Supplementary Table 1 | All 191 hit sequences for secreted proteins of the venom gland tissue (VgT) cDNA library. Contig names with isogroup number and read numbers are given. For each transcript the sequence description based on the results using BLAST nr is given including sequence length, e-value, and mean similarity. BLAST2GO results are shown including Gene ontology terms (GO's) and the InterProScan results (green background highlightspositive SignalP results) to identify signalpeptides. Additionally external SignalP search was condcuted to identify signal peptides (positive hits are highlighted in blue font color).

Nr	Contig sequence name	Isogroup	reads	Sequence description (BLAST nr, E-value= > 0.0001)	Length (aa pos.)	E-Value	mean Similarity	Gene ontology terms and annotation (GO's)	Nr. Of GO's	Interpro scan results (BLAST2GO) | - Green background = SignalP hit in BLAST2GO - SignalP 4.0 results with SignalP 3.1 sensitivity settings (externally identified siganl peptides)
1	contig00005_gene_isogroup00001_length_1165_3	1	102	chitinase 2	389	2.3E-57	57.50%	F:catalytic activity	1	IPR001223; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SSF54556 (SUPERFAMILY)
2	contig00043_gene_isogroup00001_length_791_0	1	1321	low-density lipoprotein receptor-related protein 2	264	5.4E-35	57.70%	F:scavenger receptor activity; C:integral to membrane; C:membrane	3	IPR002172; IPR023415; PR00261 (PRINTS), PTHR10529 (PANTHER), SignalP-NN(euk) (SIGNALP)
3	contig00056_gene_isogroup00001_length_1122_1	1	2058	isoform a	374	4.5E-43	53.60%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
4	contig00072_gene_isogroup00001_length_669_5	1	83	suppressor of tumorigenicity protein 14	223	2E-31	51.70%	-	0	IPR001254; IPR001314; IPR002172; IPR009003; IPR018114; IPR023415; G3DSA:2.40.10.10 (GENE3D), G3DSA:4.10.1220.10 (GENE3D), PTHR24256 (PANTHER), PTHR24256:SF20 (PANTHER)
5	contig00075_gene_isogroup00001_length_1389_4	1	5839	suppressor of tumorigenicity 14 protein homolog	463	8.9E-60	49.90%	-	0	IPR001254; IPR002172; IPR009003; IPR018114; IPR023415; PR00261 (PRINTS), G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), PTHR24256:SF20 (PANTHER), tmhmm (TMHMM)
6	contig00117_gene_isogroup00001_length_662_1	1	2059	---NA---	221			-	0	IPR004169; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF57059 (SUPERFAMILY)
7	contig00124_gene_isogroup00001_length_674_1	1	400	---NA---	225			-	0	IPR004169; SSF57059 (SUPERFAMILY)
8	contig00153_gene_isogroup00001_length_1013_4	1	190	chitinase 2	338	3.3E-56	61.70%	F:hydrolase activity; P:carbohydrate metabolic process	2	IPR001223; IPR001579; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54556 (SUPERFAMILY)
9	contig00202_gene_isogroup00001_length_740_0	1	28945	chitinase 2	247	1.3E-63	61.60%	F:hydrolase activity; P:metabolic process	2	IPR001223; IPR001579; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SSF54556 (SUPERFAMILY)
10	isotig00044_gene_isogroup00003_length_1180_numContigs_5_5	3	2341	isoform a	393	4.1E-50	56.70%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
11	isotig00045_gene_isogroup00003_length_1198_numContigs_6_5	3	2640	isoform a	399	4.5E-50	56.70%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
12	isotig00046_gene_isogroup00003_length_1167_numContigs_5_4	3	2302	isoform a	389	5.9E-50	56.70%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
13	isotig00047_gene_isogroup00003_length_1185_numContigs_6_4	3	2601	isoform a	395	7.3E-50	56.70%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)

14	isotig00048_gene_isogroup00003_length_1133_numContigs_5_5	3	1966	isoform a	377	7.9E-51	57.20%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
15	isotig00049_gene_isogroup00003_length_1151_numContigs_5_5	3	2391	isoform a	383	8.2E-51	57.20%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
16	isotig00050_gene_isogroup00003_length_1120_numContigs_5_4	3	1927	isoform a	373	1.3E-50	57.40%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
