**Supplementary materials**

**Combination of genomic and proteomic data in searching novel Tardigrade proteins responsible for radiation resistance**

1. **Functional annotation**  
     
   Downloaded the annotated genome (“.gff”):  
   wget <http://public.dobzhanskycenter.ru/mrayko/BIMM185/augustus.whole.gff>  
     
   Got only proteins using getAnnoFasta.pl script:  
   wget <http://augustus.gobics.de/binaries/scripts/getAnnoFasta.pl>  
   ./getAnnoFasta.pl augustus.whole.gff  
     
   Obtained file “.aa” and counted how many proteins are there:  
   grep -c ">" augustus.whole.aa  
   16435
2. **Physical localization**Downloaded list of peptides (chromatin fraction) from tandem mass spectrometry:  
   wget <http://public.dobzhanskycenter.ru/mrayko/BIMM185/peptides.fa>  
     
   Created a database with proteins to understand from which proteins those peptides came:  
   makeblastdb -in augustus.whole.aa -parse\_seqids -dbtype prot  
     
   Made local alignment to get the indexes of proteins:  
   blastp -db ./augustus.whole.aa -query peptides.fa -out chromatin\_proteins  
     
   Indexed file with all tardigrade proteins:  
   samtools faidx augustus.whole.aa  
     
   Extracted only protein ids:  
   grep "[\<>]" chromatin\_proteins | awk -F" " '{print $1}' | cut -c 2- | sort | uniq > file.txt  
     
   Filtered proteins:  
   xargs samtools faidx augustus.whole.aa < file.txt > proteins.fa  
     
   Proteins that were matched with peptides on 100%

from Bio import SeqIO

with open("outfile\_protein.fasta", "w") as f:

proteins = []

for peptide in SeqIO.parse("peptides.fa", "fasta"):

for protein in SeqIO.parse("augustus.whole.aa", "fasta"):

if peptide.seq in protein.seq:

if protein.seq not in proteins:

proteins.append(protein.seq)

f.write(str(">" + protein.id + "\n"))

f.write(str(protein.seq) + "\n")

else:

continue

**grep ">" outfile\_protein.fasta | wc -l**

**19**

1. **Localization prediction  
     
   3a. WoLF PSORT** **prediction of the subcellular localization**Service: <https://wolfpsort.hgc.jp/>  
     
   Hereinafter proteins that were matched with peptides on 100% are shown in yellow.  
     
   Table 1 - Results of prediction of the subcellular localization by WoLF PSORT.

