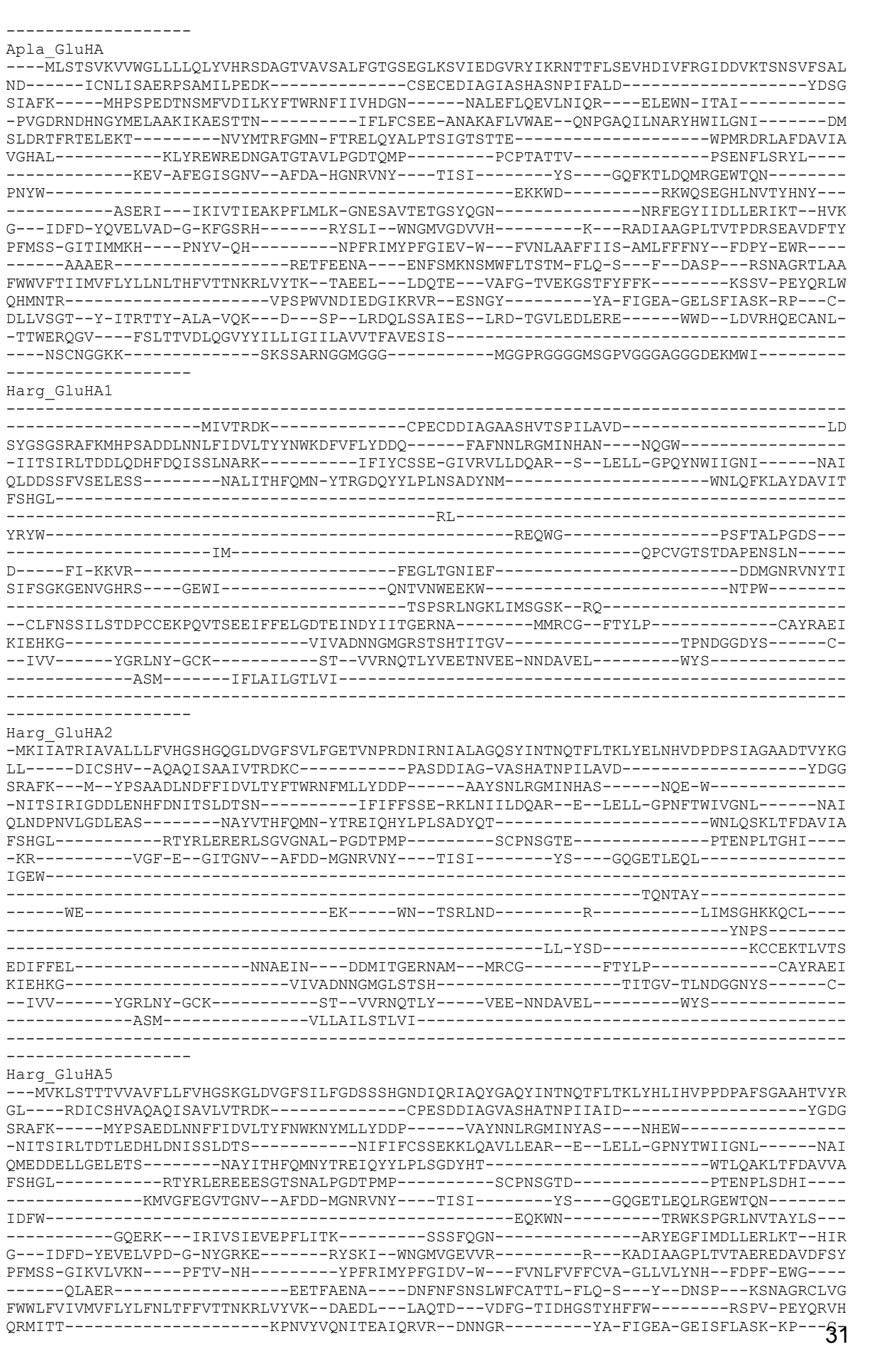
--Q---NADVAAGPLTVTDSRKGGVDFTY
PFMAA-GIQALTLN----TEYV-HH---------NPFRIVYPFTIEV-W---FLNAFIFFLVA-VMLWAFNR--FDPY-EWK----
------KAVKK-----------------NKADEGNR----DNFSFKNSLWFCSSTL-FLQ-S---F--HASP---RSNAGRCIVA
FWWLLLLALVFLYIYNLQFFVTSQKTINFIK--DTGDL---KAEKR---VLYGTTFKGSNTYHVFK--------KT---PALQSMW
HKMNND---------------------HNDPYVTTVKDGVQRVR--SSNGK---------YV-FLGES-PELRYIASQ-RP---C-
DVDVVGE--Y-LLRTQY-AFA-VAK---D---SP--LNEHISSAIEA--LRD-NGVLEDLERD------WWD--LDDRWNRCRNL-
-TAHERAGA----FSLVVNDLSGFYYLLSIGIVASLFVFLVELIF---
----YKCSGGEDK--
----
61 Ofas_GluHA4

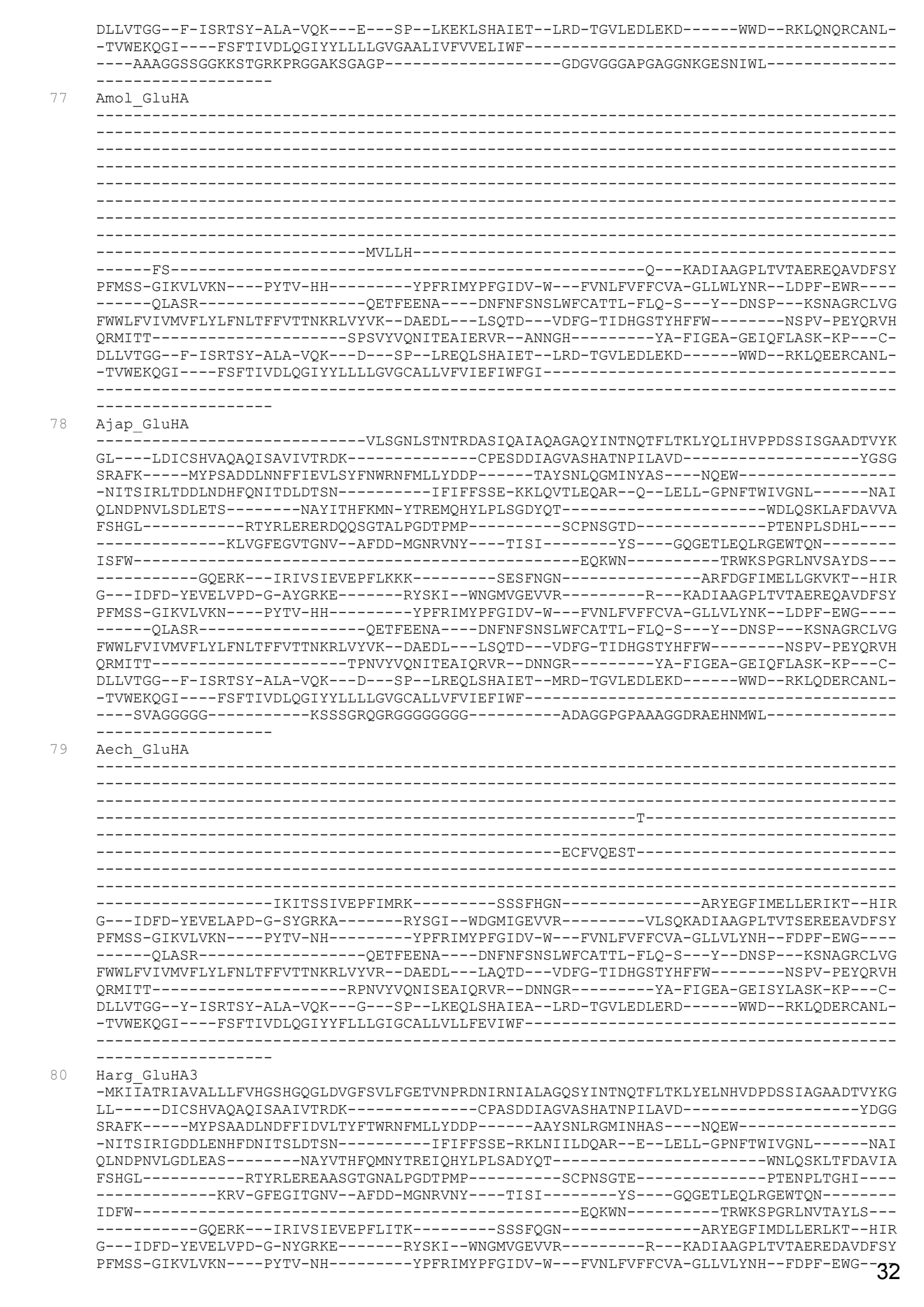

62 Ofas_GluHA2
63 Ofas_GluHA3
64 Ofas_GluHA1
65 Etri_GluHA1

```
------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------
--------------------------FFSKIQAEPFLF---------------------LREKRAAE----------------
------------------------------------------------------------------------------------------
--------------------LARLNSRQTVYTG-----------------------------NDRYEGYIMDLLSRIKS--NMR
G---IDFD-YEVELVPD-G-KYGNKD-------IFSQE--WDGMIGEIVRRVRSRFFICRVRVKADIAAGPLTVTAEREADVDFTY
SFMSG-GIKLLLKN----PYHV-NH---------YPFRLIYPFGIEV-W---FINLITFVLVA-LLLFLFNY--FDPY-EWQ----
------AAAER------------------GETFEENG----RNFNFKNSLWFCATTM-FLQ-S---Y--DNSP---RSNAGRCLTA
FWWVFALVMVFLYLFNLTFFINTNKRLVFVK--TAGDL---LNQND---VDFG-TVDEGSIYWYLF--------KSAI-PEYNRIW
QRMYSA---------------------NPSVFVNSTAQGVQRVR--DGNGF---------YS-FLGEA-GELDYAASK-PP---C-
DLIVSGG--Y-LVRTTY-ALA-VQT---D---SP--LRDQLSYAIET--LRD-SGVLEDLQRE------WWE--MEVPRYRCANL-
-TTWERQGV----FSFTVNDLQGVYFMLLLGF--------------------------------------------------
------------------------------------------------------------------------------------
-------------------
66 Lvar_GluHA1
DDTRSRRTLIQIFILTLWCFCLAESADVGISAMFGAETSIEDNYKTIIQDGVRYINRNTSFLSEVHQLVFVDPSHNRPSNSVYVAL
QE------DCEHVASSQVSALVLPRDQ-------------CTASDDIAGVISHATNPVFSID-------------------LGSG
SQAFK-----MQPSPEDMTSFFIDILSYYNWRNFTLLYDDG------GAFQNMEGIMEFAT----MNKW-----------------
-NISTVIIDEEFQNNIPMIEERGSR-----------NIFIYCSSETLLRSTIDQAI--L--LGTM-GPEYTWMIGNM-------DM
GIDRQFLEDLEDS---------NAFITRFNMN-YTREQQYALPTARNTPTGE--------------------WMFRERCAFDSVIA
VGHAL-----------RLYRLERTRAGATGSSVLPGDTPMP---------ACPTTNPV--------------VSENELTRYM----
-------------KQI-SFEGITGNI--AFDD-EGNRVNY----TITI--------RS----GQGETIDQIRGDWTQN--------
IDYW-------------------------------------------------EDRWD----------RKWESDGRLNVTTYNY---
-----------GNDRK---IKVVAIRAKPFLFLREERALELNQLVNRRQS---------STYTGNDRYEGYIMDLLARLKS--HMR
G---LDFD-YEVELVPD-G-RYGNKD-------VFSEE--WNGMIGEIVR---------R---KADIAAGPLTVTEEREEDVDFTY
SFMSG-GVKLLLQN----PYFV-QH---------YTFRLMYPFGIEV-W---FINLIVFLLVA-LLLFLFNY--FDPY-EWQ----
------AAAER------------------GETFEENG----KNFNMKNSFWFCTTTM-FLQ-S---Y--DNSP---RSNAGRTLTA
FWWVFILVMVFLYLFNLTYFINSNKRLVHVK--DAGDL---LNQDD---VVFG-TVDEGSIYWYLY--------KSSI-PEYNRIW
QRMYSA---------------------QPTAFVKNVTEGVQRVR--DSNGF---------YA-FLGEA-GELDYIASK-RP---C-
NLIVSGG--Y-IVRTTY-ALA-VQT---D---SP--LRDQLSYAIET--LRD-SGVLEDLQRE------WWEDTGVTYRYRCQNL-
-TSWERQGV----FSFTVNDLQGVYYMLLLGFLITFVVFILE----------------------------------------------
----VIVFAACGGKSKKTNSGGGGASRKKPARSGGGGP-----------VGGGQPIGGGGGASDGKEKMWI--------------
-------------------
67 Spur_GluHA1
-------------------------MSQPGALFGTETGYQDNYKTIIQDGVRYINRNTTFLSEVHQLVFVDSSINSRPSNSVYVA
LQ-----EGCDHV--ATSQVSALVLPKDR-----------CTASDDIAGVLSHATNPVFSID-------------------LGSG
STAFK-----MQPSPEDMTSFYIDILSYYSWMNFTLLYDDG------GAFANMEGVMEYAT----MNKW-----------------
-NISTVIIDEEFGNNIPMIEERGSKN----------IFIYCSSE-IILRNTIDQAL--L--FGTM-GPAYTWMIGNM-------DM
GIDRQFLEDLEDS---------NGFVTRFNMN-YTREQQYALPTARNTPTGE--------------------WQFRERCAFDAVIA
VGHGL-----------RLYRKKRVADGNTGSSVLPGDSSMP---------ACPTSSLV--------------VNENDLTYYL----
-------------KEV-TFEGITGTV--AFDD-EGNRVNY----TITV--------RS----GQGETIDQIRGDWTQN--------
IEYW-------------------------------------------------EDKWN----------RKWESEGRFNVTTYNY---
-----------GNDRK---IKVVSIEAEPFLFLREKRAQELNQYNLRQSS--------------DRYEGYIMDLLARIKS--NMR
G---IDFD-YEVELVPD-N-KYGNKD-------VFSEE--WDGMIGEVVR---------R---KADIAAGPLTVTEERERHVDFTF
SFMSG-GVKLLLQN----PYFV-QH---------YIFRLTYPFGIEV-W---FINLIVFLLVA-LLLFLFNY--FDPY-EWQ----
------AAAER------------------GETFEENG----KNFNLKNSLWFCTTTM-FLQ-S---Y--DNSP---RSNAGRTLTA
FWWVFILVMVFLYLFNLTFFINSNKRLVHVK--DAGDL---LDQDD---VVFG-TVDEGSIYWYLY--------KSSI-PEYNRIW
QRMYSA---------------------QPSAFVKNTTEGVERVR--NSNGF---------FA-FLGEA-GELDYIASK-RP---C-
NLMVSGG--Y-IDRTTY-ALA-VQT---D---SP--LRDQLSYAIET--LRD-SGVLEDLQRE------WWEESEINNRYRCNNL-
-TTWERQGV----FSFTVNDLQGVYFMLLLGFLVAFIVFLLEVIFFA-----------------------------------------
----AFGGKSKG------TRNKSRGGVSRNPPSGGGGGP-----------IGGGQPIGGGGGKSDGKEKMWI--------------
-------------------
68 Etri_GluHA2
------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------
------------------------------------------------------------Q---KSDIAAGPITITKQRQKDVEFSV
SFMSG-GIKLLLKH----PNYI-HQ---------NPFRLLYPFGIEV-W---FINFGTFLIVA-GLLCLINY--FDPY-EWK----
------AAAER------------------GETSDENG----PNFSFKNSLWYCCTTL-FLQ-G---Y--DHAP---RSNAGRALSV
FWWIFVLVMAFVYLFNLPGKIKTNKRLVYIK--SPSDL---VNQGD---VTFG-TVEDGSIHWYLF--------RAGI-PVYSRIW
HRMWHK-------------------SPSVYVKNTTEGVERVR--SSNGK---------YA-FLGEA-GELDYHASR-RP---C-
DLIVSGG--F-LERSTY-AMV-VSK---G---SP--LGDHLSYAIET--LRD-TGVLEDLQRE------WWG--LDRIHSRCRNL-
-TKWERQGM----FSYTPFDMQGIYFLLLVGFAVTILVFVLEMIAFG----------------------------------------
------------------------------------------------------------------------------------------
-------------------
69 Lvar_GluHA2
ETPSWIPGLVQILVVIWLGSLVCDAATVGISAMFGEDTGYANNYRTVINDGVLYVNRNQTFLGGIHTLEFIDKDNIIPSNTSYDGL
```


VD------ACQHIATEQISALILPADR--------------CTDHDDIAGVVSHGSNPVFSID-------------------FGSG
SKAFK-----MYPTPEEMTEFYVDIMTYFSWRAFILLYDDS------SAFANMEGLLEYAS----SQEWN----------------
-VTAVVLDEDDFENNVPTIEDEKTT-----------NIFLICTSEATLRRTLDRAI--D--LRIL-GPKYTWMIGNL---------
---------DLAMD--------RTFMETLEDTNAYITRFSMNYTRDWQYALPTTGSSQFTE-----------WEFRERNAYDAAIA
IGHAL-----------RKYRLKREADGVVGSSVLPGDTPMP---------ACPSSPSI--------------VATNVLTRYL----
-------------KNI-SFEGITGNV--AFND-NGDRTNY----TITI--------YS----GQGESVHQIRGIWTQN--------
IKHW---EDTWN----------REWQSEGRLNVTNYNY---
-----------GNDRR---IKIVTIEAEPFLFKRENYLELRRQENSLYAG-RRKRQIQTGPYTGNDRYDGYIMDLLSRIKA--YMR
G---IDFE-YEVELVPD-G-KYGHKS-------KYSKK--WDGMIGEVLR---------K---KADIAAAPITITKERLKDVEFTD
SFMSG-GIKLLLKN----PYYI-DH---------NPFRFLHPFGIEV-W---FVNLGTFLIVA-GVLCLINY--FDPY-EWK----
------AAAER-------------------GETFEENG----RNFCWKNSLWYCTTTL-FLQ-G---Y--DRAP---RSNAGHTLTA
FWWVFVLVMVFVYLFNLPGKLNTNKRLTYIK--NPDDL---TNQAD---VNIG-TVYDGSIHWYLF--------KSGI-PAYSRIW
HRMYHN---------------------PAKVYVENTTVGIQRVR--DSNGK---------YA-FLGES-GELDYAASL-RP---C-
DLIVSGG--Y-VDRSTY-AMV-VSK---G---SP--LGDHLSYAIET--LRD-TGVLEDLHRE------WWG-LDRTYWQRCRNL-
-TRYERQGM----FSFTVSDMEGIYFFLLLGFAISILVFVLEIMV---
----YGCKGREKTSGKSGGHQLNGTGRGGSSKSGGK-------------KSASGGGGAGGGGGGNDPNLWI--------------
----
Spur_GluHA2

-----------------------MGPKYTWMIGNLDLAMD---
-----------------------------------RTFMETLE-DTNAYITR--------FNMNYTRDWQYALPTT---------
-----------------------------------GSSQFTE-------------------------------WTFRERNAYDAAIA
IGHAL-----------RKYRLKREADGVVGSSVLPGDTPMP---------ACPSSPSI--------------VATNVLTSYL----
-------------QNI-SFEGITGNV--AFND-IGDRINY----TITI--------YS----GQGESVHQIRGIWTQN--------
VEHW---ENTWN----------RKWESEGKLNVTNYNY---
-----------GNDRR---IKIVTIESEPFLFKRENYLELRREQNSILNG-RRKRQIQTGPYTGNDRYDGYMMDLLSRIKA--YMR
G---IDFE-YEVELVPD-G-KYGHKS-------KYSKK--WDGMIGEVLR---------K---KADIAAAPITITKERLADVEFTD
SFMSG-GIKLLLKN----PYYI-DH---------NPFRLLHPFGIEV-W---FINLGTFLIVA-GILCLINY--FDPY-EWK----
------AAAER-------------------GETFEENG----RTFSWKNSLWYCTTTL-FLQ-G---Y--DRGP---RSNAGHTLTA
FWWVFVLVMVFVYLFNLPGKINTNKRLVYIK--NADDL---TNQAD---VNIG-TVYDGSIHWYLF--------KSGI-PAYNRIW
QRMYHN---------------------PAKVYVENTTVGIQRVR--DSNGK---------YA-FLGES-GELEYAASQ-RP---C-
DLIVSGG--F-VDRSTY-AMV-VAK---G---SP--LGDHLSYAIET--LRD-TGVLEDLQRE------WWG-LDRNYYQRCRNL-
-TRYERMGM----FSFTVSDLEGIYFFLLLGFAISILVFVLE---
----LMVCGCKGKDGRTGNSSGGRQQNGKRTFGGKKA-------------ASSGGGGVGSGGGGGNDANLWI--------------
----
Arub_GluHA
----MLSTTVKVLWSVMLMQLYVHNGEAGDVSIAALFGAASEDLKVVIDDGVRYIQRNTSFLSEVHTISFTGAEQFKPSNSVYSAL
EE------ICSLISGEIPSAMILSEDK--------------CPECEDIAGIASHASNPVFSVD-------------------YDSG
SLAFK-----MHPSPEDTNSFFVDILTYFQWRNFIIIHDGG------NALEFLQEVLSIQK----EREWN-ITA------------
-IELASSNHQSFLDVSVRIRAESTK-----------NLFVFCSAETTAKAFLVWAQ--QTPSANILTANYHWVLGNI-------DM
SLDRTFKTDLERT---------NAYITRFGMN-YTREIQFALPTSITTSTNE--------------------WPMRDRLAFDAVIS
VGHAL-----------RMYREWEESQGSSGTAVLPGDTQMP---------PCPTASAV--------------PTQNTLTTYL----
-------------RRV-AFEGISGNV--EFDD-VGNRVNY----TISI--------YS----GQFKTLDQMRGEWTQN--------
PAYW---EKKWK----------RKWESDGHLNVTYHNY---
-----------AAERT---VKIVTIEAEPFLKAR-IANSTFTETGSWVGN--------------NRYEGYIIDLLERIKT--HVK
G---IDFD-YQIELVSD-N-KFGSQH-------PYSHI--WDGMVGDVIR---------K---KADVAAGPLTVTPDRAQAVDFTY
PFMSS-GITVMMKH----PESV-QH---------NPFRIMYPLGIEV-W---IVNLVAFFIIS-AMLYFFNY--FDPY-EWR----
------AAAER-------------------QETFEENA----DNFSMKNSMWFATTSM-FLQ-S---F--DASP---RSNAGRTLAA
FWWVFVIIMVFLYLLNLTHFVTSNKRLVYAT--TAEGL---LDQTE---VAFG-SIEKGSTYYFFK--------KSSV-PEYQRLW
QHMNTR---------------------IPSPWVANIKEGIEKVR--DSNGY---------YA-FIGEA-AEMNFKASK-KP---C-
DLLVAGT--F-IARTTY-ALA-VQK---D---SP--LKDQLSSAIES--LRD-TGVLEDLERE------WWN--LDRYPLECRNL-
-TTWEKQGV----FSLTAVDLQGVYYILLMGIVIAVVTFAIESFF---
----SCGGGNKKSSSRNGMGGGQRMGGGP--------------------IGGGQPIGGGAGGGGGDEKMWI--------------
----
Pmin_GluHA
----MLSQTVKVLWSVVLLQLYVHRGDAGVVSIAALFGTESTDVKSVIQDGVQYINRNTSILSEVHSIEYTGIVGVKTSNSVFSAL
DD------VCNLISGERPSAMILPEDK--------------CPDCEDIAGIASHASNPVFSLD-------------------YDSG
SLAFK-----MHPSPEDTNNLFVDILEYFEWRNFIIVHDGG------NALEFLQEVLNIQR----VNEWN-ITAI----------
-ELGERGNHEGYMELAGKIKAESSR-----------NLFLFCSSEANAKAFIVWAQ--ANPSAQILNAKYHWVLGNI-------DI
SLDRTFRTELEKT---------NAYITRFGMN-YTREIQYAQPTSISTSTTE--------------------WPMRNRLAFDAVIA
VGHAL-----------RLYREWREDNGESGTAVLPGDTQMP---------PCPTSSAT--------------PTENALSRYL----
-------------KQV-AFEGISGNV--EFDS-KGNRVNY----TISI--------YS----GQFRTLDQMRGEWTQN--------
KAYW---EQKWK----------RKWESEGHLNVTYHNY---
-----------ASERT---IKIVTIESKPFLMLK--GNDTLTDQGSYAGN--------------NRFEGYIIDLMERIKT--HIK
G---IDFD-YQVELVAD-G-KFGSSH-------PYSKI--WDGMVGDVVR---------K---KADIAAGPLTVTPDRAAAIDFTY
PFMSS-GITILMKH----PNYV-QH---------NPFRIMYPFGIEV-W---FINLVAFFIIS-AMLYFFNY--FDPY-EWR----
------AAAER-------------------RETFEENA----ENFTMKNSLWFATTTM-FLQ-S---F--DASP---RSNAGRCLAA
FWWVFTIIMVFLYLLNLTHFVTTNKRLAYAK--TAEDL---LDQTE---VAFG-SVEKGSTYFYFK--------KSSV-PEFQRLW
QHMNTR---------------------IPSPWVKNVPEGIQRVR--DSNGY---------YA-FIGEA-GELNFLASK-RP---C-
DLLVSGT--Y-ITRTTY-ALA-VQK---G---SP--LRDQLSSAIES--LRD-TGVLEDLERE------WWD--LDIRHQECANL-
-TTWERQGV----FSLTTVDLQGVYYILVIGIILAAVTFILESISY--SCSGGKKKSSS-----------------------------
----SARNGGMG-------------------------------------GGMSGPRGGGGGAVGGPASGGGDEKMWI------


73 Apla_GluHA
74 Harg_GluHA1
75 Harg_GluHA2
76 Harg_GluHA5

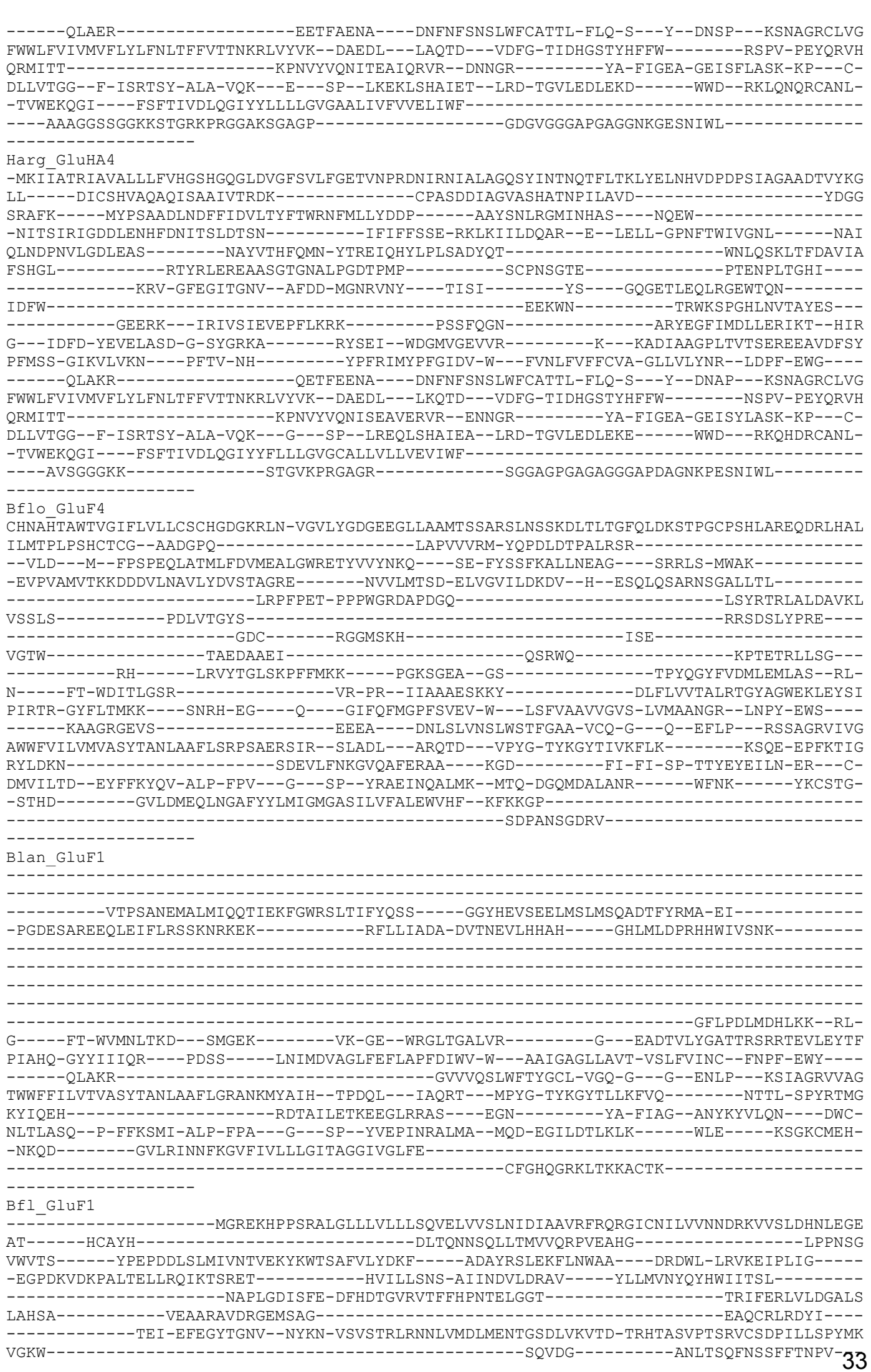

DLLVTGG--F-ISRTSY-ALA-VQK---E---SP--LKEKLSHAIET--LRD-TGVLEDLEKD------WWD--RKLQNQRCANL-
-TVWEKQGI----FSFTIVDLQGIYYLLLLGVGAALIVFVVELIWF----------
----AAAGGSSGGKKSTGRKPRGGAKSGAGP----------GDGVGGGAPGAGGNKGESNIWL----------
77 Amol_GluHA

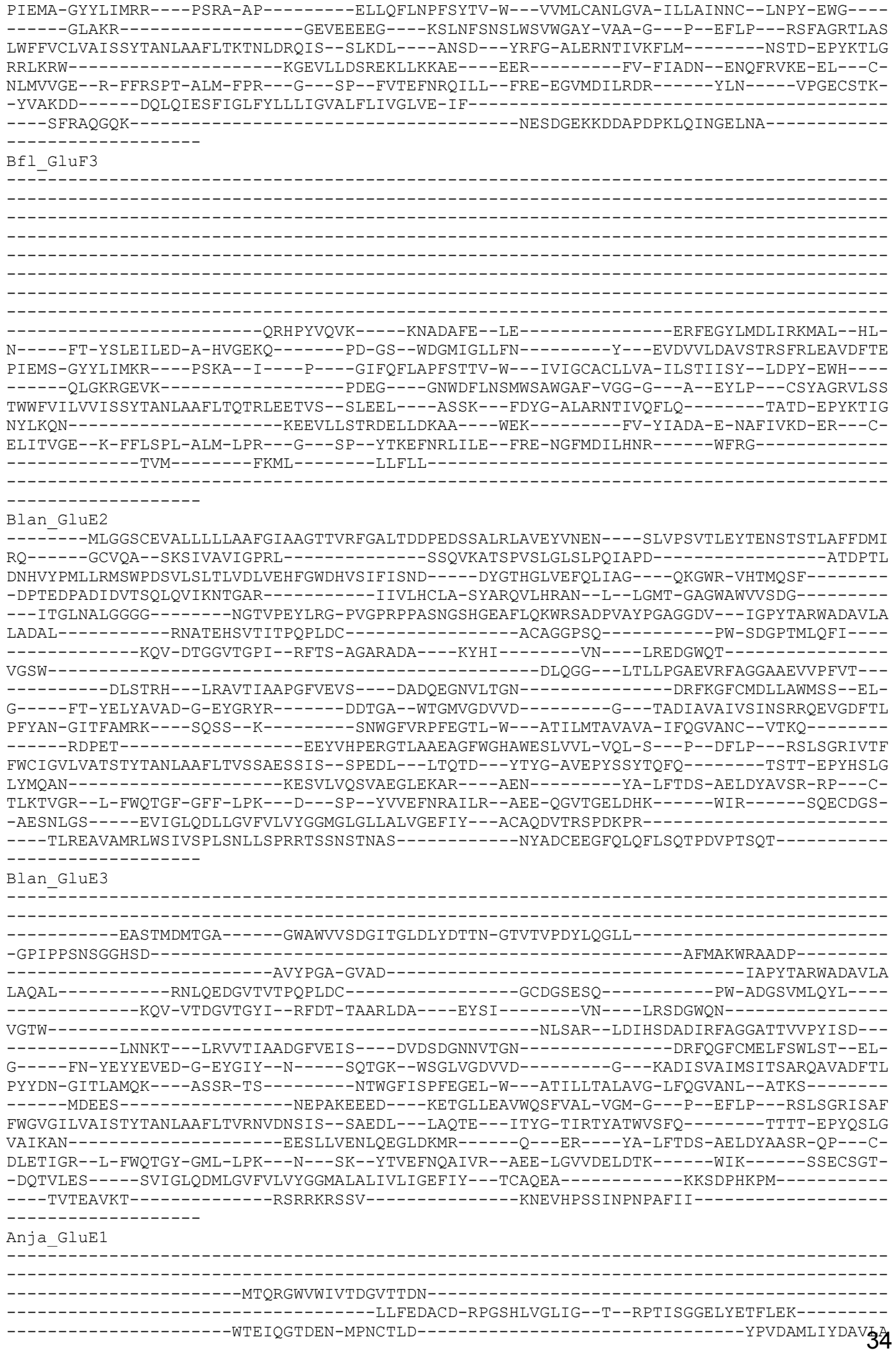
----------MVLLH----------
------FS----------Q---KADIAAGPLTVTAEREQAVDFSY
PFMSS-GIKVLVKN----PYTV-HH---------YPFRIMYPFGIDV-W---FVNLFVFFCVA-GLLWLYNR--LDPF-EWR----
------QLASR----------QETFEENA----DNFNFSNSLWFCATTL-FLQ-S---Y--DNSP---KSNAGRCLVG
FWWLFVIVMVFLYLFNLTFFVTTNKRLVYVK--DAEDL---LSQTD---VDFG-TIDHGSTYHFFW--------NSPV-PEYQRVH
QRMITT----------SPSVYVQNITEAIERVR--ANNGH---------YA-FIGEA-GEIQFLASK-KP---C-
DLLVTGG--F-ISRTSY-ALA-VQK---D---SP--LREQLSHAIET--LRD-TGVLEDLEKD------WWD--RKLQEERCANL-
-TVWEKQGI----FSFTIVDLQGIYYLLLLGVGCALLVFVIEFIWFGI----------
----
78 Ajap_GluHA
----------VLSGNLSTNTRDASIQAIAQAGAQYINTNQTFLTKLYQLIHVPPDSSISGAADTVYK
GL----LDICSHVAQAQISAVIVTRDK----------CPESDDIAGVASHATNPILAVD----------YGSG
SRAFK-----MYPSADDLNNFFIEVLSYFNWRNFMLLYDDP------TAYSNLQGMINYAS----NQEW----------
-NITSIRLTDDLNDHFQNITDLDTSN----------IFIFFSSE-KKLQVTLEQAR--Q--LELL-GPNFTWIVGNL------NAI
QLNDPNVLSDLETS--------NAYITHFKMN-YTREMQHYLPLSGDYQT----------WDLQSKLAFDAVVA
FSHGL----------RTYRLERERDQQSGTALPGDTPMP----------SCPNSGTD----------PTENPLSDHL----
----------KLVGFEGVTGNV--AFDD-MGNRVNY----TISI--------YS----GQGETLEQLRGEWTQN---------
ISFW----------EQKWN----------TRWKSPGRLNVSAYDS---
----------GQERK---IRIVSIEVEPFLKKK---------SESFNGN----------ARFDGFIMELLGKVKT--HIR
G---IDFD-YEVELVPD-G-AYGRKE-------RYSKI--WNGMVGEVVR---------R---KADIAAGPLTVTAEREQAVDFSY
PFMSS-GIKVLVKN----PYTV-HH---------YPFRIMYPFGIDV-W---FVNLFVFFCVA-GLLVLYNK--LDPF-EWG----
------QLASR----------QETFEENA----DNFNFSNSLWFCATTL-FLQ-S---Y--DNSP---KSNAGRCLVG
FWWLFVIVMVFLYLFNLTFFVTTNKRLVYVK--DAEDL---LSQTD---VDFG-TIDHGSTYHFFW--------NSPV-PEYQRVH
QRMITT----------TPNVYVQNITEAIQRVR--DNNGR---------YA-FIGEA-GEIQFLASK-KP---C-
DLLVTGG--F-ISRTSY-ALA-VQK---D---SP--LREQLSHAIET--MRD-TGVLEDLEKD------WWD--RKLQDERCANL-
-TVWEKQGI----FSFTIVDLQGIYYLLLLGVGCALLVFVIEFIWF----------
----SVAGGGGG----------KSSSGRQGRGGGGGGGG----------ADAGGPGPAAAGGDRAEHNMWL----------
----
79 Aech_GluHA

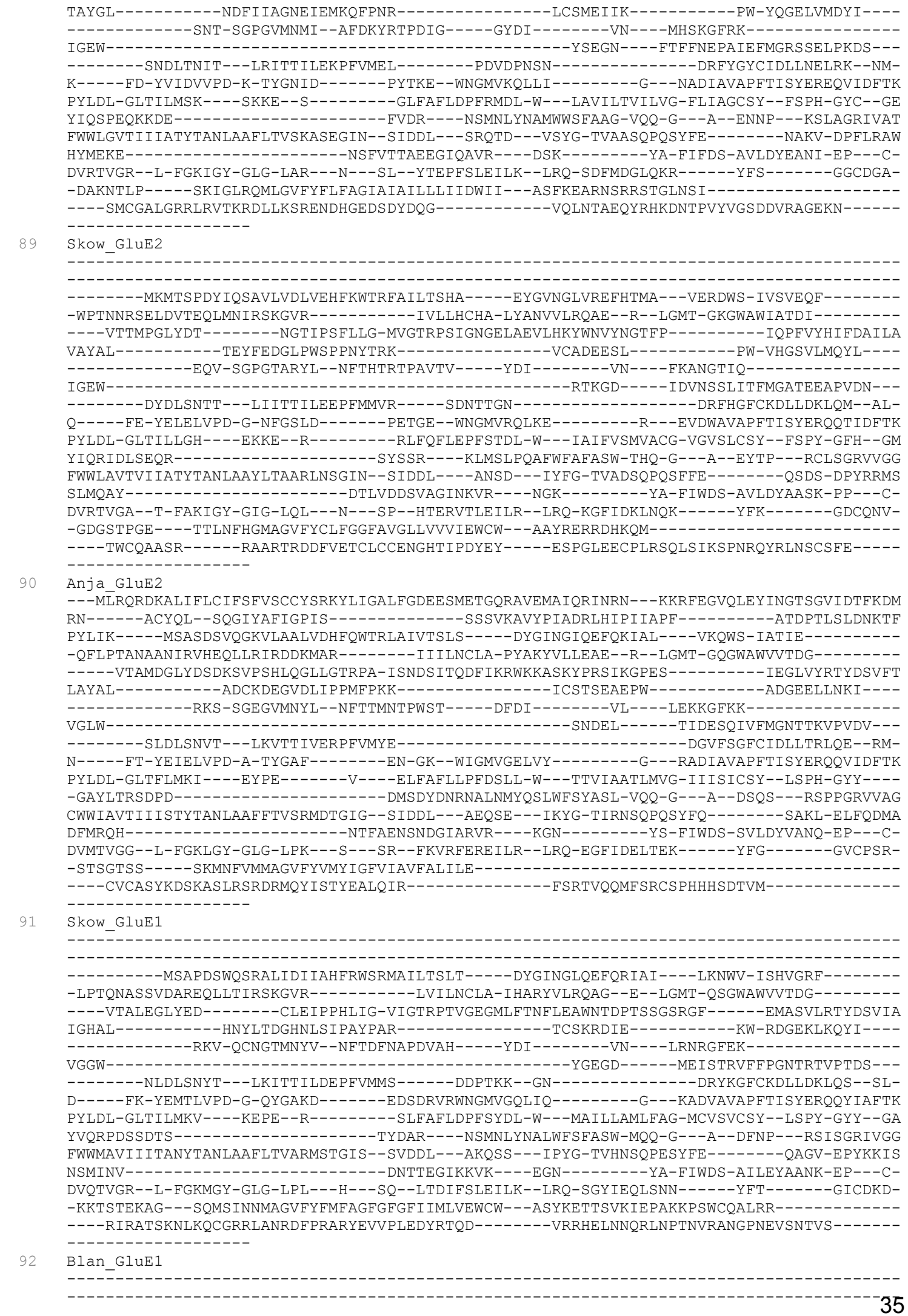
----------T----------

----------ECFVQEST----------

----------IKITSSIVEPFIMRK---------SSSFHGN----------ARYEGFIMELLERIKT--HIR
G---IDFD-YEVELAPD-G-SYGRKA-------RYSGI--WDGMIGEVVR---------VLSQKADIAAGPLTVTSEREEAVDFSY
PFMSS-GIKVLVKN----PYTV-NH---------YPFRIMYPFGIDV-W---FVNLFVFFCVA-GLLVLYNH--FDPF-EWG----
------QLASR----------QETFEENA----DNFNFSNSLWFCATTL-FLQ-S---Y--DNSP---KSNAGRCLVG
FWWLFVIVMVFLYLFNLTFFVTTNKRLVYVR--DAEDL---LAQTD---VDFG-TIDHGSTYHFFW--------NSPV-PEYQRVH
QRMITT----------RPNVYVQNISEAIQRVR--DNNGR---------YA-FIGEA-GEISYLASK-KP---C-
DLLVTGG--Y-ISRTSY-ALA-VQK---G---SP--LKEQLSHAIEA--LRD-TGVLEDLERD------WWD--RKLQDERCANL-
-TVWEKQGI----FSFTIVDLQGIYYFLLLGIGCALLVLLFEVIWF----------
----
80 Harg_GluHA3
-MKIIATRIAVALLLFVHGSHGQGLDVGFSVLFGETVNPRDNIRNIALAGQSYINTNQTFLTKLYELNHVDPDSSIAGAADTVYKG
LL-----DICSHVAQAQISAAIVTRDK----------CPASDDIAGVASHATNPILAVD----------YDGG
SRAFK-----MYPSAADLNDFFIDVLTYFTWRNFMLLYDDP------AAYSNLRGMINHAS----NQEW----------
-NITSIRIGDDLENHFDNITSLDTSN----------IFIFFSSE-RKLNIILDQAR--E--LELL-GPNFTWIVGNL------NAI
QLNDPNVLGDLEAS--------NAYVTHFQMNYTREIQHYLPLSADYQT----------WNLQSKLTFDAVIA
FSHGL----------RTYRLEREAASGTGNALPGDTPMP----------SCPNSGTE----------PTENPLTGHI----
----------KRV-GFEGITGNV--AFDD-MGNRVNY----TISI--------YS----GQGETLEQLRGEWTQN---------
IDFW----------EQKWN----------TRWKSPGRLNVTAYLS---
----------GQERK---IRIVSIEVEPFLITK---------SSSFQGN----------ARYEGFIMDLLERLKT--HIR
G---IDFD-YEVELVPD-G-NYGRKE-------RYSKI--WNGMVGEVVR---------R---KADIAAGPLTVTAEREDAVDFSY
PFMSS-GIKVLVKN----PYTV-NH---------YPFRIMYPFGIDV-W---FVNLFVFFCVA-GLLVLYNH--FDPF-EWG--



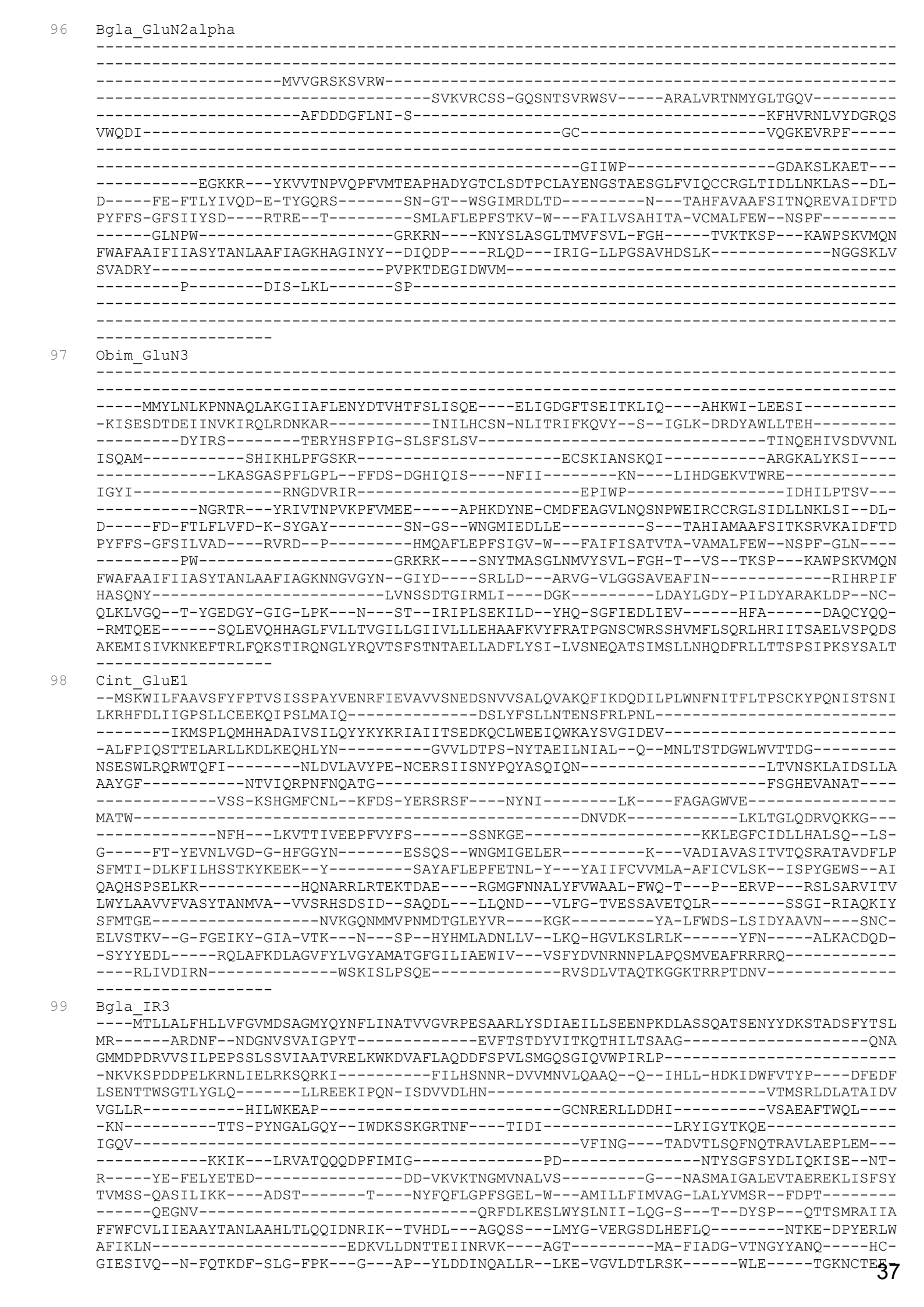

85 Bfl_GluF3
86 Blan_GluE2
87 Blan_GluE3
88 Anja_GluE1


TAYGL----------NDFIIAGNEIEMKQFPNR----------LCSMEIIK----------PW-YQGELVMDYI----
----------SNT-SGPGVMNMI--AFDKYRTPDIG-----GYDI--------VN----MHSKGFRK----------
IGEW----------YSEGN----FTFFNEPAIEFMGRSSELPKDS---
--------SNDLTNIT---LRITTILEKPFVMEL--------PDVDPNSN----------DRFYGYCIDLLNELRK--NM-
K-----FD-YVIDVVPD-K-TYGNID-------PYTKE--WNGMVKQLLI---------G---NADIAVAPFTISYEREQVIDFTK
PYLDL-GLTILMSK----SKKE--S---------GLFAFLDPFRMDL-W---LAVILTVILVG-FLIAGCSY--FSPH-GYC--GE
YIQSPEQKKDE----------FVDR----NSMNLYNAMWWSFAAG-VQQ-G---A--ENNP---KSLAGRIVAT
FWWLGVTIIIATYTANLAAFLTVSKASEGIN--SIDDL---SRQTD---VSYG-TVAASQPQSYFE--------NAKV-DPFLRAW
HYMEKE----------NSFVTTAEEGIQAVR----DSK---------YA-FIFDS-AVLDYEANI-EP---C-
DVRTVGR--L-FGKIGY-GLG-LAR---N---SL--YTEPFSLEILK--LRQ-SDFMDGLQKR------YFS-------GGCDGA-
-DAKNTLP-----SKIGLRQMLGVFYFLFAGIAIAILLLIIDWII---ASFKEARNSRRSTGLNSI----------
----SMCGALGRRLRVTKRDLLKSRENDHGEDSDYDQG----------VQLNTAEQYRHKDNTPVYVGSDDVRAGEKN------
----
89 Skow_GluE2

--------MKMTSPDYIQSAVLVDLVEHFKWTRFAILTSHA-----EYGVNGLVREFHTMA---VERDWS-IVSVEQF--------
-WPTNNRSELDVTEQLMNIRSKGVR----------IVLLHCHA-LYANVVLRQAE--R--LGMT-GKGWAWIATDI---------
----VTTMPGLYDT--------NGTIPSFLLG-MVGTRPSIGNGELAEVLHKYWNVYNGTFP----------IQPFVYHIFDAILA
VAYAL----------TEYFEDGLPWSPPNYTRK----------VCADEESL----------PW-VHGSVLMQYL----
----------EQV-SGPGTARYL--NFTHTRTPAVTV-----YDI--------VN----FKANGTIQ----------
IGEW----------RTKGD-----IDVNSSLITFMGATEEAPVDN---
--------DYDLSNTT---LIITTILEEPFMMVR-----SDNTTGN----------DRFHGFCKDLLDKLQM--AL-
Q-----FE-YELELVPD-G-NFGSLD-------PETGE--WNGMVRQLKE---------R---EVDWAVAPFTISYERQQTIDFTK
PYLDL-GLTILLGH----EKKE--R---------RLFQFLEPFSTDL-W---IAIFVSMVACG-VGVSLCSY--FSPY-GFH--GM
YIQRIDLSEQR----------SYSSR----KLMSLPQAFWFAFASW-THQ-G---A--EYTP---RCLSGRVVGG
FWWLAVTVIIATYTANLAAYLTAARLNSGIN--SIDDL----ANSD---IYFG-TVADSQPQSFFE--------QSDS-DPYRRMS
SLMQAY----------DTLVDDSVAGINKVR----NGK---------YA-FIWDS-AVLDYAASK-PP---C-
DVRTVGA--T-FAKIGY-GIG-LQL---N---SP--HTERVTLEILR--LRQ-KGFIDKLNQK------YFK-------GDCQNV-
-GDGSTPGE----TTLNFHGMAGVFYCLFGGFAVGLLVVVIEWCW---AAYRERRDHKQM----------
----TWCQAASR------RAARTRDDFVETCLCCENGHTIPDYEY-----ESPGLEECPLRSQLSIKSPNRQYRLNSCSFE-----
----
90 Anja_GluE2
---MLRQRDKALIFLCIFSFVSCCYSRKYLIGALFGDEESMETGQRAVEMAIQRINRN---KKRFEGVQLEYINGTSGVIDTFKDM
RN------ACYQL--SQGIYAFIGPIS----------SSSVKAVYPIADRLHIPIIAPF----------ATDPTLSLDNKTF
PYLIK-----MSASDSVQGKVLAALVDHFQWTRLAIVTSLS-----DYGINGIQEFQKIAL----VKQWS-IATIE---------
-QFLPTANAANIRVHEQLLRIRDDKMAR--------IIILNCLA-PYAKYVLLEAE--R--LGMT-GQGWAWVVTDG---------
-----VTAMDGLYDSDKSVPSHLQGLLGTRPA-ISNDSITQDFIKRWKKASKYPRSIKGPES----------IEGLVYRTYDSVFT
LAYAL----------ADCKDEGVDLIPPMFPKK----------ICSTSEAEPW----------ADGEELLNKI----
----------RKS-SGEGVMNYL--NFTTMNTPWST-----DFDI--------VL----LEKKGFKK----------
VGLW----------SNDEL------TIDESQIVFMGNTTKVPVDV---
--------SLDLSNVT---LKVTTIVERPFVMYE----------DGVFSGFCIDLLTRLQE--RM-
N-----FT-YEIELVPD-A-TYGAF--------EN-GK--WIGMVGELVY---------G---RADIAVAPFTISYERQQVIDFTK
PYLDL-GLTFLMKI----EYPE-------V----ELFAFLLPFDSLL-W---TTVIAATLMVG-IIISICSY--LSPH-GYY----
-GAYLTRSDPD----------DMSDYDNRNALNMYQSLWFSYASL-VQQ-G---A--DSQS---RSPPGRVVAG
CWWIAVTIIISTYTANLAAFFTVSRMDTGIG--SIDDL---AEQSE---IKYG-TIRNSQPQSYFQ--------SAKL-ELFQDMA
DFMRQH----------NTFAENSNDGIARVR----KGN---------YS-FIWDS-SVLDYVANQ-EP---C-
DVMTVGG--L-FGKLGY-GLG-LPK---S---SR--FKVRFEREILR--LRQ-EGFIDELTEK------YFG-------GVCPSR-
-STSGTSS-----SKMNFVMMAGVFYVMYIGFVIAVFALILE----------
----CVCASYKDSKASLRSRDRMQYISTYEALQIR----------FSRTVQQMFSRCSPHHHSDTVM----------
----
91 Skow_GluE1

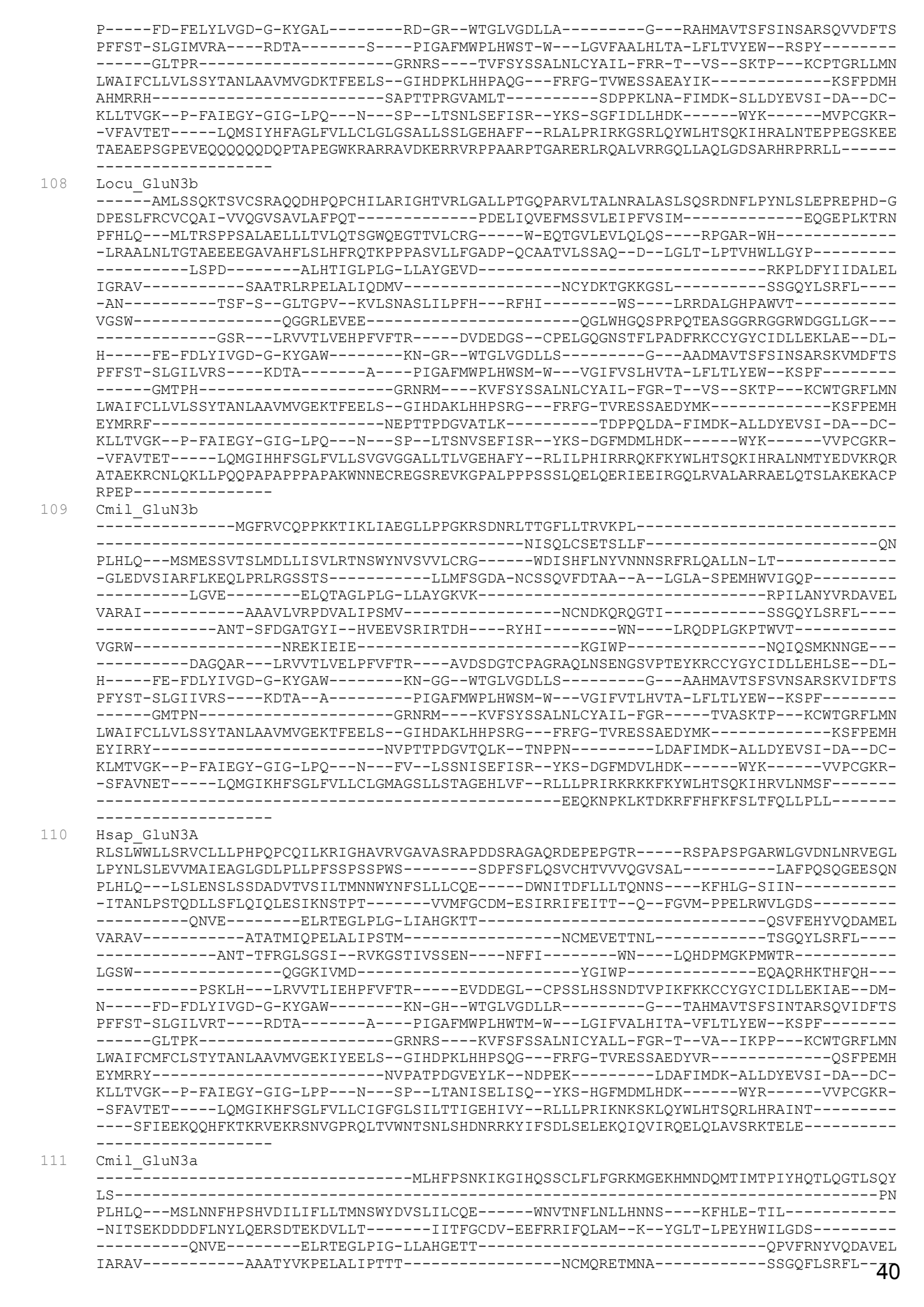
----------MSAPDSWQSRALIDIIAHFRWSRMAILTSLT-----DYGINGLQEFQRIAI----LKNWV-ISHVGRF--------
-LPTQNASSVDAREQLLTIRSKGVR----------LVILNCLA-IHARYVLRQAG--E--LGMT-QSGWAWVVTDG---------
----VTALEGLYED--------CLEIPPHLIG-VIGTRPTVGEGMLFTNFLEAWNTDPTSSGSRGF------EMASVLRTYDSVIA
IGHAL----------HNYLTDGHNLSIPAYPAR----------TCSKRDIE----------KW-RDGEKLKQYI----
----------RKV-QCNGTMNYV--NFTDFNAPDVAH-----YDI--------VN----LRNRGFEK----------
VGGW----------YGEGD------MEISTRVFFPGNTRTVPTDS---
--------NLDLSNYT---LKITTILDEPFVMMS------DDPTKK--GN----------DRYKGFCKDLLDKLQS--SL-
D-----FK-YEMTLVPD-G-QYGAKD-------EDSDRVRWNGMVGQLIQ---------G---KADVAVAPFTISYERQQYIAFTK
PYLDL-GLTILMKV----KEPE--R---------SLFAFLDPFSYDL-W---MAILLAMLFAG-MCVSVCSY--LSPY-GYY--GA
YVQRPDSSDTS----------TYDAR----NSMNLYNALWFSFASW-MQQ-G---A--DFNP---RSISGRIVGG
FWWMAVIIITANYTANLAAFLTVARMSTGIS--SVDDL---AKQSS---IPYG-TVHNSQPESYFE--------QAGV-EPYKKIS
NSMINV----------DNTTEGIKKVK----EGN---------YA-FIWDS-AILEYAANK-EP---C-
DVQTVGR--L-FGKMGY-GLG-LPL---H---SQ--LTDIFSLEILK--LRQ-SGYIEQLSNN------YFT-------GICDKD-
-KKTSTEKAG---SQMSINNMAGVFYFMFAGFGFGFIIMLVEWCW---ASYKETTSVKIEPAKKPSWCQALRR----------
----RIRATSKNLKQCGRRLANRDFPRARYEVVPLEDYRTQD--------VRRHELNNQRLNPTNVRANGPNEVSNTVS-------
----
92 Blan_GluE1


```
----------------------MRLTGVGWAWIVT----------D-GVTGMTSFRKNET----VPRHL-L----------
-----------------------------------GLLGVKPV-EDKGELFGDFM--N----------LWSTADS---------
----------NRYP--------GAGVWD-----------------------------------------IEAYPAKFVDAVLL
FAFAY----------RDLLRAGQSVTGASV-------------------QCDRFPSE----------RW-EHGDTMLQYL----
-RK----------VSE-E--GITSKI--LFTK-DGTPTQV----EFDI--------VN----LRENGWQR---------------
VGTW---------------NDTVG--------------------------LTIDN----SV------TSFMGGGQVELMDD---
----FVSDLRNRT------LRIVTHRDIPFVMKN--LNDSEGNPLH--GN--------------DQYSGLCIDLLKWLSE--QL-
G-----FR-YRLFHVAD-D-KFGNKDR------NT-GR--WNGVIGDLVY---------K---KADMAVTDLTITAEREEDVDFTL
PYIEA-GSTFIMRK----KARA--E----Y----NIMNFSRPFQPEL-W---ALVFITTLAVA-IIQSVINK--LSPY--------
------SGIPMGPGE-----------------SDED----SPYTFGESLWHSFAAL-IQQ-G---P--EFFP---RAPSGRITSI
FWGMGILIVIATYTANLAAFLTISRLETTIE--SVEDL---AAQNE---IVYG-VQRDSATQSFFD--------ESNI-EPFKTMA
AVMRAR----------------------DSYVGSMAEGIRKAK----TEN---------YA-YISDN-VLLDYQANR-----DC-
TLRTVGR--L-FKKSGF-GIA-LPK---Y---SP--YTEVFSKKILQ--ARE-SGFLDVLIKK------WKL--------------
----------------------GT-----------------------SSRRQR-----------------------------
--------------------------------------------------------------------------------
-------------------
93  Blan_GluE4
LAECPWSKMGTTTAVPFGKLMVGAAAVPARIRIGGIFAHENKIEEEAFKFAVMYVNEMMPELLPRTRIDYINRTMLLPEFAGIQA-
--------VCHQA--RSGVVAIVGPGT--------------SSGVKFSNAVCSGLHIPHIAPT----------------ATDPTLA
NREFFPYLLRMSAPDSVQSRALVDLVTHFGWTHMAILTSSD-----DYGIHGLVEFQAIAA----RKKWG-IVSV----------
-QQFQTGNDVNIVNATSQLKYIVGTGVR--------VVILNCLA-QHATRVLQQAE--H--LGMT-RKGWAWVVTDG---------
-----VTTKNTTHL--------TSPVPSYLQG-LIGTDPDIAQGTLLREVRQVWENADRSRFPHAGEFE---VESNFGQFFDAVLA
IAHAL-----------DNIFRDGHHIEEEKLE-----------------CCEEKR-------------PW-KYGKLVLEYL----
-------------KKV-EEDGVMRRL--RFSG-RGHPNNP----SYGI--------MN----LLCSGWKK----------------
VGSW-------------------------------------------SEDTR----LIMHNPVRFMGGADSVVDYVSD---
-----------LMNRT---LKVVTIEEPPFIFYS----EKDEHGRPRKGN---------------DRFYGFCKDMMEHFSK--HL-
G-----FK-YEMYMVED-E-NFGARD-------PVTGK--WNGMVRDLVV---------K---KADVAAASFTISYEREQDIDFTK
PYIDI-GLTFVLSN----KIEK-ED---------RPFKFLDVFEPNL-W---LSILLSTLAVS-FFISLVNK--LSPS-GYH--GH
FVQEEEPELVE--------------EEEDPEEIQEKKEEMIGMMSLGNALFFAVASL-LQQ-G---G--DVYP---RSTPGRITAS
LWWLVTVIIVATYTANLAAFLTVSRMDTDIN--SVEDL---VSQKL---VQYG-TVQNSQPLSFFE--------SSSI-HTFETMA
RYMKVH----------------------STLTMSSRAGIEKAR----DER---------YA-FIWDS-AVLDYVVKQ-PP---C-
NLRTVGR--L-FGKIGF-GFG-LQK---G---SA--YTDAFSIAILQ--ARE-SGYLDKLKEK------WYT-------GECHDQ-
-NSATTVTN----DKMDVSKLLGVFYIIYVGMAVSVVVLVVEWVV---ACMMAVDQTDPEAPK----------------------
----TFLEAFRKRLAILERDMEEAKRRRKQQELKDSVK-----------KRSFSRSSSRSADFKNSRSAGSLKINGNLP------
-------------------
94  Cgig_GluN3alpha
--------------MMILAGWLVYICLH-WLGGGATGLRILLICDQTFHEVCRQKQNDAKDDVIVTFFPVSDIHSYVTHVRNIDAL
LRNGTSTDVLLVF--GHS----------------------ELVSAVGT-VAQDFQRPVIAYT-------------------KDSA
PVIYQNDMLSINSNPFHLGQAMSYLINTLWLEKHTHLLTDASLLTDG-FIEGFWEGQQFNL----SHT----------------
-TVLHQDEDFDEISLFFHLRDLRENGVK--------QFVVHAQP-NQVNLLMRANR--RFEATAG-RGGYRWFLSDT---------
----------AISG--------KIDDELIPVG-ALVVKA---------------------------------VRDERALVEHTITR
LYEEI-----------EDLKDSTLSDNTP---------------------DCFRSVLLKKS----------TKNLPLCCGI----
-------------AQF----RIDNHFWRVINESSGELEWM----SAGK--------------IFYNHSKH---------------
SVQW-------------------------------------------------------------------YGSTIFGPTS---
-----------QSKHF---HRVVTTPAPPFVLVKGPIDTGDSCYGNKMCYPNTRVEDLQEVEAERYCCSGFVMDILEYLAT--DL-
A-----FD-YLVYFRDE-N-SHNATNL-------------YESLLHDVRN---------G---SAEIIAGALTVTSNRSKQLRFTE
PYYFS-GFAMIVP-----PQEA-SK----P----SMDAFTAPFDSYV-W---MAIFLSATTAA-LATSLFEW--NSPF--------
------GLNPWGRKR---------------------L----KNYTLGSALVMVYSVL-FGH-T--VS--TKSP---KSWPAKVLQN
FWAGLAIFIVASYTANLAAYLAGINRVDDMI--SIFHNTMNSKRVH--------VLRSSPAADYLR-------------VINERNR
KNIMIS----------------------EVPPDVTQLNIINNLK----NKS---------YEYYVNDR-LLLEYALAQHDN---C-
SIKFSGN--D-FGENLY-AFG-LNR---D--AVD--LTENMSSLILS--YLE-GGQVTEALQR------YVK------NRNCVGR-
-SERFT-------RKYGLDHTGGLFIILLSAMFVGAFLLVIELCVFRYYLRKKPNDSLWKNRNIEYVNQRLYRTVMSEQLVSPQQT
AQEMIRIVKERQFERLFLKNELSKHGRIQKKGVPKNNQRKASKNSPHVTRAERPEKTQLIHKSKRGANLGRAFTFYGRSMKDNRLK
S------------------
95  Cgig_GluN3beta
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
----------------------MTPEGLHRQLYNHLAEDT-----------------------------------------
-----------------------------------IVLLHLDP-PMAVLIFKS-------LPCNTSKKVRWFITEK---------
---------GYTQN--------TLLIKLYPIG-SLVMVPDS-------------------------------VTSLDDVISDSVSY
LNSAI-----------QSAPRDDKVSRGVGQ-------------------SCMNGAYRHH------------TTGLKLYRHF----
-QE----------KVY-Q--GFSMKF--EFNS-DGYLANK----NYRI--------KA----LKGMVGRSIWED------------
VGYV----------------HGEIARPR-----------------------GILWP----------------SEPDLDIRNG---
-----------RVR-----YRVVTNPVKPFVMVE----NGIEDSNQ--CILHNYENINDSSSFQLKCCRGFAVDLLNKLAS--DL-
E-----FE-YVLYIVHD-T-TYGKE--------KN-GT--WDGMMRDLTN---------G---IAHMAIAAFSITGNRLRAIDFSY
PYYFS-RFTVLYTQ----QSQK--T---------YMYAFLEPFSPEV-W---CTIFVSASLSA-LGMSMFEW--NSPF--------
------GLNPWGRKR---------------------K----QNYTIGSGMTMVYSLL-FGH-T--VS--TKSP---KSWPSKVLQN
FWASACIFIIASYTANLAAFLAGKHNGIDYN--SVFD----SRLME---IRVG-VLGGSAVEALTN-------------NINKKLY
QRSQHY----------------------LVPTTNDAINMLI------N---GNI---DA-YLGDY-PILDYARVKLDP--NC-
NLYIVPQ--S-FGEDEY-GIG-FPK---D---SP--LQKPVSEKIKH--YHE-SGYLENLIDI------HFD------EEKCFNQ-
-GINQQR------FSLTVFHHSGLFALLSIAIVCCILLVLVEHLVFKFICRGRPDDSFWKSLNVMFFSQRLHRCINSAVLVSAQES
AKEMLGIVKNGDFSRLFMKSTIRKNKLADMAKTKRINRNFPKVDSVRDYDELEYCDKRDVHSSYEGQHLLSRCESGCSSETEDIL-
------------------
```