17	isotig00051_gene_isogroup00003_length_1138_numContigs_5_4	3	2352	isoform a	379	1.4E-50	57.40%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
18	isotig00052_gene_isogroup00003_length_1149_numContigs_5_5	3	1832	isoform a	383	2.8E-50	56.90%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
19	isotig00053_gene_isogroup00003_length_1132_numContigs_2_4	3	1674	isoform a	377	9.2E-49	56.60%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
20	isotig00054_gene_isogroup00003_length_1136_numContigs_5_4	3	1793	isoform a	379	3.8E-50	57.10%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
21	isotig00055_gene_isogroup00003_length_1299_numContigs_3_0	3	398	isoform a	433	6.6E-49	56.80%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
22	isotig00056_gene_isogroup00003_length_1178_numContigs_4_3	3	1123	isoform a	393	1.4E-49	57.30%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
23	isotig00057_gene_isogroup00003_length_1131_numContigs_3_3	3	1064	isoform a	377	8E-50	57.40%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
24	isotig00059_gene_isogroup00004_length_1957_numContigs_6_5	4	7834	suppressor of tumorigenicity 14 protein homolog	652	1.2E-75	50.20%	-	0	IPR001254; IPR002172; IPR009003; IPR018114; IPR023415; PR00261 (PRINTS), G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), PTHR24256:SF20 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
25	isotig00060_gene_isogroup00004_length_1957_numContigs_6_5	4	8113	suppressor of tumorigenicity 14 protein homolog	652	1.6E-75	50.30%	-	0	IPR001254; IPR002172; IPR009003; IPR018114; IPR023415; PR00261 (PRINTS), G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), PTHR24256:SF20 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
26	isotig00061_gene_isogroup00004_length_1918_numContigs_4_5	4	6670	suppressor of tumorigenicity 14 protein homolog	639	5.5E-45	53.40%	F:catalytic activity	1	IPR001254; IPR001314; IPR002172; IPR009003; IPR018114; IPR023415; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
27	isotig00062_gene_isogroup00004_length_1918_numContigs_4_5	4	6949	suppressor of tumorigenicity 14 protein homolog	639	5.8E-45	53.40%	F:catalytic activity	1	IPR001254; IPR001314; IPR002172; IPR009003; IPR018114; IPR023415; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
28	isotig00063_gene_isogroup00004_length_1520_numContigs_7_3	4	6818	isoform a	507	2.5E-22	59.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER), tmhmm (TMHMM)
29	isotig00064_gene_isogroup00004_length_1522_numContigs_7_5	4	5879	isoform a	507	2.3E-22	59.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER), tmhmm (TMHMM)
30	isotig00065_gene_isogroup00004_length_1489_numContigs_6_3	4	5787	isoform a	497	1.7E-22	59.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER), tmhmm (TMHMM)
31	isotig00066_gene_isogroup00004_length_1491_numContigs_6_5	4	4848	isoform a	497	1.4E-22	59.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER), tmhmm (TMHMM)

32	isotig00067_gene_isogroup00005_length_1173_numContigs_8_1	5	2982	plasma kallikrein-like	391	2.9E-39	54.90%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
33	isotig00068_gene_isogroup00005_length_1172_numContigs_7_1	5	2451	plasma kallikrein-like	391	2.5E-48	56.10%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
34	isotig00069_gene_isogroup00005_length_1169_numContigs_8_1	5	2765	plasma kallikrein-like	390	3.2E-46	54.90%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
35	isotig00070_gene_isogroup00005_length_1165_numContigs_8_2	5	3316	plasma kallikrein-like	388	1.3E-39	54.90%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
36	isotig00071_gene_isogroup00005_length_1164_numContigs_7_2	5	2785	26kda protease	388	9.9E-49	56.10%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
37	isotig00072_gene_isogroup00005_length_1161_numContigs_8_2	5	3099	26kda protease	387	1.2E-46	54.60%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