| **Protein** | **Signal peptide** |
| --- | --- |
| g10513.t1 | nucl: 20, cyto\_nucl: 14.5, cyto: 7, extr: 3, E.R.: 1, golg: 1 |
| g10514.t1 | nucl: 19, cyto\_nucl: 15, cyto: 9, extr: 3, mito: 1 |
| g11320.t1 | plas: 24.5, extr\_plas: 16, extr: 6.5, lyso: 1 |
| g11513.t1 | cyto: 17, cyto\_nucl: 12.8333, cyto\_mito: 9.83333, nucl: 7.5, E.R.: 3, mito: 1.5, plas: 1, pero: 1, golg: 1 |
| g11806.t1 | nucl: 18, cyto\_nucl: 11.8333, mito: 5, extr: 4, cyto: 3.5, cyto\_pero: 2.66667, cysk\_plas: 1 |
| g11960.t1 | nucl: 32 |
| g12388.t1 | extr: 25, plas: 4, mito: 2, lyso: 1 |
| g12510.t1 | plas: 29, cyto: 3 |
| g12562.t1 | extr: 30, lyso: 2 |
| g1285.t1 | extr: 25, plas: 5, mito: 1, lyso: 1 |
| g13530.t1 | extr: 13, nucl: 6.5, lyso: 5, cyto\_nucl: 4.5, plas: 3, E.R.: 3, cyto: 1.5 |
| g14472.t1 | nucl: 28, plas: 2, cyto: 1, cysk: 1 |
| g15153.t1 | extr: 32 |
| g15484.t1 | nucl: 17.5, cyto\_nucl: 15.3333, cyto: 12, cyto\_mito: 6.83333, plas: 1, golg: 1 |
| g16318.t1 | nucl: 20.5, cyto\_nucl: 13, extr: 5, cyto: 4.5, E.R.: 1, golg: 1 |
| g16368.t1 | nucl: 20.5, cyto\_nucl: 13, extr: 5, cyto: 4.5, E.R.: 1, golg: 1 |
| g2203.t1 | plas: 29, nucl: 2, golg: 1 |
| g3428.t1 | mito: 18, cyto: 11, extr: 2, nucl: 1 |
| g3679.t1 | extr: 26, mito: 2, lyso: 2, plas: 1, E.R.: 1 |
| g4106.t1 | E.R.: 14.5, E.R.\_golg: 9.5, extr: 7, golg: 3.5, lyso: 3, pero: 2, plas: 1, mito: 1 |
| g4970.t1 | plas: 32 |
| g5237.t1 | plas: 24, mito: 8 |
| g5443.t1 | extr: 28, nucl: 3, cyto: 1 |
| g5467.t1 | extr: 27, plas: 4, mito: 1 |
| g5502.t1 | extr: 31, lyso: 1 |
| g5503.t1 | extr: 29, plas: 1, mito: 1, lyso: 1 |
| g5510.t1 | plas: 23, mito: 7, E.R.: 1, golg: 1 |
| g5616.t1 | extr: 31, mito: 1 |
| g5641.t1 | extr: 31, lyso: 1 |
| g5927.t1 | nucl: 30.5, cyto\_nucl: 16.5, cyto: 1.5 |
| g702.t1 | extr: 29, plas: 2, lyso: 1 |
| g7861.t1 | nucl: 16, cyto\_nucl: 14, cyto: 8, plas: 5, pero: 1, cysk: 1, golg: 1 |
| g8100.t1 | nucl: 16.5, cyto\_nucl: 12.5, cyto: 7.5, plas: 5, extr: 2, E.R.: 1 |
| g8312.t1 | nucl: 15.5, cyto\_nucl: 15.5, cyto: 12.5, mito: 2, plas: 1, golg: 1 |

**3b. TargetP 2.0 Server prediction of the subcellular localization**Service: <http://www.cbs.dtu.dk/services/TargetP/>  
  
Table 1 - Results of prediction of the subcellular localization by TargetP.

| **Protein** | **Signal peptide prediction** | **CS position** |
| --- | --- | --- |
| g10513.t1 | OTHER |  |
| g10514.t1 | OTHER |  |
| g11320.t1 | SP | 20-21. AYS-AG. Pr: 0.7236 |
| g11513.t1 | OTHER |  |
| g11806.t1 | OTHER |  |
| g11960.t1 | OTHER |  |
| g12388.t1 | SP | 16-17. ASA-SS. Pr: 0.6485 |
| g12510.t1 | OTHER |  |
| g12562.t1 | SP | 16-17. SYA-AN. Pr: 0.7910 |
| g1285.t1 | SP | 16-17. ASA-TS. Pr: 0.7127 |
| g13530.t1 | SP | 19-20. TIP-FT. Pr: 0.3552 |
| g14472.t1 | OTHER |  |
| g15153.t1 | SP | 16-17. AYA-AN. Pr: 0.8378 |
| g15484.t1 | OTHER |  |
| g16318.t1 | OTHER |  |
| g16368.t1 | OTHER |  |
| g2203.t1 | OTHER |  |
| g3428.t1 | OTHER |  |
| g3679.t1 | SP | 18-19. TFA-AR. Pr: 0.5523 |
| g4106.t1 | OTHER |  |
| g4970.t1 | OTHER |  |
| g5237.t1 | OTHER |  |
| g5443.t1 | OTHER |  |
| g5467.t1 | SP | 16-17. ASA-GS. Pr: 0.6543 |
| g5502.t1 | SP | 16-17. ASA-GS. Pr: 0.6833 |
| g5503.t1 | SP | 16-17. ASA-GS. Pr: 0.6833 |
| g5510.t1 | OTHER |  |
| g5616.t1 | SP | 16-17. ACA-AN. Pr: 0.5270 |
| g5641.t1 | SP | 16-17. ACA-AS. Pr: 0.4873 |
| g5927.t1 | OTHER |  |
| g702.t1 | SP | 16-17. ALA-AN. Pr: 0.8153 |
| g7861.t1 | OTHER |  |
| g8100.t1 | OTHER |  |
| g8312.t1 | OTHER |  |

