



Figure S1. Maximum likelihood trees depicting the phylogenetic relationships between several Gobiiformes and Kurtiformes species for which whole mitochondrial sequences are available, including *S. tubifer* from this study. Models based on sequences from: a) whole mitochondrial genomes excluding the control region b) *COI* only c) concatenated mitochondrial genes: *COI*, *ND4*, 16S, and *cytB*, and d) the same genes as c) excluding *cytB*. The substitution model used was GTR+F+I+G4. Bootstrap support values are included at the nodes. Scale bars indicate nucleotide substitutions per site.

Table S1. List of 506 of the 701 total protein clusters unique to *Siphamia tubifer* assigned GO annotations. The number of proteins in each cluster is indicated as is the associated SWISS-PROT ID.

Cluster ID	Proteins	SWISS-PROT ID	GO annotation
cluster20	70	P20825	GO:0015074; P:DNA integration; IEA:InterPro
cluster50	41	Q52M02	GO:0007601; P:visual perception; TAS:ProtInc
cluster71	32	P0CT41	GO:0006310; P:DNA recombination; IEA:UniProtKB-KW
cluster119	25	Q80Z10	GO:0015031; P:protein transport; IEA:UniProtKB-KW
cluster146	23	P27401	GO:0075732; P:viral penetration into host nucleus; IEA:UniProtKB-KW
cluster162	22	Q03278	GO:0003964; F:RNA-directed DNA polymerase activity; IEA:UniProtKB-KW
cluster163	22	O95125	GO:0006366; P:transcription by RNA polymerase II; TAS:ProtInc
cluster181	21	A1X283	GO:0006801; P:superoxide metabolic process; IDA:UniProtKB
cluster224	19	Q9M2N5	GO:0009791; P:post-embryonic development; IMP:TAIR
cluster275	17	O92815	GO:0006310; P:DNA recombination; IEA:UniProtKB-KW
cluster507	12	O92815	GO:0006310; P:DNA recombination; IEA:UniProtKB-KW
cluster516	12	Q68E10	GO:0006364; P:rRNA processing; IBA:GO_Central
cluster717	10	A0MSJ1	GO:0001501; P:skeletal system development; IGI:ZFIN
cluster737	10	A1X283	GO:0006801; P:superoxide metabolic process; IDA:UniProtKB
cluster868	9	O60290	GO:0006355; P:regulation of transcription, DNA-templated; IEA:InterPro
cluster1140	8	Q95218	GO:0015031; P:protein transport; IEA:UniProtKB-KW
cluster1146	8	Q14258	GO:0016032; P:viral process; IEA:UniProtKB-KW
cluster1147	8	P43353	GO:0030148; P:sphingolipid biosynthetic process; TAS:Reactome
cluster1127	8	E1C5V0	GO:0043516; P:regulation of DNA damage response, signal transduction by p53 class mediator; ISS:UniProtKB
cluster1165	8	O96006	GO:0045944; P:positive regulation of transcription by RNA polymerase II; IDA:NTNU_SB
cluster1596	7	Q1RLU1	GO:0010212; P:response to ionizing radiation; ISS:UniProtKB
cluster1552	7	Q9HCI6	GO:0016925; P:protein sumoylation; IDA:UniProtKB
cluster2199	6	Q7TN75	GO:0001890; P:placenta development; IMP:MGI
cluster2756	6	P02264	GO:0051673; P:membrane disruption in other organism; IDA:AgBase
cluster3243	5	P85521	GO:0006953; P:acute-phase response; IEA:UniProtKB-KW
cluster3432	5	Q9UPY6	GO:0008360; P:regulation of cell shape; IMP:UniProtKB
cluster3290	5	P51574	GO:0015031; P:protein transport; IEA:UniProtKB-KW
cluster3212	5	P10394	GO:0015074; P:DNA integration; IEA:InterPro

cluster3282	5	P03360	GO:0044826; P:viral genome integration into host DNA; IEA:UniProtKB-KW
cluster3245	5	O75132	GO:0046983; F:protein dimerization activity; IEA:InterPro
cluster3295	5	F8RKW0	GO:0090729; F:toxin activity; IEA:UniProtKB-KW
cluster7229	4	Q9QXS4	GO:0001702; P:gastrulation with mouth forming second; NAS:UniProtKB
cluster5270	4	Q3B8D4	GO:0003677; F:DNA binding; IEA:UniProtKB-KW
cluster5259	4	P29401	GO:0005999; P:xylulose biosynthetic process; TAS:Reactome
cluster5567	4	P11369	GO:0006310; P:DNA recombination; IEA:UniProtKB-KW
cluster5367	4	P61648	GO:0006493; P:protein O-linked glycosylation; IEA:Ensembl
cluster5315	4	Q9NU92	GO:0007165; P:signal transduction; TAS:ProtInc
cluster7149	4	Q5F4A1	GO:0007275; P:multicellular organism development; IEA:UniProtKB-KW
cluster5442	4	Q99P25	GO:0007283; P:spermatogenesis; IEA:UniProtKB-KW
cluster5543	4	Q1RLU1	GO:0010212; P:response to ionizing radiation; ISS:UniProtKB
cluster7123	4	P04323	GO:0015074; P:DNA integration; IEA:InterPro
cluster5430	4	Q14534	GO:0016126; P:sterol biosynthetic process; IBA:GO_Central
cluster5477	4	B1WC10	GO:0032185; P:septin cytoskeleton organization; ISS:UniProtKB
cluster5275	4	P11260	GO:0032197; P:transposition, RNA-mediated; IMP:UniProtKB
cluster5482	4	Q9QXR7	GO:0042060; P:wound healing; IBA:GO_Central
cluster5471	4	Q7ZXV5	GO:0043516; P:regulation of DNA damage response, signal transduction by p53 class mediator; ISS:UniProtKB
cluster7231	4	Q96TG0	GO:0045995; P:regulation of embryonic development; IEA:InterPro
cluster7076	4	Q9HAC7	GO:0047369; F:succinate-hydroxymethylglutarate CoA-transferase activity; IDA:UniProtKB
cluster5219	4	Q19546	GO:0061820; P:telomeric D-loop disassembly; IBA:GO_Central
cluster7072	4	Q09811	GO:0070914; P:UV-damage excision repair; IMP:PomBase
cluster5137	4	O94885	GO:1900044; P:regulation of protein K63-linked ubiquitination; IDA:MGI
cluster9379	3	Q91WP0	GO:0001867; P:complement activation, lectin pathway; IDA:MGI
cluster9382	3	Q4U4S6	GO:0003281; P:ventricular septum development; IMP:MGI
cluster9423	3	Q04202	GO:0006313; P:transposition, DNA-mediated; IEA:InterPro
cluster9451	3	Q9NBX4	GO:0006313; P:transposition, DNA-mediated; IMP:UniProtKB
cluster12652	3	Q61510	GO:0006511; P:ubiquitin-dependent protein catabolic process; ISO:MGI
cluster9464	3	Q9UN72	GO:0007399; P:nervous system development; TAS:ProtInc
cluster12656	3	P55067	GO:0007417; P:central nervous system development; IBA:GO_Central
cluster9405	3	Q5KQS3	GO:0008191; F:metalloendopeptidase inhibitor activity; IEA:UniProtKB-KW

