

Supplementary information for: The reference genome of the freshwater snail *Lymnaea stagnalis* reveals evolutionary and molecular implications of simultaneous hermaphroditism

Supplementary Information

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1. High Molecular Weight DNA extraction

Genomic DNA was extracted at the Genoscope, via plug-DNA extraction to obtain high molecular weight (200kb) DNA fragments.

A whole individual, flash-frozen and stored at -80°C , was removed from its shell, cleaned in a physiological water bath and then ground with a mortar in the presence of liquid nitrogen. The grinded material was then resuspended in 15ml SEB1X buffer in the presence of 0.2% β mercaptoethanol and gently stirred for 15min at 4°C . This solution resulting was passed through a specific strainer in order to remove as much mucus as possible. 0.05vol of a SEB 1X-Triton mixture was added to the 14ml of filtrate recovered, then after incubation for 10min at 4°C , centrifugation was performed for 20min at 600g at 4°C . The supernatant was removed and the resulting pellet of nuclei was washed 2 times with 1X SEB buffer, then resuspended in 300 μl of S buffer in the presence of 30 μl of SDS.

The protocol was immediately continued by embedding the nuclei in plugs. Low Melting Point agarose 2% was prepared extemporaneously and added to the nuclei suspension, volume by volume. After gentle homogenization with a vortex, avoiding bubbles, the mixture was poured into plugs at a rate of 100 μl per plug and left to polymerize on ice for 15min. The plugs were then expelled into a 50ml tube in the presence of 10ml LB buffer per plug and incubated for 1h at 37°C before undergoing proteinaseK digestion. After removal of the LB, the plugs were placed in the presence of 10ml DB buffer and proteinaseK at 40 $\mu\text{g}/\text{ml}$ final. After removal of the LB buffer, the plugs were placed in the presence of 10ml DB and proteinase K at 40 $\mu\text{g}/\text{ml}$ final and incubated in an oven at 50°C overnight. The following day, the proteinaseK solution was removed and inactivated by washing with a mixture of 10ml TE 10:1 pH8 and 23 μl PMSF 0.1M (40 $\mu\text{g}/\text{ml}$ final). Two washes of 30 min at room temperature were followed by 3 washes of 10min at room temperature with 20ml TE 10:1 pH8. The plugs were then stored in 30ml EDTA 0.5M pH8 at 4°C until extraction.

High-molecular-weight DNA was then extracted from the plugs by β -agarase treatment. After 5 washes in 20ml TE 1X buffer followed by 2 washes in 20ml MES buffer, each plug was incubated on paper, placed in a 1.5ml tube and incubated for 7min at 70°C in a dry water bath before being transferred at 42°C overnight in the presence of 16 μl β -agarase.

The following day, the entire volume ($\sim 500\ \mu\text{l}$) was transferred on to a dialysis filter using a broad tip and left for 30min at room temperature. . DNA quality was checked using Opgen QCards (Opgen, Rockville, MD, USA), and concentration determined via Qubit Fluorometric Quantitation (Thermo Fisher Scientific, Waltham, MA, USA).

2. Extraction Reagents and Buffers

- Reagents

- Tris-HCl 1M pH8 Ref : T3038 SIGMA
- KCl Ref : P3911-500g SIGMA
- Sucrose Ref : S5016-500g SIGMA
- Beta Mercaptoethanol Ref : M3148-25ml SIGMA
- Spermidine Ref : 85578-5g Fluka SIGMA
- Spermine Ref : S1141-5g SIGMA
- Ascorbic acid Ref : 255564-100G SIGMA
- NaOH Ref : S8045-1kg SIGMA
- Sodium Diethyldithio Carbamate Ref : 228680-100G SIGMA

- Concentrated solutions

- Tris-HCl 1M pH8 (dilute 121.1g Tris base in 900 ml H₂O + ~ 42 ml concentrated HCl to adjust pH 8 + H₂O qsq 1L) autoclave and conserve at room temperature.
- KCl 3M (dilute 67.09g in 300 ml H₂O) autoclave and conserve at room temperature.
- EDTA 1M pH9 (dilute 111.67g in 100 ml H₂O Adjust pH 9 with NaOH then adjust to 300 mL ; autoclave and conserve at room temperature.
- Sucrose 5X (dilute 342.3g in 300 ml H₂O), filter on 0.2 µmet ; conserve at room temperature.
- Sperminidine 100 mM (dilute 5g in 12.73 ml H₂O) filter on 0.2 µm, aliquote and conserve 1 month at -20°C.
- Spermine 100 mM (dissolve 5g in 17.4 ml H₂O dégassed) filtrer sur 0.2 µm aliquote and conserve 1 month at -20°C.
- NaOH 5M (pH adjustment: dilute 116g in 400 ml H₂O ; conserve at room temperature.

- **SEB 1X for 50 ml freshly prepared**

- Tris-HCl 1M 500 µl
- KCl 3M 1.65 ml
- EDTA 1 M pH9500 µl
- Sucrose 5X 5 ml
- Qsp 50 ml H₂O

Add extemporaneously :

- Spermine 100 mM 187.5 µl
- Spermidine 100 mM125 µl
- Ascorbic acid..... 50 mg
- Sodium Diethyldithio Carbamate 62.5 mg
- PVP40 1g
- + 0.2% βmercaptoethanol

- **Buffer S for 50 ml (stored at 4°)**

- Tris-HCl 20 mM (5ml Tris-HCl 1M)
- NaCl 100mM (1 ml NaCl 5M)
- EDTA 10 mM (5 ml EDTA 0.5M pH8)
- H₂O Nuclease free qsp 45 ml (34 ml H₂O)

Add extemporaneously :

- SDS 10% (100 µl for 1 ml)

- **SEB 1X-Triton for 2 ml freshly prepared**

- SEB 1X (RT) 1,8 ml
- Triton 200 µl

3. Mitogenome: species identification and common features in Lymnaeidae

BLAST searches showed mitogenomic sequence similarities for the full length of Lsta_scaffold2639. As indicated by a 127 bp sequence overlap at the termini, the scaffold represents a circular sequence. Nanopore reads confirmed that the assembled sequence is contiguous, and annotation revealed the complete standard gene complement for a metazoan mitogenome. The 13,834 bp mitogenome of *L. stagnalis* (Figure X) is 71.78% AT-rich. Several protein coding genes (PCGs) are delimited by downstream tRNA genes, causing the ORF to terminate with a truncated stop-codon (T- or TA-) that is completed by polyadenylation of the mRNA transcripts. The annotated *L. stagnalis* mitogenome has been deposited in GenBank (MW221941). The experimental sequence had 94% identity with another independently characterized *L. stagnalis* mitogenome sequence (13,807 bp, MT874495). The difference in length of these two mitogenomes is mostly due to indels in regions with tRNA- and rRNA genes, a two bp indel occurs at the 5' start of ND4L. The mitogenome sequences align closely but contain abundant single nucleotide variants (including several nonsynonymous substitutions) within PCGs. The organization of the 22 tRNA genes, two rRNA genes plus 13 PCGs is generally similar to that of mitogenomes of other lymnaeid (and hygrophilid) snail species, with a few minor differences in the location of tRNA genes.

The combined use of short- and long-reads provided a high coverage of the mitogenome. This approach confirms the absence of repetitive sequence elements that may “stack up” to interfere with a correct assembly when using only short-read data. Accordingly, the mitogenome of *L. stagnalis*, a panpulmonate snail, does not contain long non-coding repeat regions such as reported from two prosobranch gastropod species, *Potamopyrgus antipodarum* and *Potamopyrgus estuarinus* (<https://doi.org/10.1093/molbev/msad007>). The AT-content of the *L. stagnalis* mitogenome (71.81%) is elevated relative to the nuclear genome (62.45%). This is not unusual, as invertebrate mitogenomes tend to be AT-rich and a similar pattern (69% vs 64%) was recorded from *Physella acuta*, (family Physidae) another species of hygrophylid snail (<https://doi.org/10.1093/mollus/eyu025>). The 6% difference in nucleotide content and greater length by 27 nucleotides compared to an independently characterized *L. stagnalis* mitogenome (as yet listed by GenBank as “unverified”, MT874495) suggests considerable genetic diversity within the mitogenome of *L. stagnalis* species. The order of genes in the *L. stagnalis* mitogenome, however, conforms to the generally uniform organization of most panpulmonate gastropods (e.g. <https://doi.org/10.1093/mollus/eyu025>).

4. RNA-seq analysis of Male/female organs

Using the alignment data and annotation file as input for HTseq, we counted how many reads mapped to annotated genes. All samples and organs had similar numbers of reads, but AG reads were more frequently mapped than PG reads (ca. 80 % versus ca. 40 %). The annotation file contained 22,499 genes and the number of expressed genes was roughly similar across organs. From the total set of 422 GPCR genes present in the genome, we found 29 expressed in the female albumen gland (AG) and 31 in the male prostate gland (PG). Of these GPCRs 13 overlapped, meaning that 16 were exclusively expressed in the AG and 18 exclusively in the PG. From the total set of 55 NR genes present in the genome, we found 33 of the identified NRs expressed in the AG and 36 in the PG. Of these NRs all but 3 overlapped; the 3 non-overlapping NRs were exclusively expressed in the PG. We selected the most highly expressed transcripts, that matched a complete receptor sequence, for *in situ* expression in the prostate and albumen gland.

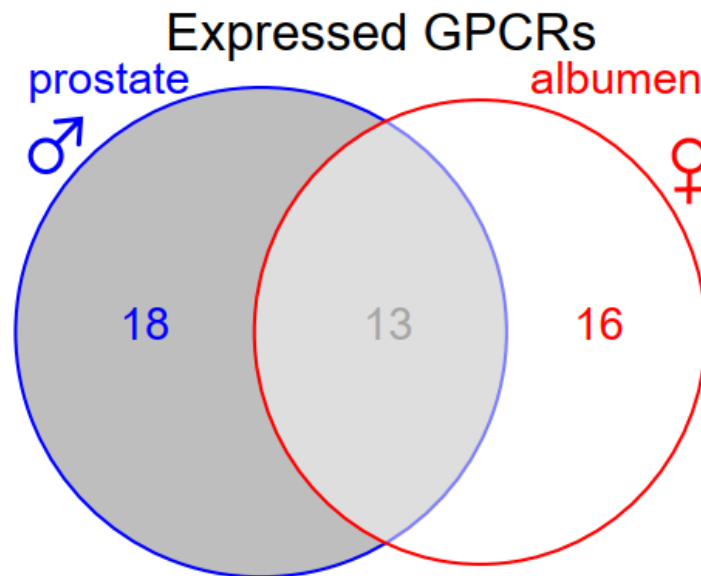


Figure 1. Distribution of GPCR genes expressed in two reproductive organs of *L. stagnalis* (prostate and albumen gland).

5. Supplementary information: Orthology

5.1. Orthology analysis at metazoan level

The set of *L. stagnalis* protein sequences predicted from the present assembly was used to determine groups of orthologues at the level of Metazoa, using predicted proteomes from 19 additional taxa representative of the main metazoan phyla (Table 1). The analysis was performed with OrthoFinder (Emms and Kelly 2020) using default parameters.

Table 1. List of species and genomic resource accessions used to infer *L. stagnalis* orthologs.

Phylum	Taxon	Bioproject	Assembly
Porifera	<i>Amphidemon queenslandica</i>	PRJNA66531	GCF_000090795.1
Placozoa	<i>Trichoplax adhaerens</i>	PRJNA12874	GCF_000150275.1
Platyhelminthes	<i>Schistosoma mansoni</i>	PRJEA36577	GCF_000237925.1
Mollusca	<i>Aplysia californica</i>	PRJNA13635	GCF_000002075.1
	<i>Biomphalaria glabrata</i>	PRJNA290623	GCA_000457365.1
	<i>Lymnaea stagnalis</i>		22499 Gene Predictions
	<i>Lottia gigantea</i>	PRJNA175706	GCF_000327385.1
	<i>Crassostrea gigas</i>	PRJNA70283	GCF_000297895.1
	<i>Octopus bimaculoides</i>	PRJNA270931	GCF_001194135.1
Annelida	<i>Helobdella robusta</i>	PRJNA175704	GCF_000326865.1_
Nematoda	<i>Caenorhabditis elegans</i>	PRJNA13758	GCF_000002985.6_WBcel235
Arthropoda	<i>Folsomia candida</i>	PRJNA299291	GCF_002217175.1
	<i>Hyalella azteca</i>	PRJNA342675	GCF_000764305.1
	<i>Daphnia pulex</i>	PRJNA12756	GCA_000187875.1
	<i>Drosophila melanogaster</i>	PRJNA13812	GCF_000001215.4
Echinodermata	<i>Apostichopus japonicus</i>	PRJNA354676	GCA_002754855.1
Hemichordata	<i>Saccoglossus kowalevskii</i>	PRJNA42857	GCF_000003605.1
Chordata	<i>Branchiostoma floridae</i>	UP000001554	GCF_000003815.1
	<i>Ciona intestinalis</i>	PRJDA65419	GCF_000224145.2
	<i>Homo sapiens</i>	PRJNA31257	GCF_000001405.37_GRCh38.p11

The dataset represents 600240 genes in total. OrthoFinder identified 17669 orthogroups (OGs; Table 2), of which 10707 included *L. stagnalis* genes (60.6%). More than 90 % of *L. stagnalis* genes (20315 out of 22499) were assigned to an OG (Fig. 2), and 28OGs were specific to *L. stagnalis*, involving 140 genes (0.6% of the total number of predicted genes). Orthogroup full content is available upon request.

Table 2. Orthogroup (OG) overall statistics (metazoan-level analysis)

Parameter	value
Number of species	20
Number of genes	600240
Number of genes in orthogroups	500283
Number of unassigned genes	99957
Percentage of genes in orthogroups	83.3
Percentage of unassigned genes	16.7
Number of orthogroups	17669
Number of species-specific orthogroups*	1947
Number of genes in species-specific orthogroups	12160
Percentage of genes in species-specific orthogroups	2
Mean orthogroup size	28.3
Median orthogroup size	14
G50 (assigned genes)	53
G50 (all genes)	40
O50 (assigned genes)	1977
O50 (all genes)	3067
Number of orthogroups with all species present	2312
Number of single-copy orthogroups	2

**Orthogroups that consist entirely of genes from one species.*

G50: The number of genes in the orthogroup such that 50% of genes are in orthogroups of that size or larger.

O50: The smallest number of orthogroups such that 50% of genes are in orthogroups of that size or larger.

Single-copy orthogroup: An orthogroup with exactly one gene (and no more) from each species.

Unassigned gene: A gene that has not been put into an orthogroup with any other genes.

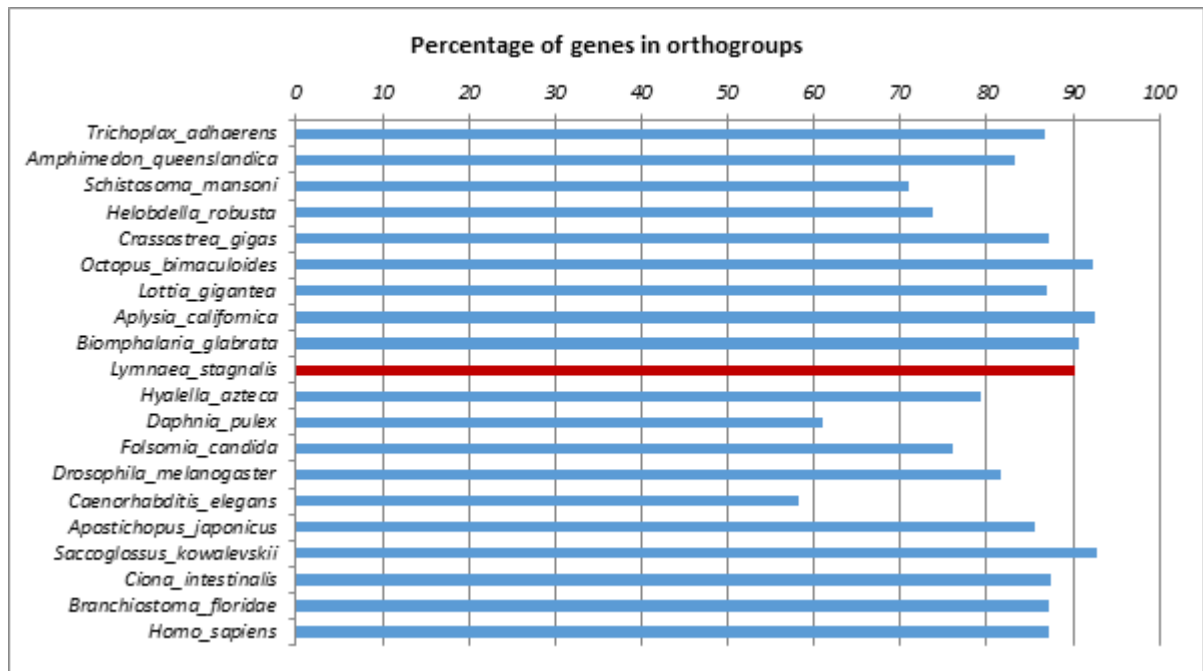


Figure 2. Percentage of genes per species attributed to an OG (orthology at metazoan level).

Gene family enrichment was explored in *L. stagnalis* using a Z-score (number of standard deviations from the mean) on the frequency of *L. stagnalis* genes that contributed to a given OG. From this test, 1149 OGs were found enriched in *L. stagnalis* genes. Among these, we selected the 53 OGs that contained at least 10 *L. stagnalis* genes and genes from at least two other species (Fig. 3), and further annotated them using InterProScan (Table 3).

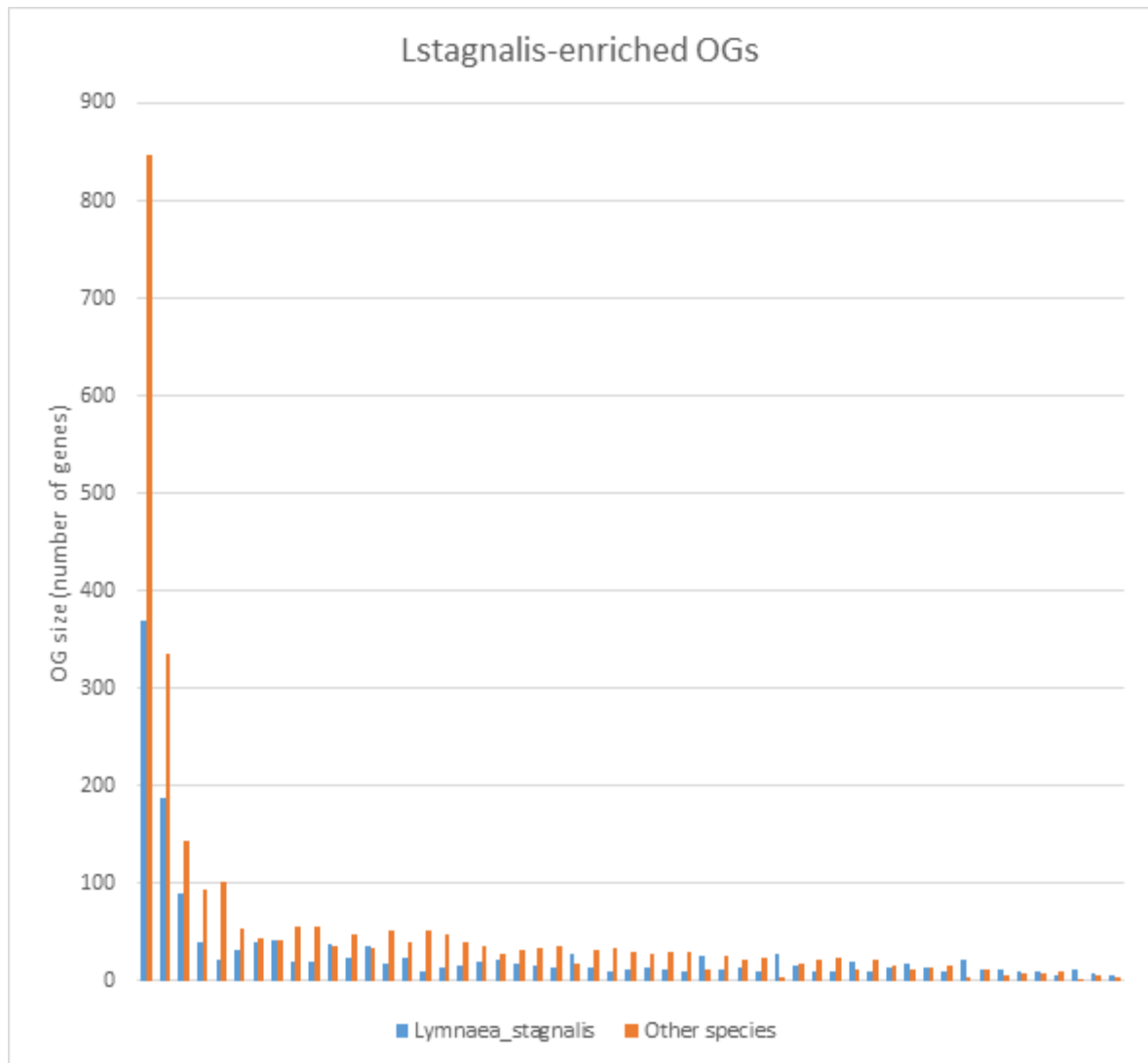


Figure 3. Size distribution of 53 OGs in which *L. stagnalis* genes were found over-represented (*L. stagnalis* Z-score>2), and contained at least 10 *L. stagnalis* genes (in blue) and genes from at least two other species (in orange). Blue and orange bars sum up to total OG size.

Table 3. InterProScan annotation of 53 OGs in which *L. stagnalis* genes were found over-represented (*L. stagnalis* Z-score>2), and contained at least 10 *L. stagnalis* genes and genes from at least two other species.

OG	OG size	Nb of molluscan* genes	IPR description	IPR accession	Proportion of <i>Lstagnalis</i> genes With IPR
OG0000008	1215	1085	GPCR, rhodopsin-like, 7TM or G protein-coupled receptor, rhodopsin-like	IPR017452 IPR000276	325/369
OG0001159	72	71			23/24
OG0002276	49	48			17/17
OG0002279	49	49			6/22
OG0004949	30	30			14/14
OG0000008	1215	1085	Serpentine type 7TM GPCR chemoreceptor Srw	IPR019427	123/369
OG0001159	72	71			10/24
OG0001501	62	58	Reactome: Signaling by GPCR	REACT_14797	4/23
OG0005798	27	24	CATH Superfamily : Rhodopsin 7-helix transmembrane proteins	1.20.1070.10	1/13
OG0005798	27	24	TMhelix (mean number per gene (sd) = 1.09 (0.30))		10/13
OG0001885	55	55	Reactome: Signaling by GPCR	REACT_14797	11/19
OG0001885	55	55	EF-Hand 1, calcium-binding site EF-hand domain pair	IPR018247 IPR011992	19/19 19/19
OG0001501	62	58	Protein of unknown function DUF1647	IPR012444	20/23
OG0001501	62	58	TMhelix (mean number per gene (SD) = 1 (0))		17/23
OG0000047	524	422	AIG1-type G domain profile	IPR006703	180/188
OG0000047	524	422	P-loop containing nucleoside triphosphate hydrolase	IPR027417	183/188
OG0000168	233	230	C-type lectin C-type lectin-like C-type lectin fold	IPR001304 IPR016186 IPR016187	87/89
OG0001607	60	32	Rho GTPase activation protein Rho GTPase-activating protein domain	IPR008936 IPR000198	13/13
OG0000400	133	94	Tumour necrosis factor domain Tumour necrosis factor-like domain	IPR006052 IPR008983	38/39
OG0006745	24	24	Tumour necrosis factor-like domain	IPR008983	20/21
OG0001293	68	62	TNFR/NGFR cysteine-rich region	IPR001368	29/35
OG0000446	123	59	Antistatin-like domain	IPR004094	19/22
OG0000834	86	75	Dermatopontin family	IPR026645	27/32
OG0000899	83	54	Nck-associated protein 5-like	IPR026163	19/39
OG0000930	82	77	EGF-type aspartate/asparagine hydroxylation site EGF-like domain EGF-like calcium-binding domain Laminin EGF domain Growth factor receptor cysteine-rich domain EGF-like, conserved site EGF-like calcium-binding, conserved site	IPR000152 IPR000742 IPR001881 IPR002049 IPR009030 IPR013032 IPR018097	27/41
OG0002579	45	43	EGF-type aspartate/asparagine hydroxylation site EGF-like domain EGF-like calcium-binding domain Growth factor receptor cysteine-rich domain EGF-like, conserved site EGF-like calcium-binding, conserved site	IPR000152 IPR000742 IPR001881 IPR009030 IPR013032 IPR018097	11/27
OG0002579	45	43	von Willebrand factor, type D domain	IPR001846	3/27

Table 3. (continued)

OG0001085	75	54	VWFC domain	IPR001007	15/19
OG0001107	74	72	Major facilitator superfamily domain	IPR020846	1/19
OG0001107	74	72	PMP-22/EMP/MP20/Claudin superfamily	IPR004031	9/19
OG0001107	74	72	TMhelix (mean number per gene (SD) = 4.05 (1.18))		19/19
OG0003108	41	22	Death-like domain	IPR011029	3/7
OG0003108	41	22	Tetratricopeptide-like helical domain	IPR011990	1/7
OG0001163	72	70	Tetratricopeptide-like helical domain	IPR011990	34/37
OG0001287	68	63	LicD family	IPR007074	15/17
OG0001545	61	21	Zinc finger, PHD-type Zinc finger, FYVE/PHD-type Zinc finger, RING/FYVE/PHD-type Zinc finger, PHD-type, conserved site Zinc finger, PHD-finger	IPR001965 IPR011011 IPR013083 IPR019786 IPR019787	7/9
OG0001802	56	21	Zinc finger, SWIM-type MULE transposase domain		5/16 2/16
OG0002283	49	46	Poly(ADP-ribose) polymerase, catalytic domain	IPR012317	16/16
OG0004505	32	30	Poly(ADP-ribose) polymerase, catalytic domain Protein of unknown function DUF3990	IPR012317 IPR025051	12/15 11/15
OG0002338	48	38	PC-Esterase, SGNH hydrolase-type esterase domain	IPR026057 IPR013830	6/16
OG0002592	45	44	CATH Superfamily : Lipase, subunit A	2.10.80.10	10/14
OG0002682	44	29	Aerolysin-like toxin, beta complex domain ETX_MTX2	pfam03318	10/10
OG0002908	41	29	Metal-dependent hydrolase TatD family	IPR032466 IPR001130	11/11 10/11
OG0003114	38	38	alpha/beta hydrolase fold Alpha/beta hydrolase fold-3	IPR029058 IPR013094	10/26 10/26
OG0003123	40	33	Neurotransmitter-gated ion-channel Neurotransmitter-gated ion-channel ligand-binding domain Neurotransmitter-gated ion-channel, conserved site Nicotinic acetylcholine-gated receptor, transmembrane domain	IPR006201 IPR006202 IPR006029 IPR027361	10/11
OG0003532	37	36	C-type lectin Kringle Metalloproteinase, catalytic domain Sushi/SCR/CCP domain	IPR001304 IPR000001 IPR024079 IPR000436	5/12 7/12 5/12 8/12
	31	31	H-type lectin domain Coil Agglutinin HPA-like	IPR019019 Coil SSF141086	8/19 17/19 11/19
OG0004265	33	33	Cadherin	IPR002126	9/9
OG0004467	32	21	Glycoside hydrolase, family 23	IPR002152	9/9
OG0004482	32	27	TMhelix (mean number per gene (SD) = 5.55 (2.55))		9/10
OG0004489	32	31	TMhelix (mean number per gene(sd) = 1.09 (0.29))		22/28
OG0008071	18	18	TMHelix (1 per gene)		1/12
OG0008494	16	16	TMHelix (1 per gene)		6/9
OG0009112	13	13	TMHelix (mean number per gene (sd) = 5.43 (2.57))		7/8
OG0004604	31	18	Pyridoxal phosphate-dependent transferase DegT/DnrJ/EryC1/StrS aminotransferase	IPR015424 IPR000653	6/9 6/9
OG0005477	28	28	Protein-tyrosine phosphatase-like	IPR029021	15/17
OG0006418	25	25	Zinc finger, MYND-type	IPR002893	9/10
OG0007246	22	20	Low-density lipoprotein (LDL) receptor class A repeat	IPR002172	9/11
OG0008325	17	17	Nucleotide-binding alpha-beta plait domain Macro domain	IPR012677 IPR002589	3/10 1/10
OG0008493	16	10	Cystine-knot cytokine	IPR029034	5/6
OG0008494	16	16	Ribosomal protein L2 domain 2	IPR014722	2/9

Table 3. (continued)

OG0009240	13	12	Peptidase M13 (incl. catalytic, N-term and C-term domains)	IPR000718	11/11
OG0009997	10	9	Zinc finger, RING/FYVE/PHD-type	IPR013083	2/6
OG0009997	10	9	Immunoglobulin-like domain	IPR007110	1/6
OG0003414	38	38	Immunoglobulin-like domain	IPR007110	17/26
OG0003872	35	35	Immunoglobulin-like domain	IPR007110	5/13
OG0004489	32	31	Immunoglobulin-like fold	IPR013783	4/28

5.2. Orthology analysis at gastropod level

This analysis focused on gastropod orthology, with the aim of testing the hypothesis of association between FMRF-amide receptor expansion and the evolution of simultaneous hermaphroditism in this lineage. To this end, we refined the analysis of orthology by focusing on gastropods, and used available genomic resources to balance hermaphroditic species (*A. californica*, *B. glabrata*, *Bulinus truncatus*, *Candidula unifasciata*, *Elysia chlorotica*, *L. stagnalis*, *Radix auricularia*, *Lottia gigantea*) and gonochoristic species (separate genders: *Batillaria attramentaria*, *Gigantopelta aegis*, *Haliotis rubra*, *Littorina saxatilis*, *Pomacea canaliculata*, *Potamopyrgus antipodarum*). Note that *L. gigantea* is a protandrous sequential hermaphrodite while all other species are simultaneously hermaphroditic.

Table 4. List of gastropod species and genomic accessions used to infer *L. stagnalis* orthologs.

Clade	Taxon	Reproductive system	Bioproject	Number of proteins (nb of unique sequences)
Euthyneura	<i>Aplysia californica</i>	<i>simultaneous hermaphrodite</i>	PRJNA209509	26643 (26643)
	<i>Biomphalaria glabrata</i>		PRJNA962856	53149 (36453)
	<i>Bulinus truncatus</i>		PRJNA680620	26279 (26252)
	<i>Candidula unifasciata</i>		PRJEB41346	22464 (22446)
	<i>Elysia chlorotica</i>		PRJNA484060	23871 (23836)
	<i>Lymnaea stagnalis</i>			
	<i>Radix auricularia</i>		PRJNA350764	17338 (17334)
Patellogastropoda	<i>Lottia gigantea</i>	<i>sequential hermaphrodite</i>	PRJNA259762	23822 (23822)
Neomphalina	<i>Gigantopelta aegis</i>	<i>gonochoric</i>	PRJNA727593	33249 (29385)
Vetigastropoda	<i>Haliotis rubra</i>		PRJNA801670	43409 (38162)
Caenogastropoda	<i>Batillaria attramentaria</i>		PRJNA640962	29795 (29144)
	<i>Littorina saxatilis</i>		TSA project GHPE01000000 (PRJNA494650)	35870 (31467)
	<i>Pomacea canaliculata</i>	PRJNA472795	40391 (40378)	
	<i>Potamopyrgus antipodarum</i>	TSA project GGFE01000000	36431 (36431)	

When available, protein sequences were directly retrieved from bioprojects. Otherwise, we used TRANSDECODER to predict the proteome from the genomic resource available. This analysis generated nearly 29,500 OGs (Table 5). Because all simultaneous hermaphrodites in our analysis are members of the Euthyneura infraclass of molluscs, we also identified various OGs specific to this clade, including FMRFamide receptors, c-type lectins, cytochrome P450 cyclodipeptide synthase-associated, etc. (see Supplementary Table ST5 for annotation details). Overall OG statistics are given in Table 5. Orthogroup full content is available upon request.

Table 5. Orthogroup (OG) overall statistics (gastropod-level analysis).

Parameter	value
Number of species	14
Number of genes	404265
Number of genes in orthogroups	364557
Number of unassigned genes	39708
Percentage of genes in orthogroups	90.2
Percentage of unassigned genes	9.8
Number of orthogroups	29428
Number of species-specific orthogroups*	9158
Number of genes in species-specific orthogroups	41817
Percentage of genes in species-specific orthogroups	10.3
Mean orthogroup size	12.4
Median orthogroup size	7
G50 (assigned genes)	19
G50 (all genes)	18
O50 (assigned genes)	5033
O50 (all genes)	6101
Number of orthogroups with all species present	3275
Number of single-copy orthogroups	154

*Orthogroups that consist entirely of genes from one species.

G50: The number of genes in the orthogroup such that 50% of genes are in orthogroups of that size or larger.

O50: The smallest number of orthogroups such that 50% of genes are in orthogroups of that size or larger.

Single-copy orthogroup: An orthogroup with exactly one gene (and no more) from each species.

Unassigned gene: A gene that has not been put into an orthogroup with any other genes.

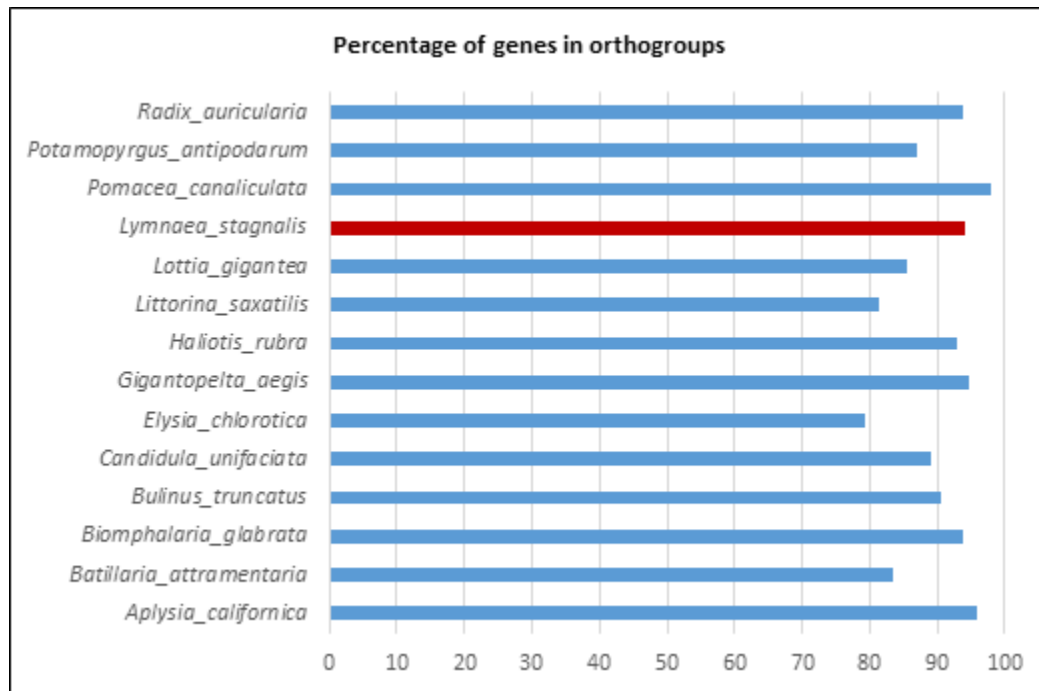


Figure 4. Percentage of genes per species attributed to an OG (orthology at gastropod level).

FMRFamide-R-like receptor distribution

CD-search produced 483 *L. stagnalis* gene predictions with a 7tmA_FMRFamide_R-like domain (405 of them with a complete domain, 37 incomplete in N terminal, 41 in C terminal and 1 in both N and C terminals). In the gastropod-level orthology analysis, these genes were distributed in 89 orthogroups, which contained in total 2596 genes (2564 excluding *Radix auricularia* genes). The contribution of each species to these 89 orthogroups was used to compare the abundance of this GPCR category in simultaneous hermaphrodites and other gastropods, in link with the hypothesis of FMRFamideR expansion in the former (Fig. 5). In this set of OGs, the cumulative abundance of genes from simultaneous hermaphroditic species (per-species mean = 329.17, SD = 117.04) was significantly higher than that of genes from gonochoric species (per-species mean = 89.17, SD = 36.88) (Fisher $F_{(1,10)} = 22.95$; $p < 0.001$). Besides, through the unique representative species *Lottia gigantea*, sequential hermaphrodite genes appeared particularly weakly represented in these OGs (total number = 54 genes).

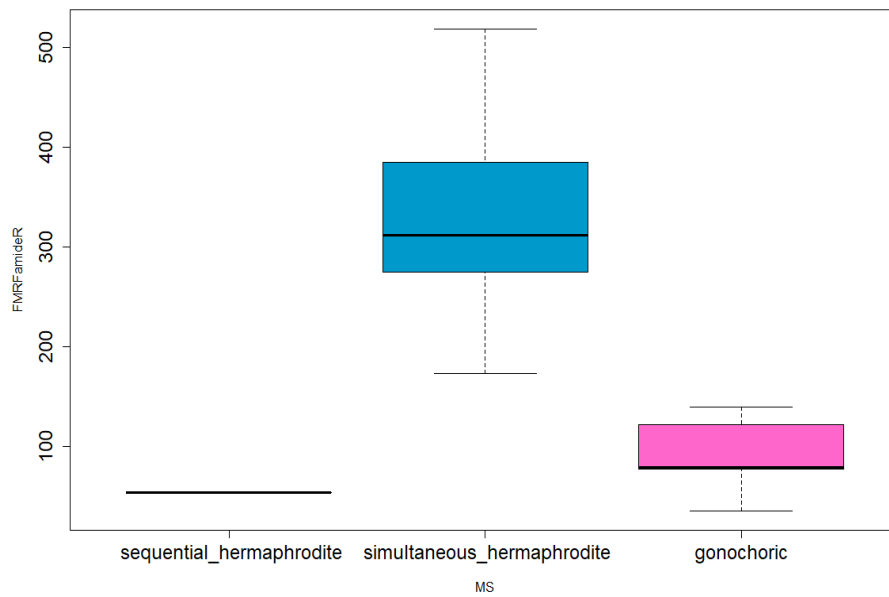


Figure 5. Mean number of FMRFamide-R like genes per species, as a function of their mating system.