1. **BLAST search**Table 3 - The best hits in UniProtKB/Swiss-Prot database.

| **Protein id** | **Description** | **Accession Number** | **E-value** | **% Ident** | **% Query coverage** |
| --- | --- | --- | --- | --- | --- |
| g10513.t1 |  |  |  |  |  |
| g10514.t1 |  |  |  |  |  |
| g11320.t1 |  |  |  |  |  |
| g11513.t1 | Full=Trafficking protein particle complex subunit 9; AltName: Full=NIK- and IKBKB-binding protein [Bos taurus] | [Q32PH0.1](https://www.ncbi.nlm.nih.gov/protein/Q32PH0.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZEUMCTR013) | 7e-83 | 28.61 | 68 |
| g11806.t1 |  |  |  |  |  |
| g11960.t1 | Full=E3 ubiquitin-protein ligase BRE1B; Short=BRE1-B; AltName: Full=RING finger protein 40; AltName: Full=RING-type E3 ubiquitin transferase BRE1B; AltName: Full=Syntaxin-1-interacting RING finger protein; Short=Protein staring [Rattus norvegicus] | [Q8CJB9.1](https://www.ncbi.nlm.nih.gov/protein/Q8CJB9.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZF67T6U013) | 6e-98 | 26.96 | 96 |
| g12388.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | [P0DPW4.1](https://www.ncbi.nlm.nih.gov/protein/P0DPW4.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZFW4TWN013) | 3e-11 | 38.1 | 50 |
| g12510.t1 |  |  |  |  |  |
| g12562.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | [P0DPW4.1](https://www.ncbi.nlm.nih.gov/protein/P0DPW4.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZG3483A013) | 7e-13 | 39.76 | 41 |
| g1285.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | [P0DPW4.1](https://www.ncbi.nlm.nih.gov/protein/P0DPW4.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZG3483A013) | 2e-12 | 37.21 | 44 |
| g13530.t1 |  |  |  |  |  |
| g14472.t1 |  |  |  |  |  |
| g15153.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | [P0DPW4.1](https://www.ncbi.nlm.nih.gov/protein/P0DPW4.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZG3483A013) | 2e-14 | 39.76 | 46 |
| g15484.t1 | Full=Vacuolar protein sorting-associated protein 51 homolog; AltName: Full=Protein fat-free [Danio rerio] | [Q155U0.1](https://www.ncbi.nlm.nih.gov/protein/Q155U0.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZGPMDY701R) | 0 | 45.03 | 78 |
| g16318.t1 | RecName: Full=Eukaryotic translation initiation factor 3 subunit A; Short=eIF3a; AltName: Full=Eukaryotic translation initiation factor 3 subunit 10; AltName: Full=eIF-3-theta [Xenopus laevis] | [A2VD00.1](https://www.ncbi.nlm.nih.gov/protein/A2VD00.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZGUSXUN013) | 4e-08 | 36.11 | 40 |
| g16368.t1 | RecName: Full=Eukaryotic translation initiation factor 3 subunit A; Short=eIF3a; AltName: Full=Eukaryotic translation initiation factor 3 subunit 10; AltName: Full=eIF-3-theta [Xenopus tropicalis] | [A4II09.1](https://www.ncbi.nlm.nih.gov/protein/A4II09.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZH0J5SG016) | 1e-05 | 39.29 | 35 |
| g2203.t1 | RecName: Full=Myogenesis-regulating glycosidase; AltName: Full=Nuclear envelope transmembrane protein 37; AltName: Full=Uncharacterized family 31 glucosidase KIAA1161 [Mus musculus] | [Q69ZQ1.2](https://www.ncbi.nlm.nih.gov/protein/Q69ZQ1.2?report=genbank&log$=prottop&blast_rank=1&RID=2ZH5ECP7016) | 2e-126 | 35.93 | 75 |
| g3428.t1 | RecName: Full=Myosin regulatory light chain; AltName: Full=Non-muscle myosin regulatory light chain; Short=nmRLC [Caenorhabditis elegans] | [Q09510.1](https://www.ncbi.nlm.nih.gov/protein/Q09510.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZH8W3N6016) | 9e-65 | 56.60 | 91 |