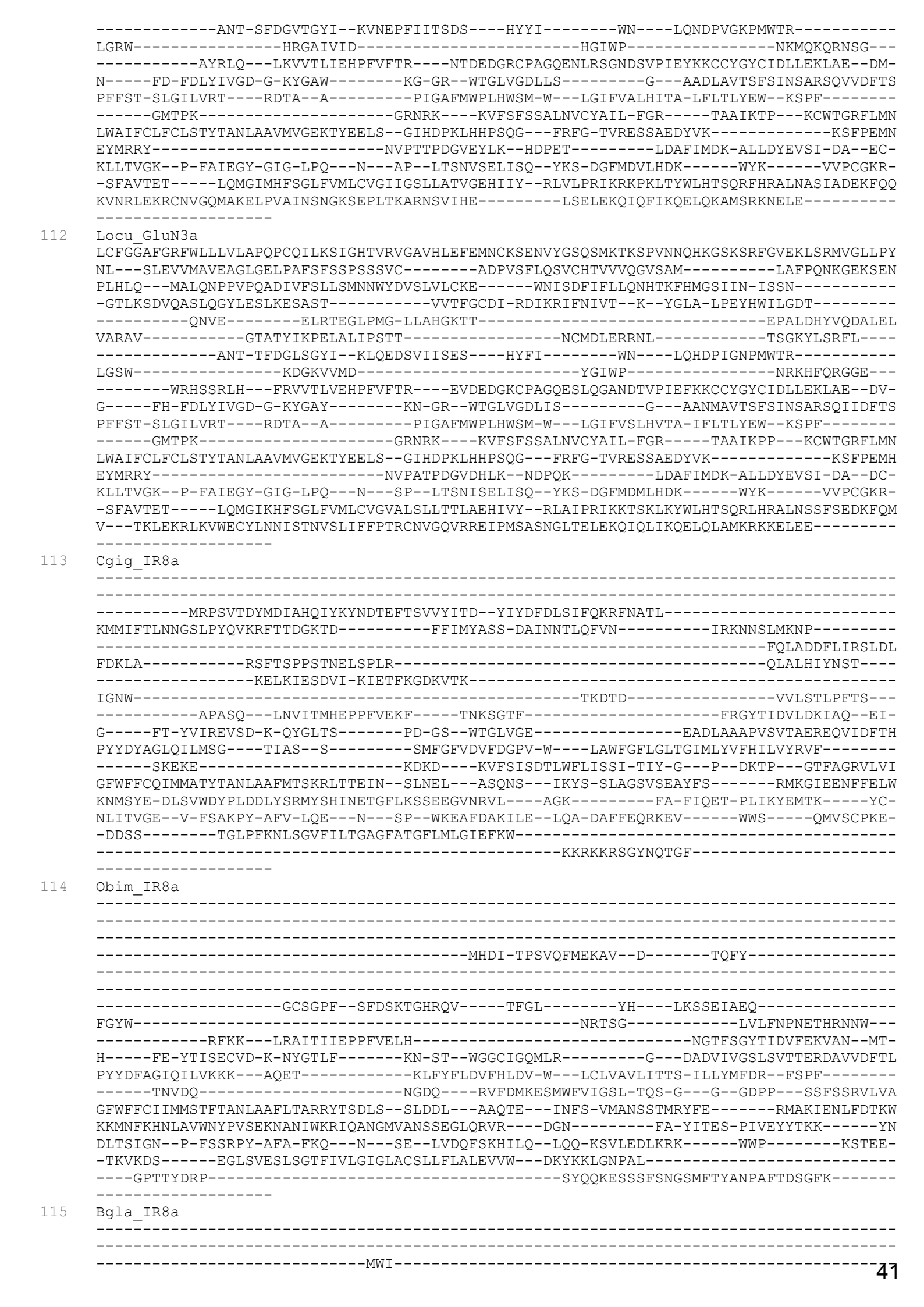

96 Bgla_GluN2alpha
97 Obim_GluN3
98 Cint_GluE1
99 Bgla_IR3

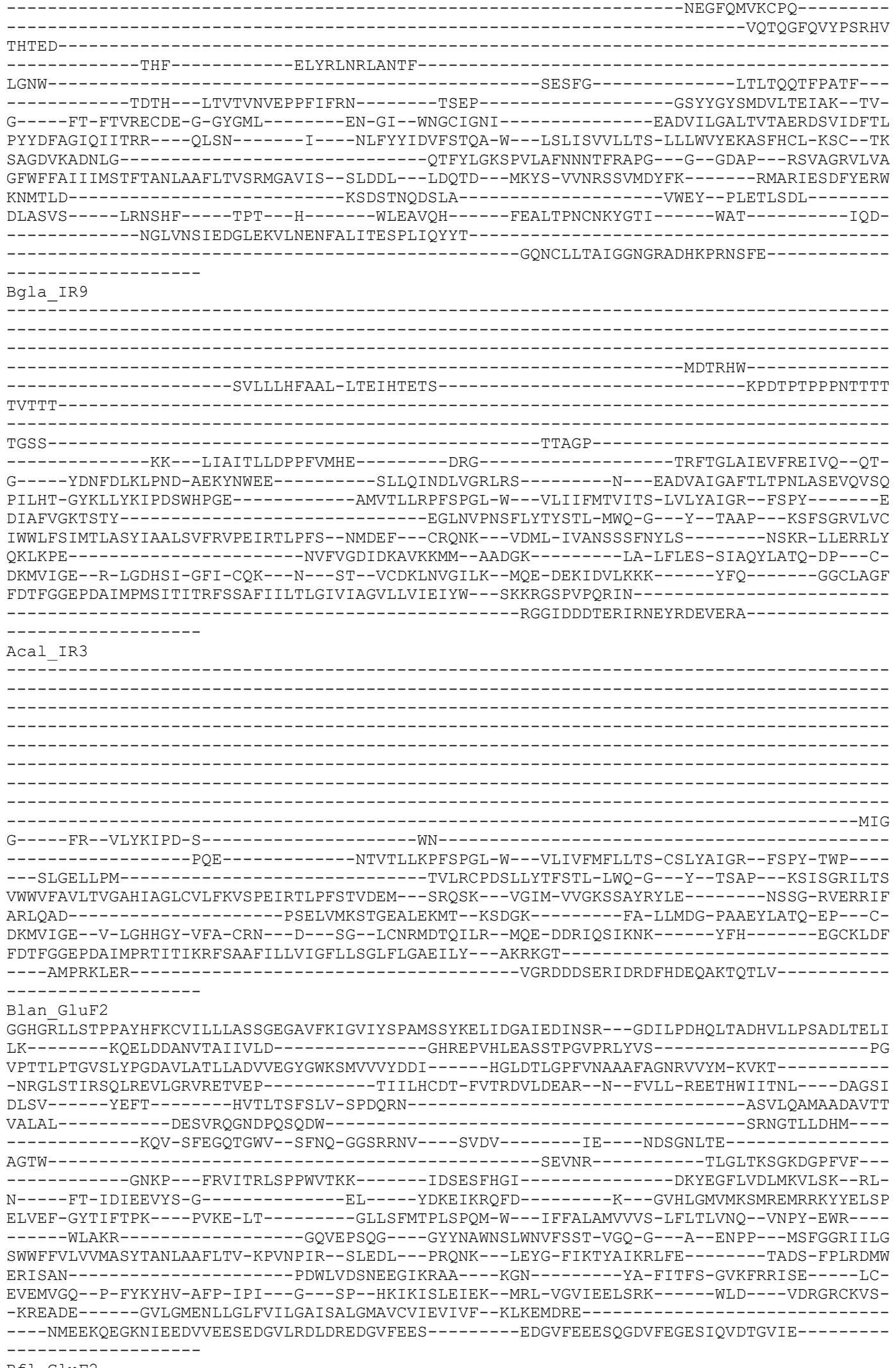
```
--DKSRSISQKTTPELELTNMIGVFIVLGVFIGVAIIVDVASRMY---KWDKNT------------------------------
----RKAKTTTE-----------------------------------LNQSCETNV---------------------------
------------------
100 Blan_GluN3
------------MANNIQTVAEDSNDDSTLTLGAVFPQENVSEFNRTMGRAIADYKRDFPNISVNPLTVTPGNNPQDMLNE----
--------TCESL--AGTNIAALLVVGE-------------ARTFQILSLYGAHLGIPVVGIS-----------LKYLSSPQKLDI
PLVVR-----LEPAFGHQAHAIVTLLERNVLYSFAALVIGQ----TSMDYEFMAKLDNLTS----GVHWQ-ASK-----------
-KISLARDDEDLSRHLMNLKQSNCR-----------AFVLHGSP-SDVMRVFRMAK--T--LGLT-GSNHAWILTQA---------
---------AVTTS--------QHVLEDYPVG-AVAVRYS-------------------------------DDSLTDKIYDGTFL
LMDSF-----------NKVHRDYNGNGALQRRKG----------------CCDASDSYNKK-----------FRSEDYYKHV----
-------------LNT-KTRSRGSLI--QFDQ-NGMSTRA----TYDL--------LD----LKREDDGHMTWAD-----------
VGQW-------------------------------------------------------------DDGTLRLKSGA---
-----------GDNLV---LFIVTIAEKPFTYVTPLMDSQHPCNSRVKCLDNLYQYDDTNSTYIIKCCEGLVVDLMEAIAT--DL-
G-----LE-YELYHVAD-S-KYGS---------NGSGT--WNGMVRDLMD---------G---NAEMAIGPISATMNRYDVIDFTE
PFAHS-GIGIIVAK----RTDS-------P----RLTWFLETLRWDN-W---LMTFVTLHFVA-VVITIFEW--FSPY--------
------GLHPR---------------------GRGRT----SNFGFPSALVNVWSIL-FSH-T--VY--TKPP---KSWSSRWVIN
FWGAFSFIFLGSYTANLASFMVAQDQYYNLA--GLHDQRISGP------LLYG-VATGTSIETYLE---------------EQTLL
TKKKDR----------------------FVSVNITEFGIRQLK----KGE---------IDAFFAGS-NLLEYHIAN-DP--EC-
EIVKVGN--V-AAAEGY-AFG-VRK---G---SA--LKDPVSSLILH--YSS-NGYLDELTQK------WYS------TGSCDKK-
-KRDPNEEK----RQLGVKHAEGLALFMIAGIGLSMIVLVLEYAVYSQALREMANIVKRGQFYLMFEKDTLMDGWMDGWMDGWMED
GWKMQGRKEGRKEGRKEGRKEGRKEGRGRKEGRKEGRKEGRKEGRKEGRKEGRKRKEGRKEGRKEGRKEGRKEGRKEGRKEGRXMD
EWM----------------
101 Skow_GluN3alpha
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
-MYLR-----LESAESFQAYAIKKILHRNGWFQYSILASEE-----TPSQAFLQYLTNVTS----SLTWT-VK-------------
-GTVFSRDKRDIDHVLHSAAKSKTR-----------VFVLHATP-EYSSLLFRAAK--D--FGLL-DAGNVWIVAET---------
---------VITNQ--------PQYLKHYPIG-LIAVQFVD-------------------------------SGHIESKIHDSVEL
IARAS---------------VNKNYISNIASNK-----------------SCWSKPTPDKL-----------EYGREFYSAL----
-------------VQT-SFMGQTGYI--NLDE-EGNLNNA----TYII--------LN----LVKDQNRLSYWKE-----------
LGKW----------------ENGDFSME-----------------------AIIWP----------------GNSVSLPNGV---
------------NTEK---VLIVANIEKPFIVVSTPLDVSFDCLTGVLCLEYDEPTVHGNYTDMKRCCSGLGIDLIESLRI--DV-
E-----FN-YNLYLVAD-E-NHGAF--------EN-GQ--WNGMVADLLN---------G---TADLALSSFSITSERSRVIDFSS
PFFHS-GFSTLVAK----KQVE-------P----QLDSFLEPLDWSV-W---ILVFVTVNIVA-IAITIFEW--MSPY--------
------GLHPR---------------------GRNRH----YTFGLPSALNIAFSIL-FSH-T--VK--SKPP---KCMTSRFLLN
VWGAFSFIFFASYTANLAAYMAGQTSHLQID--GINDEKVHSPDGS---LTIG-TVTGSSIQVYLT-------------RNHPKLA
KFMDNY-----------------------IQDCTEEAMAKLK----SGK---------LDAFIYDS-PVIEYRMAN-DP--EC-
QLVSVGK--P-FGEEGY-GIG-LPK---G---ST--MKEPLSLHILE--YET-DGYLEELQQK------WFG------TMICYKE-
-GDLGSSDIGD--NKVRLAHVAGLFIMLLFGIGVGGMILLLEYIMY--NYAVPRLHSQPDKRNWLVLSQRLHRAVNTEDLVSSKAN
MQEMITMVKKGQFTKMFQREQLRRKSMMRRESNMEMGSDASK--------RPSLQEESNHGNGFNRAKEKEMEARQDSRKASFH--
--------------------
102 Anja_GluN3
-----------------------------------MAMYFHTFANICLIFLSSQVAAQVVVFTTDNAGYEFPKIVKSHAVSKTTMT
NPGDLANRICRLT--EETDIIGIAAAAS-------------DKRLYTLSTMATYLNIPIIGIG-----------SRSLVYSNKENH
PLFLR-----FAISESKQAKVILSLLQRYALYKFALLGSRS--SSTEAFVRELRRLTSTSS------VWE-FVD------------
-YMTINENGEDVVEALQQLVIDDIR-----------VVIIHCSP-QEAAVLFKIAK--Q--KDVL-SQGYAIIATES---------
---------LLTYN--------KSLLVHYPEG-LISLRLIE-------------------------------HGNINDTFQDSKTL
MNIAV-----------NKVNVSFHNV-----------------------GCQGIGRRRS------------KEGDALYREL----
-------------LDT-SFEGITRHV--KFDK-KGDLVGA----SYEI--------IN----LMANSKKNPSMHWKV----------
VGKW----------------NHGALSLD-----------------------TLVWP------------------GKKDRPFGI---
------------DTQR---ILVVTNVEKPFLYYA-----ESSNFDCVTGKRLKTVSENDEDISSRRCCLGLCVDLLNEISR--DL-
D-----LN-YDLYLVAD-Q-NHGAI--------EN-GS--WNGMVGDLLQ---------G---TADIAISSFSITLERSEVIDFTA
PFFHS-GFSALVAK----KKRE-------L----TFGAFLAPLHGSV-W---ITIFMSAIVIS-FAITFFEW--GSPY--------
------GLHPA---------------------GRNRK----YIFGFPSALNITFAIL-FCH-T--IR--TKPP---KCMTSRTLLN
MWGGFSVIFFASYTANLAAFMAGQMSYLHIE--GINDPKLNSPNGD---INIG-TVTGSSIQSYLA-------------RLNPRLD
QFMDKF-----------------------VQPSTEQAIESLR----NGD---------LDVFLYDS-PIIDYRMLN-DP--DC-
KLVNVGS--P-FGEEGF-GIG-LPK---G---ST--LKIPLSTILLQ--YEM-DGRLEQLHRK------WFD------AVGCLKE-
-DVLNPQTGGND-SSVTVRHVAGLIVMLILGIVTGFLLLLCEFAMHKWHLRKRPRNKRNFLVISQ----------------------
----RIHNEVNS-----------------------------------GNTQSSSSNIKDLVALVKNGEFRKMLHKE---------
--------------------
103 Arub_GluN3
------------------------------------------------------------------------------------
-----------------------------------------------------------------------------QEVH
PLFLR---L--DVSVTNQAQVIKSLLQRNAWFNFSIVSSEG-----EGSNAFVQSLRDQIQ----TPGWN-I--------------
-RHDVRFPADAGTRFLRNIANDDSNDVIPVRYV---VMVLHCSP-RQAQAVFRAAR--E--LKLL-GKGHALIGTES---------
---------LLTYD--------KSILKDYPTG-LLIVKHMD-------------------------------AAPLKDHLHDAFTL
VARSA-----------GKLKWEGGVRNI-----------------------SCWLGPGSSQL-----------EYANNFYSTM----
-TN----------TSF-K--GNTGNI--KFDQ-NGDLVDS----SYHI--------MN----LIEESPTGHDWKE-----------
VGSW----------------RRGSLKLE-----------------------TVVWP----------------GNTMVMPVGV---
------------DTHK---LIIATNTEKPFIFFSNTTGMEGECTTGVQCLEFRRRPDGGNYSHDLKCCTGLCVDLIERMSQ--DL-
N-----FK-YDLYLVAD-T-NHGAI--------EN-GT--WNGMVGDLIT---------G---KADAAISSFSITRERSAVIDFTA
PFFHS-GFSTLVAK----KQRE-------Q----TLGAFLAPLHPNV-W---TLIFASALVMA-VCLTISEW--SSPY--------
------GLHPG---------------------GRNRN----STFSFPSALTITFAIL-FSN-T--IK--TKPP---KCMTSRMLLN
```

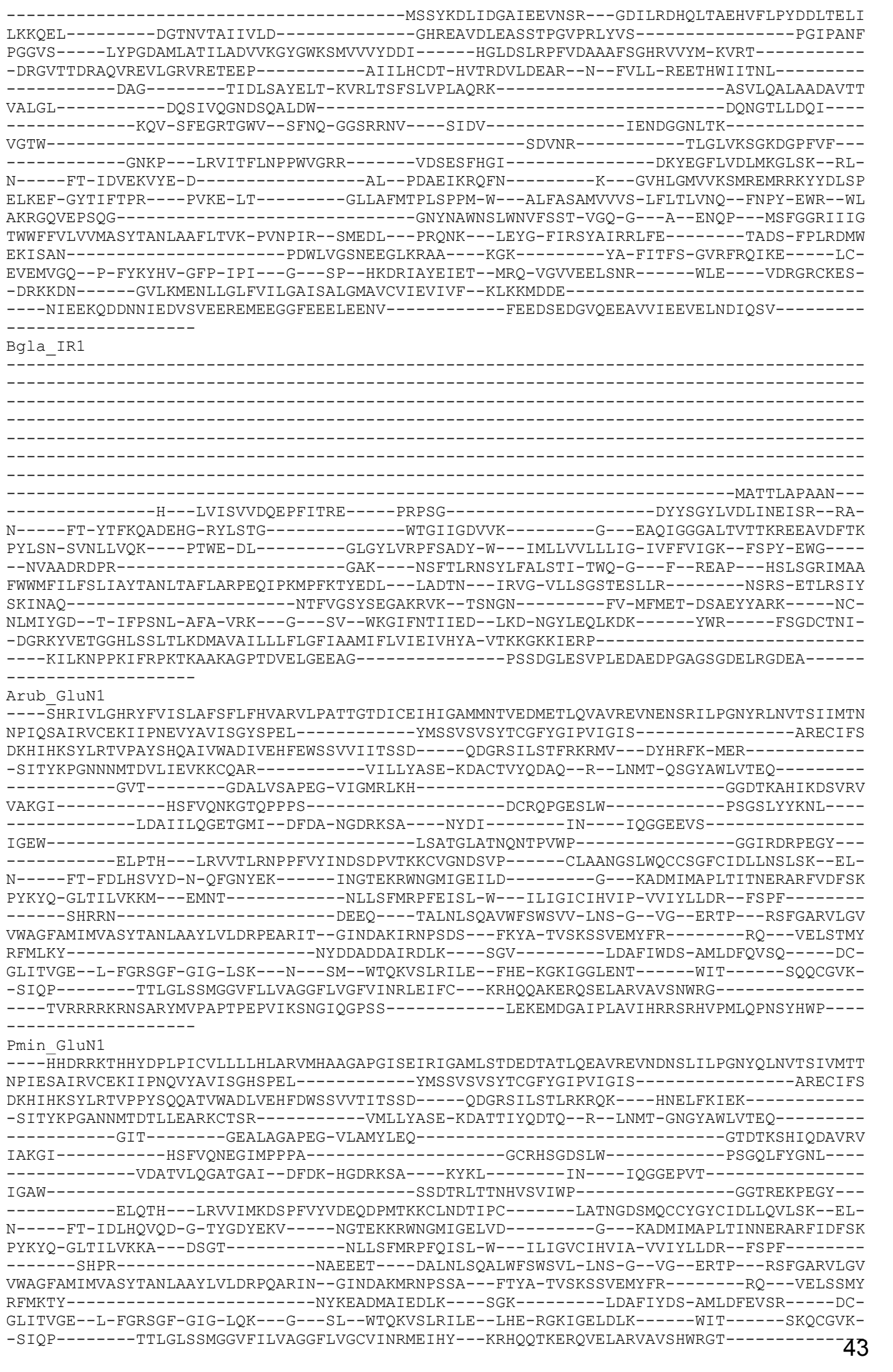
```
VWGGFSLIFFSSYTANLAAFLAGQMSYLSIE--DLNDPKLKNPTEE---TTVG-TVTGSSIQNYLM-------------SLNPGLH
RFMENY-------------------------VQLTTEEAITSLK----QGE---------LDVFIYDS-PVIEYRMAN-DP--EC-
SLVSVGK--P-FGEEGY-GIG-VSK---D---SP--LRDTVSGKILE--YEL-DGILEELQRK------WFE------TLGCMKE-
--DILDPTSGGEDNTVTIAHVGGLLLLLVSGVIISCLILLVEFAVHKYKHRRDCLVLSQRLHHEINSDYKVRSSANMRELLTLVKQ
GEFAKMLQKEQRPAAPEEIEARRDIRNAVQVDSNSYANGVGPNPYSDGVNASPETDDGTASQGHSSLSSGGAEHLPCEGATLPRTS
SLP----------------
104 Pmin_GluN3
SSQFCLTYSLIITYLPVVIFLFHTKDVLSSKLESVRVAVVSDDATNFSLFHDQVLTAIQEVNATESGMALHLGVVLSSHPNPMDVY
RQ------TCNQLAGTDVSAVVVQAD---------------ERTQFSLSVAGGFLGVPVIGLG----------------NRAFAFS
NKEVHPLFLRLDVSVTNQAHVIKSLLHRNAWFNFSVVASEG-----EGSDAFVQSLRDQIQ----TPGWNIRR-------------
-DVRFSSGEASSGRFLRNLANDDSYV----------VMVLHCSP-QEAQNVFRAAR--E--FKLL-GKGHALIGTES----------
---------LVTND--------PNILRDYPTG-LLIVKHYD--------------------------------PAPLKDHLYDAFTL
VARAA-----------QRLKWGGETRNI----------------------SCWTRPGSNQL-----------EYANNFYSTM----
-------------TNT-SLKGKIGNI--RFDQ-NGDLRDS----SYHI--------MN----LIEESPRVHAWKE-----------
VGSW----------------KRGSLNLE----------------------TVVWP----------------GNTMVMPVGV---
------------DTHK---LIIATNTEKPFIFYSDSNGIEGECTTGVQCLEFRRRPDGGNYSADLRCCTGLCVDLIKRMGQ--DL-
N-----FK-YDLYLVAD-E-NHGAL--------EN-GT--WNGMVGDLIT---------G---KADAAISSFSITRERSTVIDFTA
PFFHS-GFSTLVAK----RQRQ--Q---------TLGAFLAPLHPNV-W---MLIFASAIVMA-VCLTISEW--SSPY--------
------GLHPG----------------------GRNRN----STFSFPSALTITFAIL-F---SNTIK--TKPP---KCMTSRMLLN
VWGGFSLIFFSSYTANLAAFLAGQMSYLSIE--DINDPKLKNPTTE---TTIG-TVTGSSIQNYLR-------------SLNPNLD
AFMDNY-------------------------IQRTTEEAIDNLK----NGI---------LDVFVYDS-PVIEYRMAN-DP--QC-
NLVSVGK--P-FGEEGY-GIG-VRK---G-----------------------------------------------------------
----------------KTSH-----------------------------------------------------------------
------------------------------------------------------------------------------------
-------------------
105 Apla_GluN3
SFQYCLAYKLLFNCLPAVIFLFNTRDVLSSKLQSVRVAVVSDDVTNFSLFHEQVLTAIHEVNSTEPGMALHLGVVLSSHPNPMDVY
RE------ICCQL--AGTDVSAVVVHAD-------------EPTQFSLSVAGGFLGVPVIGLS-----------NRAFAFSNKEVH
PLFLR-----LDVSVTNQAHVIKSLLQRNAWFNFSVVASEG-----EGSDAFVQSLRDQIQ----TPGWN-IRH------------
-DVRFSSGEASSGRFLRNLANDDSYV----------VMVLHCSP-QEAQNVFRAAS--E--FKLL-GKGHALIGTES----------
---------LATSD--------PNILKDYPTG-LLIVKHYD--------------------------------TAPLRDHLYDAFTL
VARSA-----------QRLKWDGDTRNI----------------------SCWTGPDSNQL-----------EYANNFYSTM----
--------------TNTSLKGKIGNI--LFDQ-NGDLRDS----SYHI--------MN----LIENSSGIPAWKE-----------
VGSW----------------KKGSMNLD----------------------TVVWP----------------GNTMVMPVGV---
------------DTHK---LIIATNTEKPFIFYSESNGIEGECTTGVQCLEFRRRPDGGNYSADLRCCTGLCVDLIERMSQ--DL-
N-----FK-YDLYLVAD-E-NHGAV--------EN-GT--WNGMVGDLIN---------S---KADAAISSFSITRERSTVIDFTA
PFFHS-GFSTLVAK----RQRK--Q---------TLGAFLAPLHPNV-W---MLIFASAIVMA-VCLTISEW--NSPY--------
------GLHPR----------------------GRNRNSTFSFPSALTITFAIL-FSN-T----IKTKPP---KCMTSRMLLN
VWGGFSLIFFSSYTANLAAFLAGQMSYLSIE--DINDPKLKNPTSE---ITIG-TVTGSSIQNYLR-------------SLNPNLD
AFMENY-------------------------IQHSTEQAIDNLK-NGE------------LDVFIYDS-PVIEYRMAN-DP--QC-
NLVSVGK--P-FGEEGY-GIG-VPK---E---SP--LRDTVSGKILE--YEL-DGILEELQRK------WFE------STGCMKE-
--DILDPTSGGEDNTVTIAHVGGLLLLLVAGTIIACLILLVEWLVPYLKHRRDCLVLSQRLHHEINSDFKVRSSANIRDLLTLVRQ
GEFGKMLQKEQRPAAPEEIEARRDIRQAVQTRINMVSGTSTQGGTTGIEPLLSFMSDELAQSHLGRACLASTETAGGTISQGQSSA
SSDTEEPLPSEVHILSRNS
106 Skow_GluN3beta
------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------ELH
PTFLR-----MEPPLAMQSHPVVDILKRNNWYKFSIIYDDD-----PDGLSFIRELWRLTD----DEEWE-IEAF-----------
-IKIPMEYAGNISSRLTMLTQLNSK----------VIVLQVSP-QEAARIFRIAE--N--VGML-SAGYAWILTGM----------
--------------------LTMTDPTYFPVG-LIAVNNSA--------------------------------STSTAVSIKNSVRL
VAKAM-----------QKMVTQYDILNL-----------------------------------------RMGEDLTKTW-------
-------------------------------------------------------VN-----------------------------
VGSW----------------TMDDLNIN----------------------SILWP----------------GQTEIMPNLA---
-----------SERRK---LRVVTILEEPFLFISELEGDSRECYSGGLCLTFSNNMTDDMPRYAEYCCTGMAYDVLEMLSR--DM-
N-----FD-YDLYIVAD-G-NFGSIDK---------GE--WNGMVGDLIN---------G---AAEMAVGSFSINSARSQVIDFSA
PFYYT-SLGIVTAR----RKGT-------A----AIGSFMEPLEWTM-W---LGIFITLHATA-FFTTIFEW--HSPY--------
------GLTPR----------------------GRNRP----RVFSFPSALTLCWSIL-FSH-T--VP--TKSP---KCWASRFLIN
LWAIFSLVFIASYTANLAAFMVGEKQPNEIS--GINDPKLQQQSKG---FRAA-TIASSSPESFLT-------------RSYPALA
SKIAKY-----------------------AVANTSHGVDKLR----NRQ---------LEAFIWDS-AILEYTISS-DP--KC-
ELQLVGK--P-FASEGY-GIG-LPK---N---SP--LTSEVSLHIYK--YSS-AGYLEQLQRQ------WYN------RVGCSKK-
-QGLVGE------STLDLSHFIGVFILLCTGVVIASLTLILEWFVERIKWRKDAKKLNWL-------------------------
----PFTQRLH-----------------------------------------RAVHTPSVLHNNTYTARGQQIPLRNIGS--------
-------------------
107 Hsap_GluN3B
---MEFVRALWLGLALALGPGSAGGHPQPCGVLARLGGALLPRAPLARARARAALARAALAPRLPHNLSLELVVAAPPARDPASLT
RG------LCQAL-VPPGVAALLAFPEA-------------RPELLQLHFLAAATETPVLSLL-----------RREARAPLGAPN
PFHLQ---LHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGLVALWTSRAGRPPQL-------------------------
-VLDLSRRDTGDAGLRARLAPMAAPVGGEAPVPA--AVLLGCDI-ARARRVLEAV-----------PPGPHWLLGTP---------
----------LPPK--------ALPTAGLPPG-LLALGEVA---------------------------------RPPLEAAIHDIVQL
VARAL-----------GSAAQVQPKRALLPAPV-----------------NCGDLQPAGPE-----------SPGRFLARFL----
-------------ANT-SFQGRTGPV--WVTGSSQVHMSR----HFKV--------WS----LRRDPRGAPAWAT-----------
VGSW-------------------------------------------------RDGQLD-----------LEPGGASARPPPPQ---
---------GAQVWPK---LRVVTLLEHPFVFAR-----DPDEDGQ--CPLFAALANGSAPRALRKCCYGYCIDLLERLAE--DT
```


P-----FD-FELYLVGD-G-KYGAL--------RD-GR--WTGLVGDLLA---------G---RAHMAVTSFSINSARSQVVDFTS
PFFST-SLGIMVRA----RDTA-------S----PIGAFMWPLHWST-W---LGVFAALHLTA-LFLTVYEW--RSPY--------
------GLTPR---------------------GRNRS----TVFSYSSALNLCYAIL-FRR-T--VS--SKTP---KCPTGRLLMN
LWAIFCLLVLSSYTANLAAVMVGDKTFEELS--GIHDPKLHHPAQG---FRFG-TVWESSAEAYIK-------------KSFPDMH
AHMRRH-----------------------SAPTTPRGVAMLT----------SDPPKLNA-FIMDK-SLLDYEVSI-DA--DC-
KLLTVGK--P-FAIEGY-GIG-LPQ---N---SP--LTSNLSEFISR--YKS-SGFIDLLHDK------WYK------MVPCGKR-
-VFAVTET-----LQMSIYHFAGLFVLLCLGLGSALLSSLGEHAFF--RLALPRIRKGSRLQYWLHTSQKIHRALNTEPPEGSKEE
TAEAEPSGPEVEQQQQQQDQPTAPEGWKRARRAVDKERRVRPPAARPTGARERLRQALVRRGQLLAQLGDSARHRPRRLL------
----
Locu_GluN3b
------AMLSSQKTSVCSRAQQDHPQPCHILARIGHTVRLGALLPTGQPARVLTALNRALASLSQSRDNFLPYNLSLEPREPHD-G
DPESLFRCVCQAI-VVQGVSAVLAFPQT-------------PDELIQVEFMSSVLEIPFVSIM-------------EQGEPLKTRN
PFHLQ---MLTRSPPSALAELLLTVLQTSGWQEGTTVLCRG-----W-EQTGVLEVLQLQS----RPGAR-WH-------------
-LRAALNLTGTAEEEEGAVAHFLSLHFRQTKPPPASVLLFGADP-QCAATVLSSAQ--D--LGLT-LPTVHWLLGYP---------
----------LSPD--------ALHTIGLPLG-LLAYGEVD-------------------------------RKPLDFYIIDALEL
IGRAV-----------SAATRLRPELALIQDMV-----------------NCYDKTGKKGSL----------SSGQYLSRFL----
-AN----------TSF-S--GLTGPV--KVLSNASLILPFH---RFHI--------WS----LRRDALGHPAWVT-----------
VGSW----------------QGGRLEVEE----------------------QGLWHGQSPRPQTEASGGRRGGRWDGGLLGK---
-------------GSR---LRVVTLVEHPFVFTR-----DVDEDGS--CPELGQGNSTFLPADFRKCCYGYCIDLLEKLAE--DL-
H-----FE-FDLYIVGD-G-KYGAW--------KN-GR--WTGLVGDLLS---------G---AADMAVTSFSINSARSKVMDFTS
PFFST-SLGILVRS----KDTA-------A----PIGAFMWPLHWSM-W---VGIFVSLHVTA-LFLTLYEW--KSPF--------
------GMTPH---------------------GRNRM----KVFSYSSALNLCYAIL-FGR-T--VS--SKTP---KCWTGRFLMN
LWAIFCLLVLSSYTANLAAVMVGEKTFEELS--GIHDAKLHHPSRG---FRFG-TVRESSAEDYMK-------------KSFPEMH
EYMRRF-----------------------NEPTTPDGVATLK----------TDPPQLDA-FIMDK-ALLDYEVSI-DA--DC-
KLLTVGK--P-FAIEGY-GIG-LPQ---N---SP--LTSNVSEFISR--YKS-DGFMDMLHDK------WYK------VVPCGKR-
-VFAVTET-----LQMGIHHFSGLFVLLSVGVGGALLTLVGEHAFY--RLILPHIRRRQKFKYWLHTSQKIHRALNMTYEDVKRQR
ATAEKRCNLQKLLPQQPAPAPPPAPAKWNNECREGSREVKGPALPPPSSSLQELQERIEEIRGQLRVALARRAELQTSLAKEKACP
RPEP---------------
Cmil_GluN3b
---------------MGFRVCQPPKKTIKLIAEGLLPPGKRSDNRLTTGFLLTRVKPL----------------------------
---NISQLCSETSLLF-----------------------QN
PLHLQ---MSMESSVTSLMDLLISVLRTNSWYNVSVVLCRG------WDISHFLNYVNNNSRFRLQALLN-LT-------------
-GLEDVSIARFLKEQLPRLRGSSTS-----------LLMFSGDA-NCSSQVFDTAA--A--LGLA-SPEMHWVIGQP---------
----------LGVE--------ELQTAGLPLG-LLAYGKVK-------------------------------RPILANYVRDAVEL
VARAI-----------AAAVLVRPDVALIPSMV----------------NCNDKQRQGTI----------SSGQYLSRFL----
-------------ANT-SFDGATGYI--HVEEVSRIRTDH----RYHI--------WN----LRQDPLGKPTWVT-----------
VGRW----------------NREKIEIE----------------------KGIWP---------------NQIQSMKNNGE---
----------DAGQAR---LRVVTLVELPFVFTR----AVDSDGTCPAGRAQLNSENGSVPTEYKRCCYGYCIDLLEHLSE--DL-
H-----FE-FDLYIVGD-G-KYGAW--------KN-GG--WTGLVGDLLS---------G---AAHMAVTSFSVNSARSKVIDFTS
PFYST-SLGIIVRS----KDTA--A---------PIGAFMWPLHWSM-W---VGIFVTLHVTA-LFLTLYEW--KSPF--------
------GMTPN---------------------GRNRM----KVFSYSSALNLCYAIL-FGR-----TVASKTP---KCWTGRFLMN
LWAIFCLLVLSSYTANLAAVMVGEKTFEELS--GIHDAKLHHPSRG---FRFG-TVRESSAEDYMK-------------KSFPEMH
EYIRRY-----------------------NVPTTPDGVTQLK--TNPPN---------LDAFIMDK-ALLDYEVSI-DA--DC-
KLMTVGK--P-FAIEGY-GIG-LPQ---N---FV--LSSNISEFISR--YKS-DGFMDVLHDK------WYK------VVPCGKR-
-SFAVNET-----LQMGIKHFSGLFVLLCLGMAGSLLSTAGEHLVF--RLLLPRIRKRKKFKYWLHTSQKIHRVLNMSF-------
---EEQKNPKLKTDKRFFHFKFSLTFQLLPLL-------

Hsap_GluN3A
RLSLWWLLSRVCLLLPHPQPCQILKRIGHAVRVGAVASRAPDDSRAGAQRDEPEPGTR-----RSPAPSPGARWLGVDNLNRVEGL
LPYNLSLEVVMAIEAGLGDLPLLPFSSPSSPWS--------SDPFSFLQSVCHTVVVQGVSAL----------LAFPQSQGEESQN
PLHLQ---LSLENSLSSDADVTVSILTMNNWYNFSLLLCQE-----DWNITDFLLLTQNNS----KFHLG-SIIN-----------
-ITANLPSTQDLLSFLQIQLESIKNSTPT-------VVMFGCDM-ESIRRIFEITT--Q--FGVM-PPELRWVLGDS---------
----------QNVE--------ELRTEGLPLG-LIAHGKTT-------------------------------QSVFEHYVQDAMEL
VARAV-----------ATATMIQPELALIPSTM----------------NCMEVETTNL-----------TSGQYLSRFL----
-------------ANT-TFRGLSGSI--RVKGSTIVSSEN----NFFI--------WN----LQHDPMGKPMWTR-----------
LGSW----------------QGGKIVMD----------------------YGIWP--------------EQAQRHKTHFQH---
-----------PSKLH---LRVVTLIEHPFVFTR-----EVDDEGL--CPSSLHSSNDTVPIKFKKCCYGYCIDLLEKIAE--DM-
N-----FD-FDLYIVGD-G-KYGAW--------KN-GH--WTGLVGDLLR---------G---TAHMAVTSFSINTARSQVIDFTS
PFFST-SLGILVRT----RDTA-------A----PIGAFMWPLHWTM-W---LGIFVALHITA-VFLTLYEW--KSPF--------
------GLTPK---------------------GRNRS----KVFSFSSALNICYALL-FGR-T--VA--IKPP---KCWTGRFLMN
LWAIFCMFCLSTYTANLAAVMVGEKIYEELS--GIHDPKLHHPSQG---FRFG-TVRESSAEDYVR-------------QSFPEMH
EYMRRY-----------------------NVPATPDGVEYLK--NDPEK---------LDAFIMDK-ALLDYEVSI-DA--DC-
KLLTVGK--P-FAIEGY-GIG-LPP---N---SP--LTANISELISQ--YKS-HGFMDMLHDK------WYR------VVPCGKR-
-SFAVTET-----LQMGIKHFSGLFVLLCIGFGLSILTTIGEHIVY--RLLLPRIKNKSKLQYWLHTSQRLHRAINT---------
----SFIEEKQQHFKTKRVEKRSNVGPRQLTVWNTSNLSHDNRRKYIFSDLSELEKQIQVIRQELQLAVSRKTELE----------
----
Cmil_GluN3a
---------------------------------MLHFPSNKIKGIHQSSCLFLFGRKMGEKHMNDQMTIMTPIYHQTLQGTLSQY
LS---PN
PLHLQ---MSLNNFHPSHVDILIFLLTMNSWYDVSLILCQE------WNVTNFLNLLHNNS----KFHLE-TIL-----------
-NITSEKDDDDFLNYLQERSDTEKDVLLT-------IITFGCDV-EEFRRIFQLAM--K--YGLT-LPEYHWILGDS---------
----------QNVE--------ELRTEGLPIG-LLAHGETT-------------------------------QPVFRNYVQDAVEL
IARAV-----------AAATYVKPELALIPTTT----------------NCMQRETMNA-----------SSGQFLSRFL--

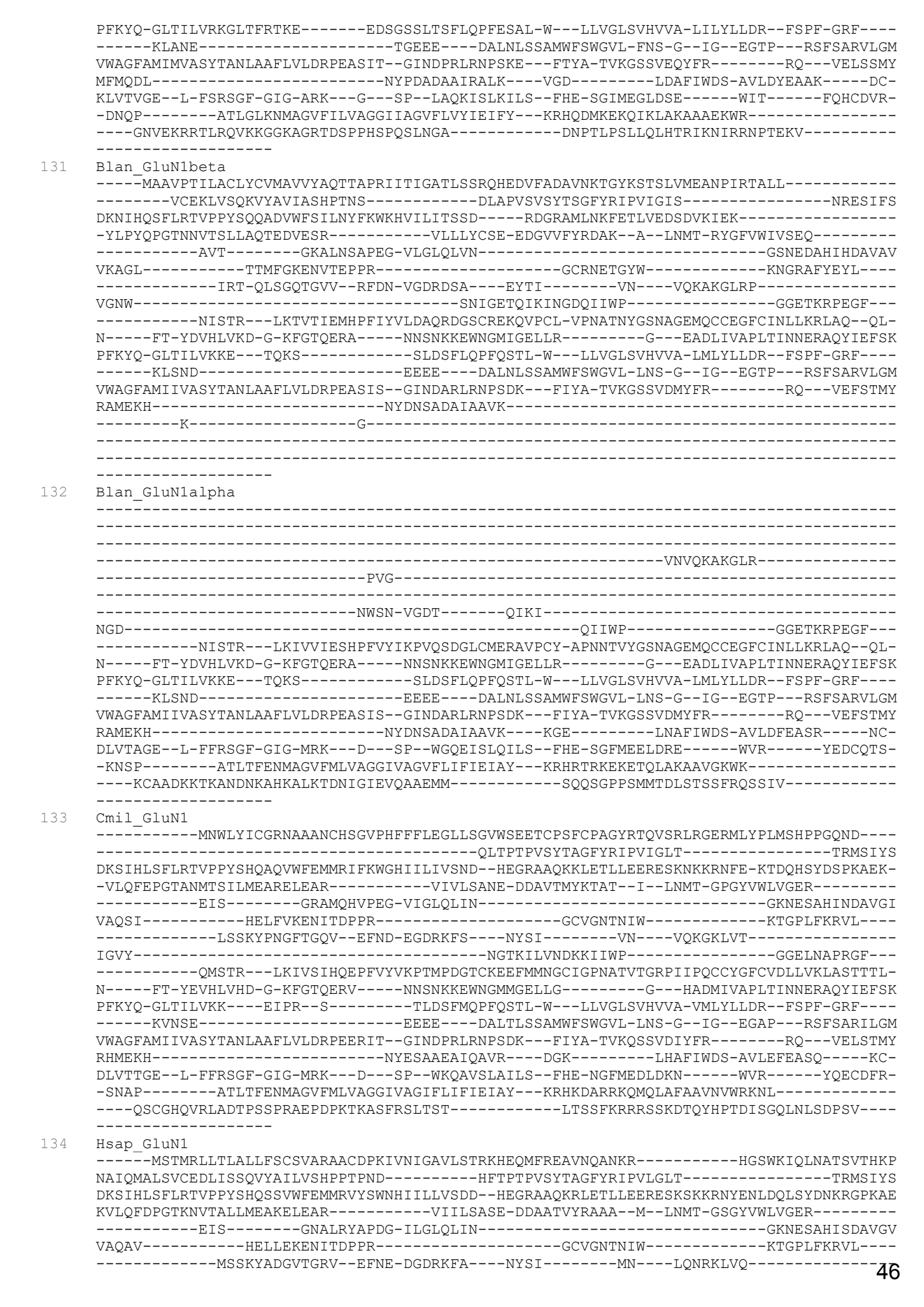

112 Locu_GluN3a
113 Cgig_IR8a
114 Obim_IR8a
115 Bgla_IR8a


116 Bgla_IR9
117 Acal_IR3
118 Blan_GluF2
119 Bfl_GluF2



```
----VRRRRKRNSSKYMVPAPTPEPVEKRNGVQGASS-------------LEKEMDGAIPLAVINRRDRTIPMLQLPSNTYRWG--
------------------
123 Apla_GluN1
----YHHRRHRKTNRYDPLPVCLLLLLHLARVMHAAPAISEIRIGAMLSTEEDIETLQAAVREVNDNSLILPGNYQLNVTSIVMTN
NPIESAIRVCVKIIPNQVYAVISGHSPEL------------YMSSVSVSYTCGFYGIPVIGIS----------------ARECIFS
DKHIHKSYLRTVPPYSQQANVWADLVDHFEWNSVVTITSSD-----QDGRAILSTLRKRLEGSARFKIEQ----------------
-SIAYKPRASNLTDTLLEVRKCRSR-----------VLLLYASE-KDATTIFQDAQ--R--LNMT-GAGYAWVVTEQ---------
-----------GIT--------GEALAEAPEG-TLGMYLEQ-------------------------------GTDTKSHIQDAVRV
IAKGI-----------HSFVQNEGIMPPPA-------------------GCRLSSGESLW-----------ASGRLFYGNL-----
-------------VDARVLQGATGAI--DFDK-HGDRKSA----KYKL--------IN----IQSGEPVT-----------------
IGAW-------------------------------------SSETRLTTTHVPIIWP-----------------GGTRDKPEGY---
-----------ELQTH---LRVVIMKDSPFVYVDEQDPETKKCMNDTLPC-------LAAKGDRMQCCYGFCIDLLVVLAK--EL-
N-----FT-FDLHQVHD-G-NYGNFEHV-----NGTERKRWTGMIGELVD---------D---KADMIMAPLTINNERARYIDFSK
PYKYQ-GLTILVKK----ADAS--T---------NLLSFMRPFQISL-W---LLIGVCIHVIA-VVIYLLDR--FSPF---------
-------SHPR--------------------NGSET----DALNLSQALWFSWSVL-LNS-G--VG--ERTP---RSFGARVLGV
VWAGFAMIMVASYTANLAAYLVLDKPHARIS--GINDAKMRNPSPA---FTYA-TVSKSSVEMYFR--------RQ---VELSSMY
RFMQTY-----------------------NYKEADNAIEDLK----SGK---------LDAFIYDS-AMLDFEVSR-----DC-
GLITVGE--L-FGRSGF-GIG-LQK---G---SL--WTQKISLRILE--LHE-KGKIGELDIK------WIT------SKQCGVK-
-SVQP--------TTLGLSSMGGVFILVAGGFLVGCIINRLEIHY---KRHQQTKERQIELARVAVSHWRS---------------
----TVRRRRKRVSSKYMVPAPSPEPMEKRNGVQGSSS------------IEKEMDGAIPLAVINRRSRTTPILQIPSNTWG----
------------------
124 Anja_GluN1
----------MRWLQIQIIVCVLPIVTS-QTPFVIGGAFEYENDRIVFEDAVREINQN---KNHVLPRGITLSVSTILTDNPLNAT
ME------LCQKV--VPNQVAALIMCLSKPNR---------LSAMSVSN-ILGSLEIPVVDIA---TRSNL--------FNDRNIH
NTYMR---T--VPAYTDQAEVWLDLIGHYRWTNVVTVTSKD-DGGSS-MLNAFIRLVNDSS----RLGIK-IEK-----------
-AVQFNKGQTNMTGVLLQVKKAQST-----------VVLLHASA-NDEVAIYSAAK--E--LGLT-APGFIWITDEQ---------
-----------GIN--------ARALRSIPDG-TLAMRLPK-------------------------------GTNRTAHINDAIML
LVKGL-----------HELVQNDNVTRPPS--------------------TCGDA--------------PW-RSGHLYYRWL----
-KD-------TKLSEM-Q--AETGAI--SFSG-RGDRISN----DYDI--------VN----LQNGDLKI----------------
VGKW-----------------TKTSKVMMNA-----------------------QVIWP-----------------GRKMTKPEGY---
-----------RLSTH---LQVVTIKSIPFVYTD-----KPHPTNG--CVDEHYLVCTDGKTGEIMCCKGFCIDLLANLSN--FL-
N-----FT-FDLHIVAD-G-HYGDLVR--VTNSTE-RR--WNGMIGELLD---------G---KADIIMAPLTINKERVKHIDFSK
PFKYQ-GLTILVKK----DVPT--N---------KLVSFLRPFETEL-W---ILMFLAIHVVA-FFLFILDR--LSPF---------
-----SRMHTG--------------------KFGREQ----DALNLSRALWFSWGVL-FNS-G--IG--EGTP---RSLSARVVGM
VWAFFSMIMLASYTANLAAFLVLDKPEGKIS--GINDARMRNPSNT---FKFA-TVKGSSVDAYFR--------RQ---VELSTMY
TFMETF-----------------------NYVNADAAVEAVR------E---GEL---DA-FIWDS-AMLDYQTSR-----DC-
NLVTVGE--L-FGKSGF-GIG-LPK---E---SL--WTQEVSLAILH--FQE-GGVMERLESE------WIS------YRNCPVV-
-GNQP--------ATLSLENMGGTFLLIAFAIVAGFFMIIIERQY---KAYHDKKEHQKELAGRVTLKWKAQRRQKQ---------
----TPSESGSE--------------EEEIALLEMEMDA-----------VNGRCTGRIDKFDYNSKSNNHI--------------
------------------
125 Cgig_GluN1
-------MTWKMENLLIAVSLIVVTSSA-KQTFKIAGIVSTDQMGRALEDAVRIANQDMPSNLQLQALYIKMDANPIRSALN----
--------LCSDV--ISKGIHTVIVSKPENSDI--------SPPISVSY-TCGFYSIPVIGIS---ARDSS--------FSDMTVH
KTFLR---T--VPPYFHQADVWLKMLEYFDWNQVVFIHSMD-TEGRM-ILNRFQSKAEEIM----IEK----------------
-VIKYPSGSKDYQPYLQQLDSLQSR-----------VVLLSATE-EDADQIFRDAE--A--LNLT-GEGYAWIVSEQ---------
----------------------ALTSTSVPEG-TLGLKLLH-------------------------------GTSEKDHIQDCVRL
IKQTV-----------KQLFNGTLTQITDTPT-----------------SCKNSSS------------SW-QAGNSILQAL----
-LA---------AKLE-N--GNTGKV--AFDS-DGDRLNP----DYYI--------QN----VKIENGQKKLED-----------
IGYY----ADPKVSSNALEIKDS-------------------------KIIWP----------------GKKTTKPSGI---
-----------NISTE---LKVVTLESVPFVYTRKMTGSDSCNWDK--NE---------------YCCWGYCIDMLIQIAD--MV-
N-----FT-YSIHLGSS-G-EFGSYKK--VNKTSE-KK--WNGVIAELIN---------K---EADMIVAPLTINPERAGHIDFSK
PFKYQ-GLTILVKK----TATE--S---------KLDSFLQPFEDTL-W---ILVALSVHVVA-LVLYLLDR--FSPF-GRF----
------KLAKN---------------------NDTEE----DALNLSSAMWFAWGVL-LNS-G--IG--EGTP---RSFSARVLGM
VWAGFAMIIVASYTANLAAFLVLDRPEASIT--GIDDARLRNPNED---FKYA-TVRNSAVEMYFK--------RQ---VELSTMY
RQMEPR-----------------------NYKTAEEAIQDIV----NANL--------QA-FIWDS-SRLEYEAGQ-----NC-
DLITVGD--L-FGRSGL-GVG-LQK---K---SP--WTSKISMAILK--LHE-KGNMEDLDNK------WILR------NDCPEK-
-DTTP--------ATLGLTNMASVFLMVAGGIIAGIILIVIEIAY---KRHRGL----KDKELELARNAADRWRGNI---------
----EKRRTLRQTLQRQRETQKKPGVEGNGSALGRGPVGQGNGYNLP---VDHPPPRVGHRLSYTEATGGQMYSPPSYR-------
------------------
126 Obim_GluN1
AIHRTAGIFWLFYLTLFTITALSLESTQPIDVYTIGGVLSSREHQQIFDEAIEHVNQK----------SSKSNIIFNSTSILMNA
NPIRSALSICEDLIPNRVYVVIASHPYDS------------DQSPISVSYTCGFYNIPVIGIS----------------SRESVYS
DNNVHNSFIRTVPPYFHQAEIWIKILQSFKWTQVMFIYSRD-----EDGQAILSHFQTLAK----AEGIS-IEK-----------
-TIRIFPGVENYTDSLVSLKALQSR-----------VILLYALK-EDSERIFTDAG--D--LELT-STGYAWLVTEQ---------
----------------------SLQASNIPVG-TLGTQLIN-------------------------------GTNEAAHIQDSISL
ISQAF-----------IRLRKEMNISEALS--------------------QCNEMNMPW-------------YEGKTILQYL----
-------------KTGYLEDGVTGQV--SFNL-DGDRKNP----VYNI--------MN----VQQTRTVA----------------
VGIYGSIKKPQPGENPLAMAENI-----------------------------NIVWP----------------GNTHKQPEGL---
-----------RKTTH---LKVVTIQEEPFIKKRPIPKGEACDSEEVFCP----HTDKSTGNLTEYCCKGYCIDLLKNLST--RV-
N-----FT-FELHLSSE-N-TYGSFERR-----NGSSDKKWNGMIGEMVS---------G---EADMIMAPLTINPERAQHIDFSK
PFKYQ-GLTILVKKT---RKDS------------SLASFLQPFQDTL-W---ILVGLSVHVVA-LVLYLLDR--FSPF-GRF----
------KLAKS---------------------DDTEE----DALNLSSAMWFAWGVL-LNS-G--IG--EGTP---RSFSARVLGM
VWAGFAMIIVASYTANLAAFLVLDRPEASIS--GIDDPRLRNPQEN---FKYA-TVKKSAVEMYFK--------RQ---VELSTMY
```