Statistics on the mean number of per species genes in FMRFamide OGs

HERMA vs GONO

	mean	SD	n
0 (gono)	89.16667	36.88044	6
1 (herma)	289.85714	149.10112	7

	mms	sdms	nms
gonochoric	89.16667	36.88044	6
herma_Seq	54.00000	NA	1
herma_Sim	329.16667	117.03575	6

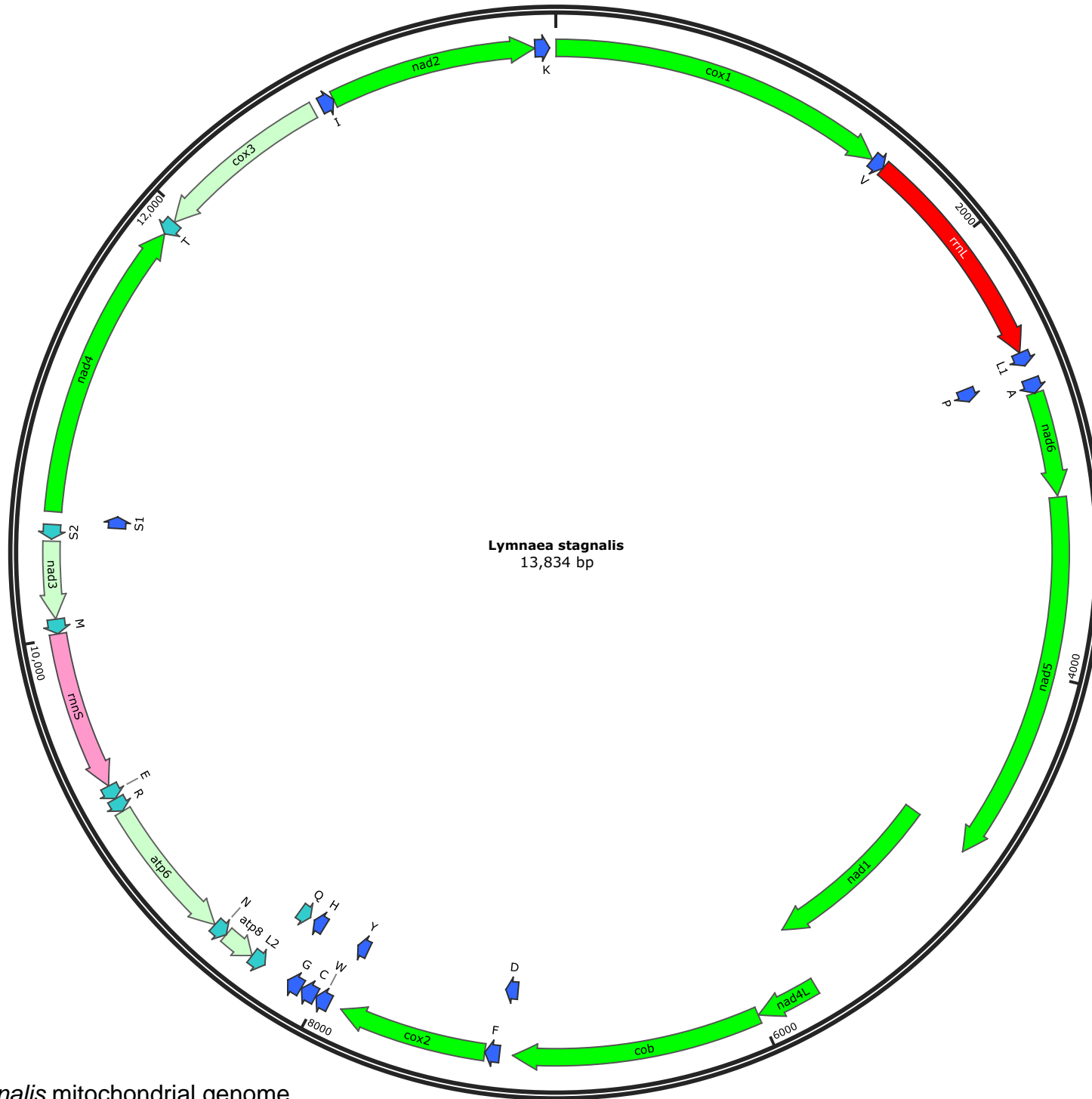
```
> h<-lm(FMRFamideR~herma, data=fmrf)
Coefficients: (Intercept)          herma
              89.17             200.69
```

```
> ah<-anova(h, test="F")
Response: FMRFamideR
      Df Sum Sq Mean Sq F value    Pr(>F)
herma  1 130125  130125   10.21 0.008525 **
Residuals 11 140188   12744
```

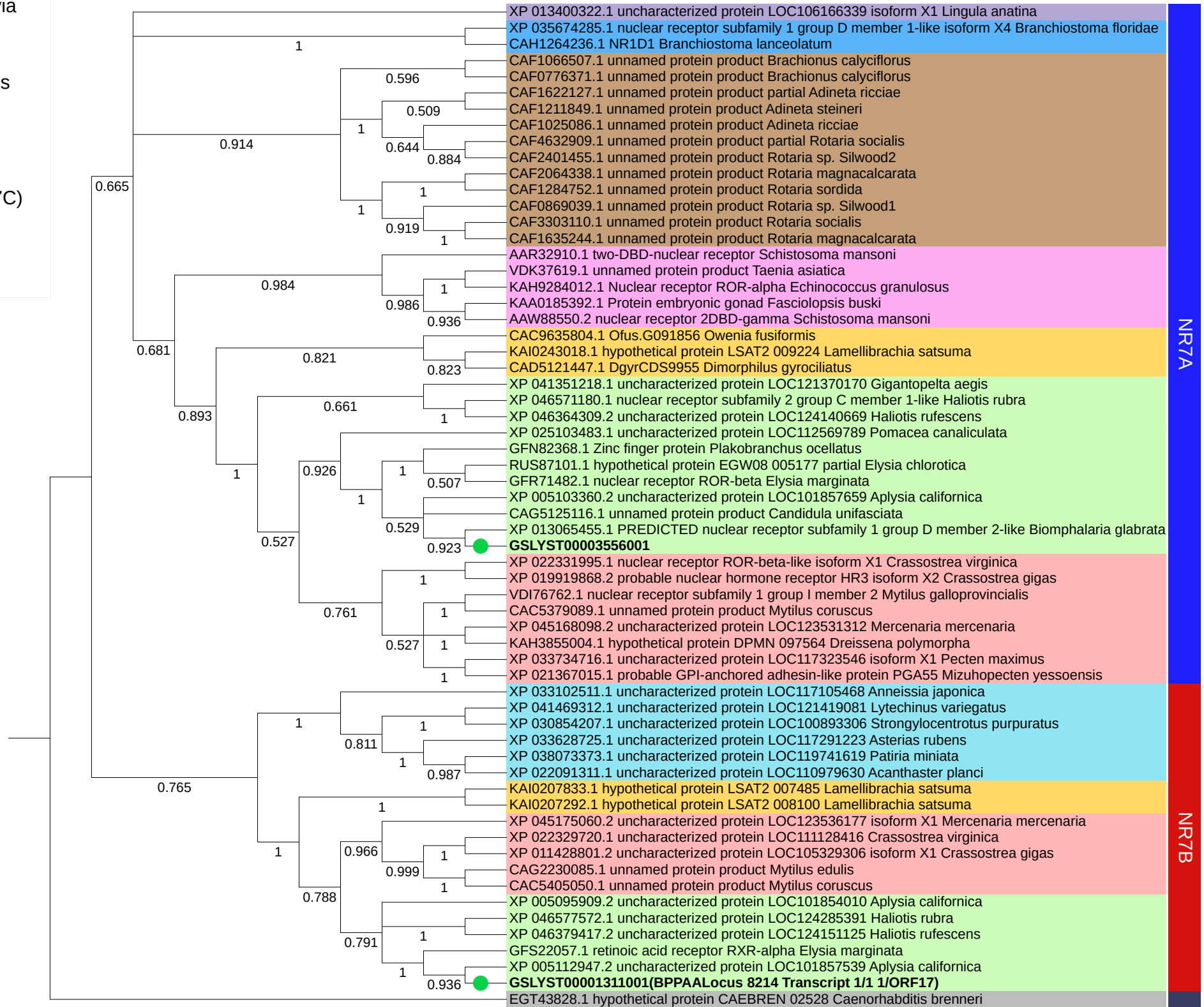
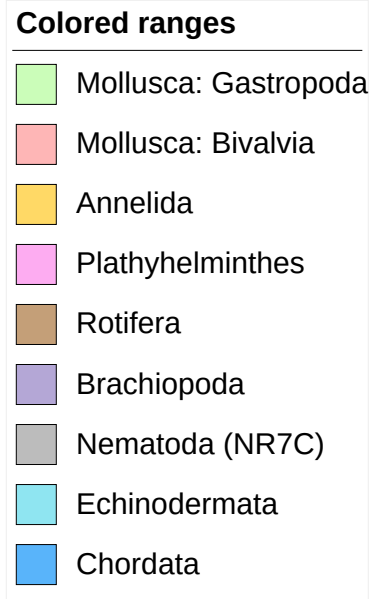
HERMASIM vs GONO (excluding *L. gigantea*)

```
> lms<-lm(FMRFamideR~MS, data=sub)
Coefficients: (Intercept)    MSherma_Si
              89.17         240.00
```

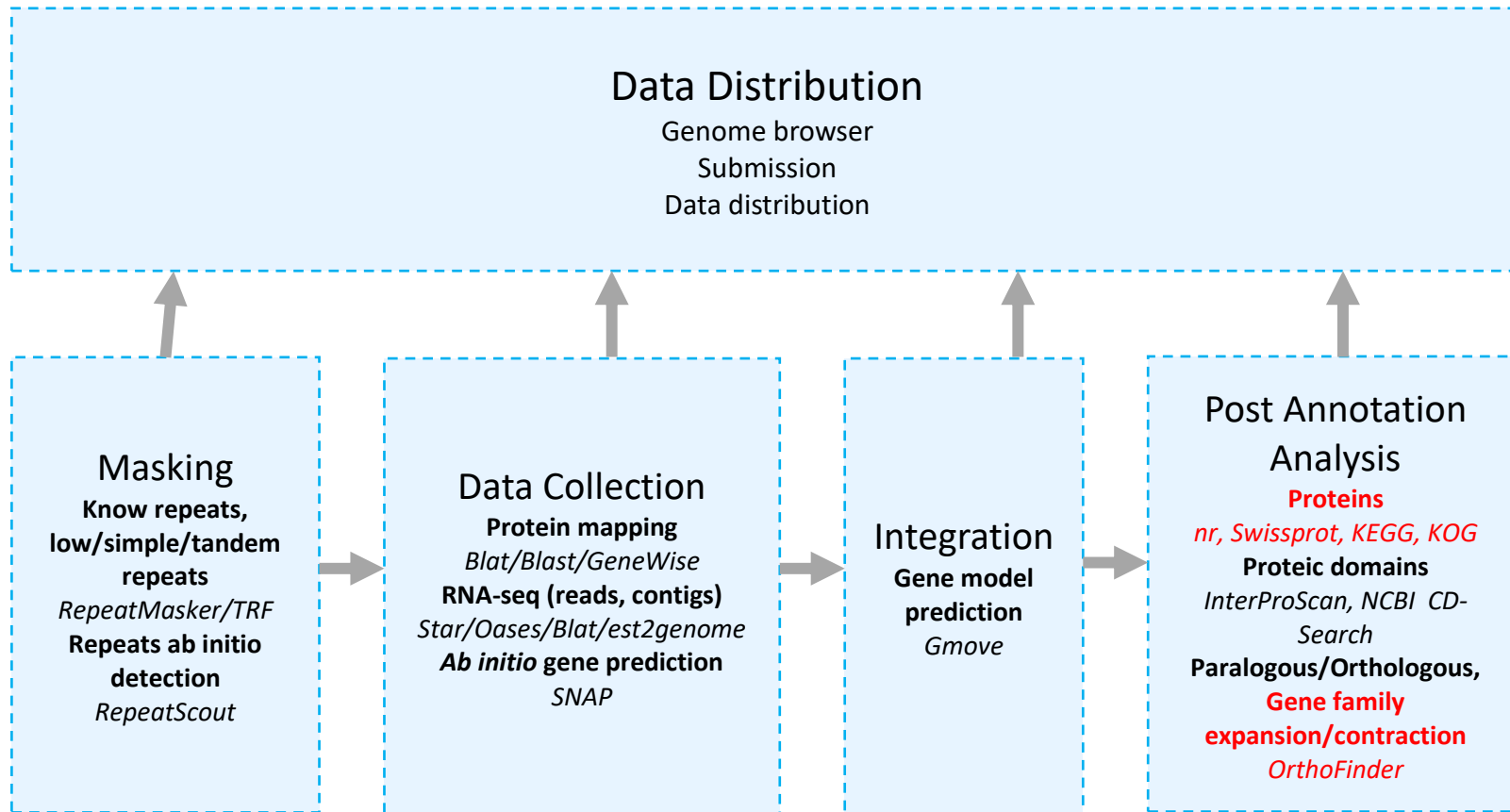
```
> alms<-anova(lms, test="F")
Response: FMRFamideR
      Df Sum Sq Mean Sq F value    Pr(>F)
MS     1 172800  172800   22.952 0.0007337 ***
Residuals 10 75288   7529
```



SF1. Map of *L. stagnalis* mitochondrial genome



SF3. Phylogenetic analysis of 2DBD-NRs relationships across metazoans (full tree) (further explanation in Figure 2, main text).



SF4. General annotation workflow applied to the *L. stagnalis* genome assembly.

ST1. Annotation of *L. stagnalis* predicted protein sequences: Receptor Tyrosine Kinases (RTKs). See HUGO gene nomenclature and conserved domain database for domain definition.

order	RTK_type	Lstagnalis GP	present domain	absent domain
?	?	GSLYST00007363001	LRR-RI, Ephrin receptor_like (partial), TNFRSF(partial), PTKc	FNIII, FNIII, SAM
?	?	GSLYST00000618001	FNIII, PTKc	
type01	Type I RTKs: ErbB (epidermal growth factor)	GSLYST00018222001	receptor L (partial), Furin-like (cystein rich), receptor L, GFR, GFR, PTKc-EGFR	
type02	Type II RTKs: Insulin	GSLYST00008439001	receptor L, Furin-like (cystein rich), receptor L, FNIII, FNIII, PTKc-Ins-like	
type02	Type II RTKs: Insulin	GSLYST00021192001	receptor L, Furin-like (cystein rich), receptor L, FNIII, FNIII, PTKc-Ins-like	
type03	Type III RTKs: PDGFR, CSFR, Kit, FLT3	no match		
type04	Type IV RTKs: VEGF (vascular endothelial growth factor)	GSLYST00004989001	Ig, Ig, Ig, Ig, PTKc_VEGFR	
type05	Type V RTKs: FGF (fibroblast growth factor)	GSLYST00001552001	Ig, Ig2-FGFR, Ig3-FGFR-2, PTKc-FGFR	
type05	Type V RTKs: FGF (fibroblast growth factor)	GSLYST00017427001	Ig, Ig3-FGFR, PTKc	
type05	Type V RTKs: FGF (fibroblast growth factor)	GSLYST00016773001+16774001	Ig, PTKc + Ig, Ig2_Kirrel3, Ig2_Robo, Ig, Ig_Kirrel3	
type06	Type VI RTKs: PTK7/CCK4	GSLYST00016093001	Ig3_Robo, Ig, Ig2_Robo, Ig, Ig3, Ig3, PTK_CCK4	
type07	Type VII RTKs: Neurotrophin receptor/Trk	GSLYST00007831001	LRR-RI, PTKc-TRK	Ig, Ig,
type07	Type VII RTKs: Neurotrophin receptor/Trk	GSLYST00008464001	PTKc_TRK, TOMM_kin_cyc	LRR, Ig, Ig
type08	Type VIII RTKs: ROR	GSLYST00009936001	IG, FZ (=CRDTR), Kringle, PTKc-ROR	
type09	Type IX RTKs: MuSK	GSLYST00008324001+8323001	FZ (8324001); Kringle (8323001), PTKc-MUSK (8323001)	Ig
type10	Type X RTKs: HGF (hepatocyte growth factor)	GSLYST00000013001	LAM-EGF x5, IPT x2, PTKc	SEMA, Psi
type10	Type X RTKs: HGF (hepatocyte growth factor)	GSLYST00003015001	Sema_plexin-like, IPT, IPT, IPT, PTKc	Psi
type10	Type X RTKs: HGF (hepatocyte growth factor)	GSLYST00003016001_17001_18001_plus_addi	Sema_plexin-like, Psi, IPT (full), IPT (partial), PTKc	
type10	Type X RTKs: HGF (hepatocyte growth factor)	GSLYST00003019001	IPT, IPT (partial), PTKc	
type10	Type X RTKs: HGF (hepatocyte growth factor)	GSLYST00003020001	IPT, IPT, IPT (partial), PTKc	
type10	Type X RTKs: HGF (hepatocyte growth factor)	GSLYST00003021001	IPT (partial) x3	PTKc
type10	Type X RTKs: HGF (hepatocyte growth factor)	GSLYST00009000001to9004001	SEMA, Psi, IPT, IPT (partial), PTKc_Met_Ron	
type11	Type XI RTKs: TAM (TYRO3-, AXL- and MER-TK)	no match		
type12	Type XII RTKs: TIE family of angiopoietin receptors	GSLYST00011095001	Ig, Ig, EGF (partial), EGF, PTKc(partial), PTKc(partial)	Ig, FNIII, FNIII, FNIII
type13	Type XIII RTKs: Ephrin	GSLYST00016855001	EphrinLBD, FNIII, FNIII, FNIII, PTKc-EPH, SAM	
type14	Type XIV RTKs: RET	GSLYST00012958001+12959001	PTKc_RET	cadherin, cyst-rich
type15	Type XV RTKs: RYK	GSLYST00007181001_extended	PTKc-RYK, WIF	
type16	Type XVI RTKs: DDR (collagen receptor) family	GSLYST00008779001	Discoidin, PTKc-DDR	Discoidin
type17	Type XVII RTKs: ROS receptors	GSLYST00009260001	FNIII, FNIII, FNIII, FNIII, PTKc_Ros	YWTD propeller
type18	Type XVIII RTKs: LMR	GSLYST00014169001	PTKc, TOMM_kin_cyc	
type19	Type XIX RTKs: Leukocyte tyrosine kinase (LTK)	GSLYST00020441001	PTKc_ALK_LTK	Mam, Lda
type20	Type XX RTKs: STYK1	GSLYST00018463001	PTKc_STYK	

ST2. Summary of *L. stagnalis* nuclear receptor annotation: BLASTp Best-Hit (BH) from *H. sapiens*-restricted or global nr NCBI database. Automatic protein predictions were manually modified where necessary (alternative ORF, combination of several gene predictions with obviously partial domains or other annotated regions, co-localised transcripts with a better annotation score, etc.). DNA- and Ligand-binding domains were identified with NCBI conserved domains database (CDD): presence/absence, completeness (full vs incomplete in N- or C-terminal region, Ninc and Cinc, respectively). Domain location and other detailed information are specified in Supplementary Table ST3. Abbreviation: P =predicted.

<i>L. stagnalis</i> predicted protein	Domain (DBD, LBD)	Gene abbreviation	BH accession (<i>H. sapiens</i>)	BH accession (nr)	BH gene name (nr)	BH taxon (nr)
GSLYST00010242001ext	DBD full no LBD	NR1A2 (THRB)	NP_00134 1643.1	Q02965.2	Thyroid hormone receptor beta	<i>Lithobates catesbeianus</i>
GSLYST00002111001	DBD full LBD full	NR1B2 (RARB)	NP_00127 7145.1	XP_0130613 59.1	^P nuclear receptor subfamily 1 group D member 2-like	<i>B. glabrata</i>
GSLYST00008490001	DBD full LBD full	NR1B2 (RARB)	NP_00127 7229.1	ADF43963.1	Retinoic acid receptor	<i>L. stagnalis</i>
GSLYST00009886001&G SLYST00009887001	DBD full LBD full	NR1B3 (RARG)	NP_00095 7.1	KAH9519321 .1	hypothetical protein Btru_075258	<i>B. truncatus</i>
GSLYST00012932001	DBD full LBD full	NR1C1 (PPARA)	NP_00502 7.2	XP_0130613 59.1	^P nuclear receptor subfamily 1 group D member 2-like	<i>B. glabrata</i>
GSLYST00020728001	DBD full LBD full	NR1C1 (PPARA)	NP_00502 7.2	XP_0130889 59.1	^P uncharacterised protein LOC106073033	<i>B. glabrata</i>
Lsta_scaffold719:49114. .65797_ORF30 (same location as GSLYST00019008001)	DBD full no LBD	NR1C1 (PPARA)	EAW7340 3.1	XP_0051056 14.2	Probable serine/threonine-protein kinase DDB_G0282963	<i>A. californica</i>
GSLYST00012709001	DBD full LBD full	NR1C2 (PPARD)	NP_00116 5290.1	XP_0130941 06.1	^P retinoic acid receptor beta-like	<i>B. glabrata</i>
GSLYST00008467001& ORF2_EX9&10_bpp1E7 5_GALME.1.1	DBD full LBD full	NR1C3 (PPARG)	NP_05695 3.2	XP_0130727 95.1	^P ecdysone-inducible protein E75-like	<i>B. glabrata</i>
GSLYST00009627001& GSLYST00009626001ext	DBD full LBD full	NR1C3 (PPARG)	KAI25283 16.1	KAH9498600 .1	hypothetical protein Btru_007742	<i>B. truncatus</i>
GSLYST00020475001	DBD full LBD full	NR1C3 (PPARG)	XP_01153 2145.1	XP_0130789 73.1	^P uncharacterised protein LOC106064881	<i>B. glabrata</i>
GSLYST00021345001	DBD Ninc LBD full	NR1C3 (PPARG)	NP_00502 8.4	XP_0129353 01.1	^P ecdysone-induced protein 78C-like	<i>A. californica</i>
GSLYST00003246001	DBD full LBD full	NR1D1 (REVERBA)	NP_06837 0.1	XP_0130788 93.1	^P nuclear receptor subfamily 1 group D member 1-like	<i>B. glabrata</i>
GSLYST00003376001	DBD full LBD full	NR1D2 (REVERBB)	NP_00113 8897.1	XP_0130777 61.1	^P flocculation protein FLO11-like	<i>B. glabrata</i>
GSLYST00005611001	no DBD LBD full	NR1D2 (REVERBB)	NP_00113 8897.1	XP_0130808 16.1	^P thyroid hormone receptor alpha-like isoform X2	<i>B. glabrata</i>
GSLYST00003356001	DBD1 full DBD2 full LBD full	NR1D2 (REVERBB) 2DBD-NR	NP_00113 8897.1	XP_0130654 55.1	^P nuclear receptor subfamily 1 group D member 2-like	<i>B. glabrata</i>
GSLYST00002203001	DBD full LBD full	NR1F1 (RORA)	XP_011520 176.1	XP_013063 338.1	^P nuclear receptor ROR-beta-like isoform X3	<i>B. glabrata</i>
GSLYST00003481001	DBD full LBD full	NR1F1 (RORA)	NP_599023 .1	XP_005111 322.2	^P uncharacterised protein LOC101857528	<i>A. californica</i>
GSLYST00003724001	DBD full LBD full	NR1F1 (RORA)	XP_011520 176.1	XP_005104 642.1	^P flocculation protein FLO11-like isoform X1	<i>A. californica</i>
GSLYST00012703001	DBD full LBD full	NR1F1 (RORA)	XP_005254 641.1	KAI878362 0.1	Nuclear receptor ROR-beta-like isoform X3	<i>B. glabrata</i>
GSLYST00007099001	DBD full LBD full	NR1F2 (RORB)	NP_008845 .2	XP_013094 161.1	^P probable nuclear hormone receptor HR3	<i>B. glabrata</i>
GSLYST00019331001	DBD full LBD full	NR1F3 (RORC)	NP_001001 523.1	XP_012935 014.1	^P nuclear receptor ROR-gamma-like	<i>A. californica</i>
GSLYST00000602001	DBD full LBD full	NR1H3 (LXRA)	XP_011518 108.1	XP_013079 217.1	^P nuclear hormone receptor HR96-like isoform X1	<i>B. glabrata</i>

ST2 (cont.)

<i>L. stagnalis</i> predicted protein	Domain (DBD, LBD)	Gene abbreviation	BH accession (<i>H. sapiens</i>)	BH accession (nr)	BH gene name (nr)	BH taxon (nr)
GSLYST00000926001	DBD full LBD full	NR1H3 (LXRA)	NP_001123 574.1	RUS8288 9.1	Hypothetical protein EGW08_009354	<i>E. chlorotica</i>
GSLYST00003412001	DBD full LBD full	NR1H3 (LXRA)	NP_001123 574.1	XP_0051 06455.2	^P nuclear hormone receptor HR96-like	<i>A. californica</i>
GSLYST00019008001	no DBD LBD full	NR1H3 (LXRA)	XP_011518 110.1	KAH9504 298.1	Hypothetical protein Btru_064571	<i>B. truncatus</i>
GSLYST00021927001	DBD full LBD full	NR1H4 (FXRA)	NP_001193 922.1	XP_0129 40090.1	^P peroxisome proliferator- activated receptor alpha- like	<i>A. californica</i>
GSLYST00016253001	DBD full LBD full	NR1I1 (VDR)	NP_000367 .1	XP_0130 74086.1	^P vitamin D3 receptor A- like	<i>B. glabrata</i>
GSLYST00020495001& GSLYST00020494001ext	DBD full LBD full	NR1I1 (VDR)	NP_000367 .1	XP_0130 73965.1	^P nuclear hormone receptor HR96-like isoform X1	<i>B. glabrata</i>
GSLYST00006772001	DBD full LBD full	NR2A1 (HNF4A)	NP_001025 174.1	XP_0129 39974.1	^P hepatocyte nuclear factor 4-gamma-like	<i>A. californica</i>
GSLYST00014050001	DBD full LBD full	NR2B1 (RXRA)	NP_002948 .1	Q5I7G2.1	Retinoid X receptor (LymRXR)	<i>L. stagnalis</i>
BPPAALocus_8214_Transcr ipt_1/1_1/ORF17 (same location as GSLYST00001311001)	DBD1 DBD2 full LBD full	NR2B2 (RXRB) 2DBD-NR	NP_001278 918.1	KAI87889 05.1	Ecdysone-induced protein 75B, partial	<i>B. glabrata</i>
GSLYST00009203001	DBD full LBD full	NR2B3 (RXRG)	NP_008848 .1	XP_0130 76268.1	^P retinoic acid receptor RXR-alpha-B-like	<i>B. glabrata</i>
GSLYST00005434001&74A A&GSLYST00005433001	DBD full LBD full	NR2C2 (TR4)	NP_001278 623.1	XP_0130 80569.1	^P orphan steroid hormone receptor 2-like isoform X4	<i>B. glabrata</i>
GSLYST00007009001	DBD full LBD Cinc	NR2E1 (TLL)	NP_003260 .1	XP_0130 64092.1	^P nuclear receptor subfamily 2 group E member 1-like	<i>B. glabrata</i>
GSLYST00012340001	DBD full LBD full	NR2E1 (TLL)	NP_003260 .1	XP_0130 96601.1	^P nuclear receptor subfamily 2 group E member 1-like	<i>B. glabrata</i>
GSLYST00013111001&GSL YST00013110001	DBD full LBD full	NR2E1 (TLL)	NP_003260 .1	XP_0130 68647.1	^P nuclear receptor subfamily 2 group E member 1-like	<i>B. glabrata</i>
GSLYST00020139001_ALT ORF	DBD full LBD full	NR2E3 (PNR)	NP_055064 .1	KAH9500 942.1	Photoreceptor-specific nuclear receptor	<i>B. truncatus</i>
GSLYST00022416001	DBD Ninc no LBD	NR2E3 (PNR)	NP_057430 .1	XP_0130 71146.1	^P photoreceptor-specific nuclear receptor-like	<i>B. glabrata</i>
GSLYST00018763001	no DBD LBD full	NR2F1 (COUP-TFI)	NP_005645 .1	XP_0130 70030.1	^P photoreceptor-specific nuclear receptor-like	<i>B. glabrata</i>
GSLYST00002895001	DBD full LBD full	NR2F2 (COUP-TFII)	NP_066285 .1	XP_0130 80128.1	^P COUP transcription factor 2-like isoform X1	<i>B. glabrata</i>
GSLYST00006228001&GSL YST00006227001& GSLYST00006226001	DBD full LBD full	NR3A1 (ESR1)	NP_000116 .2	XP_0130 94385.1	^P probable nuclear hormone receptor HR38	<i>B. glabrata</i>
GSLYST00013137001	DBD full LBD full	NR3B1 (ERRA)	XP_016872 802.1	XP_0130 84015.1	^P uncharacterised protein LOC106069003	<i>B. glabrata</i>
ORF5/bpp1T00019575001 /bpp1LOC100704106_ORE NI.2.3 (same location as GSLYST00020047001)	DBD full LBD full	NR3B3 (ERRG)	XP_011507 576.1	XP_0130 80350.1	^P steroid hormone receptor ERR2-like isoform X2	<i>B. glabrata</i>
GSLYST00017058001	DBD Ninc LBD full	NR4A2 (NURR1)	NP_006177 .1	XP_0090 45078.1	Hypothetical protein LOTGIDRAFT_136520, partial	<i>L. gigantea</i>
GSLYST00000165001	DBD full LBD full	NR5A2 (LRH1, FTZ-F1)	NP_001263 393.1	XP_0130 68514.1	^P nuclear receptor subfamily 5 group A member 2-like	<i>B. glabrata</i>
GSLYST00015414001	DBD full LBD full	NR5A2 (LRH1, FTZ-F1)	NP_003813 .1	XP_0130 64317.1	^P nuclear hormone receptor FTZ-F1 beta-like	<i>B. glabrata</i>
GSLYST00018899001&GSL YST00018898001	DBD full LBD full	NR6A1 (GCNF)	XP_005251 975.1	XP_0130 73570.1	^P hormone receptor 4-like isoform X1	<i>B. glabrata</i>

ST3. Annotation of *L. stagnalis* predicted proteins: nuclear receptor domains (DBD: DNA-binding domain; LBD: Ligand-binding domain).

protein prediction	GP_identifier	DBD start	DBD end	DBD	DBD_E-value	DBD_incomplete	LBD start	LBD end	LBD	LBD_E-value	LBD_incomplete	other domain start	other domain end	other domain	other domain E-value	other domain incomplete	gene nomenclature
modified	GSLYST00010242001extended	13	86	NR_DBD_like	6.44E-28	-	-	-	no LBD	-	no LBD	-	-	-	-	-	NR1A2 (THR8)
automatic	GSLYST00002111001	675	746	NR_DBD_like	2.06E-31	-	865	1040	NR_LBD_F1	4.97E-22	-	-	-	-	-	-	NR1B2 (RARB)
automatic	GSLYST00008490001	114	197	NR_DBD_RAR	5.50E-55	-	218	471	NR_LBD_RAR	1.76E-104	-	-	-	-	-	-	NR1B2 (RARB)
modified	GSLYST00009886001&GSLYST00009887001	13	78	NR_DBD_like	5.68E-39	-	792	936	NR_LBD superfamily	1.77E-19	-	-	-	-	-	-	NR1B3 (RARG)
automatic	GSLYST00012932001	393	464	NR_DBD_like	5.10E-31	-	570	732	NR_LBD_F1	1.31E-28	-	-	-	-	-	-	NR1C1 (PPARA)
automatic	GSLYST00020728001	35	123	NR_DBD_REV_ERB	8.29E-59	-	210	381	NR_LBD_REV_ERB	1.26E-71	-	990	1294	Med15	5.34E-05	C	NR1C1 (PPARA)
modified	Lsta_scaffold719:49114..65797_ORF30 same location as GSLYS00019008001	160	231	NR_DBD_like	4.16E-31	-	-	-	-	-	no LBD	-	-	-	-	-	NR1C1 (PPARA)
modified	Lsta_scaffold719:49114..65797_ORF30 same location as GSLYS00019008001	160	231	NR_DBD_like	4.16E-31	-	-	-	-	-	no LBD	-	-	-	-	-	NR1C1 (PPARA)
automatic	GSLYST00012709001	31	105	NR_DBD_like	9.03E-34	-	434	601	NR_LBD_F1	1.27E-19	-	-	-	-	-	-	NR1C2 (PPARD)
modified	GSLYST00008467001&ORF2_EX9&10_bpp1E75_GAL ME.1.1	35	113	NR_DBD_REV_ERB	4.49E-41	-	165	327	NR_LBD_PPAR	1.77E-23	-	-	-	-	-	-	NR1C3 (PPARG)
modified	GSLYST00009627001&GSLYST00009626001ext	67	152	NR_DBD_Ppar	1.83E-47	-	222	394	NR_LBD_F1	7.59E-21	-	-	-	-	-	-	NR1C3 (PPARG)
automatic	GSLYST00020475001	32	103	NR_DBD_like	3.33E-30	-	484	634	NR_LBD_Dme78_like	6.62E-19	-	-	-	-	-	-	NR1C3 (PPARG)
automatic	GSLYST00021345001	2	38	NR_DBD_Dme78_like	3.26E-20	N	121	313	NR_LBD_Dme78_like	2.01E-82	-	-	-	-	-	-	NR1C3 (PPARG)
automatic	GSLYST00003246001	18	89	NR_DBD_like	4.35E-42	-	437	609	NR_LBD_F1	6.96E-43	-	-	-	-	-	-	NR1D1 (REVERBA)
automatic	GSLYST00003376001	406	478	NR_DBD_like	8.24E-39	-	1089	1262	NR_LBD_F1	2.15902E-49	-	732	951	T4SS_IcmE_DotG	3.39E-16	NC	NR1D2 (REVERBB)
automatic	GSLYST00003556001	212	278	2DBD_NR_DBD1	3.62E-25	-	867	1035	NR_LBD_F1	9.84E-23	-	298	373	2DBD_NR_DBD2	1.68E-32	full	NR1D2 (REVERBB)
automatic	GSLYST00005611001	-	-	no DBD	-	no DBD	194	347	NR_LBD_F1	9.66E-38	-	-	-	-	-	-	NR1D2 (REVERBB)
automatic	GSLYST00002203001	21	92	NR_DBD_like	3.34E-28	-	480	648	NR_LBD_F1	9.99E-22	-	145	356	Herpes BLLF1	5.53E-05	NC	NR1F1 (RORA)
automatic	GSLYST00003481001	470	541	NR_DBD_like	1.93E-28	-	733	897	NR_LBD_F1	3.64E-12	-	-	-	-	-	-	NR1F1 (RORA)
automatic	GSLYST00003724001	20	93	NR_DBD_like	6.55E-32	-	764	927	NR_LBD_F1	1.13E-18	-	-	-	-	-	-	NR1F1 (RORA)
automatic	GSLYST00012703001	21	93	NR_DBD_like	5.41E-36	-	501	672	NR_LBD_F1	1.97E-17	-	-	-	-	-	-	NR1F1 (RORA)
automatic	GSLYST00007099001	91	184	NR_DBD_ROR	3.92E-65	-	272	508	NR_LBD_ROR_like	8.86E-78	-	-	-	-	-	-	NR1F2 (RORB)
automatic	GSLYST00019331001	22	93	NR_DBD_like	6.95E-37	-	368	537	NR_LBD_F1	3.65E-30	-	-	-	-	-	-	NR1F3 (RORC)
automatic	GSLYST00000602001	62	140	NR_DBD_CAR	8.44E-42	-	375	556	NR_LBD_F1	1.60E-33	-	-	-	-	-	-	NR1H3 (LXRA)
automatic	GSLYST00000926001	71	168	NR_DBD_LXR	1.32E-46	-	246	464	NR_LBD_EcR	7.74E-69	-	-	-	-	-	-	NR1H3 (LXRA)
automatic	GSLYST00003412001	96	188	NR_DBD_CAR	2.00E-46	-	254	432	NR_LBD_F1	1.13E-34	-	-	-	-	-	-	NR1H3 (LXRA)
automatic	GSLYST00019008001	-	-	no DBD	-	no DBD	358	508	NR_LBD_F1	3.78E-29	-	-	-	-	-	-	NR1H3 (LXRA)
automatic	GSLYST00021927001	13	84	NR_DBD_like	7.97E-34	-	231	388	NR_LBD_F1	1.89E-33	-	-	-	-	-	-	NR1H4 (FXRA)
automatic	GSLYST00016253001	20	111	NR_DBD_CAR	2.10E-42	-	259	447	NR_LBD_F1	1.17E-40	-	-	-	-	-	-	NR1I1 (VDR)
modified	GSLYST00020495001&GSLYST00020494001ext	58	151	NR_DBD_CAR	5.27E-45	-	258	431	NR_LBD_F1	1.11E-25	-	-	-	-	-	-	NR1I1 (VDR)
automatic	GSLYST00006772001	151	226	NR_DBD_HNF4A	3.29E-48	-	245	468	NR_LBD_HNF4_like	3.63E-128	-	-	-	-	-	-	NR2A1 (HNF4A)
automatic	GSLYST00014050001	174	253	NR_DBD_RXR	6.66E-54	-	273	476	NR_LBD_RXR_like	2.69E-152	-	98	171	Nuc_recep-AF1	0.0028077	C	NR2B1 (RXRA)
modified	BPPAALocus_8214_Transcript_1/1_1/ORF17/ same location as GSLYST00001311001	189	268	2DBD_NR_DBD1	8.47E-21	-	1145	1313	NR_LBD_F1	7.10774E-13	-	275	348	2DBD_NR_DBD2	4.473E-30	-	NR2B2 (RXRB)
automatic	GSLYST00009203001	113	196	NR_DBD_TR	3.74E-48	-	259	466	NR_LBD_Nurrr1_like	3.25E-41	-	-	-	-	-	-	NR2B3 (RXRG)
modified	GSLYST00005434001&74AA&GSLYST00005433001	152	238	NR_DBD_TR2_like	1.03E-54	-	426	647	NR_LBD_TR2_like	3.86E-103	-	-	-	-	-	-	NR2C2 (TR4)
automatic	GSLYST00007009001	2	82	NR_DBD_PNR_like_2	8.88E-50	-	143	188	NR_LBD_F2	2.32E-10	C	-	-	-	-	-	NR2E1 (TLL)
automatic	GSLYST00012340001	11	103	NR_DBD_TLX	1.06E-64	-	185	377	NR_LBD_Tlx_PNR_like	7.74E-60	-	-	-	-	-	-	NR2E1 (TLL)
modified	GSLYST00013111001&GSLYST00013110001	10	59	NR_DBD_TLX	3.80E-24	-	121	325	NR_LBD_Tlx_PNR_like	5.57E-104	-	-	-	-	-	-	NR2E1 (TLL)
modified	GSLYST00020139_altORF	1	85	NR_DBD_PNR	1.44E-62	-	141	357	NR_LBD_Tlx_PNR_like	5.2571E-107	-	-	-	-	-	-	NR2E3 (PNR)
automatic	GSLYST00022416001	3	20	NR_DBD_PNR	0.000114548	N	-	-	no LBD	-	no LBD	-	-	-	-	-	NR2E3 (PNR)
automatic	GSLYST00018763001	-	-	no DBD	-	no DBD	321	470	NR_LBD_F2	5.00E-31	-	-	-	-	-	-	NR2F1 (COUP-TFI)

ST4. List of metazoan sequences used in the phylogenetic analysis of 2DBD-NRs (see Wu and Loverde 2023).