38	isotig00073_gene_isogroup00005_length_1138_numContigs_7_1	5	1840	plasma kallikrein-like	379	4.4E-49	55.70%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
39	isotig00074_gene_isogroup00005_length_1130_numContigs_7_2	5	2174	plasma kallikrein-like	376	6.4E-49	55.70%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
40	isotig00077_gene_isogroup00007_length_2209_numContigs_5_4	7	2146	chitinase 2	736	3.5E-76	63.50%	F:hydrolase activity; P:metabolic process	2	IPR001223; IPR001579; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54556 (SUPERFAMILY)
41	isotig00078_gene_isogroup00007_length_2223_numContigs_5_4	7	2126	chitinase 2	741	7.3E-76	63.50%	F:hydrolase activity; P:metabolic process	2	IPR001223; IPR001579; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54556 (SUPERFAMILY)
42	isotig00079_gene_isogroup00007_length_2211_numContigs_6_5	7	2118	chitinase 2	737	1E-47	68.10%	P:carbohydrate metabolic process; F:hydrolase activity	2	IPR001223; IPR001579; IPR002557; IPR011583; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
43	isotig00080_gene_isogroup00007_length_2225_numContigs_6_5	7	2098	chitinase 2	741	2E-47	68.10%	P:carbohydrate metabolic process; F:hydrolase activity	2	IPR001223; IPR001579; IPR002557; IPR011583; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
44	isotig00081_gene_isogroup00007_length_2210_numContigs_5_5	7	1842	chitinase 2	736	8.6E-76	63.60%	F:hydrolase activity; P:metabolic process	2	IPR001223; IPR001579; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54556 (SUPERFAMILY)
45	isotig00082_gene_isogroup00007_length_2224_numContigs_5_5	7	1822	chitinase 2	741	1.6E-75	63.50%	F:hydrolase activity; P:metabolic process	2	IPR001223; IPR001579; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54556 (SUPERFAMILY)
46	isotig00092_gene_isogroup00010_length_2698_numContigs_5_4	10	2945	chitinase 2	899	4.8E-98	61.70%	F:hydrolase activity; P:metabolic process	2	IPR001223; IPR002557; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54556 (SUPERFAMILY)

47	isotig00093_gene_isogroup00010_length_2698_numContigs_4_4	10	3120	chitinase 2	899	3.9E-98	61.70%	F:hydrolase activity; P:metabolic process	2	IPR001223; IPR002557; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54556 (SUPERFAMILY)
48	isotig00094_gene_isogroup00010_length_2689_numContigs_4_4	10	3048	chitinase 2	896	3.5E-98	61.70%	F:hydrolase activity; P:metabolic process	2	IPR001223; IPR002557; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54556 (SUPERFAMILY)
49	isotig00095_gene_isogroup00010_length_1192_numContigs_2_4	10	1101	obstractor b	397	1.5E-09	63.70%	F:chitin binding; P:chitin metabolic process; C:extracellular region	3	IPR002557; PTHR23301 (PANTHER)
50	isotig00105_gene_isogroup00014_length_1360_numContigs_5_2	14	2809	f-box domain containing protein	453	2.5E-27	41.10%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
51	isotig00119_gene_isogroup00018_length_2330_numContigs_4_4	18	1099	venom serine carboxypeptidase-like	777	2E-124	63.50%	F:hydrolase activity	1	IPR001563; IPR018202; G3DSA:3.40.50.1820 (GENE3D), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53474 (SUPERFAMILY)
52	isotig00120_gene_isogroup00018_length_2330_numContigs_4_4	18	1100	venom serine carboxypeptidase-like	777	2E-124	63.50%	F:hydrolase activity	1	IPR001563; IPR018202; G3DSA:3.40.50.1820 (GENE3D), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53474 (SUPERFAMILY)
53	isotig00121_gene_isogroup00018_length_2330_numContigs_4_4	18	1079	venom serine carboxypeptidase-like	777	3E-124	63.50%	F:hydrolase activity	1	IPR001563; IPR018202; G3DSA:3.40.50.1820 (GENE3D), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53474 (SUPERFAMILY)
54	isotig00125_gene_isogroup00020_length_1162_numContigs_4_0	20	2211	clotting factor b-like	388	1.6E-46	54.30%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