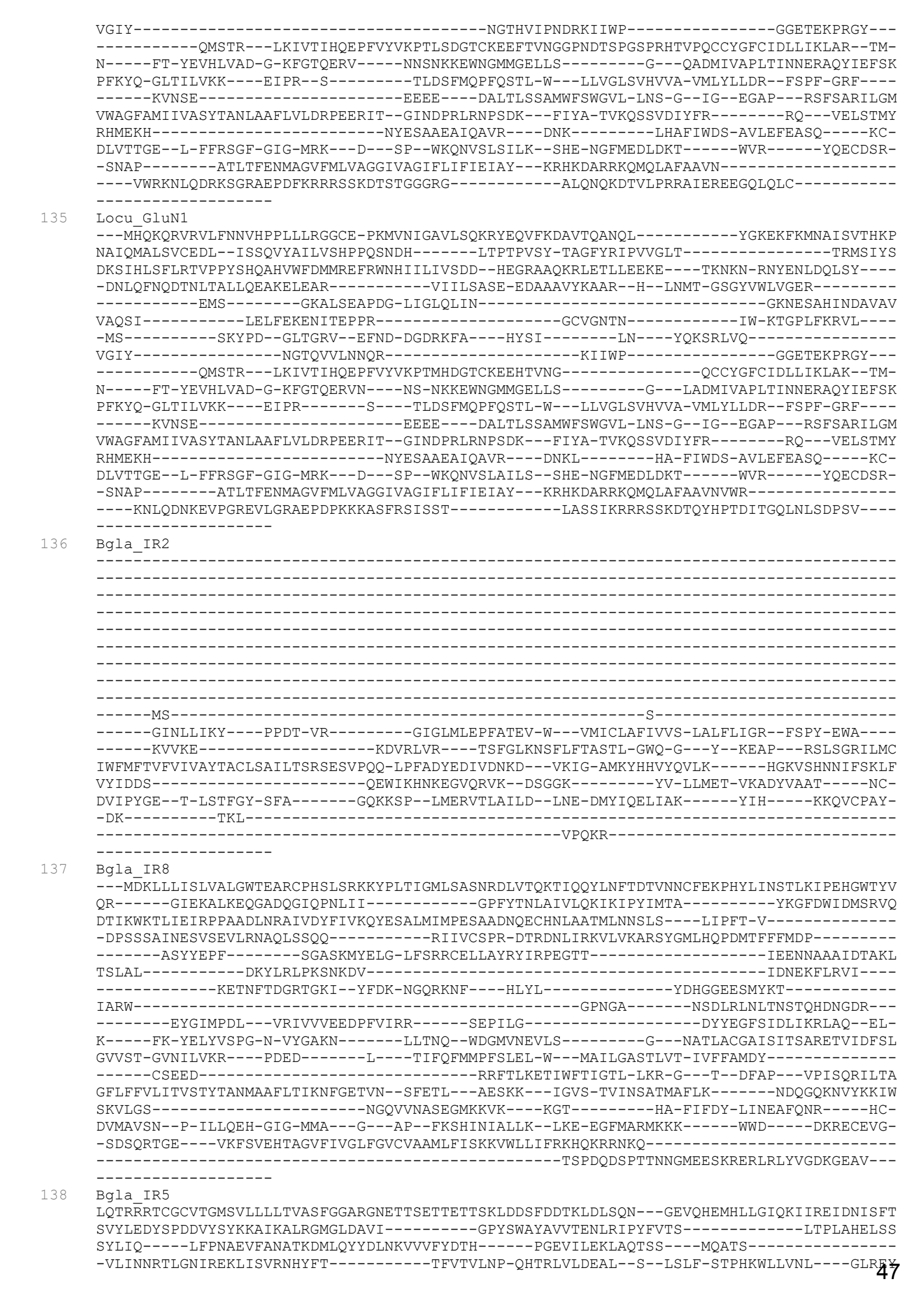
```
RTMETR------------------------NYNTAEEAIDDVR----KGK---------LQAFIWDS-SRLEFEAAN-----DC-
ELVTAGE--L-FGRSGY-GIG-LRK---H---SP--WTQEISLSILS--FHE-SGFMEDLDSK------WIL----VESHNCPER-
-DSSP--------ATLGLTNMAGVFMMVAGGIVAGVLLIFVEILYKRHRWRGNIEKRKTLRQSWRQMKDLKTLNMAPSDDANVKRR
TLRQTLQKQREAEQKLSQFSKMTPPKPAVLLQRGNSQTCGAPY-------PSDAETMGNVTGSSRPVTPGPEASVPTYP-------
------------------
127 Bgla_GluN2beta
-------------------------------------------MEFEFQQAVSHLNAK-----------SKQRHIKFQSSTILMDS
NPIRSALDICDKLLTQHVFTVVASHPNST------------DHSPISVSYTCGYYKIPVLGIS----------------ARDSAFS
DTNVHTMFLRTVPPYSHQADVWVQLLVNLSWYKVIFVYSAD-----EEGRAILSRFQTLAE-----------------------
--------EVNIRVNAEKIYHDAEL-----------------------------------MGMT-GEDWAWIVSEQ---------
----------------------AFEAYNIPVG-FLGVHLVN-------------------------------GTNEVNHIKDAVEV
IGEAF-----------IRLMSSDNISSPPT--------------------GCNESESW--------------SNGDDVYNAL----
-------------KAT-KIEGETGQV--SFNE-KGDRVNP----MYEI--------MN----INANRRAMSVGLFGHKDQAIGLRM
MGN-----------------------------------------------NLTWP----------------GNVHVKPKGE---
-----------KISRN---LTIVTLVEKPFVEVTPLPKDGVCRPVYPAKH-----AFPCKNGTQDLCCMGYCMDMLAKISK--DV-
Q-----FN-FTIHLSKD-G-LFGSFERH-----NSSDKKYWNGMMGELMR---------Q---EADLIVAPLTINPERANDIDFTK
PFKYQ-GLNILVRK----TQKD--S---------SLASFLQPFQDTL-W---ILVGLSVHVVA-LVLYLLDR--FSPF-GRF----
------KLAKS----------------------DDTEE----DALNLSSAMWFSWGVL-LNS-G--IG--EGTP---RSFSARVLGM
VWAGFAMIIVASYTANLAAFLVLDRPEALIS--GIDDPRLRNPNEK---FKYA-TVKGSAVEMYFK-------RQVELSTMYRNME
NQKKYY----------------------------TAEAAIADIR----LGE---------LQAFIWDS-PRLEYEASN-----DC-
DLTTAGD--L-FGRSGL-GIG-LPK---N---SP--WTHDVSMAVLR--MHE-SGFMEQLDNS------WIL---VDSKSNCPES-
-NSAP--------ATLGLTNMAGVFMMVAGGIVAGILLIFIEIAY---KRHRGLKEKELELARNAADRWRGNIEKRRTLRQTLQKQ
KEAVNSVAPKMNSNNTGTKTVIPPPYRRPSLLEATRERDC----------LPPPPPMDYPAPSYVPARSGRTVTWH----------
------------------
128 Lgig_GluN1
----MDTSSQFRWFLTLILIGTVNQVFSKPFSVTIGAALSSEHHQDIFRQAVAALNRHISPDVVFNSTSILMDANPIRSALD----
--------VCDKLLPQNIFAVIASHPNSS------------NQSPISVSYTCGFYNIPVIGIT----------------ARDSAFS
DQNVHSTFLRTVPPFAHQADVWVSLLQYFKWSQVVLIVGTD-----EEGRSILSRFQTVAE----PLKIT-IEK------------
-VVKYIPGESNYTGSLLNLYSAQAR-----------VILMSASL-EDAEQLYTDAN--N--LRLT-GEDFAWIVTEQ----------
----------------------AFSALSAPIG-LIGLHLIN-------------------------------GSNEDAHIRDSVSI
LGHGF-----------EKIIKEHNITKPPS--------------------QCQDISKW--------------QDGNRVMQYL----
-------------RKTKLDHGETGHV--SFND-RGDRMNP----VYEI--------QN----INMDNKVFA---------------
IGLY---------------------------------GSVKNISEQLRMMGEITWP----------------GGVTVQPKGQ---
-----------KISRN---LTVVTIAEKPFVDVLVLEPGEKCQYDDKMRT---------------HCCSGYCMDMLDEISK--IV-
N-----FT-LTIHLSTD-G-LFGSFERH-----NGTKQRHWNGMIGELLS---------N---KADLIVAPLTINPERAKVIDFTK
PFKYQ-GLTILVKK----TTKD--S---------SLASFLQPFQDTL-W---ILVGLSVHVVA-LVLYLLDR--FSPF-GRF----
------KLAKS----------------------EDTEE----DALNLSSAMWFAWGVL-LNS-G--IG--EGTP---RSFSARVLGM
VWAGFAMIIVASYTANLAAFLVLDRPEASIS--GIDDPRLRNPNDK---YHYA-TVKGSAVEMYFK--------RQ---VELSTMY
RTMENK-----------------------NYQTAEEAIEAIR----QES---------LQAFIWDS-PRLEYEAAR-----DC-
NLVTAGE--L-FGRSGL-GIG-LQK---N---SP--WTQEVSLAILK--LHE-KGFMEKLDNE------WIL---AESSSACPES-
-NSAP--------ATLGLTNMAGVFMMVAGGIVAGVLLIFVEIAY---KRHRGLKEKEL-------------------------
----ELARNAADRWRGNIEKRKKLRATWQFLHSLNDGT-----------SPPYPAGGVNFV-----------------------
------------------
129 Skow_GluN1alpha
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
-------------------------------------------------------------------------MVHLFFFRKL----
-KS----------CELPD--GDTGYV--SFDS-HGDREYV----DYDI--------VNTQRPSEGEELVAEV--------------
VGKW----------------ENKQVKIG-----------------------SVVWP---------------GGQVGKPPEGV---
-----------SLSSR---LQITTIDTKPFVMVG-----PPNSEGS--CSCAQYNKSGDGGDWSTMCCTGFCIDLLVKLAD--HL-
N-----FS-YDLHLVSD-G-KYGTLEVPKQLGMNGSYKKHWNGMVGELVD---------N---KADMIVAPLTINNERAQYIDFSV
PFKYQ-GLTILVKK----KDHG-------S----SFASFFQPFESAL-W---LLIGLAVHIVA-LILYVLDR--FSPF-GRF----
------KSGQT----------------------GDEQ----DALTLSSAMWFSWGVL-LNS-G--MG--EGTP---RSLSARVLGM
VWAGFAMIMVASYTANLAAFLVLDRPESSIT--GINDPRLRNPSES---FKYA-TVTGSSVEQYFR--------RQ---VELSTMY
RFMEDY-----------------------NYDNVSAAIAALK--NHNEL---------DA-FIWDS-AVLDYVASD-----DC-
SLVTVGE--L-FGRCGF-GLG-LQK---G---SP--WTQKVSLRILS--FHE-SGVMEGLDSE------WIS------FKHCKLS-
-DNQP--------ATLGLSNMAGVFILVAGGIIMGIPLIFVEIFY---KHHMETKEKQMELARMAAS-----------------
----RWRGTVQRRRTVRQTLLNRIPTISQMSPNMEDSL-----------HSTNEVSFVHSRHSSLKRNHFSERGDIL--------
------------------
130 Skow_GluN1beta
------TMHLPNIHCCLTSIWVFLVIFFHNFHHMHGLDNNTQIINIGAMLSSAQHEEEFLKIIEDVNTERMPGIRKLNGTFLVMNA
NPIQLALSVCRDLVSQQVYAVIASHPPNS------------DLSPVSISYTCGFYRIPVIGIS----------------CQESIFS
DKNIHMSFLRTVPPYAHHAKVWADLLDIYGWERIITITSSD-----QDGRAVLSAFKQIEEHSDGEIKIE-KS-------------
-LVYKPSSKTNMTELLMKTNDVHSR----------VFLLYANE-EDACSAYAAAK--K--LNMT-DSGNVWLVPEQ---------
-----------AIS--------GKALKEAPTG-IVGLRLVN-------------------------------GTNEVAHINDAIHI
ITRPP-------------------------------------------SSCRGTEKYW--------------TSGPQFYKYL----
-------------LKASLQNGQTGTV--EFDQ-NGDRTSA----EYEI--------IN----VVDGKDRM----------------
VGTW---------------------------------------PFHTTKKLNIVWP----------------GGQETDPEGY---
-----------QISKR---LEVVTIKSHPFVFVEEMGPDGECELPNHVRC---AAPNRTNQEDAYFCCRGFCMDLLNKLAD--SL-
N-----FT-YHVHLVSD-S-LYGAQERING---TNDKR--WNGMVGELLD---------G---KTDLIVAPLTINNERATFIDFSK
```


PFKYQ-GLTILVRKGLTFRTKE-------EDSGSSLTSFLQPFESAL-W---LLVGLSVHVVA-LILYLLDR--FSPF-GRF----
------KLANE---------------------TGEEE----DALNLSSAMWFSWGVL-FNS-G--IG--EGTP---RSFSARVLGM
VWAGFAMIMVASYTANLAAFLVLDRPEASIT--GINDPRLRNPSKE---FTYA-TVKGSSVEQYFR--------RQ---VELSSMY
MFMQDL------------------------NYPDADAAIRALK----VGD---------LDAFIWDS-AVLDYEAAK-----DC-
KLVTVGE--L-FSRSGF-GIG-ARK---G---SP--LAQKISLKILS--FHE-SGIMEGLDSE------WIT------FQHCDVR-
-DNQP--------ATLGLKNMAGVFILVAGGIIAGVFLVYIEIFY---KRHQDMKEKQIKLAKAAAEKWR----------------
----GNVEKRRTLRQVKKGGKAGRTDSPPHSPQSLNGA------------DNPTLPSLLQLHTRIKNIRRNPTEKV----------
----
131 Blan_GluN1beta
-----MAAVPTILACLYCVMAVVYAQTTAPRIITIGATLSSRQHEDVFADAVNKTGYKSTSLVMEANPIRTALL------------
--------VCEKLVSQKVYAVIASHPTNS------------DLAPVSVSYTSGFYRIPVIGIS----------------NRESIFS
DKNIHQSFLRTVPPYSQQADVWFSILNYFKWKHVILITSSD-----RDGRAMLNKFETLVEDSDVKIEK----------------
-YLPYQPGTNNVTSLLAQTEDVESR-----------VLLLYCSE-EDGVVFYRDAK--A--LNMT-RYGFVWIVSEQ---------
-----------AVT--------GKALNSAPEG-VLGLQLVN-------------------------------GSNEDAHIHDAVAV
VKAGL-----------TTMFGKENVTEPPR-------------------GCRNETGYW-------------KNGRAFYEYL----
-------------IRT-QLSGQTGVV--RFDN-VGDRDSA----EYTI--------VN----VQKAKGLRP---------------
VGNW-----------------------------------SNIGETQIKINGDQIIWP---------------GGETKRPEGF---
-----------NISTR---LKTVTIEMHPFIYVLDAQRDGSCREKQVPCL-VPNATNYGSNAGEMQCCEGFCINLLKRLAQ--QL-
N-----FT-YDVHLVKD-G-KFGTQERA-----NNSNKKEWNGMIGELLR---------G---EADLIVAPLTINNERAQYIEFSK
PFKYQ-GLTILVKKE---TQKS------------SLDSFLQPFQSTL-W---LLVGLSVHVVA-LMLYLLDR--FSPF-GRF----
------KLSND----------------------EEEE----DALNLSSAMWFSWGVL-LNS-G--IG--EGTP---RSFSARVLGM
VWAGFAMIIVASYTANLAAFLVLDRPEASIS--GINDARLRNPSDK---FIYA-TVKGSSVDMYFR--------RQ---VEFSTMY
RAMEKH-----------------------NYDNSADAIAAVK---
---------K------------------G---

----
132 Blan_GluN1alpha

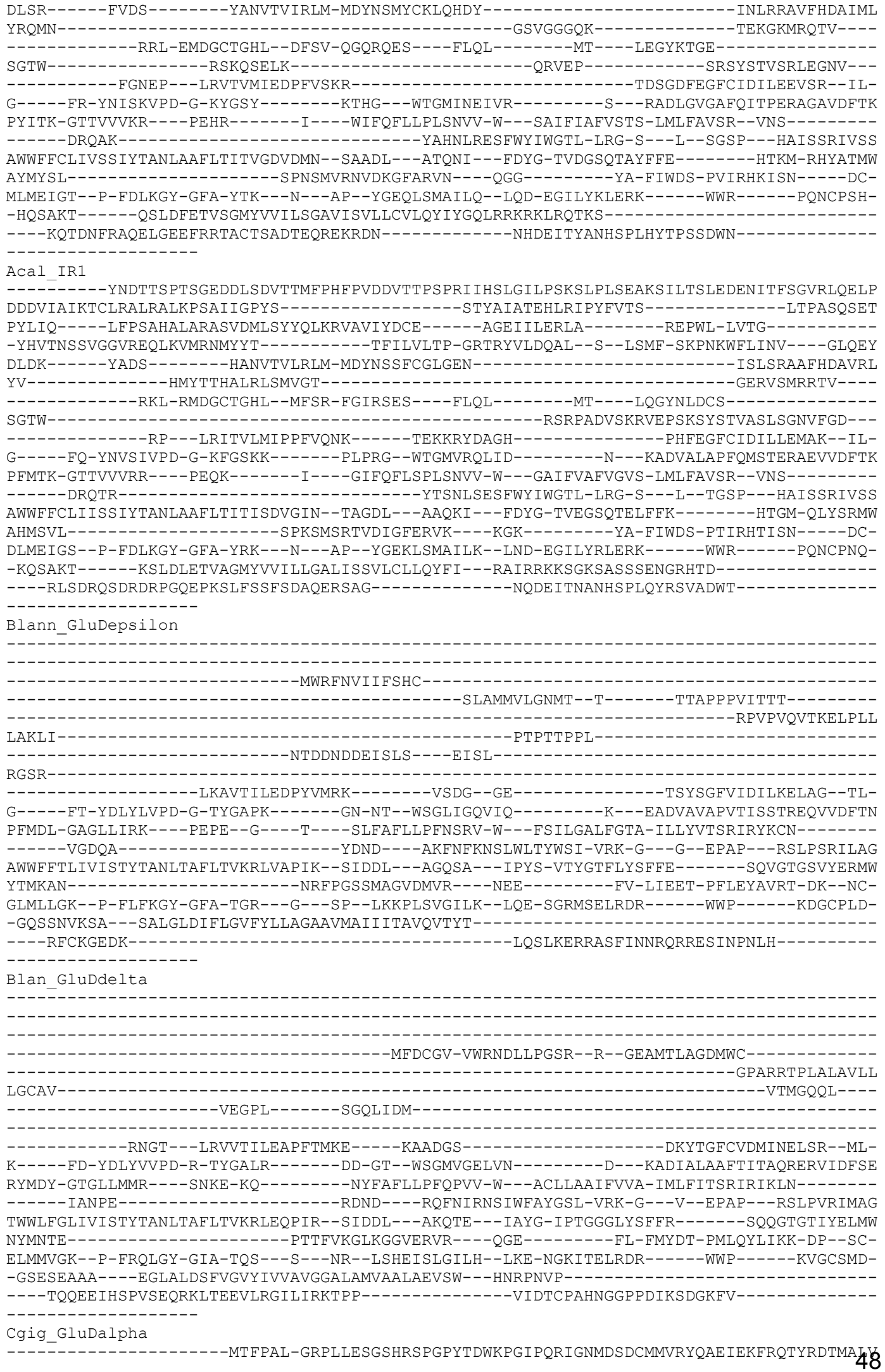
---VNVQKAKGLR---------------
----------------------------PVG---

---------------------------NWSN-VGDT-------QIKI---
NGD---QIIWP----------------GGETKRPEGF---
-----------NISTR---LKIVVIESHPFVYIKPVQSDGLCMERAVPCY-APNNTVYGSNAGEMQCCEGFCINLLKRLAQ--QL-
N-----FT-YDVHLVKD-G-KFGTQERA-----NNSNKKEWNGMIGELLR---------G---EADLIVAPLTINNERAQYIEFSK
PFKYQ-GLTILVKKE---TQKS------------SLDSFLQPFQSTL-W---LLVGLSVHVVA-LMLYLLDR--FSPF-GRF----
------KLSND----------------------EEEE----DALNLSSAMWFSWGVL-LNS-G--IG--EGTP---RSFSARVLGM
VWAGFAMIIVASYTANLAAFLVLDRPEASIS--GINDARLRNPSDK---FIYA-TVKGSSVDMYFR--------RQ---VEFSTMY
RAMEKH-----------------------NYDNSADAIAAVK----KGE---------LNAFIWDS-AVLDFEASR-----NC-
DLVTAGE--L-FFRSGF-GIG-MRK---D---SP--WGQEISLQILS--FHE-SGFMEELDRE------WVR------YEDCQTS-
-KNSP--------ATLTFENMAGVFMLVAGGIVAGVFLIFIEIAY---KRHRTRKEKETQLAKAAVGKWK----------------
----KCAADKKTKANDNKAHKALKTDNIGIEVQAAEMM------------SQQSGPPSMMTDLSTSSFRQSSIV------------
----
133 Cmil_GluN1
-----------MNWLYICGRNAAANCHSGVPHFFFLEGLLSGVWSEETCPSFCPAGYRTQVSRLRGERMLYPLMSHPPGQND----
---QLTPTPVSYTAGFYRIPVIGLT----------------TRMSIYS
DKSIHLSFLRTVPPYSHQAQVWFEMMRIFKWGHIILIVSND--HEGRAAQKKLETLLEERESKNKKRNFE-KTDQHSYDSPKAEK-
-VLQFEPGTANMTSILMEARELEAR-----------VIVLSANE-DDAVTMYKTAT--I--LNMT-GPGYVWLVGER---------
-----------EIS--------GRAMQHVPEG-VIGLQLIN-------------------------------GKNESAHINDAVGI
VAQSI-----------HELFVKENITDPPR-------------------GCVGNTNIW-------------KTGPLFKRVL----
-------------LSSKYPNGFTGQV--EFND-EGDRKFS----NYSI--------VN----VQKGKLVT----------------
IGVY-------------------------------------NGTKILVNDKKIIWP---------------GGELNAPRGF---
-----------QMSTR---LKIVSIHQEPFVYVKPTMPDGTCKEEFMMNGCIGPNATVTGRPIIPQCCYGFCVDLLVKLASTTTL-
N-----FT-YEVHLVHD-G-KFGTQERV-----NNSNKKEWNGMMGELLG---------G---HADMIVAPLTINNERAQYIEFSK
PFKYQ-GLTILVKK----EIPR--S---------TLDSFMQPFQSTL-W---LLVGLSVHVVA-VMLYLLDR--FSPF-GRF----
------KVNSE----------------------EEEE----DALTLSSAMWFSWGVL-LNS-G--IG--EGAP---RSFSARILGM
VWAGFAMIIVASYTANLAAFLVLDRPEERIT--GINDPRLRNPSDK---FIYA-TVKQSSVDIYFR--------RQ---VELSTMY
RHMEKH-----------------------NYESAAEAIQAVR----DGK---------LHAFIWDS-AVLEFEASQ-----KC-
DLVTTGE--L-FFRSGF-GIG-MRK---D---SP--WKQAVSLAILS--FHE-NGFMEDLDKN------WVR------YQECDFR-
-SNAP--------ATLTFENMAGVFMLVAGGIVAGIFLIFIEIAY---KRHKDARRKQMQLAFAAVNVWRKNL------------
----QSCGHQVRLADTPSSPRAEPDPKTKASFRSLTST------------LTSSFKRRRSSKDTQYHPTDISGQLNLSDPSV----
----
134 Hsap_GluN1
------MSTMRLLTLALLFSCSVARAACDPKIVNIGAVLSTRKHEQMFREAVNQANKR----------HGSWKIQLNATSVTHKP
NAIQMALSVCEDLISSQVYAILVSHPPTPND----------HFTPTPVSYTAGFYRIPVLGLT----------------TRMSIYS
DKSIHLSFLRTVPPYSHQSSVWFEMMRVYSWNHIILLVSDD--HEGRAAQKRLETLLEERESKSKKRNYENLDQLSYDNKRGPKAE
KVLQFDPGTKNVTALLMEAKELEAR-----------VIILSASE-DDAATVYRAAA--M--LNMT-GSGYVWLVGER---------
-----------EIS--------GNALRYAPDG-ILGLQLIN-------------------------------GKNESAHISDAVGV
VAQAV-----------HELLEKENITDPPR-------------------GCVGNTNIW-------------KTGPLFKRVL----
-------------MSSKYADGVTGRV--EFNE-DGDRKFA----NYSI--------MN----LQNRKLVQ-------------


VGIY-----------------------------------NGTHVIPNDRKIIWP----------------GGETEKPRGY---
----------QMSTR---LKIVTIHQEPFVYVKPTLSDGTCKEEFTVNGGPNDTSPGSPRHTVPQCCYGFCIDLLIKLAR--TM-
N-----FT-YEVHLVAD-G-KFGTQERV-----NNSNKKEWNGMMGELLS---------G---QADMIVAPLTINNERAQYIEFSK
PFKYQ-GLTILVKK----EIPR--S---------TLDSFMQPFQSTL-W---LLVGLSVHVVA-VMLYLLDR--FSPF-GRF----
------KVNSE----------------------EEEE----DALTLSSAMWFSWGVL-LNS-G--IG--EGAP---RSFSARILGM
VWAGFAMIIVASYTANLAAFLVLDRPEERIT--GINDPRLRNPSDK---FIYA-TVKQSSVDIYFR--------RQ---VELSTMY
RHMEKH------------------------NYESAAEAIQAVR----DNK---------LHAFIWDS-AVLEFEASQ-----KC-
DLVTTGE--L-FFRSGF-GIG-MRK---D---SP--WKQNVSLSILK--SHE-NGFMEDLDKT------WVR------YQECDSR-
-SNAP--------ATLTFENMAGVFMLVAGGIVAGIFLIFIEIAY---KRHKDARRKQMQLAFAAVN------------------
----VWRKNLQDRKSGRAEPDFKRRRSSKDTSTGGGRG------------ALQNQKDTVLPRRAIEREEGQLQLC----------
----
Locu_GluN1
---MHQKQRVRVLFNNVHPPLLLRGGCE-PKMVNIGAVLSQKRYEQVFKDAVTQANQL----------YGKEKFKMNAISVTHKP
NAIQMALSVCEDL--ISSQVYAILVSHPPQSNDH-------LTPTPVSY-TAGFYRIPVVGLT----------------TRMSIYS
DKSIHLSFLRTVPPYSHQAHVWFDMMREFRWNHIILIVSDD--HEGRAAQKRLETLLEEKE----TKNKN-RNYENLDQLSY----
-DNLQFNQDTNLTALLQEAKELEAR----------VIILSASE-EDAAAVYKAAR--H--LNMT-GSGYVWLVGER---------
----------EMS--------GKALSEAPDG-LIGLQLIN------------------------------GKNESAHINDAVAV
VAQSI----------LELFEKENITEPPR--------------------GCVGNTN-----------IW-KTGPLFKRVL----
-MS----------SKYPD--GLTGRV--EFND-DGDRKFA----HYSI--------LN----YQKSRLVQ----------------
VGIY----------------NGTQVVLNNQR---------------------KIIWP----------------GGETEKPRGY---
----------QMSTR---LKIVTIHQEPFVYVKPTMHDGTCKEEHTVNG--------------QCCYGFCIDLLIKLAK--TM-
N-----FT-YEVHLVAD-G-KFGTQERVN----NS-NKKEWNGMMGELLS---------G---LADMIVAPLTINNERAQYIEFSK
PFKYQ-GLTILVKK----EIPR-------S----TLDSFMQPFQSTL-W---LLVGLSVHVVA-VMLYLLDR--FSPF-GRF----
------KVNSE----------------------EEEE----DALTLSSAMWFSWGVL-LNS-G--IG--EGAP---RSFSARILGM
VWAGFAMIIVASYTANLAAFLVLDRPEERIT--GINDPRLRNPSDK---FIYA-TVKQSSVDIYFR--------RQ---VELSTMY
RHMEKH------------------------NYESAAEAIQAVR----DNKL--------HA-FIWDS-AVLEFEASQ-----KC-
DLVTTGE--L-FFRSGF-GIG-MRK---D---SP--WKQNVSLAILS--SHE-NGFMEDLDKT------WVR------YQECDSR-
-SNAP--------ATLTFENMAGVFMLVAGGIVAGIFLIFIEIAY---KRHKDARRKQMQLAFAAVNVWR----------------
----KNLQDNKEVPGREVLGRAEPDPKKKASFRSISST------------LASSIKRRRSSKDTQYHPTDITGQLNLSDPSV----
----
Bgla_IR2
------MS---S-------------------------
------GINLLIKY----PPDT-VR---------GIGLMLEPFATEV-W---VMICLAFIVVS-LALFLIGR--FSPY-EWA----
------KVVKE--------------------KDVRLVR----TSFGLKNSFLFTASTL-GWQ-G---Y--KEAP---RSLSGRILMC
IWFMFTVFVIVAYTACLSAILTSRSESVPQQ-LPFADYEDIVDNKD---VKIG-AMKYHHVYQVLK------HGKVSHNNIFSKLF
VYIDDS-----------------------QEWIKHNKEGVQRVK--DSGGK---------YV-LLMET-VKADYVAAT-----NC-
DVIPYGE--T-LSTFGY-SFA-------GQKKSP--LMERVTLAILD--LNE-DMYIQELIAK------YIH-----KKQVCPAY-
-DK----------TKL---
---VPQKR-----------------------------

Bgla_IR8
---MDKLLLISLVALGWTEARCPHSLSRKKYPLTIGMLSASNRDLVTQKTIQQYLNFTDTVNNCFEKPHYLINSTLKIPEHGWTYV
QR------GIEKALKEQGADQGIQPNLII------------GPFYTNLAIVLQKIKIPYIMTA----------YKGFDWIDMSRVQ
DTIKWKTLIEIRPPAADLNRAIVDYFIVKQYESALMIMPESAADNQECHNLAATMLNNSLS----LIPFT-V--------------
-DPSSSAINESVSEVLRNAQLSSQQ----------RIIVCSPR-DTRDNLIRKVLVKARSYGMLHQPDMTFFFMDP---------
-------ASYYEPF--------SGASKMYELG-LFSRRCELLAYRYIRPEGTT------------------IEENNAAAIDTAKL
TSLAL----------DKYLRLPKSNKDV---IDNEKFLRVI----
-------------KETNFTDGRTGKI--YFDK-NGQRKNF----HLYL--------------YDHGGEESMYKT------------
IARW---GPNGA-------NSDLRLNLTNSTQHDNGDR---
--------EYGIMPDL---VRIVVVEEDPFVIRR------SEPILG-------------------DYYEGFSIDLIKRLAQ--EL-
K-----FK-YELYVSPG-N-VYGAKN-------LLTNQ--WDGMVNEVLS---------G---NATLACGAISITSARETVIDFSL
GVVST-GVNILVKR----PDED-------L----TIFQFMMPFSLEL-W---MAILGASTLVT-IVFFAMDY--------------
------CSEED-----------------------------RRFTLKETIWFTIGTL-LKR-G---T--DFAP---VPISQRILTA
GFLFFVLITVSTYTANMAAFLTIKNFGETVN--SFETL---AESKK---IGVS-TVINSATMAFLK-------NDQGQKNVYKKIW
SKVLGS-----------------------NGQVVNASEGMKKVK----KGT---------HA-FIFDY-LINEAFQNR-----HC-
DVMAVSN--P-ILLQEH-GIG-MMA---G---AP--FKSHINIALLK--LKE-EGFMARMKKK------WWD-----DKRECEVG-
-SDSQRTGE----VKFSVEHTAGVFIVGLFGVCVAAMLFISKKVWLLIFRKHQKRRNKQ--------------------------
---TSPDQDSPTTNNGMEESKRERLRLYVGDKGEAV---

Bgla_IR5
LQTRRRTCGCVTGMSVLLLLTVASFGGARGNETTSETTETTSKLDDSFDDTKLDLSQN---GEVQHEMHLLGIQKIIREIDNISFT
SVYLEDYSPDDVYSYKKAIKALRGMGLDAVI----------GPYSWAYAVVTENLRIPYFVTS-------------LTPLAHELSS
SYLIQ-----LFPNAEVFANATKDMLQYYDLNKVVVFYDTH------PGEVILEKLAQTSS----MQATS----------------
-VLINNRTLGNIREKLISVRNHYFT----------TFVTVLNP-QHTRLVLDEAL--S--LSLF-STPHKWLLVNL----GLREV

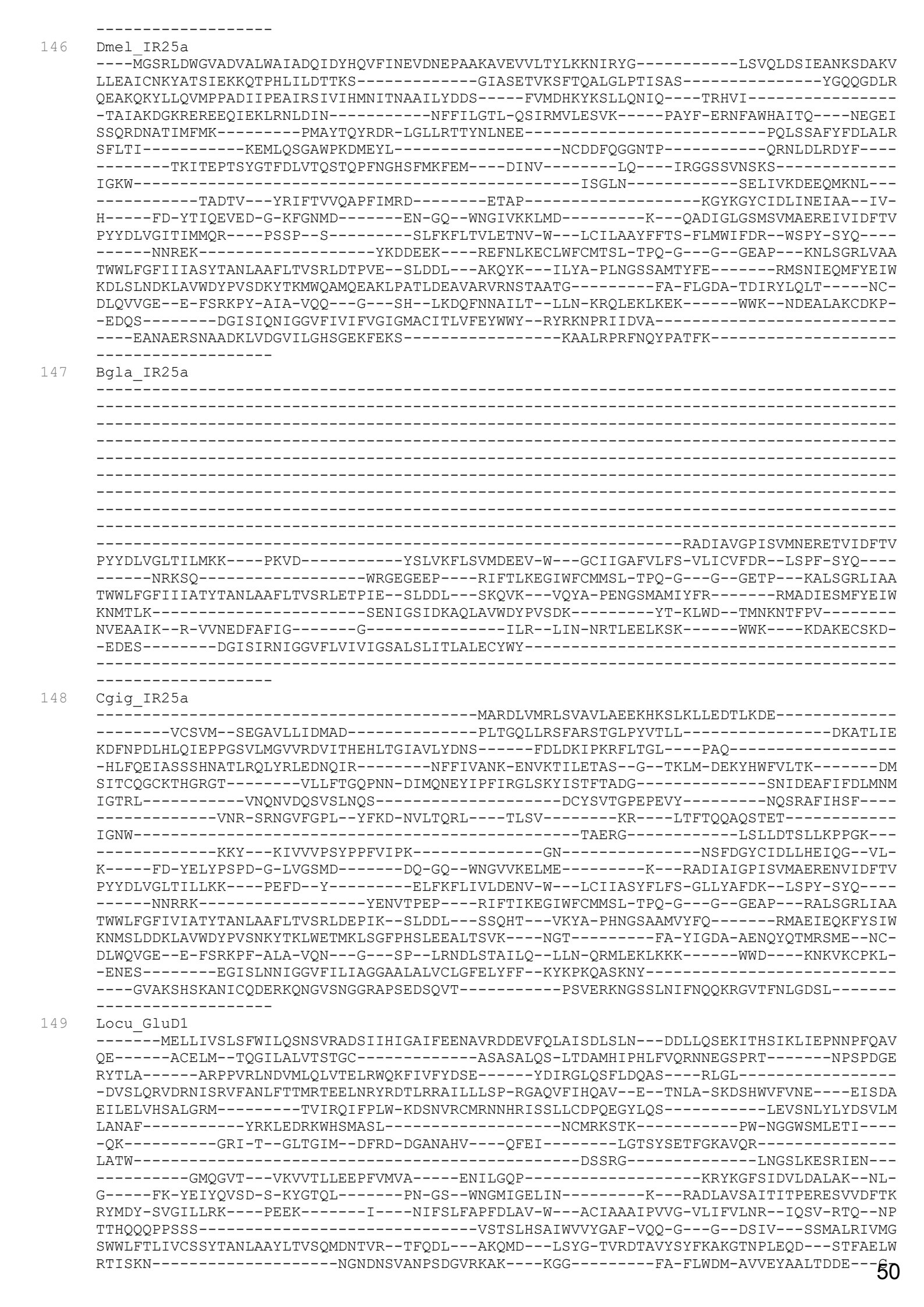

DLSR------FVDS--------YANVTVIRLM-MDYNSMYCKLQHDY------------------------INLRRAVFHDAIML
YRQMN---GSVGGGQK--------------TEKGKMRQTV----
------------RRL-EMDGCTGHL--DFSV-QGQRQES----FLQL--------MT----LEGYKTGE----------------
SGTW----------------RSKQSELK-----------------------QRVEP------------SRSYSTVSRLEGNV---
-----------FGNEP---LRVTVMIEDPFVSKR--------------------------TDSGDFEGFCIDILEEVSR--IL-
G-----FR-YNISKVPD-G-KYGSY--------KTHG---WTGMINEIVR---------S---RADLGVGAFQITPERAGAVDFTK
PYITK-GTTVVVKR----PEHR-------I----WIFQFLLPLSNVV-W---SAIFIAFVSTS-LMLFAVSR--VNS---------
------DRQAK-------------------------------YAHNLRESFWYIWGTL-LRG-S---L--SGSP---HAISSRIVSS
AWWFFCLIVSSIYTANLAAFLTITVGDVDMN--SAADL---ATQNI---FDYG-TVDGSQTAYFFE--------HTKM-RHYATMW
AYMYSL---------------------SPNSMVRNVDKGFARVN----QGG---------YA-FIWDS-PVIRHKISN-----DC-
MLMEIGT--P-FDLKGY-GFA-YTK---N---AP--YGEQLSMAILQ--LQD-EGILYKLERK------WWR------PQNCPSH-
-HQSAKT------QSLDFETVSGMYVVILSGAVISVLLCVLQYIYGQLRRKRKLRQTKS--------------------------
----KQTDNFRAQELGEEFRRTACTSADTEQREKRDN-------------NHDEITYANHSPLHYTPSSDWN--------------
----
139 Acal_IR1
----------YNDTTSPTSGEDDLSDVTTMFPHFPVDDVTTPSPRIIHSLGILPSKSLPLSEAKSILTSLEDENITFSGVRLQELP
DDDVIAIKTCLRALRALKPSAIIGPYS------------------STYAIATEHLRIPYFVTS--------------LTPASQSET
PYLIQ-----LFPSAHALARASVDMLSYYQLKRVAVIYDCE------AGEIILERLA--------REPWL-LVTG-----------
-YHVTNSSVGGVREQLKVMRNMYYT-----------TFILVLTP-GRTRYVLDQAL--S--LSMF-SKPNKWFLINV----GLQEY
DLDK------YADS--------HANVTVLRLM-MDYNSSFCGLGEN-------------------------ISLSRAAFHDAVRL
YV--------------HMYTTHALRLSMVGT---GERVSMRRTV----
-------------RKL-RMDGCTGHL--MFSR-FGIRSES----FLQL--------MT----LQGYNLDCS---------------
SGTW---RSRPADVSKRVEPSKSYSTVASLSGNVFGD---
--------------RP---LRITVLMIPPFVQNK------TEKKRYDAGH---------------PHFEGFCIDILLEMAK--IL-
G-----FQ-YNVSIVPD-G-KFGSKK-------PLPRG--WTGMVRQLID---------N---KADVALAPFQMSTERAEVVDFTK
PFMTK-GTTVVVRR----PEQK-------I----GIFQFLSPLSNVV-W---GAIFVAFVGVS-LMLFAVSR--VNS---------
------DRQTR-------------------------------YTSNLSESFWYIWGTL-LRG-S---L--TGSP---HAISSRIVSS
AWWFFCLIISSIYTANLAAFLTITISDVGIN--TAGDL---AAQKI---FDYG-TVEGSQTELFFK--------HTGM-QLYSRMW
AHMSVL---------------------SPKSMSRTVDIGFERVK----KGK---------YA-FIWDS-PTIRHTISN-----DC-
DLMEIGS--P-FDLKGY-GFA-YRK---N---AP--YGEKLSMAILK--LND-EGILYRLERK------WWR------PQNCPNQ-
-KQSAKT------KSLDLETVAGMYVVILLGALISSVLCLLQYFI---RAIRRKKSGKSASSSENGRHTD----------------
----RLSDRQSDRDRPGQEPKSLFSSFSDAQERSAG--------------NQDEITNANHSPLQYRSVADWT--------------
----
140 Blann_GluDepsilon

-----------------------------MWRFNVIIFSHC---
---SLAMMVLGNMT--T-------TTAPPPVITTT---------
---RPVPVQVTKELPLL
LAKLI---PTPTTPPL-----------------------------
---------------------------NTDDNDDEISLS----EISL---
RGSR--
-------------------LKAVTILEDPYVMRK--------VSDG--GE---------------TSYSGFVIDILKELAG--TL-
G-----FT-YDLYLVPD-G-TYGAPK-------GN-NT--WSGLIGQVIQ---------K---EADVAVAPVTISSTREQVVDFTN
PFMDL-GAGLLIRK----PEPE--G----T----SLFAFLLPFNSRV-W---FSILGALFGTA-ILLYVTSRIRYKCN--------
------VGDQA----------------------YDND----AKFNFKNSLWLTYWSI-VRK-G---G--EPAP---RSLPSRILAG
AWWFFTLIVISTYTANLTAFLTVKRLVAPIK--SIDDL---AGQSA---IPYS-VTYGTFLYSFFE-------SQVGTGSVYERMW
YTMKAN----------------------NRFPGSSMAGVDMVR----NEE---------FV-LIEET-PFLEYAVRT-DK--NC-
GLMLLGK--P-FLFKGY-GFA-TGR---G---SP--LKKPLSVGILK--LQE-SGRMSELRDR------WWP------KDGCPLD-
-GQSSNVKSA---SALGLDIFLGVFYLLAGAAVMAIIITAVQVTYT---
----RFCKGEDK---LQSLKERRASFINNRQRRESINPNLH----------
----
141 Blan_GluDdelta

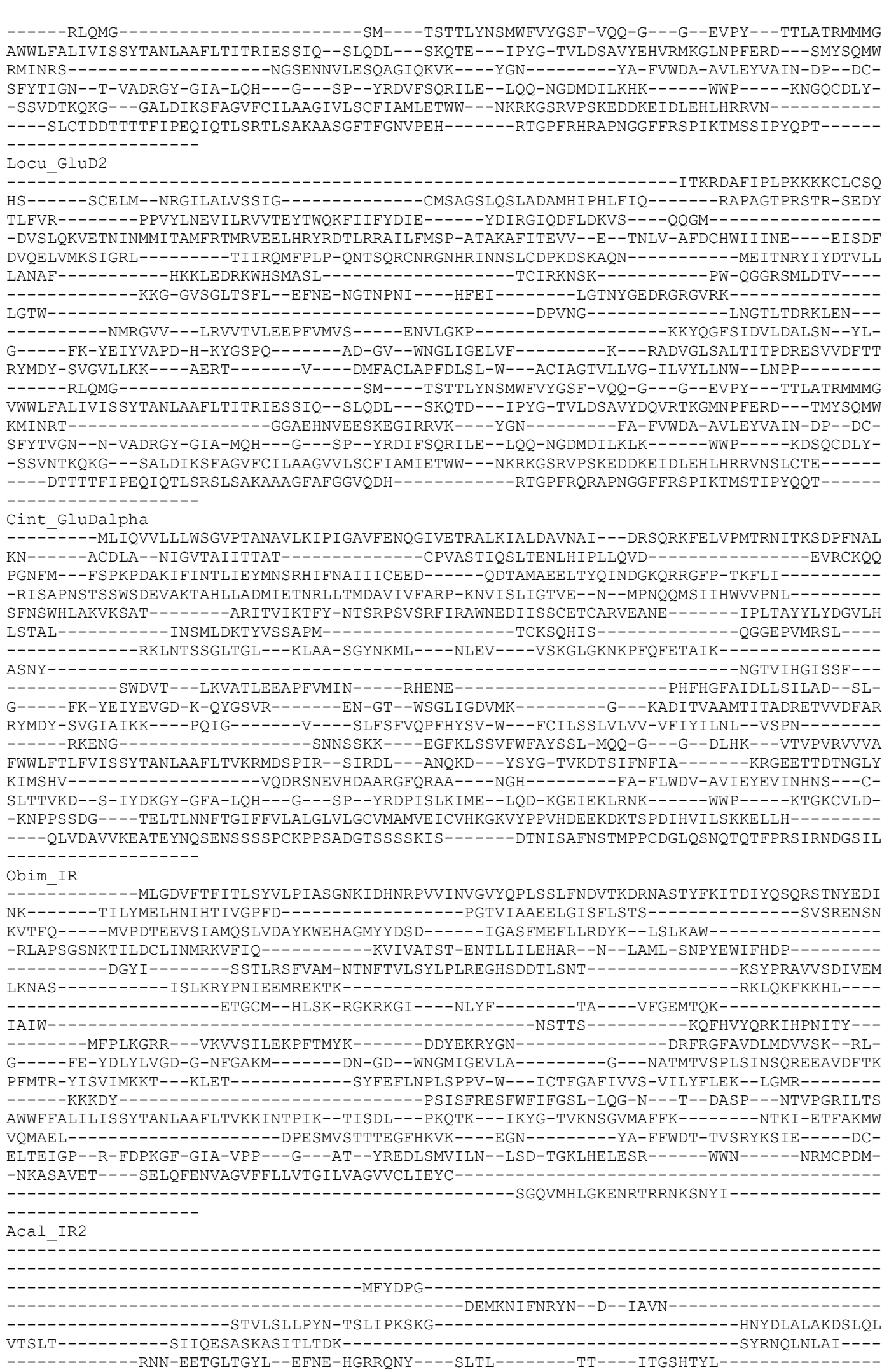
---------------------------------------MFDCGV-VWRNDLLPGSR--R--GEAMTLAGDMWC-------------
---GPARRTPLALAVLL
LGCAV---VTMGQQL----
---------------------VEGPL-------SGQLIDM---

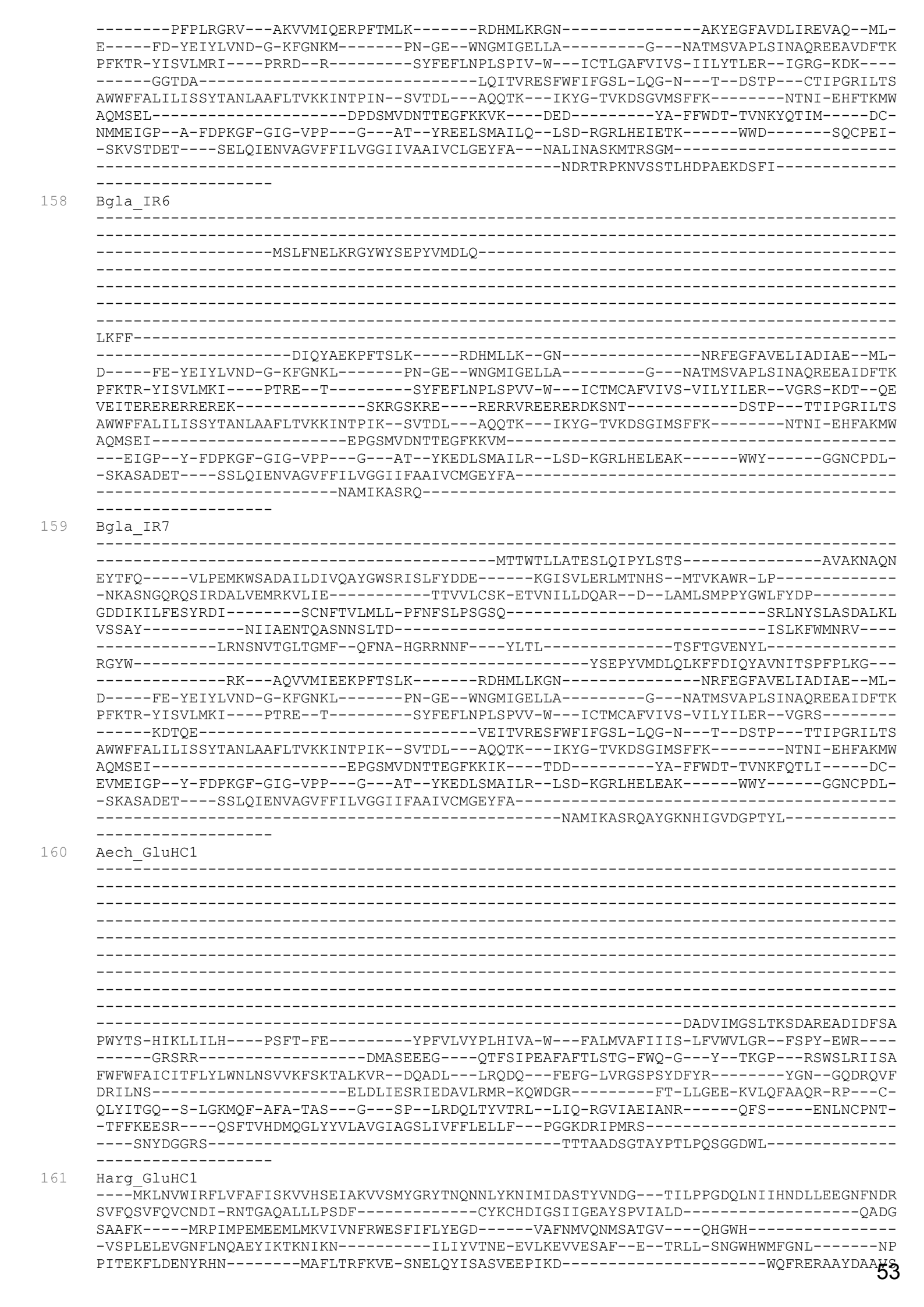
------------RNGT---LRVVTILEAPFTMKE-----KAADGS--------------------DKYTGFCVDMINELSR--ML-
K-----FD-YDLYVVPD-R-TYGALR-------DD-GT--WSGMVGELVN---------D---KADIALAAFTITAQRERVIDFSE
RYMDY-GTGLLMMR----SNKE-KQ---------NYFAFLLPFQPVV-W---ACLLAAIFVVA-IMLFITSRIRIKLN--------
------IANPE----------------------RDND----RQFNIRNSIWFAYGSL-VRK-G---V--EPAP---RSLPVRIMAG
TWWLFGLIVISTYTANLTAFLTVKRLEQPIR--SIDDL---AKQTE---IAYG-IPTGGGLYSFFR-------SQQGTGTIYELMW
NYMNTE----------------------PTTFVKGLKGGVERVR----QGE---------FL-FMYDT-PMLQYLIKK-DP--SC-
ELMMVGK--P-FRQLGY-GIA-TQS---S---NR--LSHEISLGILH--LKE-NGKITELRDR------WWP------KVGCSMD-
-GSESEAAA----EGLALDSFVGVYIVVAVGGALAMVAALAEVSW---HNRPNVP--------------------------------
----TQQEEIHSPVSEQRKLTEEVLRGILIRKTPP---------------VIDTCPAHNGGPPDIKSDGKFV--------------
----
142 Cgig_GluDalpha
----------------------MTFPAL-GRPLLESGSHRSPGPYTDWKPGIPQRIGNMDSDCMMVRYQAEIEKFRQTYRDTMALV

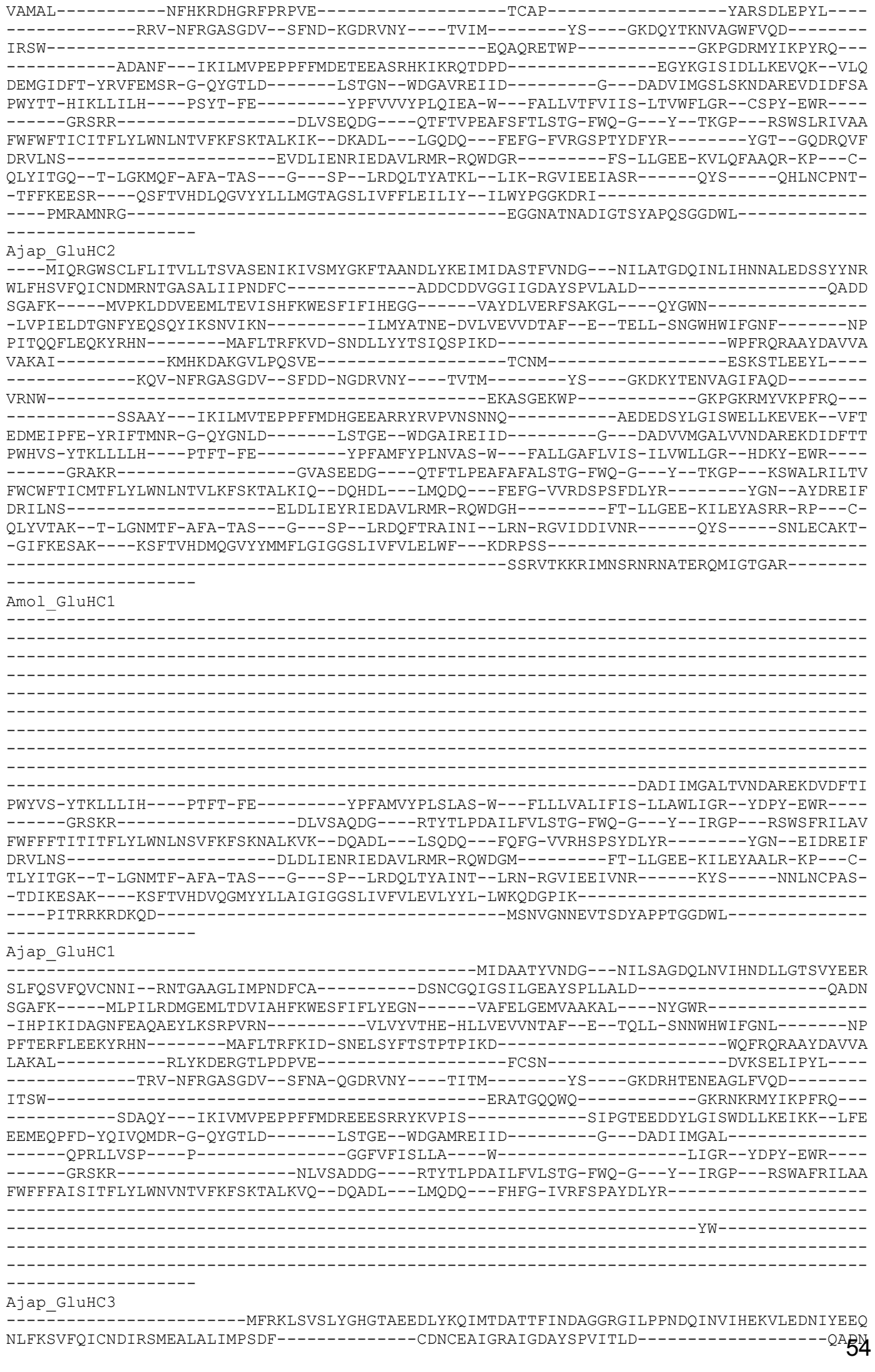

PD
RLLHSPVPVDT
FGLRQFYREHDEIMLEI
RRQHSLCIQELAQLETEVEIESDR
KYFKHTDS-SNETRLID
KESYARVFSSA
IDEETPFQEVAE
YSQEP
NSFH
VVEDRLYKCI
FKD-FGNRTLK
VVSVEDEPFQMRV
DKGN
GS
FYYYGFTYDLLNEFAK--QF-
N
FR-YEFLDSVD-G-LYGNPTN
DN-KN--ASGMIGM
EADIAVGPFTITAERRKVVDFIY
PFQEE-GSGIIVRK
VDNE-AD
RIFRVFSPLDTDS-W
LATGAAAFVAA-VVLSIIVK--LSPF
SKG
LHNKVSASFWLVFSAF-LHQ-G
E--EKSS
KSVPARLVMG
FWWVFTIIVMSLYTANLAAFLTVSLGKAPIK--NLEEL
AAQSV
YKPL-ISDGTNLHMLFK
KAEE-GIYKKIW
DMMRDM
PKFKSLKQVYEMII
KG-VIYQSTAVLDYLLHQVDN
S-
DALSMYQKVSNFSESGVIGITNLPLITIDNEVCPQTYDGHHHLSVLPNCHRQNSQFIEIVLHM
KWEVIYDSTSSYCVQEK
KNVSSNAIFLHEGQHLTLEIFPELVIYVERTLGIVSEAMTLDFFWVPYPVHEGCVLLISSGLQQNETMGSSDETGLIGKESQIRVF
SSTKDYETPFEEVAGYSQDTRNFNVADDRLYKCIFKNKMFRVFSSLGTDSLYTANLAAFLTVSLAKAPIKNLEELAAQSVYKPLIK
NGSNLHTLFKKAEGGIYKK
143
Cgig_GluDbeta
MKTTSLFGRVLYD--SKIAWTDLNNTETEK
GIVYIPYGMGENE
PFALIEKNSTCIQDLVHRLSAMGVATS
SILMTTEG-NTIKGTLSMIR--R
DDHYENVYLAL
EPHLMLNTIKN
T
NAMLKNAPYVMKG
TKENGE
TYYYGFCYDILEDYAK--AF-
N
FR-YESVDGDG-G-LFGNPT
ED-GLN-ASGMVGMVMR
G
EVDIGVAPFAVTATREQVIDYVL
PYQED-GVGILMKR
VENK-VQ
KFFRIFLPLHYTT-W
WAVVVATVVAA-YVLYFAAK--LSPE
SKE
RELQLGHNIWLIVGTV-YGQ-D
D--GQRP
SFGAGRIILG
FWWVFTILITASYTANLAAFLTISLAKPPVK--NLEEL
ASQTI
YKPL-IVQETNHHAMFK
GATT-GLYKRIW
DLMSDI
PKIKTVEEGYQLVE
TGQ
FA-LLWDY-SQFEYLINN
DC-
GSLEIAQ--ESFHKISL-SFI-IPE
K
AP--FKRAFDNHMLK--MIE-AGIIAKFKAK
WWR
KSKCVSS-
-PKTA
TALETESLSGIFALYGGILAIVLVTFILERKW
RRVSKIRQ
ETELDNRTKFMENVPSSFKYSPNT
144
Cgig_GluDgamma
MSETNDADTSLALLIRANDTKLFTMLNGNR
TEDLLHQAS--S--VDMF-SREYYWIIHND
SKFLKS
SHLLTAMEGG-NVLTASFD
KRLPDAILSDIISA
YGYGL
EYMLNHNTTFSIGKY
DCDDKKPT
IGEPGLLQII
TRN-SMQENLENI--KWTK-DGVLDATVHISSTQA
GRNGTLAE
VATY
NYTDG
FRVKDGRLYQNLFKD
FANRT
LKVVSWTSTPFTMRK
QSTNGQ
VQYHGFCYDILEEFAK--VF-
N
FR-YVMLDSVD-G-TYGGPT
NDGKN--GTGMVGMVMR
G
EADIGVGPFTVTAARETVVDFLT
PFQEE-GVGIIMKT
KDQK-ND
RMFRMFLPFQSTS-W
IATGVSIVITG-IILFVISR--CSPY
TND
ADKPIYKNFWLAFGAF-FGQ-G
G--DSTH
TSASGRIILG
IWWMCTILILELYTANLAAYLTIPPAKSPIK--NLEQL
AASSD
YKPLVKTGSNLDFLF
RRAKGGLYKQIQ
EKMDQM
PVITTTE--A
G
MIR--MIE-AGLIAKFHSK
WWP
RVSECSQD-
-SSKSA
TALQIDSMAGIFIVYAAFSGLALIFFVSE
MEEKTR
KMICNIAAFVQ
FVSVTSALLYPFHFGIKAASIAQKYP
145
Dmel_IR8a
MELPLLVLLLALRFAGSEVLKITFWIEPVQRAEFDTDIAMVLKELDALRLDVKVDDTTLTLTRSEDGLDMQR
FCEIL--STVGASAVIDLT
YSHWEEGYNLVRSLGIGYVRLE
RIMRPFLDMFGDFMRQKRANNVAMVFMNA
RDAVEAMQQMLVGYP
FRTLI-M
-DASQTDPGQHFLERIRSLRPAPT
YIALFARA-AAMNGIFEKVQKAD--LFQR-PLEWHFVFLDT
RDRVFKYRRQ
AELCTRFTLN-PRAICRSMPMPDLYCGSG
FTMQRAMLLNVLRS
LINAA
QVSPGYPLAIYQ
DCNATASSSEVSD
PLEKDDYNWL
DMVHWSNFLAYAPPLPHIQDQFQSPVPGL
TFAV
NISAGYYSSEHEAKTD
LAAW
SSVGEMRLLNETI
SPARRF
FRIGTAESIPWSYLR
REEGTGELIRD
RSGLPIWEGYCIDFIIRLSQ--KL-
N
FE-FEI-VAPEVG-HMGEL
NELGE--WDGVVGDLVR
G
ETDFAIAALKMYSEREEVIDFLP
PYYEQTGISIAIRK
PVRR--T
SLFKFMTVLRLEV-W
LSIVAALVGTA-IMIWFMDK--YSPY
SS
RNNRQAYPYAC
REFTLRESFWFALTSF-TPQ-G
G--GEAP
KAISGRMLVA
AYWLFVVLMLATFTANLAAFLTVERMQTPVQ--SLEQL
ARQSR
INYT-VVKDSDTHQYFV
NMKFAEDTLYRMW
KELALN-KFRIWDYPIKEQYGHILLAINSSQPVADAKEGFANVD-AHENAD
YA-FIHDS-AEIKYEITR
NC-
NLTEVGE--V-FAEQPY-AVA-VQQ
G
SH--LGDELSYAILE--LQK-DRFFEELKAK
YWN
QSNLPNCPLS-
-EDQ
EGITLESLGGVFIATLFGLVLAMMTLGMEVLYY--KKKQNALEITQVR
PVNDSSGSGGLEAEEKPAKVSPPPSFETATFRGKKLPARI
TLGDGKFKPRHGLYARRNLGASDSHSGYM
49