taxon	protein_ID
Annelida	CAC9635804.1 Ofus.G091856 Owenia fusiformis LBD989..1145
Annelida	CAD5121447.1 DgyrCDS9955 Dimorphilus gyrociiliatus LBD447..620
Annelida	KAI0207292.1 hypothetical protein LSAT2_008100 Lamellibrachia satsuma LBD1166..1314
Annelida	KAI0207833.1 hypothetical protein LSAT2_007485 Lamellibrachia satsuma LBD533..691
Annelida	KAI0243018.1 hypothetical protein LSAT2_009224 Lamellibrachia satsuma LBD877..1064
Brachiopoda	XP_013400322.1 uncharacterized protein LOC106166339 isoform X1 Lingula anatina LBD665..824
Chordata	CAH1264236.1 NR1D1 Branchiostoma lanceolatum LBD528..687
Chordata	ref XP_035674285.1 1-713 nuclear receptor subfamily 1 group D member 1-like isoform X4 Branchiostoma floridae LBD531..690
Echinodermata	XP_022091311.1 uncharacterized protein LOC110979630 Acanthaster planci LBD661..828
Echinodermata	XP_030854207.1 uncharacterized protein LOC100893306 Strongylocentrotus purpuratus LBD836..985
Echinodermata	XP_033102511.1 uncharacterized protein LOC117105468 Anneissia japonica LBD644..781
Echinodermata	XP_033628725.1 uncharacterized protein LOC117291223 Asterias rubens LBD657..824
Echinodermata	XP_038073373.1 uncharacterized protein LOC119741619 Patiria miniata LBD668..835
Echinodermata	XP_041469312.1 uncharacterized protein LOC121419081 Lytechinus variegatus LBD830..996
Mollusca: Gastropoda	BPPAAlocus 8214 Transcript 1/1 1/ORF17 Lymnaea stagnalis LBD1145..1313
Mollusca: Gastropoda	CAG5125116.1 unnamed protein product Candidula unifasciata LBD894..1049
Mollusca: Gastropoda	GFN82368.1 Zinc finger protein Plakobranthus ocellatus LBD1299..1474
Mollusca: Gastropoda	GFR71482.1 nuclear receptor ROR-beta Elysia marginata LBD1336..1504
Mollusca: Gastropoda	GFS22057.1 retinoic acid receptor RXR-alpha Elysia marginata LBD1228..1430
Mollusca: Gastropoda	GSLYST00003556001 Lymnaea stagnalis LBD867..1035
Mollusca: Gastropoda	RUS87101.1 hypothetical protein EGW08_005177 partial Elysia chlorotica LBD652..822
Mollusca: Gastropoda	XP_005095909.2 uncharacterized protein LOC101854010 Aplysia californica LBD1595..1740
Mollusca: Gastropoda	XP_005103360.2 uncharacterized protein LOC101857659 Aplysia californica LBD958..1128
Mollusca: Gastropoda	XP_005112947.2 uncharacterized protein LOC101857539 Aplysia californica LBD1395..1564
Mollusca: Gastropoda	XP_013065455.1 PREDICTED nuclear receptor subfamily 1 group D member 2-like Biomphalaria glabrata LBD700..868
Mollusca: Gastropoda	XP_025103483.1 uncharacterized protein LOC112569789 Pomacea canaliculata LBD676..860
Mollusca: Gastropoda	XP_041351218.1 uncharacterized protein LOC121370170 Gigantopelta aegis LBD764..933
Mollusca: Gastropoda	XP_045168098.2 uncharacterized protein LOC123531312 Mercenaria mercenaria LBD867..1014
Mollusca: Gastropoda	XP_045175060.2 uncharacterized protein LOC123536177 isoform X1 Mercenaria mercenaria LBD782..948
Mollusca: Gastropoda	XP_046364309.2 uncharacterized protein LOC124140669 Haliotis rufescens LBD786..940
Mollusca: Gastropoda	XP_046379417.2 uncharacterized protein LOC124151125 Haliotis rufescens LBD976..1111
Mollusca: Gastropoda	XP_046571180.1 nuclear receptor subfamily 2 group C member 1-like Haliotis rubra LBD739..912
Mollusca: Gastropoda	XP_046577572.1 uncharacterized protein LOC124285391 Haliotis rubra LBD925..1120
Mollusca:Bivalvia	CAC5379089.1 unnamed protein product Mytilus coruscus LBD668..832
Mollusca:Bivalvia	CAC5405050.1 unnamed protein product Mytilus coruscus LBD823..991
Mollusca:Bivalvia	CAG2230085.1 unnamed protein product Mytilus edulis LBD436..570
Mollusca:Bivalvia	KAH3855004.1 hypothetical protein DPMN_097564 Dreissena polymorpha LBD939..1086
Mollusca:Bivalvia	VDI76762.1 blastNuclear receptor subfamily 1 group I member 2 Mytilus galloprovincialis LBD669..833
Mollusca:Bivalvia	XP_011428801.2 uncharacterized protein LOC105329306 isoform X1 Crassostrea gigas LBD816..986
Mollusca:Bivalvia	XP_019919868.2 probable nuclear hormone receptor HR3 isoform X2 Crassostrea gigas LBD504..650
Mollusca:Bivalvia	XP_021367015.1 probable GPI-anchored adhesin-like protein PGA55 Mizuhopecten yessoensis LBD881..1056
Mollusca:Bivalvia	XP_022329720.1 uncharacterized protein LOC111284416 Crassostrea virginica LBD818..988
Mollusca:Bivalvia	XP_022331995.1 nuclear receptor ROR-beta-like isoform X1 Crassostrea virginica LBD504..648
Mollusca:Bivalvia	XP_033734716.1 uncharacterized protein LOC117323546 isoform X1 Pecten maximus LBD964..1113
Nematoda	EGT43828.1 hypothetical protein CAEBREN_02528 Caenorhabditis breneri
Platyhelminthes	gb AAR32910.1 1-1527 two-DBD-nuclear receptor Schistosoma mansoni LBD567..641
Platyhelminthes	gb AAW88550.2 1-1861 nuclear receptor 2DBD-gamma Schistosoma mansoni LBD479..554
Platyhelminthes	KAA0185392.1 Protein embryonic gonad Fasciolopsis buski LBD1458..1650
Platyhelminthes	KAH9284012.1 Nuclear receptor ROR-alpha Echinococcus granulosus LBD882..1069
Platyhelminthes	VDK37619.1 unnamed protein product Taenia asiatica LBD880..1070
Rotifera	CAF0776371.1 unnamed protein product Brachionus calyciflorus LBD415..557
Rotifera	CAF0869039.1 unnamed protein product Rotaria sp. Silwood1 LBD325..474
Rotifera	CAF1025086.1 unnamed protein product Adineta ricciae LBD318..469
Rotifera	CAF1066507.1 unnamed protein product Brachionus calyciflorus LBD259..408
Rotifera	CAF1211849.1 unnamed protein product Adineta steineri LBD308..480
Rotifera	CAF1284752.1 unnamed protein product Rotaria sordida LBD256..403
Rotifera	CAF1622127.1 unnamed protein product partial Adineta ricciae LBD320..471
Rotifera	CAF1635244.1 unnamed protein product Rotaria magnacalcarata LBD323..478
Rotifera	CAF2064338.1 unnamed protein product Rotaria magnacalcarata LBD299..446
Rotifera	CAF2401455.1 unnamed protein product Rotaria sp. Silwood2 LBD307..458
Rotifera	CAF3303110.1 unnamed protein product Rotaria socialis LBD325..480
Rotifera	CAF4632909.1 unnamed protein product partial Rotaria socialis LBD308..459

ST5. Annotation of *L. stagnalis* predicted proteins: GPCRs.

gp	Hit type	PSSM-ID	From	To	E-Value	Bitscore	Accession	Short name	Incomplete	Superfamily	class
GSLYST00017491001	superfamily	333717	12	152	4.89E-05	44.7022	cd28897	7tm_GPCRs superfamily	C	-	Class_?
GSLYST00000030001	specific	320187	25	388	7.79E-110	322.755	cd15059	7tm_alpha2_AR	-	cd28897	Class_A
GSLYST00000030001	non-specific	222976	25	209	2.50E-12	67.1106	PHAO3087	7tm_alpha2_AR	C	cd27963	Class_A
GSLYST00000010001	specific	320194	34	337	1.46E-166	466.468	cd15066	7tm_DmOct-betaAR-like	-	cd28897	Class_A
GSLYST00000010001	non-specific	222976	41	343	8.63E-19	86.3706	PHAO3087	7tm_alpha2_AR	-	cd27963	Class_A
GSLYST00000017001	non-specific	320190	3	330	1.23E-107	314.812	cd15062	7tm_alpha1_AR	-	cd28897	Class_A
GSLYST00000017001	non-specific	222976	5	326	3.89E-12	65.955	PHAO3087	7tm_alpha1_AR	-	cd27963	Class_A
GSLYST00000031001	non-specific	313540	38	175	0.000157492	42.5613	pfam10328	7TM_GPCR_Srx	C	cd21561	Class_A
GSLYST00000031001	non-specific	320109	34	186	1.65E-12	66.8876	cd14978	7tm_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00000031001	non-specific	165021	38	174	3.22E-07	51.5526	PHAO2638	PHAO2638	NC	cd27963	Class_A
GSLYST00000032001	non-specific	255903	2	288	0.000392063	40.6547	pfam10320	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00000032001	non-specific	320109	1	288	1.99E-17	80.3696	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000034001	non-specific	320109	3	303	4.07E-11	62.2652	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000035001	non-specific	320109	3	307	6.29E-12	64.9616	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000036001	non-specific	313536	2	311	5.31E-07	50.2884	pfam10324	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00000036001	non-specific	320109	3	307	1.19E-14	72.6656	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000037001	non-specific	320109	3	297	2.78E-15	74.2064	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000037001	non-specific	313540	85	134	0.00439945	37.9389	pfam10328	7TM_GPCR_Srx	NC	cd21561	Class_A
GSLYST00000038001	non-specific	320109	3	240	6.00E-11	60.7244	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000039001	non-specific	313536	1	302	0.000366757	41.4288	pfam10324	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00000039001	non-specific	320109	1	302	1.89E-14	71.8952	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000054001	non-specific	320109	14	278	7.05E-16	75.7472	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000055001	non-specific	320109	11	217	4.53E-15	71.8952	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00000057001	non-specific	320109	23	239	2.37E-13	68.0432	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00000058001	non-specific	320109	7	229	5.72E-09	55.7168	cd14978	7tm_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00000079001	non-specific	320109	6	272	2.10E-13	68.4284	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000082001	non-specific	320109	7	212	8.88E-15	71.1248	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00000083001	non-specific	320109	1	290	2.47E-26	105.022	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000156001	non-specific	320109	41	330	2.88E-29	114.652	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000156001	non-specific	222976	40	229	2.71E-06	48.621	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00000196001	superfamily	333717	13	308	2.17E-82	250.67	cd28897	7tm_GPCRs superfamily	-	-	Class_A
GSLYST00000196001	non-specific	320128	13	308	2.17E-82	250.67	cd14997	7tm_ETH-R	-	cd28897	Class_A
GSLYST00000196001	non-specific	222976	44	312	2.32E-12	66.3402	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00000205001	non-specific	320109	1	264	1.50E-19	86.1476	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000246001	non-specific	313536	1	298	0.000191395	42.1992	pfam10324	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00000246001	non-specific	320109	1	291	5.90E-30	114.652	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000247001	non-specific	320086	17	127	1.33E-07	48.8108	cd00637	7tm_classa_rhodopsin-like	C	cd28897	Class_A
GSLYST00000248001	non-specific	320109	3	120	1.66E-09	53.7908	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000254001	non-specific	313536	2	279	0.00790323	36.8064	pfam10324	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00000254001	non-specific	320109	1	279	1.31E-23	96.9332	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000255001	non-specific	320109	15	148	7.91E-06	44.1608	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00000256001	non-specific	320109	1	285	8.89E-23	95.0072	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000279001	specific	320086	46	399	4.98E-28	111.598	cd00637	7tm_classa_rhodopsin-like	-	cd28897	Class_A
GSLYST00000314001	non-specific	320109	13	218	2.44E-15	73.8212	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00000329001	non-specific	320112	2	276	1.78E-34	133.14	cd14981	7tm_Prostanoid_R	-	cd28897	Class_A
GSLYST00000339001	non-specific	320132	72	263	1.75E-42	146.267	cd15001	7tm_GPRna14-like	C	cd28897	Class_A
GSLYST00000339001	non-specific	222976	51	268	4.47E-16	76.7406	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00000340001	non-specific	320132	1	68	2.64E-12	61.1377	cd15001	7tm_GPRna14-like	N	cd28897	Class_A
GSLYST00000395001	specific	320086	6	159	3.43E-21	86.5604	cd00637	7tm_classa_rhodopsin-like	C	cd28897	Class_A
GSLYST00000395001	non-specific	222976	3	119	9.96E-05	40.9171	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00000443001	non-specific	320331	39	317	8.64E-45	154.685	cd15203	7tm_NPYR-like	-	cd28897	Class_A
GSLYST00000443001	non-specific	222976	51	145	1.30E-06	49.3914	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00000558001	non-specific	320098	25	158	4.71E-20	89.5444	cd14967	7tm_amine_R-like	C	cd28897	Class_A
GSLYST00000558001	non-specific	320182	409	475	1.07E-06	50.1878	cd15054	7tm_5-HT6	N	cd28897	Class_A
GSLYST00000558001	non-specific	165021	29	149	0.00378418	39.6114	PHAO2638	PHAO2638	NC	cd27963	Class_A
GSLYST00000628001	non-specific	320109	5	270	1.43E-19	86.1476	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000661001	non-specific	320109	15	310	8.04E-14	70.3544	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000751001	non-specific	320086	8	64	3.91E-05	44.1884	cd00637	7tm_classa_rhodopsin-like	C	cd28897	Class_A
GSLYST00000801001	non-specific	320109	1	306	1.89E-08	54.5612	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000803001	non-specific	320109	27	338	9.77E-09	55.7168	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000803001	non-specific	313540	32	231	0.000317006	41.7909	pfam10328	7TM_GPCR_Srx	C	cd21561	Class_A
GSLYST00000804001	non-specific	320109	6	289	3.15E-12	65.3468	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000806001	non-specific	320109	27	338	1.67E-14	73.0508	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00000806001	non-specific	313540	32	227	0.00106879	39.8649	pfam10328	7TM_GPCR_Srx	C	cd21561	Class_A
GSLYST00000919001	non-specific	320086	37	138	6.21E-06	48.4256	cd00637	7tm_classa_rhodopsin-like	C	cd28897	Class_A
GSLYST00000919001	non-specific	223633	28	128	0.00239896	40.2328	COG0559	LivH	C	cd00454	Class_A
GSLYST00000919001	superfamily	320981	28	128	0.00239896	40.2328	cd00454	TM_PBP1_branched-chain-AA_like superfamily	C	-	Class_A
GSLYST00000981001	non-specific	320124	6	257	4.57E-11	61.4612	cd14993	7tm_CCKR-like	N	cd28897	Class_A
GSLYST00000982001	non-specific	320109	16	76	0.000265815	37.9977	cd14978	7tm_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00000983001	non-specific	320109	44	386	5.14E-19	86.5328	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00001128001	non-specific	320109	21	324	2.83E-25	103.096	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00001152001	specific	320086	86	371	9.37E-56	185.171	cd00637	7tm_classa_rhodopsin-like	-	cd28897	Class_A
GSLYST00001152001	non-specific	222976	86	382	9.44E-10	59.4066	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00001155001	specific	320086	11	312	4.16E-52	172.845	cd00637	7tm_classa_rhodopsin-like	-	cd28897	Class_A
GSLYST00001155001	non-specific	222976	8	210	3.13E-10	60.177	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00001159001	non-specific	320504	60	376	1.56E-123	358.932	cd15382	7tm_AKHR	-	cd28897	Class_A
GSLYST00001159001	non-specific	222976	63	382	2.27E-17	82.1334	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00001165001	specific	320109	68	359	2.46E-85	263.725	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00001165001	non-specific	222976	72	363	5.76E-09	57.0954	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00001309001	non-specific	313536	9	274	1.34E-07	51.444	pfam10324	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00001309001	non-specific	320109	9	276	1.29E-18	83.4512	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00001318001	non-specific	320109	6	303	4.21E-28	110.03	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00001318001	non-specific	313536	150	310	1.16E-09	58.3776	pfam10324	7TM_GPCR_Srx	N	cd21561	Class_A
GSLYST00001330001	non-specific	313536	4	269	0.000715513	40.2732	pfam10324	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00001330001	non-specific	320109	4	271	4.63E-15	73.0508	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00001331001	non-specific	320109	6	273	8.04E-17	78.0584	cd14978	7tm_FMRFamide_R-like	-	cd28	

GSLYST00002054001	non-specific	320140	55	250	3.89E-60	199.207	cd15012	7tm_Trissin_R	C	cd28897	Class_A
GSLYST00002054001	non-specific	222976	52	255	2.47E-17	82.9038	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00002054001	non-specific	320245	442	501	0.00020278	43.184	cd15117	7tm_FPR-like	N	cd28897	Class_A
GSLYST00002083001	non-specific	313536	5	294	5.60E-06	46.8216	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00002083001	non-specific	320109	5	300	7.01E-19	84.6068	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002125001	non-specific	320098	3	248	2.04E-41	141.932	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00002125001	non-specific	222976	28	213	1.67E-05	44.769	PHAO3087	PHAO3087	NC	cd27963	Class_A
GSLYST00002127001	non-specific	320098	1	248	1.28E-51	168.125	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00002127001	non-specific	222976	4	216	6.98E-07	49.0062	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00002153001	non-specific	320454	96	159	4.40E-34	120.151	cd15331	7tm_5-HT1A_invertebrates	C	cd28897	Class_A
GSLYST00002154001	non-specific	320513	1	22	1.88E-05	44.4279	cd15391	7tm_NPR1-like_invertebrate	N	cd28897	Class_A
GSLYST00002193001	non-specific	320331	1	216	2.90E-68	212.465	cd15203	7tm_NPYR-like	N	cd28897	Class_A
GSLYST00002193001	non-specific	222976	1	232	0.000231647	41.6874	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00002219001	specific	320086	35	245	3.70E-28	113.524	cd00637	7tm_classA_rhodopsin-like	C	cd28897	Class_A
GSLYST00002219001	non-specific	320086	447	532	2.93E-08	54.974	cd00637	7tm_classA_rhodopsin-like	N	cd28897	Class_A
GSLYST00002219001	non-specific	165021	35	167	0.000121507	44.619	PHAO2638	PHAO2638	NC	cd27963	Class_A
GSLYST00002277001	non-specific	320132	1	262	9.65E-76	231.781	cd15001	7tm_GPRnna14-like	N	cd28897	Class_A
GSLYST00002277001	non-specific	222976	3	258	5.74E-11	62.103	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00002394001	specific	320234	71	402	2.89E-152	432.814	cd15196	7tm_Vasopressin_Oxytocin	-	cd28897	Class_A
GSLYST00002394001	non-specific	222976	65	398	1.39E-11	65.1846	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00002484001	non-specific	313536	8	308	1.34E-09	57.9924	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00002484001	non-specific	320109	4	301	4.13E-25	101.941	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002484001	non-specific	165021	8	69	0.0056634	38.0706	PHAO2638	PHAO2638	NC	cd27963	Class_A
GSLYST00002485001	non-specific	313536	8	305	4.76E-08	53.37	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00002485001	non-specific	320109	4	300	1.36E-23	97.7036	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002492001	non-specific	320109	43	332	1.35E-24	101.17	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002589001	specific	320109	70	367	3.03E-39	142.772	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002589001	non-specific	222976	76	381	3.05E-10	60.9474	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00002608001	non-specific	313536	23	316	5.93E-06	46.8216	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00002608001	non-specific	320109	16	313	1.41E-26	105.793	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002609001	non-specific	313536	23	316	1.01E-11	64.5408	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00002609001	non-specific	320109	16	313	9.80E-28	109.26	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002613001	non-specific	320109	45	335	8.25E-22	93.8516	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002638001	non-specific	320124	86	332	9.79E-75	232.875	cd14993	7tm_CCKR-like	-	cd28897	Class_A
GSLYST00002638001	non-specific	222976	87	338	1.45E-14	73.2738	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00002650001	non-specific	320236	75	376	2.48E-93	284.007	cd15198	7tm_GPR150	-	cd28897	Class_A
GSLYST00002650001	non-specific	222976	71	369	3.22E-12	67.1106	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00002670001	non-specific	320109	1	292	5.89E-27	106.948	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002670001	non-specific	222976	5	199	0.00670894	37.4503	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00002794001	non-specific	313536	66	364	8.27E-16	77.2524	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00002794001	specific	320109	59	360	1.19E-46	161.262	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002815001	non-specific	320232	7	272	7.40E-24	97.0589	cd15104	7tm_GPR119_R_insulinotropic_receptor	-	cd28897	Class_A
GSLYST00002824001	non-specific	320109	20	316	5.59E-24	99.2444	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002836001	non-specific	320336	59	359	1.13E-93	284.282	cd15208	7tm_OXR	-	cd28897	Class_A
GSLYST00002836001	non-specific	222976	62	361	2.22E-17	82.5186	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00002840001	non-specific	320109	5	289	4.34E-22	93.4664	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002847001	non-specific	320335	1	233	1.15E-37	133.13	cd15207	7tm_NPFFR	N	cd28897	Class_A
GSLYST00002847001	non-specific	222976	7	243	0.000238497	41.3022	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00002848001	non-specific	320124	3	51	7.69E-10	51.446	cd14993	7tm_CCKR-like	C	cd28897	Class_A
GSLYST00002864001	specific	320109	68	369	9.50E-48	164.728	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002865001	specific	320109	77	378	3.43E-52	176.67	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002865001	non-specific	222976	89	283	6.89E-05	44.3838	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00002884001	non-specific	320109	15	303	1.08E-23	97.7036	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00002917001	specific	320109	32	327	1.99E-44	156.254	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003090001	specific	320086	53	325	1.18E-35	132.014	cd00637	7tm_classA_rhodopsin-like	-	cd28897	Class_A
GSLYST00003162001	specific	320459	47	337	8.80E-161	458.709	cd15337	7tm_Opsin_Gq_invertebrates	-	cd28897	Class_A
GSLYST00003162001	non-specific	222976	2	288	6.06E-19	87.9114	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00003176001	non-specific	320109	35	250	8.85E-20	86.1476	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00003179001	non-specific	320513	33	300	2.54E-100	295.963	cd15391	7tm_NPR-like_invertebrate	-	cd28897	Class_A
GSLYST00003179001	non-specific	222976	34	296	3.34E-19	85.9854	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00003184001	non-specific	313536	44	338	8.74E-11	61.8444	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00003184001	non-specific	320109	37	334	8.28E-29	112.341	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003294001	non-specific	320109	13	288	5.14E-20	87.3032	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003295001	non-specific	320109	1	282	2.65E-23	96.1628	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003296001	non-specific	320109	1	288	3.54E-27	106.948	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003312001	non-specific	320109	1	270	1.40E-19	86.1476	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003313001	non-specific	320109	1	277	1.87E-18	83.066	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003314001	non-specific	320109	1	269	2.47E-20	88.0736	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003315001	non-specific	320109	14	277	1.31E-17	80.7548	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003317001	non-specific	320109	2	283	1.41E-27	108.104	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003317001	non-specific	222976	3	222	2.28E-07	50.9322	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00003385001	non-specific	320224	31	320	6.79E-108	315.774	cd15096	7tm_AstA_R_insect	-	cd28897	Class_A
GSLYST00003385001	non-specific	222976	27	330	1.39E-28	112.564	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00003386001	non-specific	320224	24	311	3.89E-106	311.152	cd15096	7tm_AstA_R_insect	-	cd28897	Class_A
GSLYST00003386001	non-specific	222976	20	315	3.16E-21	92.1486	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00003387001	non-specific	320224	24	311	2.23E-103	304.604	cd15096	7tm_AstA_R_insect	-	cd28897	Class_A
GSLYST00003387001	non-specific	222976	20	315	1.27E-20	90.6708	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00003388001	specific	320224	47	333	1.81E-144	410.919	cd15096	7tm_AstA_R_insect	-	cd28897	Class_A
GSLYST00003388001	non-specific	222976	45	337	1.66E-23	99.4674	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00003391001	non-specific	320335	3	67	1.08E-13	63.7945	cd15207	7tm_NPFFR	C	cd28897	Class_A
GSLYST00003392001	specific	320124	1	216	2.45E-80	244.816	cd14993	7tm_CCKR-like	N	cd28897	Class_A
GSLYST00003392001	non-specific	222976	1	220	9.21E-16	75.9702	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00003651001	non-specific	320109	1	309	1.07E-16	78.4436	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003651001	non-specific	313540	1	132	0.00872728	36.7833	pfam10328	7TM_GPCR_Srx	C	cd21561	Class_A
GSLYST00003704001	non-specific	320262	79	387	1.74E-128	375.515	cd15134	7tm_capaR	-	cd28897	Class_A
GSLYST00003704001	non-specific	222976	76	391	2.26E-14	74.0442	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00003771001	non-specific	320109	1	309	1.08E-17	81.5252	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003798001	non-specific	320515	1	68	3.09E-44	146.014	cd15393	7tm_Leucokinin-like	N	cd28897	Class_A
GSLYST00003798001	non-specific	222976	1	64	5.12E-05	41.3022	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00003803001	superfamily	333717	16	159	1.37E-18	80.7824	cd28897	7tm_GPCRs superfamily	C	-	Class_A
GSLYST00003899001	specific	320512	51	336	3.17E-142	406.68	cd15390	7tm_TACR	-	cd28897	Class_A
GSLYST00003899001	non-specific	222976	23	332	1.11E-18	86.3706	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00003984001	non-specific	320109	42	259	6.39E-30	113.497	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00003985001	non-specific	320109	20	318	3.69E-18	83.066	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003986001	non-specific	320109	15	312	5.21E-18	82.6808	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003987001	non-specific	320109	1	287	9.23E-21	89.6144	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00003988001	non-specific	320109	4	301	1.72E-21	91.9256	cd14978</				

GSLYST00004246001	non-specific	222976	35	114	0.00147212	37.8355	PHA03087	PHA03087	N	-	c127963	Class_A	
GSLYST00004278001	non-specific	320132	1	69	2.92E-30	108.902	cd15001	7tm_GPRnna14-like	N	-	c128897	Class_A	
GSLYST00004278001	non-specific	165177	1	74	1.14E-05	42.9693	PHA02834	PHA02834	N	-	c127963	Class_A	
GSLYST00004295001	specific	320265	645	928	2.05E-152	450.884	cd15137	7tm_Relaxin_R	-	-	-	c128897	Class_A
GSLYST00004295001	specific	278486	238	274	8.49E-10	54.562	pfam00057	Ldl_recept_a	-	-	-	c100104	Class_A
GSLYST00004295001	non-specific	278486	279	313	1.01E-06	45.7024	pfam00057	Ldl_recept_a	-	-	-	c100104	Class_A
GSLYST00004295001	non-specific	278486	5	39	1.01E-06	45.7024	pfam00057	Ldl_recept_a	-	-	-	c100104	Class_A
GSLYST00004295001	specific	238060	5	39	1.90E-10	56.4662	cd00112	LDLa	-	-	-	c100104	Class_A
GSLYST00004295001	specific	238060	279	313	1.02E-09	54.135	cd00112	LDLa	-	-	-	c100104	Class_A
GSLYST00004295001	specific	238060	240	274	1.09E-09	54.135	cd00112	LDLa	-	-	-	c100104	Class_A
GSLYST00004295001	specific	197566	5	36	5.57E-09	52.2505	smart00192	LDLa	-	-	-	c100104	Class_A
GSLYST00004295001	specific	197566	279	310	8.91E-09	51.4801	smart00192	LDLa	-	-	-	c100104	Class_A
GSLYST00004295001	specific	197566	240	271	1.21E-08	51.0949	smart00192	LDLa	-	-	-	c100104	Class_A
GSLYST00004295001	specific	197566	44	75	3.30E-06	44.1613	smart00192	LDLa	-	-	-	c100104	Class_A
GSLYST00004295001	specific	238060	44	80	3.89E-06	44.1198	cd00112	LDLa	-	-	-	c100104	Class_A
GSLYST00004295001	specific	238060	362	397	0.000110687	39.8826	cd00112	LDLa	-	-	-	c100104	Class_A
GSLYST00004295001	specific	238060	203	231	0.000265426	38.727	cd00112	LDLa	-	-	-	c100104	Class_A
GSLYST00004295001	superfamily	294076	5	39	1.90E-10	56.4462	cd00104	LDLa superfamily	-	-	-	-	Class_A
GSLYST00004295001	superfamily	294076	238	274	8.49E-10	54.562	cd00104	LDLa superfamily	-	-	-	-	Class_A
GSLYST00004295001	superfamily	294076	279	313	1.02E-09	54.135	cd00104	LDLa superfamily	-	-	-	-	Class_A
GSLYST00004295001	superfamily	294076	44	75	3.30E-06	44.1613	cd00104	LDLa superfamily	-	-	-	-	Class_A
GSLYST00004295001	superfamily	294076	362	397	0.000110687	39.8826	cd00104	LDLa superfamily	-	-	-	-	Class_A
GSLYST00004295001	superfamily	294076	203	231	0.000265426	38.727	cd00104	LDLa superfamily	-	-	-	-	Class_A
GSLYST00004295001	specific	316378	510	569	1.17E-15	71.7894	pfam13855	LRR_8	-	-	-	c125992	Class_A
GSLYST00004295001	specific	197566	362	387	0.00095324	37.2277	smart00192	LDLa	C	-	c100104	Class_A	
GSLYST00004295001	non-specific	278486	204	231	0.00579658	35.302	pfam00057	Ldl_recept_a	-	-	-	c100104	Class_A
GSLYST00004295001	specific	197566	204	228	0.00446811	35.3017	smart00192	LDLa	N	-	c100104	Class_A	
GSLYST00004295001	non-specific	238064	466	600	0.000297021	43.8834	cd00116	LRR_RI	N	-	c126161	Class_A	
GSLYST00004295001	superfamily	330982	466	600	0.000297021	43.8834	c126161	LRR_RI superfamily	N	-	-	-	Class_A
GSLYST00004295001	non-specific	165021	645	919	4.83E-05	46.545	PHA02638	PHA02638	N	-	c127963	Class_A	
GSLYST00004295001	specific	227223	460	593	6.47E-19	90.0273	COG4886	LRR	NC	-	c125992	Class_A	
GSLYST00004295001	superfamily	330813	460	593	6.47E-19	90.0273	c125992	LRR_8 superfamily	NC	-	-	-	Class_A
GSLYST00004295001	non-specific	215061	455	641	8.54E-08	56.0096	PLN00113	PLN00113	NC	-	c126793	Class_A	
GSLYST00004295001	superfamily	331614	455	641	8.54E-08	56.0096	c126793	PLN00113 superfamily	NC	-	-	-	Class_A
GSLYST00004392001	non-specific	320109	1	152	1.71E-11	61.88	cd14978	7tm_FMRFamide_R-like	N	-	c128897	Class_A	
GSLYST00004444001	non-specific	320109	9	239	7.66E-07	48.7832	cd14978	7tm_FMRFamide_R-like	N	-	c128897	Class_A	
GSLYST00004445001	non-specific	320109	25	331	2.48E-11	63.4208	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004445001	non-specific	313540	32	167	0.000458678	41.0205	pfam10328	7TM_GPCR_Srx	C	-	c121561	Class_A	
GSLYST00004448001	non-specific	320109	43	394	4.33E-07	51.0944	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004448001	non-specific	313540	107	232	0.000158289	42.9465	pfam10328	7TM_GPCR_Srx	C	-	c121561	Class_A	
GSLYST00004449001	non-specific	320109	2	296	4.54E-22	93.4664	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004477001	non-specific	320132	3	278	3.75E-59	189.409	cd15001	7tm_GPRnna14-like	-	-	-	c128897	Class_A
GSLYST00004477001	non-specific	222976	17	148	2.64E-08	54.0138	PHA03087	PHA03087	NC	-	-	c127963	Class_A
GSLYST00004508001	non-specific	313536	22	295	9.10E-05	42.9696	pfam10324	7TM_GPCR_Srw	-	-	-	c121561	Class_A
GSLYST00004508001	non-specific	320109	1	291	4.02E-18	82.2956	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004509001	non-specific	313536	1	285	1.30E-09	57.6072	pfam10324	7TM_GPCR_Srw	-	-	-	c121561	Class_A
GSLYST00004509001	non-specific	320109	1	285	8.05E-27	105.793	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004510001	non-specific	320109	16	312	1.32E-15	75.362	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004511001	non-specific	320109	23	319	9.05E-19	84.6068	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004512001	non-specific	320109	2	282	1.36E-20	88.844	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004513001	non-specific	320109	1	262	5.33E-16	76.1324	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004513001	non-specific	313536	109	269	0.000450895	40.6584	pfam10324	7TM_GPCR_Srw	N	-	c121561	Class_A	
GSLYST00004514001	non-specific	320109	18	308	4.11E-20	88.0736	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004544001	non-specific	320109	2	187	1.19E-07	50.7092	cd14978	7tm_FMRFamide_R-like	C	-	c128897	Class_A	
GSLYST00004545001	non-specific	313536	13	305	8.33E-07	49.518	pfam10324	7TM_GPCR_Srw	-	-	-	c121561	Class_A
GSLYST00004545001	non-specific	320109	8	302	3.66E-25	101.941	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004546001	non-specific	313536	13	306	0.000139017	42.5844	pfam10324	7TM_GPCR_Srw	-	-	-	c121561	Class_A
GSLYST00004546001	non-specific	320109	8	302	6.88E-24	98.474	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004547001	non-specific	313536	47	342	4.24E-08	53.7552	pfam10324	7TM_GPCR_Srw	-	-	-	c121561	Class_A
GSLYST00004547001	non-specific	320109	41	337	1.11E-25	104.252	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004548001	non-specific	320109	25	317	2.96E-17	80.3696	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004549001	non-specific	313536	22	315	5.81E-05	43.74	pfam10324	7TM_GPCR_Srw	-	-	-	c121561	Class_A
GSLYST00004549001	non-specific	320109	17	310	1.30E-25	103.482	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004562001	specific	320109	60	349	7.00E-44	153.172	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004562001	non-specific	222976	52	307	0.00556546	38.2207	PHA03087	PHA03087	-	-	-	c127963	Class_A
GSLYST00004573001	non-specific	317417	89	279	4.95E-31	115.831	pfam14997	CECR6_TMEM121	-	-	-	c120875	Class_A
GSLYST00004573001	superfamily	317417	89	279	4.95E-31	115.831	c120875	CECR6_TMEM121 superfamily	-	-	-	-	Class_A
GSLYST00004573001	superfamily	333717	14	98	0.000627281	40.4802	c128897	7tm_GPCRs superfamily	N	-	-	-	Class_A
GSLYST00004573001	non-specific	320170	14	98	0.000627281	40.4802	cd15042	7tm_C_Boss	-	-	-	c128897	Class_A
GSLYST00004584001	specific	320112	1	210	9.67E-67	220.965	cd14981	7tm_Prostanoid_R	N	-	c128897	Class_A	
GSLYST00004591001	non-specific	320140	51	250	3.61E-49	171.088	cd15012	7tm_Trissin_R	C	-	c128897	Class_A	
GSLYST00004591001	non-specific	222976	40	251	2.31E-13	70.9626	PHA03087	PHA03087	C	-	-	c127963	Class_A
GSLYST00004610001	non-specific	313536	10	316	1.23E-17	81.8748	pfam10324	7TM_GPCR_Srw	-	-	-	c121561	Class_A
GSLYST00004610001	specific	320109	6	319	5.22E-55	180.907	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004633001	specific	320086	34	276	2.58E-26	103.894	cd00637	7tm_class_rhodopsin-like	-	-	-	c128897	Class_A
GSLYST00004643001	specific	320109	67	350	1.01E-36	134.683	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004805001	non-specific	320109	15	310	1.47E-23	97.7036	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004810001	non-specific	320109	37	332	4.65E-24	99.6296	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004811001	non-specific	320109	22	319	4.06E-23	96.9332	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004911001	non-specific	320109	78	360	1.53E-23	99.2444	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00004914001	non-specific	320100	25	322	7.14E-43	149.279	cd14969	7tm_Opsins_type2_animals	-	-	-	c128897	Class_A
GSLYST00004930001	non-specific	320109	24	327	6.79E-16	76.5176	cd14978	7tm_FMRFamide_R-like	-	-	-	c128897	Class_A
GSLYST00005028001	non-specific	320334	71	149	2.05E-37	128.277	cd15206	7tm_CCK_R	C	-	c128897	Class_A	
GSLYST00005028001	non-specific	165021	46	141	1.90E-10	57.3306	PHA02638	PHA02638	C	-	-	c127963	Class_A
GSLYST00005029001	non-specific	320334	2	220	6.46E-33	120.958	cd15206	7tm_CCK_R	N	-	c128897	Class_A	
GSLYST00005029001	non-specific	222976	146	216	0.0012548	39.3763	PHA03087	PHA03087	N	-	-	c127963	Class_A
GSLYST00005067001	specific	320086	57	328	1.68E-65	217.913	cd00637	7tm_class_rhodopsin-like	-	-	-	c128897	Class_A
GSLYST00005067001	non-specific	222976	47	331	9.04E-17	82.1334	PHA03087	PHA03087	-	-	-	c127963	Class_A
GSLYST00005070001	specific	320086	45	317	2.88E-72	237.173	cd00637	7tm_class_rhodopsin-like	-	-	-	c128897	Class_A
GSLYST00005070001	non-specific	222976	42	328	8.06E-21	94.4598	PHA03087	PHA03087	-	-	-	c127963	Class_A
GSLYST00005070001	non-specific	316466	519	631	0.00191407	39.8665	pfam13945	NST1	C	-	c116492	Class_A	
GSLYST00005070001	superfamily</												