| g3679.t1 | RecName: Full=Zinc metalloproteinase nas-14; AltName: Full=Nematode astacin 14; Flags: Precursor [Caenorhabditis elegans] | [Q19269.2](https://www.ncbi.nlm.nih.gov/protein/Q19269.2?report=genbank&log$=prottop&blast_rank=1&RID=2ZHEMXJJ013) | 7e-22 | 29.72 | 72 |
| g4106.t1 |  |  |  |  |  |
| g4970.t1 | RecName: Full=Enteropeptidase; AltName: Full=Enterokinase; AltName: Full=Serine protease 7; AltName: Full=Transmembrane protease serine 15; Contains: RecName: Full=Enteropeptidase non-catalytic heavy chain; Contains: RecName: Full=Enteropeptidase catalytic light chain [Mus musculus] | [P97435.1](https://www.ncbi.nlm.nih.gov/protein/P97435.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZHNEHUW016) | 4e-16 | 25.34 | 46 |
| g5237.t1 |  |  |  |  |  |
| g5443.t1 |  |  |  |  |  |
| g5467.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | [P0DPW4.1](https://www.ncbi.nlm.nih.gov/protein/P0DPW4.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZJ0F9G1013) | 4e-13 | 44.12 | 46 |
| g5502.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | [P0DPW4.1](https://www.ncbi.nlm.nih.gov/protein/P0DPW4.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZJ3CF4X013) | 6e-14 | 39.76 | 33 |
| g5503.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | [P0DPW4.](https://www.ncbi.nlm.nih.gov/protein/P0DPW4.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZJ6FCUW016)1 | 7e-14 | 39.76 | 38 |
| g5510.t1 |  |  |  |  |  |
| g5616.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | [P0DPW4.1](https://www.ncbi.nlm.nih.gov/protein/P0DPW4.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZJCVT6R013) | 2e-14 | 40.96 | 40 |
| g5641.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | [P0DPW4.1](https://www.ncbi.nlm.nih.gov/protein/P0DPW4.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZJFSBW2016) | 5e-13 | 39.29 | 43 |
| g5927.t1 | RecName: Full=Glucosamine 6-phosphate N-acetyltransferase; AltName: Full=Phosphoglucosamine acetylase; AltName: Full=Phosphoglucosamine transacetylase [Caenorhabditis elegans] | [Q17427.1](https://www.ncbi.nlm.nih.gov/protein/Q17427.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZJMN8RE01R) | 1e-18 | 38.64 | 14 |
| g702.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | [P0DPW4.1](https://www.ncbi.nlm.nih.gov/protein/P0DPW4.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZJFSBW2016) | 1e-11 | 40.48 | 39 |
| g7861.t1 | RecName: Full=SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1; AltName: Full=HepA-related protein; AltName: Full=Sucrose nonfermenting protein 2-like 1 [Rattus norvegicus] | [B4F769.1](https://www.ncbi.nlm.nih.gov/protein/B4F769.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZJX8GK5013) | 2e-71 | 37.21 | 99 |
| g8100.t1 | RecName: Full=Inositol monophosphatase 3; Short=IMP 3; Short=IMPase 3; AltName: Full=3'(2'), 5'-bisphosphate nucleotidase 2; AltName: Full=Inositol monophosphatase domain-containing protein 1; AltName: Full=Inositol-1(or 4)-monophosphatase 3; AltName: Full=Myo-inositol monophosphatase A3 [Danio rerio] | [Q2YDR3.1](https://www.ncbi.nlm.nih.gov/protein/Q2YDR3.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZK0A3ZJ016) | 3e-46 | 36.04 | 22 |
| g8312.t1 | RecName: Full=Vacuolar protein sorting-associated protein 41 homolog; AltName: Full=VAM2 homolog; Short=mVAM2 [Mus musculus] | [Q5KU39.1](https://www.ncbi.nlm.nih.gov/protein/Q5KU39.1?report=genbank&log$=prottop&blast_rank=1&RID=2ZK2SUDC016) | 0 | 40.84 | 84 |