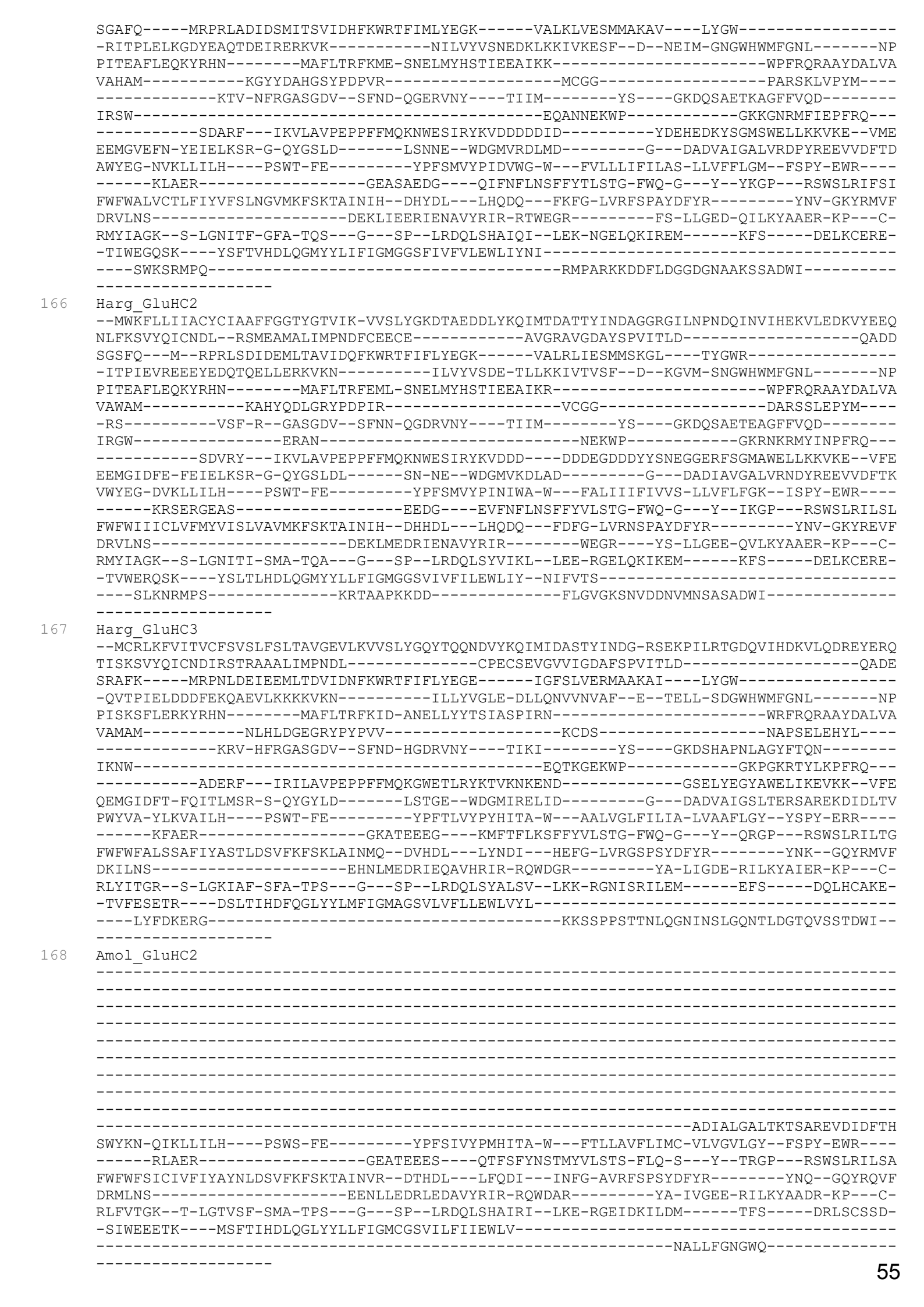


```
SVTVAGN--S-MSSKGY-GIA-LQH---G---SP--YRDLFSHKILE--LQE-KGDLDILKQK------WWP-----RTGRCDLD-
-SHGSAQPDG---RALKLHSFAGVFCILAAGLLLACLVAGLEMWWSSNRCRQEQPKEVTKDYRLARVSGPLTYNDITTASSEGRKD
IWTERERDWDEAEAIDTGQGSESGAGTPAYDQSYGRGHGTHLPPGAGSWGQHPAPASQQHLHHPLHTVQTQITQRGPLPPEPRQDT
------------------
150 Hsap_GluD1
-------MEALTLWLLPWICQCVSVRADSIIHIGAIFEENAAKDDRVFQLAVSDLSLN---DDILQSEKITYSIKVIEANNPFQAV
QE------ACDLM--TQGILALVTSTGC-------------ASANALQS-LTDAMHIPHLFVQRNPGGSPRT-------NPSPDGE
AYTLA------SRPPVRLNDVMLRLVTELRWQKFVMFYDSE------YDIRGLQSFLDQAS----RLGL-----------------
-DVSLQKVDKNISHVFTSLFTTMKTEELNRYRDTLRRAILLLSP-QGAHSFINEAV--E--TNLA-SKDSHWVFVNE----EISDP
EILDLVHSALGRM---------TVVRQIFPSA-KDNQKCTRNNHRISSLLCDPQEGYLQM------------LQISNLYLYDSVLM
LANAF-----------HRKLEDRKWHSMASL-------------------NCIRKSTK-----------PW-NGGRSMLDTI----
-KK----------GHI-T--GLTGVM--EFRE-DSSNPYV----QFEI--------LGTTYSETFGKDMRK---------------
LATW-------------------------------------------------DSEKG--------------LNGSLQERPMGS---
----------RLQGLT---LKVVTVLEEPFVMVA-----ENILGQP-------------------KRYKGFSIDVLDALAK--AL-
G-----FK-YEIYQAPD-G-RYGHQL-------HN-TS--WNGMIGELIS---------K---RADLAISAITITPERESVVDFSK
RYMDY-SVGILIKK----PEEK-------I----SIFSLFAPFDFAV-W---ACIAAAIPVVG-VLIFVLNR--IQAV--------
RAQSAAQPRPS-----------------------------ASATLHSAIWIVYGAF-VQQ-G---G--ESSV---NSMAMRIVMG
SWWLFTLIVCSSYTANLAAFLTVSRMDNPIR--TFQDL---SKQVE---MSYG-TVRDSAVYEYFRAKGTNPLEQD---STFAELW
RTISKN--------------------GGADNCVSSPSEGIRKAK----KGN----------YA-FLWDV-AVVEYAALT-DD--DC-
SVTVIGN--S-ISSKGY-GIA-LQH---G---SP--YRDLFSQRILE--LQD-TGDLDVLKQK------WWP-----HMGRCDLT-
-SHASAQADG---KSLKLHSFAGVFCILAIGLLLACLVAALELWWNN-RCHQETPKEDKEVNLEQVH-----------------
----RRMNSLMDESVSTFLPEQSSHGTSRTLSSGPSSN------------LPLPLSSSATMPSMQCKHRSPNGGLFRQSPVK----
--------------------
151 Cmil_GluD1
MQTRGSEQGSWLGLTPPPPPPSLLWLLT-EQHIGAIFEESAAKDDEVFQLAVSDLSLN---DDILQSERITYSIKFVEANNPFQTV
QE------ACDLM--TQGILALVSSTGC-------------TSATALQS-LTDTMHIPHLFVQRNNGGSPRTMR-------NNDWE
EYTLA------ARPPVRIGDVMMRLVNELRWQKFIVFYDSD-----Y-DIRGLQSFLDQAS----RQGL-----------------
-DVSLQRIDRNISRIFASLFTTMKTEELNRYRDTLRRAILLLSP-RGAQVFINEAV--E--TNLA-SKDSHWVFVNE----EISDS
EILELVHSALGRM---------TVVRQVFPAS-KDSNRRCMRNNHRISSLLCDPQEGYLQT-----------LQTSNLYLYDSVLL
LASAF-----------HRKLEDRKWHSMASL-------------------NCMRKSTK-----------PW-NGGRSMLETI----
-QK----------GLX-H--GLTGAM--EFRD-DGSNNNV----HFEI--------LGTSFSETFGKDVRR---------------
LALW-------------------------------------------------DPVKG----LN----------GSLQERRLES---
----------DMQGVT---LKVVTVLEEPFVMVA-----ENILGQP-------------------KRYKGFSIDVLDALSK--NL-
G-----FK-YEIYQATD-H-KYGNQI-------PN-GS--WNGMIGELIN---------K---RADLAISAITITPERESVVDFSK
RYMDY-SVGILLRK----PEEK-------I----NIFSVFAPFDLAV-W---ACIAAAIPVVG-VLIFVLNR--VQLI--------
--RAQSPTKPQ----------------------TPTS----NSNTLHSAIWLVYGAF-VQQ-G---G--ESAM---NSVAMRIVMG
SWWLFTLIVCSSYTANLAAFLTVSRMDNSVR--SFQDL---AKQSE---LLYG-TVKDSSVYEYFQAKGTNPLEQD---STYAELW
RTISKN--------------------SGMENCVSSASEGIKKVK----NGN----------YA-FLWDM-AVVEYAALTDDD---C-
SMTIVGN--S-VSSKGY-GIA-LQH---G---SP--YRDLFSQRILE--LQE-SGDLDVFKQK------WWP-----KMGRCNLH-
-SHTNAQPDG---RALKLQSFAGVFCILAAGLLLACLVAALEIWWNTFKCTHSHIYGISLVYSFPIQDKEVNLEQVH---------
----RRMNSLMDESVSTFLPEQ-THNTSRNMPSSGSTN------------LSLPLSSSATLPSIQCKHRSPNGGLFRQSPIK----
--------------------
152 Cmil_GluD2
EGEKEMEVFLALALAISWLLCTDTVASDSIIHIGAIFEESARKDDKMFRLAVADVNMN---EEILQNEKITFSVRFVDSNNPFQAV
QE------ACDLV--SQGILALVSSTT-------------CAPSASLQSLADGMHIPHLYIQ----------RATAGTPRSTRSN
DYTLS------VRPPDYFNEVILKVITEFSWQKFMIFYDGA------YDIRGIQEFLGQAG----RQGI-----------------
-EVSLQKVETSISSMFTSLFSTLGFDELSRFRDMLRRALLFLNP-RTAKTFISEAV--D--TNLA-AVDSHWIFINE----EINDA
DVRELGRRLTGRL---------TVIRQTFPMS-ESKSQYCLSQRHRFSSAMCNPKDPFTQH----------MEISNLYVYDSVLL
LADAF-----------HKKLEDRKWHSMASL-------------------TCIRKNSK-----------PW-QGGRSMIETI----
-------------QKG-QVSGLTGML--NFRE-DGVNANV----LFEI--------LGTSYSEDKERGIQR---------------
LGVW-------------------------------------------------SPTSG--------------FNGSLVDQKLDN---
----------RMEGVT---LRVVTVLEAPFVLVA-----ENVFGQP-------------------KEFCGYSIDVLNTLSQ--QL-
G-----FK-YQIYQVPD-R-QYGKIQ-------RN-GK--WNGMIGELIN---------K---RADLAVSALTITPERENVVDFTG
RFMDF-TLGFLLKK----PEDK-------V----DMFTCLAPFDLSV-W---ACIIGTLFIVG-LLICMFTWATPSPL--------
------QIGSV-----------------------------TSTTLYNAVWFVYGSF-VQQ-G--TG--GEIP--INTLAVRLLMG
FWWLFVFIIISTYTANLTAILTSNRIDNPIR--SFQDL---AKQTD---LPFG-TVHNSEVFQIIK---MKGQNPFEVEQTYAHMW
SMINRT--------------------EGSENRVKEVHEGIQRAK----VGN----------YA-FVWDV-AVLEYVAEN-EP--DC-
AFVTARN--S-KVDRGY-GIA-LQD---G---SP--YRDIFSHRLLE--LEQ-SGELDALKRK------WWP-----EAGMCDLQ-
-THGKGHGKG---GAMALHNFAGAFGFLALGVILALTAAMLEIWW---KNKKKTSSLTEEDKEVEMEQFEKQVD-----------
----DLCKTEFELSMVPAGETLETFSDFRNTMTMSTF-------------IPEQMRRTSACSLSAKTLSGLPMGGTPVS-------
--------------------
153 Hsap_GluD2
----MEVFPFLLVLSVWWSRTWDSANADSIIHIGAIFDESAKKDDEVFRTAVGDLNQN---EEILQTEKITFSVTFVDGNNPFQAV
QE------ACELM--NQGILALVSSIG-------------CTSAGSLQSLADAMHIPHLFIQ-------RSTAGTPR---SNRND
DYTLS------VRPPVYLHDVILRVVTEYAWQKFIIFYDSE-----Y-DIRGIQEFLDKVS----QQGM-----------------
-DVALQKVENNINKMITTLFDTMRIEELNRYRDTLRRAILVMNP-ATAKSFITEVV--E--TNLV-AFDCHWIIINE----EINDV
DVQELVRRSIGRL---------TIIRQTFPVP-QNISQRCFRGNHRISSTLCDPKDPFAQN----------MEISNLYIYDTVLL
LANAF-----------HKKLEDRKWHSMASL-------------------SCIRKNSK-----------PW-QGGRSMLETI----
-------------KKG-GVSGLTGEL--EFGE-NGGNPNV----HFEI--------LGTNYGEELGRGVRK---------------
LGCW-------------------------------------------------NPVTG--------------LNGSLTDKKLEN---
----------NMRGVV---LRVVTVLEEPFVMVS-----ENVLGKP-------------------KKYQGFSIDVLDALSN--YL-
G-----FN-YEIYVAPD-H-KYGSPQ-------ED-GT--WNGLVGELVF---------K---RADIGISALTITPDRENVVDFTT
RYMDY-SVGVLLRR----AEKT-------V----DMFACLAPFDLSL-W---ACIAGTVLLVG-LLVYLLNW--LNPP------
```


154 Locu_GluD2
155 Cint_GluDalpha
156 Obim_IR
157 Acal_IR2


158 Bgla_IR6
159 Bgla_IR7
160 Aech_GluHC1
161 Harg_GluHC1


Ajap_GluHC2
Amol_GluHC1
Ajap_GluHC1
Ajap_GluHC3

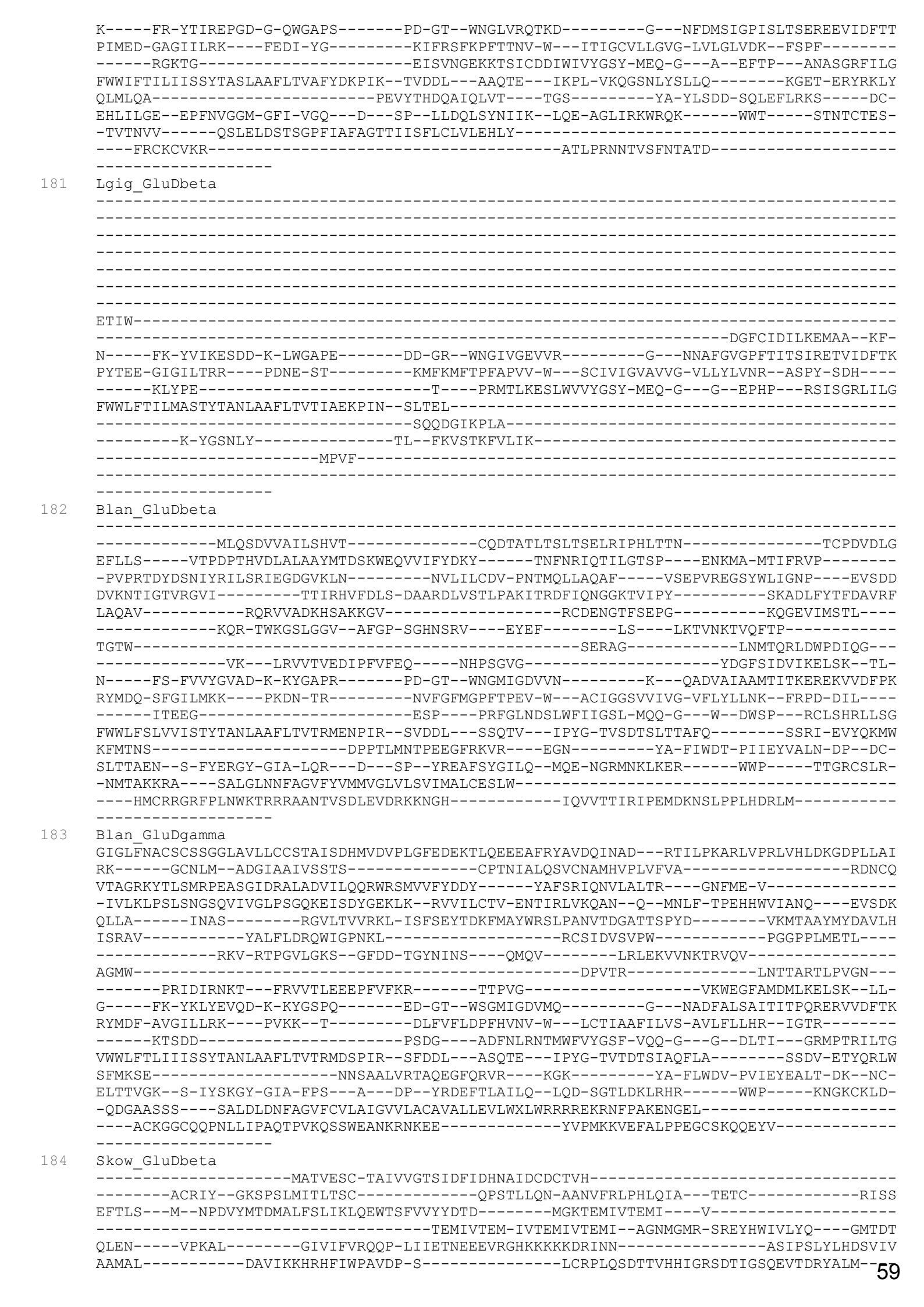

SGAFQ-----MRPRLADIDSMITSVIDHFKWRTFIMLYEGK------VALKLVESMMAKAV----LYGW----------
-RITPLELKGDYEAQTDEIRERKVK----------NILVYVSNEDKLKKIVKESF--D--NEIM-GNGWHWMFGNL-------NP
PITEAFLEQKYRHN--------MAFLTRFKME-SNELMYHSTIEEAIKK----------WPFRQRAAYDALVA
VAHAM----------KGYYDAHGSYPDPVR----------MCGG----------PARSKLVPYM----
----------KTV-NFRGASGDV--SFND-QGERVNY----TIIM--------YS----GKDQSAETKAGFFVQD--------
IRSW----------EQANNEKWP----------GKKGNRMFIEPFRQ---
----------SDARF---IKVLAVPEPPFFMQKNWESIRYKVDDDDDID----------YDEHEDKYSGMSWELLKKVKE--VME
EEMGVEFN-YEIELKSR-G-QYGSLD-------LSNNE--WDGMVRDLMD---------G---DADVAIGALVRDPYREEVVDFTD
AWYEG-NVKLLILH----PSWT-FE---------YPFSMVYPIDVWG-W---FVLLLIFILAS-LLVFFLGM--FSPY-EWR----
------KLAER----------GEASAEDG----QIFNFLNSFFYTLSTG-FWQ-G---Y--YKGP---RSWSLRIFSI
FWFWALVCTLFIYVFSLNGVMKFSKTAINIH--DHYDL---LHQDQ---FKFG-LVRFSPAYDFYR---------YNV-GKYRMVF
DRVLNS----------DEKLIEERIENAVYRIR-RTWEGR---------FS-LLGED-QILKYAAER-KP---C-
RMYIAGK--S-LGNITF-GFA-TQS---G---SP--LRDQLSHAIQI--LEK-NGELQKIREM------KFS-----DELKCERE-
-TIWEGQSK----YSFTVHDLQGMYYLIFIGMGGSFIVFVLEWLIYNI----------
----SWKSRMPQ----------RMPARKKDDFLDGGDGNAAKSSADWI----------
----
166 Harg_GluHC2
--MWKFLLIIACYCIAAFFGGTYGTVIK-VVSLYGKDTAEDDLYKQIMTDATTYINDAGGRGILNPNDQINVIHEKVLEDKVYEEQ
NLFKSVYQICNDL--RSMEAMALIMPNDFCEECE----------AVGRAVGDAYSPVITLD----------QADD
SGSFQ---M--RPRLSDIDEMLTAVIDQFKWRTFIFLYEGK------VALRLIESMMSKGL----TYGWR----------
-ITPIEVREEEYEDQTQELLERKVKN----------ILVYVSDE-TLLKKIVTVSF--D--KGVM-SNGWHWMFGNL-------NP
PITEAFLEQKYRHN--------MAFLTRFEML-SNELMYHSTIEEAIKR----------WPFRQRAAYDALVA
VAWAM----------KAHYQDLGRYPDPIR----------VCGG----------DARSSLEPYM----
-RS----------VSF-R--GASGDV--SFNN-QGDRVNY----TIIM--------YS----GKDQSAETEAGFFVQD--------
IRGW----------ERAN----------NEKWP----------GKRNKRMYINPFRQ---
----------SDVRY---IKVLAVPEPPFFMQKNWESIRYKVDDD----DDDEGDDDYYSNEGGERFSGMAWELLKKVKE--VFE
EEMGIDFE-FEIELKSR-G-QYGSLDL------SN-NE--WDGMVKDLAD---------G---DADIAVGALVRNDYREEVVDFTK
VWYEG-DVKLLILH----PSWT-FE---------YPFSMVYPINIWA-W---FALIIIFIVVS-LLVFLFGK--ISPY-EWR----
------KRSERGEAS----------EEDG----EVFNFLNSFFYVLSTG-FWQ-G---Y--IKGP---RSWSLRILSL
FWFWIIICLVFMYVISLVAVMKFSKTAINIH--DHHDL---LHQDQ---FDFG-LVRNSPAYDFYR---------YNV-GKYREVF
DRVLNS----------DEKLMEDRIENAVYRIR--------WEGR----YS-LLGEE-QVLKYAAER-KP---C-
RMYIAGK--S-LGNITI-SMA-TQA---G---SP--LRDQLSYVIKL--LEE-RGELQKIKEM------KFS-----DELKCERE-
-TVWERQSK----YSLTLHDLQGMYYLLFIGMGGSVIVFILEWLIY--NIFVTS----------
----SLKNRMPS----------KRTAAPKKDD----------FLGVGKSNVDDNVMNSASADWI----------
----
167 Harg_GluHC3
--MCRLKFVITVCFSVSLFSLTAVGEVLKVVSLYGQYTQQNDVYKQIMIDASTYINDG-RSEKPILRTGDQVIHDKVLQDREYERQ
TISKSVYQICNDIRSTRAAALIMPNDL----------CPECSEVGVVIGDAFSPVITLD----------QADE
SRAFK-----MRPNLDEIEEMLTDVIDNFKWRTFIFLYEGE------IGFSLVERMAAKAI----LYGW----------
-QVTPIELDDDFEKQAEVLKKKKVKN----------ILLYVGLE-DLLQNVVNVAF--E--TELL-SDGWHWMFGNL-------NP
PISKSFLERKYRHN--------MAFLTRFKID-ANELLYYTSIASPIRN----------WRFRQRAAYDALVA
VAMAM----------NLHLDGEGRYPYPVV----------KCDS----------NAPSELEHYL----
----------KRV-HFRGASGDV--SFND-HGDRVNY----TIKI--------YS----GKDSHAPNLAGYFTQN--------
IKNW----------EQTKGEKWP----------GKPGKRTYLKPFRQ---
----------ADERF---IRILAVPEPPFFMQKGWETLRYKTVKNKEND----------GSELYEGYAWELIKEVKK--VFE
QEMGIDFT-FQITLMSR-S-QYGYLD-------LSTGE--WDGMIRELID---------G---DADVAIGSLTERSAREKDIDLTV
PWYVA-YLKVAILH----PSWT-FE---------YPFTLVYPYHITA-W---AALVGLFILIA-LVAAFLGY--YSPY-ERR----
------KFAER----------GKATEEEG----KMFTFLKSFFYVLSTG-FWQ-G---Y--QRGP---RSWSLRILTG
FWFWFALSSAFIYASTLDSVFKFSKLAINMQ--DVHDL---LYNDI---HEFG-LVRGSPSYDFYR--------YNK--GQYRMVF
DKILNS----------EHNLMEDRIEQAVHRIR-RQWDGR---------YA-LIGDE-RILKYAIER-KP---C-
RLYITGR--S-LGKIAF-SFA-TPS---G---SP--LRDQLSYALSV--LKK-RGNISRILEM------EFS-----DQLHCAKE-
-TVFESETR----DSLTIHDFQGLYYLMFIGMAGSVLVFLLEWLVYL----------
----LYFDKERG----------KKSSPPSTTNLQGNINSLGQNTLDGTQVSSTDWI--
----
168 Amol_GluHC2

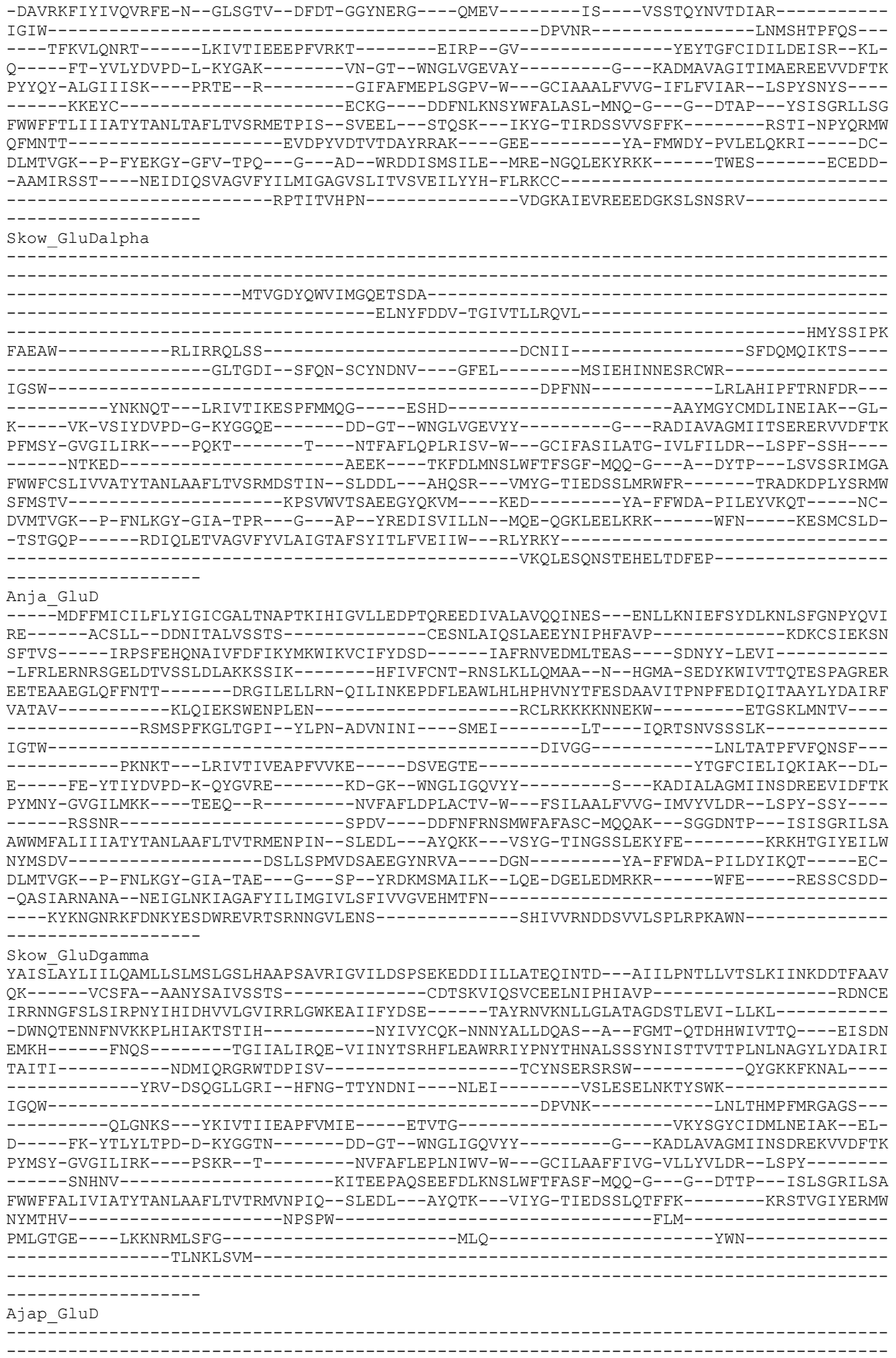
----------ADIALGALTKTSAREVDIDFTH
SWYKN-QIKLLILH----PSWS-FE---------YPFSIVYPMHITA-W---FTLLAVFLIMC-VLVGVLGY--FSPY-EWR----
------RLAER----------GEATEEES----QTFSFYNSTMYVLSTS-FLQ-S---Y--TRGP---RSWSLRILSA
FWFWFSICIVFIYAYNLDSVFKFSKTAINVR--DTHDL---LFQDI---INFG-AVRFSPSYDFYR--------YNQ--GQYRQVF
DRMLNS----------EENLLEDRLEDAVYRIR-RQWDAR---------YA-IVGEE-RILKYAADR-KP---C-
RLFVTGK--T-LGTVSF-SMA-TPS---G---SP--LRDQLSHAIRI--LKE-RGEIDKILDM------TFS-----DRLSCSSD-
-SIWEEETK----MSFTIHDLQGLYYLLFIGMCGSVILFIIEWLV----------
----------NALLFGNGWQ----------


169 Ajap_GluHC6
MCT
170 Ajap_GluHC7
MSR
171 Aech_GluHC3
E
172 Harg_GluHC6

```
-SLWEEQTR----RSFTLHDLQGLYYLLFIGMGCSAIVFVLEWLV-----------------------------------------
----SVLFLGHS--------------WQGRSPRGTGTR------------NTAALQRRNYDDREREEKTGAANTRDWL---------
--------------------
173 Amol_GluHC3
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------RITL
MSRGQ-----------------------------------------------------------------------------------
--------------------------------YGSLDLS-----------------------------------------------------
TGEW-----------------------------------------------DGMIR-----------------------------------
--------------------ELIDGVCQILYTLDI--------------------------------DQKNHYNIIILKKIKL------
---------TRLSILTT---LFGIFQ-------------------------------------DADVAIGSLTKNGAREDAIDFTG
VWYKS-QLKMAILH----PTWT-FE---------YPFSLVYPFHITA-W---AALGALFIIIS-LLVFALGY--FSPY-EYR----
------QLAER------------------GEASEEEA----DTFNFRDSLFYCMSTG-FWQ-G---Y--RKYP---RSWSLRILSI
FWFWFVICSIFLYASNISSVFKFSKTAIKIK--DVHEL---LYNDI---HDFG-AVRYSPSYDFYR--------YNK--GQYRMVF
DRILNS---------------------DKDLLEDRVEEAMYRIR-RQWDGR---------YA-VLGEE-RILSYAADR-KP---C-
RLYLSGK--T-LGKISF-SFA-TPS---G---SP--LRDQLSYALKV--LKK-RGNITRILDM------KFS-----DSLRCAKD-
-TKFEKLTK----KSFTVHDLQGMYYLIFCGMSGSVIVMILEWLF-----------------------------------------
----YVLAIDKGARPTFVARGGNRGAQPRRENNM----------------RTDFYGQDTRDIAPEKGATDWI--------------
--------------------
174 Ajap_GluHC4
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------DADVAIGSLTKVGAREDAIDFTG
TWYKS-QLKVAILH----PSWT-FE---------YPFSLVFPLHVTA-W---AALVALFVIIS-SMVFFLGY--CSPY-EYR----
------RLAER------------------GEATEEEA----GTFSIGESIFYCLSTG-FWQ-S---F--HRSP---KSWSLRLLSM
FWFWFCICTIFLYAWNVNSVFKFSKTAIKIK--DVHDL---LFNDI---HEFG-AVRNSPSYDFYR--------FNK--GQYRMVF
DRILNS---------------------DRNLLEDRIEEAIYRVR--------------------RQWDG------------------
RYAVLGK-------KGF---------------------------------YHT---------RR----------------------
-----------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------
--------------------
175 Ajap_GluHC5
-----------------------------------------------------------------------------------------
-----------------------------------------MGCTHAGRRECLAL-----------------------------------
-----------------------------WPKARIHA---------RHLERFWSTSDQPT-------------------------------
-SDPPGFVYDNKGDMARDPRPQKAP---------------YLQP-EKLSSSLSRTL--ATVYSVSSARSFAYTVALT---------
-----------------------------------------------------------------NTSARKLTSELIL-
----------------KDETEKRGKVKILL-----------------------------------------SHVRSLISFR----
--------------------GASGDV--SFND-AGDRVNY----TINI--------YS----GKDKFAQNLAGFFTQD---------
IKSW-----------------------------------------QEANGETWP------------GKPGKRTYIQPFRQ---
----------SDARV---IKVLAVPEPPFFMQKGWEQVRYRKENIKYDN----------ADRNDEPYEGYAWELIKDVKK--VFE
EEMGIDFN-FEITLMSR-G-QYGSLD-------LSTGE--WDGMIRELID---------G---DADVAIGSLTKVGAREDAIDFTG
TWYKS-QLKVAILH----PSWT-FE---------YPFSLVFPLHVTA-W---AALVALFVIIS-SMVFFLGY--FSPY-EYR----
------RLAER------------------GEATEEEA----GTFSIGESIFYCLSTG-FWQ-S---F--HRSP---KSWSLRLLSM
FWFWFCICTIFLYAWNVNSVFKFSKTAIKIK--DVHDL---LFNDI---HEFG-AVRNSPSYDFYR--------FNK--GQYRMVF
DRILNS---------------------DRNLLEDRIEEAIYRVR-RQWDGR---------YA-VLGEE-RILSYAADR-KP---C-
RLFISGK--T-LGKISF-SFA-TPS---G---SP--LRDQLSYALKV--LKK-RGNITRILDM------KFS-----NSLKCARD-
-TLWETETK----KSFTVHDLQGMYYLIFCGMGGSVIVMILEWLLYVLAIDKGARP-------------------------------
----TFVGRRGHR-----------------------------------APPQNKMTTDFYGQDPKDAAPDKGATDWI--------
--------------------
176 Harg_GluHC4
-MKRSFVASAVLALWMSLFSNGQNIIKV-ASFYGKNTGEGDVYKDIMTDATTYINDDRGGQHIIPLGDQVNVIHQNLLSNRVYENQ
TLSKSVYQICNDL--RSTIPSVVITPSDFCPTCY-----------GIGG-VLGEAYSPVFTLD-------------------QADR
SGAFK---M--RPNLDDIEEMITDVIAHFKWRTFIFLYDAR-----V-GIPLVEAMGAKAV------SYG-W--------------
-TMTPIEVEQDFEKQAEELK-KRRVKN---------ILI-YTYE-DTLEKIVNVAF--E--TMLL-SNDYHWIFGNL-------NP
PISNSFLDQYYRHN--------MAFLTRFKVV-SNDLLYYTS-----SAKPIKN------------------WRFRQRAAYDALVA
SSMAM-----------NLHFQTIGRYPDPVATC---GT-------------------------------SEKSTLEPFI----
-KQ---------V-KF-R--GASGDV--AFNE-LGDRVNY----TVNI--------YS----GKDKFAKNLAGYFVQD--------
VKSW----------------EVAN-------------------------GKKWP----GK---------PGKRTYMEPFR---
----QSDA---RF------IKVLAVPEPPFFMEK-----GWEALRY--PN---------------EQYEGYSWELLKEVKQ--FFE
EEMGIPFD-FQVTLMSK-G-QYGSL----DLTTGE-----WDGMIRELID---------G---DADVAIGSLTKRGAREKDIDFTA
GWYKS-YLKVAILH----PSWT--F----E----YPFALVYPYHRSA-W---FALLGTFIVIF-LVVFCLGN--FSPY-EYR----
------SLAARGEAS-----------------EEEG----ETFCFFDSIWFLLSTG-FWQ-S---Y--IRGP---RSWSLRILSA
```

```
FWFYFALCMIFLYSDNINSVFKFSKTAIKIK--DVHDL---LFNDV---IDFG-AVRNSPSYDFYR--------YNT--GQYRMVF
DRILNS--------------------EKNLLEDSIEQAIYRIR------R-WDGH----YA-VLGEE-RILNYAAAR-RP---C-
RIFVTGK--T-LGKISF-AFA-TPS---G---SP--LRDQLSYAIQT--LKK-RGNVSRILKM------KFSN-----NLHCEPD-
-TLFETEAK----KSFTIHDFQGLYYLMFIGMGGSVIVFILEWLVFLLFISKGS------------RPKRGIRRRGR---------
----ITGNDSKG-----------------------------------VDYYGLGPIQSTEPDNATTDWL--------------
------------------
Aech_GluHC2
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
------------------IS----------------------------------------------------------------
------FL-CRITLMSP-G-QYGTLD-------LSNGE--WDGMIRELID---------G---DADVAIGALTKNSAREEDIDFTD
KWYKS-QLKIAILH----PSWT-FE---------YPFSLVYPYHITA-W---FALLVTFIVIV-FVAFLLGY--LSPY-EWR----
------SLASR------------------GEASEEQG----ETFSFSDSIWFVLSTG-FWQ-S---Y--TRGP---RSWSLRILSG
FWFYFALCMVFLYVKNLNSVMNFSKTAIRIK--DTHDL---LFQDI---IDFG-AVRNSPSYDFYR--------YNT--GQYRMVF
DRILNS--------------------EKDLLEQRIEEAIYRIR-RQWDGR---------YA-VLGEP-EILKYAAAR-KP---C-
RIFVTGK--T-LGKITF-SFA-TPS---G---SP--LRDQLSYAIKT--LKK-RGNITRILEM------KFS-----KNLHCEKD-
-TLYETGTK----KSFTIHDFQGLYYLMFIGMSGSVIVFILEWLFY-------------------------------------
----VLFIDKESRPKIGNTRPARRPNDNELQ------------------TDYYGSGQSGSAAPVKSSTDWI--------------
------------------
Harg_GluHC5
---MLKHTFIASLVLALWMPHLSNGEILKVASFYGKYTEKDDIYKQIMTDASTYINDDRGGQQIVLSGDQVIHQNLLN-DRNFDDQ
TLSKAIYQVCNDL--RSTGASIVIMPNDF------------CDNCDDIGGVLGGAYSPVFTLD------------------QADE
SGAFK-----MRPNLGDMEEMITDVIANFKWSTFLFLYKGD------VAFGLVEAMKAKAV----NYGW----------------
-AITPIEVEDDFEKQAEELKKRRTKN----------ILIYYTNE-DMLGSIVNIAF--E--TKLL-SNGYHWIFGNL-------NP
PISKSFLEQYYRHN--------MAFLTRFKVV-ANELLYYTSLAKPVKN----------------------WRFRQRAAYDALVA
ATMAM-----------KLHRQREGRYPAAVP-------------------VCGS------------------PQKSTLEQYI----
-------------KQV-SFRGASGDI--AFNE-HGDRVNY----TINI--------YS----GKDKFAQNLAGYFVQD--------
VKSW-----------------------------------------EITSGEKWP------------GKPGKRTYIKPFRQ---
-----------SDARF---IRVLAVPEPPFFMEKDWERVRYSDTENFDNE--------------EEYQGYSWELLKEVKK--VFE
EEMGIPFD-FQITLMSP-G-QYGTLD-------LSTGE--WDGMIRELID---------G---DADVAIGSLTKNGARENDIDFTG
TWYKS-QLKVAILH----PSWT-FE---------YPFSLVYPYHITA-W---FALIIIVLGIA-LGVFCLGH--FSPY-EYR----
------SLAER------------------GQATEEEA----GTFSFFDSIWFVLSAG-FWQ-S---Y--TRGP---RSWSLRILSA
FWFYFSLCMIFLYVTNLNSVFKFSKTAIKIK--DVHDL---LFNDI---IEFG-AVRRSPSYDFYR--------YNK--GQYRMVF
DRILNS--------------------EKNLLEEKITNAIFRIR-RQWDGR---------YA-VLGEE-RILKYAAAR-KP---C-
RIYISGK--T-LGKISF-SFA-TPS---G---SP--LRDQLSYALKI--LKK-RGNISRILEM------EFS-----DRLHCAED-
-TLFETETK----KSFTIHDFQGLYYLMFIGLGGSVIVFILEWLYF-------------------------------------
----VLFVDKSSRPRIATRRTARPKANLQ--------------------TDYYGSGPGQSAAADKTPTDWI--------------
------------------
Cint_GluDbeta
-MQMIISSYISQVSVWLVATFVCSCLSM-QSTIIGILSDERLDPHLVNSAVTQAWKAT-----FADDILILSGAEFTPATEIVDIN
SASDVVGKVCQIL--EKSPAVIVVVSRC-------------GYTRSLHF-LSSALKIPVVEVS---LREHFDCP-------GTDTQ
LAQVD---SNTLMGSAGYDGLLISFFKTALWRKMIIVFDES-----V-DIGSISRVIDRMG----NRMRK-VTLQRLPATDNGEVA
TVAALSLAQDMINYAMEGVWEFDDDATAQAPLSRDVVFLILGSE-DTVKKLVLNV-----------GWKTSYFTESLLFRDGVTVI
TASDDRTVPSVVNEDVLLQTLLSKVGSVFASI-YISFVRAGTLGMDLTAHAANIT-----------------CSKLAVVELESNLW
LANSI-----------RASIFGQKENVDGEWSV-----------------SGGNSP-------------YYISHQNSMSSNVSLEL
DGCDVTEEGQIQCESL-K--AKEDRI--KFDN-QGSNPDYATTDTFNT--------HE--------------------------
LG-------------------------------------------------KEKHA----LF------DDENSDTLLYEFGK---
----RWLN---TT------FKVATLEDEPFVFVR--------KDSD--GH---------------VTFSGFSIDLLHMLSE--KI-
G-----FR-YEIYEVAD-R-KYGTF--------KD-GK--WNGLVGDVVS---------K---KADFAIAAMTITPQREKVVDFTK
RYMDY-AVGILMKK----PKAV--T---------NLFAFLNPFDNTV-W---YSIMAGLFLVS-ILLYVLNR--VSPK--------
------RMPGP------------------------PF----QDTSLHGTFWFVYSSL-VQQ-G---T--DMNL---VTISSQIVTG
VWWFFILIIISSYTANLAAHLTVTRMENHIT--SFRDL---SKQND---MVYG-TALDTSIFDFLH---TKGSNAKDLTSMYARLW
KVVNAS------------------------HSVSDPKQGIQRVK----DQN----------YA-FLWDV-AVIEYLILT-DP--EC-
SFSTVPD--S-IYDKGY-GIA-VEQ---G---NP--IREVMSMGILQ--LQD-GGEIARLKQR------WWTG-------KCPID-
-HSGSRSHS----SELTLENFAGVFCVLACGLVIASLVAVGEILQYMKKTKKLQKQKENQMESSQTSSVPPSRRPHV---------
----YVEKCVGDLKKERPPITENGSATNRDTSETKSWW------------GSHNFQRNAKSNTKERQPHKIT--------------
------------------
Lgig_GluDalpha
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------ILIFQAEPFTIKL--------------AN---------------GEYVGFCIDILNELAY--RL
```


K-----FR-YTIREPGD-G-QWGAPS-------PD-GT--WNGLVRQTKD---------G---NFDMSIGPISLTSEREEVIDFTT
PIMED-GAGIILRK----FEDI-YG---------KIFRSFKPFTTNV-W---ITIGCVLLGVG-LVLGLVDK--FSPF--------
------RGKTG----------------------EISVNGEKKTSICDDIWIVYGSY-MEQ-G---A--EFTP---ANASGRFILG
FWWIFTILIISSYTASLAAFLTVAFYDKPIK--TVDDL---AAQTE---IKPL-VKQGSNLYSLLQ--------KGET-ERYRKLY
QLMLQA----------------------PEVYTHDQAIQLVT----TGS---------YA-YLSDD-SQLEFLRKS-----DC-
EHLILGE--EPFNVGGM-GFI-VGQ---D---SP--LLDQLSYNIIK--LQE-AGLIRKWRQK------WWT-----STNTCTES-
-TVTNVV------QSLELDSTSGPFIAFAGTTIISFLCLVLEHLY----------
----FRCKCVKR----------ATLPRNNTVSFNTATD----------
181 Lgig_GluDbeta
ETIW----------DGFCIDILKEMAA--KF-
N-----FK-YVIKESDD-K-LWGAPE-------DD-GR--WNGIVGEVVR---------G---NNAFGVGPFTITSIRETVIDFTK
PYTEE-GIGILTRR----PDNE-ST---------KMFKMFTPFAPVV-W---SCIVIGVAVVG-VLLYLVNR--ASPY-SDH----
------KLYPE----------T----PRMTLKESLWVVYGSY-MEQ-G---G--EPHP---RSISGRLILG
FWWLFTILMASTYTANLAAFLTVTIAEKPIN--SLTEL----------
----------SQQDGIKPLA----------
---------K-YGSNLY---------TL--FKVSTKFVLIK----------
----------MPVF----------
182 Blan_GluDbeta
-------------MLQSDVVAILSHVT----------CQDTATLTSLTSELRIPHLTTN----------TCPDVDLG
EFLLS-----VTPDPTHVDLALAAYMTDSKWEQVVIFYDKY------TNFNRIQTILGTSP----ENKMA-MTIFRVP--------
-PVPRTDYDSNIYRILSRIEGDGVKLN---------NVLILCDV-PNTMQLLAQAF-----VSEPVREGSYWLIGNP----EVSDD
DVKNTIGTVRGVI---------TTIRHVFDLS-DAARDLVSTLPAKITRDFIQNGGKTVIPY----------SKADLFYTFDAVRF
LAQAV----------RQRVVADKHSAKKGV----------RCDENGTFSEPG----------KQGEVIMSTL----
-------------KQR-TWKGSLGGV--AFGP-SGHNSRV----EYEF--------LS----LKTVNKTVQFTP----------
TGTW----------SERAG----------LNMTQRLDWPDIQG---
--------------VK---LRVVTVEDIPFVFEQ-----NHPSGVG----------YDGFSIDVIKELSK--TL-
N-----FS-FVVYGVAD-K-KYGAPR-------PD-GT--WNGMIGDVVN---------K---QADVAIAAMTITKEREKVVDFPK
RYMDQ-SFGILMKK----PKDN-TR---------NVFGFMGPFTPEV-W---ACIGGSVVIVG-VFLYLLNK--FRPD-DIL----
------ITEEG----------ESP----PRFGLNDSLWFIIGSL-MQQ-G---W--DWSP---RCLSHRLLSG
FWWLFSLVVISTYTANLAAFLTVTRMENPIR--SVDDL---SSQTV---IPYG-TVSDTSLTTAFQ--------SSRI-EVYQKMW
KFMTNS----------DPPTLMNTPEEGFRKVR----EGN---------YA-FIWDT-PIIEYVALN-DP--DC-
SLTTAEN--S-FYERGY-GIA-LQR---D---SP--YREAFSYGILQ--MQE-NGRMNKLKER------WWP-----TTGRCSLR-
-NMTAKKRA----SALGLNNFAGVFYVMMVGLVLSVIMALCESLW----------
----HMCRRGRFPLNWKTRRRAANTVSDLEVDRKKNGH----------IQVVTTIRIPEMDKNSLPPLHDRLM----------
183 Blan_GluDgamma
GIGLFNACSCSSGGLAVLLCCSTAISDHMVDVPLGFEDEKTLQEEEAFRYAVDQINAD---RTILPKARLVPRLVHLDKGDPLLAI
RK------GCNLM--ADGIAAIVSSTS----------CPTNIALQSVCNAMHVPLVFVA----------RDNCQ
VTAGRKYTLSMRPEASGIDRALADVILQQRWRSMVVFYDDY------YAFSRIQNVLALTR----GNFME-V----------
-IVLKLPSLSNGSQVIVGLPSGQKEISDYGEKLK--RVVILCTV-ENTIRLVKQAN--Q--MNLF-TPEHHWVIANQ----EVSDK
QLLA------INAS--------RGVLTVVRKL-ISFSEYTDKFMAYWRSLPANVTDGATTSPYD--------VKMTAAYMYDAVLH
ISRAV----------YALFLDRQWIGPNKL----------RCSIDVSVPW----------PGGPPLMETL----
----------RKV-RTPGVLGKS--GFDD-TGYNINS----QMQV--------LRLEKVVNKTRVQV----------
AGMW----------DPVTR----------LNTTARTLPVGN---
-------PRIDIRNKT---FRVVTLEEEPFVFKR-------TTPVG----------VKWEGFAMDMLKELSK--LL-
G-----FK-YKLYEVQD-K-KYGSPQ-------ED-GT--WSGMIGDVMQ---------G---NADFALSAITITPQRERVVDFTK
RYMDF-AVGILLRK----PVKK--T---------DLFVFLDPFHVNV-W---LCTIAAFILVS-AVLFLLHR--IGTR--------
------KTSDD----------PSDG----ADFNLRNTMWFVYGSF-VQQ-G---G--DLTI---GRMPTRILTG
VWWLFTLIIISSYTANLAAFLTVTRMDSPIR--SFDDL---ASQTE---IPYG-TVTDTSIAQFLA--------SSDV-ETYQRLW
SFMKSE----------NNSAALVRTAQEGFQRVR----KGK---------YA-FLWDV-PVIEYEALT-DK--NC-
ELTTVGK--S-IYSKGY-GIA-FPS---A---DP--YRDEFTLAILQ--LQD-SGTLDKLRHR------WWP-----KNGKCKLD-
-QDGAASSS----SALDLDNFAGVFCVLAIGVVLACAVALLEVLWXLWRRRREKRNFPAKENGEL----------
----ACKGGCQQPNLLIPAQTPVKQSSWEANKRNKEE----------YVPMKKVEFALPPEGCSKQQEYV----------
184 Skow_GluDbeta
----------MATVESC-TAIVVGTSIDFIDHNAIDCDCTVH----------
--------ACRIY--GKSPSLMITLTSC----------QPSTLLQN-AANVFRLPHLQIA---TETC----------RISS
EFTLS---M--NPDVYMTDMALFSLIKLQEWTSFVVYYDTD--------MGKTEMIVTEMI----V----------
----------TEMIVTEM-IVTEMIVTEMI--AGNMGMR-SREYHWIVLYQ----GMTDT
QLEN-----VPKAL--------GIVIFVRQQP-LIIETNEEEVRGHKKKKKDRINN----------ASIPSLYLHDSVIV
AAMAL----------DAVIKKHRHFIWPAVDP-S----------LCRPLQSDTTVHHIGRSDTIGSQEVTDRYALM--


185 Skow_GluDalpha
186 Anja_GluD
187 Skow_GluDgamma
188 Ajap_GluD

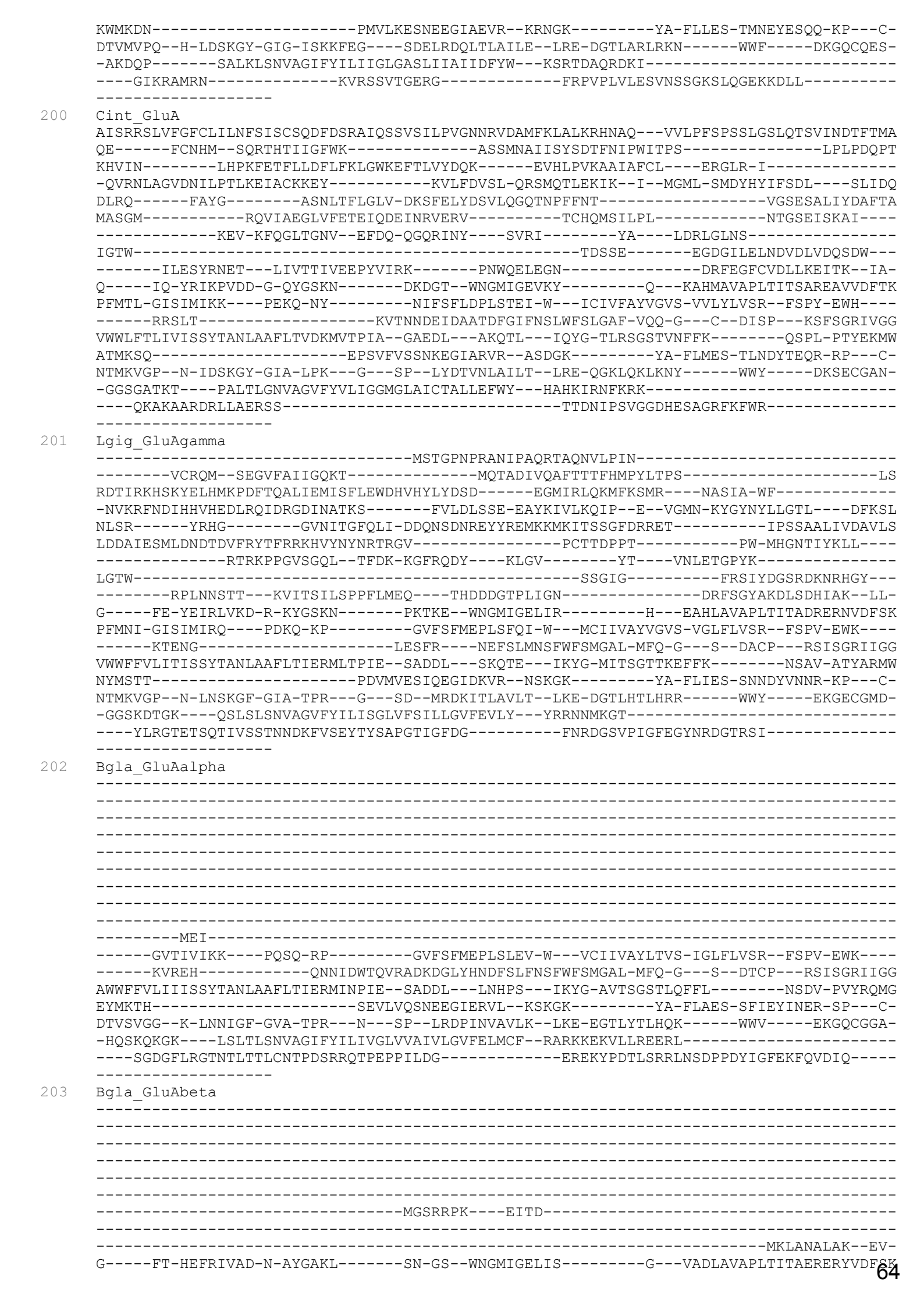
```
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
------------------------------------------------------------------------MERQKSHQTM----
------------------------------------LCTY----------------------------------------------
IGTW------------------------------------------------NSSDN------------LTLLQTPFTKSLRA---
------------MNKT---YTIVTIAEAPFVSVD-----DTVNG---------------------PKFSGFCIDMLNYISK--EL-
D-----FE-YKLYLTPD-E-KYGGQN-------LD-NT--WNGLVGEVYY---------G---RADMAVAGMIINSHREEVVDFTK
PYMNY-GVGILMRN----PNKK--A---------NPFAFLEPLDITV-W---GCVSAALVIVG-FLIFILDR--LSPY-SLY----
------GRSGG----------------------EIGY----DEFDLKNSMWFAFASC-MQQ-G------DSTP---ISMSGRILSA
FWWFFALIITATYTANLAAFLTVTRMENPIT--SLDDL---ARQSV---VVYG-TIENSSLHRFFE--------QRKEESPYDMMW
SQMNKA---------------------GVDPWVKTAENGYNRVK----TEK---------YA-FFWDA-PILDYIKQT-----EC-
DLMTVGK--P-FNLKGY-GIA-TPQ---D---VP--YTDDLSMVILK--MQE-KGIIEEYRKR------WFL-----KDSQCREE-
-QKSDANTKA---DAIQLQTIGGAFYVLMMGGILAFVAVFIEHVWHKP--------------------------------------
----SFYRKKRKELKGNREREWAEKLQGARIAECSSAKVFY---------VGLVANTIFFYHIYYTHRKFLLM-------------
-------------------
189 Etri_GluD
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------
------------------------LQEAPFVSIE-----ETVDG---------------------PKYTGFCIDMLENIAE--ML-
D-----FS-YELYLTPD-N-NYGGKN-------PD-GR--WNGLVGEVYY---------G---KADMAVAGMVINSDRETVVDFTK
PYMNY-GVGILLRK----PQKK--S---------NVFAFLEPLDIRVVW---GCVLASLFVVG-FLIYILDR--LSPY-SSY----
----GKGGPDC-----------------------DEA----NDFNLQNSLWFAFASC-LQQ-G------DNTP---ISVSGRMLSA
FWWFFALIIIATYTANLAAFLTVTRMENPIN--SLEDL---ANQNK---ILYG-TIENSSLHRFFE--------KRKNQGIYERMW
DFMSTS---------------------SRNPWVPSDKAGYKQVK----EED---------YA-FFWDA-PILDYIKQT-----EC-
DLMTVGK--P-FNLKGY-GIA-TPQ---G---AS--YRDDLSLAILK--MQE-EGILEEYRKK------WFE-----RESICPEE-
-VVNINPNTKA--SAIGLSKIAGAFYVLIIGAVLSFVAVIMEHMWH----------------------------------------
--------------------------------------------------KPPSFYKKKRQMEARKAKEKVE--------------
-------------------
190 Lvar_GluD
NAIHWQLQTRLVPGVVSLEAVRRGGDMRIQRDGVILLEDPSQKDLDIIELAFNHINND---DTILPNTRLEPRRGRVPASDPFSAV
IT------VCDILFPENITAVLSSTS---------------CETSLAVQSLVETFQIPHVEVP------------------REKCA
VERQNGFSVSIRPDYSHISRATLDLMLRLGWKQVSIFYDSDTAYKNVEDLLLLSAALTQTY----PPHFRLFRL------------
-KKNVATGKLDFVHPLHTVKDSKTF-----------NMVAYCSTMNNIKLIREAAT-----FGMT-TGEYHWIVASHPLAERFIRY
NEEPLDEFKFFNGS--------RGILTLLKQR-VKIDPTREDFYQAWLTLDPELEAQLEENATEIMPDYLQPIEYHNAYLYDAVRA
LAVSI-----------SDVVSRGRFVEPEIY-------------------RCNENPHRNT------------RGSNRLKKAL----
-------------NKV-ETEGMMGMI--QFNR-TGYNEEV----AIDI--------ISVEGRNNDTKAWQ----------------
IGSW------------------------------------------------DYESK------------LTLDQFPFIRRYDE---
-----------FHNKT---FNIVTIEEAPFVTLE-----ETVNG---------------------PKYTGFCIDMLEKIAE--KQ-
N-----FK-YNLYLVAD-N-KYGGRN-------ED-GR--WNGLVGDVYY---------G---KADMAVAGMVINSDRENVVDFTK
PYMNY-GVGILLRK----PQKK--S---------NVFAFLEPLDIKV-W---GCVLASLFVVG-FLIFILDR--LSPY-SAY----
----GKGGPEC-----------------------DEA----DDFNLLNSLWFAFASC-LQQ-G---G--DNTP---VSVSGRMLSA
FWWFFALIIIATYTANLAAFLTVTRMENPIN--SLEDL---ANQNK---IVYG-TIENSSLHRFFE--------KRKNQVTYERMW
DFMSSS---------------------SVSPWVPSDKAGYQRVK----NED---------YA-FFWDA-PILDYIKQT-----EC-
DLMTVGK--P-FNLKGY-GIA-TPQ---G---AA--YRDNLSVAILK--LQE-EGILEGIRKK------WFE-----RESICPEEI
VNNNPNTKA----SAIGLSKIAGAFYVLIIGAVLSFIAVIVEHMW-----------------------------------------
----HPPSFYKRKRQMEARKAKEKDWSEKLPSSRSA--------------MQENNSKHMVVQESESMVLQPLRPTPWS--------
-------------------
191 Spur_GluD
-----------------------------------MGNTEQNQRKGRLEREKAVRDKE----------------------------
--------ICDMF--PENITAVLSSTS--------------CETSLAVQSLVETFQIPHVEVP-------------REKCAVQRQN
GFSVS-----IRPDYSHISRATLDLMLRLGWKQVSIFYDSDTAYKNVEDLLLLSAALTETY----PPHFR-LFRL-----------
-KQNVATSKLDFVHPLHTVKDSKTF-----------NMVAYCST-MNNIKLIRQAA--M--FGMT-VGEYHWIVASH-----EWSN
AFGQPLADRFIRYN--------EEPVDEFRFF-NGSKGILTLLKQSVK------------------------IDPTREDFYQAWLT
LDPDL-----------ETQLEENAT-----------------------------------------------EIMPDYLQPI----
--------------EV-ETEGMMGII--QFNR-TGYNEEV----AIDI--------ISVEGRNNDTKAWQ----------------
IGSW------------------------------------------------DHESK------------LTLDQFPFSRRYDD---
-----------FHNKT---FNIVTIEEAPFVTLE-----DTVNG---------------------PKYTGFCIDMLEKIAE--KQ-
N-----FK-YNLYLVGD-K-NYGGRN-------ED-GR--WNGLVGDVYY---------G---KADMAVAGMVINSDRENVVDFTK
PYMNY-GVGILLRK----PQKK--S---------NVFAFLEPLDIKV-W---GCVLASLFVVG-FLIFILDR--LSPY-SAY----
----GKGGPDC-----------------------DEA----DDFNLLNSLWFAFASC-LQQ-G---G--DNTP---VSVSGRMLSA
FWWFFALIIIATYTANLAAFLTVTRMENPIN--SLEDL---ANQNK---ISYG-TIENSSLHRFFE--------KRKNQVTYERMW
DFMTST---------------------SVSPWVPSDKAGYQRVK----TED---------YA-FFWDA-PILDYIKQT-----EC-
DLMTVGK--P-FNLKGY-GIA-TPQ---G---AA--YRDNLSVAILK--LQE-EGILEGIRKK------WFE-----RESICPEEI
VNNNPNSKA----SAIGLSKIAGAFYVLIIGAVLSFIAVIVEHMW---HRPPSFYKRK----------------------------
----RQMEARKA--------------------------------------KEKNVRMCASKHPRSTSVNRNKENRL----------
-------------------
192 Arub_GluD
```

```
                                   ----------MEQPTIVEEEMIRLAFDNINID---DVILPESRLDYTIFRITSPDPFGAV
KS------ACTML--NSTMVAMVSSTG--------------CETSLALQSLTNSFDVPHIIVP-------------SEECPIEKHN
SFTVN-----VRPSLLYLSEATLELVWSLAWTKICIFYDSE------TAYKNVQQFLHLSTESDDKKPPE-V--------------
-TLFRLDDTEDSSTVIAIIRVLHKAKDSEIK-----NMITFCNT-ANSMKIIRQAA--L--FGMT-CGKFKWIVTTQDNAVGSLDW
DTLVDDEPGGFTTTGEIIEDGGMRFLNGSTGI-VTLIKQQVKVQIQPQEFYNAWRILYEDVDRENDVNATYLVQFKAAYMYDAVRV
LAVAL-----------DELVERDKYIEPESQ-------------------QCYESKPRTW-----------KGGTRLRKLL----
--------------HRTETNGLMGNI--RYNH-TNLNDEI----AVDI--------ITVESRLNQTKAWK----------------
IGSW-------------------------------------------------DPDNR-----------LNLVKTPFTR-SFE---
--------PFISNNTT---LRIVTVVEAPFVSRD-----ETVNG---------------------HKYSGFCIDMLDFIAR--EL-
N-----IK-YELYLVPD-G-LYGGKT-------ED-GT--WNGLIGEVYY---------R---RAELAVAGMVINSDREAVVDFTK
PYMNY-GVGILMRK----PQKK--T---------NIFAFLEPLDFNV-W---GCVLASLFVVG-ILIYIVDR--LSPY-SSF----
------RRENS----------------------NNQ----DAFDLKNSMWFAFASC-MQQ-G---G--DTSP---LSISGRVLSA
FWWFFALIITATYTANLAAFLTVTRMENPIN--SLEDL---AMQKT---VVYG-TIVNSSLARFFE--------KRKNQPTYERMW
SFMSDS--------------------DVNPWVPNAEAGYKRVQ----NEE---------YA-FFWDA-PILDYIKQK-----EC-
NVMTVGK--P-FNLKGY-GIA-TPQ---H---AP--WRDKISLVILK--MQE-EGHIAELRKK------WFD-----RESSCPEE-
-MDNMNAQSRA--TDINLDQIAGAFYVLILGAVLSFVVVIVEHIWHKPKKRQKETGRITL-----------------------
-----------------DWSEKLPPREIRNNGLSNIDS-----------KHLVVQENDSLALTPLRPNPWS-------------
-------------------
193  Pmin_GluD
MDLPQWIALPCLLLLHILEGVVTTERRVSPSVIKVILEQPSPDEDEMVRLSFQHLNQN---ENILPSSRLDYTVARIASTDPFAAV
KA------ACSML--NTSITAIVSSTS--------------CETSLALQSLTNSFDVPHMIVP------------------GEECP
SEKHNSFTVNVRPSLLFLSEAALDLVWKLGWEGVCIFYDSE------SAYKNVQQFLHLAAQSEERKPLEVTLYRVD---------
-ASEPSGGALGIINILHKAKDSDVK-----------HMIAFCDRTQSMKLIRQAAR-----FGMA-VGKYQWIITTQPEGFTTTSG
DISEEDGMRFLNGS--------EGIITLMKQQ-VKVQTQPPDFYGAWQILYPDIDREEDANATYLSPGYLNTVQFKAAYMYDAVRV
LAVAL-----------DEQVERDKYIEPENQ-------------------HCYDNKPKSW-----------KGGTRLRKML----
-------------HRM-ETTGLMGRI--RFNH-SGVNDEM----AVDV--------ITVESSRNQTKAWK----------------
IGTW-------------------------------------------------DPENR-----------LNLVKTPFTRSFEA---
---------FITNNTT---FRIVTVVEAPFVNRD-----ETVNG---------------------HKYSGFCIDMLELIAD--EM-
N-----AK-YELYLVPD-G-NYGGKN-------ED-GT--WNGLIGEVYY---------G---RADLAVAGMVINSDREEVVDFTK
PYMNY-GVGILMQK----PQKK--T---------NVFAFLEPLHIQV-W---GCVLASLFVVG-VLIYIVDR--LSPY--------
------SSFRR----------------------ENSPNQ----DAFDLKNSMWFAFASC-MQQ-G---G--DTSP---LSISGRVLSA
FWWFFALIITATYTANLAAFLTVTRMENPIN--SLEDL---AMQKS---VVYG-TIVNSSLHRFFE--------KRKHQGIYERMW
NFMSTS---------------------KINPWVPNAEAGYKRVQ----TED---------YA-FFWDA-PILDYIKQK-----EC-
NVMTVGK--P-FNLKGY-GIA-TPR---G---LP--WRDEISMVILR--LQE-KGILEELRKK------WFD-----RESSCAED-
-TVIMSSNRGA--ADINLDQIAGAFYVLIIGAVLSFVVVIIEHIW---HKPSFYKK-------------------------------
----REKEAGRTTLDWSDKLPPRETRNNGLSNIENKFF-----------LSPLKRQRTLASTWLEQVGKARNPYRMC---------
-------------------
194  Apla_GluD
MEIPQWIALTCLLLMYILEGVVTSERRVFPSVIKVILEQPSSDEDEMIRLSFQHINQN---GNILPSTRLDYTVARIASTDPFAAV
KA------ACSML--NTTVAALVSSTS--------------CETSLALQSLANSFDVPHIIVP------------------GEECL
SEKHNSFTVNVRPSQVYLSEAVLDLVWWLKWKSVSMFYDSE------SAYKNVQQFLHLAAQSEERKPLE-VTLYRVD---------
-DRDPASGALGMINILHKAKDSDVQ-----------HMITFCDR-AQSMRLIRQAA--R--FGMA-VGKYQWIITTQPGSFTTAGG
DISEEEGMRFLNGS--------EGIITLMKQQ-VKVQTHPLQFYSAWQMLYPDIDREEDANSTYLSPGYLNTIQFKAAYMYDAVRV
LAVAL-----------NEQVERDKYIEPEIQ-------------------HCYDNKPKSW-----------KGGIRLRKML----
-------------HRT-ETTGLMGRM--RFNH-SSLNDEI----AVDV--------IT----LESGRNQTKAWK----------
IGGW-------------------------------------------------DPENR-----------LNLVKTPFSRGFAA---
---------FISNNTT---FRIVTVVEAPFVNRD-----ETVNG---------------------YKYSGFCIDMLELIAK--EL-
N-----LK-YELYLVPD-G-NYGGKN-------DD-GT--WNGLIGEVYY---------G---RADLAVAGMVINSDREEVVDFTK
PFMNY-GVGILMQK----PKKK--A---------NIFAFLEPLHIKV-W---GCVLASLFVVG-VLIYIVDR--LSPY-SSF----
------RRENS----------------------PNP----EAFDLKNSMWFAFASC-MQQ-G---G--DTSP---LSISGRVLSA
FWWFFALIITATYTANLAAFLTVTRMENPIN--SLEDL---ATQKT---VVYG-TILNSSLHDFFE--------KRKNQGIYEKMW
NFMSTS---------------------KIDPWVPNAEAGYKRVQ----TED---------YA-FFWDA-PILDYIKQE-----EC-
DVMTVGK--P-FNLKGY-GIA-TPR---G---VP--WRDEISMVILK--MQE-RGELEELRKK------WFD-----RESSCLDE-
-TDSMNTKHRAARADINLDQIAGAFYVLIIGAVLSFVVVIVEHVW-------------------------------------------
----HKPSFYKKREKETGRTTLDWSDKLPPRETRNNG------------LSNIENKHLVVQENDSFALTPLRPNPWS---------
-------------------
195  Ajap_GluA5alphaalpha
-------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------
----------------------------------MLYKHN-------------------------------------------------
-------------------------------------------------IVLEWRMLQQ--LGMV-TYQYHYIVTNL----------
-------------------------------------------------------------------------TEAALVFDTLAI
FNETI-----------LGLGNLITLLRLRNTR-----------------QCNQIYDQVD-----------PVDDNILRAL-----
-------------LQS-QTQGITGNV--QFSE-RGERQNY----SLNI--------VG----LSRNGIMK----------------
VGEW-------------------------------------------------------------------------------
------------HSTR---KR-------------------------------------------------------------------
G-----FE---------------------------------WKD----------------K-------------------------
-------------------------------------------W--------------------TY--AKPP---------------
-----------------------------------MAIDAENATEFCEASS--QR-N---C----------------------------
---------------------------------GEPDI----------IMYS-------------------------------------
-------------------------------ATAGI--------------------YS-------TYSDINEDK---------------
-----------------------------------------VLR--ITT-VEVRIKFERK-----------------------------
------------------------IVI-------------------------------------------------------------
```