GSLYST00005481001	superfamily	330813	11	63	2.45E-06	44.4403	cd25992	LRR_8 superfamily	-	-	Class_A
GSLYST00005481001	non-specific	222976	122	342	0.000568717	41.3022	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00005491001	non-specific	320334	1	191	1.16E-90	270.416	cd15206	7tm_CCK_R	C	cd28897	Class_A
GSLYST00005491001	non-specific	222976	1	198	3.55E-20	88.6818	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00005513001	non-specific	320109	26	300	2.11E-17	80.3696	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005514001	non-specific	320109	2	281	6.60E-13	67.2728	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005515001	non-specific	313536	21	312	0.000293635	41.814	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00005515001	non-specific	320109	13	303	2.29E-19	86.1476	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005515001	non-specific	165021	15	256	0.000184638	42.693	PHAO2638	PHAO2638	NC	cd27963	Class_A
GSLYST00005516001	non-specific	320109	1	203	2.50E-10	58.4132	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00005560001	non-specific	320128	2	97	1.10E-32	115.465	cd14997	7tm_ETH-R	N	cd28897	Class_A
GSLYST00005561001	non-specific	320128	42	232	2.86E-43	147.437	cd14997	7tm_ETH-R	C	cd28897	Class_A
GSLYST00005561001	non-specific	222976	49	182	2.75E-06	47.0802	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00005562001	non-specific	320128	18	108	8.10E-31	111.228	cd14997	7tm_ETH-R	N	cd28897	Class_A
GSLYST00005563001	non-specific	320262	14	69	1.66E-10	54.2588	cd15134	7tm_capaR	NC	cd28897	Class_A
GSLYST00005564001	non-specific	320128	39	93	4.39E-05	39.9659	cd14997	7tm_ETH-R	C	cd28897	Class_A
GSLYST00005588001	non-specific	320109	5	329	1.04E-11	64.5764	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005643001	non-specific	320109	1	291	8.27E-17	78.8288	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005643001	non-specific	165021	1	243	0.00825504	37.3002	PHAO2638	PHAO2638	N	cd27963	Class_A
GSLYST00005694001	non-specific	320324	597	670	2.72E-40	148.537	cd15196	7tm_Vasopressin_Oxytocin	N	cd28897	Class_A
GSLYST00005694001	non-specific	222976	595	665	0.00120022	41.6874	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00005694001	non-specific	320324	1	114	1.15E-52	182.82	cd15196	7tm_Vasopressin_Oxytocin	NC	cd28897	Class_A
GSLYST00005779001	non-specific	320109	20	312	3.47E-08	53.7908	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005780001	non-specific	320109	19	343	4.82E-13	68.4284	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005781001	non-specific	320109	7	223	0.000521151	39.9237	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005782001	non-specific	320109	12	349	7.87E-14	70.7396	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005783001	non-specific	320109	22	284	2.71E-06	47.6276	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005784001	non-specific	320109	6	319	0.000117998	43.0052	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005785001	non-specific	320109	6	319	0.000198715	42.2348	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005786001	non-specific	320109	6	322	2.31E-05	45.3164	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005795001	non-specific	320109	1	305	3.14E-12	65.732	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005819001	specific	320098	83	282	9.04E-71	227.831	cd14967	7tm_amine_R-like	C	cd28897	Class_A
GSLYST00005819001	non-specific	320098	488	559	5.61E-24	101.1	cd14967	7tm_amine_R-like	N	cd28897	Class_A
GSLYST00005819001	non-specific	165021	75	290	1.24E-14	75.8202	PHAO2638	PHAO2638	NC	cd27963	Class_A
GSLYST00005850001	specific	320086	25	295	8.88E-11	61.5224	cd00637	7tm_classa_rhodopsin-like	-	cd28897	Class_A
GSLYST00005994001	non-specific	320109	56	345	1.94E-27	109.26	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00005994001	non-specific	222976	66	345	0.00267953	38.9911	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00006018001	non-specific	320109	60	343	1.17E-18	84.992	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006018001	non-specific	313536	131	350	0.00370475	38.7324	pfam10324	7TM_GPCR_Srw	N	cd21561	Class_A
GSLYST00006019001	non-specific	320109	5	301	1.25E-17	81.14	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006019001	non-specific	313536	89	308	0.00584775	37.5768	pfam10324	7TM_GPCR_Srw	N	cd21561	Class_A
GSLYST00006020001	non-specific	320109	20	312	5.90E-15	73.8212	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006041001	specific	320086	1	174	7.61E-31	112.369	cd00637	7tm_classa_rhodopsin-like	C	cd28897	Class_A
GSLYST00006041001	non-specific	222976	2	167	0.000972408	38.2207	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00006200001	non-specific	320109	1	317	3.04E-13	68.8136	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006201001	non-specific	320109	3	232	2.16E-05	44.1608	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006354001	specific	320331	45	341	6.12E-118	344.588	cd15203	7tm_NPYR-like	-	cd28897	Class_A
GSLYST00006354001	non-specific	222976	29	337	3.88E-22	96.0006	PHAO3087	PHAO3087	-	cd27963	Class_A
GSLYST00006494001	non-specific	320109	57	350	6.64E-15	74.5916	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006494001	non-specific	222976	1	162	0.000223032	42.843	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00006510001	non-specific	320137	20	302	1.85E-51	172.711	cd15008	7tm_GPR19	-	cd28897	Class_A
GSLYST00006510001	non-specific	222976	51	271	5.06E-07	50.9322	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00006580001	non-specific	320128	3	164	2.28E-30	111.228	cd14997	7tm_ETH-R	N	cd28897	Class_A
GSLYST00006581001	non-specific	320128	6	57	3.16E-12	61.5371	cd14997	7tm_ETH-R	N	cd28897	Class_A
GSLYST00006584001	non-specific	313536	50	283	0.00132509	39.5028	pfam10324	7TM_GPCR_Srw	N	cd21561	Class_A
GSLYST00006584001	non-specific	320109	61	283	4.25E-11	61.88	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006585001	non-specific	320109	30	322	7.39E-24	99.2444	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006707001	non-specific	320109	52	333	1.22E-24	102.326	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006789001	non-specific	320109	16	312	6.37E-27	107.334	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006861001	specific	320109	51	389	5.79E-61	199.011	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006863001	specific	320109	1	299	1.31E-32	121.971	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006886001	non-specific	320109	3	299	6.23E-26	103.867	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006887001	non-specific	320109	4	302	3.71E-24	99.2444	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006887001	non-specific	313536	9	172	5.82E-06	46.8216	pfam10324	7TM_GPCR_Srw	C	cd21561	Class_A
GSLYST00006888001	non-specific	320109	1	198	9.41E-13	65.3468	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00006888001	superfamily	330410	16	80	0.00513012	37.1243	cd25589	COG4262 superfamily	NC	cd25589	Class_A
GSLYST00006888001	non-specific	235139	16	80	0.00513012	37.1243	PRK03612	PRK03612	NC	cd25589	Class_A
GSLYST00006911001	non-specific	320109	15	324	2.90E-20	88.844	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00006911001	non-specific	313536	94	331	0.0013422	39.888	pfam10324	7TM_GPCR_Srw	N	cd21561	Class_A
GSLYST00006981001	specific	320109	1	295	6.50E-77	237.531	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00007050001	non-specific	313536	48	337	5.69E-09	56.8368	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00007050001	specific	320109	43	333	5.40E-54	180.521	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00007051001	non-specific	320098	3	251	1.10E-41	143.087	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00007051001	non-specific	222976	4	215	1.70E-08	54.0138	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00007052001	non-specific	320098	1	243	2.78E-30	113.427	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00007053001	specific	320086	1	217	2.64E-23	93.8792	cd00637	7tm_classa_rhodopsin-like	-	cd28897	Class_A
GSLYST00007053001	non-specific	222976	31	213	0.00295149	37.8355	PHAO3087	PHAO3087	N	cd27963	Class_A
GSLYST00007054001	specific	320086	2	304	3.45E-25	101.583	cd00637	7tm_classa_rhodopsin-like	-	cd28897	Class_A
GSLYST00007054001	non-specific	222976	34	124	0.000282654	41.6874	PHAO3087	PHAO3087	NC	cd27963	Class_A
GSLYST00007063001	non-specific	320098	1	299	3.60E-28	108.804	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00007063001	non-specific	222976	29	88	0.0036763	38.2207	PHAO3087	PHAO3087	NC	cd27963	Class_A
GSLYST00007064001	non-specific	320183	3	312	2.31E-20	88.7652	cd15055	7tm_TAARs	-	cd28897	Class_A
GSLYST00007064001	non-specific	222976	29	87	0.00271972	38.6059	PHAO3087	PHAO3087	NC	cd27963	Class_A
GSLYST00007065001	non-specific	320098	9	307	4.76E-34	124.983	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00007065001	non-specific	222976	82	261	0.000394093	41.3022	PHAO3087	PHAO3087	NC	cd27963	Class_A
GSLYST00007066001	specific	320086	1	299	5.40E-26	104.28	cd00637	7tm_classa_rhodopsin-like	-	cd28897	Class_A
GSLYST00007067001	non-specific	320183	2	68	1.54E-13	62.5716	cd15055	7tm_TAARs	-	cd28897	Class_A
GSLYST00007067001	non-specific	222976	1	69	0.00739806	32.8279	PHAO3087	PHAO3087	NC	cd27963	Class_A
GSLYST00007068001	non-specific	320098	1	307	5.03E-35	127.294	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00007068001	non-specific	222976	29	155	7.05E-06	46.695	PHAO3087	PHAO3087	NC	cd27963	Class_A
GSLYST00007069001	non-specific	320098	1	307	6.03E-34	124.598	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00007069001	non-specific	222976	29	155	2.81E-06	47.8506	PHAO3087	PHAO3087	NC	cd27963	Class_A
GSLYST00007070001	specific	320086	3	288	2.98E-29	111.984	cd00637	7tm_classa_rhodopsin-like	-	cd28897	Class_A
GSLYST00007070001	non-specific	222976	3	260	0.0069742	37.4503	PHAO3087	PHAO3087	C	cd27963	Class_A
GSLYST00007071001	non-specific	320109	20	300	1.75E-26	105.408	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00007191001	specific	320086	42	258	3.45E-24	102.739	cd00637	7tm_classa_rhodopsin-like	-	cd28897	Class_A
GSLYST00007191001	non-specific	320086	620	715	9.65E-09	56.9</					

GSLYST0008092001	specific	197566	68	101	2.18E-09	53.0209	smart00192	LDLa	-	cI00104	Class_A
GSLYST0008092001	specific	238060	69	105	4.94E-09	52.209	c000112	LDLa	-	cI00104	Class_A
GSLYST0008092001	superfamily	294076	68	101	2.18E-09	53.0209	c00104	LDLa superfamily	-	-	Class_A
GSLYST0008092001	specific	316378	266	326	6.00E-13	63.7002	pfam13855	LRR_8	-	cI25992	Class_A
GSLYST0008092001	non-specific	222976	405	634	5.72E-05	45.9246	PHAO3087	PHAO3087	C	cI27963	Class_A
GSLYST0008092001	specific	272223	164	403	8.07E-14	73.8489	COG4886	LRR	N	cI25992	Class_A
GSLYST0008092001	superfamily	330813	164	403	8.07E-14	73.8489	cI25992	LRR_8 superfamily	N	-	Class_A
GSLYST0008092001	non-specific	238064	219	356	1.01E-08	57.3654	c000116	LRR_RI	N	cI26161	Class_A
GSLYST0008092001	superfamily	330982	219	356	1.01E-08	57.3654	cI26161	LRR_RI superfamily	N	-	Class_A
GSLYST0008092001	superfamily	330839	145	298	0.000814717	42.7618	cI26018	NEL superfamily	NC	-	Class_A
GSLYST0008092001	non-specific	185268	145	298	0.000814717	42.7618	PRK15370	PRK15370	NC	cI26018	Class_A
GSLYST0008183001	specific	320331	38	323	6.63E-137	394.664	cd15203	7tm_NPYR-like	-	cI28897	Class_A
GSLYST0008183001	non-specific	222976	41	327	6.12E-24	101.779	PHAO3087	PHAO3087	-	cI27963	Class_A
GSLYST0008197001	specific	320086	1	119	1.27E-12	63.0632	c000637	7tm_classA_rhodopsin-like	C	cI28897	Class_A
GSLYST0008271001	non-specific	320325	1	64	2.39E-23	99.4211	cd15197	7tm_NPSR	N	cI28897	Class_A
GSLYST0008328001	non-specific	320336	1	112	8.48E-20	83.5928	cd15208	7tm_OXR	N	cI28897	Class_A
GSLYST0008336001	non-specific	320140	150	216	7.72E-18	79.4103	cd15012	7tm_Trissin_R	N	cI28897	Class_A
GSLYST0008337001	non-specific	320140	1	56	2.65E-10	52.8315	cd15012	7tm_Trissin_R	NC	cI28897	Class_A
GSLYST0008338001	non-specific	320140	1	55	3.29E-17	71.7063	cd15012	7tm_Trissin_R	C	cI28897	Class_A
GSLYST0008478001	non-specific	320109	1	175	0.00011983	41.4644	cd14978	7tm_FMRFamide_R-like	N	cI28897	Class_A
GSLYST0008531001	non-specific	320098	17	177	1.31E-05	44.7671	cd14967	7tm_amine_R-like	N	cI28897	Class_A
GSLYST0008589001	specific	320086	33	327	1.27E-13	70.382	c000637	7tm_classA_rhodopsin-like	-	cI28897	Class_A
GSLYST0008625001	specific	313429	157	411	4.65E-62	205.17	pfam10192	GpcrRhopsn4	-	cI21735	Class_A
GSLYST0008625001	superfamily	328874	157	411	4.65E-62	205.17	cI21735	Lung_7-TM_R superfamily	-	-	Class_A
GSLYST0008626001	specific	313429	166	420	6.79E-57	192.073	pfam10192	GpcrRhopsn4	-	cI21735	Class_A
GSLYST0008626001	superfamily	328874	166	420	6.79E-57	192.073	cI21735	Lung_7-TM_R superfamily	-	-	Class_A
GSLYST0008698001	non-specific	320109	8	300	1.01E-19	86.918	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0008727001	non-specific	320109	38	336	1.21E-11	64.1912	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0008729001	non-specific	313536	20	311	2.46E-07	51.0588	pfam10324	7TM_GPCR_Srw	-	cI21561	Class_A
GSLYST0008729001	non-specific	320109	14	311	8.09E-24	98.474	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0008730001	non-specific	313536	22	316	5.00E-06	47.2068	pfam10324	7TM_GPCR_Srw	-	cI21561	Class_A
GSLYST0008730001	non-specific	320109	15	312	3.46E-21	91.1552	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0008731001	non-specific	320109	16	309	3.44E-25	101.941	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0008732001	non-specific	313536	23	316	1.23E-07	52.2144	pfam10324	7TM_GPCR_Srw	-	cI21561	Class_A
GSLYST0008732001	non-specific	320109	14	313	5.09E-25	101.941	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0008733001	non-specific	313536	22	316	5.89E-11	62.2296	pfam10324	7TM_GPCR_Srw	-	cI21561	Class_A
GSLYST0008733001	non-specific	320109	16	313	6.31E-30	115.038	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0008734001	non-specific	313536	29	322	1.21E-07	52.2144	pfam10324	7TM_GPCR_Srw	-	cI21561	Class_A
GSLYST0008734001	non-specific	320109	20	319	8.58E-26	103.867	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0008740001	non-specific	320109	2	275	3.58E-16	76.5176	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0008864001	non-specific	320109	1	338	2.45E-08	54.176	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0009134001	non-specific	320265	437	718	6.18E-100	308.745	cd15137	7tm_Relaxin_R	-	cI28897	Class_A
GSLYST0009134001	non-specific	278486	21	58	2.75E-06	44.1616	pfam00057	Ldl_recept_a	-	cI00104	Class_A
GSLYST0009134001	specific	238060	25	58	2.24E-07	47.2014	c000112	LDLa	-	cI00104	Class_A
GSLYST0009134001	specific	197566	22	55	2.40E-06	44.1613	smart00192	LDLa	-	cI00104	Class_A
GSLYST0009134001	specific	238060	149	183	1.56E-05	42.1938	c000112	LDLa	-	cI00104	Class_A
GSLYST0009134001	specific	197566	149	180	0.000259287	38.3833	smart00192	LDLa	-	cI00104	Class_A
GSLYST0009134001	superfamily	294076	25	58	2.24E-07	47.2014	cI00104	LDLa superfamily	-	-	Class_A
GSLYST0009134001	superfamily	294076	149	183	1.56E-05	42.1938	cI00104	LDLa superfamily	-	-	Class_A
GSLYST0009134001	specific	316378	274	331	1.01E-07	49.0627	pfam13855	LRR_8	-	cI25992	Class_A
GSLYST0009134001	superfamily	330813	274	331	1.01E-07	49.0627	cI25992	LRR_8 superfamily	-	-	Class_A
GSLYST0009134001	non-specific	222976	438	716	2.84E-06	49.7766	PHAO3087	PHAO3087	-	cI27963	Class_A
GSLYST0009134001	specific	272223	202	359	0.00017448	44.1886	COG4886	LRR	NC	cI25992	Class_A
GSLYST0009145001	non-specific	320109	43	356	2.01E-17	81.5252	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0009145001	non-specific	313536	117	363	0.00683602	37.962	pfam10324	7TM_GPCR_Srw	N	cI21561	Class_A
GSLYST0009165001	non-specific	320109	1	242	1.94E-15	73.8212	cd14978	7tm_FMRFamide_R-like	N	cI28897	Class_A
GSLYST0009166001	non-specific	320109	19	339	2.58E-24	100.4	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0009179001	non-specific	320109	1	125	3.75E-05	43.0052	cd14978	7tm_FMRFamide_R-like	C	cI28897	Class_A
GSLYST0009341001	specific	320086	21	133	1.49E-21	93.494	c000637	7tm_classA_rhodopsin-like	C	cI28897	Class_A
GSLYST0009341001	non-specific	165021	14	123	7.96E-05	44.619	PHAO2638	PHAO2638	NC	cI27963	Class_A
GSLYST0009352001	non-specific	320109	10	299	5.68E-18	82.2956	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0009353001	specific	320109	1	292	1.42E-30	116.193	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0009353001	non-specific	222976	210	296	0.00287075	38.6059	PHAO3087	PHAO3087	N	cI27963	Class_A
GSLYST0009354001	non-specific	320109	1	294	1.05E-23	98.0888	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0009367001	specific	320109	28	318	6.94E-40	142.772	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0009367001	non-specific	165021	22	327	5.20E-07	51.1674	PHAO2638	PHAO2638	N	cI27963	Class_A
GSLYST0009368001	specific	320109	1	296	8.79E-35	127.749	cd14978	7tm_FMRFamide_R-like	-	cI28897	Class_A
GSLYST0009368001	non-specific	165021	8	300	2.68E-07	51.1674	PHAO2638	PHAO2638	N	cI27963	Class_A
GSLYST0009369001	non-specific	320431	102	354	2.52E-05	45.2755	cd15305	7tm_5-HT2C	-	cI28897	Class_A
GSLYST0009426001	specific	320086	40	318	3.50E-13	69.6116	c000637	7tm_classA_rhodopsin-like	-	cI28897	Class_A
GSLYST0009501001	non-specific	320098	1	300	4.22E-26	103.412	cd14967	7tm_amine_R-like	-	cI28897	Class_A
GSLYST0009501001	non-specific	165021	23	103	0.00309449	38.4558	PHAO2638	PHAO2638	NC	cI27963	Class_A
GSLYST0009502001	non-specific	320183	2	309	1.45E-29	113.803	cd15055	7tm_TAARs	-	cI28897	Class_A
GSLYST0009502001	non-specific	222976	4	165	0.00148863	39.7615	PHAO3087	PHAO3087	NC	cI27963	Class_A
GSLYST0009503001	specific	320086	2	280	7.28E-29	110.828	c000637	7tm_classA_rhodopsin-like	-	cI28897	Class_A
GSLYST0009503001	non-specific	165021	72	239	0.00625823	37.6854	PHAO2638	PHAO2638	NC	cI27963	Class_A
GSLYST0009504001	specific	320086	1	295	9.64E-29	110.828	c000637	7tm_classA_rhodopsin-like	-	cI28897	Class_A
GSLYST0009505001	non-specific	320098	14	282	1.88E-37	132.687	cd14967	7tm_amine_R-like	-	cI28897	Class_A
GSLYST0009505001	non-specific	222976	15	248	0.00636877	37.4503	PHAO3087	PHAO3087	C	cI27963	Class_A
GSLYST0009506001	specific	320086	2	288	4.60E-37	132.784	c000637	7tm_classA_rhodopsin-like	-	cI28897	Class_A
GSLYST0009506001	non-specific	222976	1	248	2.03E-06	48.2358	PHAO3087	PHAO3087	C	cI27963	Class_A
GSLYST0009507001	non-specific	320098	1	133	8.83E-11	58.3433	cd14967	7tm_amine_R-like	C	cI28897	Class_A
GSLYST0009508001	superfamily	333717	1	249	2.23E-35	126.909	cI28897	7tm_GPCRs superfamily	-	-	Class_A
GSLYST0009508001	non-specific	320098	1	249	2.23E-35	126.909	cd14967	7tm_amine_R-like	-	cI28897	Class_A
GSLYST0009508001	non-specific	222976	29	154	5.08E-05	43.6134	PHAO3087	PHAO3087	NC	cI27963	Class_A
GSLYST0009533001	non-specific	320109	18	92	6.21E-06	42.62	cd14978	7tm_FMRFamide_R-like	C	cI28897	Class_A
GSLYST0009643001	non-specific	320099	7	285	2.25E-81	247.166	cd14968	7tm_Adenosine_R	-	cI28897	Class_A
GSLYST0009643001	non-specific	222976	3	294	3.61E-08	53.6286	PHAO3087	PHAO3087	-	cI27963	Class_A
GSLYST0009644001	non-specific	320099	7	285	3.51E-73	225.98	cd14968	7tm_Adenosine_R	-	cI28897	Class_A
GSLYST0009644001	non-specific	222976	3	292	8.03E-06	46.3098	PHAO3087	PHAO3087	-	cI27963	Class_A
GSLYST0009645001	non-specific	320099	17	295	5.06E-84	254.099	cd14968	7tm_Adenosine_R	-	cI28897	Class_A
GSLYST0009645001	non-specific	222976	13	302	1.36E-09	57.8658	PHAO3087	PHAO3087	-	cI27963	Class_A
GSLYST0009646001	non-specific	320099	6	287	4.17E-103	315.346	cd14968	7tm_Adenosine_R	-	cI28897	Class_A
GSLYST0009646001	non-specific	222976	2	292	1.92E-14	74.8146	PHAO3087	PHAO3087	-	cI27963	Class_A
GSLYST0009659001	specific	320086	38	317	9.70E-34	124.695	c000637	7tm_classA_rhodopsin-like	-	cI28897	Class_A
GSLYST0009659001	non-specific	222976	16	239	0.00145886	39.7615	PHAO3087	PHAO3087	C	cI27963	Class_A
GSLYST0009660001	specific	320086	39	307	1.92E-35	128.932	c000637	7tm_classA_rhodopsin-like	-	cI28897	Class_A
GSLYST0009661001	specific	320086	1	279	1.14E-30	116.606	c000637	7tm_classA_rhodopsin-like	-	cI28897	Class_A
GSLYST0009662001	specific	320086	11								

GSLYST00009693001	specific	238060	400	437	1.54E-05	42.579	cd00112	LDLa	-	cd00104	Class_A
GSLYST00009693001	specific	238060	442	477	1.78E-05	42.1938	cd00112	LDLa	-	cd00104	Class_A
GSLYST00009693001	specific	197566	69	101	2.05E-05	42.2353	smart00192	LDLa	-	cd00104	Class_A
GSLYST00009693001	specific	197566	442	474	3.80E-05	41.4649	smart00192	LDLa	-	cd00104	Class_A
GSLYST00009693001	specific	197566	359	391	9.76E-05	40.3093	smart00192	LDLa	-	cd00104	Class_A
GSLYST00009693001	specific	238060	189	221	0.000276331	39.1122	cd00112	LDLa	-	cd00104	Class_A
GSLYST00009693001	specific	197566	400	432	0.000465398	38.3833	smart00192	LDLa	-	cd00104	Class_A
GSLYST00009693001	specific	197566	190	218	0.000815086	37.6129	smart00192	LDLa	-	cd00104	Class_A
GSLYST00009693001	superfamily	294076	320	355	3.39E-10	55.7176	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00009693001	superfamily	294076	30	64	8.12E-07	46.0458	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00009693001	superfamily	294076	69	104	1.48E-06	45.2754	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00009693001	superfamily	294076	360	394	3.50E-06	44.505	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00009693001	superfamily	294076	108	140	5.14E-06	43.7761	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00009693001	superfamily	294076	400	437	1.54E-05	42.579	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00009693001	superfamily	294076	442	477	1.78E-05	42.1938	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00009693001	superfamily	294076	189	221	0.000276331	39.1122	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00009693001	specific	316378	610	669	1.65E-14	68.7078	pfam13855	LRR_8	-	cd25992	Class_A
GSLYST00009693001	non-specific	222976	732	1005	0.00132777	42.0726	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00009693001	non-specific	238064	506	701	2.32E-05	47.3502	cd00116	LRR_RI	C	cd26161	Class_A
GSLYST00009693001	superfamily	330982	506	701	2.32E-05	47.3502	cd26161	LRR_RI superfamily	C	-	Class_A
GSLYST00009693001	non-specific	278486	76	104	0.00574538	35.302	pfam00057	Ldl_recept_a	N	cd00104	Class_A
GSLYST00009693001	specific	227223	538	672	3.58E-16	81.5529	COG4886	LRR	NC	cd25992	Class_A
GSLYST00009693001	superfamily	330813	538	672	3.58E-16	81.5529	cd25992	LRR_8 superfamily	NC	-	Class_A
GSLYST00009693001	non-specific	215061	536	718	7.39E-06	49.8464	PLN00113	PLN00113	NC	cd26793	Class_A
GSLYST00009693001	superfamily	331614	536	718	7.39E-06	49.8464	cd26793	PLN00113 superfamily	NC	-	Class_A
GSLYST00009799001	specific	320124	3	289	7.48E-84	254.061	cd14993	7tm_A_CCKR-like	-	cd28897	Class_A
GSLYST00009799001	non-specific	222976	7	285	1.17E-06	49.0062	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00009928001	non-specific	320109	17	314	1.87E-15	75.362	cd14978	7tm_A_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00009932001	non-specific	320128	32	330	3.63E-97	289.575	cd14997	7tm_ETH-R	-	cd28897	Class_A
GSLYST00009932001	non-specific	222976	1	334	6.86E-15	74.4294	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00009949001	specific	320109	25	307	1.80E-54	179.366	cd14978	7tm_A_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00009949001	non-specific	165021	25	262	1.48E-10	61.1826	PHA02638	PHA02638	N	cd27963	Class_A
GSLYST00009951001	non-specific	320124	17	137	1.32E-08	51.446	cd14993	7tm_A_CCKR-like	C	cd28897	Class_A
GSLYST00009969001	non-specific	320109	1	137	1.78E-07	49.9388	cd14978	7tm_A_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00009970001	non-specific	320109	3	143	1.89E-06	47.2424	cd14978	7tm_A_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00010013001	non-specific	320109	7	310	7.75E-27	106.948	cd14978	7tm_A_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00010013001	non-specific	222976	7	150	0.00193709	39.3763	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00010015001	superfamily	333717	407	688	8.96E-91	284.093	cd28897	7tm_GPCRs superfamily	-	-	Class_A
GSLYST00010015001	non-specific	320265	407	688	8.96E-91	284.093	cd15137	7tm_Relaxin_R	-	cd28897	Class_A
GSLYST00010015001	non-specific	278486	21	56	1.08E-05	42.6208	pfam00057	Ldl_recept_a	-	cd00104	Class_A
GSLYST00010015001	specific	238060	23	56	2.82E-08	49.8978	cd00112	LDLa	-	cd00104	Class_A
GSLYST00010015001	specific	197566	23	53	4.76E-08	49.1689	smart00192	LDLa	-	cd00104	Class_A
GSLYST00010015001	specific	197566	107	138	0.000204033	38.7685	smart00192	LDLa	-	cd00104	Class_A
GSLYST00010015001	specific	238060	107	138	0.00037858	37.9566	cd00112	LDLa	-	cd00104	Class_A
GSLYST00010015001	superfamily	294076	23	56	2.82E-08	49.8978	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00010015001	superfamily	294076	107	138	0.000204033	38.7685	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00010015001	specific	316378	237	303	9.66E-05	40.5883	pfam13855	LRR_8	-	cd25992	Class_A
GSLYST00010015001	superfamily	330813	237	303	9.66E-05	40.5883	cd25992	LRR_8 superfamily	-	-	Class_A
GSLYST00010015001	specific	316378	293	335	1.27E-06	45.5959	pfam13855	LRR_8	C	cd25992	Class_A
GSLYST00010015001	superfamily	330813	293	335	1.27E-06	45.5959	cd25992	LRR_8 superfamily	C	-	Class_A
GSLYST00010015001	non-specific	215061	176	328	0.000287054	44.0685	PLN00113	PLN00113	C	cd26793	Class_A
GSLYST00010015001	superfamily	331614	176	328	0.000287054	44.0685	cd26793	PLN00113 superfamily	C	-	Class_A
GSLYST00010015001	specific	227223	205	334	4.77E-06	49.1962	COG4886	LRR	NC	cd25992	Class_A
GSLYST00010016001	non-specific	278431	421	684	2.41E-15	76.192	pfam00001	7tm_1	-	cd27963	Class_A
GSLYST00010016001	superfamily	332784	421	684	2.41E-15	76.192	cd27963	7tm_1 superfamily	-	-	Class_A
GSLYST00010016001	superfamily	333717	406	685	2.87E-95	296.034	cd28897	7tm_GPCRs superfamily	-	-	Class_A
GSLYST00010016001	non-specific	320265	406	685	2.87E-95	296.034	cd15137	7tm_A_Relaxin_R	-	cd28897	Class_A
GSLYST00010016001	non-specific	278486	7	36	6.93E-06	43.006	pfam00057	Ldl_recept_a	-	cd00104	Class_A
GSLYST00010016001	specific	238060	7	36	1.11E-08	51.0534	cd00112	LDLa	-	cd00104	Class_A
GSLYST00010016001	specific	197566	7	33	9.40E-08	48.3985	smart00192	LDLa	-	cd00104	Class_A
GSLYST00010016001	specific	197566	77	108	0.00213089	36.0721	smart00192	LDLa	-	cd00104	Class_A
GSLYST00010016001	specific	238060	77	108	0.00256835	35.6454	cd00112	LDLa	-	cd00104	Class_A
GSLYST00010016001	superfamily	294076	7	36	1.11E-08	51.0534	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00010016001	superfamily	294076	77	108	0.00213089	36.0721	cd00104	LDLa superfamily	-	-	Class_A
GSLYST00010016001	specific	316378	236	301	6.66E-06	43.6699	pfam13855	LRR_8	-	cd25992	Class_A
GSLYST00010016001	superfamily	330813	236	301	6.66E-06	43.6699	cd25992	LRR_8 superfamily	-	-	Class_A
GSLYST00010016001	specific	197566	38	62	0.000743772	37.2277	smart00192	LDLa	C	cd00104	Class_A
GSLYST00010016001	specific	238060	43	62	0.00242103	35.6454	cd00112	LDLa	C	cd00104	Class_A
GSLYST00010016001	superfamily	294076	38	62	0.000743772	37.2277	cd00104	LDLa superfamily	C	-	Class_A
GSLYST00010016001	specific	238060	131	153	0.000628797	37.5714	cd00112	LDLa	N	cd00104	Class_A
GSLYST00010016001	specific	197566	131	150	0.00797114	34.1461	smart00192	LDLa	N	cd00104	Class_A
GSLYST00010016001	superfamily	294076	131	153	0.000628797	37.5714	cd00104	LDLa superfamily	N	-	Class_A
GSLYST00010016001	non-specific	238064	217	345	0.00221754	40.4166	cd00116	LRR_RI	N	cd26161	Class_A
GSLYST00010016001	superfamily	330982	217	345	0.00221754	40.4166	cd26161	LRR_RI superfamily	N	-	Class_A
GSLYST00010016001	specific	227223	179	344	0.000933359	41.8774	COG4886	LRR	NC	cd25992	Class_A
GSLYST00010016001	non-specific	165021	407	537	0.000248567	43.8486	PHA02638	PHA02638	NC	cd27963	Class_A
GSLYST00010191001	non-specific	320109	1	288	9.97E-24	97.7036	cd14978	7tm_A_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00010191001	non-specific	222976	2	298	0.000244857	41.6874	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00010192001	non-specific	320109	1	293	2.07E-27	107.719	cd14978	7tm_A_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00010192001	non-specific	222976	6	290	0.000174664	42.4578	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00010193001	non-specific	313540	9	204	8.36E-07	47.9541	pfam10328	7TM_GPCR_Srx	C	cd21561	Class_A
GSLYST00010193001	non-specific	320109	6	204	1.06E-19	84.6068	cd14978	7tm_A_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00010193001	non-specific	222976	9	204	0.00363736	37.4503	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00010333001	non-specific	320109	34	247	2.01E-12	65.3468	cd14978	7tm_A_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00010366001	specific	320086	10	267	8.75E-34	123.925	cd00637	7tm_classA_rhodopsin-like	-	cd28897	Class_A
GSLYST00010366001	non-specific	222976	17	227	4.50E-05	43.9986	PHA03087	PHA03087	NC	cd27963	Class_A
GSLYST00010367001	specific	320086	1	242	1.93E-36	129.318	cd00637	7tm_classA_rhodopsin-like	-	cd28897	Class_A
GSLYST00010367001	non-specific	222976	1	204	2.55E-11	62.103	PHA03087	PHA03087	NC	cd27963	Class_A
GSLYST00010503001	specific	320086	36	308	1.06E-61	200.965	cd00637	7tm_classA_rhodopsin-like	-	cd28897	Class_A
GSLYST00010503001	non-specific	222976	43	314	4.55E-17	81.7482	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00010503001	non-specific	223664	31	277	0.00122823	40.7478	COG0591	PutP	N	cd00456	Class_A
GSLYST00010503001	superfamily	320982	31	277	0.00122823	40.7478	cd00456	SLC5-6-like_sbd superfamily	N	-	Class_A
GSLYST00010575001	specific	320086	51	327	1.32E-50	170.919	cd00637	7tm_classA_rhodopsin-like	-	cd28897	Class_A
GSLYST00010575001	non-specific	165021	53	339	9.19E-08	53.4786	PHA02638	PHA02638	N	cd27963	Class_A
GSLYST00010803001	non-specific	320109	56	355	7.96E-29	113.112	cd14978	7tm_A_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00010803001	non-specific	165021	60	268	0.00717602	38.0706	PHA02638	PHA02638	NC	cd27963	Class_A
GSLYST00010804001	non-specific	313536	8	308	5.81E-10	59.148	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00010804001	non-specific	320109	4	303	4.61E-25	101.941	cd14978	7tm_A_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00010805001	non-specific	313536	8	311	9.23E-08	52.5996	pfam1032				

GSLYST00010924001	non-specific	320109	27	356	5.31E-11	62.6504	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011001001	non-specific	320109	66	350	1.90E-14	73.0508	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011001001	non-specific	313540	100	229	7.89E-05	43.7169	pfam10328	7TM_GPCR_Srx	C	cl21561	Class_A
GSLYST00011039001	non-specific	320109	4	125	4.21E-11	58.028	cd14978	7tm_FMRFamide_R-like	C	cl28897	Class_A
GSLYST00011049001	specific	320086	50	238	7.38E-28	111.213	cd00637	7tm_classA_rhodopsin-like	C	cl28897	Class_A
GSLYST00011049001	non-specific	322976	52	168	3.33E-07	51.7026	PHAO3087	PHAO3087	C	cl27963	Class_A
GSLYST00011049001	non-specific	320453	372	437	1.25E-05	46.5104	cd15330	7tm_5-HT1A Vertebrates	N	cl28897	Class_A
GSLYST00011074001	specific	320109	17	365	2.39E-32	122.742	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011123001	non-specific	320109	32	323	9.94E-17	78.8288	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011124001	non-specific	320109	30	327	3.24E-19	86.1476	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011218001	non-specific	320109	56	348	1.29E-22	96.548	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011227001	specific	320086	22	291	1.57E-14	71.9228	cd00637	7tm_classA_rhodopsin-like	-	cl28897	Class_A
GSLYST00011256001	non-specific	313536	40	335	1.00E-10	61.8444	pfam10324	7TM_GPCR_Srx	-	cl21561	Class_A
GSLYST00011256001	non-specific	320109	34	330	2.05E-26	106.178	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011405001	non-specific	320109	22	251	1.32E-30	115.038	cd14978	7tm_FMRFamide_R-like	N	cl28897	Class_A
GSLYST00011498001	specific	320086	17	275	3.28E-19	86.1752	cd00637	7tm_classA_rhodopsin-like	-	cl28897	Class_A
GSLYST00011508001	specific	320454	120	515	5.45E-137	396.725	cd15331	7tm_5-HT1A_invertebrates	-	cl28897	Class_A
GSLYST00011508001	non-specific	322976	134	255	1.03E-05	47.4654	PHAO3087	PHAO3087	C	cl27963	Class_A
GSLYST00011518001	specific	320086	49	389	4.86E-34	127.777	cd00637	7tm_classA_rhodopsin-like	-	cl28897	Class_A
GSLYST00011518001	non-specific	165021	51	176	4.91E-05	45.0042	PHAO2638	PHAO2638	NC	cl27963	Class_A
GSLYST00011575001	non-specific	320109	50	349	2.22E-08	54.5612	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011644001	non-specific	320109	4	24	0.00141177	34.1457	cd14978	7tm_FMRFamide_R-like	N	cl28897	Class_A
GSLYST00011645001	specific	320109	2	300	1.67E-47	160.876	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011666001	non-specific	320309	41	87	0.00905915	33.1832	cd15181	7tm_CXCR5	C	cl28897	Class_A
GSLYST00011682001	non-specific	320109	62	351	6.69E-22	94.2368	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011733001	non-specific	320429	93	282	2.32E-98	299.736	cd15302	7tm_mACHR_GAR-2-like	C	cl28897	Class_A
GSLYST00011733001	non-specific	121564	308	451	0.00833664	38.9847	cd11674	lambda-1	C	cl17035	Class_A
GSLYST00011733001	non-specific	222976	107	295	7.65E-09	57.4806	PHAO3087	PHAO3087	C	cl27963	Class_A
GSLYST00011733001	non-specific	320429	493	567	1.06E-35	134.485	cd15302	7tm_mACHR_GAR-2-like	N	cl28897	Class_A
GSLYST00011733001	non-specific	222976	491	571	0.000108476	44.3838	PHAO3087	PHAO3087	N	cl27963	Class_A
GSLYST00011749001	specific	320086	24	296	1.11E-31	118.917	cd00637	7tm_classA_rhodopsin-like	-	cl28897	Class_A
GSLYST00011750001	specific	320086	22	296	4.03E-30	114.68	cd00637	7tm_classA_rhodopsin-like	-	cl28897	Class_A
GSLYST00011751001	superfamily	333717	17	289	5.30E-30	113.427	cl28897	7tm_GPCRs superfamily	-	-	Class_A
GSLYST00011751001	non-specific	320098	17	289	5.30E-30	113.427	cd14967	7tm_amine_R-like	-	cl28897	Class_A
GSLYST00011825001	specific	320112	52	349	9.28E-88	268.345	cd14981	7tm_Prostanoid_R	-	cl28897	Class_A
GSLYST00011881001	specific	320086	49	367	2.75E-21	93.494	cd00637	7tm_classA_rhodopsin-like	-	cl28897	Class_A
GSLYST00011887001	specific	320177	100	437	8.68E-117	341.988	cd15049	7tm_mACHR	-	cl28897	Class_A
GSLYST00011887001	non-specific	222976	102	295	1.85E-13	70.9626	PHAO3087	PHAO3087	C	cl27963	Class_A
GSLYST00011888001	non-specific	320177	2	41	4.76E-20	79.6668	cd15049	7tm_mACHR	N	cl28897	Class_A
GSLYST00011952001	non-specific	320181	2	336	2.86E-87	263.052	cd15053	7tm_D2-like_dopamine_R	N	cl28897	Class_A
GSLYST00011952001	non-specific	222976	21	130	3.84E-09	57.0954	PHAO3087	PHAO3087	NC	cl27963	Class_A
GSLYST00011979001	non-specific	313536	53	374	0.000337017	41.814	pfam10324	7TM_GPCR_Srx	-	cl21561	Class_A
GSLYST00011979001	non-specific	320109	55	367	3.32E-18	83.8364	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011993001	specific	320109	1	412	3.01E-45	158.565	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00011993001	non-specific	313536	2	210	6.24E-15	74.9412	pfam10324	7TM_GPCR_Srx	C	cl21561	Class_A
GSLYST00011993001	non-specific	222976	7	148	1.90E-08	55.5546	PHAO3087	PHAO3087	C	cl27963	Class_A
GSLYST00012013001	non-specific	320109	4	292	5.89E-27	106.563	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012029001	specific	320112	42	336	3.18E-95	288.76	cd14981	7tm_Prostanoid_R	-	cl28897	Class_A
GSLYST00012029001	non-specific	222976	44	180	5.33E-05	44.769	PHAO3087	PHAO3087	C	cl27963	Class_A
GSLYST00012068001	non-specific	320109	3	120	2.33E-07	47.2424	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012097001	non-specific	320511	1	288	2.24E-131	373.982	cd15389	7tm_GPR83	-	cl28897	Class_A
GSLYST00012097001	non-specific	222976	1	289	2.22E-22	94.4598	PHAO3087	PHAO3087	-	cl27963	Class_A
GSLYST00012110001	non-specific	320222	31	310	1.10E-131	377.201	cd15094	7tm_AstC_insect	-	cl28897	Class_A
GSLYST00012110001	non-specific	165021	29	315	4.73E-34	129.748	PHAO2638	PHAO2638	N	cl27963	Class_A
GSLYST00012114001	non-specific	320109	62	329	2.15E-17	81.14	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012115001	non-specific	320109	9	306	1.58E-20	89.6144	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012117001	non-specific	320109	19	313	1.67E-24	100.4	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012119001	non-specific	320109	17	313	4.98E-22	93.4664	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012120001	non-specific	320109	1	287	8.10E-20	87.3032	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012121001	non-specific	320123	51	166	6.32E-06	44.731	cd14992	7tm_TACR_family	N	cl28897	Class_A
GSLYST00012122001	non-specific	320109	16	311	2.18E-22	94.622	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012123001	non-specific	320109	23	313	2.10E-18	83.4512	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012123001	superfamily	331954	15	92	0.00351615	38.6661	cl27133	Gcpe superfamily	NC	-	Class_A
GSLYST00012123001	non-specific	234812	15	92	0.00351615	38.6661	PRK00694	PRK00694	NC	cl27133	Class_A
GSLYST00012124001	non-specific	320109	17	311	7.20E-25	101.556	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012125001	non-specific	320109	18	313	2.56E-21	91.9256	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012126001	non-specific	320109	18	313	1.66E-20	89.6144	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012127001	non-specific	320109	15	305	1.15E-17	81.14	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012128001	non-specific	313536	18	317	1.80E-06	48.3624	pfam10324	7TM_GPCR_Srx	-	cl21561	Class_A
GSLYST00012128001	non-specific	320109	16	311	1.76E-20	89.2292	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012129001	non-specific	320109	15	309	2.75E-21	91.5404	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012130001	non-specific	320109	30	316	2.22E-24	100.015	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012131001	non-specific	320109	1	184	4.64E-09	54.176	cd14978	7tm_FMRFamide_R-like	C	cl28897	Class_A
GSLYST00012132001	non-specific	320109	23	314	6.09E-24	98.8592	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012133001	non-specific	320109	17	72	3.71E-05	44.546	cd14978	7tm_FMRFamide_R-like	C	cl28897	Class_A
GSLYST00012134001	non-specific	320109	23	317	8.00E-22	93.4664	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012135001	non-specific	320109	16	311	2.37E-23	97.3184	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012136001	non-specific	313536	22	317	1.44E-09	57.9924	pfam10324	7TM_GPCR_Srx	-	cl21561	Class_A
GSLYST00012136001	non-specific	320109	16	310	5.20E-21	90.77	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012137001	non-specific	320109	25	316	1.91E-29	114.267	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012138001	non-specific	320109	18	313	9.80E-26	103.867	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012139001	non-specific	320109	10	307	7.14E-06	46.8572	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012140001	non-specific	320109	31	330	3.01E-24	100.015	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012180001	non-specific	320109	18	313	6.37E-22	93.4664	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012217001	non-specific	320109	42	338	1.31E-23	98.474	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012218001	non-specific	320109	45	341	2.97E-25	103.096	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012228001	specific	320109	1	302	1.17E-31	119.275	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012228001	non-specific	165021	4	265	0.00865977	37.3002	PHAO2638	PHAO2638	N	cl27963	Class_A
GSLYST00012248001	non-specific	320109	26	323	1.77E-26	105.793	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012248001	non-specific	313536	213	327	7.20E-07	49.9032	pfam10324	7TM_GPCR_Srx	N	cl21561	Class_A
GSLYST00012301001	non-specific	313536	129	416	9.01E-09	56.4516	pfam10324	7TM_GPCR_Srx	-	cl21561	Class_A
GSLYST00012301001	specific	320109	122	410	9.61E-51	173.973	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012509001	non-specific	320109	5	278	1.76E-23	96.548	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012510001	non-specific	320109	15	283	6.61E-13	67.2728	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012511001	non-specific	320109	2	301	1.88E-21	91.5404	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012512001	non-specific	320109	11	290	8.21E-10	58.4132	cd14978	7tm_FMRFamide_R-like	-	cl28897	Class_A
GSLYST00012512001	non-specific	313536	254								