55	isotig00126_gene_isogroup00020_length_1162_numContigs_4_0	20	2884	clotting factor b-like	388	1.5E-46	54.50%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
56	isotig00127_gene_isogroup00020_length_1161_numContigs_4_0	20	2832	clotting factor b-like	387	9E-44	54.80%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
57	isotig00139_gene_isogroup00024_length_1686_numContigs_4_4	24	1564	isoform a	562	2E-47	55.60%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
58	isotig00140_gene_isogroup00024_length_1274_numContigs_3_4	24	1226	isoform a	425	6.4E-49	56.00%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
59	isotig00141_gene_isogroup00024_length_898_numContigs_2_3	24	591	serine proteinase stubble	300	3.6E-14	59.20%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
60	isotig00142_gene_isogroup00025_length_1561_numContigs_3_3	25	1783	pdgf- and vegf-related factor 1-like precursor	521	3.7E-39	53.20%	F:growth factor activity; P:positive regulation of cell division; C:membrane	3	IPR000072; G3DSA:2.10.90.10 (GENE3D), PTHR11633 (PANTHER), PTHR11633:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF57501 (SUPERFAMILY)
61	isotig00143_gene_isogroup00025_length_1279_numContigs_3_3	25	1155	pdgf- and vegf-related factor 1-like precursor	427	3E-10	48.38%	F:growth factor activity; P:positive regulation of cell division; C:membrane	3	IPR000072; G3DSA:2.10.90.10 (GENE3D), PTHR11633 (PANTHER), PTHR11633:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF57501 (SUPERFAMILY)
62	isotig00145_gene_isogroup00026_length_1046_numContigs_3_2	26	14	adp-ribosylation factor 5	348	9E-114	93.30%	C:intracellular; F:nucleotide binding; P:signal transduction	3	IPR003579; IPR005225; IPR006687; IPR006689; IPR024156; IPR027417; G3DSA:3.40.50.300 (GENE3D), PTHR11711 (PANTHER)
63	isotig00147_gene_isogroup00026_length_1013_numContigs_3_2	26	14	adp-ribosylation factor 2-like	337	5E-103	91.20%	C:intracellular; F:nucleotide binding; P:signal transduction	3	IPR005225; IPR006687; IPR006689; IPR024156; IPR027417; G3DSA:3.40.50.300 (GENE3D), PTHR11711 (PANTHER)

64	isotig00159_gene_isogroup00031_length_2529_numContigs_3_0	31	713	matrix metalloproteinase 9	843	4.1E-15	51.10%	F:carbohydrate binding; F:metalloendopeptidase activity; F:hydrolase activity; F:zinc ion binding; F:metallopeptidase activity; C:extracellular matrix; F:peptidase activity; P:proteolysis; F:metal ion binding; P:metabolic process; P:positive regulation of granuloma formation; P:response to bacterium	12	IPR000562; IPR001254; IPR001314; IPR009003; IPR013806; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
65	isotig00160_gene_isogroup00031_length_2495_numContigs_3_1	31	428	matrix metalloproteinase-9	832	5.2E-14	51.90%	F:carbohydrate binding	1	IPR000562; IPR013806; PTHR22918 (PANTHER), PTHR22918:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
66	isotig00161_gene_isogroup00032_length_1786_numContigs_3_5	32	7333	suppressor of tumorigenicity protein 14	595	2.2E-75	50.80%	-	0	IPR001254; IPR002172; IPR009003; IPR018114; IPR023415; PR00261 (PRINTS), G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP)
67	isotig00162_gene_isogroup00032_length_1785_numContigs_3_5	32	8674	st14a protein	595	8.3E-57	50.40%	F:catalytic activity	1	IPR001254; IPR002172; IPR009003; IPR018114; IPR023415; PR00261 (PRINTS), G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), PTHR24256:SF20 (PANTHER), SignalP-NN(euk) (SIGNALP)
68	isotig00165_gene_isogroup00034_length_1331_numContigs_3_4	34	43	annexin isoform 1	444	4.5E-47	69.50%	F:calcium ion binding; F:calcium-dependent phospholipid binding	2	IPR001464; IPR018252; IPR018502; SignalP-NN(euk) (SIGNALP)
69	isotig00166_gene_isogroup00034_length_1331_numContigs_3_4	34	44	annexin isoform 1	444	1.1E-46	69.50%	F:calcium ion binding; F:calcium-dependent phospholipid binding	2	IPR001464; IPR018252; IPR018502; SignalP-NN(euk) (SIGNALP)
70	isotig00167_gene_isogroup00035_length_1183_numContigs_3_2	35	120	allergen 5	394	1.2E-29	54.60%	-	0	IPR001283; IPR002413; IPR014044; IPR018244; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