----
196 Harg_GluAbeta
-----MDRSLPILLVFTFACFLCADCQFLKFVSLMEVMVKGDARFVGQKRACILSNVRSNRSDSPSTIVTFYQTDVFEPADVIRA-
--------WCETLKEGIGYTGQLG-----------------LSTIHTMKHYSQVVYRIPFLLYN------------------LAPT
DFWDDFESQYLISIRPSIIPVLKDVIEYHRWSKYAYLFDSD------ESFLRYANYMQKVP----SHEII-F--------------
-KRVQKSNMTSIGLVLDRIQELEVT-----------KVVVDCNH-FMTETLLSMLA--E--KEMV-TAAYHYVFLDM---------
---DINLATFPTLG--------GMNLIGFNMV-DKNSKYFEYAFGTYHKREDYNSMTTEEKF----------VGFEASLAFDSSNA
AIEAY-----------EKPENGETEITALNPPC-----------------KCDPNSKLRRS-----------PIGAVYANRL----
-------------RNV-SFTGITGHV--AFNE-GGARTNY----SVDV--------LS----LHAKTMKK----------------
IGHW--STSEG------------LKINETLKQSVHSY---
-----------SAGRV---YRVASVIGAPYFMIK--------EGNVSNGT---------------AKFEGFCVDLMEKINE--VL-
EKKGRNIS-YKFQKVED-D-NYGEPT-------VH-GK--WNGAVGDIID---------G---RADFAVAGMTITKKRQKVVDFTK
PFMDF-GISIMLKK----PEKQ--P---------RHFDFLGPFSIEI-W---ICLFFALLGIT-LTLFEVGR--FSEN-EWY----
------TQSNG--------------------GEDERI----NEFGFFNSMWYTIGAF-MQQ-G---T--EYSP---RSMAGLXAGG
VCWFFTLIILASYTANLAAFLTMQRMNTPIK--SSNDL---AKQTE---VTYG-TRSGGTTSDFFR--------DSTI-PTFQTMW
EFMDNK---------------------EPSSFAQNAEEGWRRVM-ESKDGT---------YA-YLLES-TTNKYYNQK-SP---C-
KTMMVEE--R-LSSSSY-GIA-VSK-------SLDSLTKELTLAILE--LRE-NTQITELETK------WWT-----ERGECGQD-
-DEVVSSSGT---HSLTLEQLAGLFYILLGGLTIAVLITLLH------IIKRTLVEEQINL-------------------------
----SRFTSLRFFQSLWNFGKSVQDSPRTPTISTGSS-------------SRDTAPLTLKIPRNVAERNTRDEPIA----------
----
197 Cgig_GluAdelta
-----------------------------------MLAESHDEVRSAVTYPCPLEGAKVRKYGDPTGHRALRFEQQK---------
--------VCDHL--SNGVFALVGSRS--------------YVSREVIDSYTRVFHMPYLSPC--------------TDYHPKDHK
PFSIF--------MKPDNTRAIASIINYLDWKEFHYVYDTD------YGLSRLMDLKLWLK----DGENQ-V--------------
-NVISTWRLHRIQEVHRDLRALDKQYGPPTNFTPINVVFDLSNE-TAYGAVLDKIR--N--VGMN-KKGYSYLLGSL----DIVNH
DLER------FSHG--------GVNITGFQLV-DHESATVQSFLEEWSELPRSIWEGAGST-----------VRMESALLVDTASL
LRETIHTMLKNDSTVFRSTFRRAKVYNYDLTQGI----------------PCTGNKPW--------------MHGLKIMENL----
-------------KKV-SINGLTGDV--HIDQ-DGRRQNY----SIGV--------YR----------------------------
VGFK--
---------------------ENPRKERPFLQYKKEYEYPENRKNVKNPN---------------DLYEGYCVDLIAAVSE--QLG
G-----FK-YTIRPIKS-S-VYGAK--------VN-GT--WTGMIAELVN---------G---KADLAVAPLTITKQREEDIAFTK
PFMNS-GISIMIKK----PEIQ-KP---------GVFSFLKPFSIPL-W---MCIIAGYFCVS-FGMFIVSR--FSPA-EWR----
------RKCLR--------------------VDNGVV----NKFTLESSLWFTMGAL-MLQ-G---S--DTCP---RSVAGRIIGG
TWWFAVLIVISSYTANLAAFLTIDKLLTPIQ--NADDL---AAQTE---ITYG-TLESGSTQSFFK--------DSKV-PTYQKMW
AYMSTA---------------------YPRVFVKTTAEGVRKVR--EMKGK---------YA-FLLES-VYNEYFGQR-EP---C-
DVMQVGP--P-LNTKGY-GIA-TPKTSKH---QE--LSEKMSIAILQ--LKE-NGSLIKMKRR------WWI-----DKGECGVQ-
-EDNQGNKKK---KSLSLSNLAGVFFILISGLVFSIILAVCHFL----RSRSNNKQG-----------------------------
--VGKLESISRKTGNHIDASVKWA--------------
----
198 Ajap_GluAalphabeta

------------------------MKEQPFLMRI--------EGAQEKNG---------------KEYEGYCIDLLDEIRN--IF-
N-----FT-YKIEVVPG-N-IYGNEL-------EN-GT--WTGMIGQLME----------------------------QEVVQTN-
------GHRCSIPR----PIDD----------------PNAMEPMGIEKRM-----------------------------------
---NNFSFSNSVWFSLGAL-MQQ-G---G--DTTP---RSLAGRIVGG
VWWFFTLILISSYTANLAAFLTVERMESPIN--SVKEL----QESD---IDYG-ILRTGATFQLFE--------QSEI-PLYRDMF
TYMQAH----------------------TENYKDSNEDGIAEVR--RRNGK---------YA-FLLES-TINEYESQQ-KP---C-
DTIMVPQ--H-LDSKSY-GIG-ISR---GYEGFEV-LRDQLTLAILQ--LRE-DGTLARLRKT------WWF-----DKGKCQES-
-AKDNA-------SALSLSNVAGIFYILIVGLAAALLIAIIDFYW---KSRKDASRDKI---------------------------
----GLVRAMRN--------------KVRASVTGERGFR-----------PVPVLMESVASSGKEEKKDLLKREHGQT--------
----
199 Harg_GluAalpha

------------------MEGMQRFYALTRLKKFEQKGFDV---
-VLKRVSTDEEILETMTAIRRMQMK-----------RIIIDVDL-QGIDGILDKVK--Q--LGMV-TVDYHYIITNM----DLVKV
NLDE------FLVG--------GMNLTGFNLI-DRTDPTYTKFMKTWTKQRVAKGLEAEP------------METESALVFDTIGI
FAKTV-----------VGLGNVVDLLRLRNQR------------------RCDQNYKKSEGGVD--------AIDDNILNSL----
-------------LDS-QTQGLSGNV--QFNR-NGERTNY----TLDI--------LG----LTQDGLMKVGEWYSEGEPEERFQW
EDTW---VQAGSFDGSSLVQVKTPFLTSEENVTNVTDHAA
TRKLYSDNLWGNKDKV---YYITTVLEKPFLMLK-------EEKSRGEGN---------------DRFEGYCMDLLKGITK--IF-
N-----FS-YVIKPEPN-N-VYGNEL-------DD-GS--WSGMLGDLLD---------E---RAHIAVAPLTITSVREEVIDFTK
PYMSL-GVSIMIKK----PMSS-KP---------DVFSFMQPLSSDI-W---MCVAFAFMGVS-VVLFLVSR--FSSQ-EWFSETI
HTNGHRCSLPR-------------PIDDPNALEPMVIEKRMNNFSFSNSIWFSLGAL-MQQ-G---G--DTTP---RSLAGRIVGG
IWWFFTLILISSYTANLAAFLTVERRESPIN--SAKDL----YESE---MEYG-ILKTGSTYELFR--------NSNI-PLYQNMY

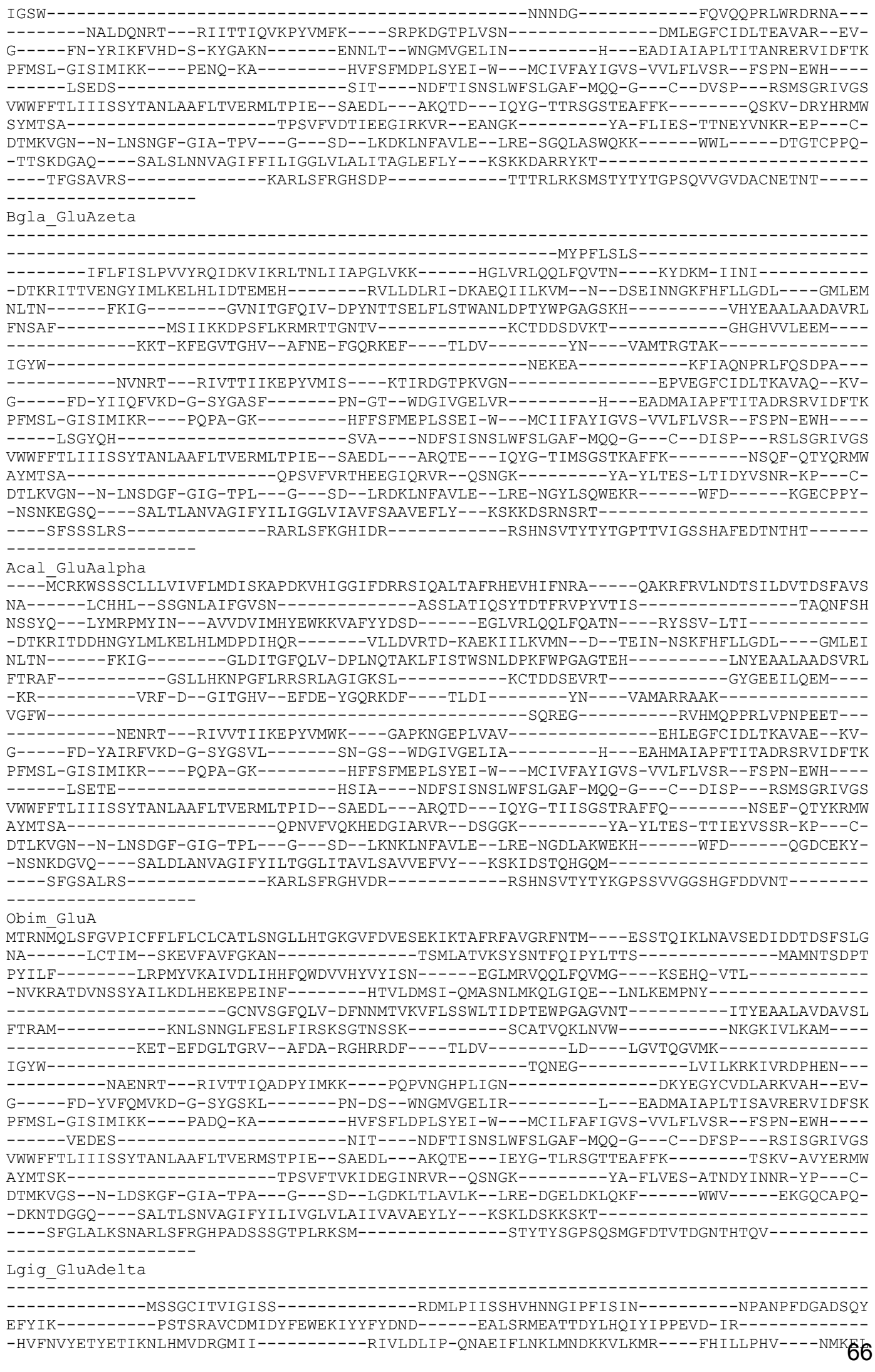

KWMKDN----------PMVLKESNEEGIAEVR--KRNGK---------YA-FLLES-TMNEYESQQ-KP---C-
DTVMVPQ--H-LDSKGY-GIG-ISKKFEG----SDELRDQLTLAILE--LRE-DGTLARLRKN------WWF-----DKGQCQES-
-AKDQP-------SALKLSNVAGIFYILIIGLGASLIIAIIDFYW---KSRTDAQRDKI----------
----GIKRAMRN----------KVRSSVTGERG----------FRPVPLVLESVNSSGKSLQGEKKDLL----------
----
200 Cint_GluA
AISRRSLVFGFCLILNFSISCSQDFDSRAIQSSVSILPVGNNRVDAMFKLALKRHNAQ---VVLPFSPSSLGSLQTSVINDTFTMA
QE------FCNHM--SQRTHTIIGFWK----------ASSMNAIISYSDTFNIPWITPS----------LPLPDQPT
KHVIN--------LHPKFETFLLDFLFKLGWKEFTLVYDQK------EVHLPVKAAIAFCL----ERGLR-I----------
-QVRNLAGVDNILPTLKEIACKKEY----------KVLFDVSL-QRSMQTLEKIK--I--MGML-SMDYHYIFSDL----SLIDQ
DLRQ------FAYG--------ASNLTFLGLV-DKSFELYDSVLQGQTNPFFNT----------VGSESALIYDAFTA
MASGM----------RQVIAEGLVFETEIQDEINRVERV----------TCHQMSILPL----------NTGSEISKAI----
----------KEV-KFQGLTGNV--EFDQ-QGQRINY----SVRI--------YA----LDRLGLNS----------
IGTW----------TDSSE-------EGDGILELNDVDLVDQSDW---
-------ILESYRNET---LIVTTIVEEPYVIRK-------PNWQELEGN----------DRFEGFCVDLLKEITK--IA-
Q-----IQ-YRIKPVDD-G-QYGSKN-------DKDGT--WNGMIGEVKY---------Q---KAHMAVAPLTITSAREAVVDFTK
PFMTL-GISIMIKK----PEKQ-NY---------NIFSFLDPLSTEI-W---ICIVFAYVGVS-VVLYLVSR--FSPY-EWH----
------RRSLT----------KVTNNDEIDAATDFGIFNSLWFSLGAF-VQQ-G---C--DISP---KSFSGRIVGG
VWWLFTLIVISSYTANLAAFLTVDKMVTPIA--GAEDL---AKQTL---IQYG-TLRSGSTVNFFK--------QSPL-PTYEKMW
ATMKSQ----------EPSVFVSSNKEGIARVR--ASDGK---------YA-FLMES-TLNDYTEQR-RP---C-
NTMKVGP--N-IDSKGY-GIA-LPK---G---SP--LYDTVNLAILT--LRE-QGKLQKLKNY------WWY-----DKSECGAN-
-GGSGATKT----PALTLGNVAGVFYVLIGGMGLAICTALLEFWY---HAHKIRNFKRK----------
----QKAKAARDRLLAERSS----------TTDNIPSVGGDHESAGRFKFWR----------
----
201 Lgig_GluAgamma
----------MSTGPNPRANIPAQRTAQNVLPIN----------
--------VCRQM--SEGVFAIIGQKT----------MQTADIVQAFTTTFHMPYLTPS----------LS
RDTIRKHSKYELHMKPDFTQALIEMISFLEWDHVHYLYDSD------EGMIRLQKMFKSMR----NASIA-WF----------
-NVKRFNDIHHVHEDLRQIDRGDINATKS-------FVLDLSSE-EAYKIVLKQIP--E--VGMN-KYGYNYLLGTL----DFKSL
NLSR------YRHG--------GVNITGFQLI-DDQNSDNREYYREMKKMKITSSGFDRRET----------IPSSAALIVDAVLS
LDDAIESMLDNDTDVFRYTFRRKHVYNYNRTRGV----------PCTTDPPT----------PW-MHGNTIYKLL----
----------RTRKPPGVSGQL--TFDK-KGFRQDY----KLGV--------YT----VNLETGPYK----------
LGTW----------SSGIG----------FRSIYDGSRDKNRHGY---
--------RPLNNSTT---KVITSILSPPFLMEQ----THDDDGTPLIGN----------DRFSGYAKDLSDHIAK--LL-
G-----FE-YEIRLVKD-R-KYGSKN-------PKTKE--WNGMIGELIR---------H---EAHLAVAPLTITADRERNVDFSK
PFMNI-GISIMIRQ----PDKQ-KP---------GVFSFMEPLSFQI-W---MCIIVAYVGVS-VGLFLVSR--FSPV-EWK----
------KTENG----------LESFR----NEFSLMNSFWFSMGAL-MFQ-G---S--DACP---RSISGRIIGG
VWWFFVLITISSYTANLAAFLTIERMLTPIE--SADDL---SKQTE---IKYG-MITSGTTKEFFK--------NSAV-ATYARMW
NYMSTT----------PDVMVESIQEGIDKVR--NSKGK---------YA-FLIES-SNNDYVNNR-KP---C-
NTMKVGP--N-LNSKGF-GIA-TPR---G---SD--MRDKITLAVLT--LKE-DGTLHTLHRR------WWY-----EKGECGMD-
-GGSKDTGK----QSLSLSNVAGVFYILISGLVFSILLGVFEVLY---YRRNNMKGT----------
----YLRGTETSQTIVSSTNNDKFVSEYTYSAPGTIGFDG----------FNRDGSVPIGFEGYNRDGTRSI----------
----
202 Bgla_GluAalpha

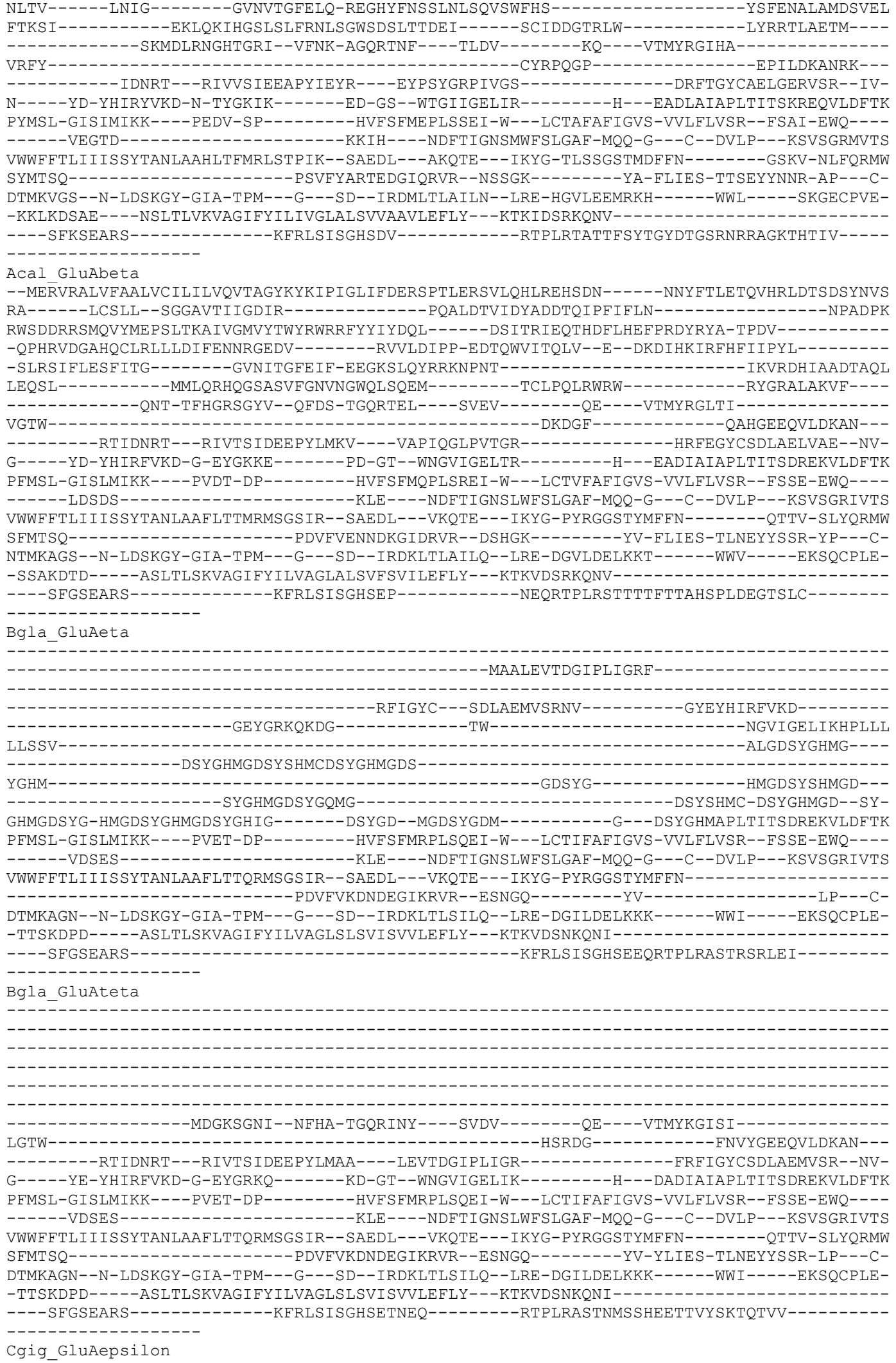
---------MEI----------
------GVTIVIKK----PQSQ-RP---------GVFSFMEPLSLEV-W---VCIIVAYLTVS-IGLFLVSR--FSPV-EWK----
------KVREH----------QNNIDWTQVRADKDGLYHNDFSLFNSFWFSMGAL-MFQ-G---S--DTCP---RSISGRIIGG
AWWFFVLIIISSYTANLAAFLTIERMINPIE--SADDL---LNHPS---IKYG-AVTSGSTLQFFL--------NSDV-PVYRQMG
EYMKTH----------SEVLVQSNEEGIERVL--KSKGK---------YA-FLAES-SFIEYINER-SP---C-
DTVSVGG--K-LNNIGF-GVA-TPR---N---SP--LRDPINVAVLK--LKE-EGTLYTLHQK------WWV-----EKGQCGGA-
-HQSKQKGK----LSLTLSNVAGIFYILIVGLVVAIVLGVFELMCF--RARKKEKVLLREERL----------
----SGDGFLRGTNTLTTLCNTPDSRRQTPEPPILDG----------EREKYPDTLSRRLNSDPPDYIGFEKFQVDIQ-----
----
203 Bgla_GluAbeta

----------MGSRRPK----EITD----------

----------MKLANALAK--EV-
G-----FT-HEFRIVAD-N-AYGAKL-------SN-GS--WNGMIGELIS---------G---VADLAVAPLTITAERERYVDFSK

```
HFMEI-GVTIVIKK----PQSQ---------------------RPGV-W---VCIIVAYLTVS-IGLFLVSR--FSPV-EWK----
------KVREH-----------------------------QNNIDWTQVRADKDGL-YHN--------DFS----LSISGRIIGG
AWWFFVLIIISSYTANLAAFLTIERMINPIE--SADDL---LNHPS---IKYG-AVTSGSTLQFFL--------NSDV-PVYRQMG
EYMKTH----------------------SEVLVQSNEEGIERVL--KSKGK---------YA-FLAES-SFIEYINER-SP---C-
DTVSVGG--K-LNNIGF-GVA-TPR---N---SP--LRDPINVAVLK--LKE-EGTLYTLHQK------WWV-----EKGQCGGA-
-------------HQSKRLSGDGF----LRGTNTLTTLCNTP------NDREDGMLPYD-------------------------
-------------------------------------------------SRRQTPEPPILDGEREKYPDTLSRRL----------
-------------------
204 Arub_GluAalpha
PLGDLWRGSALLLVAILVACLVSFCQGARQLSIGAIFTDKLTTSFFGFRRGAILHNVA-----NNGTDSVQFVEKYVSDSNSFELG
QK------VCDLF--TNGILLIGADIE--------------TPLIPTALSYSGTFHIPIIITS------------------LSKRD
MGLNTGTRDYLVSLMPSLVPVVVDLVRFHQWKRFAFIYDGD------KGLLRLHALMERLS----FKTYD-V-------------
-AFRKINNRSSIIQTLREFRDTKRQ-----------QIICDTSN-KNTKLLMEQIP--L--LGMV-TASYHYIFMDL----DIDKI
NMEK------FQYG--------GMNVTGFNIL-NETSFNFIQMKRAWDYIKLQNTSTISRQKNV--------LTHRSGLMMDLVDV
MDKTV-----------KILKQEKKLEQFDNRGQR----------------SCDDDPFR-----------PW-EFDKNVLRFL----
-KR----------VSF-T--GATGPI--SFNN-FGERSNY----VFNI--------LS----LFDDGMQK----------------
IGTW-------------------------------------------------DAKAV--------KQLKFDNVAYANGNGPGN---
-----------SKNKT---YLVTSVIEPPYLMLK-----EPRHLYF--GN---------------NRYQGYAIDLLEEIVK--KT-
P-----FK-YKINLVHD-K-AYGIP--------IN-GT--WNGMVGELVD---------G---KADLAVAPLTITSDRERVIDFTK
PFMSL-GISIMIKK----PQTT-KP---------DVFSFMHPLSYEI-W---MCIVLAYAGVS-VVLFLVSR--FSPK-EWY--PI
EYTRVPTDEAP---------------SGTNQLNDKTT----NDFGITNSLWFSFGAL-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVTNIK--SAQDL---VQSKD---VSYG-MLGEGSTLEFFK--------QSKI-PLYMDMW
TYMNNS---------------------ERSVLMTSNEQGAERVR--HMNGK---------FA-FLIES-TINEYFSQQ-KP---C-
DTMKVGQ--N-LDSKSY-GIG-VSR-------NLIKFSDDLTLAILQ--LRE-EGVLDALQKR------WWF-----DKGECHEA-
-NADASS------NALSLSNVAGVFYILVGGLSMALFSAIIEFYW---KSRSQSRKQKT-------------------------
----SLAAAMRA--------------KVRLSVTGENAL------------ASQLHPKGNASAPSTETETTPIDKSKDSSPEGNHT-
-------------------
205 Pmin_GluAalpha
GRLSSFVGVVCLFGYWQAICLFTCCDAVPQIPIGSIFSANPNASVFGFRRATINQNVH------NKSFQFMGFEKSVSSANCFEMG
QK------ICDLF--TNGVLLIGADVE--------------PPLITTTASYSSTFHMPIIIPS------------------QSKRD
LGFKDANTKYLVSLMPSLVPVLFDIIQFHQWNRFAFIYDTD------KGLLRLHALMEMLS----FRKFD-V-------------
-AFRKVNGSESMIQNLREFRDTDRH-----------RIICDTNV-QNTRLLMEQIP--L--LGML-TSSYHYIFLDL----DIDKV
NLEK------FQLG--------GMNITGFSII-NETSRRFQLLKTGLEILREQNRSVVSKMEF---------VSYRSALMMDLVDV
MARTV-----------KILIRENKLVQFEKRGQR----------------SCDDDRFR-----------PW-GFDKNVLKFL----
-KT----------VSF-N--GATGPI--SFDS-FGERSNY----VVRI--------LS----LFSDGMRE----------------
VGTW-------------------------------------------------RSEAK----------TRLKFNAGTFGDGTGR---
---------ADFNNKT---IIVTSILEQPYLMRK-----EPRHLYS--GN---------------DRFQGYAIDLLEEIVQ--KF-
P-----FK-YKIQLVRD-N-TYGIP--------VN-GT--WNGMVGELVR---------G---EADIAVAPLTIISDRERVIDFTK
PFMSL-GISIMIKK----PQTT-KP---------DVFSFMHPLSYEI-W---MCIVLAYAGVS-VVLFLVSR--FSPK-EWY--PV
EYTRVPTDEPN----------------GAIPPKEQTT----NDFGITNSLWFSFGAL-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVTDIQ--SAEDL---VASKD---VSYG-MVAAGSTEEFFR--------QSKI-PLYMDMW
NYMNST---------------------ERAVLMTTNDQGLERLR--HMNGK---------FA-FLMES-TMNEYFSQQ-KP---C-
DTLKVGQ--N-LDSKSY-GIG-VSR-------NLTRFSDELTLAILQ--LRE-EGVLDALKKR------WWF-----DKGQCHEA-
-DADSGS------NALSLSNVAGVFYILVGGLALALMSAIMEFYW---KSRSQSRKQKT-------------------------
----SLAAAMRA--------------KVRLSVTGENAL------------ARQLHPKANASVPSTDTETTPVDKPKVEPKDGSQT-
-------------------
206 Apla_GluAalpha
VENAWWTKRLFSPSVDLSPCGQLPTLLSGMGTSGAIFADNPNASFLGFKRAIFYQNGL------NDSFQFACLVKSVSSSNSFEMA
QK------VCSLFSIGKGALLISADVE--------------PPLIGTAASYSGTFQMPIIIPS------------------LSKRD
LGYQDPSTKYLVSLMPSLVPVLFDVIQFRQWTRFAFIYDSD------KGLLRLHALMEKLS----FRKFD-V-------------
-AFRKAEGEVSMIQILREFRDSDYH-----------RIICDTNV-ANTRLLMEKIP--L--LGML-TSSYHYIFLDL----DIGKV
NLEK------FQLG--------GMNITGFSIV-NETSQRFQLLKTYYEELRRNNMSITRNMEY---------VSYRSALMMDLVNV
MAKTM-----------YILIRDNKFKLFKDRGQR----------------SCGSDGSR-----------HW-GIDKTVLKSL----
-KT----------VSF-D--GASGPV--SFDS-FGERSNY----VVRI--------LN----LFSNGMRE----------------
VGTW-------------------------------------------------QSDAK----------TRLKFSAGAYGDGTDR---
---------VDFNNKT---IIVTSILEEPYMMRK-----EPRHLYS--GN---------------DRFHGYAIDLLEEIVK--KF-
P-----FK-YRIQLVRD-N-TYGIL--------VN-NT--WNGMVGELVR---------G---EADIAVAPLTIISDRERVIDFTK
PFMSL-GISIMIKK----PHTT-KP---------DVFSFMHPLSYEI-W---MCIVLAYAGVS-VVLFLVSR--FSPK-EWY--PV
EYTRVPTDETN---------------------GASPSQGQTTNDFSITNSLWFSFGAL-MQQ-G---S--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVTDIQ--SAQDL---VNSKD---VSYG-MVGAGSTEEFFR--------QSNI-PLYVDMW
NYMNST---------------------ERSVLVTSNEQGVERVR--HMNGK---------FA-FLVES-TLNEYFSQQ-KP---C-
DTMKVGQ--N-LDSKSY-GIG-VSR-------NFTTFRDDLTLAVLQ--LRE-EGVLDALKKR------WWF-----DKGQCHEA-
-NSDSGS------NALTLSNVAGVFYILVGGLALALLSAIVEFYC---KSRSQSRKQKT-------------------------
----SLAAAMRA--------------KVRLSVTGENAL------------ASQLHPKANTSAPSTETETTPVDKPKVPPKDGSQT-
-------------------
207 Lgig_GluAepsilon
-----------------------------------IFDRNSGQVHTAFRHEVQSFNRA---YSGAHRYRLENITKELDVTDSFAVS
NA------LCSHL--SKGVLAIFGVSN--------------ASSLATIQSYSNTFKVPFITIS----------------MAQNTSS
KDSYQ------IYMRPLYIHAIIKVLEHFDWRKVSYIYDSD------EGLIRLQQLFQSTN----LYEYD-LHI-----------
-GAKRITTVDNCFNVLYELHKKDEEEDQ--------RIILDLQI-EKAEEVIKQIM--R--YSDVSNARFHFLLGEL----GMLEM
NLTN------FETG--------GINITGFQLM-DPKNQTVEMFLNSWANLDPLEWPGAGTKK----------IKYEAALAVDAVRL
FTRSF---SGILGMEPNFLHRQSSLNENKGI-------------------KCTDDSLVTS-----------RQGDKIIKQM----
-------------KSV-NFDGVTGRV--AFDE-NGHRKDF----TLGV--------YD----VAMNRGIAK-----------
```

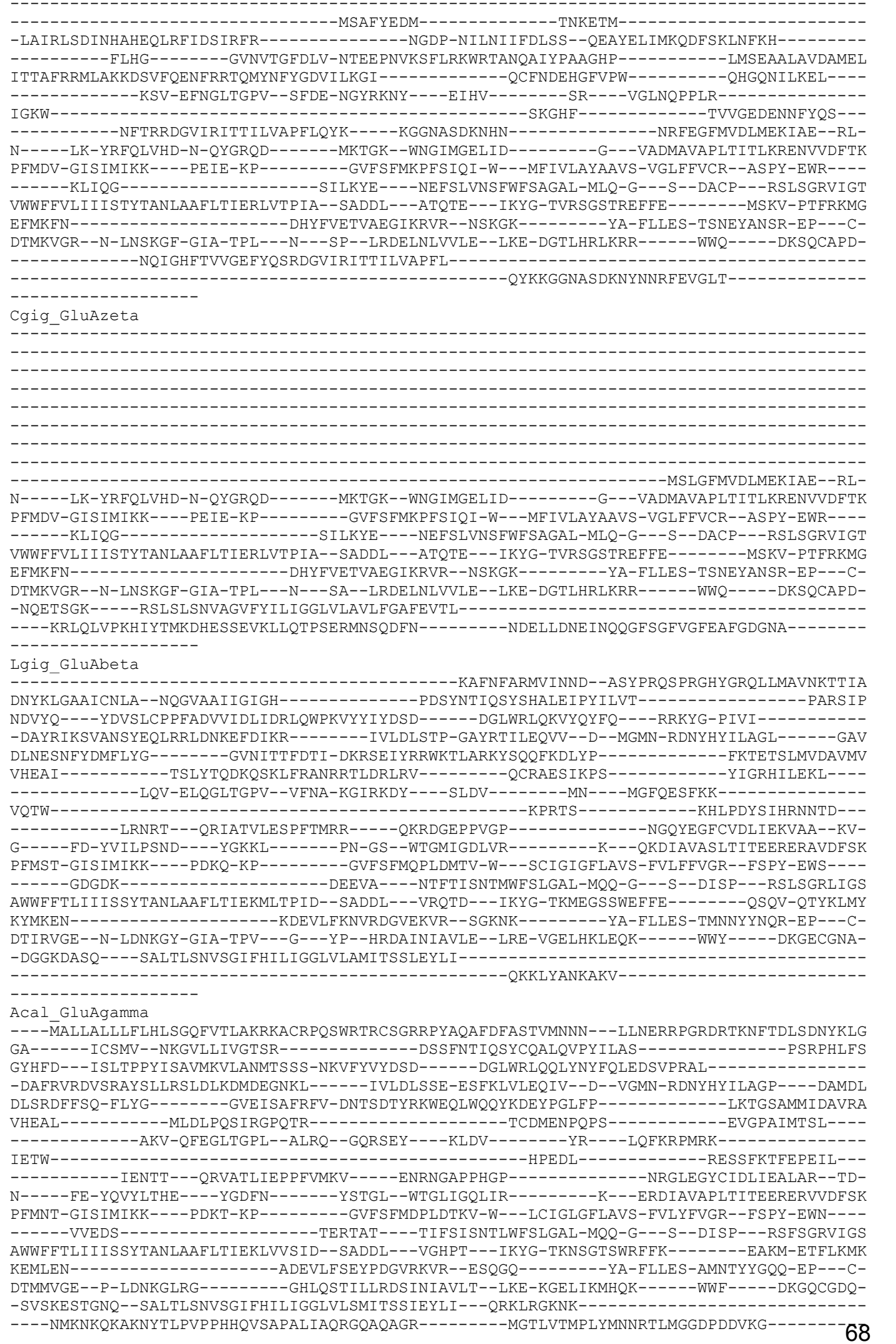

IGSW----------NNNDG----------FQVQQPRLWRDRNA---
--------NALDQNRT---RIITTIQVKPYVMFK----SRPKDGTPLVSN----------DMLEGFCIDLTEAVAR--EV-
G-----FN-YRIKFVHD-S-KYGAKN-------ENNLT--WNGMVGELIN---------H---EADIAIAPLTITANRERVIDFTK
PFMSL-GISIMIKK----PENQ-KA---------HVFSFMDPLSYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPN-EWH----
------LSEDS----------SIT----NDFTISNSLWFSLGAF-MQQ-G---C--DVSP---RSMSGRIVGS
VWWFFTLIIISSYTANLAAFLTVERMLTPIE--SAEDL---AKQTD---IQYG-TTRSGSTEAFFK--------QSKV-DRYHRMW
SYMTSA----------TPSVFVDTIEEGIRKVR--EANGK---------YA-FLIES-TTNEYVNKR-EP---C-
DTMKVGN--N-LNSNGF-GIA-TPV---G---SD--LKDKLNFAVLE--LRE-SGQLASWQKK------WWL-----DTGTCPPQ-
-TTSKDGAQ----SALSLNNVAGIFFILIGGLVLALITAGLEFLY---KSKKDARRYKT----------
----TFGSAVRS----------KARLSFRGHSDP----------TTTRLRKSMSTYTYTGPSQVVGVDACNETNT-----
----
208 Bgla_GluAzeta
----------MYPFLSLS----------
--------IFLFISLPVVYRQIDKVIKRLTNLIIAPGLVKK------HGLVRLQQLFQVTN----KYDKM-IINI----------
-DTKRITTVENGYIMLKELHLIDTEMEH--------RVLLDLRI-DKAEQIILKVM--N--DSEINNGKFHFLLGDL----GMLEM
NLTN------FKIG--------GVNITGFQIV-DPYNTTSELFLSTWANLDPTYWPGAGSKH----------VHYEAALAADAVRL
FNSAF----------MSIIKKDPSFLKRMRTTGNTV----------KCTDDSDVKT----------GHGHVVLEEM----
----------KKT-KFEGVTGHV--AFNE-FGQRKEF----TLDV--------YN----VAMTRGTAK----------
IGYW----------NEKEA----------KFIAQNPRLFQSDPA---
----------NVNRT---RIVTTIIKEPYVMIS----KTIRDGTPKVGN----------EPVEGFCIDLTKAVAQ--KV-
G-----FD-YIIQFVKD-G-SYGASF-------PN-GT--WDGIVGELVR---------H---EADMAIAPFTITADRSRVIDFTK
PFMSL-GISIMIKR----PQPA-GK---------HFFSFMEPLSSEI-W---MCIIFAYIGVS-VVLFLVSR--FSPN-EWH----
-----LSGYQH----------SVA----NDFSISNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGS
VWWFFTLIIISSYTANLAAFLTVERMLTPIE--SAEDL---ARQTE---IQYG-TIMSGSTKAFFK--------NSQF-QTYQRMW
AYMTSA----------QPSVFVRTHEEGIQRVR--QSNGK---------YA-YLTES-LTIDYVSNR-KP---C-
DTLKVGN--N-LNSDGF-GIG-TPL---G---SD--LRDKLNFAVLE--LRE-NGYLSQWEKR------WFD------KGECPPY-
-NSNKEGSQ----SALTLANVAGIFYILIGGLVIAVFSAAVEFLY---KSKKDSRNSRT----------
----SFSSSLRS----------RARLSFKGHIDR----------RSHNSVTYTYTGPTTVIGSSHAFEDTNTHT------
----
209 Acal_GluAalpha
----MCRKWSSSCLLLVIVFLMDISKAPDKVHIGGIFDRRSIQALTAFRHEVHIFNRA-----QAKRFRVLNDTSILDVTDSFAVS
NA------LCHHL--SSGNLAIFGVSN----------ASSLATIQSYTDTFRVPYVTIS----------TAQNFSH
NSSYQ---LYMRPMYIN---AVVDVIMHYEWKKVAFYYDSD------EGLVRLQQLFQATN----RYSSV-LTI----------
-DTKRITDDHNGYLMLKELHLMDPDIHQR-------VLLDVRTD-KAEKIILKVMN--D--TEIN-NSKFHFLLGDL----GMLEI
NLTN------FKIG--------GLDITGFQLV-DPLNQTAKLFISTWSNLDPKFWPGAGTEH----------LNYEAALAADSVRL
FTRAF----------GSLLHKNPGFLRRSRLAGIGKSL----------KCTDDSEVRT----------GYGEEILQEM----
-KR----------VRF-D--GITGHV--EFDE-YGQRKDF----TLDI--------YN----VAMARRAAK----------
VGFW----------SQREG----------RVHMQPPRLVPNPEET---
----------NENRT---RIVVTIIKEPYVMWK----GAPKNGEPLVAV----------EHLEGFCIDLTKAVAE--KV-
G-----FD-YAIRFVKD-G-SYGSVL-------SN-GS--WDGIVGELIA---------H---EAHMAIAPFTITADRSRVIDFTK
PFMSL-GISIMIKR----PQPA-GK---------HFFSFMEPLSYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPN-EWH----
------LSETE----------HSIA----NDFSISNSLWFSLGAF-MQQ-G---C--DISP---RSMSGRIVGS
VWWFFTLIIISSYTANLAAFLTVERMLTPID--SAEDL---ARQTD---IQYG-TIISGSTRAFFQ--------NSEF-QTYKRMW
AYMTSA----------QPNVFVQKHEDGIARVR--DSGGK---------YA-YLTES-TTIEYVSSR-KP---C-
DTLKVGN--N-LNSDGF-GIG-TPL---G---SD--LKNKLNFAVLE--LRE-NGDLAKWEKH------WFD------QGDCEKY-
-NSNKDGVQ----SALDLANVAGIFYILTGGLITAVLSAVVEFVY---KSKIDSTQHGQM----------
----SFGSALRS----------KARLSFRGHVDR----------RSHNSVTYTYKGPSSVVGGSHGFDDVNT--------
----
210 Obim_GluA
MTRNMQLSFGVPICFFLFLCLCATLSNGLLHTGKGVFDVESEKIKTAFRFAVGRFNTM----ESSTQIKLNAVSEDIDDTDSFSLG
NA------LCTIM--SKEVFAVFGKAN----------TSMLATVKSYSNTFQIPYLTTS----------MAMNTSDPT
PYILF--------LRPMYVKAIVDLIHHFQWDVVHYVYISN------EGLMRVQQLFQVMG----KSEHQ-VTL----------
-NVKRATDVNSSYAILKDLHEKEPEINF--------HTVLDMSI-QMASNLMKQLGIQE--LNLKEMPNY----------
----------GCNVSGFQLV-DFNNMTVKVFLSSWLTIDPTEWPGAGVNT----------ITYEAALAVDAVSL
FTRAM----------KNLSNNGLFESLFIRSKSGTNSSK----------SCATVQKLNVW----------NKGKIVLKAM----
----------KET-EFDGLTGRV--AFDA-RGHRRDF----TLDV--------LD----LGVTQGVMK----------
IGYW----------TQNEG----------LVILKRKIVRDPHEN---
----------NAENRT---RIVTTIQADPYIMKK----PQPVNGHPLIGN----------DKYEGYCVDLARKVAH--EV-
G-----FD-YVFQMVKD-G-SYGSKL-------PN-DS--WNGMVGELIR---------L---EADMAIAPLTISAVRERVIDFSK
PFMSL-GISIMIKK----PADQ-KA---------HVFSFLDPLSYEI-W---MCILFAFIGVS-VVLFLVSR--FSPN-EWH----
------VEDES----------NIT----NDFTISNSLWFSLGAF-MQQ-G---C--DFSP---RSISGRIVGS
VWWFFTLIIISSYTANLAAFLTVERMSTPIE--SAEDL---AKQTE---IEYG-TLRSGTTEAFFK--------TSKV-AVYERMW
AYMTSK----------TPSVFTVKIDEGINRVR--QSNGK---------YA-FLVES-ATNDYINNR-YP---C-
DTMKVGS--N-LDSKGF-GIA-TPA---G---SD--LGDKLTLAVLK--LRE-DGELDKLQKF------WWV-----EKGQCAPQ-
-DKNTDGGQ----SALTLSNVAGIFYILIVGLVLAIIVAVAEYLY---KSKLDSKKSKT----------
----SFGLALKSNARLSFRGHPADSSSGTPLRKSM----------STYTYSGPSQSMGFDTVTDGNTHTQV----------
----
211 Lgig_GluAdelta
----------MSSGCITVIGISS----------RDMLPIISSHVHNNGIPFISIN----------NPANPFDGADSQY
EFYIK----------PSTSRAVCDMIDYFEWEKIYYFYDND------EALSRMEATTDYLHQIYIPPEVD-IR----------
-HVFNVYETYETIKNLHMVDRGMII----------RIVLDLIP-QNAEIFLNKLMNDKKVLKMR----FHILLPHV----NMKEL

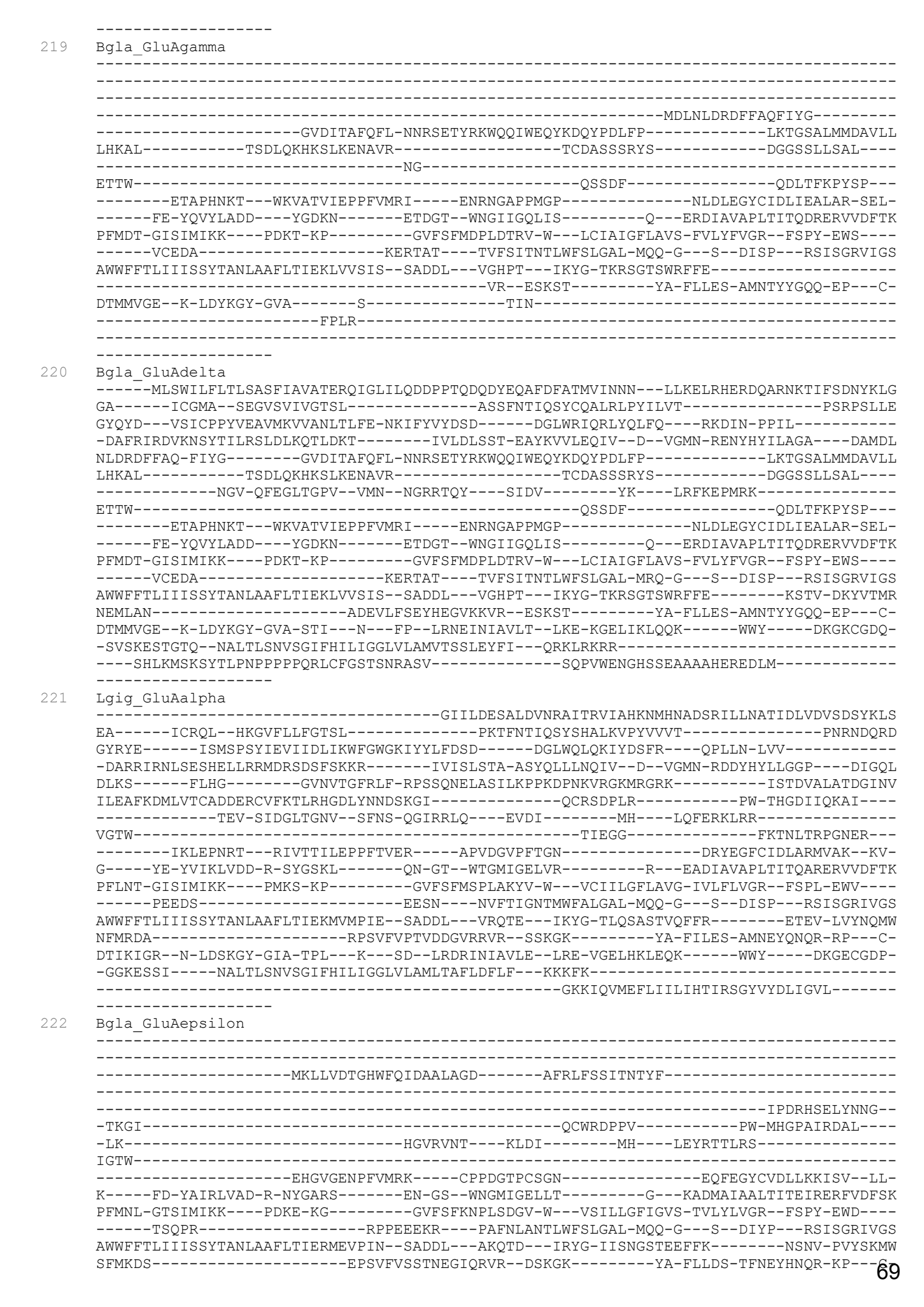

NLTV------LNIG--------GVNVTGFELQ-REGHYFNSSLNLSQVSWFHS-------------------YSFENALAMDSVEL
FTKSI-----------EKLQKIHGSLSLFRNLSGWSDSLTTDEI------SCIDDGTRLW------------LYRRTLAETM----
-------------SKMDLRNGHTGRI--VFNK-AGQRTNF----TLDV--------KQ----VTMYRGIHA---------------
VRFY---CYRPQGP----------------EPILDKANRK---
-----------IDNRT---RIVVSIEEAPYIEYR----EYPSYGRPIVGS---------------DRFTGYCAELGERVSR--IV-
N-----YD-YHIRYVKD-N-TYGKIK-------ED-GS--WTGIIGELIR---------H---EADLAIAPLTITSKREQVLDFTK
PYMSL-GISIMIKK----PEDV-SP---------HVFSFMEPLSSEI-W---LCTAFAFIGVS-VVLFLVSR--FSAI-EWQ----
------VEGTD----------------------KKIH----NDFTIGNSMWFSLGAF-MQQ-G---C--DVLP---KSVSGRMVTS
VWWFFTLIIISSYTANLAAHLTFMRLSTPIK--SAEDL---AKQTE---IKYG-TLSSGSTMDFFN--------GSKV-NLFQRMW
SYMTSQ----------------------PSVFYARTEDGIQRVR--NSSGK---------YA-FLIES-TTSEYYNNR-AP---C-
DTMKVGS--N-LDSKGY-GIA-TPM---G---SD--IRDMLTLAILN--LRE-HGVLEEMRKH------WWL-----SKGECPVE-
-KKLKDSAE----NSLTLVKVAGIFYILIVGLALSVVAAVLEFLY---KTKIDSRKQNV----------------------------
----SFKSEARS--------------KFRLSISGHSDV------------RTPLRTATTFSYTGYDTGSRNRRAGKTHTIV-----
----
212 Acal_GluAbeta
--MERVRALVFAALVCILILVQVTAGYKYKIPIGLIFDERSPTLERSVLQHLREHSDN------NNYFTLETQVHRLDTSDSYNVS
RA------LCSLL--SGGAVTIIGDIR--------------PQALDTVIDYADDTQIPFIFLN-----------------NPADPK
RWSDDRRSMQVYMEPSLTKAIVGMVYTWYRWRRFYYIYDQL------DSITRIEQTHDFLHEFPRDYRYA-TPDV-----------
-QPHRVDGAHQCLRLLLDIFENNRGEDV--------RVVLDIPP-EDTQWVITQLV--E--DKDIHKIRFHFIIPYL---------
-SLRSIFLESFITG--------GVNITGFEIF-EEGKSLQYRRKNPNT------------------------IKVRDHIAADTAQL
LEQSL-----------MMLQRHQGSASVFGNVNGWQLSQEM---------TCLPQLRWRW------------RYGRALAKVF----
-------------QNT-TFHGRSGYV--QFDS-TGQRTEL----SVEV--------QE----VTMYRGLTI---------------
VGTW---DKDGF-------------QAHGEEQVLDKAN---
---------RTIDNRT---RIVTSIDEEPYLMKV----VAPIQGLPVTGR---------------HRFEGYCSDLAELVAE--NV-
G-----YD-YHIRFVKD-G-EYGKKE-------PD-GT--WNGVIGELTR---------H---EADIAIAPLTITSDREKVLDFTK
PFMSL-GISLMIKK----PVDT-DP---------HVFSFMQPLSREI-W---LCTVFAFIGVS-VVLFLVSR--FSSE-EWQ----
------LDSDS----------------------KLE----NDFTIGNSLWFSLGAF-MQQ-G---C--DVLP---KSVSGRIVTS
VWWFFTLIIISSYTANLAAFLTTMRMSGSIR--SAEDL---VKQTE---IKYG-PYRGGSTYMFFN--------QTTV-SLYQRMW
SFMTSQ----------------------PDVFVENNDKGIDRVR--DSHGK---------YV-FLIES-TLNEYYSSR-YP---C-
NTMKAGS--N-LDSKGY-GIA-TPM---G---SD--IRDKLTLAILQ--LRE-DGVLDELKKT------WWV-----EKSQCPLE-
-SSAKDTD-----ASLTLSKVAGIFYILVAGLALSVFSVILEFLY---KTKVDSRKQNV----------------------------
----SFGSEARS--------------KFRLSISGHSEP------------NEQRTPLRSTTTTFTTAHSPLDEGTSLC---------
----
213 Bgla_GluAeta

---MAALEVTDGIPLIGRF----------------------

-----------------------------------RFIGYC---SDLAEMVSRNV----------GYEYHIRFVKD---------
----------------------GEYGRKQKDG-------------TW------------------------NGVIGELIKHPLLL
LLSSV---ALGDSYGHMG----
-----------------DSYGHMGDSYSHMCDSYGHMGDS---
YGHM---GDSYG---------------HMGDSYSHMGD---
--------------------SYGHMGDSYGQMG-------------------------DSYSHMC-DSYGHMGD--SY-
GHMGDSYG-HMGDSYGHMGDSYGHIG-------DSYGD--MGDSYGDM-----------G---DSYGHMAPLTITSDREKVLDFTK
PFMSL-GISLMIKK----PVET-DP---------HVFSFMRPLSQEI-W---LCTIFAFIGVS-VVLFLVSR--FSSE-EWQ----
------VDSES----------------------KLE----NDFTIGNSLWFSLGAF-MQQ-G---C--DVLP---KSVSGRIVTS
VWWFFTLIIISSYTANLAAFLTTQRMSGSIR--SAEDL---VKQTE---IKYG-PYRGGSTYMFFN------------------
--------------------------PDVFVKDNDEGIKRVR--ESNGQ---------YV-----------------LP---C-
DTMKAGN--N-LDSKGY-GIA-TPM---G---SD--IRDKLTLSILQ--LRE-DGILDELKKK------WWI-----EKSQCPLE-
-TTSKDPD-----ASLTLSKVAGIFYILVAGLSLSVISVVLEFLY---KTKVDSNKQNI----------------------------
----SFGSEARS---KFRLSISGHSEEQRTPLRASTRSRLEI---------
----
214 Bgla_GluAteta