cluster12672	3	Q8BV66	GO:0009617; P:response to bacterium; IEP:MGI
cluster9435	3	Q1RLU1	GO:0010212; P:response to ionizing radiation; ISS:UniProtKB
cluster12653	3	P36514	GO:0015020; F:glucuronosyltransferase activity; IEA:UniProtKB-EC
cluster9449	3	Q9UKJ4	GO:0016032; P:viral process; IEA:UniProtKB-KW
cluster9469	3	Q7LHG5	GO:0032197; P:transposition, RNA-mediated; ISS:SGD
cluster12646	3	Q9PTM4	GO:0034765; P:regulation of ion transmembrane transport; IEA:UniProtKB-KW
cluster9447	3	Q92820	GO:0046900; P:tetrahydrofolylpolyglutamate metabolic process; IBA:GO_Central
cluster9444	3	Q96DH6	GO:0048864; P:stem cell development; IEA:Ensembl
cluster9365	3	Q9Y5F6	GO:0050808; P:synapse organization; IEA:Ensembl
cluster9402	3	P02264	GO:0051673; P:membrane disruption in other organism; IDA:AgBase
cluster9367	3	P20693	GO:0051770; P:positive regulation of nitric-oxide synthase biosynthetic process; ISO:MGI
cluster9431	3	F1QH17	GO:0055114; P:oxidation-reduction process; ISS:UniProtKB
cluster9430	3	E9Q401	GO:0086005; P:ventricular cardiac muscle cell action potential; IMP:BHF-UCL
cluster12657	3	O54898	GO:0086018; P:SA node cell to atrial cardiac muscle cell signaling; ISS:BHF-UCL
cluster9436	3	Q8R4F1	GO:0099560; P:synaptic membrane adhesion; IDA:SynGO
cluster9369	3	Q16820	GO:1901998; P:toxin transport; IEA:Ensembl
cluster18310	2	Q66124	GO:0000050; P:urea cycle; ISS:UniProtKB
cluster19257	2	Q9H6P0	GO:0000122; P:negative regulation of transcription by RNA polymerase II; IDA:BHF-UCL
cluster18344	2	Q86VZ6	GO:0000122; P:negative regulation of transcription by RNA polymerase II; IDA:MGI
cluster19277	2	Q86VZ6	GO:0000122; P:negative regulation of transcription by RNA polymerase II; IDA:MGI
cluster18351	2	Q6P0B1	GO:0000381; P:regulation of alternative mRNA splicing, via spliceosome; IBA:GO_Central
cluster18358	2	Q7T2T1	GO:0000381; P:regulation of alternative mRNA splicing, via spliceosome; IBA:GO_Central
cluster19259	2	Q7T2T1	GO:0000381; P:regulation of alternative mRNA splicing, via spliceosome; IBA:GO_Central
cluster19182	2	A1A4K8	GO:0000398; P:mRNA splicing, via spliceosome; IBA:GO_Central
cluster18403	2	Q8QGX4	GO:0000723; P:telomere maintenance; IBA:GO_Central
cluster19154	2	Q9Y6X0	GO:0000981; F:DNA-binding transcription factor activity, RNA polymerase II-specific; ISM:NTNU_SB
cluster18275	2	Q8VHG2	GO:0001570; P:vasculogenesis; IMP:MGI

cluster18319	2	E9PCK8	GO:0001657; P:ureteric bud development; ISS:BHF-UCL
cluster18409	2	P48645	GO:0001659; P:temperature homeostasis; IEA:Ensembl
cluster18490	2	Q9JI18	GO:0001701; P:in utero embryonic development; IMP:MGI
cluster18317	2	Q96II1	GO:0001764; P:neuron migration; IBA:GO_Central
cluster18350	2	Q96II1	GO:0001764; P:neuron migration; IBA:GO_Central
cluster19162	2	Q61137	GO:0001764; P:neuron migration; IDA:MGI
cluster18460	2	P98064	GO:0001867; P:complement activation, lectin pathway; IMP:UniProtKB
cluster19296	2	Q9Z2W9	GO:0001919; P:regulation of receptor recycling; ISO:MGI
cluster19326	2	O15399	GO:0001964; P:startle response; IEA:Ensembl
cluster18303	2	Q96SG3	GO:0001967; P:suckling behavior; IEA:Ensembl
cluster19243	2	Q96SG3	GO:0001967; P:suckling behavior; IEA:Ensembl
cluster19400	2	A1XQX1	GO:0002040; P:sprouting angiogenesis; IMP:ZFIN
cluster19165	2	Q56JV1	GO:0002181; P:cytoplasmic translation; ISS:UniProtKB
cluster18456	2	A6QLK5	GO:0002437; P:inflammatory response to antigenic stimulus; ISS:UniProtKB
cluster19261	2	P13789	GO:0003009; P:skeletal muscle contraction; IBA:GO_Central
cluster18346	2	P22004	GO:0003323; P:type B pancreatic cell development; IDA:BHF-UCL
cluster19205	2	Q04906	GO:0003323; P:type B pancreatic cell development; IEA:Ensembl
cluster18324	2	P32018	GO:0003429; P:growth plate cartilage chondrocyte morphogenesis; IBA:GO_Central
cluster19244	2	P13944	GO:0003429; P:growth plate cartilage chondrocyte morphogenesis; IBA:GO_Central
cluster19216	2	A6H7H1	GO:0003723; F:RNA binding; IEA:UniProtKB-KW
cluster18383	2	Q8MJU9	GO:0003774; F:motor activity; IEA:InterPro
cluster18477	2	Q00962	GO:0003964; F:RNA-directed DNA polymerase activity; IEA:UniProtKB-KW
cluster18401	2	Q7SIG3	GO:0004252; F:serine-type endopeptidase activity; IEA:InterPro
cluster18282	2	B6ZK76	GO:0004908; F:interleukin-1 receptor activity; IEA:InterPro
cluster18448	2	Q8NGI2	GO:0004984; F:olfactory receptor activity; IBA:GO_Central
cluster18504	2	P51856	GO:0005198; F:structural molecule activity; IEA:InterPro
cluster18365	2	P98157	GO:0005509; F:calcium ion binding; IEA:InterPro
cluster18425	2	O02751	GO:0005634; C:nucleus; IEA:UniProtKB-SubCell
cluster18533	2	Q6DDT5	GO:0005737; C:cytoplasm; ISS:UniProtKB
cluster19208	2	A0JM08	GO:0005874; C:microtubule; IEA:UniProtKB-KW
cluster18498	2	Q2M3C6	GO:0005886; C:plasma membrane; IDA:HPA
cluster19283	2	F1P4W9	GO:0005886; C:plasma membrane; IEA:UniProtKB-KW
cluster19276	2	Q6IPM2	GO:0005929; C:cilium; TAS:Reactome

cluster18421	2	B5DGQ7	GO:0006096; P:glycolytic process; IEA:UniProtKB-UniPathway
cluster18304	2	Q7TQ07	GO:0006261; P:DNA-dependent DNA replication; ISO:MGI
cluster19339	2	Q7TQ07	GO:0006261; P:DNA-dependent DNA replication; ISO:MGI
cluster19192	2	O93309	GO:0006275; P:regulation of DNA replication; ISS:UniProtKB
cluster18356	2	Q92089	GO:0006304; P:DNA modification; IEA:UniProtKB-KW
cluster18523	2	P0CT41	GO:0006310; P:DNA recombination; IEA:UniProtKB-KW
cluster18377	2	Q9NBX4	GO:0006313; P:transposition, DNA-mediated; IMP:UniProtKB
cluster19354	2	Q9NBX4	GO:0006313; P:transposition, DNA-mediated; IMP:UniProtKB
cluster19179	2	Q9NTU8	GO:0006351; P:transcription, DNA-templated; IEA:InterPro
cluster18245	2	P40645	GO:0006355; P:regulation of transcription, DNA-templated; IDA:MGI
cluster18441	2	Q9GL32	GO:0006357; P:regulation of transcription by RNA polymerase II; IBA:GO_Central
cluster19297	2	Q86UJ9	GO:0006366; P:transcription by RNA polymerase II; TAS:ProtInc
cluster18357	2	P42568	GO:0006368; P:transcription elongation from RNA polymerase II promoter; TAS:Reactome
cluster19327	2	Q9C0J8	GO:0006369; P:termination of RNA polymerase II transcription; TAS:Reactome
cluster18261	2	Q92005	GO:0006414; P:translational elongation; IBA:GO_Central
cluster19349	2	Q8BWD8	GO:0006468; P:protein phosphorylation; IBA:GO_Central
cluster18309	2	Q15208	GO:0006468; P:protein phosphorylation; IDA:UniProtKB
cluster18408	2	Q8WX83	GO:0006468; P:protein phosphorylation; IMP:UniProtKB
cluster18510	2	Q8WX83	GO:0006468; P:protein phosphorylation; IMP:UniProtKB
cluster19310	2	O62830	GO:0006470; P:protein dephosphorylation; ISS:UniProtKB
cluster19196	2	E6ZGB4	GO:0006482; P:protein demethylation; ISS:UniProtKB
cluster19273	2	E6ZGB4	GO:0006482; P:protein demethylation; ISS:UniProtKB
cluster18535	2	Q6P9A2	GO:0006493; P:protein O-linked glycosylation; IDA:UniProtKB
cluster19378	2	O08688	GO:0006508; P:proteolysis; IBA:GO_Central
cluster19313	2	Q9ULZ9	GO:0006508; P:proteolysis; TAS:ParkinsonsUK-UCL
cluster18414	2	O70263	GO:0006511; P:ubiquitin-dependent protein catabolic process; IDA:MGI
cluster19207	2	Q14974	GO:0006610; P:ribosomal protein import into nucleus; IDA:UniProtKB
cluster19223	2	F1QXD3	GO:0006612; P:protein targeting to membrane; IBA:GO_Central
cluster18355	2	P50416	GO:0006641; P:triglyceride metabolic process; IEA:Ensembl
cluster18345	2	Q9HBU6	GO:0006646; P:phosphatidylethanolamine biosynthetic process; IDA:UniProtKB
cluster19357	2	Q9D4V0	GO:0006646; P:phosphatidylethanolamine biosynthetic process; ISO:MGI
cluster19345	2	Q9JJY3	GO:0006684; P:sphingomyelin metabolic process; IDA:MGI