71	isotig00168_gene_isogroup00035_length_1183_numContigs_3_2	35	122	allergen 5	394	2.2E-30	55.00%	-	0	IPR001283; IPR002413; IPR014044; IPR018244; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
72	isotig00181_gene_isogroup00043_length_2198_numContigs_2_5	43	3936	suppressor of tumorigenicity 14 protein homolog	732	9.1E-73	50.40%	-	0	IPR001254; IPR002172; IPR009003; IPR018114; IPR023415; PR00261 (PRINTS), G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP)
73	isotig00182_gene_isogroup00043_length_1819_numContigs_2_5	43	4043	suppressor of tumorigenicity 14 protein homolog	606	2.4E-73	50.50%	-	0	IPR001254; IPR002172; IPR009003; IPR018114; IPR023415; PR00261 (PRINTS), G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP)
74	isotig00183_gene_isogroup00044_length_1968_numContigs_3_3	44	43	peptidyl-prolyl cis-trans isomerase fkbp14-like	656	4.8E-94	80.00%	P:protein metabolic process; F:calcium ion binding	2	IPR001179; IPR002048; IPR011992; IPR018247; IPR023566; G3DSA:3.10.50.40 (GENE3D), PTHR10516:SF20 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF47473 (SUPERFAMILY), SSF54534 (SUPERFAMILY)
75	isotig00184_gene_isogroup00044_length_1795_numContigs_2_3	44	45	peptidyl-prolyl cis-trans isomerase fkbp14-like	599	9.2E-96	81.60%	P:protein metabolic process; F:calcium ion binding	2	IPR001179; IPR002048; IPR011992; IPR018247; IPR023566; G3DSA:3.10.50.40 (GENE3D), PTHR10516:SF20 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF47473 (SUPERFAMILY), SSF54534 (SUPERFAMILY)
76	isotig00185_gene_isogroup00045_length_1937_numContigs_2_4	45	144	suppressor of tumorigenicity 14 protein homolog	646	7.7E-44	52.00%	P:biological_process; P:response to external stimulus; P:response to stress; F:catalytic activity	4	IPR001254; IPR001314; IPR002172; IPR009003; IPR018114; IPR023415; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
77	isotig00186_gene_isogroup00045_length_1798_numContigs_2_4	45	143	suppressor of tumorigenicity 14 protein homolog	599	6.4E-44	52.40%	P:biological_process; P:response to external stimulus; P:response to stress; F:catalytic activity	4	IPR001254; IPR001314; IPR002172; IPR009003; IPR018114; IPR023415; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

78	isotig00191_gene_isogroup00048_length_1578_numContigs_2_4	48	168	glyceraldehyde-3-phosphate dehydrogenase	526	0	89.90%	F:nucleotide binding; P:carbohydrate metabolic process; F:catalytic activity; P:metabolic process	4	IPR006424; IPR016040; IPR020828; IPR020829; IPR020830; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF51735 (SUPERFAMILY), SSF55347 (SUPERFAMILY)
79	isotig00192_gene_isogroup00048_length_1423_numContigs_2_4	48	179	glyceraldehyde-3-phosphate dehydrogenase	474	0	90.20%	F:nucleotide binding; P:carbohydrate metabolic process; F:catalytic activity; P:metabolic process	4	IPR006424; IPR016040; IPR020828; IPR020829; IPR020830; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF51735 (SUPERFAMILY), SSF55347 (SUPERFAMILY)
80	isotig00195_gene_isogroup00050_length_1574_numContigs_2_1	50	28	leukocyte elastase inhibitor	525	4.8E-85	62.30%	C:extracellular space	1	IPR000215; IPR023796; G3DSA:2.30.39.10 (GENE3D), G3DSA:3.30.497.10 (GENE3D)
81	isotig00196_gene_isogroup00050_length_1413_numContigs_2_1	50	28	leukocyte elastase inhibitor	471	1E-90	61.50%	C:extracellular space	1	IPR000215; IPR023795; IPR023796; G3DSA:2.30.39.10 (GENE3D), G3DSA:3.30.497.10 (GENE3D)
82	isotig00199_gene_isogroup00052_length_2084_numContigs_2_4	52	210	disulfide isomerase	695	0	82.70%	F:electron carrier activity; P:cellular homeostasis; P:regulation of biological process; P:metabolic process; F:catalytic activity; F:transferase activity; C:endoplasmic reticulum	7	IPR005746; IPR005788; IPR005792; IPR012336; IPR013766; IPR017937; PTHR18929 (PANTHER), PTHR18929:SF32 (PANTHER), PF13848 (PFAM), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