------------------MDGKSGNI--NFHA-TGQRINY----SVDV--------QE----VTMYKGISI---------------
LGTW---HSRDG------------FNVYGEEQVLDKAN---
---------RTIDNRT---RIVTSIDEEPYLMAA----LEVTDGIPLIGR---------------FRFIGYCSDLAEMVSR--NV-
G-----YE-YHIRFVKD-G-EYGRKQ-------KD-GT--WNGVIGELIK---------H---DADIAIAPLTITSDREKVLDFTK
PFMSL-GISLMIKK----PVET-DP---------HVFSFMRPLSQEI-W---LCTIFAFIGVS-VVLFLVSR--FSSE-EWQ----
------VDSES----------------------KLE----NDFTIGNSLWFSLGAF-MQQ-G---C--DVLP---KSVSGRIVTS
VWWFFTLIIISSYTANLAAFLTTQRMSGSIR--SAEDL---VKQTE---IKYG-PYRGGSTYMFFN--------QTTV-SLYQRMW
SFMTSQ----------------------PDVFVKDNDEGIKRVR--ESNGQ---------YV-YLIES-TLNEYYSSR-LP---C-
DTMKAGN--N-LDSKGY-GIA-TPM---G---SD--IRDKLTLSILQ--LRE-DGILDELKKK------WWI-----EKSQCPLE-
-TTSKDPD-----ASLTLSKVAGIFYILVAGLSLSVISVVLEFLY---KTKVDSNKQNI----------------------------
----SFGSEARS--------------KFRLSISGHSETNEQ---------RTPLRASTNMSSHEETTVYSKTQTVV----------
----
215 Cgig_GluAepsilon





```
NTMKVGR--D-LDVKGY-GIA-TPR---G---SD--LRAEINIVVLQ--LNE-IGELLKLYQK------WWY-----DKGQCAPD-
--------------------AGK-------------------------------------------------------------
-------------------------------------------------------------------------------------
------------------
223 Acal_GluAdelta
---------MAQPFLHVCFCFILTLAYTQHIPIGIIVDVDERDVITILKRMIARHNSE---QTSSNHIIISPSWYIANINNNCDLI
RA------ICQRL--DAGVFLLLGSSS--------------SRSYNIIQSYSHALHVPYVVYS---------------QNVNQPRD
GYDYD------VTVSPGYVTAVAELIKFFNWEKVYYVFDSD------DALWELQRLHDYVR----LPPND-VMI-----------
-DARRLRNVTSSHDFLRQLDRFSTHTKR--------IILNLSSR-DAYQKVLNQLV--D--VGMN-RDNYHYLLSGP---------
-YIDSLDLRSFLYG--------GVNVTGFRLP-IDLQEVTPSWARVPALELEPLLNKR--------------ISTDAALAADGLQL
VINALNDLKVSNATRHIFKTFRHSELYNNGTRGV----------------QCWRHPPL-----------PW-VHGPVIRQAL----
-------------LKS-NFTGITGPL--TINS-HGQRVGH----RLDL--------MQ----LDYRNPLRK---------------
VGSW-------------------------------------------------SETLG-----------LTTNLTRPKANRVQL---
-----------DVNRT---RVVTTILENPFVMRK-----CPSDGTPCQGH---------------AQYEGYCIDLLKKVAE--IV-
K-----FD-YAIKLVND-T-TYGTRL-------DD-GS--WNGMIGELIS---------S---EADIAIASLTITEVRERVVDFSK
PFMDL-GTSIMIKK----PDKE-KG---------GVFSFKNPLSDGV-W---ISIICGFFGVS-VVLFFVGR--FSPY-EWA--AV
PGVKDGRHRAK-----------------------------PAFSLANTVWFALGAL-MQQ-G---S--DIYP---RSISGRIVGS
VWWFFTLIIISSYTANLAAFLTIERMDVTIN--SVDDL---ARQTE---IRYG-ITANGSTEDFFS--------QSNV-SVYEKMW
NFMKNT---------------------EPSVFVKTTQEGIERVR--NSKGK---------YA-FLLDS-SFNEYHNQR-KP---C-
NTMKVGR--N-LDVKGY-GIA-TPL---G---SD--LRASINIAVLE--LNE-IGELLKLHQK------WWY-----DKGQCAAE-
-SGKESKT-----SALTLSNVSGIFHILIGGLILSMVTAFFDFIL---KNRMRSEKKITVVVK-----------------------
----TSGNHSRD-------------TRGRRTSDENGDCRY----------ATLDAQSAFDIEHHHCRHRDRDEP------------
------------------
224 Skow_GluA
-------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------
-----------------------------------MV----------------------------TRKYHFVVLDF----DVYHI
DLEN------FKYG--------GANVTGFRMV-DETNTRLKEYRDVWNQFTEKYAEFENITY----------VKFQAALVYDAVSV
ITEAF-----------RLMKNDHVDIDSELI--------------------NCDNKHQK-----------PW-RDGEKMNNYL----
-------------KEV-DIQGLTGPI--RFDK-LGRRTNY----TMDI--------LS----LVPDETGKARFDKCHDYFIVVP--
CGKW-------------------------------------------------DSSGE--------GHIGIGSDGEVLSFPADS---
------------FNRT---LRVTTIDDDPYFMLK-----KNADEFE--GM---------------DKYEGYCVDLMAKIAD--VL-
K-----IK-YEWQIVED-G-NYGRLN-------EDTNR--WDGMIGELIE---------N---KADLVVAPLTITSDREPYVEFTT
PFMGL-GISIMIKK----PQNT-KP---------GVFSFLHPLSHEI-W---MCIVFAYVGVS-VVLFLVSR--FSPY-EWH--AV
DAPPPLFDDTG--------------------DRQEMA----NDFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SADDL---ATQTE---ISYG-TLTSGSTTSFFE--------KSTV-PTYTRMW
AYMSTT---------------------QPSVFTNSIKEGIERVR--RQKGR---------YA-FLLES-TMNEYINQR-KP---C-
DTIKVGN--N-LNSRXH-GKMTIKR-------SA--LKENLTLAILT--LRE-RGELHKMEKK------WWY-----EKGECGDG-
-DSKSQETA----NALSLSNVAGVFYILVGGLGLAMVVALMEFCY---KSRKEARRAKTSLSIAMRAKARM---------------
----SIKGDNGLRTPPKANSGNMFSRKKSLTPCPSEEDL-----------LAKVKKEEVYLRENVKMLHIEGLDSCNGTNT-----
------------------
225 Blan_GluAbeta
APTRPLTRSRFLLVLTICTQCTFAAFPQ-NVPIGAIFSDQSREETTAFRNRLDMLNKA-----KDASFKIVSDPKIVDTSNSFNMV
NA------VCSQI--KRGSGG----VYAIFGMYD------MPALDAIQA-YSRNLQVSFITPS----------------YPPAYSK
RSDFV---VYMRPNLARPLVDLINQV--YKWSSFTYVYDDD-----E-GLSSLEQVMDLVQ----MKDTE-V--------------
-IARKLYGVDNVNATITTIDGEGERK----------VIIDLDR--RTTEIFLKKIS--E--RNMW-TSYYHYIFMNL----DFHLL
NKAN------LTYG--------QAKVTSFQI---VDPLRDDR-----KDFQKIGKN----------------IGFKAALTYDAAGI
ISTAF-----------NSLKQDGADINLSDNTS----------------PACEKEDN-----------IW-RFGDGIRSSL----
-KK----------VKT-M--GVTGWV--EFDR-FGRRQNY----TVHC--------LE----LQRRQM-----------------
IPVW-------------------------------------------------RWR----NS------KLTKVEVKVTAPTS---
----PLRD---RV------LRVTSIFEPPYLMNKSAEDMARCPPNK--VN---------------CQYEGYAVDMLEEIAK--IV-
N-----FT-YKIHIVAD-G-VYGSENE------TT-GK--WNGMVGELIE---------G---KADLAVAPLTITLVRERVIDFSK
PYTST-GISIMIKK----PQKS--K----P----GVFSFLDPLAYEI-W---MCILFAYIGVS-VVLFLVSR--FSPY-EWH----
------PAESCGVGS----------------EDEEQT----NDFGIWNSLWFSLGAF-MQQ-G---C--DISP---RSISGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVTPIE--SADDL---AKQTE---IRYG-IVKSGSTEAFFK--------SSTI-PVYQKMW
NFMSKA---------------------EPSPLMNNNNEGITNVR----QSK---GK----YA-FLLES-AINDYIAQR-KP---C-
DTIKTGS--N-LDSKGY-GIG-MPK---E---SP--WRHKITLAVLK--LRE-DGKLSRS--------------------------
----------------ALPKVNAL---------------ISNMFH-----------------------------------------
-------------------------------------------------------------------------------------
------------------
226 Blan_GluAalpha
-------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------
----------------MELRRPRGYLTK---------------------------------------------------------
-------------------------------------------------------------------------------------
VAEW-------------------------------------------------RKITL---------------SDIDRPPVKE---
----------NRSEGL---VRVTSILEAPFLMVK-----SAEDLEKEKCD---------------CKYEGYCVDMLKKVAT--LV-
G-----FN-YTIREVAD-G-KYGAVD-------GN-GT--WNGMVGELIS---------R---KADLAVAPLTINMAREEVIEFSK
PYMSV-GISIMIKK----PQKS-KP---------GVFSFLDPLAYEI-W---MCILFAYIGVS-VVLFLVSR--FSPY-EWH--
```

```
      ------TADSA-------------------GGASIEEEQINDFGIWNSLWFSLGAF-MQQ-G---C--DISP---RSVSGRMVGG
      AWWFFTLIIISSYTANLAAFLTVERMVTPIE--SADDL---AKQTE---IAYG-TVTSGSTEAFFK--------SATI-PVYMKMW
      TYMSNA--------------------NPSPMVSSNGDGIAKVR--SSKGK---------YA-FLLES-AQNEYIEQR-KP---C-
      DTMKAGS--N-LDSKGY-GIG-MPK---N---SS--RRQAITLAVLE--LRE-EGVLQSLETK------WWY-----DKGECGPS-
      -ESSNKGET----NALSLSNVAGVFYILVGGLGLAMMAALLEFCY-----------------------------------------
      ----------------------------------------------KSKVEAKKTKVAPFITTCLCTLQ-----------------
      --------------------
227   Cmil_GluA2
      -----MANNPPVQWIIHLLAIEWDIAVRKLSATFTKYTVTTLNCKYYAVFRHSSNVIRHCVKHNNNNNNKIAFIERLSRPRRWTVG
      SGPEQGGNVCSQF--SRGVYAIFGFYD-------------KKSVNTLTSFCGTLHVSFITPS----------------FPADGLH
      QFVIQ--------MRPDLKGALLSLIEYYQWTKFAYLYDSD------RGLSVLQAVLDSAA----ENKWQ-VTAINVG--------
      -NIKDERKDEAYRSLFQDLENKKER-----------RVILDCER-DKVNDIMDQVI--T--IGKH-VKGYHYIFANL----GFTDG
      DLSK------IQYG--------GANVSGFQIV-DYDDPVVMKFMQRWLALDEKEYPGGKTSK----------IKYTSALTYDAVQV
      MTEAF-----------RYLRKQRIDISRRGSTG-----------------DCLANPAV-----------PW-GQGIEIERAL----
      -KL----------VRI-D--GLTGNI--QFDQ-FGRRVNY----TVNI--------ME----LTNNGPRK---------------
      IGYW----------------------------------------------NEVDK-----------MVLTATDFLGGNDT---
      ---------AAMENKT---VVVTTIMEAPYVMLK-----KNHEQFE--GN--------------DQYEGYCVDLAAEIAK--HC-
      G-----FK-YKLSIVPD-G-KYGARD-------AETKV--WNGMVGELVY---------G---KADIAVAPLTITLVREEVIDFSK
      PFMSL-GISIMIKK----PQKS-KP---------GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWH--TE
      EYEDGRETQTS----------------------EQT----NEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
      VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE---IAYG-TLDSGSTKEFFR--------RSKI-ALFEKMW
      AYMKSA--------------------EPSVFVKTTAEGVARVR--KSKGK---------YA-YLLES-TMNEYIEQR-KP---C-
      DTMKVGG--N-LDSKGY-GIA-TPK---G---SS--LRTPINLAVLK--LSE-QGILDKLKNK------WWY-----DKGECGAK-
      -DSGSKEKT----SALSLSNVAGVFYILVGGLGLAMLVALIEFCY---KSRAEA--------------------------------
      ----KRMKVAKN-----------------------------------AQAINPTSSQSQNFATYKEGYNVYGIESVKI-------
      --------------------
228   Hsap_GluA2
      ----MQKIMHISVLLSPVLWGLIFGVSSNSIQIGGLFPRGADQEYSAFRVGMVQFSTS--------EFRLTPHIDNLEVANSFAVT
      NA------FCSQF--SRGVYAIFGFYD-------------KKSVNTITSFCGTLHVSFITPS----------------FPTDGTH
      PFVIQ--------MRPDLKGALLSLIEYYQWDKFAYLYDSD------RGLSTLQAVLDSAA----EKKWQ-VTAINVG--------
      -NINNDKKDEMYRSLFQDLELKKER-----------RVILDCER-DKVNDIVDQVI--T--IGKH-VKGYHYIIANL----GFTDG
      DLLK------IQFG--------GANVSGFQIV-DYDDSLVSKFIERWSTLEEKEYPGAHTTT----------IKYTSALTYDAVQV
      MTEAF-----------RNLRKQRIEISRRGNAG-----------------DCLANPAV-----------PW-GQGVEIERAL----
      -KQ----------VQV-E--GLSGNI--KFDQ-NGKRINY----TINI--------ME----LKTNGPRK---------------
      IGYW----------------------------------------------SEVDK-------------MVVTLTELPSGN---
      -------DTSGLENKT---VVVTTILESPYVMMK-----KNHEMLE--GN--------------ERYEGYCVDLAAEIAK--HC-
      G-----FK-YKLTIVGD-G-KYGARD-------ADTKI--WNGMVGELVY---------G---KADIAIAPLTITLVREEVIDFSK
      PFMSL-GISIMIKK----PQKS--K----P----GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWH--TE
      EFEDGRETQSS----------------------EST----NEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
      VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---SKQTE---IAYG-TLDSGSTKEFFR--------RSKI-AVFDKMW
      TYMRSA--------------------EPSVFVRTTAEGVARVR--KSKGK---------YA-YLLES-TMNEYIEQR-KP---C-
      DTMKVGG--N-LDSKGY-GIA-TPK---G---SS--LRNAVNLAVLK--LNE-QGLLDKLKNK------WWY-----DKGECGSG-
      -GGDSKEKT----SALSLSNVAGVFYILVGGLGLAMLVALIEFCY---KSRAEAKRMKM--------------------------
      ----TLNDAMRN-------------KARLSITGSTGV-----------MTPEFPKAVHAVPYVSPGMGMNVSVTDLS-------
      --------------------
229   Locu_GluA2
      -----MHKIMNISLFLLPVLWGLVFGGSPSVQIGGLFPRGADQEYSAFRIGMVQFGTS--------EFRLTPHIDNLEVANSFAVT
      NC------FCSQF--SRGVYAIFGFYD-------------KKSVNTITSFCGTLHVSFITPS----------------FPADGLH
      QFILQ--------MRPDIKGPLLSLIEYYKWDKFAYLYDSD------RGLSTLQVVLDTAA----EKKWQVTAINVG---------
      -NLKDEKKDEAYRSLFQDLENKKER-----------RVILDCEQ-DKVKDIMEQVI--T--IGRH-VKGYHYIIANL----GFVDG
      DLSK------IQYG--------GANVSGFQIV-DFDDPLVSKFDQRWEALEEKEYPGADSR----------IRYTSALTYDAVQV
      MTEAF-----------RYLHKQRIDISRRGNNG-----------------DCLANPAVPW-----------AQGVEIERAL----
      -------------KQV-HVEGLTGNI--QFDQ-YGKRVNY----TVNV--------ME----LKNSGPVK---------------
      IGYW----------------------------------------------NEVDK------------MAVTKPDILPNES---
      ---------MGLENKT---VIVTTILEAPYVMLK-------KNADLFVDN--------------DRYEGYCVDLAAEIAK--HC-
      G-----FK-YKLSIVGD-G-KYGARD-------AETKI--WNGMVGELVY---------G---KADIAVAPLTITLVREEVIDFSK
      PFMSL-GISIMIKK----PQKS-KP---------GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWHTEEY
      EDGQIQTNEST-------------------------------NEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
      VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE---IAYG-TLDSGSTKEFFR--------RSKI-ALFDKMW
      TYMKSA--------------------EPSVFVKTTAEGVLRVR--KSKGK---------YA-YLLES-TMNEYIEQR-KP---C-
      DTMKVGG--N-LDSKGY-GIA-TPK---G---SS--LRNAVNLAVLK--LNE-QGLLDKLKNK------WWY-----DKGECGSG-
      -GGDSKEKT----SALSLSNVAGVFYILVGGLGLAMLVALIEFCY---KSRAEAKRMKM--------------------------
      ----TFGDAMRS-------------KARLSITGSTGV-----------MTPEFPKAVHAVPYVRPGMGMNVSVTDLS-------
      --------------------
230   Cmil_GluA4
      ---MREVDRQIVLLCSGFLGLAMGAFPT-SVQIGGLFMRYSDQEYSAFRFAIYLHNTN--PNTTEAPFNLVPHVDNIETANSFAVT
      NA------FCSQY--ARGVFAIFGMYD-------------KRSVHTLTSFCGALHISLITPS----------------FPTEGES
      QFVLQ---L--RPSLRG---ALLSLLDHYEWKKFVFLYDTD------RGYSILQSIMEKAG----QNGWQ-VSA-----------
      -ICIENFDDASYRRLLEDLERKQEK-----------RFVVDCEV-ERLHNIMEQIV--S--VGKH-VRGYHYVLANL----GFKDI
      ALDR------FMHG--------GANVTGFQIV-DYSKPIVTKFMQRWKKLDQREFPGTDNAQ----------LKYTSALTYDGILV
      MAEAF-----------RYLRRQRIDISRKGNAG-----------------DCLANPAA-----------PW-IQGIDTERAL----
      -KQ----------VRI-Q--GLTGNV--QFDN-YGRRTNF----TIDV--------LE----LKNTGHRK---------------
      IGYW----------------------------------------------NDVDK-----------LVLIQNEMLFPNDS-
```

```
---------SALENRT---VYVTTILEGPYVMLK-----KNHDTME--GN---------------DRYEGYCVDLASEIAK--HI-
G-----IK-YELKIVPD-G-KYGARDP------ET-KI--WNGMVGELVY---------G---RAQIGVAPLTITLVREEVIDFSK
PFMSL-GISIMIKK----PQKS--K----P----GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWH--TE
EPEDGQDSPPS---------------------DQPP----NEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---SKQTE---IAYG-TLDSGSTKEFFR--------RSKI-AVYEKMW
AYMKSA---------------------EPSVFTKTTAEGVARVR--KSKGK---------FA-FLLES-TMNEYIEQR-KP---C-
DTMKVGG--N-LDSKGY-GVA-TPK---S---SP--LRNAVNLAVLK--LNE-QGLLDKLKNK------WWY-----DKGECGSG-
-GGDSKDKT----SALSLSNVAGVFYILVGGLGLAMLVALVEFCY---KSRAEAKRMKL-------------------------
----TFSEAMRN--------------KARLSITGSVGV------------LTPDCPKAVHTVPTIRQNPGLAIVASDLP-------
-------------------
---MRIISRQIVLLFSGFWGLAMGAFPS-SVQIGGLFIRNTDQEYTAFRLAIFLHNTS--PNASEAPFNLVPHVDNIETANSFAVT
NA------FCSQY--SRGVFAIFGLYD--------------KRSVHTLTSFCSALHISLITPS----------------FPTEGES
QFVLQ---L--RPSLRG---ALLSLLDHYEWNCFVFLYDTD------RGYSILQAIMEKAG----QNGWH-VSA------------
-ICVENFNDVSYRQLLEELDRRQEK-----------KFVIDCEI-ERLQNILEQIV--S--VGKH-VKGYHYIIANL----GFKDI
SLER------FIHG--------GANVTGFQLV-DFNTPMVIKLMDRWKKLDQREYPGSETP-----------PKYTSALTYDGVLV
MAETF-----------RSLRRQKIDISRRGNAG-----------------DCLANPAA-----------PW-GQGIDMERTL----
-KQ----------VRI-Q--GLTGNV--QFDH-YGRRVNY----TMDV--------FE----LKSTGPRK----------------
VGYW-------------------------------------------------NDMDK------------LVLIQDVPTLGNDT---
---------AAIENRT---VVVTTIMESPYVMYK-----KNHEMFE--GN---------------DKYEGYCVDLASEIAK--HI-
G-----IK-YKIAIVPD-G-KYGARD-------ADTKI--WNGMVGELVY---------G---KAEIAIAPLTITLVREEVIDFSK
PFMSL-GISIMIKK----PQKS--K----P----GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWH--TE
EPEDGKEGPSD----------------------QPP----NEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE---IAYG-TLDSGSTKEFFR--------RSKI-AVYEKMW
TYMRSA---------------------EPSVFTRTTAEGVARVR--KSKGK---------FA-FLLES-TMNEYIEQR-KP---C-
DTMKVGG--N-LDSKGY-GVA-TPK---G---SS--LRTPVNLAVLK--LSE-AGVLDKLKNK------WWY-----DKGECGPK-
-DSGSKDKT----SALSLSNVAGVFYILVGGLGLAMLVALIEFCY---KSRAEAKRMKL-------------------------
----TFSEAIRN--------------KARLSITGSVGV------------LTPDCPKAVHTGTAIRQSSGLAVIASDLP-------
-------------------
----MRITCRQLLLLFSSFWGLTMGAFPSSVQIGGLFIRNTDQEYTAFRLAIFLHNTS--PNATEAPFNLVPHVDNIETANSFAVT
NA------FCSQY--SRGVFAIFGLYD--------------KRSVHTLTSFCSALHISLITPS----------------FPTEGES
QFVLQ--------LRPSLRGALLSLLDHYDWNRFVFLYDTD------RGYSILQAIMEKAG----QNGWQVSA-------------
-ICVENFNDASYRRLLEDLDRRQEK-----------KFVIDCEA-ERLQNILEQIV--S--VGKH-VKGYHYIMANL----GFKDI
SLER------FMHG--------GANVTGFQLV-DFNTPMVIKLMQRWNKLDQREYPGSESP-----------PKYTSALTYDGVLV
MAEAF-----------RNLRRQKIDISRRGNAG-----------------DCLANPAAPW-----------NQGIDMERTL----
-------------KQV-RIQGLTGNV--QFDH-YGRRVNY----TMDV--------FE----LKSNGPRR----------------
IGYW-------------------------------------------------NDNDK------------LVLIQNEILLPNET---
---------AAMENRT---VVVTTIMEGPYVMLK-------KNWEMFEGN---------------DQYEGYCVDLASEIAK--HI-
G-----IK-YKISIVPD-G-KYGARD-------PETKI--WNGMVGELVY---------G---KAEIAVAPLTITLVREEVIDFSK
PFMSL-GISIMIKK----PQKS-KP---------GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWH----
------TEEPE--------------DGNEGPPSDQPP----NEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE---IAYG-TLDSGSTKEFFR--------RSKI-AVYEKMW
TYMKSA---------------------EPSVFTKTTAEGVARVR--KSKGK---------FA-FLLES-TMNEYIEQR-KP---C-
DTMKVGG--N-LDSKGY-GVA-TPK---G---SQ--LRTPVNLAVLK--LSE-SGVLDKLKNK------WWY-----DKGECGPK-
-DSGSKDKT----SALSLSNVAGVFYILVGGLGLAMLVALIEFCY---KSRAEAKRMKL-------------------------
----TFTEAMRN--------------KARLSITGSVGV------------LTPDCPKAVHTGPSQRQSSGLAVVSSEYQ-------
-------------------
---MGRDLLQSVLLGLNLLLGAVLGAFPSNVQIGGLFARSTDQENSAFRFGIYLHNTN---PNISEAPFALTPVDNLESSNSFSVT
NA------FCSQY--SKGVYAIFGFYD--------------KRSVNTLTSFCGALHTSFITPS----------------FPTEGEI
QFVIQ--------LRPPLHGALLGLLSHYKWKKFVYLYDTD------RGYSILQVIMEAAV----QNNWQ-VTAK-----------
-SVGSITDVIEYRRIFEEMDKRQER-----------RFLIDCEL-GRLNTIMDQVSHLS-------RSSWHLGFSDL---------
------MLDKFMET--------GVNVTGFQLV-NYEDPMVQKFMQRWTKLDQREYPGTAAST----------LKFTAALTYDGIFV
IAEAF-----------RYLRKQRIDISRRVTTG-----------------DCLANPAV-----------PW-SQGIDIERAL----
-------------KQV-RSQGLTGNL--QFDN-YGRRTNY----TIDV--------YE----LRPTGPRK----------------
IGYW-------------------------------------------------NEYEK--------------LVSTVEVQPTNE---
--------STSMENRT---IVVTTIMESPYVMLK-----KNFEQFD--AN---------------DRYEGYCVDLAFEIAK--HV-
G-----IN-YKLSVVPD-G-KYGARD-------PDTKI--WNGMVGELVY---------G---RADIAVAPLTITLVREEMIDFSK
PFMSL-GISIMIKK----PQKS-KP---------GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWH--ME
DNEEGRDPQNT----------------------EPP----NEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE---IAYG-TLDSGSTKEFFR--------RSKI-GVYEKMW
SYMKSA---------------------EPSVFTKTTADGVAKVR--KSKGK---------FA-FLLES-TMNEYIEQR-KP---C-
DTMKVGG--N-LDSKGY-GVA-TPK---G---AS--LRNAVNLAVLK--LNE-QGLLDKLKNK------WWY-----DKGECGSG-
-GGDSKDKT----SALSLSNVAGVFYILVGGLGLAMMVALIEFCY---KSRAEAKRL-------------------------
----KVAKSAQN--------------FKPAPTMGGG-------------GEGGCTTNPIKVTFFSMIPEREQKIC----------
-------------------
QKKMGQSVLRAVFFLVLGLLGHSHGGFPNTISIGGLFMRNTVQEHSAFRFAVQLYNTN--QNTTEKPFHLNYHVDHLDSSNSFSVT
NA------FCSQF--SRGVYAIFGFYD--------------QMSMNTLTSFCGALHTSFVTPS----------------FPTDADV
QFVIQ--------MRPALKGAILSLLGHYKWEKFVYLYDTE------RGFSILQAIMEAAV----QNNWQ-VTAR-----------
-SVGNIKDVQEFRRIIEEMDRRQEK-----------RYLIDCEV-ERINTILEQVV--I--LGKH-SRGYHYMLANL----GFTDI
LLER------VMHG--------GANITGFQIV-NNENPMVQQFIQRWVRLDEREFPEAKNAP----------LKYTSALTHDAILV
```

```
IAEAF-----------RYLRRQRVDVSRRGSAG-----------------DCLANPAV-----------PW-SQGIDIERAL----
--------------KMVQVQGMTGNI--QFDT-YGRRTNY----TIDV--------YE----MKVSGSRK----------------
AGYW-------------------------------------------------NEYER-----------FVPFSDQQISNDSAS---
-----------SENRT---IVVTTILESPYVMYK-----KNHEQLE--GN---------------ERYEGYCVDLAYEIAK--HV-
R-----IK-YKLSIVGD-G-KYGARD-------PETKI--WNGMVGELVY---------G---RADIAVAPLTITLVREEVIDFSK
PFMSL-GISIMIKK----PQKS-KP---------GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWH--LE
DNNEEPRDPQS----------------------PPDPP----NEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE---IAYG-TLDSGSTKEFFR--------RSKI-AVYEKMW
SYMKSA----------------------EPSVFTKTTADGVARVR--KSKGK---------FA-FLLES-TMNEYIEQR-KP---C-
DTMKVGG--N-LDSKGY-GVA-TPK---G---SA--LRNAVNLAVLK--LNE-QGLLDKLKNK------WWY-----DKGECGSG-
-GGDSKDKT----SALSLSNVAGVFYILVGGLGLAMMVALIEFCY---KSRAES--------------------------------
----KRMKLTKN--------------TQNFKPAPATTQ------------NYATYREGYNVYGTESVKI----------------
--------------------
```

235 Locu_GluA3

```
RLQKMGRRILHTVLFLTILFGKSLAGFPNQINIGGLFMRSTVQEHSAFRFAVQLYNTN--QNVTEKPFHLNYHVDHLESSNSFSVT
HA------FCSQF--SRGVYAIFGFYD--------------KKSMNTLTSFCGALHTSFVTPS----------------YPTDADV
QFVIQ--------MRPALRGAVLSLLSHYKWEKFVYLYDTD------RGFSILQAIMESAV----ANNWQ-VTAR-----------
-SVGSISDPQEFRRIIEEMDRRQEK-----------RYLIDCEV-ERINAILEQVV--I--LGKN-SRGYHYILANL----GFSNV
SLDK------VFLG--------GANITGFQII-NTENPIVQQFLQRWDRLDEREFPEARNTP----------LKYTSALTHDAILV
IAEAF-----------RYLRRQRVDVSRRGSAG-----------------DCLANPAVPW-----------SQGIDIERAL----
--------------KMVQVQGMTGNI--QFDN-FGRRSNY----TIDV--------YE----MKPGGPRK----------------
IGYW-------------------------------------------------NEYER-----------FVYIMDQQVTNDTSS---
-----------VENRT---IVVTTIMEAPYVMYK-----KNSDHLE--GN---------------EKYEGYCVDLASEIAK--HV-
G-----IK-YKLSIVTD-G-KYGARD-------PETKT--WNGMVGELVY---------G---RADIAVAPLTITLVREEVIDFSK
PFMSL-GISIMIKK----PQKS-KP---------GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWHLDDS
DEARDPQTPPD-----------------------PP----NDFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE---IAYG-TLDSGSTKEFFR--------RSKI-AVYEKMW
SYMKSA----------------------EPSVFAKTTAEGVARVR--KSKGK---------FA-FLLES-TMNEYIEQR-KP---C-
DTMKVGG--N-LDSKGY-GVA-TPK---G---SA--LRTPVNLAVLK--LSE-QGILDKLKNK------WWY-----DKGECGTK-
-DSGSKDKT----SALSLSNVAGVFYILVGGLGLAMMVALIEFCY---KSRAESKRL--------------------------------
----KLAKNAQN-----------------------------------FKPAPPTNTQNFATYREGYNVYGTESV---------
--------------------
```

236 Cmil_GluA1

```
---MSTSGIQALLCVSGACVCLCAIPSEAGLGAWLPRLPLHHQESIRPRGAHTRLYSCRLSLFLESSAAVSVETENVDISNSFAVT
HA------FCSLF--QRGVYAIFGFYD--------------RKTVNTLRSFCGALHLSFITPS----------------FPVDTSN
QFVIQ--------MRPGLHDALLSLITHYKWQKFVYIYDAD------RGLSVLQKVLDTAA----EKNWQ-VTA-----------
-VSLETTTEEGYRMLFKDLDKRKER-----------HVVIDCES-DKLNAIMNQVN--STTSEIHTSLCLIFVLRFG-----FLDV
NLDK------FQYA--------GANVTGFQIV-LPTNIQVTKFLQRWEKLDPKEYQGVEGSR----------LKYTSAMTFDGILV
LSEAF-----------KYLRKTRIDISRRGNAG-----------------DCLANPAV-----------PW-GQGIDIQRAL----
-------------QQV-RAEGLTGNI--QFNE-FGQRTNY----TVSV--------LE----LKSSGVRK----------------
IGYW-------------------------------------------------NEDDR-----------FMPTSTDPHSSNET---
---------SGIQNRT---YIVTTILEAPYVMLK-----KNHEQLE--GN---------------DKYEGYCVELATEIGK--HV-
S-----FN-YKLAIVAD-G-KYGARD-------PETKV--WNGMVGELVY---------S---KADIAVAPLTITLVREEVIDFSK
PFMSL-GISIMIKK----PQKS-KP---------GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWH--TE
EYEEGQDPQNS----------------------DQT----NEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE---IAYG-TLDAGSTKEFFR--------RSKI-AVFEKMW
AYMKSA----------------------EPSVFVKTTEEGVARVR--KSKGK---------YA-YLLES-TMNEYIEQR-KP---C-
DTMKVGG--N-LDSKGY-GVA-TPK---G---SA--LRTTVNLAVLK--LSE-QGILDKLKNK------WWY-----DKGECGSK-
-DSASKDKT----SALSLSNVAGVFYILIGGLGLAMLVALVEFCY---KSRSETRRM--------------------------------
----KVAKSTQTL-----------------------------------NAPSLQYATCKEGYNVFGMESV---------------
--------------------
```

237 Hsap_GluA1

```
------MQHIFAFFCTGFLGAVVGANFPNNIQIGGLFPNQQSQEHAAFRFALSQLTEP---------PKLLPQIDIVNISDSFEMT
YR------FCSQF--SKGVYAIFGFYE--------------RRTVNMLTSFCGALHVCFITPS----------------FPVDTSN
QFVLQ--------LRPELQDALISIIDHYKWQKFVYIYDAD------RGLSVLQKVLDTAA----EKNWQ-VTA-----------
-VNILTTTEEGYRMLFQDLEKKKER-----------LVVVDCES-ERLNAILGQII--K--LEKN-GIGYHYILANL----GFMDI
DLNK------FKES--------GANVTGFQLV-NYTDTIPAKIMQQWKNSDARDHTRVDWKR----------PKYTSALTYDGVKV
MAEAF-----------QSLRRQRIDISRRGNAG-----------------DCLANPAV-----------PW-GQGIDIQRAL----
-QQ----------VRF-E--GLTGNV--QFNE-KGRRTNY----TLHV--------IE----MKHDGIRK----------------
IGYW-------------------------------------------------NEDDK-------------FVPAATDAQAGGD---
--------NSSVQNRT---YIVTTILEDPYVMLK-----KNANQFE--GN---------------DRYEGYCVELAAEIAK--HV-
G-----YS-YRLEIVSD-G-KYGARD-------PDTKA--WNGMVGELVY---------G---RADVAVAPLTITLVREEVIDFSK
PFMSL-GISIMIKK----PQKS-KP---------GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWH--SE
EFEEGRDQTTS----------------------DQS----NEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE---IAYG-TLEAGSTKEFFR--------RSKI-AVFEKMW
TYMKSA----------------------EPSVFVRTTEEGMIRVR--KSKGK---------YA-YLLES-TMNEYIEQR-KP---C-
DTMKVGG--N-LDSKGY-GIA-TPK---G---SA--LRNPVNLAVLK--LNE-QGLLDKLKNK------WWY-----DKGECGSG-
-GGDSKDKT----SALSLSNVAGVFYILIGGLGLAMLVALIEFCY---KSRSESKRMK--------------------------------
----GFCLIPQQSINEAIRTSTLPRNSGAGASSGGSGENGRV--------VSHDFPKSMQSIPCMSHSSGMPLGAT----------
--------------------
```

238 Locu_GluA1

```
------MQRSFTLFYTSFLGVCLGSSFPSNINIGGLFPT-NSHEYEVFRFALSHHQDI---------PKLVPQVDMVHIGNSFAMT
YA------FCSQF--SKGVYAIIGLYD--------------KKTVNMLMSFCGALHVCFVTPS----------------FPIETSN
```

```
QFVIQ--------LRPELQDALVSVIDHYKWTKFVYIYSSD------SGLTVLQKVLDTAP----EKNWF-VTS-----------
-VNLETMTEAAFLKVFQDLDKKKEG-----------QIVIDCET-DKLNSILKLIA--S--HGKN-VKSYHYILANL----GFLDI
DLTE------FRNG--------GANVTGFQLV-NYTDQNVSRIVQQWMDFDSKDTKSPKKR-----------LKYTGALTYDGVSV
MSAAF-----------QNLRKQRIDISRRGNAG-----------------DCLANPPAPW-----------GQGIDIQRAL----
-------------QQV-RLEGMTGHV--QFNE-KGRRTNY----TVGV--------ME----LGPNRPKK----------------
VGYW-------------------------------------------------NEDEG-----------YVSTASYSHAGNDT---
---------TGLQNRT---YIVTTILESPYVMLK-----KNHDQLT--GN--------------EKYEGYCVELAAEIAK--HV-
G-----YR-YKLEIVSD-G-KYGARD-------PETKM--WNGMVGELVY---------G---KADVAVAPLTITLVREEVIDFSK
PFMSL-GISIMIKK----PQKS-KP---------GVFSFLDPLAYEI-W---MCIVFAYIGVS-VVLFLVSR--FSPY-EWH--AE
DFEDGQDPPQQ-------------QQQQHQQQQQQNQEQTNEFGIFNSLWFSLGAF-MQQ-G---C--DISP---RSLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE---IAYG-TLDAGSTKEFFR--------RSKI-AVFEKMW
SYMKSA---------------------DPSVFVKTTDEGVFRVR--KSKGK---------YA-YLLES-TMNEYIEQR-RP---C-
DTMKVGG--N-LDSKGY-GIA-TPK---G---SP--LRNPVNLAVLK--LNE-QGLLDKLKNK------WWY-----DKGECGSG-
-GGDSKDKT----SALSLSNVAGVFYILIGGLGLAMLVALVEFCY---KSRTESRRMKQ----------------------------
----SINDAMRTST------------LTRMSGNGSGGI------------VTHDFPKSMQTLPCMSHAAGLGLSATGM--------
--------------------
```

239 Blann_GluDalpha

```
-MTTHGLPATLFVLAFIGNLLQATHGYPDKVTIGAFFEEPTTAEETAFKYAVDQINRN---SSILPGVKLLYKKEVMDRSNPFLAT
IK------VCSLM--TSQIAALVSITS-------------QSTNSVLQSMTNTMTLPHLYVP----------------RPSCNCK
VLEPKGYSMSMRPRQSQLDQALLTLIKQQHWRSIVLIYDES------YDFERLQTLIIEGT----NHEWD-MLILRV---------
-SSKDVLNSKDFRKKLRSIDERNFRYN---------NVVVLCSP-DTTVEVLYQAN--E--MHMV-GNQYLWVIANE----EISDR
HLDSINITTGMITGIRKRIPTDGYHLNGFLAH-LQKMHPGYSLSFVLPTLQD--------------------FPLSAAYSYDAVWA
LARTF-----------DILIKERNWTAATPL-------------------ICHKPTPW--------------LGGKNLLGSL----
-------------RKN-NMSGLNGPV--YFNN-EGYNDNA----EMEL--------LS----LTTNDENITKFWA-----------
IGTW-------------------------------------------------NVQGG-----------LNLTEPAFTREIHS---
-----------FENTT---LTVVTLTEKPFIFKD-----IPEDGPP--------------------AFRGFLIDVLNELKT--QL-
K-----FS-YTIFETPD-Q-KYGAKK-------ED-GE--WNGMVGQLVQ---------K---RAHIAVSALTITSEREDVVDFTK
PYMDY-GATILLRK----PEQK--Y---------NVFAFLEPFNFQV-W---ACILGSILIVG-FILYILNR--ISPY--------
------SSFGT---------------------DEPDA----DAFNLSNSVWFAYGSL-VQQ-G---G--ESNP---RASSGRMLSG
FWWFFTLIMISTYTANLAAFLTVTRMDTPVR--SVDDL---AAQTT---MPYG-TVEDSSLYTFFK--------TSKI-GVYERMW
DFMNNS----------------------NTFVNTVEAGYDKVL----SEM---------YA-FIWEN-PSLDYLKLT-----NC-
DYTTIGR--P-FNMKGY-GIA-LQE---G---MS--LRDQLSISILK--MQE-SGKMDELKSK------WWP----SENAKCPAE-
-SSSQKSKA----SELGLNSLAGVFYVLALGVGISIVIVLIEIIWW--LLRGEGKLKRP----------------------------
----KPKNDKIV-------------------------------------LEEVERIEIKHIPNDSTSSNGKRKIWT---------
--------------------
```

240 Lvar_GluAbeta

```
--MANQARKLHFMMCVLLSLVYVTSAGYQITIFGIFDEDVTEHDPKSVGFRRGMIKYNVQSNSTGSPFQLMGFEVRIPVNNSFILT
NL------ICGAL--SDNRMLIAGDAD-------------VNTIYNAAYASREVKIPYFITS--------------------FAPR
DVYPDFSAEYLLAMQPQVLQPLVDYIGYFHWSSLAYIYEGQ------TGFLRLHNFLDLIR----PLGIE----------------
-VTHRRINIDSVNETLNELKDTGKH-----------RIICDANL-PLTDTVLRNSI--D--LEMT-TASYHMVYLNL----DFDTI
DTSN------MSFG--------GMNLTGFSLITNKSSEAYHELFGDWSDKFRYSHPTLANTE----------VGYEAILAHDLCRV
AVAAA-----------RSIHESGRQLPLPKVNTFH---------------TCFKHVRDGTDIMTETVSS---TVGPELLDAI----
-------------KRT-ATDQLSGRV--QFDE-NGSRTNY----SLQI--------LG----LHNGVLEQ----------------
VGTW-------------------------------------------------NQKND----------PSISFFDSDTHGRKGS---
---------HDYENRT---FTITSVLDDPFLMNV-----TLPDGT--------------------SRYEGFCVDLLKKIVE--IY-
P-----FK-YRIQLVKD-G-NYGTQQ-------KN-GK--WDGMIGELMY---------G---SADISVAPLTINTDRERVVAFTK
PYMSF-GISIMIKK----MKSP-RP---------SGFSFFQPFTNEI-W---ICLALATCGVS-MIMFQICR--FSSS-EWRIETD
NSDDVSNGNRV--------------------AGAGKGVKWTNDFYILNSLWFALGAL-MQQ-G---S--DILP---RSISGRIMGG
VWWFFTLIIISSYTANLAAFLTTQSMQSPIK--SAEDL---AAQTK---IQYG-VHKGGSTVEFFR--------KSSH-PLYRKMW
SFMANT---------------------EPSPLAESTEDGVNRVR--ESDGK---------YA-YLLES-KMNEYRETQ-KP---C-
DTMAVGD--P-IGTSSY-GIA-VSK-------HLVELQKELTVAILE--LRE-RDILRRLEEK------YWV-----NRSQCVKD-
-DTDGTDT-----RALNLDKLAGVFYILLAGTAVALLVSIVDLIY---RSKKQIREEL----------------------------
----GSCGLRRIWLNVRAPAPTKSPSDGTSETGTDELSTPATA-------QKSIVPSIASEEGNVNSALCKKKSGSQGSAV-----
--------------------
```

241 Spur_GluAbeta

```
--MAIQHGKLHLTICILSSVLYVASAGYQITIFGIFDQDVTTDDPKSVGFRRGMIKYNVQSNSTGSPFQLMGFEVRVQVNNSFILT
NL------ICGAL--SQNRMLIAGDAD-------------VTTIYNAASASREVKIPYFITS--------------------FAPR
DVYPDFTAEYLLAMQPQVLQPLVDYIEYFHWTSLAYVYEGQ------TGFLRLHNFLELIR----PLGIE----------------
-VSHRRINVDTVNETLVELKDTGKH-----------RIICDTGL-ALTNTVLRTSL--D--LEMV-TASFHMVYLNL----DFDTI
DTSN------MSFG--------GMNLTGFSLITNKSSEAYQDLFGDWSDKFRDSHPTLANSN----------VGYEAILAHDLCRV
AVSAA-----------RSIHESGRELPLPRVNTYH---------------RCFKQVKEGTETVAS-------TVGPELLDAI----
-------------KRT-ATNQLSGRV--QFDG-NGSRTNY----SLQI----------------------------------------
VGLH-------------------------------------------------NGVVE-----------------------------
------------------------QDDPFLMNV-----TLPDGT--------------------FRFEGFCVDLLKKIVE--IY-
P-----FK-YRIQLVKD-G-NYGTLQ-------RN-GK--WDGMIGEVMY---------G---TADISVAPLTINTDRERVVAFTK
PYMSF-GISIMVKK----SKAP-RP---------SGFSFFQPFTNEI-W---ICLALATCGVS-IIMFQICR--FSTA-EWRIETD
NSSSDDVSNGN-----------------RATGAGKGVKWTNDFYVMNSFWFALGAL-MQQ-G---S--DILP---RSISGRIMGG
VWWFFTLIIISSYTANLAAFLTTQSMQSPIK--SAEDL---AAQTK---IQYG-VHKGGSTVEFFR--------KSSS-PLYRKMW
SFMANT---------------------EPSPLAESTEDGVRRVR----ESD-------------------------------------
---------------------------G--------KKELTVAILE--LRE-RDTLRRLEEK------YWV-----NRSQCVKD-
-TTDATET-----RALNLDKLAGVFYILLAGTAVALLVSIVDLVY---RSKEQVRNEL----------------------------
----SSCGFRRMWLNLRARI-----------------------------AHIASEEGNMNSALSKKKSGSAGSAVTHT-------
--------------------
```

```
242  Arub_GluAbeta
     -MELSSVVHGVLLLELAVFLVFPTSEAVEFYSLGGIFDDGPPPNPERMIFVQSSIRNN---IRSNSSSSSRPFLQHTKLENNAAVL
     RK------MCVVL--AYNVSLTVGMVD--------------FNVANMVASTSQQIQVPFITPS-------------------FASK
     ESFPDMDFDYVISMRPSLIQPLLDLLEYHKWKDFAYIYDGQ------RGLRRSDTFMQMFP----QYGYN-V--------------
     -VFKNLLKDRNITETLKSMAELGNH-----------LVVFDLNL-ENSVEVLRKAN--G--LGMV-TASYHYIFMDL----DISEM
     NLTE------FQAG--------GLNITGFRLL-DKNSDAYQDFIWEWRSYVKNSSYQEVDINYF--------HLSNPALSVDMMDV
     ALEAL-----------DLYRMDPSSNIKRKEKSL----------------SCNLGSSSRVIPN---------PDGPNLKEVI----
     -------------KKV-KLQGLTGNI--EFDS-DGNRANY----SLQI--------LG----LRGKTLMK----------------
     VGTW-------------------------------------------------NGANK---------QRLTFDSQGDTEAPISP---
     -----------GEGRM---YTITSILNPPFLMRK-------PGGKP-------------------NEYQGYCVDLLIEIAR--VYR
     G---PKFN-YKIELVSD-S-EFGSQM-------AN-GK--WNGMIGELMY---------G---KADIAVAPLTINVQRERVIGFTK
     PFMSV-GVSIMIKK----PMDN-KP---------SVFAFMQPLAPEI-W---MCVIFACCIVS-VVLFQVSR--FSPK-EWHRVDH
     PPSTPSGTGDY--------SSEKPGERFVTEDQEETE----NDFGIFNSLWFTVGAL-MQQ-G---C--ELCP---RSMSGRLTGG
     VWWFFTLIIVSSYTANLAAFLTAKRMVMPIS--SASDL---VDQTA---ITYG-ILKSGSSQTFFQ--------TSTV-PLYRHMW
     EFMRNS--------------------ERSPFANTTQEGVERVR--KSNGK---------YA-FLLES-AMNDYYNSQ-PP---C-
     DTMMVGS--L-LDSKSY-GIG-VSK-------HLVEVRELLTLAILE--LRE-QAALDTLQKK------WWS---GNGSSSCKVQ-
     -KVPEHLQKT---SALNLDTLAGVFYILLGGLAGALLVAGIHLFW---RSRHEIIAAKD-------------------------
     ----RYLQARRELL-------------------------------------PESKKQTLPMNKGAQSKSSGTGSHTV----------
     ------------------
243  Pmin_GluAbeta
     -------MRGVMLLVLPIAVIFSTCKAVEFYSIGGIFGDGPPPNPERMIFVQSAIRNNIRSNSSAFRPFHLQHTKLANNAAVLRK-
     --------MCVLL--AYNVSLIVGVAD--------------FDVVNMVATTSQKIQLPFITPS-------------------FALK
     ESFPDMEFDYVVSLRPSLVQPLLDMLEYNRWKQFAYIYDGK------RGMRRADTFMQIFS----RYDYD-V--------------
     -IFKHLLTEEPITETLKNMRDSGRH-----------HIIFDLSL-DASENALRKLQAND--LGMV-TASYHYIFMDL----DIGEI
     DMNQ------FQLG--------GLNLTGFRLL-DKDSDAYQDFILDWRSYVKNSSYIEVDTNYF--------HLSNPAISVDMMDV
     ALEAL-----------DMFRLDSRGSVRKKERAL----------------SCNLGTSYAPVPN---------RDGPKLIEII----
     -------------KKV-KLQGLTGNI--EFDS-RGDRTNY----SVQI--------LG----LRQTGLEK----------------
     VGTW-------------------------------------------------NGQNE---------NRLTFDTFTEDESPADA---
     -----------MSGRI---YTVTSILSPPFLMLK-------KDADQRRGI---------------DKYEGYCVDLLEEIVK--VY-
     KSKHSIFR-YKIKLVAD-G-EYGAQM-------EN-GK--WNGMIGELIY---------G---KADIAVAPLTINVQRERMVGFTK
     PFMSL-GVSIMIKK----PQDN-QP---------GVFTFMQPLAPEI-W---MSIVFACIIVS-VVLFQVSR--FSPK-EWHPVEH
     PPPTPSGTGEF--------NLNKPGERFVTEDREETE----NDFGIFNSLWFTVGAL-MQQ-G---C--ELCP---RSFAGRVTGS
     VWWFFTLILVSSYTANLAAFLTAKRMVMPIS--SAADL---VDQTT---ITYG-ILKSGSTETFLK--------TSTV-PVYRHMW
     EFMANS--------------------EDSPFANTTEEGVERVR--KSNGK---------FA-FLLES-AMNDYYSQQ-PP---C-
     NTVRVGN--L-LDSKSY-GIG-VNKQLVD-------VRELVTLAILE--LQE-QAILTRLEKK------WWT----SNNESCRIP-
     -NIPDHMSKT---SALNLVTLAGIFYILLGGLAVALLVAGGNLFW---RSRHEIIAAKS-------------------------
     ----RYIEKHKA-------------------------------------RSPENKKLPANPEAQTKGNGSHTPV----------
     ------------------
244  Apla_GluAbeta
     ---MALTVYGVILLILPIAVVFPTSQAIEFYSIGGIFDDGPPPNPERLIFVQSVICNNIRCNRSEERPFQLQHTKLANNAAVLQT-
     --------MCVLL--ANNATLTVGVAD--------------LDVVNMIATASKQIKVPFITPS-------------------FALK
     ESFPDMKFDYVVSLRPSLIQPLLDLLDYNHWKQFAYIYDGK------RGMRRADTLMRIFP----RYGYD-V--------------
     -TFKHLRMEEPITETLKNMRDSGRH-----------HIIFDLSL-EASERALRKLQAND--LGMV-TASYHYIFMDL----DIGEI
     DMNQ------FQLG--------GLNLTGFRLL-DKESDVYQDFIVDWRSCVRNNSYIDVDTKYF--------HLSNPALSLDMMEV
     ALEAL-----------NKFRLDKRESVKKKERTR----------------TCKLGMSSALVPS---------SEGPILINII----
     -------------KKV-KYQGLTGNI--EFDS-QGDRVNY----SVQI--------LG----LRQTGLEK----------------
     IGTW-------------------------------------------------NGQNE---------NRLTFDTFTDDETSTDA---
     -----------MSGRI---YTITSILSPPFLMLK-------PDADQRRGI---------------DKYKGYCVDLLEEIAK--VY-
     RNKHSTFR-YKIKLVAD-G-EYGTQM-------EN-GK--WNGMVGELMY---------G---KADIAVAPLTINVQRERVVGFTK
     PFMSL-GVSIMIKK----PQDN-QP---------GVFTFMQPLAPEI-W---MSVFFACVIVS-VVLFQVSR--FSPK-EWH----
     -RVEHPPPTPS---GIGEFSLNNPSERFVTEDREETE----NDFGIFNSLWFTVGAL-MQQ-G---C--ELCP---RSFSGRLTGS
     VWWFFTLILVSSYTANLAAFLTAKRMVMPIS--SASDL---AEQTS---ITYG-TLASGASETFFK--------TSSV-PIYRHMW
     EFMSNS--------------------EDMPFANTTEEGVERVR--KSNGK---------YA-FLLES-AMNDYYNQQ-PP---C-
     NTMRAGN--L-LDSKSY-GIG-VNKQLVD-------VREFLTLAILE--LQE-GAILNDLQKR------WWT----SQNESCRIP-
     -PVPDHMTKT---SALNLETLAGIFYILLGGLAVALLVAGGNLFL---RSRHELIAAKN-------------------------
     ----RYIAKRKE-------------------------------------RIQGNNVQANLKACCKGASSHTPV----------
     ------------------
245  Cgig_GluKdelta
     RRVPNIKMPWIIPLCLLCFTPVICGTSFQQFRVDGFFGDSNIGAINMFKWAMQQLNME---NLKHPGTPNANYTQSVTGDDPFEAG
     NH------VCEAI--NNGSRVIFGPFT--------------RASANHVQSVGRSLQIPVLQAH---------------WDPRDLIT
     NRDRIPAHVNLYPSYGNLSQGFREIIQQFGWKNLTVLYEDD------DGLIRAQEILKLEP----DIHVY----------------
     -LRKMEDHPEMLYRMFIDMKDKKEY-----------RVVLDCKT-SNIFSILQKAL--Q--CNAL-TEDFHYFLTNL----DLHMV
     DLES------FKYS--------GANITGVSLI-DINSRVVAEVKSKIAESFSSNDAPYSPFYNGPQE-----ITTELAFIYDSVRL
     LGEAL-----------NGTLASRKKLNFSQAV-----------------GCGRSPAW--------------EDGRDFYDFI----
     -------------KSSTVFDGLTGKV--QLGN-FGERNMF----KLNI--------YQ----LSNSNLKH----------------
     IGFW-------------------------------------------------EPPNS----------LTMQLIHRNKTRNPGL---
     --------------AT---YKVVVVLVEPYVIKK-------------------------------EGKYEGFCIDIMDALAQ--RL-
     N-----FR-YEVIESPN-N-VYGNCME------FNNGTVSCDGMVKMLVD---------Q---QVDMAITGFTITHSRAKYIDFTK
     PFMNL-GITVLFRK----PKPD-PP---------QLMSFLAPLDNTV-W---AGIITVFLGIS-LVLLITAR--FTPY-EWI----
     ------NPHPC-------------------DPTTEEVE----NQFTPLSSLWYVIAAL-MQQ-G---C--ELAP---VAVSTRTLAA
     VWWFFTLILISSYTANLAAFLTVENVVSPIE--SAEDL---ASQTE---IKFG-TTEGGSTMDFFK--------SSNN-PTYLKMF
     DIMERA--------------------NPPVWANIEEGERRVL----QGD---------YA-YLSES-SSIEYRVER-----NC-
     DLMQVGN--W-LDSKGY-GIG-LPK---D---SD--LTDEVSREVIK--LQE-EQIIQSMYDK------WWK---QKKDVDCSGG
```

```
-KTQTT-------NPLTMENVGGIFLVLMIGTFFGLIVALGEFLW---IARQNARKYKS--------------------------
----HWRSEICK--------------EFRFEWKCG---------------KSNVLQSIPLTKSYVKANGGQDITYDTNTSDDV---
--------------------
246 Lvar_GluAalphaalpha
-----MEGKILQSIVIACLIILLWTSYSASSSTIMVGGVFDRYRDFGFERGIISHNTQ---KNKSSAFQFMAYVLPALLEDPFNVT
RR------LCKLY--DQNTIITGGHSK--------------LVCLPTLQSYANNFLIPYVTVS------------------QSKSD
MGLTFSSSDYLVSMMPSLVPPVEDCVRYFGWDKFVYIYSSA------EGLQRYNTLSARFP----PDKYD-I--------------
-LVRRVGSEIETRNLLKRFRDSGHH-----------RIIFDTTG-NDTQLVLKQVD--A--LGMI-TKSFHYIFLDL----DLADV
SVDE------FLFG--------GMNITGFQLV-NKTDPYYQNIENMWYKRQAYLRQGNVTSNPS---SALGYLKTLTALTYDVTRV
FWETI-----------VLLKTTGRLPSLTARQRR----------------LCSSTGFLKI------------PQDREVLEYI----
-------------KKL-SFKSATGNV--EFDE-NGERSNY----TLRV--------LG----LKPSGLKE----------------
VGTW-------------------------------------------------QSNNK---------TRLTINEEDPKLFLQDI---
-------------NKT---FIITSVFESPFMMLK-----DEKDQTP--GN---------------GRYEGYCVDLLHAINE--HH-
P-----FK-FIFRVRND-S-AYGNAD-------EN-GT--WDGMVSDIMT---------K---KADIAVAPLTINSERQRVIDFTK
PYMSL-GISIMIKK----PQHT-HP---------SVFSFMHPLSYEI-W---LSIIFAYLGVS-VVMFLISR--FSPD-EWY--PV
EKGSLKSAPST------------EGDLDRVEPGDKKE----NNFGIQNSMWFSLGAL-MQQ-G---C--EVSP---RCLSGRIVGA
VWWLFTLIIISSYTANLAAFLTVQRMSTPVN--SADDL---VKRKD---ISYG-IQGGGSTENFFS--------SSNI-PLYMTMW
KSMTSA-------------------Q--PSPITNSSVQGIDRVR--NANGK---------YA-FLLES-TMNEYQNQQ-KP---C-
DTMKVGS--N-LDSKSY-GIG-VAR-------DLTMLRDELTLAILQ--LGE-DGVLDNLKKK------WWY-----DKGKCEPE-
-SESIDMQA----SALSLSSVAGIFYILMAGMGTAIGVALIEFYWRNHRNRSQSNKEKT--------------------------
----SLSLALKA--------------KIRMSVTGEKGIPTYPI-------MREVNAMACEKALLSKDRESPSAIRRGQTSV-----
--------------------
247 Lvar_GluAalphabeta
-----MAGKMSHALVVVCMGTLFRTCCSAGSSTIMVGAVFDRYLDFGFERGIISHNTQ---KNKSNSFQFMALELPALLEDTFNVT
RR------LCTLY--SQNTLITGGHSK--------------QVCLPTLQSYANYFLIPYVTVS------------------QSKSD
MGLTISSSDYLLSMMPSLVPPVEDCVKYFKWDKFAYVYSSQ------EGLQRYQTLSSRFP----SKQYD-I--------------
-TVRRVGSEPETRLLLKSFRDSGRH-----------RIIFDTTG-NDTQLVLRQAS--M--LGMI-TSSFHYLFLDL----DLADV
NMDD------FIFG--------GMNVTGFQLV-NKTDPHYKSLEMMWYKRQAYLRQGNQTFDWPQNISSLGYLKTMTALSYDVTRV
FWETI-----------SMLKKNKRIQLLTVRAAR----------------SCGNPGFKKI------------PQDKDVLEYI----
--------------KLISFKSATGHI--EFDE-NGERANY----TLKV--------LA----LKPTGLQE----------------
VGTW-------------------------------------------------MPNVP-NSNSNSPLLSRLVLKGENSENSFQN---
------------VNKT---FIITSVLERPFMMLK-----NEKARTP--DN---------------GRYEGYCMDLLHAINE--HH-
P-----FK-FIIRVRND-S-AYGTAD-------DN-GT--WNGMVSELIN---------K---EADIAVAPLTINSDRERVIDFTK
PYMSL-GVSIMIKK----PQNT-RP---------SVFSFMHPLSYEI-W---LSIIFAYLGVS-VVLFLVSR--FSPD-EWYTVEQ
GTLSSAPSTEG--------------EIDRDEPRDKKA----NNFGIQNSLWFSMGAL-MQQ-G---C--EVSP---RCLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMSFPIN--SAEDL---VKRKD---ISYG-IQRGGSTQSFFS--------TSKI-PLYNTMW
RSMSNN-------------------NTLPSPMTNSSVQGIERVR--HSNGK---------YA-FLLES-TMNEYQNQQ-KP---C-
DTMKVGS--N-LDSKSY-GIG-VAR-------DLTLLRDELTLAILQ--LGE-DGVLDNLKKK------WWY-----DKGECDPQ-
-SQAMDQA-----SALSLSNVAGIFYILVVGMGVAIGVALTEFYW---RTRSQSNKEKI--------------------------
----SLSNALKA--------------KIRMSVTGEKG-----I-------MRQVNPMACEKALLSKDRESPSAIRRGQTSV-----
--------------------
248 Spur_GluAalpha
-----MAGKMFQALVIVCATILMWTTYSNGSSTIIVGGVFDRIRDFGFERGIISHNTQ---KNKTSAFQFMAYVYPALLEDTFNVT
RR------LCTLY--AQNTLITGGHSK--------------QVCLPTFQSYANYFLIPYVTVS------------------QSKSD
MGLTIGPSDYLVSMMPSLVPPVEDCVKYFKWEKFAYVYSSA------EGLQRYQTLSLKFP----PRKYD-I--------------
-MVRRVGSEVETRRLLKSFRDSGRH-----------RIIFDTSA-NDTVLVLKQAN--V--LGMI-TSSFHYIFLDL----DLADV
NMDN------FLFG--------GLNVTGFQLV-NKTDPYYKNLELMWYKRQAYLRQGNTTFDPSQDNSAMGYLKTMSALTYDVTRV
FWETI-----------SMLKKNKRLPILTVRGAR----------------SCSNPGFKKI------------PQDKDVLEYI----
--------------KMLSLKSATGNI--EFDE-NGERANY----TLRV--------LG----LKPSGLQE----------------
VGTW-------------------------------------------------LPNAN----------PRLTIKGEDKQNFLQD---
------------INKT---FIITSLFERPFMMLK-----NEKDRTP--GN---------------GMYEGYCMDLLKAIND--HH-
P-----FR-FVIRVRND-S-AYGSAN-------EN-GT--WDGMVSELIN---------K---EADIAVAPLTINSERERVIDFTK
PYMSL-GVSIMIKK----PQNT-RP---------SVFSFMHPLSYEI-W---LSIIFAYLGVS-VVLFLVSR--FSPD-EWYTVEQ
GTLSSAPSTEG--------------EIDRVEPRDKKA----NNFGIQNSLWFSMGAL-MQQ-G---C--EVSP---RCLSGRIVGG
VWWFFTLIIISSYTANLAAFLTVERMSTPIN--SAEDL---VKRKD---ISYG-IQGGGATEVFFS--------------------
-------------------------------------GIERVR--HANGK---------YA-FLLES-TMNEYSNQQ-KP---C-
DTMKVGS--N-LDSKSY-GIG-VAR-------DLTLLRDELTLAILQ--LGE-DGVLDNLKKK------WWY-----DKGECEPQ-
-SESMISLS----NALKAKIRMSV----TGEKGMPTYPIMRQ----------------------------------------------
-------------------------------------------------VNPMACEKALLSKDRESPSAIRRGQTSV--------
--------------------
249 Anja_GluA
------MRHCEGLTVSLFLVYVGLCKTYGKYMIGGLFPEGYMHNQTMISYKRALIQHNVRSNSTLHKYQIAALSDRGDLSDSFVVS
GLICKCFNTCKYIKNTGPLCFAAVVH---------------SNTVQTMASYSTAFAVPFITPS--------------------FAKT
EALNKDNLDFMVSVRPPLIDALIDLMKFKKWNAFAYFYGHD------EALFRLQALIERLS----LKDFN-V--------------
-AFRRIGDRNEIEAALRELMRLKIY-----------NIVIDADV-PITQSTMEIVD--V--VGVN-TALYTFVLLQL---------
-DSQTIDKESMKYR--------GATTLAFRLS-FQTTDIIYKGLEEKWEKHRKLHPDAFKNQGT--------LLATAILTYDMVDT
IVEAL-----------RLAEEKNVSLIAPPQ----------------------NCQEKVAW--------------SRGPLMLEYM----
-------------KKV-DIQGLSGRI--AFNA-IGDRTNY----TLDV--------LR----LRGTGLVK----------------
IGVW-------------------------------------------------NSSLT------------EAERQKVFSTPDNN---
---------ETLQNRT---FTVTSILEKPFLIKK-------VGTTPADGN---------------EQYEGYCKDLLDELSK--HL-
K-----FK-YKLQLVKD-G-EYGTYD-------ETLGR--WNGMIGEIKD---------G---TADMAVASLTINAQRERDVLFTK
PFMTL-GISIMVKK----PLDP-SP---------DPFSFLRPLSTEI-W---LCIIFAYTGVS-VVLFLVSR--FSPT-EWYTVRE
DGDVSPTPVED----------------SSTEEDEPKT----NDFGIFNSLWFSMGAF-MQQ-G---C--EISP---RSLSGRIVGG
```

```
VWWFFTLIIISSYTANLAAFLTVERMDSPIE--SAEDL---AKQTD---ITYG-TLASGASFEFFK--------NSKI-HVYERMW
NFMQST--------------------DPPPFVKTNQQGVNRVR--QSDGK---------YA-FLLES-TVNEYHNQQ-LP---C-
DTLKVGS--N-LDSKGY-GIAVSPN-------LPK-LREQLTLALLE--LRDWNNTLQHLQKK------WWY-----FKGNCDPT-
-DSNSQGTA----SALTLSSVAGVFYILICGLALAIIVAILEFCM-----------------------------------------
----RSRKHMRQTRKPSKSTSYPTISKAALRDDDPANHP----------MLQTREQMLKLHGMETRCSNRR--------------
------------------
Lgig_GluKalpha
---------------MPLGLQHGDRLSAVFRLGALFEPEFDGQKQSFEWAVEKINLR---TDILGQTLVLDDDQVVQAQDSFGAQ
RK------VCRMV--QQGVAAIFGPIS-------------SLSAAHVQSMCNAFEIPHLQWH----------------WDPRDS
RDYYS---ISLYPHYLTLSGAYKDLVKFWAWEEFTVLYEDN------DGLTRLQEVLKAPE----GNTAR-LT-------------
-VRKLRVINNDYVNLFKDLKERRAT----------RIIIDCHV-SRVKKILHAAL--K--VHMV-SEYYHYLFTTL----DLGLV
DLED------YRHG--------GANITALRLI-DPERREVIDVRTEWLLEERRSGKSPLMGQSE--------IQTETALAYDAVHL
FARAL----------HELSQAQDVTTSIL--------------------SCDKSQTW--------------NHGNSLLNYM----
-------------KSM-NFDGLSGNI--RYEK--GERVDF----SLEV--------ME----LTENGLKK----------------
TGTW-------------------------------------------------NRLSG---------VNITLDYKEKQVERAKS---
----------LSNHT---LVILVKLDEPYVIKR-------------GE--------------GDYIGFCIDLLRIIAK--KR-
N-----FT-YVIKEADG----YGSQ--------RN-GK--WDGIVGQLMD---------R---KADIGLGGMSITHEREEVIDFTK
PFLTL-GITILFAK----PVPK-AP---------QLFSFLSPLSVEV-W---VYVIAAYLCVS-FMLFVIAR--FSPY-EWC----
------NPHPC-----------------NENTDIVE----NQFTILNSLWFTIGSL-MQQ-G---C--EIAP---RAISTRLVAG
MWWFFTLIIISSYTANLAAFLTVERMISPIT--GAEDL---AKQSS---IAYG-TVRGGSTMSFFA--------NSKI-DTFKRMW
SFMNSS----------------------SDNFVDSNKEGVARVK----AGG---------YA-YLAES-TAVEYTVER-----NC-
ELEQVGG--L-LDSKGY-GIA-TPR---N---SP--YRELITESILK--LQE-EQEIHRLHSV------WWK--QYGKAGKCRQD-
-DGGAKSKA----NELGVDNVGGVFVVLLGGVGAGFIVSLCEFIW---KARKNAREDEQ--------------------------
----TLCSEMAE-------------EFRFAVRCVSSKKPSKNR------TKDVTDNGLQFMPLTGYGHNSVGGKEV---------
------------------
Bgla_GluKalpha
---MQPRYDLHFRIVIVMVAVKLATSLPERLLIGALVEKEYEGHWRAIEKAVENLNLN-----LFQNMVVIVDRDTIQPQDSFQAQ
KK------VCRMS--QTGIAAMFGPVS-------------SLAAGHVQSICNAFEIPHLQWR----------------WDARDN
RDYFS---INLYPHYLTLSKAYKDAIQHWGWDQFTILYENN------DGLTRLQEVLKTSDEIKTPQITV---------------
-RKLEAISNSDYVSVLKDLKRRGEF----------RFIIDCDL-RSITKILHAAL--K--IKMI-SELFHYFFITL----DLGLL
DLED------YRYG--------SANITAYRLI-DPARDKVVNVKTDWLRHAKKGHESPLMGYAEIEGNSSHTLLTETALAYDAYEL
FAYAL----------MAYSKVQEVATMNQ--------------------PCDKMYTW--------------RHGNSLLNYM----
-------------KSS-AIEGLSGLI--KYDG--GERMDF----VLDL--------LS----LTPKGLEV----------------
VGKW-------------------------------------------------DRKHR-----------LNITRENVTPTDTK---
----------ITNKK---LIVTTYITKPYVMKD--------------------------NVTGQYYGFCIDLLNEIAK--TR-
N-----FT-YEIQIESKVGKRIGNN--------NN-----WDGVMGALVN---------R---KADIGIGDLTINLVREQAVDFTK
PFLTL-GITILFKK----PAPK-AL---------NLFSFLSPLSFDV-W---VYMIAAYLCVS-FMLFVIAR--FSPY-EWC----
------NPHPC-----------------NPDTDEVE----NQFSVMNSLWFTIGSL-MQQ-G---C--EIAP---RALSTRLVAG
MWWFFTLIMISSYTANLAAFLTVERMVSDIN--SADDL---AKQSK---IKYG-LYGGGATQEFFE--------KNQL-PLYIGMW
EYMNRT---------------------KEHNFVKSLDEAIQKVK----KGD---------YA-YITES-TTAEFVIHR-----HC-
DLMKVGG--L-LDSKGY-GFA-TPT---G---SP--WREDLTEEILR--LKE-NQFIDQLYTR------WWT--KEMEAANCDTE-
-KSASASSA----NELGVENVGGVFVVLMGGVVVGFFVSLCEFIW---KARKNAKKDKQ--------------------------
----TLCSEMSE-------------EFRFAVHCFGSKKT----------KKKQDDEITDNGLQFMPLTGSRQHVHNKEV------
------------------
Acal_GluK
---MQFMTSLWLCLVCMVALIHLTKAMPERLRIGALFEPDYEGQWRALEWAVEEINLK---SDLLAGTLVLVDRDTVPPQDSFTAQ
RK------VCRMS--QEGIAAMFGPVS-------------AMTAAHVQSMCNAFEIPHLQWR----------------WDPRDK
RDYFS---ISLYPHYLTLSTAYKDVVQYWNWNRFTILYEDN------EGLTRLQEVLKAAE----RTPAQ-IT-------------
-VRKLEMVNSDYLVLLKELQNRGEY----------RFIVDCNV-KTVTRFLHAGL--K--LKMI-SELYHFFFTTL----DLGLL
DLSD------YMHG--------GANITAYRLI-DPDREKVISVRTSWLFRSKIGDKSPLMEYSE--------IDTETALAYDAYVL
FAKAL----------HSLSEAQEVNTISL--------------------PCDKVHTW--------------RYGNSLLNYM----
-------------KAM-KFEGLSGTV--KYE--NGERYDF----DLDL--------LY----LTQNGLHK----------------
VGKW-------------------------------------------------NRKSG-----------LNVSLQAAEAVDQG---
----------PGNKV---YVVSAYETEPYVIRN--------ASSP------------------SGFSGFCVELLDMIAK--AK-
N-----FS-YRIELTDT----VGKEQ-------SN-GS--WNGVMGALID---------R---KADIGIGDLTINLVREQQVDFTK
PFLTL-GITILYKR----PAPK-SL---------NLFSFLQPLSVDV-W---VYMIAAYLCVS-FMLFVIAR--FSPY-EWC----
------NPHPC-----------------NPDTDEVE----NQFTVMNSLWFTIGSL-MQQ-G---C--EIAP---RALSTRMVAG
MWWFFTLIMISSYTANLAAFLTVERMVSDIN--SADDL---AKQTK---IKYG-TFAGGATQEFFQ--------KSNM-PPFDRMW
NFMNAT---------------------GESAFVQNLTEAVERVK----TGD---------YA-YITES-TTVKFVVER-----NC-
NLMQIGG--L-LDTKGY-GFA-TPQ---G---SS--LREHLTEEILR--LTE-LQDIERLRVK------WWE--KELGGGKCHKE-
-EGSMAGKA----NELGVENVGGVFVFLMGGVVIGFFVSICEFVW---KAKKNAKKDKQ--------------------------
----TLCSEMSE-------------EFRFAVRCLGSKKS----------KKKENDEITDNGLQFMPLTGYNQNAYGKE-------
------------------
Cgig_GluKalpha
-----------------------------MSNHAMVGYEDTALELAFKETMNKAQQS---LLYGNKNLKIEDFSRVNLEDSYEVS
GE------VCKVI--SFGSEVIFGTHS-------------RSSSEYVTSLCNQLSIPNLQIH----------WDSREVVTSKRPD
RDHMT---LNLYPDHHTLSAAQRDLIKFWDWKKFAVLYEDN------DGLIRLQSILKLSF----KGRVA-ITT-----------
-RKINFLNPESVKNVLKDLKNTEHQ----------RIIVDCHY-DRVHDILKEAA--E--TEAL-SEYFHYHFMTL----DLGVT
DISE------FSEY--------GANITALRLV-NPEHGAVKNLTEEWKQLQFNIRGNRSPLRKGQLQ-----IPTETALMHDAVWV
LTEAA----------LALNEANPTALASYSRA-----------------SCDKAAPW--------------EFGADLLGYM----
-------------KSV-NVDGLSGTI--QFGQ-YGQRENF----ELEV--------------VKFSHEFKKVQK------------
IGTW-------------------------------------------------NSLSF--------------LNITDDNESLS---
----------QLNKT---LKVLTVLEMPYAGKK----------IDEYGN--------------VKYEGFCIDILDYIAE--SM-
```

```
K-----FK-YEIQEEPTYG-NCDEKE--------------CTGMYQKLID---------R---EADLAVAGITITSAREKFVDFTK
PFWNL-GITILFRK----PKAK-------PV---RLFSFLDPFHEDV-W---VYMIAIYLCVS-FMFFVIAR--LTPY-EWC----
------NPYPC------------------NQEEDIVE----NQFSVLNSMWLTIGSI-LQQ-G---C--ELAP---RTVSTRMVAG
VWWFFTLIIISSYTANLAAFLTAGRMQSPIE--SAEDL---SKQTD---IKYG-TLQTGSTYSFFQ---------NSIFPIYQRMF
TFMKNQ--------------------NPPVFVKNSNEGEKRVL----QGD---------YA-YFAES-TTVEYKVER-----NC-
DLTQIGN--W-LNSVGY-GIA-LPK---G---SP--YKDKISQRILY--LQD-KQVIKQLYSK------WWT--KMYINQTCDNE-
-KKEPS-------NALSIQNLGGVFVVLVGGIGVSIVIAVFEFIYYYSDRWKKDLERSSFSLSPIGRDQTQVSIGAALMYDAIKVL
YRALDLLTTMRNVDFKRKISCDEGTVEYRTARNCDLMQVGQQLDSKGYGIKFCDNTKTPSTKALELRNVGGVFVLVLTGTFCGFVI
ALIEFVCNARKISRKGEST
```