GSLYST00012818001	non-specific	320086	1	92	8.52E-13	61.1372	cd00637	7tm_classA_rhodopsin-like	C	cd28897	Class_A
GSLYST00012822001	superfamily	330316	510	600	0.00202923	41.4278	cd25495	Endomucin superfamily	C	-	Class_A
GSLYST00012822001	non-specific	165513	510	600	0.00202923	41.4278	PHA03255	PHA03255	C	cd25495	Class_A
GSLYST00012822001	non-specific	226685	969	1077	0.00040736	44.6696	CG04232	DsbD	NC	cd26469	Class_A
GSLYST00012842001	specific	320086	1	110	2.21E-18	83.864	cd00637	7tm_classA_rhodopsin-like	C	cd28897	Class_A
GSLYST00012853001	non-specific	320109	24	227	2.67E-08	52.6352	cd14978	7tmA_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00012854001	non-specific	320109	1	293	1.13E-16	78.4436	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00012855001	non-specific	320109	23	157	3.62E-10	58.028	cd14978	7tmA_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00012855001	non-specific	313540	20	154	0.00305508	37.5537	pfam10328	7TM_GPCR_Srx	C	cd21561	Class_A
GSLYST00012855001	non-specific	320216	100	219	0.000396179	40.1282	cd15088	7tmA_MCHR-like	NC	cd28897	Class_A
GSLYST00012980001	specific	320191	51	271	3.14E-101	308.656	cd15063	7tmA_Octopamine_R	C	cd28897	Class_A
GSLYST00012980001	non-specific	222976	53	165	2.33E-12	68.2662	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00012980001	non-specific	320191	512	583	1.72E-40	148.413	cd15063	7tmA_Octopamine_R	N	cd28897	Class_A
GSLYST00012980001	non-specific	222976	508	587	7.29E-06	48.2358	PHA03087	PHA03087	N	cd27963	Class_A
GSLYST00012995001	non-specific	320262	2	249	4.79E-96	283.838	cd15134	7tmA_copaR	-	cd28897	Class_A
GSLYST00012995001	non-specific	222976	15	258	4.85E-07	49.7766	PHA03087	PHA03087	N	cd27963	Class_A
GSLYST00012998001	non-specific	320109	13	310	5.40E-16	76.5176	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013082001	non-specific	320109	1	336	1.34E-08	54.9464	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013147001	non-specific	320101	390	458	1.21E-05	46.5189	cd14970	7tmA_Opioid_R-like	N	cd28897	Class_A
GSLYST00013147001	specific	320086	3	124	8.67E-15	74.2384	cd00637	7tm_classA_rhodopsin-like	NC	cd28897	Class_A
GSLYST00013148001	non-specific	320109	40	365	2.08E-18	84.2216	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013149001	non-specific	320109	2	338	3.24E-08	53.7908	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013150001	non-specific	320109	2	336	1.26E-09	58.028	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013151001	non-specific	320109	1	320	5.54E-08	53.0204	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013152001	non-specific	320109	13	373	1.34E-10	61.4948	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013153001	non-specific	320109	1	328	9.84E-08	52.25	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013154001	non-specific	320086	5	209	1.08E-05	46.1144	cd00637	7tm_classA_rhodopsin-like	C	cd28897	Class_A
GSLYST00013155001	non-specific	320086	5	209	3.17E-05	44.5736	cd00637	7tm_classA_rhodopsin-like	C	cd28897	Class_A
GSLYST00013156001	non-specific	320086	5	209	7.84E-05	43.418	cd00637	7tm_classA_rhodopsin-like	C	cd28897	Class_A
GSLYST00013157001	non-specific	320109	1	196	0.00732235	37.6125	cd14978	7tmA_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00013158001	non-specific	320109	1	194	0.00712905	37.6125	cd14978	7tmA_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00013159001	non-specific	320109	1	196	0.0047944	37.9977	cd14978	7tmA_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00013160001	non-specific	320109	244	338	0.000595037	41.0793	cd14978	7tmA_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00013161001	non-specific	320086	38	223	1.51E-07	51.8924	cd00637	7tm_classA_rhodopsin-like	C	cd28897	Class_A
GSLYST00013162001	non-specific	320109	1	347	2.31E-06	48.398	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013163001	non-specific	320109	1	343	2.64E-06	48.0128	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013164001	non-specific	320109	1	343	5.77E-05	44.1608	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013167001	non-specific	320109	1	341	1.71E-06	48.7832	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013168001	non-specific	320109	1	341	1.15E-07	52.25	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013169001	non-specific	320109	1	343	3.43E-08	53.7908	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013170001	non-specific	320109	1	146	2.16E-06	48.398	cd14978	7tmA_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00013171001	non-specific	320109	1	345	6.11E-09	56.102	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013172001	non-specific	320109	1	146	3.27E-06	48.0128	cd14978	7tmA_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00013173001	non-specific	320109	1	340	1.31E-06	49.1684	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013174001	non-specific	320109	1	344	1.86E-06	48.7832	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013229001	non-specific	320109	2	309	1.31E-15	75.362	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013244001	non-specific	320109	55	365	7.18E-12	65.3468	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013245001	non-specific	320109	4	237	0.000346781	40.6941	cd14978	7tmA_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00013260001	non-specific	320109	148	459	4.59E-22	95.7776	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013260001	non-specific	313536	148	463	0.00600514	38.3472	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00013329001	non-specific	320109	2	288	3.92E-27	106.948	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013329001	non-specific	313540	2	237	0.000675631	40.2501	pfam10328	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00013330001	non-specific	320109	1	295	6.17E-17	79.214	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013331001	non-specific	320109	1	294	5.86E-17	78.8288	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013332001	non-specific	320109	1	291	1.45E-17	80.7548	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013366001	non-specific	320109	18	130	2.65E-05	42.2348	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013367001	non-specific	320180	280	472	2.11E-102	318.488	cd15052	7tmA_5-HT2	NC	cd28897	Class_A
GSLYST00013367001	non-specific	222976	277	466	2.61E-13	71.733	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00013367001	non-specific	320180	756	828	1.01E-36	138.985	cd15052	7tmA_5-HT2	N	cd28897	Class_A
GSLYST00013423001	non-specific	320109	2	305	2.20E-27	108.104	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013424001	non-specific	320109	2	299	1.79E-22	94.622	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013424001	non-specific	313536	12	290	4.58E-08	53.37	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00013424001	non-specific	222976	12	137	0.000860263	40.1467	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00013425001	non-specific	320109	7	298	2.64E-22	93.8516	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013425001	non-specific	313536	4	293	1.07E-11	64.1556	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00013426001	non-specific	320109	46	341	7.63E-20	88.0736	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013426001	non-specific	313536	54	211	3.77E-07	50.6736	pfam10324	7TM_GPCR_Srw	C	cd21561	Class_A
GSLYST00013427001	non-specific	320109	2	302	1.61E-28	111.186	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013427001	non-specific	313536	12	308	9.64E-11	61.4592	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00013430001	non-specific	320109	35	327	4.95E-23	96.9332	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013532001	specific	320109	82	393	2.09E-65	211.337	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013532001	non-specific	313536	86	397	2.35E-17	82.26	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00013565001	non-specific	320325	37	343	2.38E-121	352.497	cd15197	7tmA_NPSR	-	cd28897	Class_A
GSLYST00013565001	non-specific	222976	18	333	2.30E-16	79.0518	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00013609001	non-specific	320109	109	385	2.11E-16	78.8288	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013628001	non-specific	320109	17	339	5.77E-12	65.3468	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013629001	non-specific	320109	15	348	3.83E-11	63.0356	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013635001	non-specific	320109	1	330	1.05E-12	67.2728	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00013731001	non-specific	320109	4	64	2.11E-05	39.5385	cd14978	7tmA_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00013732001	non-specific	320109	116	214	9.60E-14	68.0432	cd14978	7tmA_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00013737001	non-specific	320126	27	335	3.86E-118	345.139	cd14995	7tmA_TRH-R	-	cd28897	Class_A
GSLYST00013737001	non-specific	222976	29	340	1.17E-20	92.1486	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00013809001	non-specific	320336	83	403	3.53E-135	390.597	cd15208	7tmA_OXR	-	cd28897	Class_A
GSLYST00013809001	non-specific	222976	59	405	4.33E-14	72.8886	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00013839001	specific	320109	42	340	1.23E-35	131.601	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014035001	non-specific	320109	23	316	1.43E-19	86.918	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014045001	non-specific	320109	1	126	1.44E-05	44.1608	cd14978	7tmA_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00014051001	non-specific	320109	3	305	4.95E-28	109.645	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014054001	specific	320086	1	291	5.37E-34	124.31	cd00637	7tm_classA_rhodopsin-like	-	cd28897	Class_A
GSLYST00014054001	non-specific	222976	2	134	0.0037989	38.2207	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00014055001	non-specific	320098	6	301	4.42E-39	137.694	cd14967	7tmA_amine_R-like	-	cd28897	Class_A
GSLYST00014055001	non-specific	222976	15	295	3.71E-07	50.547	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00014126001	non-specific	320109	34	327	3.55E-26	105.793	cd14978	7tmA_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014137001	specific	320086	65	343	4.94E-19	85.79	cd00637	7tm_classA_rhodopsin-like	-	cd28897	Class_A
GSLYST00014155001	non-specific	320211	2	169	1.44E-50	163.658	cd15083	7tmA_Melanopsin-like	N	cd28897	Class_A
GSLYST00014207001	specific	320086	34	180	2.12E-27	111.598	cd00637	7tm_classA_rhodopsin-like	C	cd2	

GSLYST00014777001	non-specific	320109	9	300	7.63E-16	76.1324	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014796001	non-specific	320109	52	351	2.51E-29	114.652	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014823001	non-specific	320109	9	284	1.40E-16	78.0584	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014912001	non-specific	320109	12	305	7.03E-29	111.956	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014912001	non-specific	222976	17	296	0.000682412	40.5319	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00014916001	specific	320109	70	358	2.87E-31	119.66	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014916001	non-specific	313536	144	362	2.77E-07	51.444	pfam10324	7TM_GPCR_Srw	N	cd21561	Class_A
GSLYST00014920001	non-specific	320109	5	301	4.56E-20	88.0736	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014920001	non-specific	313536	86	308	8.21E-07	49.518	pfam10324	7TM_GPCR_Srw	N	cd21561	Class_A
GSLYST00014922001	specific	320109	21	338	6.52E-69	218.656	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014922001	non-specific	313536	24	345	2.08E-32	123.476	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00014922001	non-specific	222976	33	163	0.00784854	37.8355	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00014960001	non-specific	320086	16	264	7.70E-08	52.2776	cd00637	7tm_class_rhodopsin-like	-	cd28897	Class_A
GSLYST00014961001	specific	320086	2	253	2.11E-15	73.8488	cd00637	7tm_class_rhodopsin-like	-	cd28897	Class_A
GSLYST00014962001	specific	320086	99	321	2.56E-16	77.7008	cd00637	7tm_class_rhodopsin-like	N	cd28897	Class_A
GSLYST00014963001	non-specific	320109	22	308	9.11E-29	111.956	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00014963001	non-specific	222976	2	318	5.66E-05	43.9986	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00014964001	non-specific	320109	15	310	7.93E-20	87.3032	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015021001	non-specific	320109	1	289	2.21E-19	85.7624	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015021001	non-specific	313536	1	289	0.000894857	39.888	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00015022001	non-specific	320109	1	289	3.71E-16	76.5176	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015049001	non-specific	320109	35	340	1.04E-21	93.0812	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015068001	non-specific	320109	14	359	2.34E-06	48.398	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015069001	non-specific	320109	28	369	2.43E-08	54.5612	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015124001	non-specific	320109	10	327	2.61E-12	66.1172	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015125001	non-specific	320109	2	297	8.38E-16	75.7472	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015126001	non-specific	320086	5	97	0.00203951	38.4104	cd00637	7tm_class_rhodopsin-like	C	cd28897	Class_A
GSLYST00015127001	non-specific	320109	1	208	4.27E-07	48.7832	cd14978	7tm_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00015128001	non-specific	320109	1	310	3.04E-15	74.5916	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015129001	non-specific	320109	45	316	2.59E-06	48.0128	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015131001	non-specific	320109	1	320	3.11E-15	74.5916	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015132001	non-specific	320109	1	320	6.26E-15	73.8212	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015133001	non-specific	320109	1	315	3.55E-14	71.51	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015168001	non-specific	320109	1	211	2.45E-12	64.1912	cd14978	7tm_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00015190001	specific	320514	98	381	3.91E-158	449.118	cd15392	7tm_PR4-like	-	cd28897	Class_A
GSLYST00015190001	non-specific	222976	97	383	5.42E-22	96.3858	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00015213001	non-specific	320109	5	92	2.66E-06	43.3904	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00015319001	non-specific	320109	5	284	3.85E-21	90.3848	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015320001	non-specific	320109	2	301	1.03E-20	89.6144	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015331001	non-specific	320098	7	305	8.18E-38	134.613	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00015331001	non-specific	222976	8	218	7.22E-05	43.6134	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00015332001	non-specific	320098	1	254	5.60E-31	115.738	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00015332001	non-specific	222976	40	251	0.000625136	40.5319	PHA03087	PHA03087	N	cd27963	Class_A
GSLYST00015333001	non-specific	320098	9	296	3.14E-42	146.169	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00015333001	non-specific	222976	86	249	2.69E-06	47.8506	PHA03087	PHA03087	NC	cd27963	Class_A
GSLYST00015334001	non-specific	320098	1	292	5.10E-39	137.309	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00015334001	non-specific	165021	7	284	0.000975637	40.3818	PHA02638	PHA02638	N	cd27963	Class_A
GSLYST00015335001	non-specific	320098	1	287	2.30E-33	122.672	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00015336001	specific	320086	1	296	4.52E-36	130.088	cd00637	7tm_class_rhodopsin-like	-	cd28897	Class_A
GSLYST00015337001	specific	320086	1	296	6.96E-35	127.006	cd00637	7tm_class_rhodopsin-like	-	cd28897	Class_A
GSLYST00015338001	specific	320086	2	332	6.51E-36	130.858	cd00637	7tm_class_rhodopsin-like	-	cd28897	Class_A
GSLYST00015339001	non-specific	320098	1	296	3.31E-34	124.598	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00015360001	non-specific	320098	1	265	7.15E-41	141.932	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00015361001	non-specific	320098	7	281	1.99E-39	138.08	cd14967	7tm_amine_R-like	-	cd28897	Class_A
GSLYST00015479001	non-specific	278431	47	292	1.66E-08	54.6208	pfam00001	7tm_1	-	cd27963	Class_A
GSLYST00015537001	non-specific	320334	2	84	8.52E-36	121.343	cd15206	7tm_CCK_R	C	cd28897	Class_A
GSLYST00015537001	non-specific	222976	5	80	3.03E-08	48.621	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00015538001	non-specific	320334	2	282	6.20E-69	217.643	cd15206	7tm_CCK_R	N	cd28897	Class_A
GSLYST00015538001	non-specific	222976	204	278	0.00104077	40.5319	PHA03087	PHA03087	N	cd27963	Class_A
GSLYST00015603001	specific	320124	1	270	2.87E-80	243.661	cd14993	7tm_CCKR-like	-	cd28897	Class_A
GSLYST00015603001	non-specific	222976	2	238	8.44E-15	72.8886	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00015744001	non-specific	320109	90	402	4.68E-09	56.8724	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015745001	non-specific	320109	1	284	9.04E-26	103.096	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00015745001	non-specific	165021	1	227	0.00818097	37.3002	PHA02638	PHA02638	NC	cd27963	Class_A
GSLYST00015782001	non-specific	320110	12	113	8.90E-12	65.4542	cd14979	7tm_NTSR-like	NC	cd28897	Class_A
GSLYST00015783001	non-specific	320128	69	167	4.95E-08	50.7515	cd14997	7tm_ETH-R	N	cd28897	Class_A
GSLYST00015784001	specific	320086	38	152	1.80E-15	72.6932	cd00637	7tm_class_rhodopsin-like	C	cd28897	Class_A
GSLYST00015785001	non-specific	320131	1	68	1.35E-06	43.568	cd15000	7tm_BNGR-A34-like	N	cd28897	Class_A
GSLYST00015787001	non-specific	320638	1	68	0.00268481	34.3927	cd15972	7tm_SSTR3	N	cd28897	Class_A
GSLYST00015788001	non-specific	320331	11	148	5.67E-12	61.4663	cd15203	7tm_NPYR-like	C	cd28897	Class_A
GSLYST00015789001	non-specific	320335	50	70	0.000566556	36.0601	cd15207	7tm_NPFFR	N	cd28897	Class_A
GSLYST00015791001	specific	320086	23	160	1.40E-17	76.9304	cd00637	7tm_class_rhodopsin-like	C	cd28897	Class_A
GSLYST00015791001	non-specific	165021	23	148	0.00127753	38.0706	PHA02638	PHA02638	NC	cd27963	Class_A
GSLYST00015884001	non-specific	320593	82	376	3.76E-133	383.926	cd15927	7tm_Bombesin_R-like	-	cd28897	Class_A
GSLYST00015884001	non-specific	222976	81	391	1.33E-17	83.289	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00016128001	specific	320086	1	134	9.80E-23	96.9008	cd00637	7tm_class_rhodopsin-like	C	cd28897	Class_A
GSLYST00016128001	non-specific	320133	360	419	3.09E-05	45.0938	cd15002	7tm_GPR151	N	cd28897	Class_A
GSLYST00016169001	non-specific	320514	96	392	2.40E-116	344.344	cd15392	7tm_PR4-like	-	cd28897	Class_A
GSLYST00016169001	non-specific	165021	16	399	1.18E-18	87.7614	PHA02638	PHA02638	-	cd27963	Class_A
GSLYST00016218001	specific	320086	25	238	5.69E-16	76.5452	cd00637	7tm_class_rhodopsin-like	N	cd28897	Class_A
GSLYST00016378001	non-specific	320134	237	554	4.03E-105	319.403	cd15005	7tm_SREB-like	-	cd28897	Class_A
GSLYST00016378001	non-specific	165177	228	434	1.11E-07	53.7548	PHA02834	PHA02834	C	cd27963	Class_A
GSLYST00016446001	non-specific	320086	21	96	8.78E-08	47.6552	cd00637	7tm_class_rhodopsin-like	C	cd28897	Class_A
GSLYST00016447001	non-specific	320086	328	411	4.70E-08	53.8184	cd00637	7tm_class_rhodopsin-like	N	cd28897	Class_A
GSLYST00016447001	specific	320086	1	125	2.48E-12	66.53	cd00637	7tm_class_rhodopsin-like	NC	cd28897	Class_A
GSLYST00016448001	specific	320086	60	262	2.10E-30	119.302	cd00637	7tm_class_rhodopsin-like	C	cd28897	Class_A
GSLYST00016448001	non-specific	222976	61	175	0.000291153	42.843	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00016448001	non-specific	320101	427	511	0.00310927	39.5853	cd14970	7tm_Opioid_R-like	C	cd28897	Class_A
GSLYST00016567001	specific	320109	3	156	2.45E-31	120.816	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00016646001	specific	320109	2	278	2.94E-37	134.298	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00016675001	non-specific	320109	1	311	1.48E-16	78.4436	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00016690001	non-specific	320124	9	83	7.69E-21	82.6472	cd14993	7tm_CCKR-like	C	cd28897	Class_A
GSLYST00016690001	non-specific	165021	10	79	1.33E-06	43.8486	PHA02638	PHA02638	NC	cd27963	Class_A
GSLYST00016691001	non-specific	320109	20	310	8.93E-23	95.7776	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00016691001	non-specific	313536	22	317	3.16E-12	66.0816	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00016692001	non-specific	320109	1	272	6.76E-17	78.8288	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00016718001	non-specific	320109	1	296	4.39E-20	88.0736	cd14978	7tm_F			

GSLYST00016915001	non-specific	320109	22	319	7.69E-24	98.8592	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00016916001	non-specific	320109	40	339	1.23E-21	93.8516	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00016916001	non-specific	313536	68	346	4.21E-09	57.222	pfam10324	7TM_GPCR_Srw	-	cd121561	Class_A
GSLYST00017157001	non-specific	320109	1	359	5.95E-07	50.324	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST0001719001	non-specific	320109	59	347	1.82E-17	81.5252	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST0001719001	non-specific	313536	59	351	0.000646882	41.0436	pfam10324	7TM_GPCR_Srw	-	cd121561	Class_A
GSLYST00017180001	non-specific	320109	11	211	4.08E-07	49.1684	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017240001	non-specific	320109	45	333	7.55E-26	104.637	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017240001	non-specific	313536	45	338	4.06E-10	59.9184	pfam10324	7TM_GPCR_Srw	-	cd121561	Class_A
GSLYST00017249001	specific	320086	46	250	4.38E-28	114.295	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00017249001	non-specific	165021	4	176	2.50E-06	50.397	PHA02638	PHA02638	C	cd127963	Class_A
GSLYST00017249001	non-specific	320086	673	767	6.57E-09	57.6704	cd00637	7tm_classA_rhodopsin-like	N	cd128897	Class_A
GSLYST00017250001	specific	320086	129	330	3.32E-19	88.4864	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00017250001	non-specific	165021	6	280	7.51E-09	58.8714	PHA02638	PHA02638	C	cd127963	Class_A
GSLYST00017250001	non-specific	320086	910	993	3.44E-09	58.826	cd00637	7tm_classA_rhodopsin-like	N	cd128897	Class_A
GSLYST00017251001	non-specific	320086	5	75	0.000230256	37.2548	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00017252001	non-specific	320086	7	83	2.41E-06	43.8032	cd00637	7tm_classA_rhodopsin-like	N	cd128897	Class_A
GSLYST00017253001	non-specific	320109	2	81	0.0038313	34.1457	cd14978	7tm_FMRFamide_R-like	N	cd128897	Class_A
GSLYST00017254001	non-specific	320086	4	99	1.16E-08	49.9664	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00017255001	non-specific	320124	205	277	1.93E-05	44.8976	cd14993	7tm_CCKR-like	N	cd128897	Class_A
GSLYST00017256001	non-specific	320086	5	101	2.45E-09	52.2776	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00017257001	non-specific	320124	10	82	2.12E-06	43.3568	cd14993	7tm_CCKR-like	N	cd128897	Class_A
GSLYST00017258001	non-specific	320086	31	106	3.32E-10	54.5888	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00017258001	non-specific	165021	27	93	0.00778886	34.2186	PHA02638	PHA02638	NC	cd127963	Class_A
GSLYST00017259001	non-specific	320428	2	80	4.73E-08	47.8952	cd15301	7tm_mAChr_DM1-like	N	cd128897	Class_A
GSLYST00017260001	specific	320086	5	139	1.21E-14	69.2264	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00017261001	non-specific	320124	4	76	1.27E-06	43.742	cd14993	7tm_CCKR-like	N	cd128897	Class_A
GSLYST00017262001	non-specific	320110	11	117	3.05E-05	41.1866	cd14978	7tm_NTSR-like	C	cd128897	Class_A
GSLYST00017283001	non-specific	320109	25	321	9.89E-27	106.563	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017283001	non-specific	313536	28	328	5.63E-11	62.2296	pfam10324	7TM_GPCR_Srw	-	cd121561	Class_A
GSLYST00017295001	specific	320086	7	131	1.29E-16	73.0784	cd00637	7tm_classA_rhodopsin-like	NC	cd128897	Class_A
GSLYST00017296001	non-specific	320086	4	118	3.05E-11	58.0556	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00017329001	non-specific	320109	17	312	8.40E-28	109.26	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017330001	non-specific	320109	15	313	1.18E-27	108.874	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017330001	non-specific	313536	23	320	4.09E-06	47.592	pfam10324	7TM_GPCR_Srw	-	cd121561	Class_A
GSLYST00017331001	non-specific	320109	16	312	6.61E-27	106.948	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017331001	non-specific	313536	46	316	1.11E-06	49.1328	pfam10324	7TM_GPCR_Srw	-	cd121561	Class_A
GSLYST00017391001	non-specific	320109	9	265	2.32E-19	85.3772	cd14978	7tm_FMRFamide_R-like	N	cd128897	Class_A
GSLYST00017392001	non-specific	320109	1	48	2.59E-09	50.324	cd14978	7tm_FMRFamide_R-like	C	cd128897	Class_A
GSLYST00017531001	specific	320452	71	410	4.56E-148	422.835	cd15329	7tm_5-HT7	-	cd128897	Class_A
GSLYST00017531001	non-specific	322976	85	417	7.12E-10	60.177	PHA03087	PHA03087	-	cd127963	Class_A
GSLYST00017736001	non-specific	320098	1	315	1.99E-36	131.531	cd14967	7tm_amine_R-like	-	cd128897	Class_A
GSLYST00017737001	specific	320086	1	253	6.17E-25	99.272	cd00637	7tm_classA_rhodopsin-like	-	cd128897	Class_A
GSLYST00017737001	non-specific	165021	1	225	0.000461506	40.767	PHA02638	PHA02638	N	cd127963	Class_A
GSLYST00017738001	specific	320086	1	282	1.24E-31	118.147	cd00637	7tm_classA_rhodopsin-like	-	cd128897	Class_A
GSLYST00017738001	non-specific	222976	2	244	4.85E-06	47.0802	PHA03087	PHA03087	C	cd127963	Class_A
GSLYST00017739001	non-specific	320098	10	364	2.75E-32	121.516	cd14967	7tm_amine_R-like	-	cd128897	Class_A
GSLYST00017739001	non-specific	222976	2	180	0.00139966	40.1467	PHA03087	PHA03087	C	cd127963	Class_A
GSLYST00017803001	non-specific	320109	3	298	3.94E-23	96.9332	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017803001	non-specific	313536	3	302	1.32E-05	46.0512	pfam10324	7TM_GPCR_Srw	-	cd121561	Class_A
GSLYST00017809001	non-specific	320109	21	275	1.24E-19	86.918	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017809001	non-specific	313540	28	243	0.00393963	37.9389	pfam10328	7TM_GPCR_Srx	C	cd121561	Class_A
GSLYST00017834001	non-specific	320109	13	303	1.42E-13	69.584	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017834001	non-specific	313540	13	138	0.000800179	40.2501	pfam10328	7TM_GPCR_Srx	C	cd121561	Class_A
GSLYST00017836001	specific	320324	1	302	3.42E-125	363.093	cd15196	7tm_Vasopressin_Oxytocin	-	cd128897	Class_A
GSLYST00017836001	non-specific	222976	1	170	5.30E-07	50.9322	PHA03087	PHA03087	NC	cd127963	Class_A
GSLYST00017880001	specific	320109	43	340	4.79E-56	185.144	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017895001	non-specific	320109	23	342	3.07E-06	48.0128	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00017958001	specific	320086	6	197	1.51E-34	123.154	cd00637	7tm_classA_rhodopsin-like	N	cd128897	Class_A
GSLYST00017958001	non-specific	222976	5	205	1.20E-05	44.769	PHA03087	PHA03087	N	cd127963	Class_A
GSLYST00018112001	non-specific	291157	203	307	0.00226939	38.4475	pfam14468	DUF4427	-	cd169033	Class_A
GSLYST00018112001	non-specific	320109	49	248	1.85E-27	111.956	cd14978	7tm_FMRFamide_R-like	C	cd128897	Class_A
GSLYST00018112001	non-specific	222976	53	222	2.96E-05	45.9246	PHA03087	PHA03087	C	cd127963	Class_A
GSLYST00018148001	specific	315159	283	450	1.20E-38	138.099	pfam12430	ABA_GPCR	-	cd113817	Class_A
GSLYST00018148001	specific	315250	143	210	1.01E-29	110.295	pfam12537	GPHR_N	-	cd113913	Class_A
GSLYST00018259001	non-specific	320124	1	113	3.55E-15	70.3208	cd14993	7tm_CCKR-like	N	cd128897	Class_A
GSLYST00018259001	non-specific	222976	3	130	5.43E-08	50.547	PHA03087	PHA03087	N	cd127963	Class_A
GSLYST00018296001	non-specific	320109	121	266	2.76E-14	73.0508	cd14978	7tm_FMRFamide_R-like	C	cd128897	Class_A
GSLYST00018296001	non-specific	222976	125	283	0.00186769	40.1467	PHA03087	PHA03087	C	cd127963	Class_A
GSLYST00018320001	specific	320086	42	258	7.82E-29	115.45	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00018321001	specific	320086	22	223	2.74E-21	88.8716	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00018324001	non-specific	320086	1	68	0.00454154	33.0176	cd00637	7tm_classA_rhodopsin-like	N	cd128897	Class_A
GSLYST00018384001	specific	320086	1	265	1.74E-47	159.363	cd00637	7tm_classA_rhodopsin-like	-	cd128897	Class_A
GSLYST00018384001	non-specific	222976	2	165	5.43E-08	52.8582	PHA03087	PHA03087	NC	cd127963	Class_A
GSLYST00018433001	non-specific	320109	2	290	3.15E-19	85.7624	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00018481001	non-specific	320336	1	66	2.72E-10	54.3176	cd15208	7tm_OXR	NC	cd128897	Class_A
GSLYST00018494001	non-specific	320117	54	432	1.54E-92	288.505	cd14986	7tm_Vasopressin-like	-	cd128897	Class_A
GSLYST00018494001	non-specific	222976	13	244	5.71E-18	85.6002	PHA03087	PHA03087	C	cd127963	Class_A
GSLYST00018494001	superfamily	331068	455	554	0.0011059	42.0699	cd26247	DNA_pol3_delta2 superfamily	NC	-	Class_A
GSLYST00018494001	non-specific	237874	455	554	0.0011059	42.0699	PRK14971	PRK14971	NC	cd126247	Class_A
GSLYST00018530001	specific	320086	18	315	4.65E-58	187.868	cd00637	7tm_classA_rhodopsin-like	-	cd128897	Class_A
GSLYST00018530001	non-specific	222976	13	316	8.04E-16	76.7406	PHA03087	PHA03087	-	cd127963	Class_A
GSLYST00018558001	non-specific	320117	1	286	2.68E-96	290.816	cd14986	7tm_Vasopressin-like	-	cd128897	Class_A
GSLYST00018656001	specific	320086	44	177	8.82E-27	108.517	cd00637	7tm_classA_rhodopsin-like	C	cd128897	Class_A
GSLYST00018656001	non-specific	222976	50	186	0.00188057	40.1467	PHA03087	PHA03087	C	cd127963	Class_A
GSLYST00018656001	non-specific	320226	385	454	2.66E-07	51.6505	cd15098	7tm_Gal1_R	N	cd128897	Class_A
GSLYST00018718001	non-specific	320109	1	302	5.43E-27	106.948	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00018718001	non-specific	313536	4	306	5.26E-10	59.148	pfam10324	7TM_GPCR_Srw	-	cd121561	Class_A
GSLYST00018755001	non-specific	320325	45	352	2.88E-107	318.985	cd15197	7tm_NPSR	-	cd128897	Class_A
GSLYST00018764001	specific	320086	39	293	4.45E-13	68.0708	cd00637	7tm_classA_rhodopsin-like	-	cd128897	Class_A
GSLYST00018795001	non-specific	320109	21	316	9.46E-23	95.7776	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00018795001	non-specific	313536	101	321	2.21E-05	45.2808	pfam10324	7TM_GPCR_Srw	N	cd121561	Class_A
GSLYST00018796001	non-specific	320109	30	325	1.98E-23	97.7036	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00018796001	non-specific	313536	30	330	0.000795781	40.6584	pfam10324	7TM_GPCR_Srw	-	cd121561	Class_A
GSLYST00018797001	non-specific	320109	21	316	4.96E-26	104.637	cd14978	7tm_FMRFamide_R-like	-	cd128897	Class_A
GSLYST00018797001	non-specific	313536	21	321	0.00132571	39.888	pfam1032				