cluster19409	2	P79386	GO:0006694; P:steroid biosynthetic process; ISS:HGNC
cluster19294	2	Q86YH6	GO:0006744; P:ubiquinone biosynthetic process; IDA:HGNC
cluster19312	2	P30561	GO:0006805; P:xenobiotic metabolic process; TAS:MGI
cluster19334	2	Q3YAW7	GO:0006811; P:ion transport; IEA:UniProtKB-KW
cluster18393	2	Q99250	GO:0006814; P:sodium ion transport; TAS:ProtInc
cluster18532	2	Q99250	GO:0006814; P:sodium ion transport; TAS:ProtInc
cluster18388	2	P53992	GO:0006886; P:intracellular protein transport; IEA:InterPro
cluster19263	2	Q9NZR2	GO:0006898; P:receptor-mediated endocytosis; TAS:ProtInc
cluster18306	2	Q8WU76	GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro
cluster18497	2	A0JMW6	GO:0006915; P:apoptotic process; IEA:UniProtKB-KW
cluster19169	2	O09127	GO:0006929; P:substrate-dependent cell migration; IDA:UniProtKB
cluster19362	2	Q9UIT1	GO:0006939; P:smooth muscle contraction; TAS:ProtInc
cluster18470	2	Q2VLH6	GO:0006953; P:acute-phase response; IEA:UniProtKB-KW
cluster19226	2	Q2VLG6	GO:0006953; P:acute-phase response; IEA:UniProtKB-KW
cluster18431	2	P98093	GO:0006954; P:inflammatory response; IEA:UniProtKB-KW
cluster19346	2	Q9WU60	GO:0006979; P:response to oxidative stress; ISO:MGI
cluster18392	2	Q5KR47	GO:0007015; P:actin filament organization; IBA:GO_Central
cluster18273	2	Q7Z668	GO:0007018; P:microtubule-based movement; IBA:GO_Central
cluster19161	2	E9PYY5	GO:0007018; P:microtubule-based movement; IBA:GO_Central
cluster19194	2	Q7Z668	GO:0007018; P:microtubule-based movement; IBA:GO_Central
cluster19228	2	Q9NQ86	GO:0007051; P:spindle organization; IMP:UniProtKB
cluster18243	2	Q9DDD0	GO:0007155; P:cell adhesion; IEA:UniProtKB-KW
cluster18339	2	A1XQY1	GO:0007155; P:cell adhesion; IEA:UniProtKB-KW
cluster18361	2	A2AVA0	GO:0007155; P:cell adhesion; IEA:UniProtKB-KW
cluster18482	2	P0C6B8	GO:0007155; P:cell adhesion; IEA:UniProtKB-KW
cluster18318	2	P24503	GO:0007156; P:homophilic cell adhesion via plasma membrane adhesion molecules; IBA:GO_Central
cluster18458	2	P24503	GO:0007156; P:homophilic cell adhesion via plasma membrane adhesion molecules; IBA:GO_Central
cluster19398	2	Q5DRB1	GO:0007156; P:homophilic cell adhesion via plasma membrane adhesion molecules; IEA:InterPro
cluster18487	2	P28472	GO:0007165; P:signal transduction; IBA:GO_Central
cluster19338	2	Q13191	GO:0007165; P:signal transduction; IBA:GO_Central

cluster18395	2	Q8TCX5	GO:0007165; P:signal transduction; IEA:InterPro
cluster18491	2	A6NI28	GO:0007165; P:signal transduction; IEA:InterPro
cluster19174	2	Q6DRG7	GO:0007165; P:signal transduction; IEA:InterPro
cluster19240	2	Q6TLK4	GO:0007165; P:signal transduction; IEA:InterPro
cluster19350	2	Q61302	GO:0007165; P:signal transduction; IEA:InterPro
cluster18269	2	Q9UJF2	GO:0007165; P:signal transduction; TAS:ProtInc
cluster18437	2	Q92915	GO:0007165; P:signal transduction; TAS:ProtInc
cluster18544	2	Q9NU92	GO:0007165; P:signal transduction; TAS:ProtInc
cluster19199	2	Q8WUQ3	GO:0007165; P:signal transduction; TAS:ProtInc
cluster19211	2	O14514	GO:0007165; P:signal transduction; TAS:ProtInc
cluster19363	2	O15484	GO:0007165; P:signal transduction; TAS:ProtInc
cluster18509	2	O97814	GO:0007166; P:cell surface receptor signaling pathway; IEA:InterPro
cluster19164	2	Q9UM73	GO:0007169; P:transmembrane receptor protein tyrosine kinase signaling pathway; IEA:InterPro
cluster19181	2	P43026	GO:0007179; P:transforming growth factor beta receptor signaling pathway; TAS:ProtInc
cluster18517	2	P97751	GO:0007187; P:G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger; ISO:MGI
cluster18283	2	O75899	GO:0007194; P:negative regulation of adenylate cyclase activity; TAS:ProtInc
cluster19250	2	P28335	GO:0007210; P:serotonin receptor signaling pathway; IMP:UniProtKB
cluster19371	2	Q2KI97	GO:0007218; P:neuropeptide signaling pathway; IBA:GO_Central
cluster19332	2	Q8C0Q9	GO:0007264; P:small GTPase mediated signal transduction; IEA:InterPro
cluster19245	2	Q91Z69	GO:0007266; P:Rho protein signal transduction; IDA:MGI
cluster18270	2	Q02084	GO:0007275; P:multicellular organism development; IEA:UniProtKB-KW
cluster18399	2	Q6VNB8	GO:0007275; P:multicellular organism development; IEA:UniProtKB-KW
cluster18436	2	Q90304	GO:0007275; P:multicellular organism development; IEA:UniProtKB-KW
cluster18492	2	Q6DN12	GO:0007275; P:multicellular organism development; IEA:UniProtKB-KW
cluster18541	2	P79777	GO:0007275; P:multicellular organism development; IEA:UniProtKB-KW
cluster19265	2	Q8R508	GO:0007275; P:multicellular organism development; IEA:UniProtKB-KW
cluster19405	2	A0A1L8GSA2	GO:0007275; P:multicellular organism development; IEA:UniProtKB-KW
cluster18417	2	Q6ZWR6	GO:0007283; P:spermatogenesis; IEA:UniProtKB-KW
cluster19176	2	Q08E27	GO:0007286; P:spermatid development; IEA:Ensembl
cluster19254	2	Q9MYW0	GO:0007338; P:single fertilization; IBA:GO_Central