83	isotig00209_gene_isogroup00057_length_1276_numContigs_3_4	57	72	carboxypeptidase	425	3.4E-59	63.00%	-	0	IPR000834; IPR003146; IPR009020; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF53187 (SUPERFAMILY)
84	isotig00210_gene_isogroup00057_length_1219_numContigs_2_4	57	71	carboxypeptidase	406	2.4E-59	62.80%	-	0	IPR000834; IPR003146; IPR009020; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF53187 (SUPERFAMILY)
85	isotig00213_gene_isogroup00059_length_1402_numContigs_2_1	59	6019	coagulation factor xi	467	7.7E-41	54.30%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
86	isotig00214_gene_isogroup00059_length_1004_numContigs_2_1	59	4798	secreted salivary gland	335	1.8E-29	54.20%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24258 (PANTHER), SignalP-NN(euk) (SIGNALP)
87	isotig00235_gene_isogroup00070_length_855_numContigs_2_5	70	237	---NA---	285			-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF30 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
88	isotig00236_gene_isogroup00070_length_795_numContigs_2_5	70	262	---NA---	265			-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF30 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
89	isotig00273_gene_isogroup00089_length_600_numContigs_3_4	89	10	thioredoxin-1	200	2.5E-51	83.40%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; IPR017937; SignalP-NN(euk) (SIGNALP)
90	isotig00274_gene_isogroup00089_length_495_numContigs_2_4	89	14	thioredoxin-like protein	165	2E-24	82.00%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
91	isotig00326_gene_isogroup00117_length_2441_numContigs_1_0	117	70	y-box factor-like protein	814	1.1E-37	89.90%	F:DNA binding; P:regulation of biological process;	3	IPR002059; IPR011129; IPR012340; IPR019844; PTHR11544 (PANTHER), PTHR11544:SF8 (PANTHER), tmhmm (TMHMM)
92	isotig00328_gene_isogroup00119_length_2317_numContigs_1_3	119	329	heat shock 70 kda protein cognate 4	773	0	96.30%	-	0	IPR013126; IPR018181; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)

93	isotig00330_gene_isogroup00121_length_2210_numContigs_1_4	121	891	plasma kallikrein-like	737	3.1E-40	52.80%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
94	isotig00331_gene_isogroup00122_length_2182_numContigs_1_2	122	57	protein disulfide-isomerase a3-like	727	0	78.50%	F:electron carrier activity; P:cellular homeostasis; P:regulation of biological process; P:metabolic process; F:catalytic activity; F:transferase activity; C:endoplasmic reticulum	7	IPR005746; IPR005788; IPR005792; IPR012336; IPR013766; IPR017937; PTHR18929 (PANTHER), PTHR18929:SF32 (PANTHER), PF13848 (PFAM), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
95	isotig00332_gene_isogroup00123_length_2124_numContigs_1_1	123	21	zinc metalloprotease	708	5E-116	61.90%	P:proteolysis; F:peptidase activity; F:metalloendopeptidase activity; F:metallopeptidase activity	4	IPR001570; IPR007280; IPR013856; IPR023612; G3DSA:1.10.390.10 (GENE3D), SSF55486 (SUPERFAMILY)
96	isotig00333_gene_isogroup00124_length_2101_numContigs_1_2	124	112	membrane metallo-endopeptidase-like 1-like	700	0	66.80%	-	0	IPR000718; IPR008753; IPR018497; IPR024079; SSF55486 (SUPERFAMILY)
97	isotig00336_gene_isogroup00127_length_2085_numContigs_1_4	127	143	---NA---	695			-	0	IPR000436; IPR002035; G3DSA:2.10.70.10 (GENE3D), PTHR10579 (PANTHER), PTHR10579:SF4 (PANTHER), tmhmm (TMHMM), SSF53300 (SUPERFAMILY)
98	isotig00338_gene_isogroup00129_length_2045_numContigs_1_1	129	148	enolase	682	0	89.40%	C:cytosol; C:protein complex; F:catalytic activity; F:binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process	7	IPR000941; IPR020809; IPR020810; IPR020811; G3DSA:3.20.20.120 (GENE3D), G3DSA:3.30.390.10 (GENE3D), tmhmm (TMHMM), SSF51604 (SUPERFAMILY), SSF54826 (SUPERFAMILY)
99	isotig00340_gene_isogroup00131_length_2033_numContigs_1_4	1313	59	peptidyl-prolyl cis-trans isomerase 5	678	9E-100	89.20%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF63 (PANTHER), SignalP-NN(euk) (SIGNALP)