1. **Pfam prediction**Table 4 - Results of the protein prediction by Pfam.

| **Protein** | **Top hit** | **Description** |
| --- | --- | --- |
| g10513.t1 |  |  |
| g10514.t1 |  |  |
| g11320.t1 |  |  |
| g11513.t1 | TRAPPC9-Trs120 | Transport protein Trs120 or TRAPPC9, TRAPP II complex subunit |
| g11806.t1 |  |  |
| g11960.t1 | zf-C3HC4 | Zinc finger, C3HC4 type (RING finger) |
| g12388.t1 | CBM\_14 | Chitin binding Peritrophin-A domain |
| g12510.t1 |  |  |
| g12562.t1 | CBM\_14 | Chitin binding Peritrophin-A domain |
| g1285.t1 | CBM\_14 | Chitin binding Peritrophin-A domain |
| g13530.t1 |  |  |
| g14472.t1 |  |  |
| g15153.t1 | CBM\_14 | Chitin binding Peritrophin-A domain |
| g15484.t1 | Vps51 | Vps51/Vps67 |
| g16318.t1 |  |  |
| g16368.t1 |  |  |
| g2203.t1 | Glyco\_hydro\_31 | Glycosyl hydrolases family 31 |
| g3428.t1 |  |  |
| g3679.t1 | Astacin | Astacin (Peptidase family M12A) |
| g4106.t1 |  |  |
| g4970.t1 | Trypsin | Trypsin |
| g5237.t1 |  |  |
| g5443.t1 |  |  |
| g5467.t1 | CBM\_14 | Chitin binding Peritrophin-A domain |
| g5502.t1 | CBM\_14 | Chitin binding Peritrophin-A domain |
| g5503.t1 | CBM\_14 | Chitin binding Peritrophin-A domain |
| g5510.t1 | MARVEL | Membrane-associating domain |
| g5616.t1 | CBM\_14 | Chitin binding Peritrophin-A domain |
| g5641.t1 | CBM\_14 | Chitin binding Peritrophin-A domain |
| g5927.t1 |  |  |
| g702.t1 | CBM\_14 | Chitin binding Peritrophin-A domain |
| g7861.t1 | SNF2\_N | SNF2 family N-terminal domain |
| g8100.t1 | Inositol\_P | Inositol monophosphatase family |
| g8312.t1 | Clathrin | Region in Clathrin and VPS |

1. **Integration of the evidence**Table 5 - Obtained information about proteins of interest.