254 Ajap_GluKalphaalpha

```
----------------------------------------------------------------------------------------
----------------------------------------------------------------------------------------
-----------------------------------------------MDLRRYSEGGAELA---------------------------
-VFHLIDKSDEYSLDIVNTWRGNAT-------------------------------------IEVI-GNGTEYQLAGM---------
----------------------------------------------------------------------------STDAALSYDAIHA
VSRAL-----------WALNVSRDVTAESL--------------------SCDNVRRRS-------------VNGVSLYDSI----
-------------KNV-NFDGLTGRV--NFT--NGMRSVP----HLHV--------SS----ITEGGLTK----------------
RGSW-------------------------------------------------NTSSG------------------IFLKPLAR---
-------DEILNFNRT---LRITTVLENPYVMRR-----HSEGGTPLTGN---------------DQYEGYCIDLMRNIAK--IV-
N-----FD-YEIHLVAD-G-DYGSED-------PETGE-------------------------------------------------
----------------------------------------------------------------------------------------
----------------------------------------------------------------------------------------
----------------------------------------------------------------------------------------
----------------------------------------------------------------------------------------
----------------------------------------------------------------------------------------
----------------------------------------------------------------------------------------
----------------------------------------------------------------------------------------
--------------------
```

255 Cmil_GluK4

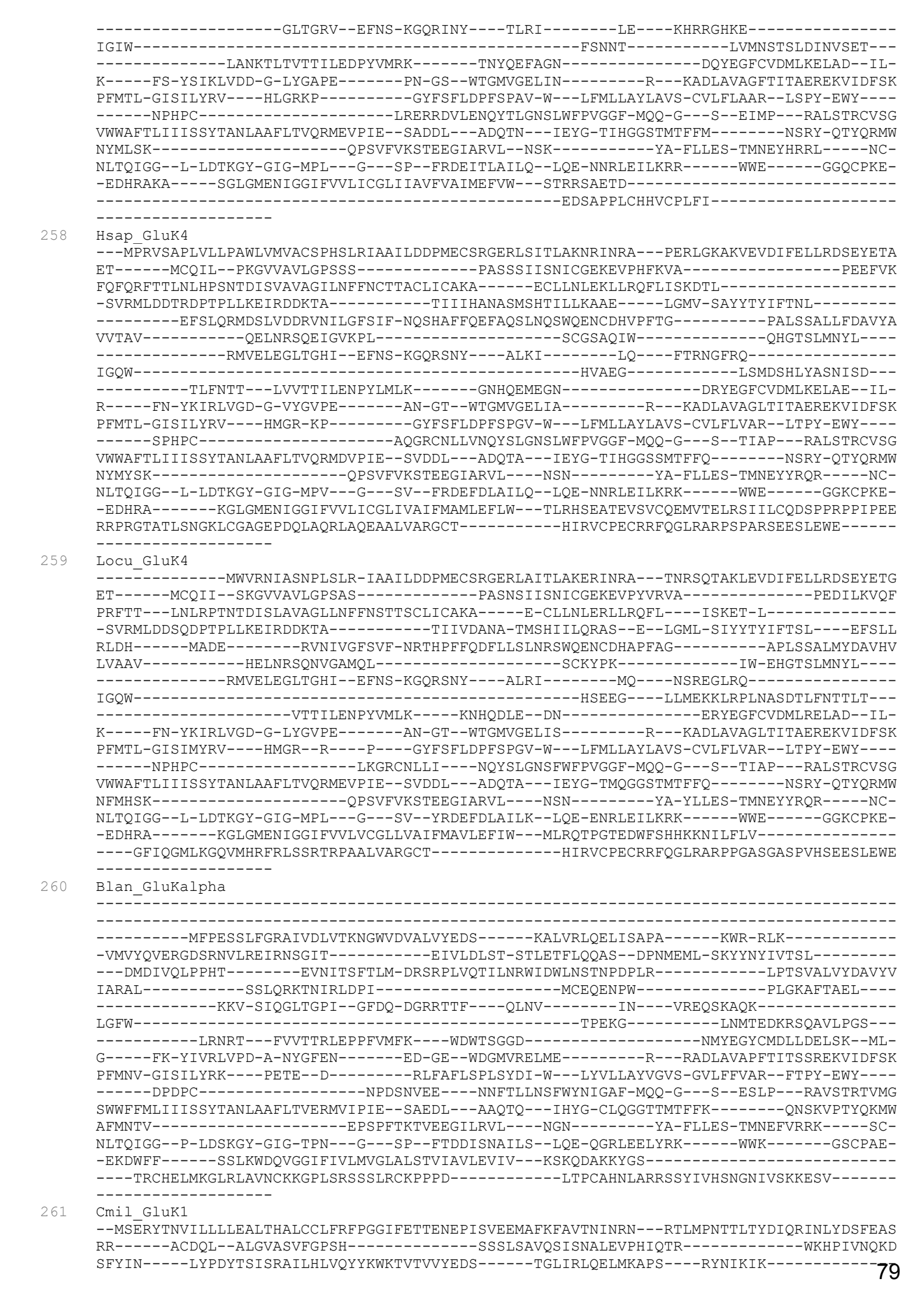
```
---SPSILYFLIIILFTTTCIILKSKQRQMYCFTADQMECSRGERLAITLAKNHINRL---LELSDNPKLEIDIFELLRDSEYETA
ET------TCQIL--PKGVVAILGPSSS-------------PASASIISHICGEKEVPHVKVA-----------------AEEIPK
WQYLRFTALNLHPSNTDISHAVTSILTFFNRSVACLICAKA------ECLLNLEKLLRQFL----ISKDT-L--------------
-SIRMLDSSQDSTPLLKEIRDDKIV-----------TIIIDASA-LVSRSILKKAV--E--LGMT-SVSYKYIFTSL----EFPLL
QLDE------LIED--------HMNILGFSIT-DSNHLHFSDFVYNLNRSWQENCAHAAYPG----------PALSSALLFDAVHV
VVTAV-----------HQLNRSQEIAIRSL--------------------SCGSAQIW--------------QHGTSLMNYL----
--------------RMVELEGLTGHI--EFSS-KGQRVNY----VLKI--------VQ----HSKEGLREVRQM------------
LGVC-------------------------------------------------------------LLLEAFILMLRFSKDC---
---------------------DVSPQENPYVMLK-------LNHQQLEGN---------------ERYEGFCVEMLQELSN--LL-
R-----FK-YKIQLVAD-G-VYGVAE-------PN-GT--WTGMIGELVT---------R---KADLAVAGLTITAEREKVIDFSK
PFMTL-GISILYRV----HMSR-KP---------GYFSFLDPFSPGV-W---LFMVLAYLAVS-CVLFLIAR--LTPY-EWY----
------MPHSC---------------------LKGKCNMLVNQYSLGNSLWFPVGGF-MQQ-G---S--EIMP---RALSTRCVTG
VWWAFTLIIISSYTANLAAFLTVQRMDVPIE--SVDDL---ADQTN---IGYG-TIQGGSTMTFFQ--------NSRY-QTYQRMW
NYMHSK---------------------QPSVFVKSTDEGIARVL----KSN---------YA-FLLES-TMNEYHRQR-----SC-
NLTQIGS--L-LDTKGY-GIG-LPI---G---SV--FRNEFDLAILQ--LQE-NNRLEILKRK------WWE------GGKCPKE-
-GDHGA-------KGLGMENIGGIFVVLICGLFVAIVIAVVEFIW---KMRQSTETEISVCQEMLREVRSIVLCQESPSNTEPPLT
GNSRALSNGKLYAGHLTDSISQHLAHSAAMTVRRCT--------------HIRVCPECRRFQGLRPRPMGSPLQRR----------
--------------------
```

256 Hsap_GluK5

```
----MPAELLLLLIVAFASPSCQVLSSLRMAAILDDQTVCGRGERLALALAREQINGI---IEVPAKARVEVDIFELQRDSQYETT
DT------MCQIL--PKGVVSVLGPSSS-------------PASASTVSHICGEKEIPHIKVG-----------------PEETPR
LQYLRFASVSLYPSNEDVSLAVSRILKSFNYPSASLICAKA------ECLLRLEELVRGFLISKETL--------------------
-SVRMLDDSRDPTPLLKEIRDDKVS-----------TIIIDANA-SISHLILRKAS--E--LGMT-SAFYKYILTTM----DFPIL
HLDG------IVED--------SSNILGFSMF-NTSHPFYPEFVRSLNMSWRENCEASTYLG----------PALSAALMFDAVHV
VVSAV-----------RELNRSQEIGVKPL--------------------ACTSANIW--------------PHGTSLMNYL----
--------------RMVEYDGLTGRV--EFNS-KGQRTNY----TLRI--------LE----KSRQGHRE----------------
IGVW-------------------------------------------------YSNRT------------LAMNATTLDINLSQ---
----------TLANKT---LVVTTILENPYVMRR-------PNFQALSGN---------------ERFEGFCVDMLRELAE--LL-
R-----FR-YRLRLVED-G-LYGAPE-------PN-GS--WTGMVGELIN---------R---KADLAVAAFTITAEREKVIDFSK
PFMTL-GISILYRV----HMGR-KP---------GYFSFLDPFSPAV-W---LFMLLAYLAVS-CVLFLAAR--LSPY-EWY----
------NPHPC---------------------LRARPHILENQYTLGNSLWFPVGGF-MQQ-G---S--EIMP---RALSTRCVSG
VWWAFTLIIISSYTANLAAFLTVQRMEVPVE--SADDL---ADQTN---IEYG-TIHAGSTMTFFQ--------NSRY-QTYQRMW
NYMQSK---------------------QPSVFVKSTEEGIARVL----NSR---------YA-FLLES-TMNEYHRRL-----NC-
NLTQIGG--L-LDTKGY-GIG-MPL---G---SP--FRDEITLAILQ--LQE-NNRLEILKRK------WWE------GGRCPKE-
-EDHRA-------KGLGMENIGGIFIVLICGLIIAVFVAVMEFIW---STRRSAESEETPALHPAACQCS----------------
----ALFSSLKPSPDLTFPPSHRPLSSLLFTALAAVGGLPD---------ASSFFFPPISSCPPLQSGIGPCHSTEA---------
--------------------
```

257 Locu_GluK5

```
----------------------------------------------------------------------------------------
----------------------------------------------------------------------------------------
----------------------------------------------------------------------------------------
-------------------------------------MFVHLSACLFVHLSLCLPV-----------------------------
---------------------SLPVSDLRA-------------------------------------------PISPSQVEYD----
----------------------------------------------------------------------------------------
```

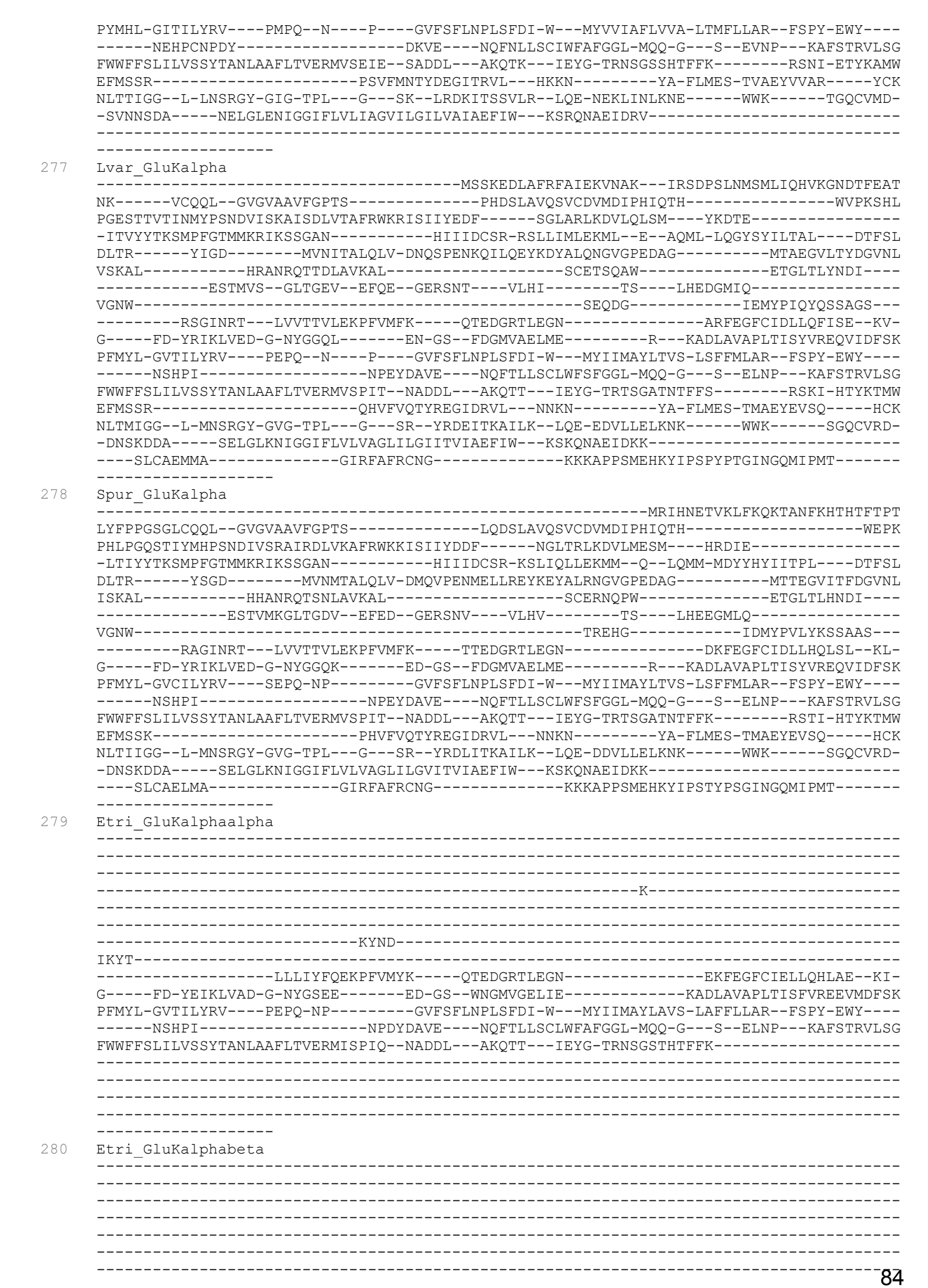

------------------GLTGRV--EFNS-KGQRINY----TLRI--------LE----KHRRGHKE----------
IGIW---FSNNT----------LVMNSTSLDINVSET---
-------------LANKTLTVTTILEDPYVMRK-------TNYQEFAGN--------------DQYEGFCVDMLKELAD--IL-
K-----FS-YSIKLVDD-G-LYGAPE-------PN-GS--WTGMVGELIN---------R---KADLAVAGFTITAEREKVIDFSK
PFMTL-GISILYRV----HLGRKP----------GYFSFLDPFSPAV-W---LFMLLAYLAVS-CVLFLAAR--LSPY-EWY----
------NPHPC---------------------LRERRDVLENQYTLGNSLWFPVGGF-MQQ-G---S--EIMP---RALSTRCVSG
VWWAFTLIIISSYTANLAAFLTVQRMEVPIE--SADDL---ADQTN---IEYG-TIHGGSTMTFFM--------NSRY-QTYQRMW
NYMLSK---------------------QPSVFVKSTEEGIARVL--NSK----------YA-FLLES-TMNEYHRRL-----NC-
NLTQIGG--L-LDTKGY-GIG-MPL---G---SP--FRDEITLAILQ--LQE-NNRLEILKRR------WWE------GGQCPKE-
-EDHRAKA-----SGLGMENIGGIFVVLICGLIIAVFVAIMEFVW---STRRSAETD-------------------------
---EDSAPPLCHHVCPLFI--------------------
----
258 Hsap_GluK4
---MPRVSAPLVLLPAWLVMVACSPHSLRIAAILDDPMECSRGERLSITLAKNRINRA---PERLGKAKVEVDIFELLRDSEYETA
ET------MCQIL--PKGVVAVLGPSSS------------PASSSIISNICGEKEVPHFKVA----------------PEEFVK
FQFQRFTTLNLHPSNTDISVAVAGILNFFNCTTACLICAKA------ECLLNLEKLLRQFLISKDTL--------------------
-SVRMLDDTRDPTPLLKEIRDDKTA----------TIIIHANASMSHTILLKAAE-----LGMV-SAYYTYIFTNL---------
---------EFSLQRMDSLVDDRVNILGFSIF-NQSHAFFQEFAQSLNQSWQENCDHVPFTG----------PALSSALLFDAVYA
VVTAV----------QELNRSQEIGVKPL--------------------SCGSAQIW--------------QHGTSLMNYL----
--------------RMVELEGLTGHI--EFNS-KGQRSNY----ALKI--------LQ----FTRNGFRQ----------------
IGQW---HVAEG-----------LSMDSHLYASNISD---
----------TLFNTT---LVVTTILENPYLMLK-------GNHQEMEGN---------------DRYEGFCVDMLKELAE--IL-
R-----FN-YKIRLVGD-G-VYGVPE-------AN-GT--WTGMVGELIA---------R---KADLAVAGLTITAEREKVIDFSK
PFMTL-GISILYRV----HMGR-KP---------GYFSFLDPFSPGV-W---LFMLLAYLAVS-CVLFLVAR--LTPY-EWY----
------SPHPC---------------------AQGRCNLLVNQYSLGNSLWFPVGGF-MQQ-G---S--TIAP---RALSTRCVSG
VWWAFTLIIISSYTANLAAFLTVQRMDVPIE--SVDDL---ADQTA---IEYG-TIHGGSSMTFFQ--------NSRY-QTYQRMW
NYMYSK---------------------QPSVFVKSTEEGIARVL----NSN----------YA-FLLES-TMNEYYRQR-----NC-
NLTQIGG--L-LDTKGY-GIG-MPV---G---SV--FRDEFDLAILQ--LQE-NNRLEILKRK------WWE------GGKCPKE-
-EDHRA-------KGLGMENIGGIFVVLICGLIVAIFMAMLEFLW---TLRHSEATEVSVCQEMVTELRSIILCQDSPPRPPIPEE
RRPRGTATLSNGKLCGAGEPDQLAQRLAQEAALVARGCT----------HIRVCPECRRFQGLRARPSPARSEESLEWE------
----
259 Locu_GluK4
--------------MWVRNIASNPLSLR-IAAILDDPMECSRGERLAITLAKERINRA---TNRSQTAKLEVDIFELLRDSEYETG
ET------MCQII--SKGVVAVLGPSAS-------------PASNSIISNICGEKEVPYVRVA--------------PEDILKVQF
PRFTT---LNLRPTNTDISLAVAGLLNFFNSTTSCLICAKA-----E-CLLNLERLLRQFL----ISKET-L--------------
-SVRMLDDSQDPTPLLKEIRDDKTA----------TIIVDANA-TMSHIILQRAS--E--LGML-SIYYTYIFTSL----EFSLL
RLDH------MADE--------RVNIVGFSVF-NRTHPFFQDFLLSLNRSWQENCDHAPFAG----------APLSSALMYDAVHV
LVAAV----------HELNRSQNVGAMQL--------------------SCKYPK-------------IW-EHGTSLMNYL----
--------------RMVELEGLTGHI--EFNS-KGQRSNY----ALRI--------MQ----NSREGLRQ----------------
IGQW---HSEEG----LLMEKKLRPLNASDTLFNTTLT---
--------------------VTTILENPYVMLK-----KNHQDLE--DN---------------ERYEGFCVDMLRELAD--IL-
K-----FN-YKIRLVGD-G-LYGVPE-------AN-GT--WTGMVGELIS---------R---KADLAVAGLTITAEREKVIDFSK
PFMTL-GISIMYRV----HMGR--R----P----GYFSFLDPFSPGV-W---LFMLLAYLAVS-CVLFLVAR--LTPY-EWY----
------NPHPC-----------------LKGRCNLLI----NQYSLGNSFWFPVGGF-MQQ-G---S--TIAP---RALSTRCVSG
VWWAFTLIIISSYTANLAAFLTVQRMEVPIE--SVDDL---ADQTA---IEYG-TMQGGSTMTFFQ--------NSRY-QTYQRMW
NFMHSK---------------------QPSVFVKSTEEGIARVL----NSN----------YA-YLLES-TMNEYYRQR-----NC-
NLTQIGG--L-LDTKGY-GIG-MPL---G---SV--YRDEFDLAILK--LQE-ENRLEILKRK------WWE------GGKCPKE-
-EDHRA-------KGLGMENIGGIFVVLVCGLLVAIFMAVLEFIW---MLRQTPGTEDWFSHHKKNILFLV---------------
----GFIQGMLKGQVMHRFRLSSRTRPAALVARGCT--------------HIRVCPECRRFQGLRARPPGASGASPVHSEESLEWE
----
260 Blan_GluKalpha
---------MFPESSLFGRAIVDLVTKNGWVDVALVYEDS------KALVRLQELISAPA------KWR-RLK------------
-VMVYQVERGDSRNVLREIRNSGIT----------EIVLDLST-STLETFLQQAS--DPNMEML-SKYYNYIVTSL---------
---DMDIVQLPPHT--------EVNITSFTLM-DRSRPLVQTILNRWIDWLNSTNPDPLR-----------LPTSVALVYDAVYV
IARAL----------SSLQRKTNIRLDPI--------------------MCEQENPW--------------PLGKAFTAEL----
-------------KKV-SIQGLTGPI--GFDQ-DGRRTTF----QLNV--------IN----VREQSKAQK---------------
LGFW---TPEKG----------LNMTEDKRSQAVLPGS---
-----------LRNRT---FVVTTRLEPPFVMFK----WDWTSGGD-------------------NMYEGYCMDLLDELSK--ML-
G-----FK-YIVRLVPD-A-NYGFEN-------ED-GE--WDGMVRELME---------R---RADLAVAPFTITSSREKVIDFSK
PFMNV-GISILYRK----PETE--D---------RLFAFLSPLSYDI-W---LYVLLAYVGVS-GVLFFVAR--FTPY-EWY----
------DPDPC------------------NPDSNVEE----NNFTLLNSFWYNIGAF-MQQ-G---S--ESLP---RAVSTRTVMG
SWWFFMLIIISSYTANLAAFLTVERMVIPIE--SAEDL---AAQTQ---IHYG-CLQGGTTMTFFK--------QNSKVPTYQKMW
AFMNTV---------------------EPSPFTKTVEEGILRVL----NGN----------YA-FLLES-TMNEFVRRK-----SC-
NLTQIGG--P-LDSKGY-GIG-TPN---G---SP--FTDDISNAILS--LQE-QGRLEELYRK------WWK-------GSCPAE-
-EKDWFF------SSLKWDQVGGIFIVLMVGLALSTVIAVLEVIV---KSKQDAKKYGS-------------------------
----TRCHELMKGLRLAVNCKKGPLSRSSSLRCKPPPD------------LTPCAHNLARRSSYIVHSNGNIVSKKESV-------
----
261 Cmil_GluK1
--MSERYTNVILLLLEALTHALCCLFRFPGGIFETTENEPISVEEMAFKFAVTNINRN---RTLMPNTTLTYDIQRINLYDSFEAS
RR------ACDQL--ALGVASVFGPSH--------------SSSLSAVQSISNALEVPHIQTR------------WKHPIVNQKD
SFYIN-----LYPDYTSISRAILHLVQYYKWKTVTVVYEDS------TGLIRLQELMKAPS----RYNIKIK----------

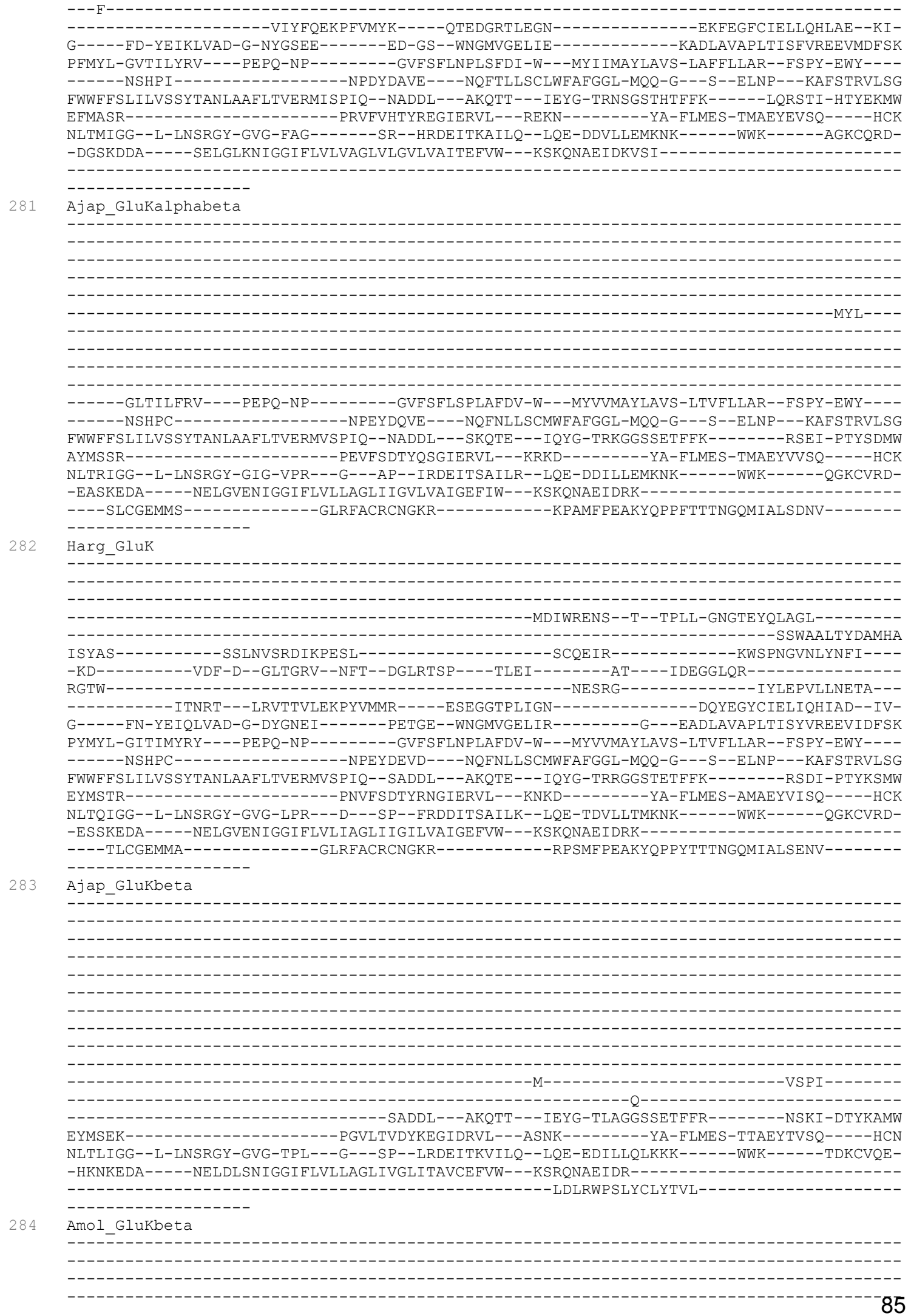
```
-IRQLPTDNRDPKPLLKEMKRGKEF----------YVIFDCTY-ETAAGMLKQLL--S--MGMM-TEYYHYFFTTL----DLFAL
NLEP------YRYS--------GVNMTGFRLL-NIDNPHIASVIDKWSMERLQAPPKPESGLLDGM------MTTDAALMYDAVYV
VSIAF---------------QRASQMTVSSL------------------QCHRHKPW--------------RFGSRFMNLI----
-------------KEA-QWDGLTGHI--AFNKTDGLRKDF----DLDV--------IS----LKEEGLEK----------------
IGIW-------------------------------------------------NSNTG------------LNMTDSMKEKPSNI---
--------SVSMSNRS---LIVTTILEDPYVMYK-------KSDKPLYGN---------------DRFEGYCLDLLKELSN--IL-
G-----FT-YEVRLVAD-G-KYGAQ--------NDKGQ--WNGMVRELVD---------H---IADLAVAPLTITYVREKVIDFSK
PFLTL-GISILYRK----PNGT-NP---------GVFSFLNPLSPDI-W---MYVLLACLGVS-CVLFVIAR--FTPY-EWY----
------NPHPC------------------NPDSDVVE----NNFTLLNSFWFGVGAL-MQQ-G---S--ELMP---KALSTRIVGG
IWWFFTLIIISSYTANLAAFLTVERMESPID--SADDL---AKQTK---IEYG-AVGDGSTMTFFK--------KSKI-STYEKMW
AFMSSR--------------------QQTALVKNNDVGIQRVL----TTD---------YA-LLMES-TNIEFVTQR-----NC-
NLTQIGG--L-IDSKGY-GVG-TPL---G---SP--YRDKITIAILQ--LQE-EGKLHMMKEK------WWR------GNGCPEE-
-DSKEA-------SALGVENIGGIFIVLAAGLVLSVFVAIGEFIY---KSRRNSDIEQV----------------------------
----SFIILIMHLQCGVLVKSFYLTNKHVINIKCITI-------------LTPISIYHNIIHRKNIGKTGWE--------------
-------------------
262 Hsap_GluK1
GLWTRDTSWALLYFLCYILPQTAPQVLRIGGIFETVENEPVNVEELAFKFAVTSINRN---RTLMPNTTLTYDIQRINLFDSFEAS
RR------ACDQL--ALGVAALFGPSH--------------SSSVSAVQSICNALEVPHIQTR-------------WKHPSVDNKD
LFYIN-----LYPDYAAISRAILDLVLYYNWKTVTVVYEDS------TGLIRLQELIKAPS----RYNIKIK--------------
-IRQLPSGNKDAKPLLKEMKKGKEF----------YVIFDCSH-ETAAEILKQIL--F--MGMM-TEYYHYFFTTL----DLFAL
DLEL------YRYS--------GVNMTGFRLL-NIDNPHVSSIIEKWSMERLQAPPRPETGLLDGM------MTTEAALMYDAVYM
VAIAS---------------HRASQLTVSSL------------------QCHRHKPW--------------RLGPRFMNLI----
-------------KEA-RWDGLTGHI--TFNKTNGLRKDF----DLDI--------IS----LKEEGTEKAAGEVSKHLYKVWKK-
IGIW-------------------------------------------------NSNSG------------LNMTDSNKDKSSNI---
--------TDSLANRT---LIVTTILEEPYVMYR-------KSDKPLYGN---------------DRFEGYCLDLLKELSN--IL-
G-----FI-YDVKLVPD-G-KYGAQ--------NDKGE--WNGMVKELID---------H---RADLAVAPLTITYVREKVIDFSK
PFMTL-GISILYRK----PNGT-NP---------GVFSFLNPLSPDI-W---MYVLLACLGVS-CVLFVIAR--FTPY-EWY----
------NPHPC------------------NPDSDVVE----NNFTLLNSFWFGVGAL-MQQ-G---S--ELMP---KALSTRIVGG
IWWFFTLIIISSYTANLAAFLTVERMESPID--SADDL---AKQTK---IEYG-AVRDGSTMTFFK--------KSKI-STYEKMW
AFMSSR--------------------QQTALVRNSDEGIQRVL----TTD---------YA-LLMES-TSIEYVTQR-----NC-
NLTQIGG--L-IDSKGY-GVG-TPI---G---SP--YRDKITIAILQ--LQE-EGKLHMMKEK------WWR------GNGCPEE-
-DNKEA-------SALGVENIGGIFIVLAAGLVLSVFVAIGEFIY---KSRKNNDIEQKGKSSRIRF----------------------
----YFRNKVRKQSLGVEKCLSFNAIMEELGISLK---------------NQKKIKKKSRTKGKSSFTSILT--------------
-------------------
263 Locu_GluK1
---------------MAEFYLSSQQVLRIGGIFETLENEPISVEELAFKFAVTNINRN---RTLMPNTTLTYDIQRINLFDSFEAS
RR------ACDQL--ALGVAAVFGPSH--------------SSSVSAVQSICNALEVPHIQTR-------------WKHPSVDNKD
SFYIN-----LYPDYASISRAILDMVQYYKWKTVTVVYEDS------TGLIRLQELIKAPS----RYNIK-IK-------------
-IRQLPTGNKDARPLLKEMKKGKEF----------YVIFDCTY-ETAADILKQIL--S--MGMM-TEYYHFFFTTL----DLFAL
DLEP------YRYS--------GVNMTGFRLL-NIDNPGVASVIEKWSMERLQAPPKPESGLLDGM------MTTEAALMYDAVYM
V---------------AVISQRATQMTVSSL------------------QCHRHKPW--------------RFGPRFMNMF----
-------------KEA-QWDGLTGHI--TINKTDGLRKDF----DLDI--------IS----LKEEGTEKPAGESSSRLNKVWKK-
IGVW-------------------------------------------------NSNSG------------LNMTDSYKEKSTNI---
--------TDSMANRT---LIVTTILEDPYVMYK-------KSDKPLYGN---------------DRFEGYCLDLLKELSN--IL-
G-----FS-YEVKLVSD-G-KYGAQ--------NDKGE--WNGMVRELID---------H---IADLAVAPLTITYVREKVIDFSK
PFMTL-GISILYRK----PNGT-NP---------GVFSFLNPLSPDI-W---MYVLLACLGVS-CVLFVIAR--FTPY-EWY----
------NPHPC------------------NPDSDVVE----NNFTLLNSFWFGVGAL-MQQ-G---S--ELMP---KALSTRIVGG
IWWFFTLIIISSYTANLAAFLTVERMDSPID--SADDL---AKQTK---IEYG-AVRDGSTMTFFK--------KSKI-STYEKMW
AFMSSR--------------------KQTALIKNNDEGIQRVL----TTD---------YA-LLMES-TSIEYVTQR-----NC-
NLTQIGG--L-IDSKGY-GVG-TPI---G---SP--YRDKVTIAILQ--LQE-EGKLHMMKEK------WWR------GNGCPEE-
-DSKEA-------SALGVENIGGIFIVLAAGLVLSVFVAIGEFIY---KSRQNTDIEQDNVT----------------------------
----KISGLILSLMQCKQTHPSNSTSGISFSAVMEELG-----------ISLKCHKSVKKRSRIKGRAGISSILM----------
-------------------
264 Cmil_GluK2
LLSNPVFECSTRLFLCLLWMGYSQGMPHVLRFGGIVEKTPSGAEELAFKFALNTINRN---RTLLPNTTLTYDIQRINIYDSFEAS
RK------ACDQL--SLGVAAIFGPSH--------------SSSANAVQSICNALGVPHIQTR-------------WKHQVSDNRD
SFFVN-----LYPDFTSLSQAILDLVHFFKWKTVTVVYDDS------TGLIRLQELIKAPS----RYSIRLK--------------
-IRQLPSDTKDSKPLLKEMKRNKEF----------HVIFDCGH-EMAAGILKQAL--S--MGMM-TEYYHYIFTTL----DIFAL
DLEP------YRYS--------GVNMTGFQIL-NTENSQVASIIEKWSMERLQAPPKPGSGLLDGF------MTTNAALMYDAVHV
VSVAV---------------QQSPQMTVSSL------------------QCNRHKPW--------------RFGNRFMKFI----
-------------KEA-HWEGLTGRI--IFNSSNGLRTDF----DLDV--------IS----LKEEGLER----------------
VGTW-------------------------------------------------ETSTG------------LNMTENRKGKTANI---
--------TDSLSNRS---LVVTTILEEPYVMFK-------KSDKPLYGN---------------GRFEGYCIDLLKELSN--IL-
G-----FT-YEVRLVDD-G-KYGAQ--------DEKGQ--WNGMVRELMD---------H---KADLAVAPLTITYVREKVIDFSK
PFMTL-GISILYRK----PNGT-NP---------GVFSFLNPLSPDI-W---MYILLAYLGVS-CVLFVIAR--FSPY-EWY----
------NPHPC------------------NPDSDVVE----NNFTLLNSFWFGVGAL-MQQ-G---S--ELMP---KALSTRIVGG
IWWFFTLIIISSYTANLAAFLTVERMESPID--SADDL---AKQTK---IEYG-AVADGATVTFFR--------KSKI-STYEKMW
AFMSSR--------------------QQTALVKNNDEGIQRVL----TTD---------YA-LLMES-TTIEFVTQR-----NC-
NLTQIGG--L-IDSKGY-GIG-TPM---G---SP--YREKITIAILQ--LQE-EGKLHMMKEK------WWR------GNGCPEE-
-ESKEA-------SALGVQNIGGIFIVLAAGLVLSIFVAVGEFLY---KSKKNAQLEKR----------------------------
----SFCSAMVE-------------ELRLSLKCQRRK-----------HRPQAPVIVKTEEVINMHTFNDRRLPGKETM-------
-------------------
265 Hsap_GluK2
```

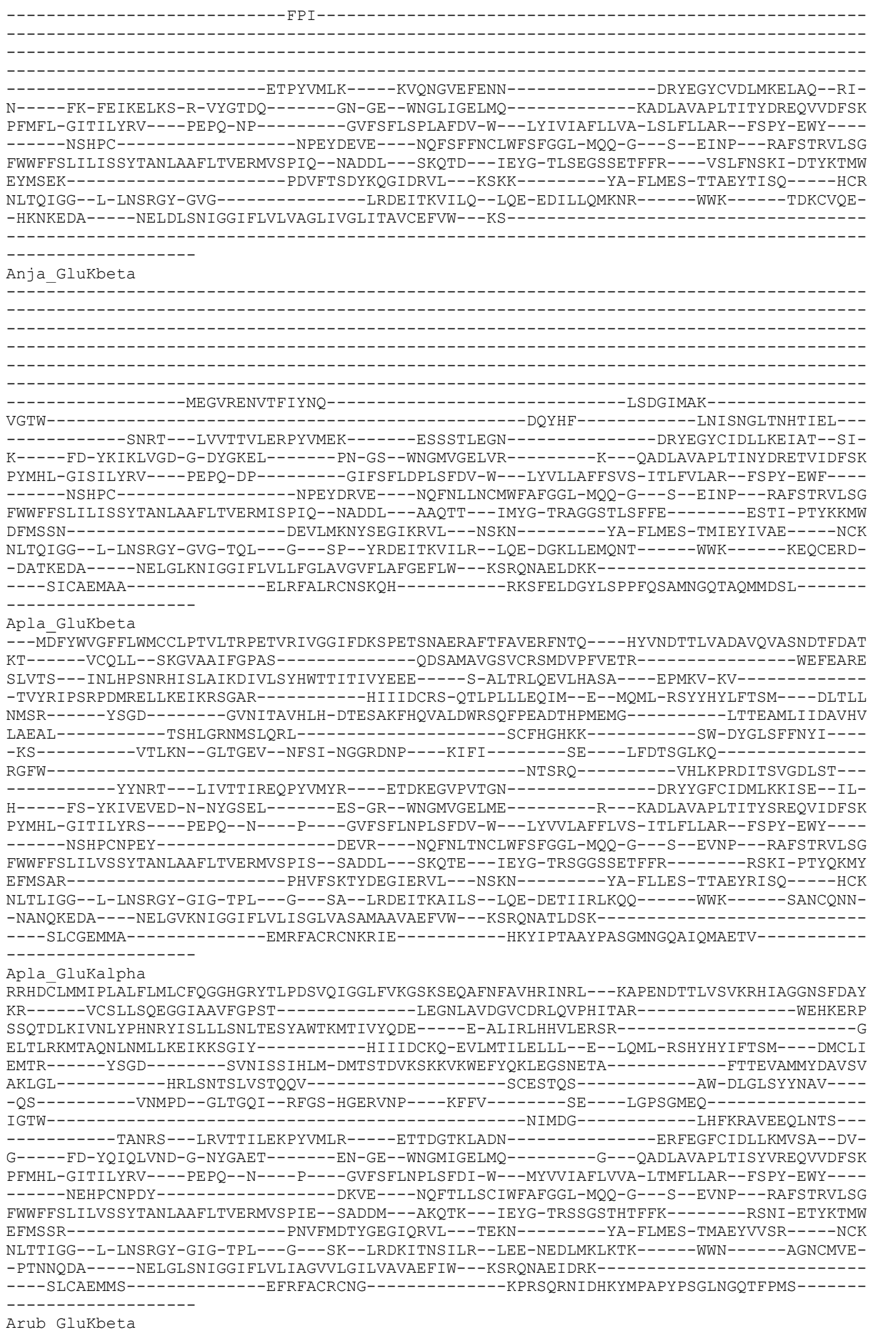
```
ILSNPVFRRTVKLLLCLLWIGYSQGTTHVLRFGGIVESGPMGAEELAFRFAVNTINRN---RTLLPNTTLTYDTQKINLYDSFEAS
KK------ACDQL--SLGVAAIFGPSH--------------SSSANAVQSICNALGVPHIQTR-------------WKHQVSDNKD
SFYVS-----LYPDFSSLSRAILDLVQFFKWKTVTVVYDDS------TGLIRLQELIKAPS----RYNLRLK--------------
-IRQLPADTKDAKPLLKEMKRGKEF-----------HVIFDCSH-EMAAGILKQAL--A--MGMM-TEYYHYIFTTL----DLFAL
DVEP------YRYS--------GVNMTGFRIL-NTENTQVSSIIEKWSMERLQAPPKPDSGLLDGF------MTTDAALMYDAVHV
VSVAV---------------QQFPQMTVSSL-------------------QCNRHKPW--------------RFGTRFMSLI----
-------------KEA-HWEGLTGRI--TFNKTNGLRTDF----DLDV--------IS----LKEEGLEK----------------
IGTW-------------------------------------------------DPASG------------LNMTESQKGKPANI---
--------TDSLSNRS---LIVTTILEEPYVLFK-------KSDKPLYGN---------------DRFEGYCIDLLRELST--IL-
G-----FT-YEIRLVED-G-KYGAQD-------DANGQ--WNGMVRELID---------H---KADLAVAPLAITYVREKVIDFSK
PFMTL-GISILYRK----PNGT-NP---------GVFSFLNPLSPDI-W---MYILLAYLGVS-CVLFVIAR--FSPY-EWY----
------NPHPC-------------------NPDSDVVE----NNFTLLNSFWFGVGAL-MQQ-G---S--ELMP---KALSTRIVGG
IWWFFTLIIISSYTANLAAFLTVERMESPID--SADDL---AKQTK---IEYG-AVEDGATMTFFK--------KSKI-STYDKMW
AFMSSR---------------------RQSVLVKSNEEGIQRVL----TSD---------YA-FLMES-TTIEFVTQR-----NC-
NLTQIGG--L-IDSKGY-GVG-TPM---G---SP--YRDKITIAILQ--LQE-EGKLHMMKEK------WWR------GNGCPEE-
-ESKEA-------SALGVQNIGGIFIVLAAGLVLSVFVAVGEFLY---KSKKNAQLEKR--------------------------
----AKTKLPQDYV-------------------------------------FLPILESVSISTVLSSSPSSSSLS------------
--------------------
266  Locu_GluK2
---------CLSRCNSKYQALMLHFSFFLGGIFESIESGPSGAEELAFKFALNTINRN---RTLLPNTTLTYDIQRINIYDSFEAS
RK------ACDQL--SLGVAAIFGPSH--------------SSSANAVQSICNALGVPHIQTK-------------WKHQVSDNRD
SFYVS-----LYPDFSSLSRAILDLVHFFKWRTVTVVYDDS---TVPQGLIRLQELIKAPS----RYNIR-LK--------------
-IRQLPADTKDAKPLLKEMKRGKEF-----------HVIFDCGH-EMAAGILKQAL--A--MGMM-TEYYHYIFTTL----DLFAL
DVEP------YRYS--------GVNMTGFRIL-NTENTQVASIIEKWSMERLQAPPKPDSGLLDGF------MTTDAALMYDAVHV
VAVAV---------------QQSQQITVSSL-------------------QCNRHKPW--------------RFGNRFMALI----
-------------KEA-HWEGLTGRI--TFNKTNGLRTDF----DLDV--------IS----LKEEGLEK----------------
IGTW-------------------------------------------------DPASS---------LNMTESQKGKMANITDS---
-----------LTNRS---LIVSTILEEPYVMFK-------KSDKPLHGN---------------DRFEGYCIDLLKELAN--IL-
G-----FT-YEIKLVED-G-KYGAQE-------ETTGQ--WNGMVKELMD---------H---KADLAVAPLAITYVREKVIDFSK
PFMTL-GISILYRK----PNGT-NP---------GVFSFLNPLSPDI-W---MYILLAYLGVS-CVLFVIAR--FSPY-EWY----
------NPHPC-------------------NPDSDVVE----NNFTLLNSFWFGVGAL-MQQ-G---S--ELMP---KALSTRIVGG
IWWFFTLIIISSYTANLAAFLTVERMESPID--SADDL---AKQTK---IEYG-VVEDGATMTFFK--------KTKI-STYDKMW
EFMSSR---------------------RHSVLVKNNEEGIQRVL----TSD---------YA-FLMES-TTIEFVTQR-----NC-
NLTQIGG--L-IDSKAY-GVG-TPM---G---SP--YRDKITIAILQ--LQE-EGKLHMMKEK------WWR------GNGCPEE-
-ESKEA-------SALGVQNIGGIFIVLAAGLVLSVFVAVGEFLY---KSKQNAQLEKR--------------------------
----SFCSAMVD-------------ELRVSLKCQRRK------------HKPQAPVVVKTEEVINMHTFNDRRLPGKETM-----
--------------------
267  Cmil_GluK3
EFQAGLVYPIERAAIYYHPTFDYRCFSLPGGIFELVEGGTVGAEELAFKFAVNNINRN---RTLLPNTTLTYDIQRINIYDSFEAS
RK------ACDQL--SLGVVAIFGPSH--------------SSSSNAVQSICNALEVPHIQIR-------------WKHHPMDNRD
SFYAN-----FYPNYSSLSHAILDLIQFLKWRTATVVYDDS------TGLIRLQELITAPS----RYNIR-LK--------------
-IRQLPSDSNDARPLLKEMKRGREF-----------RVIFDCGY-AMAAQILKQAM--A--MGMM-TEYYHYIFTSL----DLFAL
DLDS------YRYC--------GVNMTGFRIL-NTENPYVASVIEKWSMERLQAPPSPASGLLDGI------MTTDAALTYDAVHI
VSMSY---------------QRAPQMTVNSL-------------------QCHRHKPW--------------RFGSRFMAFI----
-------------KEA-QWEGLTGRI--TFNRSTGLRTDF----DLDV--------IS----LKEEGLEK----------------
VGTW-------------------------------------------------DVTNG---------LNITEMSRGRGSNITDS---
-----------LTNRS---LIVTTALEEPYVMFK-------KSDKPLSGN---------------DRFEGFCIDLLKELAN--IL-
G-----FS-YEIRLIQD-G-KYGTQD-------EK-GQ--WNGMVKELID---------H---KADLAVAPFTITYAREKVIDFSK
PFMTF-GISILYRK----SNGT-NA---------GVFSFLNPLSPDI-W---MYILLAYLGVS-CVLFVIAR--FSPY-EWY----
------DAHPC-------------------NPGSDVVE----NNFTLLNSFWFGVGAL-MQQ-G---S--ELMP---KALSTRIIGS
IWWFFTLIIISSYTANLAAFLTIERMESPIN--SADDL---AKQTK---IEYG-TVKDGATMAFFK--------KSKI-STFEKMW
AFMSSR---------------------HQSALVKSIEEGIQRVL----TAD---------YA-LLMES-TTLEYTTQR-----NC-
NLTQIGG--L-IDSKGF-GIG-TPL---G---SP--YKEKITIALLE--LQE-DGKLHMIKEK------WWR------GSGCPEE-
-DSKEA-------SALSIQNIGGIFIVLAAGLVLSVFVAIGEFVY---KLRKTAEQEQR--------------------------
----SLCSTMAE-------------ELRLSLTCQRRK------------HKPQAPVMVKTEAVINMHTFNDRRLPGKDSMSCNTG
--------------------
268  Hsap_GluK3
RLRSLVWEYWAGLLVCAFWIPDSRGMPHVIRIGGIPNAQVMNAEEHAFRFSANIINRN---RTLLPNTTLTYDIQRIHFHDSFEAT
KK------ACDQL--ALGVVAIFGPSQ--------------GSCTNAVQSICNALEVPHIQLR-------------WKHHPLDNKD
TFYVN-----LYPDYASLSHAILDLVQYLKWRSATVVYDDS------TGLIRLQELIMAPS----RYNIR-LK--------------
-IRQLPIDSDDSRPLLKEMKRGREF-----------RIIFDCSH-TMAAQILKQAM--A--MGMM-TEYYHFIFTTL----DLYAL
DLEP------YRYS--------GVNLTGFRIL-NVDNPHVSAIVEKWSMERLQAAPRSESGLLDGV------MMTDAALLYDAVHI
VSVCY---------------QRAPQMTVNSL-------------------QCHRHKAW--------------RFGGRFMNFI----
-------------KEA-QWEGLTGRI--VFNKTSGLRTDF----DLDI--------IS----LKEDGLEK----------------
VGVW-------------------------------------------------SPADG---------LNITEVAKGRGPNVTDS---
-----------LTNRS---LIVTTVLEEPFVMFR-------KSDRTLYGN---------------DRFEGYCIDLLKELAH--IL-
G-----FS-YEIRLVED-G-KYGAQ--------DDKGQ--WNGMVKELID---------H---KADLAVAPLTITHVREKAIDFSK
PFMTL-GVSILYRK----PNGT-NP---------SVFSFLNPLSPDI-W---MYVLLAYLGVS-CVLFVIAR--FSPY-EWY----
------DAHPC-------------------NPGSEVVE----NNFTLLNSFWFGMGSL-MQQ-G---S--ELMP---KALSTRIIGG
IWWFFTLIIISSYTANLAAFLTVERMESPID--SADDL---AKQTK---IEYG-AVKDGATMTFFK--------KSKI-STFEKMW
AFMSSK---------------------PSALVKNNEEGIQRAL----TAD---------YA-LLMES-TTIEYVTQR-----NC-
NLTQIGG--L-IDSKGY-GIG-TPM---G---SP--YRDKITIAILQ--LQE-EDKLHIMKEK------WWR------GSGCPEE-
-ENKEA-------SALGIQKIGGIFIVLAAGLVLSVLVAVGEFVY---KLRKTAEREQR----------------------
```

```
----SFCSTVAD--------------EIRFSLTCQRRK------------HKPQPPMMVKTDAVINMHTFNDRRLPGKDSMACSTS
-------------------
269 Locu_GluK3
SSRSVILEYWKALILCLFWIQYSRGMPHVIRIGGISPGPVVSAEEQAFKFAVNNINRN---RTLLPNTTLTYDIQRINIYDSFEAS
RK------ACDQL--SLGVVAIFGPSH--------------SSSSNAVQSICNALEVPHIQVR------------WKHHPMDNRD
TFYAN-----LYPDYSSLSYAILDLVQFLKWKTATVVYDDS------TGLIRLQELIMAPS----RYNIR-LK------------
-IRQLPLDTDDTRPLLKEMKRGREF-----------RIIFDCSH-TMAAQILKQAL--A--MGMM-TEYYHYIFTTL----DLFAL
DLEP------YRYC--------GVNMTGFRIL-NTDNPQVASIVEKWSMERLQAAPKPESGLLDGI------MTTDAALTYDAVHI
VSVSY---------------QRAPQMTVNSL-------------------QCHRHKPW--------------RFGGRFMNFI----
-------------KES-HWEGLTGRL--VFNKTSGLRTDF----DLDI--------IS----LKEDGLEK----------------
VGKW-------------------------------------------------SPSGG--------------LNITEVPRPRGV---
------NITDSLSNRS---LVITTILEEPYVMFK-----KSDKALA--GN---------------DRFEGFCIDLLKELAN--IL-
G-----FM-YEIRLVPD-G-KYGSQD-------EK-GQ--WNGMVKELMD---------H---KADLAVAPLTISYVREKVIDFSK
PFMTL-GISILYRK----PNGT-NN---------GVFSFLNPLSPDI-W---MYILLAYLGVS-CVLFVIAR--FSPY-EWY----
------DAHPC-----------------NPGSDIVE----NNFTLLNSFWFGVGSL-MQQ-G---S--ELMP---KALSTRIIGG
IWWFFTLIIISSYTANLAAFLTVERMESPVE--TADDL---AKQTK---IEYG-VVKDGATMTFFK--------KSKI-STFEKMW
AFMSSK--------------------QNTALVKNNEEGIQRVL----KAD---------YA-LLMES-TTIEYVTQR-----NC-
NLTQIGG--L-IDTKGY-GIG-TPM---G---SP--YRDKISIAILH--LLE-DGKLHVLKEK------WWR------GNGCPDD-
-DTKEI-------RALGIQNIGGIFIVLAAGLVLSVFVAIGEFIY---KLRKTAEREQR-------------------------
----SFCSAMAN--------------EIRLSFTCERRK------------HKPQPPVMVKTDAVINMHTFNDRRLPGKDNMTCNTG
-------------------
270 Anja_GluKalpha
MLKSRKTCNIGLWILCLFLQHTVSQNPSLKLGAVFKDGDNGTDEEFMFQYAINKTSIEGDTIYLQPDENILDFKEKVCLEH-----
---------------KGGMISLIGPST--------------SYNAFKVKTVCSSLGIPYIDTK---------------WAPYRSEK
QLILN-----MMPDNNLFSKAILDLIEFYDWTTLTLLYEDD------AGLMKFKELFESAS----EIGI-----------------
-NIMLSRLVGEYEVVLKNVKKMSTIS----------NVIIDCRQ-ESLEHILTKMN-----ENKM-FEYYHLIFTSL-------DF
HIFSSIIEGITTV---------EFKVTSLQMF-DLNEEPVRDLQNSLNDARSIFD-----------------LTIQSALIYDAVNL
VGRAL-----------NYSSAQGKDIKKIKNL-------------------DCDLIVTNQTW-----------RHGTKMFNAL----
-------------KKAAGYNGITGKL--SFNG-NGMREDV----KLYI--------YE----YTQTGKNM----------------
IGTW-------------------------------------------------NKTDG--------------FAKREVKIIEKP---
-----------NIKKI---LRITSVLAKPFVMLK-----DTTESQG-------------------RMYEGFCIELLNYLAQ--MM-
D-----FE-YKLTLVED-G-MYGTLVN------ADTNE--WNGMVKELID---------K---KADLAVAPLTINLAREKVIGFSK
PYMYL-GLSILYNI----HEAK-SP---------GIFSFLNPLSFDV-W---LYILIAFLSVS-IMLFLVAR--FSPY-EWY----
------NSHPC-----------------NPECDVVE----NQFTFLNCMWFSFGGI-MQQ-G---S--ELTP---KAFSTRALSG
FYWFFSLILLCSYTANLAAFLTVNRMTSPIQ--NADDL---ARQTA---IEYG-TLSSGATQLFFK--------RSSI-PTFEKMW
QFMSNK----------------------PEVFVDREEDGVNRVL--SDEED---------YA-FLMES-TATEYYISQ-----YCR
NLTRIGG--L-LNTISY-GIG-TPL---G---SH--LRDRVTQSILQ--LQE-NGTLIEMENK------WWH-KGSYKKDSCKAY-
-EIGDDD------NRLGYENIGGVFVVLVIGIAFSLFAVVSEFLW---KSRQYAEIEKR-------------------------
----SMCQEMRS--------------SMWFAMNCKQNQ------------RRKRLDSNIDRDHKIINPFTTSV-------------
-------------------
271 Blan_GluKbeta
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
-----------------------------------------------------------ME----LREAGLTK----------------
IGTW-------------------------------------------------QAGER----------QALNITDRSLAGSNVT---
---------NSLRNKT---LIVTTILEKPYVMQR-------RSDEELLGN---------------DRFEGFCIDLLNEIAR--IL-
G-----FK-YEIYLVPD-G-QYGAPM-------ED-GE--WSGMVKELID---------Q---RADLAVAPLTISFMREQVIDFSK
PFMNV-GVTIMYRV----PNRT-NP---------GVFSFLNPLSYDI-W---LYILLSYLAVS-GVLFVLAR--FSPY-EWY----
------NPHPC-----------------NPNSDYLE----NQFTLLNSMWFSIGAF-MQQ-G---S--EIMP---RALSTRLVSG
AWWFFTLIMISSYTANLAAFLTVERMESPIE--SADDL---AKQTK---IKYG-TLDSGATQTFFK--------NSKI-PTYEKMW
AFMSSQ----------------------EPSVFTKSTEEGIDRVL----NEN---------YA-FLLES-AMNEYFTHR-----NC-
NLTRVGG--L-LDSKGY-GIG-TPE---G---SP--IRDKITIAILQ--LQE-AGQIQMLYNK------WWV-----NMGQCSNE-
-DKNKEA------SALGVANVGGIFIVLIAGLVVGILVAIIEFIW---KSRSSQERDKQHMQNLSD-------------------
----VFKGSLSS-----------------------------------------PNFVLPTNTNIIPRLKTQKTDYDDYCLS--------
-------------------
272 Skow_GluK
--------------------------------------------------------------------------------
---------------MGVAAVFGPPT--------------SKSATAVQSVLKELEVPHVEAN-----------------WDHRRL
HDRFS---INLYPAPSLISRAIADAVGHYKWKKIAVLYENE------ESLVRLQDVIKLSS----QLHIT----------------
-ISVRQLVPPNFKSVLKEIKNRGLS-----------HVIVDCEF-VHVIEVLEQAL--E--VQML-THNFHYFFTSP----DFHLL
DVER------YSEG--------GVNLTSFRMI-NEDDPKVQTLLREWRIRQREEDVPLQRRN----------MTTEVALIYDAVDV
FTQAL-----------ESLDIGQSLTVREL--------------------SCQKPTTW--------------HYGLSLFNHL----
-------------SYVNNWQGITGRI--QFDE-NGLRTYV----KMDL--------ME----LVGSRLQK----------------
VGFW-------------------------------------------------EPATG---------TNYTMKSGRTDDNSTES---
----------LKNKT---FIVTTILENPYVMRK-----KAENGKVLVGN---------------DQYEGFCVDLLEEISQ--IL-
G-----FK-YKIELVPD-G-KYGAPE-------ED-GQ--WNGMVGQLIA---------R---KADLAVAPLTISYIREKVIDFAK
PYMNT-GISILYRV----PESK-NP---------GVFSFLSPLDFDI-W---LYMLLAYLGVS-VSLFILAR--FSPY-EWY----
------NPHPC-----------------NPEYDMVE----NQFNLMNSLWYSFGGL-MQQ-G---S--EVAP---RALSTRVVSG
MWWFFSLIIISSYTANLAAFLTVERMVSPIK--DVDDL---ASQTK---IEYG-TLSSGSTTTFFK--------NSNI-EIYQRMW
```

```
SFMSSR--------------------QPSVFVSTTEAGIERVL---NSKN---------YA-FLMEV-TFNEYVTAR-----NC-
NLTQIGG--L-LDSKFY-GIG-TPL---G---AS--YRDDITIAILQ--LQE-GGALQEMKKK------WWY-----SEGSCERK-
-DKKQEA------NALGFGNIGGIFFVLIGGIVLGVICAFGEFIW---KSKQNAALDRK-------------------------
----SLCAEMGQ--------------ELSFAIRCQSKE------------MAQIGPPQRHNPTSPNLKNGSTITMRENV-------
-------------------
Bgla_GluKbeta
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
-------------------------------------------------------------------------MDKENPTPD---
-----------------------------------------------------------ELYEGFCIDLTKELAR--IV-
G-----FN-FRIELVPD-G-NYGSP--------NTQGE--WDGMVREIID---------R---RADLAIAPLTITYLREQVIDFTK
PFLNL-GISILFKV----PRKE-KP---------GLFSFLNPLAIEIWW---LYVIGAYLIVS-FTIFTLAR--FSPY-EWY----
------NPHPC------------------NPDTDVVE----NTFNLSNSLWFTVGTL-MQQ-GSDINVADINP---RAVSTRLVGG
IWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTE-------------------------------------
------------------------------------------------------------------------------------
---------I--------------------------------------------------------------------------
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
-------------------
Lgig_GluKbeta
------------------------------GGLFGEGDEDLRVANAFRYAVYRVNHE---RDLLPQTRLVYDIQNLPVNDGFRAS
KK------ICYQV--ELNTVAVLGPRS--------------SNLAGFVNSLCASLQLPHLELR----------------MDTIANP
APGLS---INLYPDIETLSKAFIDVIRYYGWKQMLVIYGTK-----D-DLLKVQSVIRGAY----DQAFE----------------
-IMVRQVDKYNMRNVLKECKEKKWT-----------KLLIDLSV-DDTGLFLKMAL--Q--EGMI-DPYHHYIISNL----DIESI
DMED------YRHN--------YVNLTGFRLV-NPRDRLTQELMKDMEIYEMQTELKLLNKSGYLS------VPHEVALIFDAVFL
LAHAL-----------EAYDRGAVLRPVNV--------------------SCDIPQ-------------PW-SSGPSLYTYL----
-------------TQV-SMRGMTGNI--KLQ--KGRRYDF----QLDI--------LQ----LKPPGLLK----------------
SGTW-------------------------------------------------KYDKG----VN-----FTYVPGTKHMNPFGN---
-----------KT------LVVTTILGEPFIMEK-----KVIGSDG------------------VKYEGFCIDLLNEIAK--IV-
K-----FN-YFIEKVPD-G-KFGSKDE------KT-GE--WNGLVKQIID---------R---KADLAVAPLTISYVREQVIDFTK
PFLNL-GITILFKI----PKSE--K----P----GLFSFLNPLAIEI-W---LYVIGAYLLVS-FTIFVLAR--FSPY-EWY----
------NPHPCNPDS------------------DTVE----NTFNLANSFWFTVGTL-MQQ-G---S--DVNP---RAVSTRIVGG
TWWFFTLIIISSYTANLAAFLTVERMVSPIE--SAEDL---AKQTD---ILYG-TLAAGSTMTFFR--------DSNI-DIYKRMW
AFMEEN---------------------SKDVLMDSYIDGIDRVM----KGN---------YA-FFMES-TSIDYVIQR-----NC-
ELMQVGG--L-LDTKGY-GIG-TPI---D---SP--YRDKLSMAILE--LQE-NGKIQMLYNK------WWK-----STGTCNKD-
-DQKDQKA-----NALGVENVGGIFVVLMAGLALAVMVAMFEFIW---KSRKNAEDDRQSLCTEMAQELRFAI-------------
----RCHGSTKDKDHGGQGTSNSPNGIIQLKEVRKSP-------------LPGREYETEFRPGYSKDFNGDY---------------
-------------------
Pmin_GluK
ISMKRNVVVGAVTVLFLIFTVQTAEERQPDEVRIGGIFIKNSKYEQAFRFAVNRINRK---RVPVNGAPANDTVEHVAGKNSFDAY
KK------VCRLLAQEGGVAALFGPST--------------AEGNLAVEGVSDRLDVPHIIAR-----------------WEHKDR
PDGNQHRFVNLYPHNRYISVLLSNLTEAYAWKKMTIVYQDE-----E-ALLRLHHVLERSR-----------------------G
ELTLRKMTGHNLNMLLKEIKRSGTY-----------HIIIDCRQ-EMLRPALELLL--E--LQML-QSHYHYIFPSM----DTCLI
DMMR------YTGG---------SVNITSFHLM-NMNSIRVKTTRRDWHHYQALEGAPYNETP----------FTTDIAFMFDAVSV
AKQGL-----------HDFSGPVSTQQL---------------------SCDAGQQ------------DW-DVGLSYFNAL----
-KS----------VNMLD--GLTGEI--RFDS-NGERVEP----TFYV--------SE----VRGDGLEQ----------------
VGSW-------------------------------------------------SAMQG------------LRFDPIIEPTSNIS---
-----------KVNRT---LKVTTIMEKPYVMLR-----EPTDGTQLEGN--------------DRYEGYCIDLLKMISE--EV-
G-----FE-YEIQLVND-G-NYGAE--------VD-GR--WNGMIGELIE---------G---VADMAVAPLTITYVREQVVDFSK
PYMHL-GITILYRV----PEPQ--N----P----GVFSFLNPLSFDI-W---MYVVIAFLVVA-LTMFLIAR--FSPY-EWY----
------NEHPCNPDY------------------DKVE----NQFNLLSCIWFAFGGL-MQQ-G---S--EVNP---RAFSTRVLSG
FWWFFSLILVSSYTANLAAFLTVERMVSPID--GADDL---AKQTK---IQYG-TRSSGSSHTFFK--------RSNI-ETYKTMW
EFMSSR----------------------PNVFMNTYTDGVLRVL---REKN---------YA-FLMES-TMAEYVVAR-----HCK
NLTTIGG--L-LNSRGY-GIG-TPL---G---SK--LRDRITSAVLK--AQE-NESLMKLKSK------WWN------SEQCIVE-
-GANNSDA-----NELGLENIGGIFLVLIAGVVLGILVAVAEFIW---KSRQNAEIDRK-------------------------
----SLCAEMMA--------------EFRFACRCNGKP------------RATQRNIDHKYMPAPYPSGGMNGQTFPMS-------
-------------------
Arub_GluKalpha
------------------------------------------------------------------------------------
------------------------------------------------------------------------------------
---------------------------------MTIMYQDE-----E-ALLRIQHILEASR-----------------------G
ELTIRKIHHENINIVLKEVKRSGTY-----------RVVIDCGY-DLLREILERLL--E--LQML-RSHYHYIFTSM----DLCLM
DVAR------YGQD---------SVNMTTIHLM-NMKSKRVQTLTKEWRHYQALNGFPYNETL----------FTTEAALMFDAVNV
AKRAL-----------HSVGQTKPVSTAEL--------------------SCNSGQQ------------PW-DLGLSYFNAL----
-KS----------VDMPE--GLTGEI--RFDI-HGERDNP----SYFI--------SE----LGPLGMEQ----------------
IGTW-------------------------------------------------DSIQG------------FEFRRKVDDRTNET---
-----------GTNRT---YKVTTILESPYVMMR-----ETAEGVELHGN--------------EQFEGYCIDLLELIAK--DI-
G-----FK-YEIQLVED-G-NYGAE--------VD-GT--WNGMIGELIS---------G---KADLVVAPLTISYVREQVVDFSK
```