GSLYST00018955001	non-specific	222976	39	238	4.04E-11	64.4142	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00018955001	non-specific	139494	280	406	3.08E-05	46.2726	PRK13335	PRK13335	C	cd27863	Class_A
GSLYST00018955001	superfamily	332684	280	406	3.08E-05	46.2726	cd27863	SSL_OB superfamily	C	-	Class_A
GSLYST00018992001	non-specific	320109	51	335	8.26E-25	101.941	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00018992001	non-specific	222976	13	178	0.00576617	37.8355	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00018993001	superfamily	332784	12	121	7.22E-05	40.3684	cd27963	7tm_1 superfamily	C	-	Class_A
GSLYST00018994001	specific	320086	3	283	2.18E-15	74.234	cd00637	7tm_class_rhodopsin-like	-	cd28897	Class_A
GSLYST00018995001	specific	320086	11	273	1.52E-13	68.8412	cd00637	7tm_class_rhodopsin-like	-	cd28897	Class_A
GSLYST00019017001	non-specific	320109	58	359	1.30E-21	93.4664	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019017001	non-specific	255903	66	363	0.0027569	38.7287	pfam10320	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00019107001	non-specific	320109	33	340	3.94E-10	86.1476	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019107001	non-specific	313536	42	346	9.29E-05	43.3548	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00019108001	non-specific	320109	1	291	1.23E-19	86.5328	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019108001	non-specific	313536	6	298	1.78E-06	48.3624	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00019116001	non-specific	320109	6	223	2.08E-14	70.7396	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00019154001	non-specific	320108	20	76	0.00743315	37.4017	cd14977	7tm_ET_R-like	C	cd28897	Class_A
GSLYST00019383001	non-specific	320109	25	334	2.53E-07	51.0944	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019384001	non-specific	320109	51	365	2.28E-09	57.6428	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019385001	non-specific	320109	43	365	2.63E-06	48.398	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019386001	non-specific	320109	21	339	2.22E-11	63.4208	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019387001	non-specific	320109	45	352	7.04E-08	53.0204	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019388001	non-specific	320109	9	331	1.33E-06	49.1684	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019389001	non-specific	320109	27	341	4.36E-11	62.6504	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019390001	non-specific	320109	9	316	1.29E-07	51.8648	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019391001	non-specific	320109	21	335	4.29E-12	65.732	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019392001	non-specific	320109	20	338	4.69E-09	56.4872	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019393001	non-specific	320109	34	346	9.16E-10	58.7984	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019394001	non-specific	320109	34	346	4.32E-09	56.4872	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019395001	non-specific	320109	33	346	9.71E-10	58.7984	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019396001	non-specific	320109	33	345	1.20E-09	58.4132	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019397001	non-specific	320109	33	345	2.96E-10	60.3392	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019398001	non-specific	320109	51	377	1.48E-09	58.4132	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019477001	superfamily	333717	35	270	1.59E-05	45.6673	cd28897	7tm_GPCRs superfamily	-	-	Class_A
GSLYST00019477001	non-specific	320420	35	270	1.59E-05	45.6673	cd15293	7tm_C_GPR158-like	-	cd28897	Class_A
GSLYST00019502001	specific	320086	15	280	1.41E-33	123.54	cd00637	7tm_class_rhodopsin-like	-	cd28897	Class_A
GSLYST00019502001	non-specific	222976	7	136	8.47E-05	43.2282	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00019519001	specific	320086	60	263	6.69E-27	110.828	cd00637	7tm_class_rhodopsin-like	C	cd28897	Class_A
GSLYST00019519001	non-specific	320086	653	744	8.86E-10	59.9816	cd00637	7tm_class_rhodopsin-like	N	cd28897	Class_A
GSLYST00019636001	non-specific	320132	95	435	3.58E-75	237.174	cd15001	7tm_GPRna14-like	-	cd28897	Class_A
GSLYST00019636001	non-specific	222976	99	437	1.72E-17	83.289	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00019782001	non-specific	320109	29	347	2.90E-14	71.8952	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019783001	non-specific	320109	47	362	2.59E-13	69.584	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019784001	non-specific	320109	21	340	3.95E-11	62.6504	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019785001	non-specific	320109	4	170	0.000477576	39.9237	cd14978	7tm_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00019786001	non-specific	320109	22	331	3.65E-09	56.8724	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019787001	non-specific	320109	13	334	4.92E-11	62.2652	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019788001	non-specific	320109	22	331	9.43E-10	58.4132	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019789001	non-specific	320109	13	334	3.08E-10	59.954	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019791001	non-specific	320109	22	335	2.13E-10	60.3392	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019793001	non-specific	320109	10	316	4.63E-11	62.2652	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019794001	non-specific	320109	20	294	2.84E-06	47.6276	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019795001	non-specific	320109	13	327	4.54E-06	47.2424	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019796001	non-specific	320109	42	356	4.70E-10	59.5688	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019797001	non-specific	320109	15	328	5.98E-09	56.102	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019798001	non-specific	320109	22	337	8.91E-14	70.7396	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019799001	non-specific	320109	3	309	2.63E-09	57.2576	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019857001	specific	320109	8	247	7.92E-46	155.869	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00019857001	non-specific	313536	16	251	3.08E-16	76.8672	pfam10324	7TM_GPCR_Srw	N	cd21561	Class_A
GSLYST00019858001	specific	320109	63	365	2.19E-71	225.59	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019858001	non-specific	313536	66	369	9.98E-32	122.321	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00019858001	non-specific	222976	74	250	1.57E-05	46.3098	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00019942001	non-specific	320109	3	283	3.74E-24	98.474	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019942001	non-specific	222976	3	228	1.23E-05	45.9246	PHA03087	PHA03087	C	cd27963	Class_A
GSLYST00019944001	non-specific	320109	1	287	3.45E-22	94.2368	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019944001	non-specific	222976	7	296	0.00031979	41.6874	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00019973001	non-specific	320109	5	92	2.66E-06	43.3904	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00019981001	non-specific	320109	6	281	9.15E-16	75.7472	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019982001	non-specific	320109	13	322	1.61E-18	84.2216	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00019982001	non-specific	313536	45	328	0.000218147	42.1992	pfam10324	7TM_GPCR_Srw	-	cd21561	Class_A
GSLYST00019985001	non-specific	320109	2	327	1.09E-15	76.1324	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020000001	non-specific	320109	1	319	1.47E-13	69.584	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020000001	non-specific	313540	1	196	1.55E-05	45.6429	pfam10328	7TM_GPCR_Srx	C	cd21561	Class_A
GSLYST00020001001	non-specific	320109	30	309	3.78E-11	62.6504	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020017001	non-specific	320109	17	288	7.28E-10	58.4132	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020055001	non-specific	320109	31	351	1.32E-21	93.0812	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020084001	non-specific	320109	1	315	4.59E-17	79.9844	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020136001	non-specific	320109	2	285	8.85E-16	75.7472	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020197001	non-specific	320109	5	129	4.92E-15	73.436	cd14978	7tm_FMRFamide_R-like	C	cd28897	Class_A
GSLYST00020204001	non-specific	320109	11	280	4.26E-16	76.5176	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020205001	non-specific	320109	13	314	5.08E-24	99.2444	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020268001	specific	320420	102	303	2.85E-85	256.371	cd15293	7tm_C_GPR158-like	C	cd28897	Class_A
GSLYST00020280001	non-specific	320109	25	321	1.67E-26	106.178	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020280001	non-specific	222976	20	274	0.000600807	40.9171	PHA03087	PHA03087	-	cd27963	Class_A
GSLYST00020285001	non-specific	320109	1	200	4.72E-16	74.5916	cd14978	7tm_FMRFamide_R-like	N	cd28897	Class_A
GSLYST00020305001	non-specific	320109	4	291	5.59E-24	98.8592	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020316001	non-specific	320109	12	310	7.92E-26	104.252	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020340001	non-specific	320109	4	303	9.90E-24	98.0888	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020340001	non-specific	313540	11	246	4.35E-08	52.9617	pfam10328	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00020340001	non-specific	165021	11	218	0.0098339	37.3002	PHA02638	PHA02638	NC	cd27963	Class_A
GSLYST00020341001	non-specific	320109	28	327	1.15E-21	93.0812	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020342001	non-specific	320109	4	303	3.81E-22	93.8516	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020342001	non-specific	313540	11	246	2.34E-09	56.8137	pfam10328	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00020342001	non-specific	165021	10	254	0.0018087	39.6114	PHA02638	PHA02638	N	cd27963	Class_A
GSLYST00020343001	non-specific	320109	4	303	1.10E-22	95.3924	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020343001	non-specific	313540	11	246	7.28E-08	52.5765	pfam10328	7TM_GPCR_Srx	-	cd21561	Class_A
GSLYST00020344001	non-specific	320109	1	291	7.38E-18	81.5252	cd14978	7tm_FMRFamide_R-like	-	cd28897	Class_A
GSLYST00020345001	non-specific	320109	2</								

GSLYST00020795001	superfamily	314733	151	426	3.76E-83	257.174	c13359	GPCR_chapero_1 superfamily	-	-	Class_A
GSLYST00020795001	specific	238125	7	85	4.28E-21	88.2094	cd00204	ANK	C	d102529	Class_A
GSLYST00020795001	superfamily	321973	7	85	4.28E-21	88.2094	cd02529	ANK superfamily	C	-	Class_A
GSLYST00020795001	specific	315466	8	80	2.26E-15	70.9089	pfam12796	Ank_2	C	d126073	Class_A
GSLYST00020795001	superfamily	330894	8	80	2.26E-15	70.9089	cd26073	Ank_2 superfamily	C	-	Class_A
GSLYST00020795001	specific	223738	7	92	2.24E-10	60.2231	COG0666	ANKYR	N	d126073	Class_A
GSLYST00020795001	non-specific	165205	8	89	3.42E-10	61.518	PHAO2874	PHAO2874	NC	d126073	Class_A
GSLYST00020840001	non-specific	320109	74	211	9.19E-25	98.8592	cd14978	7tmA_FMRFamide_R-like	C	d128897	Class_A
GSLYST00020840001	non-specific	313536	77	212	8.05E-06	45.666	pfam10324	7tm_GPCR_Srw	C	d121561	Class_A
GSLYST00020843001	non-specific	222976	21	223	1.41E-09	59.0214	PHAO3087	PHAO3087	C	d127963	Class_A
GSLYST00020843001	non-specific	320101	355	418	0.00038265	41.8965	cd14970	7tmA_Opioid_R-like	N	d128897	Class_A
GSLYST00020845001	non-specific	222976	12	176	9.06E-08	54.399	PHAO3087	PHAO3087	C	d127963	Class_A
GSLYST00020845001	non-specific	320117	642	766	1.61E-06	50.4519	cd14986	7tmA_Vasopressin-like	N	d128897	Class_A
GSLYST00020925001	non-specific	320109	35	336	1.32E-21	93.0812	cd14978	7tmA_FMRFamide_R-like	C	d128897	Class_A
GSLYST00021115001	non-specific	320109	62	97	1.00E-10	56.102	cd14978	7tmA_FMRFamide_R-like	C	d128897	Class_A
GSLYST00021231001	non-specific	320086	12	139	0.00384677	35.714	cd00637	7tm_classA_rhodopsin-like	C	d128897	Class_A
GSLYST00021326001	non-specific	320109	47	362	3.95E-16	78.0584	cd14978	7tmA_FMRFamide_R-like	-	d128897	Class_A
GSLYST00021360001	non-specific	320109	1	210	1.21E-07	50.7092	cd14978	7tmA_FMRFamide_R-like	N	d128897	Class_A
GSLYST00021362001	non-specific	320109	20	318	9.79E-19	84.6068	cd14978	7tmA_FMRFamide_R-like	-	d128897	Class_A
GSLYST00021363001	non-specific	320109	20	312	4.07E-19	85.3772	cd14978	7tmA_FMRFamide_R-like	C	d128897	Class_A
GSLYST00021412001	non-specific	320124	1	208	6.42E-36	128.101	cd14993	7tmA_CCKR-like	N	d128897	Class_A
GSLYST00021412001	non-specific	165021	12	226	9.63E-11	60.4122	PHAO2638	PHAO2638	NC	d127963	Class_A
GSLYST00021539001	non-specific	320109	1	135	6.97E-06	44.9312	cd14978	7tmA_FMRFamide_R-like	N	d128897	Class_A
GSLYST00021540001	non-specific	320109	10	135	1.33E-12	62.6504	cd14978	7tmA_FMRFamide_R-like	C	d128897	Class_A
GSLYST00021592001	non-specific	320124	1	234	2.16E-62	196.666	cd14993	7tmA_CCKR-like	N	d128897	Class_A
GSLYST00021592001	non-specific	222976	3	230	4.90E-06	46.3098	PHAO3087	PHAO3087	N	d127963	Class_A
GSLYST00021598001	non-specific	320109	18	276	2.67E-14	71.1248	cd14978	7tmA_FMRFamide_R-like	-	d128897	Class_A
GSLYST00021598001	non-specific	313536	18	264	1.29E-05	45.666	pfam10324	7TM_GPCR_Srw	C	d121561	Class_A
GSLYST00021661001	specific	320109	1	240	7.01E-53	172.432	cd14978	7tmA_FMRFamide_R-like	-	d128897	Class_A
GSLYST00021869001	specific	320086	147	403	1.04E-26	109.672	cd00637	7tm_classA_rhodopsin-like	C	d128897	Class_A
GSLYST00021869001	non-specific	222976	113	281	3.04E-08	55.5546	PHAO3087	PHAO3087	C	d127963	Class_A
GSLYST00021869001	non-specific	320646	515	568	0.00012627	44.1072	cd15980	7tmA_NPFFR2	N	d128897	Class_A
GSLYST00021930001	non-specific	320098	28	299	2.24E-39	138.465	cd14967	7tmA_amine_R-like	-	d128897	Class_A
GSLYST00021943001	specific	320100	3	219	4.91E-71	218.229	cd14969	7tmA_Opsins_type2_animals	-	d128897	Class_A
GSLYST00021943001	non-specific	222976	19	198	3.09E-14	70.1922	PHAO3087	PHAO3087	NC	d127963	Class_A
GSLYST00022238001	non-specific	320109	1	350	2.06E-08	54.5612	cd14978	7tmA_FMRFamide_R-like	-	d128897	Class_A
GSLYST00022429001	non-specific	320109	101	316	1.07E-07	52.25	cd14978	7tmA_FMRFamide_R-like	N	d128897	Class_A
GSLYST00000610001	non-specific	306508	69	327	2.27E-58	188.614	pfam00002	7tm_2	-	d121561	Class_B
GSLYST00000610001	superfamily	328797	69	327	2.27E-58	188.614	cd121561	7tm_2 superfamily	-	-	Class_B
GSLYST00000610001	superfamily	333717	70	343	1.40E-93	280.044	cd128897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00000610001	non-specific	320400	70	343	1.40E-93	280.044	cd15272	7tmB1_PTH-R_related	-	d128897	Class_B
GSLYST00000610001	specific	214468	1	63	2.88E-13	64.0728	smart00008	HormR	-	d102422	Class_B
GSLYST00000610001	specific	308439	1	58	9.80E-18	75.8885	pfam02793	HRM	-	d102422	Class_B
GSLYST00000610001	superfamily	321928	1	58	9.80E-18	75.8885	cd102422	HRM superfamily	-	-	Class_B
GSLYST00000732001	specific	306508	157	410	6.77E-75	239.846	pfam00002	7tm_2	-	d121561	Class_B
GSLYST00000732001	superfamily	328797	157	410	6.77E-75	239.846	cd121561	7tm_2 superfamily	-	-	Class_B
GSLYST00000732001	superfamily	333717	151	431	4.90E-126	373.647	cd128897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00000732001	non-specific	320400	151	431	4.90E-126	373.647	cd15272	7tmB1_PTH-R_related	-	d128897	Class_B
GSLYST00000732001	specific	214468	70	142	4.59E-15	69.8508	smart00008	HormR	-	d102422	Class_B
GSLYST00000732001	specific	308439	70	140	1.15E-17	77.0441	pfam02793	HRM	-	d102422	Class_B
GSLYST00000732001	superfamily	321928	70	140	1.15E-17	77.0441	cd102422	HRM superfamily	-	-	Class_B
GSLYST00000732001	superfamily	320873	274	429	6.09E-05	45.9148	cd100275	Heme_Cu_Oxidase_1 superfamily	NC	-	Class_B
GSLYST00000732001	non-specific	225795	274	429	6.09E-05	45.9148	COG3256	NorB	NC	cd100275	Class_B
GSLYST00001176001	superfamily	333717	1414	1641	6.57E-25	105.733	cd128897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00001176001	non-specific	320168	1414	1641	6.57E-25	105.733	cd15040	7tmB2_Adhesion	-	d128897	Class_B
GSLYST00001176001	non-specific	197594	683	802	5.46E-08	51.8715	smart00237	Calc_beta	-	d102522	Class_B
GSLYST00001176001	non-specific	197594	207	289	0.00241062	38.7747	smart00237	Calc_beta	-	d102522	Class_B
GSLYST00001176001	non-specific	308663	556	647	9.16E-09	54.1779	pfam03160	Calc-beta	-	d102522	Class_B
GSLYST00001176001	superfamily	321969	207	289	0.00241062	38.7747	cd102522	Calc-beta superfamily	-	-	Class_B
GSLYST00001176001	non-specific	197639	1320	1366	0.00043664	40.8338	smart00303	GPS	-	d102559	Class_B
GSLYST00001176001	specific	307782	1319	1365	0.000646729	38.8871	pfam01825	GPS	-	d102559	Class_B
GSLYST00001176001	superfamily	321989	1320	1366	0.00043664	40.8338	cd102559	GPS superfamily	-	-	Class_B
GSLYST00001176001	non-specific	306508	1374	1565	3.14E-12	68.0467	pfam00002	7tm_2	C	d121561	Class_B
GSLYST00001176001	superfamily	328797	1374	1565	3.14E-12	68.0467	cd121561	7tm_2 superfamily	C	-	Class_B
GSLYST00001176001	non-specific	273296	552	804	3.11E-14	78.2952	TIGR00845	coca	NC	d102522	Class_B
GSLYST00001176001	non-specific	273296	10	160	0.000169486	46.3236	TIGR00845	coca	NC	d102522	Class_B
GSLYST00001176001	superfamily	321969	552	804	3.11E-14	78.2952	cd102522	Calc-beta superfamily	NC	-	Class_B
GSLYST00001176001	superfamily	321969	10	160	0.000169486	46.3236	cd102522	Calc-beta superfamily	NC	-	Class_B
GSLYST00001547001	non-specific	306508	1	87	1.27E-13	63.0391	pfam00002	7tm_2	C	d121561	Class_B
GSLYST00001547001	superfamily	328797	1	87	1.27E-13	63.0391	cd121561	7tm_2 superfamily	C	-	Class_B
GSLYST00001547001	superfamily	333717	1	87	5.82E-31	109.4	cd128897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00001547001	non-specific	320400	1	87	5.82E-31	109.4	cd15272	7tmB1_PTH-R_related	C	d128897	Class_B
GSLYST00001548001	non-specific	306508	1	81	2.14E-19	79.2175	pfam00002	7tm_2	N	d121561	Class_B
GSLYST00001548001	superfamily	328797	1	81	2.14E-19	79.2175	cd121561	7tm_2 superfamily	N	-	Class_B
GSLYST00001548001	superfamily	333717	1	102	2.17E-44	144.839	cd128897	7tm_GPCRs superfamily	N	-	Class_B
GSLYST00001548001	non-specific	320400	1	102	2.17E-44	144.839	cd15272	7tmB1_PTH-R_related	N	d128897	Class_B
GSLYST00001571001	superfamily	333717	2	171	5.31E-17	75.7236	cd128897	7tm_GPCRs superfamily	N	-	Class_B
GSLYST00001571001	non-specific	320167	2	171	5.31E-17	75.7236	cd15039	7tmB3_Methuselah-like	N	d128897	Class_B
GSLYST00001572001	superfamily	333717	1	154	3.44E-15	70.716	cd128897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00001572001	non-specific	320167	1	154	3.44E-15	70.716	cd15039	7tmB3_Methuselah-like	C	d128897	Class_B
GSLYST00001573001	superfamily	333717	1	142	4.49E-20	83.0424	cd128897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00001573001	non-specific	320167	1	142	4.49E-20	83.0424	cd15039	7tmB3_Methuselah-like	C	d128897	Class_B
GSLYST00001575001	superfamily	333717	1	90	4.85E-14	64.5528	cd128897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00001575001	non-specific	320167	1	90	4.85E-14	64.5528	cd15039	7tmB3_Methuselah-like	C	d128897	Class_B
GSLYST00001619001	superfamily	333717	2	37	0.0033525	34.8924	cd128897	7tm_GPCRs superfamily	NC	-	Class_B
GSLYST00001619001	non-specific	320167	2	37	0.0033525	34.8924	cd15039	7tmB3_Methuselah-like	NC	d128897	Class_B
GSLYST00001859001	non-specific	306508	204	464	1.86E-36	135.842	pfam00002	7tm_2	-	d121561	Class_B
GSLYST00001859001	superfamily	328797	204	464	1.86E-36	135.842	cd121561	7tm_2 superfamily	-	-	Class_B
GSLYST00001859001	superfamily	333717	204	485	4.28E-115	342.281	cd128897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00001859001	specific	320169	204	485	4.28E-115	342.281	cd15041	7tmB1_hormone_R	-	d128897	Class_B
GSLYST00001859001	specific	214468	132	179	1.27E-11	60.2208	smart00008	HormR	C	d102422	Class_B
GSLYST00001859001	specific	308439	132	179	1.47E-12	62.4065	pfam02793	HRM	C	d102422	Class_B
GSLYST00001859001	superfamily	321928	132	179	1.47E-12	62.4065	cd102422	HRM superfamily	C	-	Class_B
GSLYST00001860001	specific	306508	141	399	9.24E-80	252.943	pfam00002	7tm_2	-	d121561	Class_B
GSLYST00001860001	superfamily	328797	141	399	9.24E-80	252.943	cd121561	7tm_2 superfamily	-	-	Class_B
GSLYST00001860001	superfamily	333717	138	420	4.88E-139	407.16	cd128897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00001860001	non-specific	320400	138	420	4.88E-139	407.16	cd15272	7tmB1_PTH-R_related	-	d128897	Class_B
GSLYST00001860001	specific	214468	59	131	6.59E-25	97.9704	smart00008	HormR	-	d102422	Class_B
GSLYST00001860001	specific	30843									

GSLYST00004304001	non-specific	306508	198	424	1.52E-20	90.0031	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00004304001	superfamily	328797	198	424	1.52E-20	90.0031	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00004304001	superfamily	333717	192	436	6.65E-40	143.16	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00004304001	non-specific	320557	192	436	6.65E-40	143.16	cd15441	7tmB2_CELSR_Adhesion_IV	-	cl28897	Class_B
GSLYST00005400001	non-specific	306508	1010	1305	5.16E-15	76.1359	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00005400001	superfamily	328797	1010	1305	5.16E-15	76.1359	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00005400001	superfamily	333717	999	1320	4.26E-79	261.775	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00005400001	specific	320167	999	1320	4.26E-79	261.775	cd15039	7tmB3_Methuselah-like	-	cl28897	Class_B
GSLYST00005590001	non-specific	306508	143	388	4.39E-49	169.354	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00005590001	superfamily	328797	143	388	4.39E-49	169.354	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00005590001	superfamily	333717	142	403	1.53E-100	303.34	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00005590001	specific	320168	142	403	1.53E-100	303.34	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00005590001	specific	307782	88	128	1.78E-10	55.8359	pfam01825	GPS	-	cl02559	Class_B
GSLYST00005590001	specific	197639	86	133	2.04E-09	53.1602	smart00303	GPS	-	cl02559	Class_B
GSLYST00005590001	superfamily	321989	88	128	1.78E-10	55.8359	cl02559	GPS superfamily	-	-	Class_B
GSLYST00005707001	non-specific	306508	976	1214	5.11E-38	142.775	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00005707001	superfamily	328797	976	1214	5.11E-38	142.775	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00005707001	superfamily	333717	977	1229	1.90E-100	320.289	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00005707001	specific	320168	977	1229	1.90E-100	320.289	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00005707001	non-specific	214480	41	179	0.000361987	41.4314	smart00034	CLECT	-	cl02432	Class_B
GSLYST00005707001	specific	153057	44	181	0.00339538	38.755	cd00037	CLECT	-	cl02432	Class_B
GSLYST00005707001	superfamily	321932	41	179	0.000361987	41.4314	cl02432	CLECT superfamily	-	-	Class_B
GSLYST00005707001	specific	307782	919	962	2.43E-15	70.8586	pfam01825	GPS	-	cl02559	Class_B
GSLYST00005707001	specific	197639	918	963	2.20E-09	53.9306	smart00303	GPS	-	cl02559	Class_B
GSLYST00005707001	superfamily	321989	919	962	2.43E-15	70.8586	cl02559	GPS superfamily	-	-	Class_B
GSLYST00005709001	non-specific	306508	2	225	2.00E-25	99.6331	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00005709001	superfamily	328797	2	225	2.00E-25	99.6331	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00005709001	superfamily	333717	1	240	4.16E-81	242.864	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00005709001	specific	320168	1	240	4.16E-81	242.864	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00005710001	non-specific	306508	2	236	1.22E-33	123.515	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00005710001	superfamily	328797	2	236	1.22E-33	123.515	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00005710001	superfamily	333717	1	251	1.46E-90	270.213	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00005710001	specific	320168	1	251	1.46E-90	270.213	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00005851001	non-specific	306508	119	360	1.39E-56	187.459	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00005851001	superfamily	328797	119	360	1.39E-56	187.459	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00005851001	superfamily	333717	118	380	4.00E-110	326.152	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00005851001	non-specific	320388	118	380	4.00E-110	326.152	cd15260	7tmB1_NPR_B4_insect-like	-	cl28897	Class_B
GSLYST00005851001	specific	214468	36	99	1.81E-11	59.4504	smart00008	HorrmR	-	cl02422	Class_B
GSLYST00005851001	specific	308439	37	102	6.71E-14	65.8733	pfam02793	HRM	-	cl02422	Class_B
GSLYST00005851001	superfamily	321928	37	102	6.71E-14	65.8733	cl02422	HRM superfamily	-	-	Class_B
GSLYST00006197001	non-specific	306508	70	258	1.47E-26	103.1	pfam00002	7tm_2	C	cl21561	Class_B
GSLYST00006197001	superfamily	328797	70	258	1.47E-26	103.1	cl21561	7tm_4 superfamily	C	-	Class_B
GSLYST00006197001	superfamily	333717	76	258	2.11E-33	121.281	cl28897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00006197001	non-specific	320599	76	258	2.11E-33	121.281	cd15933	7tmB2_GPR133-like_Adhesion_V	C	cl28897	Class_B
GSLYST00006197001	non-specific	197639	32	61	2.49E-06	43.5302	smart00303	GPS	N	cl02559	Class_B
GSLYST00006197001	specific	307782	32	60	0.00239033	35.0351	pfam01825	GPS	N	cl02559	Class_B
GSLYST00006197001	superfamily	321989	32	61	2.49E-06	43.5302	cl02559	GPS superfamily	N	-	Class_B
GSLYST00006198001	superfamily	333717	1	60	1.63E-14	65.0416	cl28897	7tm_GPCRs superfamily	N	-	Class_B
GSLYST00006198001	non-specific	320599	1	60	1.63E-14	65.0416	cd15933	7tmB2_GPR133-like_Adhesion_V	N	cl28897	Class_B
GSLYST00006940001	non-specific	306508	299	540	4.19E-24	101.174	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00006940001	superfamily	328797	299	540	4.19E-24	101.174	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00006940001	superfamily	333717	298	555	9.31E-77	243.285	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00006940001	specific	320167	298	555	9.31E-77	243.285	cd15039	7tmB3_Methuselah-like	-	cl28897	Class_B
GSLYST00007655001	non-specific	306508	64	301	5.55E-43	147.783	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00007655001	superfamily	328797	64	301	5.55E-43	147.783	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00007655001	superfamily	333717	67	312	1.17E-86	261.004	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00007655001	specific	320169	67	312	1.17E-86	261.004	cd15041	7tmB1_hormone_R	-	cl28897	Class_B
GSLYST00007655001	specific	214468	2	65	1.68E-11	58.68	smart00008	HorrmR	-	cl02422	Class_B
GSLYST00007655001	specific	308439	2	63	5.73E-14	65.4881	pfam02793	HRM	-	cl02422	Class_B
GSLYST00007655001	superfamily	321928	2	63	5.73E-14	65.4881	cl02422	HRM superfamily	-	-	Class_B
GSLYST00008178001	superfamily	333717	2	154	7.19E-12	61.086	cl28897	7tm_GPCRs superfamily	N	-	Class_B
GSLYST00008178001	non-specific	320167	2	154	7.19E-12	61.086	cd15039	7tmB3_Methuselah-like	N	cl28897	Class_B
GSLYST00008179001	non-specific	320167	1	181	1.40E-27	104.614	cd15039	7tmB3_Methuselah-like	N	cl28897	Class_B
GSLYST00008179001	superfamily	333717	1	181	1.40E-27	104.614	cl28897	7tm_GPCRs superfamily	N	-	Class_B
GSLYST00008902001	non-specific	306508	1365	1599	4.22E-53	186.688	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00008902001	superfamily	328797	1365	1599	4.22E-53	186.688	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00008902001	superfamily	333717	1364	1612	5.26E-83	272.91	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00008902001	specific	320168	1364	1612	5.26E-83	272.91	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00008902001	non-specific	214520	664	728	0.000107224	42.3367	smart00112	CA	-	cl09101	Class_B
GSLYST00008902001	superfamily	333701	642	730	2.69E-10	58.8641	cl28881	CA_like superfamily	-	-	Class_B
GSLYST00008902001	non-specific	278457	642	728	2.17E-08	53.073	pfam00028	Cadherin	-	cl09101	Class_B
GSLYST00008902001	specific	206637	642	730	2.69E-10	58.8641	cd11304	Cadherin_repeat	-	cl28881	Class_B
GSLYST00008902001	superfamily	324323	642	728	2.17E-08	53.073	cl09101	E_set superfamily	-	-	Class_B
GSLYST00008902001	specific	306513	153	179	0.00512071	36.2067	pfam00008	EGF	-	cl21504	Class_B
GSLYST00008902001	specific	238011	146	180	3.25E-07	48.0166	cd00054	EGF_CA	-	cl21504	Class_B
GSLYST00008902001	specific	214542	146	180	1.19E-05	43.7748	smart00179	EGF_CA	-	cl21504	Class_B
GSLYST00008902001	superfamily	328759	146	180	3.25E-07	48.0166	cl21504	EGF_CA superfamily	-	-	Class_B
GSLYST00008902001	non-specific	318649	1098	1283	1.74E-07	53.3947	pfam16489	GAIN	-	cl24904	Class_B
GSLYST00008902001	superfamily	318649	1098	1283	1.74E-07	53.3947	cl24904	GAIN superfamily	-	-	Class_B
GSLYST00008902001	specific	307782	1309	1354	8.99E-12	61.2287	pfam01825	GPS	-	cl02559	Class_B
GSLYST00008902001	specific	197639	1307	1355	1.55E-10	57.7826	smart00303	GPS	-	cl02559	Class_B
GSLYST00008902001	superfamily	321989	1309	1354	8.99E-12	61.2287	cl02559	GPS superfamily	-	-	Class_B
GSLYST00009392001	specific	306508	741	978	3.52E-64	217.119	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00009392001	superfamily	328797	741	978	3.52E-64	217.119	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00009392001	superfamily	333717	740	998	1.46E-128	390.47	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00009392001	specific	320556	740	998	1.46E-128	390.47	cd15440	7tmB2_latrophilin-like_invertebrate	-	cl28897	Class_B
GSLYST00009392001	non-specific	318649	447	597	1.33E-18	84.9811	pfam16489	GAIN	-	cl24904	Class_B
GSLYST00009392001	superfamily	318649	447	597	1.33E-18	84.9811	cl24904	GAIN superfamily	-	-	Class_B
GSLYST00009392001	specific	307782	678	722	4.45E-15	69.703	pfam01825	GPS	-	cl02559	Class_B
GSLYST00009392001	specific	197639	678	727	4.36E-13	64.331	smart00303	GPS	-	cl02559	Class_B
GSLYST00009392001	superfamily	321989	678	722	4.45E-15	69.703	cl02559	GPS superfamily	-	-	Class_B
GSLYST00009392001	non-specific	214468	340	392	0.00147713	37.8793	smart00008	HorrmR	-	cl02422	Class_B
GSLYST00009392001	non-specific	308439	340	392	0.00252348	36.9834	pfam02793	HRM	-	cl02422	Class_B
GSLYST00009392001	superfamily	321928	340	392	0.00147713	37.8793	cl02422	HRM superfamily	-	-	Class_B
GSLYST00009392001	non-specific	223885	803	981	0.000535411	43.5525	COG0815	Lnt	C	cl25421	Class_B
GSLYST00009392001	superfamily	330242	803	981	0.000535411	43.5525	cl25421	Lnt superfamily	C	-	Class_B
GSLYST00009392001	superfamily	330571	68	201	0.000304165	43.7773	cl25750	DamX superfamily	NC	-	Class_B
GSLYST00009392001	non-specific	236792	68	201	0.000304165	43.7773	PRK10905	PRK10905	NC	cl25750	Class_B
GSLYST00009674001	non-specific	306508	1	150	3.16E-18	78.8323	pfam00002	7tm_2	N	cl21561	Class_B
GSLYST00009674001	superfamily	328797	1	150	3.16E-18	78.8323					

GSLYST00011530001	specific	214542	171	207	2.93E-06	45.3156	smart00179	EGF_CA	-	cl21504	Class_B
GSLYST00011530001	specific	238011	462	493	0.00411893	36.0754	cd00054	EGF_CA	-	cl21504	Class_B
GSLYST00011530001	superfamily	328759	172	207	4.15E-08	50.3278	cl21504	EGF_CA superfamily	-	-	Class_B
GSLYST00011530001	superfamily	328759	462	492	0.000396987	38.9031	cl21504	EGF_CA superfamily	-	-	Class_B
GSLYST00011530001	non-specific	318649	853	1064	2.68E-15	76.1215	pfam16489	GAIN	-	cl24904	Class_B
GSLYST00011530001	superfamily	318649	853	1064	2.68E-15	76.1215	cl24904	GAIN superfamily	-	-	Class_B
GSLYST00011530001	non-specific	197639	1092	1153	8.90E-06	44.3006	smart00303	GPS	-	cl02559	Class_B
GSLYST00011530001	specific	307782	1096	1150	7.58E-05	41.5835	pfam01825	GPS	-	cl02559	Class_B
GSLYST00011530001	superfamily	321989	1092	1153	8.90E-06	44.3006	cl02559	GPS superfamily	-	-	Class_B
GSLYST00011530001	specific	238058	259	436	6.01E-25	102.111	cd00110	LamG	-	cl22861	Class_B
GSLYST00011530001	specific	214598	278	438	1.79E-20	88.5505	smart00282	LamG	-	cl22861	Class_B
GSLYST00011530001	specific	238058	509	642	3.18E-14	71.2952	cd00110	LamG	-	cl22861	Class_B
GSLYST00011530001	specific	214598	527	644	3.07E-11	62.3569	smart00282	LamG	-	cl22861	Class_B
GSLYST00011530001	superfamily	328935	259	436	6.01E-25	102.111	cl22861	LamG superfamily	-	-	Class_B
GSLYST00011530001	superfamily	328935	509	642	3.18E-14	71.2952	cl22861	LamG superfamily	-	-	Class_B
GSLYST00011530001	specific	308045	283	438	5.89E-21	89.8007	pfam02210	Laminin_G_2	-	cl22861	Class_B
GSLYST00011530001	specific	308045	527	644	1.49E-12	65.9183	pfam02210	Laminin_G_2	-	cl21561	Class_B
GSLYST00012075001	non-specific	306508	1	237	4.19E-56	182.066	pfam00002	7tm_2	-	-	Class_B
GSLYST00012075001	superfamily	328797	1	237	4.19E-56	182.066	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00012075001	superfamily	333717	1	257	1.39E-103	304.34	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00012075001	non-specific	320392	1	257	1.39E-103	304.34	cd15264	7tmB1_CRF-R	-	cl28897	Class_B
GSLYST00012348001	non-specific	306508	1059	1312	1.01E-58	202.481	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00012348001	superfamily	328797	1059	1312	1.01E-58	202.481	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00012348001	superfamily	333717	1058	1327	7.33E-113	356.498	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00012348001	specific	320168	1058	1327	7.33E-113	356.498	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00012348001	specific	307782	997	1041	1.49E-14	68.9326	pfam01825	GPS	-	cl02559	Class_B
GSLYST00012348001	specific	197639	995	1045	5.10E-14	67.4126	smart00303	GPS	-	cl02559	Class_B
GSLYST00012348001	superfamily	321989	997	1041	1.49E-14	68.9326	cl02559	GPS superfamily	-	-	Class_B
GSLYST00012348001	specific	316378	89	147	3.65E-12	62.5446	pfam13855	LRR_8	-	cl25992	Class_B
GSLYST00012348001	specific	316378	136	199	0.000636353	39.0475	pfam13855	LRR_8	-	cl25992	Class_B
GSLYST00012348001	superfamily	330813	89	147	3.65E-12	62.5446	cl25992	LRR_8 superfamily	-	-	Class_B
GSLYST00012348001	superfamily	330813	136	199	0.000636353	39.0475	cl25992	LRR_8 superfamily	-	-	Class_B
GSLYST00012348001	specific	272223	67	303	7.72E-06	49.9666	COG4886	LRR	N	cl25992	Class_B
GSLYST00012348001	non-specific	238064	66	200	8.17E-05	46.1946	cd00116	LRR_RI	N	cl26161	Class_B
GSLYST00012348001	superfamily	330982	66	200	8.17E-05	46.1946	cl26161	LRR_RI superfamily	N	-	Class_B
GSLYST00012348001	superfamily	330317	601	691	0.000294229	44.4437	cl25496	Herpes BLLF1 superfamily	NC	-	Class_B
GSLYST00012348001	non-specific	319112	601	691	0.000294229	44.4437	pfam17061	PARM	NC	cl25496	Class_B
GSLYST00012405001	non-specific	306508	592	822	1.34E-43	158.183	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00012405001	superfamily	328797	592	822	1.34E-43	158.183	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00012405001	superfamily	333717	590	836	3.75E-61	207.811	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00012405001	specific	320168	590	836	3.75E-61	207.811	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00012405001	specific	306538	25	106	8.96E-07	47.4097	pfam00041	fn3	-	cl21522	Class_B
GSLYST00012405001	specific	214495	25	103	1.68E-05	43.7573	smart00060	FN3	-	cl21522	Class_B
GSLYST00012405001	specific	238020	25	103	0.000411445	40.1723	cd00063	FN3	-	cl21522	Class_B
GSLYST00012405001	superfamily	328772	25	106	8.96E-07	47.4097	cl21522	FN3 superfamily	-	-	Class_B
GSLYST00012405001	specific	307782	536	578	4.62E-09	52.7543	pfam01825	GPS	-	cl02559	Class_B
GSLYST00012405001	non-specific	197639	538	579	4.22E-08	50.0786	smart00303	GPS	-	cl02559	Class_B
GSLYST00012405001	superfamily	321989	536	578	4.62E-09	52.7543	cl02559	GPS superfamily	-	-	Class_B
GSLYST00012405001	non-specific	308439	245	297	0.00940083	35.4426	pfam02793	HRM	-	cl02422	Class_B
GSLYST00012405001	superfamily	321928	245	297	0.00940083	35.4426	cl02422	HRM superfamily	-	-	Class_B
GSLYST00012592001	non-specific	306508	668	902	2.56E-15	76.5211	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00012592001	superfamily	328797	668	902	2.56E-15	76.5211	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00012592001	superfamily	333717	668	916	1.15E-54	190.898	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00012592001	specific	320167	668	916	1.15E-54	190.898	cd15039	7tmB3_Methuselah-like	-	cl28897	Class_B
GSLYST00012609001	non-specific	306508	28	187	1.18E-43	145.087	pfam00002	7tm_2	C	cl21561	Class_B
GSLYST00012609001	superfamily	328797	28	187	1.18E-43	145.087	cl21561	7tm_4 superfamily	C	-	Class_B
GSLYST00012609001	superfamily	333717	27	189	1.04E-58	184.003	cl28897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00012609001	non-specific	320556	27	189	1.04E-58	184.003	cd15440	7tmB2_latrophilin-like_invertebrate	C	cl28897	Class_B
GSLYST00012609001	specific	307782	3	14	0.00200697	34.6499	pfam01825	GPS	N	cl02559	Class_B
GSLYST00012609001	non-specific	197639	3	19	0.00350338	33.9002	smart00303	GPS	N	cl02559	Class_B
GSLYST00012609001	superfamily	321989	3	14	0.00200697	34.6499	cl02559	GPS superfamily	N	-	Class_B
GSLYST00012813001	non-specific	306508	122	361	1.78E-41	147.398	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00012813001	superfamily	328797	122	361	1.78E-41	147.398	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00012813001	superfamily	333717	117	382	2.85E-93	282.624	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00012813001	non-specific	320388	117	382	2.85E-93	282.624	cd15260	7tmB1_NPR_B4_insect-like	-	cl28897	Class_B
GSLYST00012813001	specific	214468	45	111	1.88E-15	70.6212	smart00008	HorMR	-	cl02422	Class_B
GSLYST00012813001	specific	308439	45	111	4.71E-17	74.7329	pfam02793	HRM	-	cl02422	Class_B
GSLYST00012813001	superfamily	321928	45	111	4.71E-17	74.7329	cl02422	HRM superfamily	-	-	Class_B
GSLYST00012996001	non-specific	306508	651	886	5.23E-26	107.337	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00012996001	superfamily	328797	651	886	5.23E-26	107.337	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00012996001	superfamily	333717	648	901	5.82E-75	245.946	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00012996001	specific	320168	648	901	5.82E-75	245.946	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00012996001	specific	307782	591	634	5.25E-14	66.6214	pfam01825	GPS	-	cl02559	Class_B
GSLYST00012996001	non-specific	197639	590	634	5.85E-07	46.6118	smart00303	GPS	-	cl02559	Class_B
GSLYST00012996001	superfamily	321989	591	634	5.25E-14	66.6214	cl02559	GPS superfamily	-	-	Class_B
GSLYST00012997001	superfamily	333717	1	208	7.12E-70	213.589	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00012997001	specific	320168	1	208	7.12E-70	213.589	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00012997001	non-specific	306508	12	193	4.56E-25	98.0923	pfam00002	7tm_2	N	cl21561	Class_B
GSLYST00012997001	superfamily	328797	12	193	4.56E-25	98.0923	cl21561	7tm_4 superfamily	N	-	Class_B
GSLYST00013103001	non-specific	306508	705	941	3.88E-41	151.25	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00013103001	superfamily	328797	705	941	3.88E-41	151.25	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00013103001	superfamily	333717	703	956	1.58E-101	318.363	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00013103001	specific	320168	703	956	1.58E-101	318.363	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00013103001	specific	307782	646	688	2.07E-13	65.0806	pfam01825	GPS	-	cl02559	Class_B
GSLYST00013103001	specific	197639	643	690	1.92E-10	56.627	smart00303	GPS	-	cl02559	Class_B
GSLYST00013103001	superfamily	321989	646	688	2.07E-13	65.0806	cl02559	GPS superfamily	-	-	Class_B
GSLYST00014513001	specific	306508	166	429	6.73E-83	258.335	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00014513001	superfamily	328797	166	429	6.73E-83	258.335	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00014513001	superfamily	333717	166	450	1.09E-160	459.162	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00014513001	specific	320400	166	450	1.09E-160	459.162	cd15272	7tmB1_PTH-R_related	-	cl28897	Class_B
GSLYST00014513001	specific	214468	84	146	1.93E-19	82.1772	smart00008	HorMR	-	cl02422	Class_B
GSLYST00014513001	specific	308439	84	146	6.60E-21	86.2889	pfam02793	HRM	-	cl02422	Class_B
GSLYST00014513001	superfamily	321928	84	146	6.60E-21	86.2889	cl02422	HRM superfamily	-	-	Class_B
GSLYST00014738001	non-specific	306508	1043	1279	1.74E-45	164.347	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00014738001	superfamily	328797	1043	1279	1.74E-45	164.347	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00014738001	specific	320090	1042	1292	5.85E-71	237.856	cl13952	7tm_classB	-	cl28897	Class_B
GSLYST00014738001	superfamily	333717	1042	1292	5.85E-71	237.856	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00014738001	superfamily	333701	489	578	0.000846805	39.9894	cl28881	CA_like superfamily	-	-	Class_B
GSLYST00014738001	specific	206637	489	578	0.000846805	39.9894	cd11304	Cadherin_repeat	-	cl28881	Class_B
GSLYST00014738001	specific	197639	988	1036	6.68E-11	58.553	smart00303				