cluster18472	2	Q5DID0	GO:0007338; P:single fertilization; IEA:Ensembl
cluster18464	2	O57682	GO:0007367; P:segment polarity determination; IEA:UniProtKB-KW
cluster18244	2	O60542	GO:0007399; P:nervous system development; TAS:ProtInc
cluster18364	2	Q9Y5I4	GO:0007399; P:nervous system development; TAS:ProtInc
cluster19255	2	Q63374	GO:0007416; P:synapse assembly; ISS:BHF-UCL
cluster18281	2	Q02566	GO:0007522; P:visceral muscle development; IMP:MGI
cluster19158	2	Q02566	GO:0007522; P:visceral muscle development; IMP:MGI
cluster18241	2	Q8JIR8	GO:0007601; P:visual perception; IEA:InterPro
cluster18522	2	Q8N6F1	GO:0007601; P:visual perception; IEA:UniProtKB-KW
cluster19212	2	Q13402	GO:0007601; P:visual perception; IMP:UniProtKB
cluster18378	2	O73700	GO:0007605; P:sensory perception of sound; IEA:Ensembl
cluster19262	2	Q9UM54	GO:0007605; P:sensory perception of sound; IEA:UniProtKB-KW
cluster19264	2	Q9YH85	GO:0007605; P:sensory perception of sound; IEA:UniProtKB-KW
cluster18302	2	Q01668	GO:0007605; P:sensory perception of sound; IMP:BHF-UCL
cluster19300	2	Q9JK97	GO:0007605; P:sensory perception of sound; IMP:MGI
cluster19287	2	P56696	GO:0007605; P:sensory perception of sound; TAS:ProtInc
cluster19329	2	Q8BHR2	GO:0007624; P:ultradian rhythm; IEA:InterPro
cluster19235	2	Q08C92	GO:0008033; P:tRNA processing; IEA:UniProtKB-KW
cluster19299	2	P81018	GO:0008061; F:chitin binding; IDA:AgBase
cluster19219	2	Q96FA3	GO:0008063; P:Toll signaling pathway; IBA:GO_Central
cluster19210	2	Q96Q29	GO:0008104; P:protein localization; IBA:GO_Central
cluster18341	2	Q8NFP9	GO:0008104; P:protein localization; IEA:Ensembl
cluster18370	2	Q64GL0	GO:0008154; P:actin polymerization or depolymerization; ISS:UniProtKB
cluster18412	2	Q64GL0	GO:0008154; P:actin polymerization or depolymerization; ISS:UniProtKB
cluster18521	2	Q60467	GO:0008201; F:heparin binding; IEA:UniProtKB-KW
cluster19408	2	Q9BY12	GO:0008270; F:zinc ion binding; IEA:InterPro
cluster18473	2	Q5VXN8	GO:0008360; P:regulation of cell shape; IMP:CAFA
cluster19352	2	Q5VXN8	GO:0008360; P:regulation of cell shape; IMP:CAFA
cluster19303	2	Q7YQM1	GO:0008380; P:RNA splicing; IEA:UniProtKB-KW
cluster18423	2	E7FCN8	GO:0008589; P:regulation of smoothened signaling pathway; ISS:UniProtKB
cluster18484	2	Q6NS52	GO:0009617; P:response to bacterium; IEP:MGI
cluster19173	2	Q9UQR0	GO:0009653; P:anatomical structure morphogenesis; TAS:ProtInc
cluster18256	2	P0DM44	GO:0009755; P:hormone-mediated signaling pathway; IBA:GO_Central

cluster18287	2	Q8WXI1	GO:0009966; P:regulation of signal transduction; IEA:InterPro
cluster18424	2	Q6PJ69	GO:0010508; P:positive regulation of autophagy; IMP:UniProtKB
cluster19153	2	P43243	GO:0010608; P:posttranscriptional regulation of gene expression; IDA:CACAO
cluster19317	2	Q91VF5	GO:0010811; P:positive regulation of cell-substrate adhesion; IBA:GO_Central
cluster19286	2	Q76HP3	GO:0010923; P:negative regulation of phosphatase activity; ISS:UniProtKB
cluster19206	2	Q9R1J8	GO:0010976; P:positive regulation of neuron projection development; IDA:ParkinsonsUK-UCL
cluster19353	2	Q9ULH0	GO:0010976; P:positive regulation of neuron projection development; ISS:UniProtKB
cluster19365	2	Q13556	GO:0014733; P:regulation of skeletal muscle adaptation; TAS:UniProtKB
cluster18246	2	P70414	GO:0014829; P:vascular smooth muscle contraction; IMP:BHF-UCL
cluster18400	2	P46939	GO:0014894; P:response to denervation involved in regulation of muscle adaptation; IEA:Ensembl
cluster18267	2	A0MGZ7	GO:0015015; P:heparan sulfate proteoglycan biosynthetic process, enzymatic modification; IBA:GO_Central
cluster19301	2	A0MGZ7	GO:0015015; P:heparan sulfate proteoglycan biosynthetic process, enzymatic modification; IBA:GO_Central
cluster18328	2	O60318	GO:0015031; P:protein transport; IEA:UniProtKB-KW
cluster18359	2	Q9NWI9	GO:0015031; P:protein transport; IEA:UniProtKB-KW
cluster18381	2	Q9JIP7	GO:0015031; P:protein transport; IEA:UniProtKB-KW
cluster18406	2	Q811G0	GO:0015031; P:protein transport; IEA:UniProtKB-KW
cluster18465	2	Q9UPQ3	GO:0015031; P:protein transport; IEA:UniProtKB-KW
cluster18508	2	Q9NWI9	GO:0015031; P:protein transport; IEA:UniProtKB-KW
cluster19267	2	O60318	GO:0015031; P:protein transport; IEA:UniProtKB-KW
cluster18293	2	P04323	GO:0015074; P:DNA integration; IEA:InterPro
cluster19221	2	Q96ES6	GO:0015295; F:solute:proton symporter activity; IBA:GO_Central
cluster18374	2	Q0VCM6	GO:0015804; P:neutral amino acid transport; IBA:GO_Central
cluster19316	2	Q06185	GO:0015986; P:ATP synthesis coupled proton transport; IEA:InterPro
cluster18242	2	Q68CR7	GO:0016021; C:integral component of membrane; IEA:UniProtKB-KW
cluster18264	2	Q6ZVL6	GO:0016021; C:integral component of membrane; IEA:UniProtKB-KW
cluster18453	2	Q5GH64	GO:0016021; C:integral component of membrane; IEA:UniProtKB-KW
cluster18474	2	Q6PGS5	GO:0016021; C:integral component of membrane; IEA:UniProtKB-KW
cluster19394	2	Q8BMD6	GO:0016021; C:integral component of membrane; IEA:UniProtKB-KW
cluster18462	2	Q9NPG3	GO:0016032; P:viral process; IEA:UniProtKB-KW