277 Lvar_GluKalpha
278 Spur_GluKalpha
279 Etri_GluKalphaalpha
280 Etri_GluKalphabeta


281 Ajap_GluKalphabeta
282 Harg_GluK
283 Ajap_GluKbeta
284 Amol_GluKbeta


285 Anja_GluKbeta
286 Apla_GluKbeta
287 Apla_GluKalpha
288 Arub_GluKbeta

KT------VCRQL--SKGVAAVFGPNS--------------RESSETIASVCNSMDMPLVETR----------------WDYRERG
SMVTS---INLHPNNRQISRAIRDVVYYYRWSAITIVYQDD-----S-ALTRLQEVLRASA----PRKIK-L--------------
-TIYKLPTNPDVRTLLKEIKTSGAR-----------HIIIDCRS-EMLYPLLEQIM--E--VQML-RSYYHFLFTSM----DVTML
NMSR------YSGD--------GVNLTTFHLY-DRESAVFHRIVAEWRARFKRSETNPMERG----------LTLESALMYDAVHV
MAKGL-----------LAMSVGRNMTVQSM--------------------ACFHGDQKK----------SW-DDGRSFYNYL----
-KS----------VELRE--GLTGHV--AFDT-HGERDRP----KLFI--------SE----LSDVHGMEQ---------------
RGYW--NYDDG----------VYLRPKDKELIVNNAS---
-----------VINRT---LIVTTIIELPYVMKK----DRDADGELLVGN---------------ARYYGYCIDMLESISK--HV-
G-----FQ-YEIVEVDD-N-NYGSPM-------ED-GS--WNGMVGKLMT---------R---KADLAVAPLTITYSREQVVDFSK
PYMHL-GITILYRA----PEPQ--N----P----GVFSFLNPLSFDV-W---LYVVIAFFLVS-ITLFLLAR--FSPY-EWY----
------NSHPC------------------NPAFDEVA----NQFNLTNCLWFAFGGL-MQQ-G---S--EVNP---RAFSTRVLSG
FWWFFSLILVSSYTANLAAFLTVERMVSPIS--SADDL---AKQTE---IEYG-TRSGGSTETFFR--------RSNI-PTYQTMY
EFMSAR----------------------PHVFSKTYDEGIERVL---NSKN---------YA-FLLES-TTAEYRISQ-----HCS
NLTLIGG--L-LNSRGY-GIG-TPL---Q---SG--IRDEITKAILI--LQE-DDTLLKLKDK------WWK------TSNCQST-
-INQKEDA-----SELGVKNIGGIFLVLISGLVAGVMAAVAEFVW---KSRQNANLDRK---------------------------
----SLCGEMMA--------------ELRFACRCNKRIE-----------HKYIPATAFPTASINGQAIQMTETV-----------
----

289 Lvar_GluKbeta

--MIVLFAVVEMGCEDNGHGTFVAHICYVAGLHRGPRHMAGSPEEAAFKLAVDRVGKT---MRSAMDNTSTLSIRYIQHNDSFEAT
RA------VCAQLQHANGIAAVIGPTS--------------TDGALAVRSVCKTVDVPHVDTR-------------------RQFG
GMETLSNTISLYPHASYISSLLVDIVQHYKWQKVTVMYDED------EALERLQGVFKLSS----SVHMQ----------------
-LSVERMQGSNHKTILKRIKTSGSN-----------HVIVDCKR-ETLPILLEQML--E--LQML-RSYYHYLFVSL----DLYLI
NMSR------YTGD--------KVNLTTLHML-NLYDQYTEAFMEEWNNMQMGPRSVTMTTRNFSI------LTTEAALLYDAVHV
VAHGL-----------QELGDSRNISLRSL--------------------SCFGEQSEW-------------TDGLTYYNFL----
-------------QGT-NVNGLTGPI--TFDR-NGFRDNP----RFFI--------SE----LQDSQSVMFKT-------------
VGQW--DANGL------------NIFPVDMHIDKNTT---
-----------LTNKT---LIVTTILEPPYCMKR-----KSPDGEPLEGN---------------ARFEGFIIDLLDYISQ--RM-
N-----FN-YVITLVPD-G-DYGS---------EVDGR--WNGMVGELVE---------R---RADLAAAPLTITYVREKVIDFSK
PWMYL-GVTILFRV----PEPQ-NP---------GVFSFLNPLSPDV-W---LYVILAFLLVS-FVLFVLAR--FSPY-EWY----
------NSHPC------------------NPDYDTVE----NQFNFFNCLWFSFGGL-MQQ-G---S--EINP---RAFSTRVLSG
FWWFFSLILISSYTANLAAFLTVERMVSPIQ--TADDL---AKQTS---IEYG-TRKGGSTEEFFS--------RSKI-PTYMKMW
EFMSSR----------------------QHVFTNTYMDGIERVL---NNRN---------YA-YLMES-AMADYVVSQ-----HCN
NLTAIGG--L-LNSRGY-GIG-TPL---G---SV--YRDEITKSILQ--LQE-EDILLELKNK------WWR------TDQCHKN-
-TGQSDEA-----NSLGLKNIGGIFLVLITGLVCGLIAAFAEFIW---KSRQNALIDRK---------------------------
----SLCGEMMS--------------ELRFAFRCNNKRRNS---------KPVIEHKYIPTTTYPPNINGRQSMQM----------
----

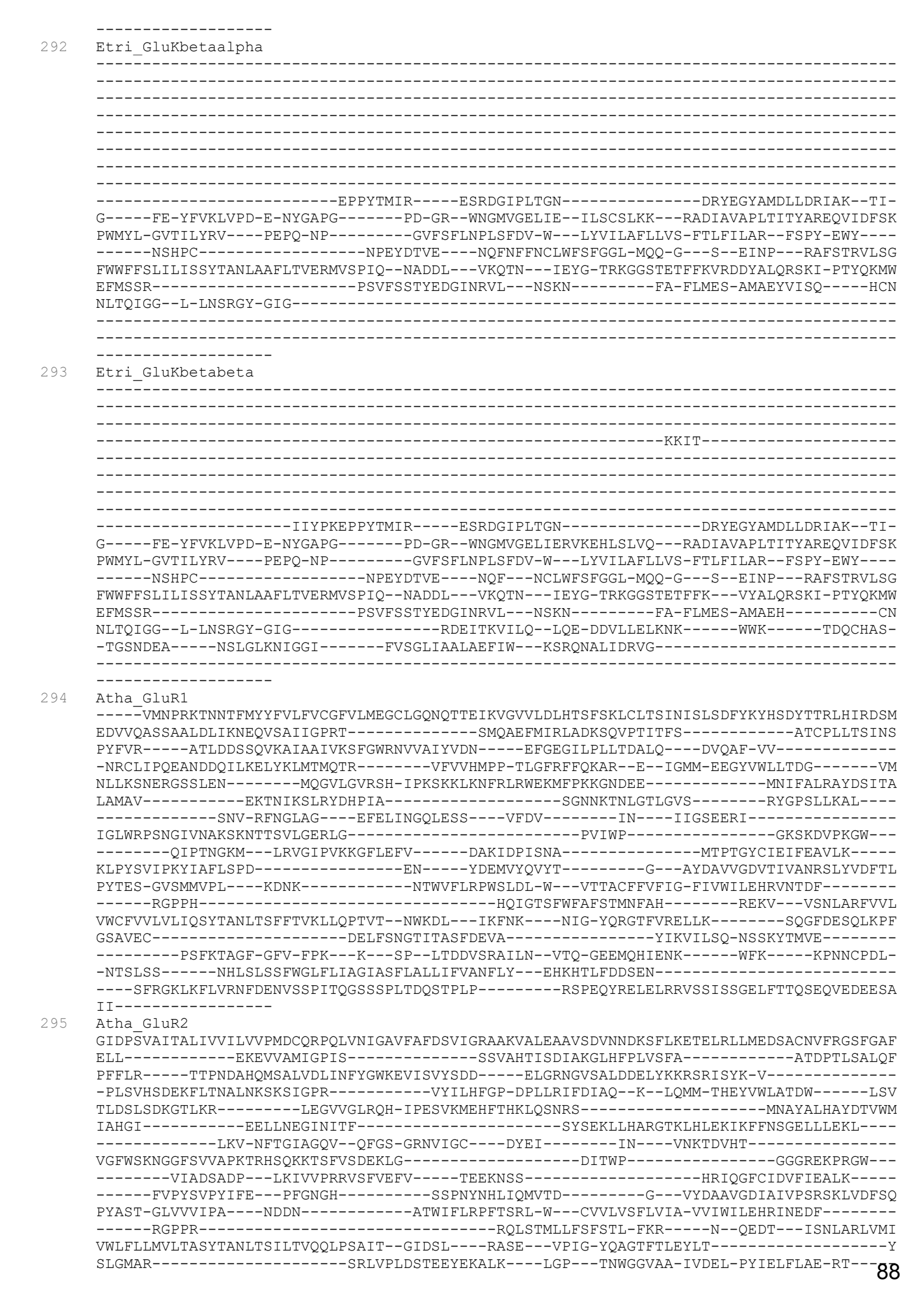
290 Spur_GluKbeta

---------------------MLELQMLRSYFHYLFVSLDL-------YLLNMSRYTGDKV-------------------------
------------------------------------NLTTLHML-NLYDQLVEAFM-------------AEWNAMQI---------
----------------------GPRSVTMTTR-NFSI-----------------------------------LTTEAALLYDAVSV
VANGL-----------EALGSTRNISLRSL--------------------SCFGEQA------------EW-NDGLTFYNFL----
-QS----------TSI-N--GLTGPI--TFDR-NGERENP----RFFI--------SE----LMEQVGFKT---------------
VGEW----------------DENG----------------------------LNIFP----------------VEMHTDKNST---
-----------FNNKT---LIITTILEPPYCMRR-----KSPDGELLEGN---------------ARFEGFIIDLLDHISR--YM-
S-----FN-YIIKLVPD-G-DYGSEI-------SE-GQ--WNGMVGELVE---------R---RADLAAAPLTISYAREKVIDFSK
PWMYL-GVTILFRV----PEPQ--N----P----GVFSFLNPLSPDV-W---LYVILAFLLVS-FVLFVLAR--FSPY-EWY----
------NSHPCNPDY------------------DTVE----NQFNFFNCLWFSFGGL-MQQ-G---S--EINP---RAFSTRVLSG
FWWFFSLILISSYTANLAAFLTVERMVSPIQ--TADDL---AKQTS---IEYG-TRKGGSTEEFFS--------RSKI-PTYMKMW
EFMSSR----------------------QHVFTNTYNDGIQQVL---NNRK---------YA-YLMES-AMADYVISQ-----HCN
NLTAIGG--L-LNSRGY-GIG-TPL---G---SV--YRDEITKVILQ--LQE-DDVLLELKTK------WWR------TDQCHKS-
-TGQSDEA-----NSLGLKNIGGIFLVLITGLVCGLIAAFAEFIW---KSRQNAMIDRK---------------------------
----SLCGEMMS--------------ELRFAFRCNNKR------------RNSKPVIEHKYIPTTTYPPNINGRQSMQM-------
----

291 Ofas_GluK

--NFLI--------------------------------------

-------------------FL-------PF--
------FQ---KADMALAPLTITYAREQVIDFSK
PYMYL-GITILFRQ----PEPQ-NP---------GVFSFLNPLSFDV-W---LYVVLAFLLVS-ITLFLLAR--FSPY-EWY----
------NEHPC------------------NPEYDNVE----NQFTLPNCLWFSFGGL-MQQ-G---S--EVNP---RAFSTRVLSG
FWWFFSLILISSYTANLAAFLTVERMVSPIQ--GADDM---VKQTT---IEYG-TRNSGSTYSFFK--------------------
----
----------------------VSA---N---


292 Etri_GluKbetaalpha
293 Etri_GluKbetabeta
294 Atha_GluR1
295 Atha_GluR2

```
GFKIVGE--P-FMHRGW-GFA-FKR---D---SP--LAIDMSTAILK--LSE-TRKLQEIRKK------WLC------KTNCAGK-
-SNWNPEP-----NQLHLKSFKGLYLVCIAITVSAFLVFVLR------MIRQFV---------------------------------
----RYRRMERTSSMPRASWSASPTLRKRMFRRSDDSN------------NNPSHVGEVQADTEVP--------------------
------------------
;

END;

BEGIN ASSUMPTIONS;
EXSET * UNTITLED  = ;
END;

BEGIN CODONS;
CODONPOSSET * CodonPositions =
 N:,
 1: 1-1480\3,
 2: 2-1481\3,
 3: 3-1479\3;
CODESET  * UNTITLED = Universal: all ;
END;

BEGIN SETS;
END;
```

Supplementary data 2

Gene expression data set (tentacles, radial nerve and nerve ring) followed by three-way analysis of variance with sex, tissue and receptor subunit as factors to compare differences in expression levels (FPKM), followed by the multicomparison Holm-Sidak a posteriori test when main effects were statistically significant. Statistical analysis was performed using SigmaPlot software (version 14.0, Systat Software, Inc).

Sex	Tissue	Gene	Expression (FPKM)	Expression (FPKM+1)	Expression Log2(FPKM+1)
Male	Tentacles	GRIHC6	0	1	0
Male	Tentacles	GRIHC6	0	1	0
Male	Tentacles	GRIHC6	0	1	0
Male	Tentacles	GRIHC6	0	1	0
Male	Tentacles	GRIHC6	0	1	0
Male	Tentacles	GRIHC6	0	1	0
Male	Tentacles	GRIHC6	0	1	0
Male	Tentacles	GRIHC6	0.32	1.32	0.40053793
Male	Tentacles	GRIHC6	0.09	1.09	0.124328135
Male	Tentacles	GRIHC6	0.35	1.35	0.432959407
Male	Tentacles	GRIHC6	0	1	0
Male	Tentacles	GRIHC6	0	1	0
Male	Radial Nerve	GRIHC6	0	1	0
Male	Radial Nerve	GRIHC6	0	1	0
Male	Radial Nerve	GRIHC6	0	1	0
Male	Radial Nerve	GRIHC6	0.24	1.24	0.310340121
Male	Radial Nerve	GRIHC6	0	1	0
Male	Radial Nerve	GRIHC6	0	1	0
Male	Radial Nerve	GRIHC6	0	1	0
Male	Radial Nerve	GRIHC6	0.1	1.1	0.137503524
Male	Radial Nerve	GRIHC6	0.32	1.32	0.40053793
Male	Radial Nerve	GRIHC6	0.28	1.28	0.35614381
Male	Radial Nerve	GRIHC6	0	1	0
Male	Radial Nerve	GRIHC6	0	1	0
Male	Nerve Ring	GRIHC6	0	1	0
Male	Nerve Ring	GRIHC6	0	1	0
Male	Nerve Ring	GRIHC6	0	1	0
Male	Nerve Ring	GRIHC6	1.6	2.6	1.378511623
Male	Nerve Ring	GRIHC6	0.01	1.01	0.014355293
Male	Nerve Ring	GRIHC6	0	1	0
Male	Nerve Ring	GRIHC6	0	1	0
Male	Nerve Ring	GRIHC6	1.09	2.09	1.063502942
Male	Nerve Ring	GRIHC6	0	1	0
Male	Nerve Ring	GRIHC6	0.27	1.27	0.344828497
Male	Nerve Ring	GRIHC6	0	1	0
Male	Nerve Ring	GRIHC6	0.12	1.12	0.163498732
Male	Tentacles	GRIHC5	6.05	7.05	2.817623258
Male	Tentacles	GRIHC5	0.15	1.15	0.201633861
Male	Tentacles	GRIHC5	0	1	0
Male	Tentacles	GRIHC5	0	1	0
Male	Tentacles	GRIHC5	0.84	1.84	0.879705766
Male	Tentacles	GRIHC5	1.01	2.01	1.007195501
Male	Tentacles	GRIHC5	0.79	1.79	0.839959587
Male	Tentacles	GRIHC5	0.04	1.04	0.056583528
Male	Tentacles	GRIHC5	1.69	2.69	1.427606173

Male	Tentacles	GRIHC5	0.33	1.33	0.411426246
Male	Tentacles	GRIHC5	1.22	2.22	1.150559677
Male	Tentacles	GRIHC5	0	1	0
Male	Radial Nerve	GRIHC5	0	1	0
Male	Radial Nerve	GRIHC5	0.13	1.13	0.176322773
Male	Radial Nerve	GRIHC5	0	1	0
Male	Radial Nerve	GRIHC5	1.69	2.69	1.427606173
Male	Radial Nerve	GRIHC5	0	1	0
Male	Radial Nerve	GRIHC5	0.05	1.05	0.070389328
Male	Radial Nerve	GRIHC5	0	1	0
Male	Radial Nerve	GRIHC5	0.18	1.18	0.23878686
Male	Radial Nerve	GRIHC5	0	1	0
Male	Radial Nerve	GRIHC5	0.23	1.23	0.298658316
Male	Radial Nerve	GRIHC5	0.08	1.08	0.111031312
Male	Radial Nerve	GRIHC5	3.82	4.82	2.269033146
Male	Nerve Ring	GRIHC5	0.14	1.14	0.189033824
Male	Nerve Ring	GRIHC5	2.98	3.98	1.992768431
Male	Nerve Ring	GRIHC5	0.08	1.08	0.111031312
Male	Nerve Ring	GRIHC5	0	1	0
Male	Nerve Ring	GRIHC5	0	1	0
Male	Nerve Ring	GRIHC5	0	1	0
Male	Nerve Ring	GRIHC5	0	1	0
Male	Nerve Ring	GRIHC5	0	1	0
Male	Nerve Ring	GRIHC5	0	1	0
Male	Nerve Ring	GRIHC5	0.78	1.78	0.831877241
Male	Nerve Ring	GRIHC5	0.41	1.41	0.495695163
Male	Nerve Ring	GRIHC5	0.42	1.42	0.50589093
Male	Tentacles	GRIHC4	27.05	28.05	4.809928866
Male	Tentacles	GRIHC4	2.6	3.6	1.847996907
Male	Tentacles	GRIHC4	0	1	0
Male	Tentacles	GRIHC4	8.14	9.14	3.192194165
Male	Tentacles	GRIHC4	13.43	14.43	3.850999395
Male	Tentacles	GRIHC4	16.94	17.94	4.165107985
Male	Tentacles	GRIHC4	5	6	2.584962501
Male	Tentacles	GRIHC4	2.8	3.8	1.925999419
Male	Tentacles	GRIHC4	6.07	7.07	2.821710215
Male	Tentacles	GRIHC4	7.67	8.67	3.116031993
Male	Tentacles	GRIHC4	7.25	8.25	3.044394119
Male	Tentacles	GRIHC4	3.54	4.54	2.182692298
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Radial Nerve	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0

Male	Nerve Ring	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0
Male	Nerve Ring	GRIHC4	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Tentacles	GRIHC3	0	1	0
Male	Radial Nerve	GRIHC3	23.81	24.81	4.63284983
Male	Radial Nerve	GRIHC3	0	1	0
Male	Radial Nerve	GRIHC3	0	1	0
Male	Radial Nerve	GRIHC3	0	1	0
Male	Radial Nerve	GRIHC3	0	1	0
Male	Radial Nerve	GRIHC3	0.04	1.04	0.056583528
Male	Radial Nerve	GRIHC3	0	1	0
Male	Radial Nerve	GRIHC3	0	1	0
Male	Radial Nerve	GRIHC3	0	1	0
Male	Radial Nerve	GRIHC3	0.07	1.07	0.097610797
Male	Radial Nerve	GRIHC3	0	1	0
Male	Radial Nerve	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Nerve Ring	GRIHC3	0	1	0
Male	Tentacles	GRIHC2	46.34	47.34	5.564987801
Male	Tentacles	GRIHC2	8.89	9.89	3.305970521
Male	Tentacles	GRIHC2	6.01	7.01	2.809414444
Male	Tentacles	GRIHC2	6.24	7.24	2.855989697
Male	Tentacles	GRIHC2	65.66	66.66	6.058749412
Male	Tentacles	GRIHC2	15.17	16.17	4.015247774
Male	Tentacles	GRIHC2	15.1	16.1	4.008988783
Male	Tentacles	GRIHC2	25.43	26.43	4.72410452
Male	Tentacles	GRIHC2	17.73	18.73	4.227278994
Male	Tentacles	GRIHC2	18.92	19.92	4.316145742
Male	Tentacles	GRIHC2	4.06	5.06	2.339137385

Male	Tentacles	GRIHC2	51.03	52.03	5.701271802
Male	Radial Nerve	GRIHC2	0	1	0
Male	Radial Nerve	GRIHC2	3.03	4.03	2.010779839
Male	Radial Nerve	GRIHC2	0	1	0
Male	Radial Nerve	GRIHC2	12.1	13.1	3.711494907
Male	Radial Nerve	GRIHC2	1.68	2.68	1.422233001
Male	Radial Nerve	GRIHC2	1.95	2.95	1.560714954
Male	Radial Nerve	GRIHC2	1.2	2.2	1.137503524
Male	Radial Nerve	GRIHC2	4.1	5.1	2.350497247
Male	Radial Nerve	GRIHC2	3.07	4.07	2.025028794
Male	Radial Nerve	GRIHC2	3	4	2
Male	Radial Nerve	GRIHC2	2.18	3.18	1.669026766
Male	Radial Nerve	GRIHC2	4.96	5.96	2.575312331
Male	Nerve Ring	GRIHC2	2.39	3.39	1.761285273
Male	Nerve Ring	GRIHC2	19.82	20.82	4.379898164
Male	Nerve Ring	GRIHC2	1.35	2.35	1.232660757
Male	Nerve Ring	GRIHC2	10.21	11.21	3.486714373
Male	Nerve Ring	GRIHC2	1.17	2.17	1.117695043
Male	Nerve Ring	GRIHC2	17.9	18.9	4.240314329
Male	Nerve Ring	GRIHC2	2.09	3.09	1.627606838
Male	Nerve Ring	GRIHC2	13.05	14.05	3.812498225
Male	Nerve Ring	GRIHC2	12	13	3.700439718
Male	Nerve Ring	GRIHC2	35.01	36.01	5.170325694
Male	Nerve Ring	GRIHC2	5.07	6.07	2.601696516
Male	Nerve Ring	GRIHC2	13.76	14.76	3.883620816
Male	Tentacles	GRIHC1	23.25	24.25	4.599912842
Male	Tentacles	GRIHC1	28.47	29.47	4.881175155
Male	Tentacles	GRIHC1	0	1	0
Male	Tentacles	GRIHC1	30.73	31.73	4.987775616
Male	Tentacles	GRIHC1	0.48	1.48	0.565597176
Male	Tentacles	GRIHC1	63.64	64.64	6.014355293
Male	Tentacles	GRIHC1	12.72	13.72	3.778208576
Male	Tentacles	GRIHC1	10.3	11.3	3.498250868
Male	Tentacles	GRIHC1	40.96	41.96	5.390942773
Male	Tentacles	GRIHC1	87.87	88.87	6.473624583
Male	Tentacles	GRIHC1	69.8	70.8	6.145677455
Male	Tentacles	GRIHC1	59.52	60.52	5.919340082
Male	Radial Nerve	GRIHC1	0	1	0
Male	Radial Nerve	GRIHC1	0.07	1.07	0.097610797
Male	Radial Nerve	GRIHC1	0.03	1.03	0.042644337
Male	Radial Nerve	GRIHC1	4.7	5.7	2.510961919
Male	Radial Nerve	GRIHC1	0	1	0
Male	Radial Nerve	GRIHC1	2.24	3.24	1.695993813
Male	Radial Nerve	GRIHC1	0	1	0
Male	Radial Nerve	GRIHC1	0.45	1.45	0.5360529
Male	Radial Nerve	GRIHC1	1.42	2.42	1.275007047
Male	Radial Nerve	GRIHC1	1.71	2.71	1.438292852
Male	Radial Nerve	GRIHC1	0.09	1.09	0.124328135
Male	Radial Nerve	GRIHC1	0.04	1.04	0.056583528
Male	Nerve Ring	GRIHC1	4.93	5.93	2.568032105
Male	Nerve Ring	GRIHC1	0.84	1.84	0.879705766
Male	Nerve Ring	GRIHC1	3.68	4.68	2.22650853
Male	Nerve Ring	GRIHC1	0.44	1.44	0.526068812
Male	Nerve Ring	GRIHC1	7.88	8.88	3.150559677
Male	Nerve Ring	GRIHC1	0	1	0

Male	Nerve Ring	GRIHC1	2.51	3.51	1.811471031
Male	Nerve Ring	GRIHC1	0.33	1.33	0.411426246
Male	Nerve Ring	GRIHC1	0.29	1.29	0.367371066
Male	Nerve Ring	GRIHC1	17.51	18.51	4.21023299
Male	Nerve Ring	GRIHC1	0	1	0
Male	Nerve Ring	GRIHC1	0.18	1.18	0.23878686
Male	Tentacles	GRIHB	45.31	46.31	5.533251852
Male	Tentacles	GRIHB	114.88	115.88	6.856487779
Male	Tentacles	GRIHB	0.55	1.55	0.632268215
Male	Tentacles	GRIHB	83.07	84.07	6.393519168
Male	Tentacles	GRIHB	2.9	3.9	1.963474124
Male	Tentacles	GRIHB	128.57	129.57	7.017587912
Male	Tentacles	GRIHB	68.61	69.61	6.12122267
Male	Tentacles	GRIHB	91.89	92.89	6.537451388
Male	Tentacles	GRIHB	112.74	113.74	6.829595899
Male	Tentacles	GRIHB	160.1	161.1	7.331812684
Male	Tentacles	GRIHB	86.47	87.47	6.450716389
Male	Tentacles	GRIHB	169.28	170.28	7.411765185
Male	Radial Nerve	GRIHB	9.44	10.44	3.384049807
Male	Radial Nerve	GRIHB	15.06	16.06	4.005399988
Male	Radial Nerve	GRIHB	5.91	6.91	2.788685711
Male	Radial Nerve	GRIHB	35.79	36.79	5.201241771
Male	Radial Nerve	GRIHB	2.78	3.78	1.918386234
Male	Radial Nerve	GRIHB	103.86	104.86	6.712320641
Male	Radial Nerve	GRIHB	6.26	7.26	2.859969548
Male	Radial Nerve	GRIHB	5.6	6.6	2.722466024
Male	Radial Nerve	GRIHB	11.11	12.11	3.59812696
Male	Radial Nerve	GRIHB	11.05	12.05	3.590961241
Male	Radial Nerve	GRIHB	3.68	4.68	2.22650853
Male	Radial Nerve	GRIHB	0.14	1.14	0.189033824
Male	Nerve Ring	GRIHB	181.87	182.87	7.514674609
Male	Nerve Ring	GRIHB	10.33	11.33	3.502075956
Male	Nerve Ring	GRIHB	90.5	91.5	6.515699838
Male	Nerve Ring	GRIHB	12.41	13.41	3.745237332
Male	Nerve Ring	GRIHB	290.8	291.8	8.188836073
Male	Nerve Ring	GRIHB	7.05	8.05	3.008988783
Male	Nerve Ring	GRIHB	177.46	178.46	7.479456935
Male	Nerve Ring	GRIHB	9.48	10.48	3.389566812
Male	Nerve Ring	GRIHB	2.99	3.99	1.996388746
Male	Nerve Ring	GRIHB	9.89	10.89	3.444932049
Male	Nerve Ring	GRIHB	1.69	2.69	1.427606173
Male	Nerve Ring	GRIHB	9.26	10.26	3.358958826
Male	Tentacles	GRIHA5	34.02	35.02	5.130107179
Male	Tentacles	GRIHA5	9.65	10.65	3.412781525
Male	Tentacles	GRIHA5	36.18	37.18	5.216454865
Male	Tentacles	GRIHA5	5.62	6.62	2.726831217
Male	Tentacles	GRIHA5	53.38	54.38	5.765004246
Male	Tentacles	GRIHA5	3.35	4.35	2.121015401
Male	Tentacles	GRIHA5	23.05	24.05	4.587964989
Male	Tentacles	GRIHA5	7.41	8.41	3.0721058
Male	Tentacles	GRIHA5	2.48	3.48	1.799087306
Male	Tentacles	GRIHA5	28.41	29.41	4.878234879
Male	Tentacles	GRIHA5	1.23	2.23	1.15704371
Male	Tentacles	GRIHA5	2.33	3.33	1.735522177
Male	Radial Nerve	GRIHA5	0	1	0

Male	Radial Nerve	GRIHA5	0	1	0
Male	Radial Nerve	GRIHA5	0	1	0
Male	Radial Nerve	GRIHA5	0	1	0
Male	Radial Nerve	GRIHA5	0	1	0
Male	Radial Nerve	GRIHA5	0	1	0
Male	Radial Nerve	GRIHA5	0	1	0
Male	Radial Nerve	GRIHA5	0	1	0
Male	Radial Nerve	GRIHA5	0	1	0
Male	Radial Nerve	GRIHA5	0	1	0
Male	Radial Nerve	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Nerve Ring	GRIHA5	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Tentacles	GRIHA4	0	1	0
Male	Radial Nerve	GRIHA4	0	1	0
Male	Radial Nerve	GRIHA4	13.71	14.71	3.878725341
Male	Radial Nerve	GRIHA4	2.43	3.43	1.778208576
Male	Radial Nerve	GRIHA4	41.7	42.7	5.416164165
Male	Radial Nerve	GRIHA4	9.36	10.36	3.372952098
Male	Radial Nerve	GRIHA4	57.76	58.76	5.876762491
Male	Radial Nerve	GRIHA4	4.09	5.09	2.347665656
Male	Radial Nerve	GRIHA4	2.64	3.64	1.86393845
Male	Radial Nerve	GRIHA4	8.27	9.27	3.212569339
Male	Radial Nerve	GRIHA4	6.7	7.7	2.944858446
Male	Radial Nerve	GRIHA4	2.64	3.64	1.86393845
Male	Radial Nerve	GRIHA4	0.09	1.09	0.124328135
Male	Nerve Ring	GRIHA4	0	1	0
Male	Nerve Ring	GRIHA4	0	1	0
Male	Nerve Ring	GRIHA4	0	1	0
Male	Nerve Ring	GRIHA4	0	1	0
Male	Nerve Ring	GRIHA4	0	1	0
Male	Nerve Ring	GRIHA4	0	1	0
Male	Nerve Ring	GRIHA4	0	1	0
Male	Nerve Ring	GRIHA4	0	1	0
Male	Nerve Ring	GRIHA4	0	1	0

Male	Nerve Ring	GRIHA4	0	1	0
Male	Nerve Ring	GRIHA4	0	1	0
Male	Nerve Ring	GRIHA4	0	1	0
Male	Tentacles	GRIHA3	0	1	0
Male	Tentacles	GRIHA3	2.04	3.04	1.604071324
Male	Tentacles	GRIHA3	0.06	1.06	0.084064265
Male	Tentacles	GRIHA3	0	1	0
Male	Tentacles	GRIHA3	0	1	0
Male	Tentacles	GRIHA3	0.46	1.46	0.545968369
Male	Tentacles	GRIHA3	0.06	1.06	0.084064265
Male	Tentacles	GRIHA3	0.06	1.06	0.084064265
Male	Tentacles	GRIHA3	0.02	1.02	0.028569152
Male	Tentacles	GRIHA3	0.38	1.38	0.464668267
Male	Tentacles	GRIHA3	0	1	0
Male	Tentacles	GRIHA3	0.1	1.1	0.137503524
Male	Radial Nerve	GRIHA3	63.27	64.27	6.006073567
Male	Radial Nerve	GRIHA3	51.53	52.53	5.715069679
Male	Radial Nerve	GRIHA3	2.82	3.82	1.933572638
Male	Radial Nerve	GRIHA3	87.73	88.73	6.471350063
Male	Radial Nerve	GRIHA3	3.83	4.83	2.272023189
Male	Radial Nerve	GRIHA3	61.66	62.66	5.969472865
Male	Radial Nerve	GRIHA3	27.69	28.69	4.842476063
Male	Radial Nerve	GRIHA3	65.15	66.15	6.047669251
Male	Radial Nerve	GRIHA3	51.07	52.07	5.702380502
Male	Radial Nerve	GRIHA3	96.31	97.31	6.604516165
Male	Radial Nerve	GRIHA3	89.96	90.96	6.507160349
Male	Radial Nerve	GRIHA3	86.39	87.39	6.449396297
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Nerve Ring	GRIHA3	0	1	0
Male	Tentacles	GRIHA2	0.39	1.39	0.475084883
Male	Tentacles	GRIHA2	3.05	4.05	2.017921908
Male	Tentacles	GRIHA2	2.16	3.16	1.659924558
Male	Tentacles	GRIHA2	1.79	2.79	1.480265122
Male	Tentacles	GRIHA2	0.32	1.32	0.40053793
Male	Tentacles	GRIHA2	1.43	2.43	1.280956314
Male	Tentacles	GRIHA2	0.29	1.29	0.367371066
Male	Tentacles	GRIHA2	1.23	2.23	1.15704371
Male	Tentacles	GRIHA2	0.72	1.72	0.782408565
Male	Tentacles	GRIHA2	5.56	6.56	2.713695815
Male	Tentacles	GRIHA2	0.68	1.68	0.748461233
Male	Tentacles	GRIHA2	0.84	1.84	0.879705766
Male	Radial Nerve	GRIHA2	0	1	0
Male	Radial Nerve	GRIHA2	0	1	0
Male	Radial Nerve	GRIHA2	0	1	0
Male	Radial Nerve	GRIHA2	0	1	0

Male	Radial Nerve	GRIHA2	0	1	0
Male	Radial Nerve	GRIHA2	0	1	0
Male	Radial Nerve	GRIHA2	0	1	0
Male	Radial Nerve	GRIHA2	0	1	0
Male	Radial Nerve	GRIHA2	0	1	0
Male	Radial Nerve	GRIHA2	0	1	0
Male	Radial Nerve	GRIHA2	0	1	0
Male	Radial Nerve	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Nerve Ring	GRIHA2	0	1	0
Male	Tentacles	GRIHA1	0.44	1.44	0.526068812
Male	Tentacles	GRIHA1	0	1	0
Male	Tentacles	GRIHA1	0	1	0
Male	Tentacles	GRIHA1	1.07	2.07	1.049630768
Male	Tentacles	GRIHA1	1.5	2.5	1.321928095
Male	Tentacles	GRIHA1	0.85	1.85	0.887525271
Male	Tentacles	GRIHA1	0.68	1.68	0.748461233
Male	Tentacles	GRIHA1	0.07	1.07	0.097610797
Male	Tentacles	GRIHA1	1.44	2.44	1.286881148
Male	Tentacles	GRIHA1	1.09	2.09	1.063502942
Male	Tentacles	GRIHA1	0	1	0
Male	Tentacles	GRIHA1	0.15	1.15	0.201633861
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Radial Nerve	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0
Male	Nerve Ring	GRIHA1	0	1	0

Male	Nerve Ring	GRIHA1	0	1	0
Male	Tentacles	GRIK2	0.53	1.53	0.613531653
Male	Tentacles	GRIK2	0	1	0
Male	Tentacles	GRIK2	0	1	0
Male	Tentacles	GRIK2	0.16	1.16	0.214124805
Male	Tentacles	GRIK2	0	1	0
Male	Tentacles	GRIK2	0.26	1.26	0.333423734
Male	Tentacles	GRIK2	0	1	0
Male	Tentacles	GRIK2	0.08	1.08	0.111031312
Male	Tentacles	GRIK2	0.12	1.12	0.163498732
Male	Tentacles	GRIK2	0.21	1.21	0.275007047
Male	Tentacles	GRIK2	0.21	1.21	0.275007047
Male	Tentacles	GRIK2	0.16	1.16	0.214124805
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Radial Nerve	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Nerve Ring	GRIK2	0	1	0
Male	Tentacles	GRIAbeta	0	1	0
Male	Tentacles	GRIAbeta	0.51	1.51	0.59454855
Male	Tentacles	GRIAbeta	0	1	0
Male	Tentacles	GRIAbeta	0.16	1.16	0.214124805
Male	Tentacles	GRIAbeta	0.64	1.64	0.713695815
Male	Tentacles	GRIAbeta	0.06	1.06	0.084064265
Male	Tentacles	GRIAbeta	0	1	0
Male	Tentacles	GRIAbeta	0.11	1.11	0.150559677
Male	Tentacles	GRIAbeta	0.2	1.2	0.263034406
Male	Tentacles	GRIAbeta	0.08	1.08	0.111031312
Male	Tentacles	GRIAbeta	0.19	1.19	0.250961574
Male	Tentacles	GRIAbeta	0	1	0
Male	Radial Nerve	GRIAbeta	1.01	2.01	1.007195501
Male	Radial Nerve	GRIAbeta	0.11	1.11	0.150559677
Male	Radial Nerve	GRIAbeta	0	1	0
Male	Radial Nerve	GRIAbeta	0.93	1.93	0.948600847
Male	Radial Nerve	GRIAbeta	0.07	1.07	0.097610797
Male	Radial Nerve	GRIAbeta	0.42	1.42	0.50589093

Male	Radial Nerve	GRIAbeta	0.22	1.22	0.286881148
Male	Radial Nerve	GRIAbeta	0.09	1.09	0.124328135
Male	Radial Nerve	GRIAbeta	0.6	1.6	0.678071905
Male	Radial Nerve	GRIAbeta	0.65	1.65	0.722466024
Male	Radial Nerve	GRIAbeta	1.36	2.36	1.23878686
Male	Radial Nerve	GRIAbeta	0.09	1.09	0.124328135
Male	Nerve Ring	GRIAbeta	1.77	2.77	1.469885976
Male	Nerve Ring	GRIAbeta	0.45	1.45	0.5360529
Male	Nerve Ring	GRIAbeta	0.41	1.41	0.495695163
Male	Nerve Ring	GRIAbeta	0.42	1.42	0.50589093
Male	Nerve Ring	GRIAbeta	0.65	1.65	0.722466024
Male	Nerve Ring	GRIAbeta	0	1	0
Male	Nerve Ring	GRIAbeta	0.1	1.1	0.137503524
Male	Nerve Ring	GRIAbeta	3.74	4.74	2.244887059
Male	Nerve Ring	GRIAbeta	0.17	1.17	0.22650853
Male	Nerve Ring	GRIAbeta	0.29	1.29	0.367371066
Male	Nerve Ring	GRIAbeta	0	1	0
Male	Nerve Ring	GRIAbeta	0.04	1.04	0.056583528
Male	Tentacles	GRIAalpha	0.66	1.66	0.731183242
Male	Tentacles	GRIAalpha	0	1	0
Male	Tentacles	GRIAalpha	1	2	1
Male	Tentacles	GRIAalpha	0.09	1.09	0.124328135
Male	Tentacles	GRIAalpha	0.09	1.09	0.124328135
Male	Tentacles	GRIAalpha	0.16	1.16	0.214124805
Male	Tentacles	GRIAalpha	0.18	1.18	0.23878686
Male	Tentacles	GRIAalpha	0.19	1.19	0.250961574
Male	Tentacles	GRIAalpha	0.37	1.37	0.454175893
Male	Tentacles	GRIAalpha	0.09	1.09	0.124328135
Male	Tentacles	GRIAalpha	0.15	1.15	0.201633861
Male	Tentacles	GRIAalpha	0.07	1.07	0.097610797
Male	Radial Nerve	GRIAalpha	0	1	0
Male	Radial Nerve	GRIAalpha	0.1	1.1	0.137503524
Male	Radial Nerve	GRIAalpha	0	1	0
Male	Radial Nerve	GRIAalpha	0.07	1.07	0.097610797
Male	Radial Nerve	GRIAalpha	0	1	0
Male	Radial Nerve	GRIAalpha	0.05	1.05	0.070389328
Male	Radial Nerve	GRIAalpha	0.59	1.59	0.669026766
Male	Radial Nerve	GRIAalpha	0	1	0
Male	Radial Nerve	GRIAalpha	0.17	1.17	0.22650853
Male	Radial Nerve	GRIAalpha	0.08	1.08	0.111031312
Male	Radial Nerve	GRIAalpha	0.04	1.04	0.056583528
Male	Radial Nerve	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Male	Nerve Ring	GRIAalpha	0	1	0
Female	Tentacles	GRIHC6	0	1	0

Female	Tentacles	GRIHC6	0	1	0
Female	Tentacles	GRIHC6	0	1	0
Female	Tentacles	GRIHC6	0	1	0
Female	Tentacles	GRIHC6	0	1	0
Female	Radial Nerve	GRIHC6	0	1	0
Female	Radial Nerve	GRIHC6	1.61	2.61	1.384049807
Female	Radial Nerve	GRIHC6	0	1	0
Female	Radial Nerve	GRIHC6	0	1	0
Female	Radial Nerve	GRIHC6	0	1	0
Female	Nerve Ring	GRIHC6	0	1	0
Female	Nerve Ring	GRIHC6	0	1	0
Female	Nerve Ring	GRIHC6	0	1	0
Female	Nerve Ring	GRIHC6	0	1	0
Female	Nerve Ring	GRIHC6	0	1	0
Female	Tentacles	GRIHC5	0.07	1.07	0.097610797
Female	Tentacles	GRIHC5	1.31	2.31	1.207892852
Female	Tentacles	GRIHC5	7	8	3
Female	Tentacles	GRIHC5	0.31	1.31	0.389566812
Female	Tentacles	GRIHC5	0.17	1.17	0.22650853
Female	Radial Nerve	GRIHC5	0	1	0
Female	Radial Nerve	GRIHC5	5.57	6.57	2.715893371
Female	Radial Nerve	GRIHC5	3.94	4.94	2.304511042
Female	Radial Nerve	GRIHC5	0.78	1.78	0.831877241
Female	Radial Nerve	GRIHC5	7.79	8.79	3.135863165
Female	Nerve Ring	GRIHC5	0.18	1.18	0.23878686
Female	Nerve Ring	GRIHC5	0.06	1.06	0.084064265
Female	Nerve Ring	GRIHC5	0	1	0
Female	Nerve Ring	GRIHC5	0	1	0
Female	Nerve Ring	GRIHC5	0	1	0
Female	Tentacles	GRIHC4	3.64	4.64	2.214124805
Female	Tentacles	GRIHC4	6.44	7.44	2.895302621
Female	Tentacles	GRIHC4	6.02	7.02	2.811471031
Female	Tentacles	GRIHC4	6.84	7.84	2.970853654
Female	Tentacles	GRIHC4	9.77	10.77	3.428946345
Female	Radial Nerve	GRIHC4	0	1	0
Female	Radial Nerve	GRIHC4	0.51	1.51	0.59454855
Female	Radial Nerve	GRIHC4	0.07	1.07	0.097610797
Female	Radial Nerve	GRIHC4	0	1	0
Female	Radial Nerve	GRIHC4	0	1	0
Female	Nerve Ring	GRIHC4	0	1	0
Female	Nerve Ring	GRIHC4	0	1	0
Female	Nerve Ring	GRIHC4	0	1	0
Female	Nerve Ring	GRIHC4	0	1	0
Female	Nerve Ring	GRIHC4	0	1	0
Female	Tentacles	GRIHC3	0	1	0
Female	Tentacles	GRIHC3	0	1	0
Female	Tentacles	GRIHC3	0	1	0
Female	Tentacles	GRIHC3	0	1	0
Female	Tentacles	GRIHC3	0	1	0
Female	Radial Nerve	GRIHC3	0	1	0
Female	Radial Nerve	GRIHC3	0	1	0
Female	Radial Nerve	GRIHC3	0	1	0
Female	Radial Nerve	GRIHC3	0	1	0
Female	Radial Nerve	GRIHC3	0	1	0
Female	Nerve Ring	GRIHC3	0	1	0

Female	Nerve Ring	GRIHC3	0	1	0
Female	Nerve Ring	GRIHC3	0	1	0
Female	Nerve Ring	GRIHC3	0	1	0
Female	Nerve Ring	GRIHC3	0	1	0
Female	Tentacles	GRIHC2	45.18	46.18	5.529196268
Female	Tentacles	GRIHC2	63.6	64.6	6.01346226
Female	Tentacles	GRIHC2	18.21	19.21	4.263785614
Female	Tentacles	GRIHC2	11.77	12.77	3.67468662
Female	Tentacles	GRIHC2	57.41	58.41	5.86814348
Female	Radial Nerve	GRIHC2	11.07	12.07	3.593353771
Female	Radial Nerve	GRIHC2	20.53	21.53	4.428276414
Female	Radial Nerve	GRIHC2	1.64	2.64	1.40053793
Female	Radial Nerve	GRIHC2	3.62	4.62	2.207892852
Female	Radial Nerve	GRIHC2	0.91	1.91	0.933572638
Female	Nerve Ring	GRIHC2	10.59	11.59	3.534808661
Female	Nerve Ring	GRIHC2	10.49	11.49	3.522306893
Female	Nerve Ring	GRIHC2	30.14	31.14	4.960697039
Female	Nerve Ring	GRIHC2	10.22	11.22	3.488000771
Female	Nerve Ring	GRIHC2	7.3	8.3	3.053111336
Female	Tentacles	GRIHC1	0.45	1.45	0.5360529
Female	Tentacles	GRIHC1	55.92	56.92	5.830863757
Female	Tentacles	GRIHC1	54.65	55.65	5.798309782
Female	Tentacles	GRIHC1	27.34	28.34	4.824767853
Female	Tentacles	GRIHC1	83.23	84.23	6.396262261
Female	Radial Nerve	GRIHC1	0.22	1.22	0.286881148
Female	Radial Nerve	GRIHC1	51.93	52.93	5.726013749
Female	Radial Nerve	GRIHC1	6.74	7.74	2.952333566
Female	Radial Nerve	GRIHC1	8.34	9.34	3.22342255
Female	Radial Nerve	GRIHC1	23.22	24.22	4.59812696
Female	Nerve Ring	GRIHC1	153.53	154.53	7.271743136
Female	Nerve Ring	GRIHC1	0.99	1.99	0.992768431
Female	Nerve Ring	GRIHC1	0.07	1.07	0.097610797
Female	Nerve Ring	GRIHC1	0.16	1.16	0.214124805
Female	Nerve Ring	GRIHC1	41.67	42.67	5.415150205
Female	Tentacles	GRIHB	1.75	2.75	1.459431619
Female	Tentacles	GRIHB	123.27	124.27	6.957334247
Female	Tentacles	GRIHB	186.49	187.49	7.55066984
Female	Tentacles	GRIHB	134.3	135.3	7.080018029
Female	Tentacles	GRIHB	170.51	171.51	7.422148886
Female	Radial Nerve	GRIHB	3.53	4.53	2.17951105
Female	Radial Nerve	GRIHB	205.21	206.21	7.687970487
Female	Radial Nerve	GRIHB	54.05	55.05	5.782670659
Female	Radial Nerve	GRIHB	54.95	55.95	5.806066226
Female	Radial Nerve	GRIHB	176.3	177.3	7.470048726
Female	Nerve Ring	GRIHB	387.95	388.95	8.603440897
Female	Nerve Ring	GRIHB	3.94	4.94	2.304511042
Female	Nerve Ring	GRIHB	16.88	17.88	4.160274831
Female	Nerve Ring	GRIHB	6	7	2.807354922
Female	Nerve Ring	GRIHB	253.57	254.57	7.991918604
Female	Tentacles	GRIHA5	230.49	231.49	7.854806062
Female	Tentacles	GRIHA5	2.6	3.6	1.847996907
Female	Tentacles	GRIHA5	2.5	3.5	1.807354922
Female	Tentacles	GRIHA5	2.65	3.65	1.867896464
Female	Tentacles	GRIHA5	62.34	63.34	5.985044962
Female	Radial Nerve	GRIHA5	0	1	0

Female	Radial Nerve	GRIHA5	0	1	0
Female	Radial Nerve	GRIHA5	0	1	0
Female	Radial Nerve	GRIHA5	0	1	0
Female	Radial Nerve	GRIHA5	0	1	0
Female	Nerve Ring	GRIHA5	0	1	0
Female	Nerve Ring	GRIHA5	0	1	0
Female	Nerve Ring	GRIHA5	0	1	0
Female	Nerve Ring	GRIHA5	0	1	0
Female	Nerve Ring	GRIHA5	0	1	0
Female	Tentacles	GRIHA4	0	1	0
Female	Tentacles	GRIHA4	0	1	0
Female	Tentacles	GRIHA4	0	1	0
Female	Tentacles	GRIHA4	0	1	0
Female	Tentacles	GRIHA4	0	1	0
Female	Radial Nerve	GRIHA4	8.19	9.19	3.200064862
Female	Radial Nerve	GRIHA4	202.52	203.52	7.669026766
Female	Radial Nerve	GRIHA4	66.54	67.54	6.077670274
Female	Radial Nerve	GRIHA4	82.09	83.09	6.376602952
Female	Radial Nerve	GRIHA4	161.38	162.38	7.34323014
Female	Nerve Ring	GRIHA4	0	1	0
Female	Nerve Ring	GRIHA4	0	1	0
Female	Nerve Ring	GRIHA4	0	1	0
Female	Nerve Ring	GRIHA4	0	1	0
Female	Nerve Ring	GRIHA4	0	1	0
Female	Tentacles	GRIHA3	0.17	1.17	0.22650853
Female	Tentacles	GRIHA3	0.12	1.12	0.163498732
Female	Tentacles	GRIHA3	0.47	1.47	0.555816155
Female	Tentacles	GRIHA3	0	1	0
Female	Tentacles	GRIHA3	0.3	1.3	0.378511623
Female	Radial Nerve	GRIHA3	2.01	3.01	1.589763487
Female	Radial Nerve	GRIHA3	74.28	75.28	6.234194723
Female	Radial Nerve	GRIHA3	106.9	107.9	6.753551055
Female	Radial Nerve	GRIHA3	82.56	83.56	6.384740587
Female	Radial Nerve	GRIHA3	119.3	120.3	6.910492832
Female	Nerve Ring	GRIHA3	0	1	0
Female	Nerve Ring	GRIHA3	0	1	0
Female	Nerve Ring	GRIHA3	0	1	0
Female	Nerve Ring	GRIHA3	0	1	0
Female	Nerve Ring	GRIHA3	0	1	0
Female	Tentacles	GRIHA2	37.12	38.12	5.252476214
Female	Tentacles	GRIHA2	6.06	7.06	2.819668183
Female	Tentacles	GRIHA2	0.42	1.42	0.50589093
Female	Tentacles	GRIHA2	2.91	3.91	1.967168608
Female	Tentacles	GRIHA2	1.25	2.25	1.169925001
Female	Radial Nerve	GRIHA2	0	1	0
Female	Radial Nerve	GRIHA2	0	1	0
Female	Radial Nerve	GRIHA2	0	1	0
Female	Radial Nerve	GRIHA2	0	1	0
Female	Radial Nerve	GRIHA2	0	1	0
Female	Nerve Ring	GRIHA2	0	1	0
Female	Nerve Ring	GRIHA2	0	1	0
Female	Nerve Ring	GRIHA2	0	1	0
Female	Nerve Ring	GRIHA2	0	1	0
Female	Nerve Ring	GRIHA2	0	1	0
Female	Tentacles	GRIHA1	1.39	2.39	1.257010618

Female	Tentacles	GRIHA1	5.46	6.46	2.691534165
Female	Tentacles	GRIHA1	0.58	1.58	0.659924558
Female	Tentacles	GRIHA1	0.36	1.36	0.443606651
Female	Tentacles	GRIHA1	3.97	4.97	2.313245852
Female	Radial Nerve	GRIHA1	0	1	0
Female	Radial Nerve	GRIHA1	0	1	0
Female	Radial Nerve	GRIHA1	0	1	0
Female	Radial Nerve	GRIHA1	0	1	0
Female	Radial Nerve	GRIHA1	0	1	0
Female	Nerve Ring	GRIHA1	0	1	0
Female	Nerve Ring	GRIHA1	0	1	0
Female	Nerve Ring	GRIHA1	0	1	0
Female	Nerve Ring	GRIHA1	0	1	0
Female	Nerve Ring	GRIHA1	0	1	0
Female	Tentacles	GRIK2	0.06	1.06	0.084064265
Female	Tentacles	GRIK2	0.19	1.19	0.250961574
Female	Tentacles	GRIK2	0.51	1.51	0.59454855
Female	Tentacles	GRIK2	0.09	1.09	0.124328135
Female	Tentacles	GRIK2	0.02	1.02	0.028569152
Female	Radial Nerve	GRIK2	0	1	0
Female	Radial Nerve	GRIK2	0	1	0
Female	Radial Nerve	GRIK2	0	1	0
Female	Radial Nerve	GRIK2	0	1	0
Female	Radial Nerve	GRIK2	0	1	0
Female	Nerve Ring	GRIK2	0	1	0
Female	Nerve Ring	GRIK2	0	1	0
Female	Nerve Ring	GRIK2	0	1	0
Female	Nerve Ring	GRIK2	0	1	0
Female	Nerve Ring	GRIK2	0	1	0
Female	Nerve Ring	GRIK2	0	1	0
Female	Tentacles	GRIAbeta	0.62	1.62	0.695993813
Female	Tentacles	GRIAbeta	0.6	1.6	0.678071905
Female	Tentacles	GRIAbeta	0.05	1.05	0.070389328
Female	Tentacles	GRIAbeta	0	1	0
Female	Tentacles	GRIAbeta	0.36	1.36	0.443606651
Female	Radial Nerve	GRIAbeta	0.46	1.46	0.545968369
Female	Radial Nerve	GRIAbeta	1.1	2.1	1.070389328
Female	Radial Nerve	GRIAbeta	1.91	2.91	1.541019153
Female	Radial Nerve	GRIAbeta	0.69	1.69	0.757023247
Female	Radial Nerve	GRIAbeta	0.88	1.88	0.910732662
Female	Nerve Ring	GRIAbeta	3.05	4.05	2.017921908
Female	Nerve Ring	GRIAbeta	3.33	4.33	2.114367025
Female	Nerve Ring	GRIAbeta	0.18	1.18	0.23878686
Female	Nerve Ring	GRIAbeta	0.36	1.36	0.443606651
Female	Nerve Ring	GRIAbeta	0.14	1.14	0.189033824
Female	Tentacles	GRIAalpha	0.22	1.22	0.286881148
Female	Tentacles	GRIAalpha	0.37	1.37	0.454175893
Female	Tentacles	GRIAalpha	0.52	1.52	0.604071324
Female	Tentacles	GRIAalpha	0.19	1.19	0.250961574
Female	Tentacles	GRIAalpha	0.39	1.39	0.475084883
Female	Radial Nerve	GRIAalpha	0.62	1.62	0.695993813
Female	Radial Nerve	GRIAalpha	0.6	1.6	0.678071905
Female	Radial Nerve	GRIAalpha	0.05	1.05	0.070389328
Female	Radial Nerve	GRIAalpha	0	1	0
Female	Radial Nerve	GRIAalpha	0.36	1.36	0.443606651

Female	Nerve Ring	GRIAalpha	0	1	0
Female	Nerve Ring	GRIAalpha	0	1	0
Female	Nerve Ring	GRIAalpha	0	1	0
Female	Nerve Ring	GRIAalpha	0	1	0
Female	Nerve Ring	GRIAalpha	0	1	0