| Protein | BLAST | BLAST E-value | Pfam | WoLF PSORT | TargetP |
| --- | --- | --- | --- | --- | --- |
| g10513.t1 |  |  |  | nucl: 20, cyto\_nucl: 14.5, cyto: 7, extr: 3, E.R.: 1, golg: 1 |  |
| g10514.t1 |  |  |  | nucl: 19, cyto\_nucl: 15, cyto: 9, extr: 3, mito: 1 |  |
| g11320.t1 |  |  |  | plas: 24.5, extr\_plas: 16, extr: 6.5, lyso: 1 | 20-21. AYS-AG. Pr: 0.7236 |
| g11513.t1 | Full=Trafficking protein particle complex subunit 9; AltName: Full=NIK- and IKBKB-binding protein [Bos taurus] | 7e-83 | Transport protein Trs120 or TRAPPC9, TRAPP II complex subunit | cyto: 17, cyto\_nucl: 12.8333, cyto\_mito: 9.83333, nucl: 7.5, E.R.: 3, mito: 1.5, plas: 1, pero: 1, golg: 1 |  |
| g11806.t1 |  |  |  | nucl: 18, cyto\_nucl: 11.8333, mito: 5, extr: 4, cyto: 3.5, cyto\_pero: 2.66667, cysk\_plas: 1 |  |
| g11960.t1 | Full=E3 ubiquitin-protein ligase BRE1B; Short=BRE1-B; AltName: Full=RING finger protein 40; AltName: Full=RING-type E3 ubiquitin transferase BRE1B; AltName: Full=Syntaxin-1-interacting RING finger protein; Short=Protein staring [Rattus norvegicus] | 6e-98 | Zinc finger, C3HC4 type (RING finger) | nucl: 32 |  |
| g12388.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | 3e-11 | Chitin binding Peritrophin-A domain | extr: 25, plas: 4, mito: 2, lyso: 1 | 16-17. ASA-SS. Pr: 0.6485 |
| g12510.t1 |  |  |  | plas: 29, cyto: 3 |  |
| g12562.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | 7e-13 | Chitin binding Peritrophin-A domain | extr: 30, lyso: 2 | 16-17. SYA-AN. Pr: 0.7910 |
| g1285.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | 2e-12 | Chitin binding Peritrophin-A domain | extr: 25, plas: 5, mito: 1, lyso: 1 | 16-17. ASA-TS. Pr: 0.7127 |
| g13530.t1 |  |  |  | extr: 13, nucl: 6.5, lyso: 5, cyto\_nucl: 4.5, plas: 3, E.R.: 3, cyto: 1.5 | 19-20. TIP-FT. Pr: 0.3552 |
| g14472.t1 |  |  |  | nucl: 28, plas: 2, cyto: 1, cysk: 1 |  |
| g15153.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | 2e-14 | Chitin binding Peritrophin-A domain | extr: 32 | 16-17. AYA-AN. Pr: 0.8378 |
| g15484.t1 | Full=Vacuolar protein sorting-associated protein 51 homolog; AltName: Full=Protein fat-free [Danio rerio] | 0 | Vps51/Vps67 | nucl: 17.5, cyto\_nucl: 15.3333, cyto: 12, cyto\_mito: 6.83333, plas: 1, golg: 1 |  |
| g16318.t1 | RecName: Full=Eukaryotic translation initiation factor 3 subunit A; Short=eIF3a; AltName: Full=Eukaryotic translation initiation factor 3 subunit 10; AltName: Full=eIF-3-theta [Xenopus laevis] | 4e-08 |  | nucl: 20.5, cyto\_nucl: 13, extr: 5, cyto: 4.5, E.R.: 1, golg: 1 |  |
| g16368.t1 | RecName: Full=Eukaryotic translation initiation factor 3 subunit A; Short=eIF3a; AltName: Full=Eukaryotic translation initiation factor 3 subunit 10; AltName: Full=eIF-3-theta [Xenopus tropicalis] | 1e-05 |  | nucl: 20.5, cyto\_nucl: 13, extr: 5, cyto: 4.5, E.R.: 1, golg: 1 |  |
| g2203.t1 | RecName: Full=Myogenesis-regulating glycosidase; AltName: Full=Nuclear envelope transmembrane protein 37; AltName: Full=Uncharacterized family 31 glucosidase KIAA1161 [Mus musculus] | 2e-126 | Glycosyl hydrolases family 31 | plas: 29, nucl: 2, golg: 1 |  |
| g3428.t1 | RecName: Full=Myosin regulatory light chain; AltName: Full=Non-muscle myosin regulatory light chain; Short=nmRLC [Caenorhabditis elegans] | 9e-65 |  | mito: 18, cyto: 11, extr: 2, nucl: 1 |  |