GSLYST00014739001	superfamily	321989	469	512	1.11E-12	62.7694	cl02559	GPS superfamily	-	-	Class_B
GSLYST00014740001	specific	306508	1919	2153	2.38E-63	216.349	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00014740001	superfamily	328797	1919	2153	2.38E-63	216.349	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00014740001	superfamily	333717	1918	2166	1.28E-92	300.644	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00014740001	specific	320168	1918	2166	1.28E-92	300.644	cd15040	7tmB2_Adhesion	-	cl28897	Class_B
GSLYST00014740001	specific	307643	2	40	0.000328206	40.0862	pfam01607	CBM_14	-	cl02629	Class_B
GSLYST00014740001	superfamily	322027	2	40	0.000154349	40.8902	cl02629	CBM_14 superfamily	-	-	Class_B
GSLYST00014740001	specific	214696	2	40	0.000154349	40.8902	smart00049	ChtBD2	-	cl02629	Class_B
GSLYST00014740001	specific	306513	1183	1209	0.00303764	36.9771	pfam00008	EGF	-	cl21504	Class_B
GSLYST00014740001	specific	306513	686	713	0.00511636	36.2067	pfam00008	EGF	-	cl21504	Class_B
GSLYST00014740001	specific	238011	1175	1210	9.05E-10	55.3354	cd00054	EGF_CA	-	cl21504	Class_B
GSLYST00014740001	specific	238011	679	714	4.46E-09	53.4094	cd00054	EGF_CA	-	cl21504	Class_B
GSLYST00014740001	specific	214542	1175	1211	6.44E-09	53.0196	smart00179	EGF_CA	-	cl21504	Class_B
GSLYST00014740001	specific	214542	679	715	8.06E-09	53.0196	smart00179	EGF_CA	-	cl21504	Class_B
GSLYST00014740001	specific	238011	177	211	2.99E-05	42.6238	cd00054	EGF_CA	-	cl21504	Class_B
GSLYST00014740001	specific	214542	177	211	5.01E-05	42.234	smart00179	EGF_CA	-	cl21504	Class_B
GSLYST00014740001	superfamily	328759	1175	1210	9.05E-10	55.3354	cl21504	EGF_CA superfamily	-	-	Class_B
GSLYST00014740001	superfamily	328759	679	714	4.46E-09	53.4094	cl21504	EGF_CA superfamily	-	-	Class_B
GSLYST00014740001	superfamily	328759	177	211	2.99E-05	42.6238	cl21504	EGF_CA superfamily	-	-	Class_B
GSLYST00014740001	non-specific	318649	1654	1839	1.72E-06	50.6983	pfam16489	GAIN	-	cl24904	Class_B
GSLYST00014740001	superfamily	318649	1654	1839	1.72E-06	50.6983	cl24904	GAIN superfamily	-	-	Class_B
GSLYST00014740001	specific	307782	1863	1908	1.30E-12	63.925	pfam01825	GPS	-	cl02559	Class_B
GSLYST00014740001	specific	197639	1861	1911	4.91E-12	62.405	smart00303	GPS	-	cl02559	Class_B
GSLYST00014740001	superfamily	321989	1863	1908	1.30E-12	63.925	cl02559	GPS superfamily	-	-	Class_B
GSLYST00014740001	non-specific	214468	1565	1618	1.70E-06	47.124	smart00008	HormR	-	cl02422	Class_B
GSLYST00014740001	superfamily	321928	1565	1618	1.70E-06	47.124	cl02422	HRM superfamily	-	-	Class_B
GSLYST00014740001	non-specific	224214	2007	2156	0.0096616	40.3729	COG1295	BrkB	N	cl07918	Class_B
GSLYST00014740001	specific	308439	1578	1618	0.000430361	40.4502	pfam02793	HRM	N	cl02422	Class_B
GSLYST00014740001	superfamily	324181	2007	2156	0.0096616	40.3729	cl07918	Virul_fac_BrkB superfamily	N	-	Class_B
GSLYST00014882001	non-specific	197639	129	190	1.49E-06	43.9154	smart00303	GPS	-	cl02559	Class_B
GSLYST00014882001	specific	307782	133	187	2.20E-05	40.8131	pfam01825	GPS	-	cl02559	Class_B
GSLYST00014882001	superfamily	321989	129	190	1.49E-06	43.9154	cl02559	GPS superfamily	-	-	Class_B
GSLYST00014882001	superfamily	333717	229	258	0.000176686	41.4676	cl28897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00014882001	non-specific	320557	229	258	0.000176686	41.4676	cl15441	7tmB2_CELSR_Adhesion_IV	C	cl28897	Class_B
GSLYST00014882001	non-specific	318649	1	101	4.06E-05	42.9943	pfam16489	GAIN	N	cl24904	Class_B
GSLYST00014882001	superfamily	318649	1	101	4.06E-05	42.9943	cl24904	GAIN superfamily	N	-	Class_B
GSLYST00015600001	non-specific	306508	1	246	4.09E-06	46.4755	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00015600001	superfamily	328797	1	246	4.09E-06	46.4755	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00015600001	superfamily	333717	1	261	6.91E-46	154.304	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00015600001	specific	320167	1	261	6.91E-46	154.304	cd15039	7tmB3_Methuselah-like	-	-	Class_B
GSLYST00015912001	non-specific	306508	29	260	5.84E-24	97.7071	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00015912001	superfamily	328797	29	260	5.84E-24	97.7071	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00015912001	superfamily	333717	28	275	2.66E-52	172.512	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00015912001	non-specific	320599	28	275	2.66E-52	172.512	cd15933	7tmB2_GPR133-like_Adhesion_V	-	cl28897	Class_B
GSLYST00016055001	non-specific	306508	1	104	2.21E-05	41.4679	pfam00002	7tm_2	N	cl21561	Class_B
GSLYST00016055001	superfamily	328797	1	104	2.21E-05	41.4679	cl21561	7tm_4 superfamily	N	-	Class_B
GSLYST00016055001	superfamily	333717	1	106	1.05E-18	77.7532	cl28897	7tm_GPCRs superfamily	N	-	Class_B
GSLYST00016055001	non-specific	320599	1	106	1.05E-18	77.7532	cd15933	7tmB2_GPR133-like_Adhesion_V	N	cl28897	Class_B
GSLYST00016055001	non-specific	306508	1	104	2.21E-05	41.4679	pfam00002	7tm_2	N	cl21561	Class_B
GSLYST00016056001	superfamily	328797	1	104	2.21E-05	41.4679	cl21561	7tm_4 superfamily	N	-	Class_B
GSLYST00016056001	superfamily	333717	1	106	1.05E-18	77.7532	cl28897	7tm_GPCRs superfamily	N	-	Class_B
GSLYST00016056001	non-specific	320599	1	106	1.05E-18	77.7532	cd15933	7tmB2_GPR133-like_Adhesion_V	N	cl28897	Class_B
GSLYST00016478001	non-specific	306508	300	412	0.00367517	38.3864	pfam00002	7tm_2	C	cl21561	Class_B
GSLYST00016478001	superfamily	328797	300	412	0.00367517	38.3864	cl21561	7tm_4 superfamily	C	-	Class_B
GSLYST00016478001	superfamily	333717	296	406	2.42E-09	57.6569	cl28897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00016478001	non-specific	320654	296	406	2.42E-09	57.6569	cd15988	7tmB2_BAI2	C	cl28897	Class_B
GSLYST00016693001	superfamily	333717	2	147	3.96E-22	88.4352	cl28897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00016693001	non-specific	320167	2	147	3.96E-22	88.4352	cd15039	7tmB3_Methuselah-like	C	cl28897	Class_B
GSLYST00016827001	non-specific	306508	16	66	4.48E-06	44.9347	pfam00002	7tm_2	N	cl21561	Class_B
GSLYST00016827001	superfamily	328797	16	66	4.48E-06	44.9347	cl21561	7tm_4 superfamily	N	-	Class_B
GSLYST00016827001	superfamily	333717	2	87	9.81E-30	109.62	cl28897	7tm_GPCRs superfamily	N	-	Class_B
GSLYST00016827001	non-specific	320169	2	87	9.81E-30	109.62	cd15041	7tmB1_hormone_R	N	cl28897	Class_B
GSLYST00018277001	non-specific	197639	40	101	2.34E-06	43.5302	smart00303	GPS	-	cl02559	Class_B
GSLYST00018277001	specific	307782	44	98	2.06E-05	40.8131	pfam01825	GPS	-	cl02559	Class_B
GSLYST00018277001	superfamily	321989	40	101	2.34E-06	43.5302	cl02559	GPS superfamily	-	-	Class_B
GSLYST00018277001	non-specific	306508	118	263	1.56E-29	111.189	pfam00002	7tm_2	C	cl21561	Class_B
GSLYST00018277001	superfamily	328797	118	263	1.56E-29	111.189	cl21561	7tm_4 superfamily	C	-	Class_B
GSLYST00018277001	superfamily	333717	114	263	5.81E-62	195.162	cl28897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00018277001	non-specific	320557	114	263	5.81E-62	195.162	cd15441	7tmB2_CELSR_Adhesion_IV	C	cl28897	Class_B
GSLYST00018774001	non-specific	306508	33	150	5.68E-14	67.2763	pfam00002	7tm_2	N	cl21561	Class_B
GSLYST00018774001	superfamily	328797	33	150	5.68E-14	67.2763	cl21561	7tm_4 superfamily	N	-	Class_B
GSLYST00018774001	superfamily	333717	1	164	6.19E-32	114.732	cl28897	7tm_GPCRs superfamily	N	-	Class_B
GSLYST00018774001	non-specific	320599	1	164	6.19E-32	114.732	cd15933	7tmB2_GPR133-like_Adhesion_V	N	cl28897	Class_B
GSLYST00020067001	non-specific	306508	225	486	3.18E-61	204.407	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00020067001	superfamily	328797	225	486	3.18E-61	204.407	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00020067001	superfamily	333717	226	510	3.15E-106	323.571	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00020067001	non-specific	320400	226	510	3.15E-106	323.571	cl15272	7tmB1_PTH-R_related	-	cl28897	Class_B
GSLYST00020067001	specific	214468	144	213	2.91E-19	81.792	smart00008	HormR	-	cl02422	Class_B
GSLYST00020067001	specific	308439	144	213	5.68E-22	89.3705	pfam02793	HRM	-	cl02422	Class_B
GSLYST00020067001	superfamily	321928	144	213	5.68E-22	89.3705	cl02422	HRM superfamily	-	-	Class_B
GSLYST00020718001	non-specific	306508	30	140	2.05E-14	67.2763	pfam00002	7tm_2	C	cl21561	Class_B
GSLYST00020718001	superfamily	328797	30	140	2.05E-14	67.2763	cl21561	7tm_4 superfamily	C	-	Class_B
GSLYST00020718001	superfamily	333717	24	141	3.48E-34	120.02	cl28897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00020718001	non-specific	320169	24	141	3.48E-34	120.02	cl15041	7tmB1_hormone_R	C	cl28897	Class_B
GSLYST0002075001	superfamily	333717	4	76	4.72E-10	55.7817	cl28897	7tm_GPCRs superfamily	N	-	Class_B
GSLYST0002075001	non-specific	320598	4	76	4.72E-10	55.7817	cd15932	7tmB2_GPR116-like_Adhesion_VI	N	cl28897	Class_B
GSLYST00021398001	non-specific	306508	44	154	2.37E-13	64.9651	pfam00002	7tm_2	C	cl21561	Class_B
GSLYST00021398001	superfamily	328797	44	154	2.37E-13	64.9651	cl21561	7tm_4 superfamily	C	-	Class_B
GSLYST00021398001	superfamily	333717	47	136	1.36E-17	76.5326	cl28897	7tm_GPCRs superfamily	C	-	Class_B
GSLYST00021398001	non-specific	320556	47	136	1.36E-17	76.5326	cl15440	7tmB2_latrophilin-like_invertebrate	C	cl28897	Class_B
GSLYST00021398001	non-specific	197639	6	35	0.00144507	34.6706	smart00303	GPS	N	cl02559	Class_B
GSLYST00021398001	superfamily	321989	6	35	0.00144507	34.6706	cl02559	GPS superfamily	N	-	Class_B
GSLYST00021790001	specific	306508	540	777	2.49E-69	232.142	pfam00002	7tm_2	-	cl21561	Class_B
GSLYST00021790001	superfamily	328797	540	777	2.49E-69	232.142	cl21561	7tm_4 superfamily	-	-	Class_B
GSLYST00021790001	superfamily	333717	539	797	5.42E-137	415.893	cl28897	7tm_GPCRs superfamily	-	-	Class_B
GSLYST00021790001	specific	320556	539	797	5.42E-137	415.893	cd15440	7tmB2_latrophilin-like_invertebrate	-	cl28897	Class_B
GSLYST00021790001	specific	197639	482	529	1.68E-17	77.0426	smart00303	GPS	-	cl02559	Class_B
GSLYST00021790001	specific	307782	482	526	2.46E-17	76.2514	pfam01825	GPS	-	cl02559	Class_B
GSLYST00021790001	superfamily	321989	482	529	1.68E-17	77.0426	cl02559	GPS superfamily	-	-	Class_B
GSLYST00021790001	specific	214468	156								

GSLYST00022112001	superfamily	328797	1	89	1.87E-13	62.6539	cl21561	7tm_4 superfamily	NC	-	Class_B
GSLYST00022112001	superfamily	333717	1	89	2.92E-19	78.1384	cl28897	7tm_GPCRs superfamily	NC	-	Class_B
GSLYST00022112001	non-specific	320599	1	89	2.92E-19	78.1384	cd15933	7tmB2_GPR133-like_Adhesion_V	NC	d128897	Class_B
GSLYST00022150001	non-specific	306508	1	67	6.16E-06	41.0828	pfam00002	7tm_2	NC	d121561	Class_B
GSLYST00022150001	superfamily	328797	1	67	6.16E-06	41.0828	cl21561	7tm_4 superfamily	NC	-	Class_B
GSLYST00022150001	superfamily	333717	1	66	1.01E-11	57.2726	cl28897	7tm_GPCRs superfamily	NC	-	Class_B
GSLYST00022150001	non-specific	320556	1	66	1.01E-11	57.2726	cd15440	7tmB2_Latrophilin-like_invertebrate	NC	d128897	Class_B
GSLYST00000580001	superfamily	333717	381	628	1.08E-87	275.631	cl28897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00000580001	specific	320420	381	628	1.08E-87	275.631	cd15293	7tmC_GPR158-like	-	d128897	Class_C
GSLYST00000580001	specific	214542	270	321	0.00696773	34.53	smarT00179	EGF_CA	-	d121504	Class_C
GSLYST00000580001	non-specific	311536	270	320	0.00541751	35.0211	pfam07645	EGF_CA	C	d121504	Class_C
GSLYST00000580001	superfamily	328759	270	320	0.00541751	35.0211	cl21504	EGF_CA superfamily	C	-	Class_C
GSLYST00000580001	specific	306509	540	624	1.52E-12	64.1209	pfam00003	7tm_3	N	cl02802	Class_C
GSLYST00000580001	superfamily	306509	540	624	1.52E-12	64.1209	cl02802	7tm_3 superfamily	N	-	Class_C
GSLYST00000807001	specific	320091	383	625	2.61E-43	156.243	cd13953	7tm_classC_mGluR-like	-	d128897	Class_C
GSLYST00000807001	superfamily	333717	383	625	2.61E-43	156.243	cl28897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00000807001	specific	306509	544	624	2.88E-12	63.3505	pfam00003	7tm_3	N	cl02802	Class_C
GSLYST00000807001	superfamily	306509	544	624	2.88E-12	63.3505	cl02802	7tm_3 superfamily	N	-	Class_C
GSLYST00000807001	non-specific	107370	119	267	2.52E-06	50.1527	cd06375	PBP1_mGluR_group1	N	d10011	Class_C
GSLYST00000807001	superfamily	324556	119	267	2.52E-06	50.1527	cl10011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00000853001	specific	306509	109	194	2.23E-16	73.3657	pfam00003	7tm_3	N	cl02802	Class_C
GSLYST00000853001	superfamily	306509	109	194	2.23E-16	73.3657	cl02802	7tm_3 superfamily	N	-	Class_C
GSLYST00000853001	superfamily	333717	1	197	2.18E-93	277.557	cl28897	7tm_GPCRs superfamily	N	-	Class_C
GSLYST00000853001	specific	320420	1	197	2.18E-93	277.557	cd15293	7tmC_GPR158-like	N	d128897	Class_C
GSLYST00000854001	superfamily	333717	125	155	0.000198054	39.8893	cl28897	7tm_GPCRs superfamily	C	-	Class_C
GSLYST00000854001	non-specific	320420	125	155	0.000198054	39.8893	cd15293	7tmC_GPR158-like	C	d128897	Class_C
GSLYST00001391001	superfamily	333717	1	53	4.86E-07	43.3178	cl28897	7tm_GPCRs superfamily	N	-	Class_C
GSLYST00001391001	non-specific	320175	1	53	4.86E-07	43.3178	cd15047	7tmC_GABA-B-like	N	d128897	Class_C
GSLYST00001392001	superfamily	333717	3	100	1.49E-28	103.024	cl28897	7tm_GPCRs superfamily	C	-	Class_C
GSLYST00001392001	non-specific	320175	3	100	1.49E-28	103.024	cd15047	7tmC_GABA-B-like	C	d128897	Class_C
GSLYST00001393001	superfamily	333717	9	61	2.14E-06	42.1622	cl28897	7tm_GPCRs superfamily	N	-	Class_C
GSLYST00001393001	non-specific	320175	9	61	2.14E-06	42.1622	cd15047	7tmC_GABA-B-like	N	d128897	Class_C
GSLYST00001475001	specific	320091	543	809	8.79E-58	197.459	cd13953	7tm_classC_mGluR-like	-	d128897	Class_C
GSLYST00001475001	superfamily	333717	543	809	8.79E-58	197.459	cl28897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00001475001	specific	307306	56	423	1.15E-37	143.272	pfam01094	ANF_receptor	-	d127603	Class_C
GSLYST00001475001	superfamily	307306	56	423	1.15E-37	143.272	cl27603	ANF_receptor superfamily	-	-	Class_C
GSLYST00001475001	specific	311495	472	521	7.23E-13	63.4118	pfam07562	NCD3G	-	cl08456	Class_C
GSLYST00001475001	superfamily	311495	472	521	7.23E-13	63.4118	cl08456	NCD3G superfamily	-	-	Class_C
GSLYST00001475001	non-specific	107357	29	431	9.08E-79	261.023	cd06362	PBP1_mGluR	-	d10011	Class_C
GSLYST00001475001	superfamily	324556	29	431	9.08E-79	261.023	cl10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00001475001	specific	306509	726	808	2.25E-18	81.0697	pfam00003	7tm_3	N	cl02802	Class_C
GSLYST00001475001	superfamily	306509	726	808	2.25E-18	81.0697	cl02802	7tm_3 superfamily	N	-	Class_C
GSLYST00001475001	specific	223755	105	317	2.23E-15	78.2497	COG0683	LivK	N	d10011	Class_C
GSLYST00001476001	specific	307306	39	435	6.70E-53	184.488	pfam01094	ANF_receptor	-	d127603	Class_C
GSLYST00001476001	superfamily	307306	39	435	6.70E-53	184.488	cl27603	ANF_receptor superfamily	-	-	Class_C
GSLYST00001476001	specific	223755	112	433	1.59E-09	60.1453	COG0683	LivK	-	d10011	Class_C
GSLYST00001476001	specific	311495	468	517	1.78E-11	59.1747	pfam07562	NCD3G	-	cl08456	Class_C
GSLYST00001476001	superfamily	311495	468	517	1.78E-11	59.1747	cl08456	NCD3G superfamily	-	-	Class_C
GSLYST00001476001	non-specific	107357	5	434	2.62E-95	301.084	cd06362	PBP1_mGluR	-	d10011	Class_C
GSLYST00001476001	superfamily	324556	5	434	2.62E-95	301.084	cl10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00001476001	non-specific	320091	540	664	4.43E-30	118.878	cd13953	7tm_classC_mGluR-like	C	d128897	Class_C
GSLYST00001476001	superfamily	333717	540	664	4.43E-30	118.878	cl28897	7tm_GPCRs superfamily	C	-	Class_C
GSLYST00005217001	specific	307306	53	443	1.67E-42	156.368	pfam01094	ANF_receptor	-	d127603	Class_C
GSLYST00005217001	superfamily	307306	53	443	1.67E-42	156.368	cl27603	ANF_receptor superfamily	-	-	Class_C
GSLYST00005217001	specific	223755	107	450	1.72E-06	50.5153	COG0683	LivK	-	d10011	Class_C
GSLYST00005217001	specific	311495	494	543	4.39E-12	61.1006	pfam07562	NCD3G	-	cl08456	Class_C
GSLYST00005217001	superfamily	311495	494	543	4.39E-12	61.1006	cl08456	NCD3G superfamily	-	-	Class_C
GSLYST00005217001	non-specific	107357	19	446	4.96E-93	295.691	cd06362	PBP1_mGluR	-	d10011	Class_C
GSLYST00005217001	superfamily	324556	19	446	4.96E-93	295.691	cl10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00005217001	non-specific	320091	595	690	6.93E-26	106.937	cd13953	7tm_classC_mGluR-like	C	d128897	Class_C
GSLYST00005217001	superfamily	333717	595	690	6.93E-26	106.937	cl28897	7tm_GPCRs superfamily	C	-	Class_C
GSLYST00005791001	specific	306509	577	667	1.01E-27	107.263	pfam00003	7tm_3	-	cl02802	Class_C
GSLYST00005791001	superfamily	306509	577	667	1.01E-27	107.263	cl02802	7tm_3 superfamily	-	-	Class_C
GSLYST00005791001	superfamily	333717	418	670	2.85E-145	422.792	cl28897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00005791001	specific	320600	418	670	2.85E-145	422.792	cd15934	7tmC_mGluRs_group2_3	-	d128897	Class_C
GSLYST00005791001	specific	311495	351	398	1.44E-15	70.7306	pfam07562	NCD3G	-	cl08456	Class_C
GSLYST00005791001	superfamily	311495	351	398	1.44E-15	70.7306	cl08456	NCD3G superfamily	-	-	Class_C
GSLYST00005791001	specific	307306	8	313	2.89E-49	174.858	pfam01094	ANF_receptor	N	d127603	Class_C
GSLYST00005791001	superfamily	307306	8	313	2.89E-49	174.858	cl27603	ANF_receptor superfamily	N	-	Class_C
GSLYST00005791001	non-specific	107357	2	337	3.62E-147	435.519	cd06362	PBP1_mGluR	N	d10011	Class_C
GSLYST00005791001	superfamily	324556	2	337	3.62E-147	435.519	cl10011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00005791001	specific	223755	10	172	1.51E-10	63.2269	COG0683	LivK	NC	d10011	Class_C
GSLYST00007018001	specific	320091	552	801	1.43E-59	203.237	cd13953	7tm_classC_mGluR-like	-	d128897	Class_C
GSLYST00007018001	superfamily	333717	552	801	1.43E-59	203.237	cl28897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00007018001	specific	307306	46	442	1.13E-54	191.807	pfam01094	ANF_receptor	-	d127603	Class_C
GSLYST00007018001	superfamily	307306	46	442	1.13E-54	191.807	cl27603	ANF_receptor superfamily	-	-	Class_C
GSLYST00007018001	specific	223755	84	451	6.10E-14	74.0125	COG0683	LivK	-	d10011	Class_C
GSLYST00007018001	specific	311495	481	530	8.16E-15	68.8046	pfam07562	NCD3G	-	cl08456	Class_C
GSLYST00007018001	superfamily	311495	481	530	8.16E-15	68.8046	cl08456	NCD3G superfamily	-	-	Class_C
GSLYST00007018001	non-specific	107357	13	439	2.27E-99	317.262	cd06362	PBP1_mGluR	-	d10011	Class_C
GSLYST00007018001	superfamily	324556	13	439	2.27E-99	317.262	cl10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00007018001	specific	306509	718	800	1.11E-21	90.6996	pfam00003	7tm_3	N	cl02802	Class_C
GSLYST00007018001	superfamily	306509	718	800	1.11E-21	90.6996	cl02802	7tm_3 superfamily	N	-	Class_C
GSLYST00007018001	superfamily	328932	483	541	0.00302911	38.9951	cl28855	TNFRSF superfamily	N	-	Class_C
GSLYST00007018001	non-specific	276903	483	541	0.00302911	38.9951	cd10577	TNFRSF1B	N	d122855	Class_C
GSLYST00007621001	specific	133033	1085	1451	3.09E-90	293.445	cd04190	Chitin_synth_C	-	cl11394	Class_C
GSLYST00007621001	superfamily	325014	1085	1451	3.09E-90	293.445	cl11394	Glyco_tranf_GTA_type superfamily	-	-	Class_C
GSLYST00007621001	superfamily	333717	1476	1613	0.00717179	40.2362	cl28897	7tm_GPCRs superfamily	N	-	Class_C
GSLYST00007621001	non-specific	320175	1476	1613	0.00717179	40.2362	cd15047	7tmC_GABA-B-like	N	d128897	Class_C
GSLYST00007621001	specific	224136	1287	1626	3.22E-17	86.5297	COG1215	BcsA	N	cl26112	Class_C
GSLYST00007621001	superfamily	330933	1287	1626	3.22E-17	86.5297	cl26112	Glyco_tranf_2_3 superfamily	N	-	Class_C
GSLYST00007621001	superfamily	330933	1294	1528	7.48E-07	53.7856	cl26112	Glyco_tranf_2_3 superfamily	N	-	Class_C
GSLYST00007621001	non-specific	275076	1290	1497	1.37E-12	71.6907	TIGR04242	nodulat_NodC	N	d126109	Class_C
GSLYST00007621001	non-specific	236171	1482	1591	0.00913813	40.837	PRK08168	PRK08168	N	d127656	Class_C
GSLYST00007621001	non-specific	236882	1294	1528	7.48E-07	53.7856	PRK11204	PRK11204	N	d126112	Class_C
GSLYST00007621001	superfamily	332477	1482	1591	0.00913813	40.837	cl27656	Proton_antipo_N superfamily	N	-	Class_C
GSLYST00007621001	non-specific	308649	1275	1456	8.65E-23	104.833	pfam03142	Chitin_synth_2	NC	d126109	Class_C
GSLYST00007621001	superfamily	330930	1275	1456	8.65E-23	104.833	cl26109	Chitin_synth_2 superfamily	NC	-	Class_C
GSLYST00007621001	non-specific	308925	1481	1610	0.0						

GSLYST00007723001	superfamily	324556	1519	1984	1.81E-62	221.733	c10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00007723001	superfamily	324556	46	522	9.03E-53	193.613	c10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00007723001	superfamily	324556	565	995	1.34E-51	190.147	c10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00007723001	superfamily	324556	2038	2494	3.24E-51	188.991	c10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00007723001	superfamily	324556	1046	1446	1.15E-48	181.287	c10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00007723001	non-specific	307306	597	800	1.06E-14	77.7876	pfam01094	ANF_receptor	C	d127603	Class_C
GSLYST00007723001	superfamily	307306	597	800	1.06E-14	77.7876	ct27603	ANF_receptor superfamily	C	-	Class_C
GSLYST00007723001	specific	223755	1547	1750	6.69E-09	60.5305	COG0683	LivK	C	d10011	Class_C
GSLYST00007723001	specific	223755	1046	1274	2.56E-08	58.6045	COG0683	LivK	C	d10011	Class_C
GSLYST00007723001	non-specific	237959	133	241	0.00279038	42.7008	PRK15404	PRK15404	C	d10011	Class_C
GSLYST00007723001	specific	223755	145	287	1.14E-10	65.9233	COG0683	LivK	NC	d10011	Class_C
GSLYST00007723001	specific	223755	2138	2333	1.97E-05	49.3597	COG0683	LivK	NC	d10011	Class_C
GSLYST00007723001	specific	223755	665	793	0.000908209	43.967	COG0683	LivK	NC	d10011	Class_C
GSLYST00008612001	specific	306509	919	1016	3.30E-22	93.0108	pfam00003	7tm_3	-	ct02802	Class_C
GSLYST00008612001	superfamily	306509	919	1016	3.30E-22	93.0108	ct02802	7tm_3 superfamily	-	-	Class_C
GSLYST00008612001	superfamily	333717	771	1019	1.00E-131	408.564	ct28897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00008612001	specific	320412	771	1019	1.00E-131	408.564	cd15285	7tm_mGluR_group1	-	d128897	Class_C
GSLYST00008612001	specific	307306	216	646	2.57E-69	235.719	pfam01094	ANF_receptor	-	ct27603	Class_C
GSLYST00008612001	superfamily	307306	216	646	2.57E-69	235.719	ct27603	ANF_receptor superfamily	-	-	Class_C
GSLYST00008612001	specific	311495	691	740	2.63E-14	68.4194	pfam07562	NCD3G	-	d108456	Class_C
GSLYST00008612001	superfamily	311495	691	740	2.63E-14	68.4194	ct08456	NCD3G superfamily	-	-	Class_C
GSLYST00008612001	specific	107357	182	673	0	611.17	cd06362	PBP1_mGluR	-	d10011	Class_C
GSLYST00008612001	superfamily	324556	182	673	0	611.17	ct10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00008612001	specific	223755	302	525	9.12E-15	77.8645	COG0683	LivK	NC	d10011	Class_C
GSLYST00009087001	specific	306509	32	114	4.43E-15	66.4321	pfam00003	7tm_3	N	ct02802	Class_C
GSLYST00009087001	superfamily	306509	32	114	4.43E-15	66.4321	ct02802	7tm_3 superfamily	N	-	Class_C
GSLYST00009087001	superfamily	333717	8	119	4.61E-55	173.767	ct28897	7tm_GPCRs superfamily	N	-	Class_C
GSLYST00009087001	non-specific	320421	8	119	4.61E-55	173.767	cd15294	7tmC_GABA-B-R2	N	d128897	Class_C
GSLYST00009472001	superfamily	333717	81	323	6.94E-132	375.43	ct28897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00009472001	specific	320173	81	323	6.94E-132	375.43	cd15045	7tmC_mGluRs	-	d128897	Class_C
GSLYST00009472001	specific	311495	2	51	1.02E-07	47.6187	pfam07562	NCD3G	-	d108456	Class_C
GSLYST00009472001	superfamily	311495	2	51	1.02E-07	47.6187	ct08456	NCD3G superfamily	-	-	Class_C
GSLYST00009472001	specific	306509	234	320	9.95E-24	93.396	pfam00003	7tm_3	N	ct02802	Class_C
GSLYST00009472001	superfamily	306509	234	320	9.95E-24	93.396	ct02802	7tm_3 superfamily	N	-	Class_C
GSLYST00009734001	superfamily	333717	285	544	1.91E-86	267.889	ct28897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00009734001	specific	320175	285	544	1.91E-86	267.889	cd15047	7tmC_GABA-B-like	-	d128897	Class_C
GSLYST00009734001	specific	306509	462	544	2.14E-14	69.1285	pfam00003	7tm_3	N	ct02802	Class_C
GSLYST00009734001	superfamily	306509	462	544	2.14E-14	69.1285	ct02802	7tm_3 superfamily	N	-	Class_C
GSLYST00009734001	non-specific	307306	1	237	1.85E-10	61.9944	pfam01094	ANF_receptor	N	ct27603	Class_C
GSLYST00009734001	superfamily	307306	1	237	1.85E-10	61.9944	ct27603	ANF_receptor superfamily	N	-	Class_C
GSLYST00009734001	non-specific	107361	8	234	5.17E-18	85.3913	cd06366	PBP1_GABAB_receptor	N	-	Class_C
GSLYST00009734001	superfamily	324556	8	234	5.17E-18	85.3913	ct10011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00011784001	specific	306509	1	23	0.000728487	39.4681	pfam00003	7tm_3	N	ct02802	Class_C
GSLYST00011784001	superfamily	306509	1	23	0.000728487	39.4681	ct02802	7tm_3 superfamily	N	-	Class_C
GSLYST00011784001	superfamily	333717	3	27	0.000236745	43.3178	ct28897	7tm_GPCRs superfamily	N	-	Class_C
GSLYST00011784001	non-specific	320175	3	27	0.000236745	43.3178	cd15047	7tmC_GABA-B-like	N	d128897	Class_C
GSLYST00015156001	non-specific	320091	2506	2728	8.24E-31	123.116	cd13953	7tm_classC_mGluR-like	-	ct28897	Class_C
GSLYST00015156001	superfamily	333717	2506	2728	8.24E-31	123.116	ct28897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00015156001	specific	307306	91	462	2.56E-29	120.93	pfam01094	ANF_receptor	-	ct27603	Class_C
GSLYST00015156001	non-specific	307306	1042	1418	2.50E-22	100.129	pfam01094	ANF_receptor	-	ct27603	Class_C
GSLYST00015156001	superfamily	307306	91	462	2.56E-29	120.93	ct27603	ANF_receptor superfamily	-	-	Class_C
GSLYST00015156001	superfamily	307306	1042	1418	2.50E-22	100.129	ct27603	ANF_receptor superfamily	-	-	Class_C
GSLYST00015156001	non-specific	107357	1467	1884	3.50E-73	252.934	cd06362	PBP1_mGluR	-	d10011	Class_C
GSLYST00015156001	non-specific	107357	42	485	5.34E-52	191.302	cd06362	PBP1_mGluR	-	d10011	Class_C
GSLYST00015156001	non-specific	107357	530	965	3.00E-43	165.494	cd06362	PBP1_mGluR	-	d10011	Class_C
GSLYST00015156001	non-specific	107357	1006	1433	2.31E-40	157.019	cd06362	PBP1_mGluR	-	d10011	Class_C
GSLYST00015156001	non-specific	107357	1971	2325	5.13E-17	86.5279	cd06362	PBP1_mGluR	-	d10011	Class_C
GSLYST00015156001	superfamily	324556	1467	1884	3.50E-73	252.934	ct10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00015156001	superfamily	324556	42	485	5.34E-52	191.302	ct10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00015156001	superfamily	324556	530	965	3.00E-43	165.494	ct10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00015156001	superfamily	324556	1006	1433	2.31E-40	157.019	ct10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00015156001	superfamily	324556	1971	2325	5.13E-17	86.5279	ct10011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00015156001	specific	307306	1497	1713	7.12E-26	110.915	pfam01094	ANF_receptor	C	d127603	Class_C
GSLYST00015156001	non-specific	307306	560	778	2.62E-18	88.5732	pfam01094	ANF_receptor	C	d127603	Class_C
GSLYST00015156001	superfamily	307306	2065	2202	2.67E-05	48.5125	pfam01094	ANF_receptor superfamily	C	ct27603	Class_C
GSLYST00015156001	superfamily	307306	2065	2202	2.67E-05	48.5125	ct27603	ANF_receptor superfamily	C	-	Class_C
GSLYST00015156001	specific	223755	619	822	3.62E-10	64.3825	COG0683	LivK	C	d10011	Class_C
GSLYST00015156001	specific	223755	2047	2206	0.00104872	43.967	COG0683	LivK	C	d10011	Class_C
GSLYST00015156001	specific	223755	137	471	8.65E-06	50.5153	COG0683	LivK	N	d10011	Class_C
GSLYST00015156001	specific	223755	1564	1742	2.19E-08	58.6045	COG0683	LivK	NC	d10011	Class_C
GSLYST00015156001	specific	223755	1108	1243	1.19E-06	53.2117	COG0683	LivK	NC	d10011	Class_C
GSLYST00016294001	specific	311495	307	358	4.24E-08	49.1595	pfam07562	NCD3G	-	d108456	Class_C
GSLYST00016294001	superfamily	311495	307	358	4.24E-08	49.1595	ct08456	NCD3G superfamily	-	-	Class_C
GSLYST00016294001	non-specific	320091	380	512	2.67E-23	98.8481	cd13953	7tm_classC_mGluR-like	C	d128897	Class_C
GSLYST00016294001	superfamily	333717	380	512	2.67E-23	98.8481	ct28897	7tm_GPCRs superfamily	C	-	Class_C
GSLYST00016294001	non-specific	307306	1	256	8.21E-11	63.15	pfam01094	ANF_receptor	N	ct27603	Class_C
GSLYST00016294001	superfamily	307306	1	256	8.21E-11	63.15	ct27603	ANF_receptor superfamily	N	-	Class_C
GSLYST00016294001	non-specific	107357	19	259	1.97E-17	84.6019	cd06362	PBP1_mGluR	N	d10011	Class_C
GSLYST00016294001	superfamily	324556	19	259	1.97E-17	84.6019	ct10011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00016626001	specific	306509	539	622	5.55E-07	48.3277	pfam00003	7tm_3	-	ct02802	Class_C
GSLYST00016626001	superfamily	306509	539	622	5.55E-07	48.3277	ct02802	7tm_3 superfamily	-	-	Class_C
GSLYST00016626001	non-specific	320091	376	629	1.20E-22	97.6925	cd13953	7tm_classC_mGluR-like	-	d128897	Class_C
GSLYST00016626001	superfamily	333717	376	629	1.20E-22	97.6925	ct28897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00016626001	specific	311495	308	353	5.88E-09	52.2411	pfam07562	NCD3G	-	d108456	Class_C
GSLYST00016626001	superfamily	311495	308	353	5.88E-09	52.2411	ct08456	NCD3G superfamily	-	-	Class_C
GSLYST00016626001	non-specific	307306	3	250	1.14E-12	69.3132	pfam01094	ANF_receptor	N	ct27603	Class_C
GSLYST00016626001	superfamily	307306	3	250	1.14E-12	69.3132	ct27603	ANF_receptor superfamily	N	-	Class_C
GSLYST00016626001	non-specific	107357	4	250	1.59E-19	91.9207	cd06362	PBP1_mGluR	N	d10011	Class_C
GSLYST00016626001	superfamily	324556	4	250	1.59E-19	91.9207	ct10011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00016627001	non-specific	307306	3	300	2.35E-18	85.8768	pfam01094	ANF_receptor	-	ct27603	Class_C
GSLYST00016627001	superfamily	307306	3	300	2.35E-18	85.8768	ct27603	ANF_receptor superfamily	-	-	Class_C
GSLYST00016627001	specific	311495	359	405	1.60E-07	47.6187	pfam07562	NCD3G	-	d108456	Class_C
GSLYST00016627001	superfamily	311495	359	405	1.60E-07	47.6187	ct08456	NCD3G superfamily	-	-	Class_C
GSLYST00016627001	non-specific	320091	431	556	2.00E-09	58.0169	cd13953	7tm_classC_mGluR-like	C	d128897	Class_C
GSLYST00016627001	superfamily	333717	431	556	2.00E-09	58.0169	ct28897	7tm_GPCRs superfamily	C	-	Class_C
GSLYST00016627001	non-specific	107357	2	293	5.21E-24	104.632	cd06362	PBP1_mGluR	N	d10011	Class_C
GSLYST00016627001	superfamily	324556	2	293	5.21E-24	104.632	ct10011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00016628001	specific	320091	388	634	2.90E-37	138.909	cd13953	7tm_classC_mGluR-like	-	d128897	Class_C
GSLYST00016628001	superfamily	333717	388	634	2.90E-37	138.9					