cluster19315	2	P08047	GO:0016032; P:viral process; IEA:UniProtKB-KW
cluster19293	2	Q80TJ1	GO:0016050; P:vesicle organization; IMP:MGI
cluster19159	2	P43446	GO:0016055; P:Wnt signaling pathway; IBA:GO_Central
cluster19311	2	Q00993	GO:0016055; P:Wnt signaling pathway; IBA:GO_Central
cluster18284	2	B0R0I6	GO:0016055; P:Wnt signaling pathway; IEA:UniProtKB-KW
cluster18336	2	B0R0I6	GO:0016055; P:Wnt signaling pathway; IEA:UniProtKB-KW
cluster19166	2	Q8R4V4	GO:0016055; P:Wnt signaling pathway; IEA:UniProtKB-KW
cluster19230	2	Q6ZSJ9	GO:0016055; P:Wnt signaling pathway; IEA:UniProtKB-KW
cluster19318	2	Q9UKE0	GO:0016055; P:Wnt signaling pathway; IEA:UniProtKB-KW
cluster19347	2	Q9UPM3	GO:0016055; P:Wnt signaling pathway; IEA:UniProtKB-KW
cluster19358	2	Q8QGP3	GO:0016055; P:Wnt signaling pathway; IEA:UniProtKB-KW
cluster18299	2	Q8BY04	GO:0016082; P:synaptic vesicle priming; IDA:SynGO
cluster18537	2	Q62769	GO:0016082; P:synaptic vesicle priming; IMP:ParkinsonsUK-UCL
cluster18263	2	Q1LYM3	GO:0016192; P:vesicle-mediated transport; IEA:InterPro
cluster18471	2	O60229	GO:0016192; P:vesicle-mediated transport; TAS:ProtInc
cluster19340	2	Q9NY28	GO:0016266; P:O-glycan processing; TAS:Reactome
cluster18439	2	Q6GLZ5	GO:0016476; P:regulation of embryonic cell shape; IMP:UniProtKB
cluster18493	2	Q7L273	GO:0016567; P:protein ubiquitination; IEA:UniProtKB-UniPathway
cluster18506	2	Q6PDK8	GO:0016567; P:protein ubiquitination; IEA:UniProtKB-UniPathway
cluster19391	2	Q7L273	GO:0016567; P:protein ubiquitination; IEA:UniProtKB-UniPathway
cluster19410	2	Q96M02	GO:0016567; P:protein ubiquitination; ISS:UniProtKB
cluster18301	2	Q6ZTM0	GO:0016579; P:protein deubiquitination; IEA:InterPro
cluster19275	2	Q6IE24	GO:0016579; P:protein deubiquitination; IEA:InterPro
cluster19403	2	Q91VV4	GO:0017112; F:Rab guanyl-nucleotide exchange factor activity; ISS:UniProtKB
cluster19395	2	A4IGD2	GO:0017188; F:aspartate N-acetyltransferase activity; IEA:UniProtKB-EC
cluster19249	2	Q9JKF6	GO:0019062; P:virion attachment to host cell; IEA:InterPro
cluster18278	2	P62955	GO:0019226; P:transmission of nerve impulse; IBA:GO_Central
cluster18367	2	P62955	GO:0019226; P:transmission of nerve impulse; IBA:GO_Central
cluster19325	2	Q5QT56	GO:0019227; P:neuronal action potential propagation; IEA:Ensembl
cluster18291	2	Q9ET38	GO:0019227; P:neuronal action potential propagation; IMP:MGI
cluster19374	2	Q9NZV8	GO:0019233; P:sensory perception of pain; IEA:Ensembl
cluster18258	2	Q02294	GO:0019233; P:sensory perception of pain; IMP:RGD
cluster18433	2	O55017	GO:0019233; P:sensory perception of pain; ISO:MGI

cluster19366	2	Q61115	GO:0021522; P:spinal cord motor neuron differentiation; IGI:MGI
cluster18300	2	P23759	GO:0021527; P:spinal cord association neuron differentiation; IEA:Ensembl
cluster18268	2	Q8NFP4	GO:0021527; P:spinal cord association neuron differentiation; ISS:HGNC
cluster18389	2	P70120	GO:0021537; P:telencephalon development; IGI:MGI
cluster19281	2	Q61380	GO:0021762; P:substantia nigra development; HEP:UniProtKB
cluster18295	2	O75093	GO:0022028; P:tangential migration from the subventricular zone to the olfactory bulb; IEA:Ensembl
cluster19341	2	Q8N7C0	GO:0022414; P:reproductive process; IEA:Ensembl
cluster19187	2	A5D7D1	GO:0030050; P:vesicle transport along actin filament; IEA:Ensembl
cluster19188	2	A5D7D1	GO:0030050; P:vesicle transport along actin filament; IEA:Ensembl
cluster18451	2	O43707	GO:0030050; P:vesicle transport along actin filament; IMP:UniProtKB
cluster19387	2	P57780	GO:0030050; P:vesicle transport along actin filament; ISO:MGI
cluster18331	2	Q9R1E6	GO:0030334; P:regulation of cell migration; ISO:MGI
cluster19167	2	Q96FX7	GO:0030488; P:tRNA methylation; IBA:GO_Central
cluster18525	2	Q92859	GO:0030513; P:positive regulation of BMP signaling pathway; IEA:InterPro
cluster19171	2	Q90Y54	GO:0030878; P:thyroid gland development; IMP:ZFIN
cluster18461	2	O95747	GO:0031098; P:stress-activated protein kinase signaling cascade; IBA:GO_Central
cluster18513	2	Q863I2	GO:0031098; P:stress-activated protein kinase signaling cascade; IBA:GO_Central
cluster18413	2	Q62845	GO:0031175; P:neuron projection development; IDA:UniProtKB
cluster19291	2	P22411	GO:0031295; P:T cell costimulation; ISS:UniProtKB
cluster18420	2	Q90YM8	GO:0031529; P:ruffle organization; ISS:UniProtKB
cluster18285	2	O43739	GO:0032012; P:regulation of ARF protein signal transduction; IEA:InterPro
cluster19383	2	O08967	GO:0032012; P:regulation of ARF protein signal transduction; IEA:InterPro
cluster18257	2	Q32NR9	GO:0032185; P:septin cytoskeleton organization; IMP:UniProtKB
cluster18398	2	Q13796	GO:0032438; P:melanosome organization; ISS:HGNC
cluster18372	2	Q96S21	GO:0032482; P:Rab protein signal transduction; IBA:GO_Central
cluster18503	2	Q96S21	GO:0032482; P:Rab protein signal transduction; IBA:GO_Central
cluster19319	2	O08680	GO:0032496; P:response to lipopolysaccharide; IEP:RGD
cluster18469	2	P07812	GO:0032570; P:response to progesterone; IDA:AgBase
cluster18271	2	P15146	GO:0032570; P:response to progesterone; IEP:RGD
cluster19302	2	Q4L1J4	GO:0032947; F:protein-containing complex scaffold activity; IEA:InterPro
cluster19386	2	P34942	GO:0032981; P:mitochondrial respiratory chain complex I assembly; ISS:UniProtKB
cluster18480	2	Q8C8R3	GO:0033292; P:T-tubule organization; IMP:BHF-UCL