| g3679.t1 | RecName: Full=Zinc metalloproteinase nas-14; AltName: Full=Nematode astacin 14; Flags: Precursor [Caenorhabditis elegans] | 7e-22 | Astacin (Peptidase family M12A) | extr: 26, mito: 2, lyso: 2, plas: 1, E.R.: 1 | 18-19. TFA-AR. Pr: 0.5523 |
| g4106.t1 |  |  |  | E.R.: 14.5, E.R.\_golg: 9.5, extr: 7, golg: 3.5, lyso: 3, pero: 2, plas: 1, mito: 1 |  |
| g4970.t1 | RecName: Full=Enteropeptidase; AltName: Full=Enterokinase; AltName: Full=Serine protease 7; AltName: Full=Transmembrane protease serine 15; Contains: RecName: Full=Enteropeptidase non-catalytic heavy chain; Contains: RecName: Full=Enteropeptidase catalytic light chain [Mus musculus] | 4e-16 | Trypsin | plas: 32 |  |
| g5237.t1 |  |  |  | plas: 24, mito: 8 |  |
| g5443.t1 |  |  |  | extr: 28, nucl: 3, cyto: 1 |  |
| g5467.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | 4e-13 | Chitin binding Peritrophin-A domain | extr: 27, plas: 4, mito: 1 | 16-17. ASA-GS. Pr: 0.6543 |
| g5502.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | 6e-14 | Chitin binding Peritrophin-A domain | extr: 31, lyso: 1 | 16-17. ASA-GS. Pr: 0.6833 |
| g5503.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | 7e-14 | Chitin binding Peritrophin-A domain | extr: 29, plas: 1, mito: 1, lyso: 1 | 16-17. ASA-GS. Pr: 0.6833 |
| g5510.t1 |  |  | Membrane-associating domain | plas: 23, mito: 7, E.R.: 1, golg: 1 |  |
| g5616.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | 2e-14 | Chitin binding Peritrophin-A domain | extr: 31, mito: 1 | 16-17. ACA-AN. Pr: 0.5270 |
| g5641.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | 5e-13 | Chitin binding Peritrophin-A domain | extr: 31, lyso: 1 | 16-17. ACA-AS. Pr: 0.4873 |
| g5927.t1 | RecName: Full=Glucosamine 6-phosphate N-acetyltransferase; AltName: Full=Phosphoglucosamine acetylase; AltName: Full=Phosphoglucosamine transacetylase [Caenorhabditis elegans] | 1e-18 |  | nucl: 30.5, cyto\_nucl: 16.5, cyto: 1.5 |  |
| g702.t1 | RecName: Full=U-scoloptoxin(01)-Er1a; Short=U-SLPTX(01)-Er1a; Flags: Precursor [Ethmostigmus rubripes] | 1e-11 | Chitin binding Peritrophin-A domain | extr: 29, plas: 2, lyso: 1 | 16-17. ALA-AN. Pr: 0.8153 |
| g7861.t1 | RecName: Full=SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1; AltName: Full=HepA-related protein; AltName: Full=Sucrose nonfermenting protein 2-like 1 [Rattus norvegicus] | 2e-71 | SNF2 family N-terminal domain | nucl: 16, cyto\_nucl: 14, cyto: 8, plas: 5, pero: 1, cysk: 1, golg: 1 |  |
| g8100.t1 | RecName: Full=Inositol monophosphatase 3; Short=IMP 3; Short=IMPase 3; AltName: Full=3'(2'), 5'-bisphosphate nucleotidase 2; AltName: Full=Inositol monophosphatase domain-containing protein 1; AltName: Full=Inositol-1(or 4)-monophosphatase 3; AltName: Full=Myo-inositol monophosphatase A3 [Danio rerio] | 3e-46 | Inositol monophosphatase family | nucl: 16.5, cyto\_nucl: 12.5, cyto: 7.5, plas: 5, extr: 2, E.R.: 1 |  |
| g8312.t1 | RecName: Full=Vacuolar protein sorting-associated protein 41 homolog; AltName: Full=VAM2 homolog; Short=mVAM2 [Mus musculus] | 0 | Region in Clathrin and VPS | nucl: 15.5, cyto\_nucl: 15.5, cyto: 12.5, mito: 2, plas: 1, golg: 1 |  |