GSLYST00016629001	superfamily	324556	14	302	3.06E-27	114.647	c10011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00016630001	non-specific	307306	10	323	3.34E-17	82.41	pfam01094	ANF_receptor	-	c127603	Class_C
GSLYST00016630001	superfamily	307306	10	323	3.34E-17	82.41	c127603	ANF_receptor superfamily	-	-	Class_C
GSLYST00016630001	specific	311495	368	413	1.20E-07	48.0039	pfam07562	NCD3G	-	c108456	Class_C
GSLYST00016630001	superfamily	311495	368	413	1.20E-07	48.0039	c108456	NCD3G superfamily	-	-	Class_C
GSLYST00016630001	superfamily	333717	438	560	6.72E-20	89.2269	c128897	7tm_GPCRs superfamily	C	-	Class_C
GSLYST00016630001	non-specific	320173	438	560	6.72E-20	89.2269	cd15045	7tm_mGluRs	C	c128897	Class_C
GSLYST00016630001	specific	223755	10	78	0.00012989	44.3522	COG0683	LivK	C	c110011	Class_C
GSLYST00016630001	non-specific	107357	14	302	5.23E-28	116.573	cd06362	PBP1_mGluR	N	c110011	Class_C
GSLYST00016630001	superfamily	324556	14	302	5.23E-28	116.573	c110011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00016631001	non-specific	307306	1	312	1.49E-21	95.5068	pfam01094	ANF_receptor	-	c127603	Class_C
GSLYST00016631001	superfamily	307306	1	312	1.49E-21	95.5068	c127603	ANF_receptor superfamily	-	-	Class_C
GSLYST00016631001	specific	311495	358	403	7.16E-07	46.0779	pfam07562	NCD3G	-	c108456	Class_C
GSLYST00016631001	superfamily	311495	358	403	7.16E-07	46.0779	c108456	NCD3G superfamily	-	-	Class_C
GSLYST00016631001	non-specific	320091	426	550	2.01E-19	87.6773	cd13953	7tm_classC_mGluR-like	C	c128897	Class_C
GSLYST00016631001	superfamily	333717	426	550	2.01E-19	87.6773	c128897	7tm_GPCRs superfamily	C	-	Class_C
GSLYST00016631001	non-specific	107357	4	312	6.33E-30	122.351	cd06362	PBP1_mGluR	N	c110011	Class_C
GSLYST00016631001	superfamily	324556	4	312	6.33E-30	122.351	c110011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00016631001	specific	223755	4	97	9.44E-07	50.9005	COG0683	LivK	NC	c110011	Class_C
GSLYST00016725001	specific	311495	310	358	2.31E-07	47.2335	pfam07562	NCD3G	-	c108456	Class_C
GSLYST00016725001	superfamily	311495	310	358	2.31E-07	47.2335	c108456	NCD3G superfamily	-	-	Class_C
GSLYST00016725001	non-specific	320091	383	476	1.53E-14	73.0397	cd13953	7tm_classC_mGluR-like	C	c128897	Class_C
GSLYST00016725001	superfamily	333717	383	476	1.53E-14	73.0397	c128897	7tm_GPCRs superfamily	C	-	Class_C
GSLYST00016725001	non-specific	307306	2	172	4.00E-07	51.5941	pfam01094	ANF_receptor	N	c127603	Class_C
GSLYST00016725001	superfamily	307306	2	172	4.00E-07	51.5941	c127603	ANF_receptor superfamily	N	-	Class_C
GSLYST00016725001	specific	153137	2	137	5.53E-13	69.0812	cd06269	PBP1_glutamate_receptors_like	N	c110011	Class_C
GSLYST00016725001	superfamily	324556	2	137	5.53E-13	69.0812	c110011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00016725001	non-specific	276900	315	370	0.00398225	36.4183	cd00185	TNFRSF	N	c122855	Class_C
GSLYST00016725001	superfamily	328932	315	370	0.00398225	36.4183	c12855	TNFRSF superfamily	N	-	Class_C
GSLYST00016726001	non-specific	320091	428	637	2.61E-32	125.042	cd13953	7tm_classC_mGluR-like	C	c128897	Class_C
GSLYST00016726001	superfamily	333717	428	637	2.61E-32	125.042	c128897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00016726001	non-specific	307306	10	243	0.00221961	40.4233	pfam01094	ANF_receptor	-	c127603	Class_C
GSLYST00016726001	superfamily	307306	10	243	0.00221961	40.4233	c127603	ANF_receptor superfamily	-	-	Class_C
GSLYST00016726001	specific	311495	359	400	1.55E-06	45.3075	pfam07562	NCD3G	-	c108456	Class_C
GSLYST00016726001	superfamily	311495	359	400	1.55E-06	45.3075	c108456	NCD3G superfamily	-	-	Class_C
GSLYST00016726001	non-specific	107357	4	293	1.18E-08	57.6379	cd06362	PBP1_mGluR	N	c110011	Class_C
GSLYST00016726001	superfamily	324556	4	293	1.18E-08	57.6379	c110011	Periplasmic_Binding_Protein_Type_1 superfamily	N	-	Class_C
GSLYST00016726001	specific	306509	591	637	7.61E-08	50.6389	pfam00003	7tm_3	NC	c102802	Class_C
GSLYST00016726001	superfamily	306509	591	637	7.61E-08	50.6389	c102802	7tm_3 superfamily	NC	-	Class_C
GSLYST00017437001	specific	320091	566	841	1.61E-42	155.472	cd13953	7tm_classC_mGluR-like	-	c128897	Class_C
GSLYST00017437001	superfamily	333717	566	841	1.61E-42	155.472	c128897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00017437001	non-specific	307306	88	276	1.77E-07	53.9053	pfam01094	ANF_receptor	C	c127603	Class_C
GSLYST00017437001	superfamily	307306	88	276	1.77E-07	53.9053	c127603	ANF_receptor superfamily	C	-	Class_C
GSLYST00017437001	non-specific	153138	52	293	4.49E-17	83.5744	cd06350	PBP1_GPCR_family_C_like	C	c110011	Class_C
GSLYST00017437001	superfamily	324556	52	293	4.49E-17	83.5744	c110011	Periplasmic_Binding_Protein_Type_1 superfamily	C	-	Class_C
GSLYST00017437001	specific	306509	749	837	1.26E-08	53.3353	pfam00003	7tm_3	N	c102802	Class_C
GSLYST00017437001	superfamily	306509	749	837	1.26E-08	53.3353	c102802	7tm_3 superfamily	N	-	Class_C
GSLYST00017437001	non-specific	314458	302	356	0.00101577	40.3498	pfam11568	Med29	N	c113081	Class_C
GSLYST00017437001	superfamily	314458	302	356	0.00101577	40.3498	c113081	Med29 superfamily	N	-	Class_C
GSLYST00021081001	specific	306509	673	762	4.82E-22	91.8552	pfam00003	7tm_3	-	c102802	Class_C
GSLYST00021081001	superfamily	306509	673	762	4.82E-22	91.8552	c102802	7tm_3 superfamily	-	-	Class_C
GSLYST00021081001	specific	333717	494	765	5.24E-138	412.884	c128897	7tm_GPCRs superfamily	-	-	Class_C
GSLYST00021081001	superfamily	320418	494	765	5.24E-138	412.884	cd15291	7tmC_GABA-B-R1	-	c128897	Class_C
GSLYST00021081001	specific	307306	90	446	1.56E-60	208.755	pfam01094	ANF_receptor	-	c127603	Class_C
GSLYST00021081001	superfamily	307306	90	446	1.56E-60	208.755	c127603	ANF_receptor superfamily	-	-	Class_C
GSLYST00021081001	specific	223755	69	451	2.72E-17	84.4129	COG0683	LivK	-	c110011	Class_C
GSLYST00021081001	superfamily	107361	74	467	1.55E-123	378.143	cd06366	PBP1_GABAb_receptor	-	c110011	Class_C
GSLYST00021081001	non-specific	324556	74	467	1.55E-123	378.143	c110011	Periplasmic_Binding_Protein_Type_1 superfamily	-	-	Class_C
GSLYST00021081001	superfamily	226400	766	835	0.000396355	43.1686	COG3883	CwlO1	C	c125603	Class_C
GSLYST00021081001	non-specific	226400	766	835	0.000396355	43.1686	c125603	CwlO1 superfamily	C	-	Class_C
GSLYST00021081001	superfamily	327530	717	846	0.00241108	40.732	c119252	MreC superfamily	C	-	Class_C
GSLYST00021081001	non-specific	327560	717	846	0.00241108	40.732	PRK13922	PRK13922	C	c119252	Class_C
GSLYST00021081001	superfamily	318842	774	822	0.00116572	38.5511	pfam16716	BST2	N	c125063	Class_C
GSLYST00021081001	non-specific	318842	774	822	0.00116572	38.5511	c125063	BST2 superfamily	N	-	Class_C
GSLYST00007366001	superfamily	333717	274	333	0.000176231	42.3385	c128897	7tm_GPCRs superfamily	N	-	Class_E
GSLYST00007366001	non-specific	320094	274	333	0.000176231	42.3385	cd14940	7tmE_cAMP_R_Slime_mold	N	c128897	Class_E
GSLYST00007366001	superfamily	307974	241	331	0.0011058	40.5151	pfam02101	Ocular_alb	NC	c124143	Class_E
GSLYST00007366001	non-specific	307974	241	331	0.0011058	40.5151	c124143	Ocular_alb superfamily	NC	-	Class_E
GSLYST00011209001	specific	320095	39	311	2.76E-14	72.4366	cd14964	7tm_GPCRs	-	c128897	Class_E
GSLYST00011209001	superfamily	333717	39	311	2.76E-14	72.4366	c128897	7tm_GPCRs superfamily	-	-	Class_E
GSLYST00011209001	non-specific	283188	49	191	0.000125125	43.621	pfam05462	Dicty_CAR	C	c127462	Class_E
GSLYST00011209001	superfamily	283188	49	191	0.000125125	43.621	c127462	Dicty_CAR superfamily	C	-	Class_E
GSLYST00012669001	superfamily	328797	24	191	6.19E-12	63.4547	c121561	7tm_4 superfamily	-	-	Class_E
GSLYST00012669001	non-specific	333717	20	278	2.77E-83	252.657	c128897	7tm_GPCRs superfamily	-	-	Class_E
GSLYST00012669001	superfamily	320094	20	278	2.77E-83	252.657	cd14940	7tmE_cAMP_R_Slime_mold	-	c128897	Class_E
GSLYST00012669001	non-specific	314555	24	191	6.19E-12	63.4547	pfam11710	Git3	-	c121561	Class_E
GSLYST00004197001	superfamily	328797	196	517	3.11E-94	291.426	c121561	7tm_4 superfamily	-	-	Class_F
GSLYST00004197001	non-specific	333717	186	518	1.36E-177	505.291	c128897	7tm_GPCRs superfamily	-	-	Class_F
GSLYST00004197001	superfamily	320158	186	518	1.36E-177	505.291	cd15030	7tmF_SMO_homolog	-	c128897	Class_F
GSLYST00004197001	non-specific	321937	32	162	7.35E-56	184.493	cd02447	CRD_FZ superfamily	-	-	Class_F
GSLYST00004197001	superfamily	143560	32	162	7.35E-56	184.493	cd07451	CRD_SMO	-	c102447	Class_F
GSLYST00004197001	non-specific	214498	33	136	1.30E-26	104.315	smart00063	FRI	-	c102447	Class_F
GSLYST00004197001	superfamily	307603	196	517	3.11E-94	291.426	pfam01534	Frizzled	-	c121561	Class_F
GSLYST00004197001	non-specific	307517	33	135	1.05E-18	81.7618	pfam01392	Fz	-	c102447	Class_F
GSLYST00004507001	superfamily	328797	253	570	0	530.635	c121561	7tm_4 superfamily	-	-	Class_F
GSLYST00004507001	non-specific	333717	245	570	0	643.624	c128897	7tm_GPCRs superfamily	-	-	Class_F
GSLYST00004507001	superfamily	320162	245	570	0	643.624	cd15034	7tmF_FZD1_2_7-like	-	c128897	Class_F
GSLYST00004507001	non-specific	321937	49	164	4.45E-78	241.932	cd02447	CRD_FZ superfamily	-	-	Class_F
GSLYST00004507001	superfamily	143567	49	164	4.45E-78	241.932	cd07458	CRD_FZ1_like	-	c102447	Class_F
GSLYST00004507001	non-specific	214498	51	162	1.96E-48	164.021	smart00063	FRI	-	c102447	Class_F
GSLYST00004507001	superfamily	307603	253	570	0	530.635	pfam01534	Frizzled	-	c121561	Class_F
GSLYST00004507001	non-specific	307517	51	155	1.20E-43	151.098	pfam01392	Fz	-	c102447	Class_F
GSLYST00008596001	superfamily	328797	264	564	1.19E-163	469.774	c121561	7tm_4 superfamily	-	-	Class_F
GSLYST00008596001	non-specific	333717	256	564	0	525.098	c128897	7tm_GPCRs superfamily	-	-	Class_F
GSLYST00008596001	superfamily	320166	256	564	0	525.098	cd15038	7tmF_FZD4	-	c128897	Class_F
GSLYST00008596001	non-specific	321937	54	178	5.79E-80	248.145	cd02447	CRD_FZ superfamily	-	-	Class_F
GSLYST00008596001	superfamily	143557	54	178	5.79E-80	248.145	cd07448	CRD_F2	-	c102447	Class_F
GSLYST00008596001	non-specific	214498	56	172	5.72E-48	163.251	smart00063	FRI	-	c102447	Class_F
GSLYST00008596001	superfamily	307603	264	564	1.19E-163	469.774	pfam01534	Frizzled	-	c121561	Class_F
GSLYST00008596001</											

ST6. Orthology analyses (summary statistics) of the *L. stagnalis* predicted proteome, as performed at two distinct levels, metazoans and gastropods.

Parameter	Metazoa-level Orthology analysis	Gastropoda-level Orthology analysis
Number of species	20	14
Number of genes	600240	404265
Number of genes in orthogroups	500283	364557
Number of unassigned genes	99957	39708
Percentage of genes in orthogroups	83.3	90.2
Percentage of unassigned genes	16.7	9.8
Number of orthogroups	17669	29428
Number of species-specific orthogroups*	1947	9158
Number of genes in species-specific orthogroups	12160	41817
Percentage of genes in species-specific orthogroups	2	10.3
Mean orthogroup size	28.3	12.4
Median orthogroup size	14	7
G50 (assigned genes)	53	19
G50 (all genes)	40	18
O50 (assigned genes)	1977	5033
O50 (all genes)	3067	6101
Number of orthogroups with all species present	2312	3275
Number of single-copy orthogroups	2	154

*Orthogroups that consist entirely of genes from one species.

G50: The number of genes in the orthogroup such that 50% of genes are in orthogroups of that size or larger.

O50: The smallest number of orthogroups such that 50% of genes are in orthogroups of that size or larger.

Single-copy orthogroup: An orthogroup with exactly one gene (and no more) from each species.

Unassigned gene: A gene that has not been put into an orthogroup with any other genes.

ST7. Gastropod orthology analysis. Conserved domains associated with the main OGs exclusively contributed by euthyneuran taxa (number of proteins per species). The list is reduced to OGs containing at least 18 sequences, and present in at least 5 of 6 euthyneuran taxa (*R. auricularia* was a posteriori discarded, see text for explanation).

conserved domain	OG_14Gastropoda														
		<i>Lymnaea_stagnalis</i>	<i>Biomphalaria_glabrata</i>	<i>Bulinus_truncatus</i>	<i>Elysia_chlorotica</i>	<i>Candidula_unifaciata</i>	<i>Aplysia_californica</i>	TOTAL-EUTHYNEURA	<i>Littorina_saxatilis</i>	<i>Potamopyrgus_antipodarum</i>	<i>Pomacea_canaliculata</i>	<i>Batillaria_attramentaria</i>	<i>Lottia_gigantea</i>	<i>Gigantopelta_aegis</i>	<i>Haliotis_rubra</i>
CLECT	OG0000086	46	35	24	1	0	19	125	0	0	0	0	0	0	0
7tmA_FMRFamide_R-like	OG0000164	20	28	17	6	13	23	107	0	0	0	0	0	0	0
7tmA_FMRFamide_R-like	OG0000194	35	18	8	4	23	10	98	0	0	0	0	0	0	0
BTB, BACK,Kelch-like	OG0000263	57	9	10	0	3	2	81	0	0	0	0	0	0	0
P450_cycloAA_1	OG0000313	7	18	32	4	1	6	68	0	0	0	0	0	0	0
Aerolysin	OG0000438	12	25	14	1	0	9	61	0	0	0	0	0	0	0
7tmA_NTSR-like	OG0000474	7	22	12	1	7	10	59	0	0	0	0	0	0	0
Galactosyltransferase	OG0000590	16	14	8	0	5	11	54	0	0	0	0	0	0	0
BIR	OG0000641	17	17	9	1	1	4	49	0	0	0	0	0	0	0
IG_like	OG0000779	7	8	7	21	1	3	47	0	0	0	0	0	0	0
OATP	OG0000504	6	15	9	2	9	6	47	0	0	0	0	0	0	0
LRR_8	OG0000760	9	16	3	0	4	13	45	0	0	0	0	0	0	0
7tmA_ET_R-like	OG0000843	12	13	3	4	9	3	44	0	0	0	0	0	0	0
7tmA_FMRFamide_R-like	OG0000969	1	4	3	19	0	14	41	0	0	0	0	0	0	0
Amelogenin / Glutenin	OG0001218	23	7	5	1	2	0	38	0	0	0	0	0	0	0
7tm_classA_rhodopsin-like	OG0001291	31	1	4	0	1	0	37	0	0	0	0	0	0	0
TNFR	OG0001290	12	8	9	2	3	0	34	0	0	0	0	0	0	0
MFS_1	OG0001548	3	5	6	4	10	3	31	0	0	0	0	0	0	0
SGL / atrophin_1	OG0001383	4	8	5	2	9	2	30	0	0	0	0	0	0	0
TNF	OG0001622	8	14	5	1	1	1	30	0	0	0	0	0	0	0
no domain	OG0001447	6	10	6	3	3	0	28	0	0	0	0	0	0	0
7tmA_FMRFamide_R-like	OG0002416	7	9	4	0	1	6	27	0	0	0	0	0	0	0
7tmB3_Methuselah-like	OG0002357	1	7	6	10	2	1	27	0	0	0	0	0	0	0
CBM_14 / Glutenin_hmw / VWA	OG0002345	5	14	5	2	0	1	27	0	0	0	0	0	0	0
Fasciclin	OG0001545	6	5	6	6	0	4	27	0	0	0	0	0	0	0
no domain	OG0001574	7	10	2	5	0	3	27	0	0	0	0	0	0	0
SH3_and_anchor / DNA_pol3_γ3	OG0001940	11	8	6	0	1	1	27	0	0	0	0	0	0	0
MATH_TRAF_C	OG0002388	3	10	6	2	1	4	26	0	0	0	0	0	0	0
7tmA_FMRFamide_R-like	OG0002778	5	4	3	1	4	8	25	0	0	0	0	0	0	0
UBQ	OG0002344	2	3	3	0	4	13	25	0	0	0	0	0	0	0
no domain	OG0003169	1	19	2	1	0	1	24	0	0	0	0	0	0	0
Trypsin	OG0002794	2	6	7	2	1	6	24	0	0	0	0	0	0	0
HtrL_YibB	OG0003057	5	2	4	2	8	2	23	0	0	0	0	0	0	0
IG_like	OG0002826	4	13	3	1	1	1	23	0	0	0	0	0	0	0
EFh	OG0003457	1	5	7	5	3	1	22	0	0	0	0	0	0	0
no domain	OG0003800	4	5	11	1	0	1	22	0	0	0	0	0	0	0
Globin	OG0003205	5	8	4	2	1	0	20	0	0	0	0	0	0	0
MFS	OG0004044	1	1	1	15	0	2	20	0	0	0	0	0	0	0
Cyt_c_Oxidase_VIIC	OG0005628	3	7	6	1	1	0	18	0	0	0	0	0	0	0
HLH	OG0004461	5	7	1	2	2	1	18	0	0	0	0	0	0	0

ST8. InterProscan annotation of OG0000001 *L. stagnalis* gene predictions (139 gene predictions). In bold: annotations shared with those of OG0000121.

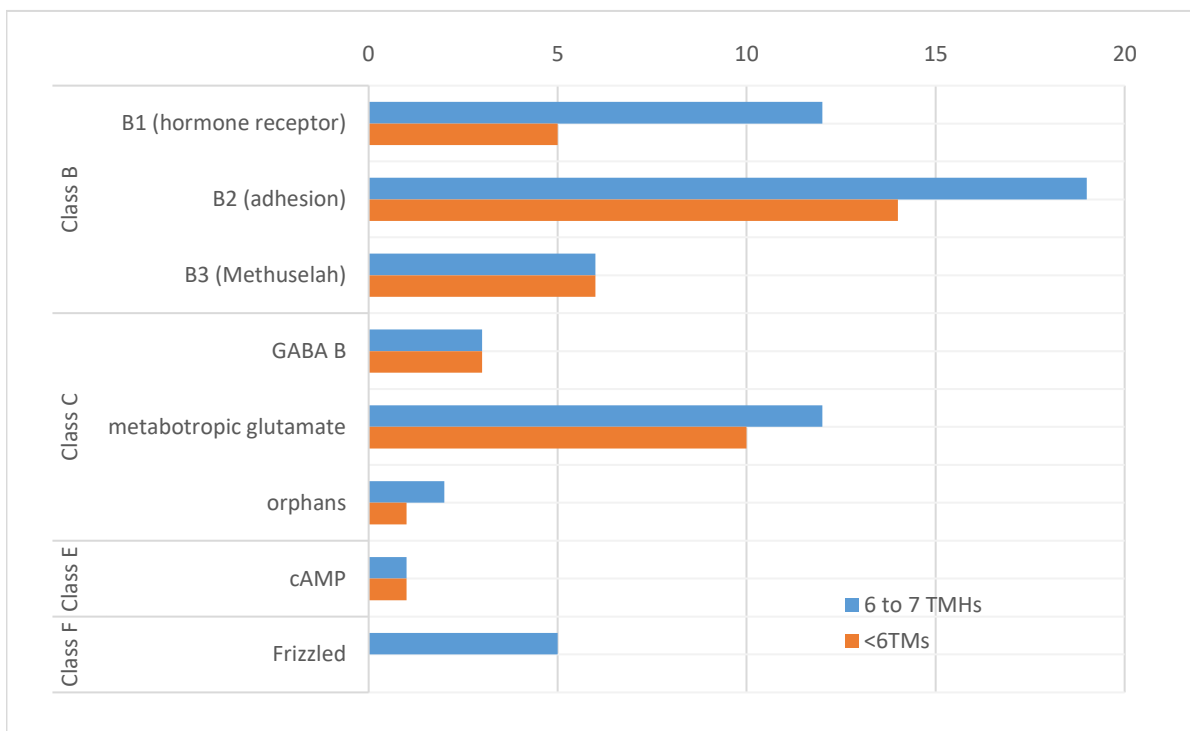
InterProscan	gene prediction number
7tm_1	139
7tmA_amine_R-like	23
7tmA_CCKR-like	7
7tmA_ETH-R	6
7tmA_GPRnna14-like	6
7tmA_Trissin_R	6
7tmA_CCK_R	5
7tmA_Adenosine_R	4
7tmA_AstA_R_insect	4
7tmA_capaR	4
7tmA_NPYR-like	4
7tmA_5-HT1A_invertebrates	3
7tmA_OXR	3
7tmA_TAARs	3
7tmA_5-HT2	2
7tmA_mAChR	2
7tmA_mAChR_GAR-2-like	2
7tmA_NPR-like_invertebrate	2
7tmA_Octopamine_R	2
7tmA_Opsin_Gq_invertebrates	2
7tmA_Opsins_type2_animals	2
7tmA_PR4-like	2
7tmA_5-HT4	1
7tmA_5-HT7	1
7tmA_alpha1_AR	1
7tmA_alpha2_AR	1
7tmA_Ap5-HTB1-like	1
7tmA_AstC_insect	1
7tmA_Bombesin_R-like	1
7tmA_D2-like_dopamine_R	1
7tmA_DmOct-betaAR-like	1
7tmA_Dop1R2-like	1
7tmA_FPR-like	1
7tmA_GPR119_R_insulinotropic_receptor	1
7tmA_GPR83	1
7tmA_GPR84-like	1
7tmA_Histamine_H1R	1
7tmA_KiSS1R	1
7tmA_Melanopsin-like	1
7tmA_NPFFR	1
7tmA_TACR	1
7tmA_TRH-R	1
HTH_XRE superfamily	1
lambda-1	1
NST1	1

ST9. Annotation of *L. stagnalis* GPCRs found organized in clusters in the genome assembly. Groups of tandem genes (clusters) are named as a function of their size (4 to 26 genes) and further numbered from 1 to n (e.g., C16-2 is the 2nd cluster of 16 genes, as based on gene prediction identifier). "a" or "b" indicates a subdivision of the group into two different GPCR classes (e.g., C06-6a: class_A and C06-6b: class_C).

Cluster	annotation	6 to 7 TMHs	< 6 TMHs	alternative or additional annotations
C26-2	7tmA_FMRFamide_R-like	13	13 (0 to 5 TMHs)	PHA02638;7tmA_TACR_family
C26-1	7tmA_FMRFamide_R-like	23	3 (2;2;4 TMHs)	
C16-2	7tmA_FMRFamide_R-like	15	1 (4 TMHs)	
C16-1	7tmA_FMRFamide_R-like	15	1 (5 TMHs)	
C14	7tmA_CCKR-like	2	12 (2 to 4 TMHs)	PHA02638;7tmA_mAChR_DM1-like;7tmA_NTSR-like;7tmA_FMRFamide_R-like
C13	7tmA_FMRFamide_R-like	12	1 (3 TMHs)	MECDP_synthase
C11	7tmA_FMRFamide_R-like	10	1 (3 TMHs)	7TM_GPCR_Srw
C09-5	7tmA_FMRFamide_R-like	8	1 (5TMHs)	7TM_GPCR_Srw
C09-4	7tmA_amine_R-like	9	0	PHA03087;PHA02638
C09-3	7tmA_FMRFamide_R-like	6	3 (2;2;4 TMHs)	
C09-2	7tmA_TAARs	7	2 (2;5 TMHs)	7tmA_FMRFamide_R-like; PHA03087
C09-1	7tmA_FMRFamide_R-like	7	2 (5 TMHs)	
		0 (but see		
C08-5	7tm_classA_rhodopsin-like	colocated transcript)	7 (2 to 4 TMHs)	PHA03087;PHA02638;7tmA_NTSR-like;7tmA_ETH-R;7tmA_BNGR-A34-like;7tmA_SSTR3;7tmA_NPYR-like;7tmA_NPFFR
C08-4	7tmA_FMRFamide_R-like	7	1 (5TMHs)	7TM_GPCR_Srw
C08-4	7tmA_amine_R-like	6	2 (3;5 TMHs)	PHA03087;PHA02638;7tmA_TAARs
C08-3	7tmA_FMRFamide_R-like	7	1 (4 TMHs)	
C08-2	7tmA_FMRFamide_R-like	7	1 (5 TMHs)	7tmF_FZD1_2_7-like;7TM_GPCR_Srw
C08-1	7tmA_FMRFamide_R-like	5	3 (4 to 5 TMHs)	PHA02638;7TM_GPCR_Srx;7TM_GPCR_Srw;
C06-8	7tm_classA_rhodopsin-like	4	2 (5TMHs)	PHA03087
C06-7	7tmA_FMRFamide_R-like	6	0	PHA02638;7TM_GPCR_Srx
C06-6b	7tm_classC_mGluR-like	1	1 (3 TMHs)	NCD3G;PBP1_mGluR
C06-6a	7tmA_FMRFamide_R-like	3	1 (4TMHs)	
C06-5	7tm_classC_mGluR-like	2	4 (3 TMHs)	NCD3G;PBP1_mGluR
C06-4	7tmA_FMRFamide_R-like	6	0	PHA03087;7TM_GPCR_Srw
C06-3	7tmA_FMRFamide_R-like	5	1 (2TMHs)	7TM_GPCR_Srw
C06-2	7tmA_AstA_R_insect	4	2 (2;5 TMHs)	PHA03087;7tmA_NPFFR;7tmA_CCKR-like
C06-1	7tmA_FMRFamide_R-like	2	4(2 to 3 TMHs)	7TM_GPCR_Srw;PHA02638
C05-6	7tm_classA_rhodopsin-like	2	3 (5 TMHs)	PHA03087; 7tmA_FMRFamide_R-like
C05-5	7tmA_amine_R-like	2	3 (4 to 5 TMHs)	PHA03087; 7tmA_FMRFamide_R-like;7TM_GPCR_Srw
C05-4	7tmA_ETH-R	0	5 (1 to 5TMHs)	7tmA_capaR; PHA03087
C05-3	7tmA_FMRFamide_R-like	5	0	PHA03087
C05-2b	7tm_classA_rhodopsin-like	0	1 (4TMHs)	
C05-2a	7tmB3_Methuselah-like	0	4 (3 to 4 TMHs)	
C05-1b	7tm_classC_mGluR-like	1	0	PBP1_mGluR_groupII
C05-1a	7tmA_FMRFamide_R-like	4	0	7TM_GPCR_Srx
C04-9b	7tmB2_Adhesion	1	1 (5TMHs)	GPS
C04-9a	7tmA_FMRFamide_R-like	1	1 (5TMHs)	7tmA_capaR;PHA03087
C04-8	7tmA_FMRFamide_R-like	4	0	7TM_GPCR_Srw
C04-7	7tmA_FMRFamide_R-like	4	0	7TM_GPCR_Srw
C04-6	7tmA_Adenosine_R	4	0	PHA03087
C04-5	7tmA_FMRFamide_R-like	3	1 (4TMHs)	PHA02638;7TM_GPCR_Srw
C04-4	7tmA_FMRFamide_R-like	3	1 (4TMHs)	PHA02638;PHA03087
C04-3	7tmA_FMRFamide_R-like	3	1 (4TMHs)	7TM_GPCR_Srx
C04-2	7tmA_FMRFamide_R-like	1	3 (4 to 5 TMHs)	
C04-14	7tm_classA_rhodopsin-like	2	2 (2;5 TMHs)	7tmA_FMRFamide_R-like; PHA03087
C04-13	7tmA_FMRFamide_R-like	2	2 (2;3 TMHs)	7tmB3_Methuselah-like;PHA02638;7tmA_CCKR-like;
C04-12	7tmA_FMRFamide_R-like	4	0	PHA02638;7TM_GPCR_Srw
C04-11	7tm_classA_rhodopsin-like	4	0	
C04-10	7tmA_FMRFamide_R-like	4	0	7TM_GPCR_Srw
C04-1	7tmA_amine_R-like	4	0	PHA03087; 7tm_classA_rhodopsin-like

ST10. Distribution of *L. stagnalis* GPCRs across B, C, E, and F families. Number of proteins with a full domain (6 to 7 transmembrane helices) versus incomplete domain (less than 6 tms).

class	group	6 to 7 TMHs	<6TMs
Class B	B1 (hormone receptor)	12	5
	B2 (adhesion)	19	14
	B3 (Methuselah)	6	6
Class C	GABA B	3	3
	metabotropic glutamate	12	10
	orphans	2	1
Class E	cAMP	1	1
Class F	Frizzled	5	0



ST11.List of genes selected for the *in situ* expression study during *L. stagnalis* development. Expression in albumen gland and prostate from RNAseq data.

Gene prediction	Annotation	Expression in albumen gland	Expression in prostate
GSLYST00001331001	7tmA_FMRFamide_R-like (6TM)	0	19
GSLYST00016909001	7tmA_FMRFamide_R-like (7TM)	67	0
GSLYST00019383001	7tmA_FMRFamide_R-like (6TM)	0	10
GSLYST00019397001	7tmA_FMRFamide_R-like (6TM)	16	0
GSLYST00001311001	2DBD-NR (NR7A)	16	9
GSLYST00003556001	2DBD-NR (NR7B)	205	183
GSLYST00008490001	NR1B2 (RARB) (retinoic acid receptor)	0	5
GSLYST00009627001&9626001ext	NR1C3 (PPARG) (retinoid X receptor)	0	2
GSLYST00020139001_ALTORF	NR2E3 (PNR) (photoreceptor specific NR)	0	1

ST12. Descriptive statistics of the various transcriptomic cDNA libraries used for the *L. stagnalis* genome annotation.

Sample	Individual	Sample id	Nb of Reads	% assembly	Nb of Contigs	Mean Size	N50
<i>TruSeq libraries</i>							
Stomach	Ind. 1	BPP-AA	23M	93	56527	916	1601
Reproductive system	Ind. 1	BPP-AC	24M	94	42958	776	1210
Digestive gland 1	Ind. 1	BPP-AE	27M	94	46760	856	1413
Digestive gland 2	Ind. 1	BPP-AF	31M	95	45656	807	1322
Other (remaining body part) 1	Ind. 1	BPP-AH	25M	89	60589	889	1469
Other (remaining body part) 2	Ind. 1	BPP-AAI	28M	90	65191	827	1341
Digestive gland	Ind. 2	BPP-BA	20M	89	54924	805	1293
Ovotestis	Ind. 2	BPP-BB	22M	92	50809	864	1368
Foot	Ind. 2	BPP-BC	21M	93	50364	952	1616
Other (remaining) parts	Ind. 2	BPP-BD	27M	95	46491	769	1157
Stomach	Ind. 2	BPP-BE	24M	94	61347	102	1843
<i>SMARTer libraries</i>							
Neural ganglia (CNS)	Ind. 1	BPP-ABA	24M	89	28576	1269	2227
Head (mouth)	Ind. 1	BPP-ADA	22M	88	36413	1389	2472
Mantel	Ind. 1	BPP-AGB	23M	89	35755	1371	2511
Head (mouth)	Ind. 2	BPP-BFB	29M	91	33470	1386	2495

ST13. Genomic DNA library coverage, *L. stagnalis* genome project.

Library	Sequencer	Fragment size	Read size	Coverage
Short	MiSeq	400 bp	300 bp	2
Short	HiSeq2500	600 bp	250 bp	39
Short	MiSeq	700 bp	300 bp	10
Short library coverage				51
Long (manual sizing)	HiSeq2000	3-5 kb	101 bp	24
Long (SAGE-ELF)	HiSeq2000	3 kb	101 bp	8
Long (SAGE-ELF)	HiSeq2000	4 kb	101 bp	9
Long (SAGE-ELF)	HiSeq2000	5 kb	101 bp	8
Long (manual sizing)	HiSeq2000	5-8 kb	101 bp	21
Long (SAGE-ELF)	HiSeq2000	6 kb	101 bp	9
Long (SAGE-ELF)	HiSeq2000	7 kb	101 bp	7
Long (SAGE-ELF)	HiSeq2000	8 kb	101 bp	8
Long (manual sizing)	HiSeq2000	8-11 kb	101 bp	18
Long (SAGE-ELF)	HiSeq2000	10 kb	101 bp	7
Long (SAGE-ELF)	HiSeq2000	15 kb	101 bp	6
Long read coverage				125

ST14. TE annotation of the *L. stagnalis* genome assembly.

	<i>1st de novo</i> library (all consensus sequences)	<i>2nd de novo</i> library (FLC consensus sequences)
NTE20	114763	131723
LTE20	773	670
Consensus sequences	5085	2643
informative consensus sequences	5061	2643
FLC consensus sequences	2643	2604
FLF consensus sequences	2534	2510
Copies	1114023	883147
FLC copies	23211	24190
FLF copies	21865	22621

ST15. Classification of transposable elements detected in the *L. stagnalis* genome assembly.

Consensus classification	<i>1st de novo</i> library (all consensus sequences)	<i>2nd de novo</i> library (FLC consensus sequences)
Consensus sequences	5085	2643
Class I TEs	2428 (47.75%)	1517 (57.40%)
Class II TEs	1799 (35.38%)	774 (29.28%)
TEs unassigned to a class	1 (0.02%)	1 (0.04%)
PH (gene match)	181 (3.56%)	105 (3.97%)
noCat (no annotation, within Class I)	246 (4.83%)	14 (0.53%)
Chimeric (annotated, other classification)	631 (12.41%)	232 (8.78%)

ST16. Primer sequences used to clone fragments for *in situ* hybridisation.

Accession	Primer (5' – 3')	Amplicon size (bp)
GSLYST00008490001	TCCAGTAACCATGGCAACAACG (Fwd)	964
	ACAGGCCATTGGAAAACATGCAT (Rev)	
GSLYST00009627001	TTCCACTACGGGGTGCATTCTT (Fwd)	974
	GCCTCTATGAGATTGGCCTGGA (Rev)	
GSLYST00020139001	CAGGACCAATGTGAGACGATGG (Fwd)	898
	AGCACTCGTACAGCGTCTCGTG (Rev)	
GSLYST00019397001	AAGAGTCGGGGAGCCCTT (Fwd)	913
	ATCCGGAACCAGGGCGAT (Rev)	
GSLYST00016909001	GCACAGGCTCTGTTCAGC (Fwd)	900
	ATCCGATGGACCAAGTGGC (Rev)	
GSLYST00019383001	ATTGTCCACCTGGGGGCT (Fwd)	869
	GTTCCGAGTGGGCCTTGG (Rev)	
GSLYST00001331001	TCCGACCTCTGCTGCTCT (Fwd)	857
	TGAAGCAGCCAGGATTTGAAC (Rev)	
GSLYST00000615001	GCTCTTACAGCAGTCCTTGCAG (Fwd)	514
	CGTAACCCTCGAAATATGGGCAGG (Rev)	
GSLYST00001311001	CGCACTTGCCCCAGTAA (Fwd)	953
	CTCTGGTTTGAGGGCCGG (Rev)	
GSLYST00003556001	ATCAGGAAATGGGTCACAGC (Fwd)	979
	AGCAGGGTGGAGTCCCTAAT (Rev)	