100	isotig00343_gene_isogroup00134_length_1981_numContigs_1_4	134	1616	suppressor of tumorigenicity 14 protein homolog	600	3.3E-61	43.70%	-	0	IPR001254; IPR002172; IPR009003; IPR023415; PR00261 (PRINTS), G3DSA:2.40.10.10 (GENE3D), PTHR10529 (PANTHER), SignalP-NN(euk) (SIGNALP)
101	isotig00345_gene_isogroup00136_length_1965_numContigs_1_1	136	78	gamma-glutamyltranspeptidase 1-like	655	0	65.70%	F:gamma-glutamyltransferase activity	1	IPR000101; SignalP-NN(euk) (SIGNALP), SSF56235 (SUPERFAMILY)
102	isotig00346_gene_isogroup00137_length_1948_numContigs_1_1	137	84	plasminogen activator spa	649	2.6E-59	55.70%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), tmhmm (TMHMM)
103	isotig00347_gene_isogroup00138_length_1946_numContigs_1_4	138	237	calreticulin	649	9E-173	87.00%	-	0	IPR001580; IPR008985; IPR013320; IPR018124; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
104	isotig00348_gene_isogroup00139_length_1937_numContigs_1_0	139	69	aldehyde mitochondrial-like isoform 1	646	0	81.60%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016160; IPR016161; IPR016162; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER), tmhmm (TMHMM)
105	isotig00349_gene_isogroup00140_length_1932_numContigs_1_1	140	58	heat shock cognate 70-2 protein	644	0	96.00%	F:nucleotide binding	1	IPR013126; IPR018181; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375 (PANTHER), tmhmm (TMHMM), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
106	isotig00357_gene_isogroup00148_length_1894_numContigs_1_4	148	120	chitinase 2	631	2E-120	59.30%	F:catalytic activity	1	IPR001223; IPR001579; IPR002557; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54556 (SUPERFAMILY)
107	isotig00361_gene_isogroup00152_length_1826_numContigs_1_2	152	44	myosin heavy muscle	608	2.6E-89	93.70%	C:cytoskeleton; C:protein complex; F:motor activity	3	IPR002928; PTHR13140 (PANTHER), PTHR13140:SF106 (PANTHER), tmhmm (TMHMM)

108	isotig00362_gene_isogroup00153_length_1816_numContigs_1_5	153	24	gamma-glutamyl hydrolase-like	605	3.5E-80	65.10%	F:peptidase activity; P:metabolic process	2	IPR011697; IPR015527; G3DSA:3.40.50.880 (GENE3D), PTHR11315:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF52317 (SUPERFAMILY)
109	isotig00366_gene_isogroup00157_length_1805_numContigs_1_4	157	138	tissue factor pathway inhibitor 2	602	1.1E-23	60.30%	F:peptidase inhibitor activity; P:blood coagulation; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; F:metallopeptidase activity; C:extracellular matrix; F:zinc ion binding; C:proteinaceous extracellular matrix; F:metalloendopeptidase activity	10	IPR002223; IPR020901; PTHR10083 (PANTHER), tmhmm (TMHMM)
110	isotig00369_gene_isogroup00160_length_1795_numContigs_1_5	160	1583	suppressor of tumorigenicity 14 protein homolog	598	7.3E-75	50.80%	-	0	IPR001254; IPR002172; IPR009003; IPR018114; IPR023415; PR00261 (PRINTS), G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
111	isotig00371_gene_isogroup00162_length_1771_numContigs_1_3	162	665	muscle protein 20-like protein	591	2.5E-83	80.00%	-	0	IPR000557; IPR001715; IPR001997; IPR003096; PTHR18959 (PANTHER), PTHR18959:SF3 (PANTHER)
112	isotig00372_gene_isogroup00163_length_1756_numContigs_1_4	163	27	low quality protein: twitchin-like	585	8.4E-95	76.00%	F:protein kinase activity	1	IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; IPR020675; PTHR22964:SF3 (PANTHER), tmhmm (TMHMM), SSF48726 (SUPERFAMILY)
113	isotig00374_gene_isogroup00165_length_1743_numContigs_1_5	165	45	cathepsin b	581	4E-162	78.20%	P:protein metabolic process; P:catabolic process; P:biological_process; F:peptidase activity	4	IPR000169; IPR000668; IPR012599; IPR013128; IPR015643; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