cluster18524	2	P02468	GO:0034446; P:substrate adhesion-dependent cell spreading; ISO:MGI
cluster18294	2	Q7Z3S7	GO:0034765; P:regulation of ion transmembrane transport; IEA:UniProtKB-KW
cluster18394	2	Q99454	GO:0034765; P:regulation of ion transmembrane transport; IEA:UniProtKB-KW
cluster18407	2	Q99244	GO:0034765; P:regulation of ion transmembrane transport; IEA:UniProtKB-KW
cluster18422	2	Q15878	GO:0034765; P:regulation of ion transmembrane transport; IEA:UniProtKB-KW
cluster18463	2	Q99454	GO:0034765; P:regulation of ion transmembrane transport; IEA:UniProtKB-KW
cluster18495	2	Q64347	GO:0034765; P:regulation of ion transmembrane transport; IEA:UniProtKB-KW
cluster19304	2	Q99244	GO:0034765; P:regulation of ion transmembrane transport; IEA:UniProtKB-KW
cluster18438	2	P23735	GO:0034987; F:immunoglobulin receptor binding; IPI:AgBase
cluster18530	2	Q8TEF5	GO:0035023; P:regulation of Rho protein signal transduction; IEA:InterPro
cluster18519	2	Q9Z0U4	GO:0035094; P:response to nicotine; IEP:RGD
cluster18297	2	Q3TYL1	GO:0035176; P:social behavior; IMP:MGI
cluster19224	2	Q3TYL1	GO:0035176; P:social behavior; IMP:MGI
cluster19298	2	Q3TYL1	GO:0035176; P:social behavior; IMP:MGI
cluster18534	2	Q61626	GO:0035249; P:synaptic transmission, glutamatergic; IMP:MGI
cluster19376	2	Q03391	GO:0035249; P:synaptic transmission, glutamatergic; ISO:MGI
cluster18466	2	P42262	GO:0035249; P:synaptic transmission, glutamatergic; TAS:ARUK-UCL
cluster18265	2	Q96MS0	GO:0035385; P:Roundabout signaling pathway; IEA:InterPro
cluster18404	2	Q9JJ00	GO:0035456; P:response to interferon-beta; ISO:MGI
cluster18430	2	O70507	GO:0035725; P:sodium ion transmembrane transport; ISO:MGI
cluster18442	2	Q5XXA6	GO:0035774; P:positive regulation of insulin secretion involved in cellular response to glucose stimulus; IMP:UniProtKB
cluster19284	2	Q6Y636	GO:0036324; P:vascular endothelial growth factor receptor-2 signaling pathway; IMP:UniProtKB
cluster18405	2	Q8CGE9	GO:0038032; P:termination of G protein-coupled receptor signaling pathway; ISO:MGI
cluster18307	2	P56581	GO:0040029; P:regulation of gene expression, epigenetic; IMP:UniProtKB
cluster19369	2	Q9TSZ3	GO:0042391; P:regulation of membrane potential; IBA:GO_Central
cluster18314	2	Q5JR59	GO:0042803; F:protein homodimerization activity; IPI:UniProtKB
cluster19322	2	Q8VC88	GO:0042803; F:protein homodimerization activity; ISO:MGI
cluster18335	2	Q8CG09	GO:0042908; P:xenobiotic transport; IMP:RGD
cluster18396	2	Q9P2T1	GO:0043101; P:purine-containing compound salvage; TAS:Reactome
cluster18440	2	Q9NYB5	GO:0043252; P:sodium-independent organic anion transport; IBA:GO_Central
cluster18489	2	Q9NPD5	GO:0043252; P:sodium-independent organic anion transport; IBA:GO_Central

cluster18511	2	Q9NPD5	GO:0043252; P:sodium-independent organic anion transport; IBA:GO_Central
cluster18435	2	Q7SY48	GO:0043487; P:regulation of RNA stability; IMP:ZFIN
cluster18429	2	Q63054	GO:0043496; P:regulation of protein homodimerization activity; IMP:RGD
cluster19396	2	Q80U12	GO:0043547; P:positive regulation of GTPase activity; ISO:MGI
cluster18347	2	Q6TEN6	GO:0043551; P:regulation of phosphatidylinositol 3-kinase activity; ISS:UniProtKB
cluster19247	2	Q6TEN6	GO:0043551; P:regulation of phosphatidylinositol 3-kinase activity; ISS:UniProtKB
cluster19308	2	A0ZSK4	GO:0044179; P:hemolysis in other organism; IEA:UniProtKB-KW
cluster18518	2	Q9BSF8	GO:0044342; P:type B pancreatic cell proliferation; ISS:UniProtKB
cluster18486	2	P03360	GO:0044826; P:viral genome integration into host DNA; IEA:UniProtKB-KW
cluster18529	2	Q07954	GO:0045056; P:transcytosis; IMP:ARUK-UCL
cluster19203	2	Q9Y219	GO:0045061; P:thymic T cell selection; IDA:UniProtKB
cluster19404	2	Q6PVZ1	GO:0045110; P:intermediate filament bundle assembly; ISS:UniProtKB
cluster18416	2	Q8CJ99	GO:0045162; P:clustering of voltage-gated sodium channels; IMP:RGD
cluster18542	2	G5E861	GO:0045162; P:clustering of voltage-gated sodium channels; ISO:MGI
cluster18499	2	Q9H604	GO:0045214; P:sarcomere organization; IEA:Ensembl
cluster19236	2	Q9H604	GO:0045214; P:sarcomere organization; IEA:Ensembl
cluster19337	2	Q9H987	GO:0045214; P:sarcomere organization; ISS:BHF-UCL
cluster19170	2	P07221	GO:0045214; P:sarcomere organization; ISS:UniProtKB
cluster18371	2	B6RSP1	GO:0045218; P:zonula adherens maintenance; ISS:UniProtKB
cluster18248	2	P55283	GO:0045773; P:positive regulation of axon extension; IEA:Ensembl
cluster19227	2	P55283	GO:0045773; P:positive regulation of axon extension; IEA:Ensembl
cluster18443	2	Q60821	GO:0045893; P:positive regulation of transcription, DNA-templated; IDA:MGI
cluster19160	2	Q92172	GO:0045893; P:positive regulation of transcription, DNA-templated; IDA:UniProtKB
cluster18515	2	Q08DL5	GO:0045944; P:positive regulation of transcription by RNA polymerase II; IBA:GO_Central
cluster19253	2	O60422	GO:0045944; P:positive regulation of transcription by RNA polymerase II; IBA:GO_Central
cluster19375	2	P17926	GO:0045944; P:positive regulation of transcription by RNA polymerase II; IBA:GO_Central
cluster18476	2	Q03413	GO:0045944; P:positive regulation of transcription by RNA polymerase II; IEA:InterPro
cluster19225	2	Q8NHV1	GO:0046039; P:GTP metabolic process; IDA:UniProtKB
cluster19342	2	P28037	GO:0046654; P:tetrahydrofolate biosynthetic process; TAS:RGD
cluster18290	2	P54760	GO:0046777; P:protein autophosphorylation; IDA:UniProtKB

cluster18312	2	A5X7A0	GO:0046872; F:metal ion binding; IEA:UniProtKB-KW
cluster18496	2	Q8R0A2	GO:0046872; F:metal ion binding; IEA:UniProtKB-KW
cluster19368	2	A5D6U8	GO:0046872; F:metal ion binding; IEA:UniProtKB-KW
cluster18342	2	Q5I2B1	GO:0046931; P:pore complex assembly; IEA:InterPro
cluster18376	2	O08764	GO:0046982; F:protein heterodimerization activity; IEA:InterPro
cluster18494	2	Q80WQ9	GO:0046983; F:protein dimerization activity; IEA:InterPro
cluster19320	2	Q642M9	GO:0047115; F:trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity; IEA:UniProtKB-EC
cluster19328	2	Q9HAC7	GO:0047369; F:succinate-hydroxymethylglutarate CoA-transferase activity; IDA:UniProtKB
cluster19272	2	Q9UI94	GO:0047496; P:vesicle transport along microtubule; IEA:Ensembl
cluster18249	2	O14576	GO:0047496; P:vesicle transport along microtubule; IMP:UniProtKB
cluster18363	2	Q5SZD4	GO:0047961; F:glycine N-acyltransferase activity; IEA:InterPro
cluster19229	2	Q5SZD4	GO:0047961; F:glycine N-acyltransferase activity; IEA:InterPro
cluster18279	2	Q8N9V7	GO:0048137; P:spermatocyte division; IEA:Ensembl
cluster18247	2	B8PYG1	GO:0048168; P:regulation of neuronal synaptic plasticity; IEA:InterPro
cluster18272	2	B3DHW5	GO:0048172; P:regulation of short-term neuronal synaptic plasticity; ISS:UniProtKB
cluster19348	2	Q00975	GO:0048265; P:response to pain; IEA:Ensembl
cluster18323	2	Q9WTU6	GO:0048511; P:rhythmic process; IEA:UniProtKB-KW
cluster19209	2	Q91018	GO:0048511; P:rhythmic process; IEA:UniProtKB-KW
cluster19241	2	Q90327	GO:0048511; P:rhythmic process; IEA:UniProtKB-KW
cluster19213	2	P40424	GO:0048538; P:thymus development; IEA:Ensembl
cluster18434	2	A3RK74	GO:0048745; P:smooth muscle tissue development; IMP:ZFIN
cluster19360	2	Q28019	GO:0050436; F:microfibril binding; IDA:AgBase
cluster19279	2	Q9Y2C2	GO:0050770; P:regulation of axonogenesis; IEA:Ensembl
cluster18454	2	P01780	GO:0050776; P:regulation of immune response; TAS:Reactome
cluster18426	2	Q9ET54	GO:0050808; P:synapse organization; IBA:GO_Central
cluster19356	2	Q9ET54	GO:0050808; P:synapse organization; IBA:GO_Central
cluster19321	2	O35927	GO:0050808; P:synapse organization; ISO:MGI
cluster18326	2	Q5PYH5	GO:0050808; P:synapse organization; NAS:UniProtKB
cluster18449	2	Q5PYH5	GO:0050808; P:synapse organization; NAS:UniProtKB
cluster19314	2	Q6R005	GO:0050808; P:synapse organization; NAS:UniProtKB
cluster19389	2	Q5PYH7	GO:0050808; P:synapse organization; NAS:UniProtKB

cluster18311	2	Q9WU42	GO:0050872; P:white fat cell differentiation; IMP:MGI
cluster18274	2	Q9ESZ0	GO:0050882; P:voluntary musculoskeletal movement; IEA:Ensembl
cluster19393	2	Q9P2F8	GO:0051056; P:regulation of small GTPase mediated signal transduction; IEA:InterPro
cluster19237	2	Q8TF74	GO:0051127; P:positive regulation of actin nucleation; IBA:GO_Central
cluster18478	2	Q9ULH7	GO:0051145; P:smooth muscle cell differentiation; IBA:GO_Central
cluster18308	2	Q1LY46	GO:0051260; P:protein homooligomerization; ISS:UniProtKB
cluster18418	2	Q9IAC6	GO:0051414; P:response to cortisol; IDA:AgBase
cluster19288	2	Q9R1N3	GO:0051453; P:regulation of intracellular pH; IBA:GO_Central
cluster19282	2	Q62920	GO:0051963; P:regulation of synapse assembly; IDA:UniProtKB
cluster19234	2	Q14833	GO:0051966; P:regulation of synaptic transmission, glutamatergic; IBA:GO_Central
cluster19290	2	Q27991	GO:0055015; P:ventricular cardiac muscle cell development; IEA:Ensembl
cluster18349	2	Q5F364	GO:0055085; P:transmembrane transport; IBA:GO_Central
cluster18543	2	Q92887	GO:0055085; P:transmembrane transport; IBA:GO_Central
cluster19292	2	Q8VI47	GO:0055085; P:transmembrane transport; IBA:GO_Central
cluster18340	2	Q0VGW6	GO:0055085; P:transmembrane transport; IEA:InterPro
cluster18288	2	Q9GZV3	GO:0055085; P:transmembrane transport; TAS:Reactome
cluster18483	2	P11615	GO:0055117; P:regulation of cardiac muscle contraction; IEA:InterPro
cluster18380	2	Q9NYQ7	GO:0060071; P:Wnt signaling pathway, planar cell polarity pathway; NAS:ParkinsonsUK-UCL
cluster19248	2	P18845	GO:0060084; P:synaptic transmission involved in micturition; ISS:UniProtKB
cluster19309	2	Q17QN4	GO:0060307; P:regulation of ventricular cardiac muscle cell membrane repolarization; IEA:Ensembl
cluster19367	2	Q9WVQ1	GO:0060395; P:SMAD protein signal transduction; IDA:UniProtKB
cluster18333	2	Q9UDU1	GO:0060395; P:SMAD protein signal transduction; ISS:UniProtKB
cluster18366	2	Q99PP9	GO:0060416; P:response to growth hormone; ISO:MGI
cluster18455	2	P31579	GO:0060468; P:prevention of polyspermy; IBA:GO_Central
cluster18411	2	Q9H9B1	GO:0060992; P:response to fungicide; IEA:Ensembl
cluster18338	2	Q90ZE4	GO:0061053; P:somite development; IMP:ZFIN
cluster18485	2	Q1LVF0	GO:0061053; P:somite development; IMP:ZFIN
cluster18292	2	Q96QZ7	GO:0065003; P:protein-containing complex assembly; NAS:ProtInc
cluster18360	2	A1CQG2	GO:0070086; P:ubiquitin-dependent endocytosis; IEA:EnsemblFungi
cluster18373	2	B0LPN4	GO:0070296; P:sarcoplasmic reticulum calcium ion transport; IMP:RGD

cluster18488	2	Q9UHV7	GO:0070328; P:triglyceride homeostasis; IEA:Ensembl
cluster19406	2	Q9UHV7	GO:0070328; P:triglyceride homeostasis; IEA:Ensembl
cluster19392	2	O73737	GO:0070507; P:regulation of microtubule cytoskeleton organization; IBA:GO_Central
cluster18479	2	Q86YQ8	GO:0071277; P:cellular response to calcium ion; IBA:GO_Central
cluster19195	2	Q86YQ8	GO:0071277; P:cellular response to calcium ion; IBA:GO_Central
cluster18386	2	O70141	GO:0071526; P:semaphorin-plexin signaling pathway; IBA:GO_Central
cluster18254	2	Q9P2S2	GO:0071625; P:vocalization behavior; IMP:BHF-UCL
cluster19183	2	Q9C081	GO:0071625; P:vocalization behavior; IMP:BHF-UCL
cluster19364	2	Q9P2S2	GO:0071625; P:vocalization behavior; IMP:BHF-UCL
cluster19379	2	Q9P2S2	GO:0071625; P:vocalization behavior; IMP:BHF-UCL
cluster18446	2	Q9CPW0	GO:0071625; P:vocalization behavior; ISO:MGI
cluster19202	2	E9Q7X7	GO:0071625; P:vocalization behavior; ISO:MGI
cluster18415	2	P58392	GO:0071805; P:potassium ion transmembrane transport; IBA:GO_Central
cluster19180	2	Q9UGI6	GO:0071805; P:potassium ion transmembrane transport; IBA:GO_Central
cluster19343	2	Q9UGI6	GO:0071805; P:potassium ion transmembrane transport; IBA:GO_Central
cluster18501	2	Q9Z0U1	GO:0071847; P:TNFSF11-mediated signaling pathway; IMP:MGI
cluster18276	2	P82264	GO:0072350; P:tricarboxylic acid metabolic process; ISS:UniProtKB
cluster18334	2	Q86TV6	GO:0072659; P:protein localization to plasma membrane; IDA:UniProtKB
cluster19215	2	Q8BGB2	GO:0072659; P:protein localization to plasma membrane; ISS:UniProtKB
cluster18390	2	P0C796	GO:0075732; P:viral penetration into host nucleus; IEA:UniProtKB-KW
cluster19175	2	Q92736	GO:0086005; P:ventricular cardiac muscle cell action potential; ISS:BHF-UCL
cluster18330	2	O97831	GO:0090129; P:positive regulation of synapse maturation; ISS:UniProtKB
cluster18516	2	Q80TR1	GO:0090129; P:positive regulation of synapse maturation; ISS:UniProtKB
cluster19333	2	Q3MHM6	GO:0090136; P:epithelial cell-cell adhesion; IEA:InterPro
cluster18325	2	Q91X85	GO:0097037; P:heme export; IBA:GO_Central
cluster18520	2	A4IFW2	GO:0097374; P:sensory neuron axon guidance; IMP:ZFIN
cluster18250	2	Q09Y11	GO:0098871; C:postsynaptic actin cytoskeleton; IEA:Ensembl
cluster19285	2	P70175	GO:0099072; P:regulation of postsynaptic membrane neurotransmitter receptor levels; IDA:SynGO
cluster19163	2	Q8JZP2	GO:0099504; P:synaptic vesicle cycle; IDA:SynGO
cluster19372	2	A5GFW5	GO:1900026; P:positive regulation of substrate adhesion-dependent cell spreading; ISS:UniProtKB
cluster19407	2	P59808	GO:1900044; P:regulation of protein K63-linked ubiquitination; ISO:MGI

cluster18397	2	Q9Y540	GO:1900535; P:palmitic acid biosynthetic process; IDA:BHF-UCL
cluster18259	2	Q96IZ0	GO:1901300; P:positive regulation of hydrogen peroxide-mediated programmed cell death; IEA:Ensembl
cluster18262	2	Q9QX29	GO:1902630; P:regulation of membrane hyperpolarization; ISO:MGI
cluster18280	2	E9PV86	GO:1902883; P:negative regulation of response to oxidative stress; ISO:MGI
cluster18337	2	P52797	GO:1902961; P:positive regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process; IGI:ARUK-UCL
cluster18316	2	Q9HCP3	GO:1903358; P:regulation of Golgi organization; IDA:UniProtKB
cluster18452	2	Q9W6S8	GO:1904396; P:regulation of neuromuscular junction development; IMP:ZFIN
cluster18512	2	G5ECD6	GO:1904778; P:positive regulation of protein localization to cell cortex; IMP:UniProtKB
cluster18531	2	Q9Y2L9	GO:2000405; P:negative regulation of T cell migration; IMP:UniProtKB
cluster18368	2	A5D8S5	GO:2000564; P:regulation of CD8-positive, alpha-beta T cell proliferation; ISS:UniProtKB
cluster18475	2	Q6NRE7	GO:2000583; P:regulation of platelet-derived growth factor receptor-alpha signaling pathway; ISS:UniProtKB
cluster19274	2	Q8IWQ3	GO:2000807; P:regulation of synaptic vesicle clustering; TAS:ARUK-UCL
cluster19307	2	Q6UXZ4	GO:2001222; P:regulation of neuron migration; IEA:Ensembl
cluster18320	2	Q8TB45	GO:2001236; P:regulation of extrinsic apoptotic signaling pathway; IMP:UniProtKB
cluster18507	2	Q9NSC5	GO:2001256; P:regulation of store-operated calcium entry; IBA:GO_Central

Table S2. Biological process GO terms assigned to the unique clusters identified for *S. tubifer*. The number of assigned to each term is listed.

ID	Description	Number
GO:0008150	biological process	291
GO:0009987	cellular process	178
GO:0065007	biological regulation	144
GO:0050896	response to stimulus	84
GO:0032501	multicellular organismal process	74
GO:0008152	metabolic process	71
GO:0032502	developmental process	71
GO:0007154	cell communication	67
GO:0044237	cellular metabolic process	56
GO:0043170	macromolecule metabolic process	51
GO:0016043	cellular component organization	44
GO:0044238	primary metabolic process	42
GO:0006810	transport	41
GO:0051234	establishment of localization	41
GO:0006807	nitrogen compound metabolic process	39
GO:0051179	localization	39
GO:0006725	cellular aromatic compound metabolic process	34
GO:0046483	heterocycle metabolic process	34
GO:0006139	nucleobase-containing compound metabolic process	32
GO:0016070	RNA metabolic process	25
GO:0051641	cellular localization	18
GO:0006464	cellular protein modification process	17
GO:0006811	ion transport	17
GO:0006928	movement of cell or subcellular component	17
GO:0050877	neurological system process	17
GO:0051704	multi-organism process	17
GO:0006793	phosphorus metabolic process	14
GO:0007155	cell adhesion	14
GO:0006996	organelle organization	13
GO:0015031	protein transport	13
GO:0032989	cellular component morphogenesis	13
GO:0000003	reproduction	9
GO:0002376	immune system process	9
GO:0019538	protein metabolic process	9
GO:0006259	DNA metabolic process	8
GO:0016032	viral process	8
GO:0016192	vesicle-mediated transport	8

GO:0040011	locomotion	8
GO:0051640	organelle localization	8
GO:0006396	RNA processing	7
GO:0006508	proteolysis	7
GO:0006629	lipid metabolic process	7
GO:0065003	macromolecular complex assembly	7
GO:0006936	muscle contraction	6
GO:0022607	cellular component assembly	6
GO:0044255	cellular lipid metabolic process	6
GO:0005975	carbohydrate metabolic process	5
GO:0008015	blood circulation	5
GO:0001775	cell activation	4
GO:0009117	nucleotide metabolic process	4
GO:0032196	transposition	4
GO:0043412	macromolecule modification	4
GO:0043603	cellular amide metabolic process	4
GO:0044419	interspecies interaction between organisms	4
GO:0046903	secretion	4
GO:0048511	rhythmic process	4
GO:0051186	cofactor metabolic process	4
GO:0006082	organic acid metabolic process	3
GO:0009116	nucleoside metabolic process	3
GO:0015074	DNA integration	3
GO:0034622	cellular macromolecular complex assembly	3
GO:0040007	growth	3
GO:0006260	DNA replication	2
GO:0006412	translation	2
GO:0006518	peptide metabolic process	2
GO:0006836	neurotransmitter transport	2
GO:0008283	cell proliferation	2
GO:0043500	muscle adaptation	2
GO:0046794	transport of virus	2
GO:0048469	cell maturation	2
GO:0050879	multicellular organismal movement	2
GO:0051705	multi-organism behavior	2
GO:0001906	cell killing	1
GO:0006091	generation of precursor metabolites and energy	1
GO:0006281	DNA repair	1
GO:0006304	DNA modification	1
GO:0006354	DNA-templated transcription, elongation	1

GO:0006805	xenobiotic metabolic process	1
GO:0006818	hydrogen transport	1
GO:0006865	amino acid transport	1
GO:0006914	autophagy	1
GO:0007005	mitochondrion organization	1
GO:0007030	Golgi organization	1
GO:0007049	cell cycle	1
GO:0007588	excretion	1
GO:0009914	hormone transport	1
GO:0015833	peptide transport	1
GO:0015849	organic acid transport	1
GO:0016049	cell growth	1
GO:0016050	vesicle organization	1
GO:0022406	membrane docking	1
GO:0022610	biological adhesion	1
GO:0031640	killing of cells of other organism	1
GO:0042180	cellular ketone metabolic process	1
GO:0042254	ribosome biogenesis	1
GO:0042908	xenobiotic transport	1
GO:0043101	purine-containing compound salvage	1
GO:0048753	pigment granule organization	1
GO:0051181	cofactor transport	1
GO:0051258	protein polymerization	1
GO:0051276	chromosome organization	1
GO:0051301	cell division	1
GO:0051703	intraspecies interaction between organisms	1

Table S3. GenBank accession numbers NCBI for phylo tree

Accession	Species	Family
MH678615.1	<i>Acentrogobius caninus</i>	Gobiiformes
MG744345.1	<i>Eugnathogobius polylepis</i>	Gobiiformes
MG018480.1	<i>Gymnogobius petschiliensis</i>	Gobiiformes
MK409978.1	<i>Istigobius campbelli</i>	Gobiiformes
MH678617.1	<i>Paratrypauchen microcephalus</i>	Gobiiformes
MF663787.1	<i>Tridentiger obscurus</i>	Gobiiformes
AP005996.1	<i>Apogon semilineatus</i>	Kurtiformes
MH102356.1	<i>Cheilodipterus quinquelineatus</i>	Kurtiformes
MN937193.1	<i>Jaydia lineata</i>	Kurtiformes
AP006030.1	<i>Kurtus gulliveri</i>	Kurtiformes
MN381712.1	<i>Ostorhinchus fleurieu</i>	Kurtiformes
MW007385.1	<i>Ostorhinchus novemfasciatus</i>	Kurtiformes
AP018928.1	<i>Pristicon trimaculatus</i>	Kurtiformes
AP005997.1	<i>Pterapogon kauderni</i>	Kurtiformes
AP018927.1	<i>Sphaeramia orbicularis</i>	Kurtiformes
MF541546.1	<i>Hippocampus hippocampus</i>	Syngnathiformes
MF663787.1	<i>Trachyrhamphus serratus</i>	Syngnathiformes