114	isotig00384_gene_isogroup00175_length_1639_numContigs_1_0	175	15	angiotensin-converting enzyme	547	2E-180	74.50%	P:regulation of biological process; P:protein metabolic process; P:catabolic process; F:peptidase activity; P:biological_process; P:response to external stimulus; F:binding; P:multicellular organismal development; C:cell; F:receptor binding; P:transport; C:extracellular space; F:actin binding; C:plasma membrane; C:endosome; P:cell differentiation; P:response to stress; P:anatomical structure morphogenesis; P:cell proliferation	19	IPR001548; SSF55486 (SUPERFAMILY)
115	isotig00389_gene_isogroup00180_length_1617_numContigs_1_3	180	117	suppressor of tumorigenicity 14 protein homolog	539	9.5E-52	49.60%	-	0	IPR001254; IPR002172; IPR009003; IPR018114; IPR023415; PR00261 (PRINTS), G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP)
116	isotig00390_gene_isogroup00181_length_1600_numContigs_1_1	181	17	cathepsin l-like	533	2E-102	85.40%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000169; IPR000668; IPR013128; IPR025660; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
117	isotig00393_gene_isogroup00184_length_1579_numContigs_1_5	184	37	c-type lectin	526	4.2E-30	50.00%	F:catalytic activity	1	IPR001223; IPR002557; IPR013781; IPR017853; PTHR11177 (PANTHER), tmhmm (TMHMM)
118	isotig00395_gene_isogroup00186_length_1565_numContigs_1_4	186	549	neurogenic locus	522	4.2E-10	49.17%	F:calcium ion binding; F:transferase activity; F:hydrolase activity; F:transmembrane receptor protein tyrosine kinase activity	4	IPR000436; IPR002035; G3DSA:2.10.70.10 (GENE3D), PTHR10579 (PANTHER), PTHR10579:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53300 (SUPERFAMILY)

119	isotig00397_gene_isogroup00188_length_1557_numContigs_1_3	188	23	superoxide dismutase	519	3.4E-52	86.90%	-	0	IPR001424; IPR018152; IPR024134; tmhmm (TMHMM)
120	isotig00400_gene_isogroup00191_length_1523_numContigs_1_5	191	89	ame: full=otogelin-like protein	507	1.4E-11	45.50%	P:cell adhesion; C:extracellular region	2	IPR001007; IPR006207; PTHR11339 (PANTHER), PTHR11339:SF42 (PANTHER), tmhmm (TMHMM), SSF57603 (SUPERFAMILY)
121	isotig00401_gene_isogroup00192_length_1514_numContigs_1_4	192	80	low quality protein: mucin-5ac	505	3.2E-16	44.70%	P:cell adhesion	1	IPR001007; IPR006207; PTHR11339 (PANTHER), PTHR11339:SF25 (PANTHER), SSF57603 (SUPERFAMILY)
122	isotig00403_gene_isogroup00194_length_1493_numContigs_1_3	194	14	low-density lipoprotein receptor-related protein 2	498	8.7E-22	50.10%	F:calcium ion binding; F:receptor activity; C:integral to membrane; C:membrane	4	IPR000152; IPR000436; IPR000742; IPR001254; IPR001881; IPR002172; IPR009003; IPR013032; IPR018097; IPR018114; IPR023415; IPR026823; PR00261 (PRINTS), G3DSA:2.10.25.10 (GENE3D), G3DSA:2.10.70.10 (GENE3D), G3DSA:2.40.10.10 (GENE3D), PTHR10529 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF57196 (SUPERFAMILY)
123	isotig00407_gene_isogroup00198_length_1468_numContigs_1_3	198	632	transmembrane protease serine 6	490	2.5E-44	49.30%	-	0	IPR001254; IPR001314; IPR002172; IPR009003; IPR018114; IPR023415; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
124	isotig00409_gene_isogroup00200_length_1463_numContigs_1_1	200	1046	carboxypeptidase b-like	488	6E-127	63.00%	-	0	IPR000834; IPR003146; IPR009020; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF53187 (SUPERFAMILY)
125	isotig00410_gene_isogroup00201_length_1458_numContigs_1_4	201	1322	carboxypeptidase b-like	486	9E-122	63.20%	-	0	IPR000834; IPR003146; IPR009020; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
126	isotig00413_gene_isogroup00204_length_1450_numContigs_1_4	204	86	cyclophilin a	483	8E-99	92.90%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
127	isotig00414_gene_isogroup00205_length_1450_numContigs_1_4	205	49	phospholipid-hydroperoxide glutathione peroxidase	483	8.3E-80	79.80%	F:antioxidant activity; F:catalytic activity; P:response to stress; P:metabolic process	4	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
128	isotig00416_gene_isogroup00207_length_1440_numContigs_1_4	207	10	clotting factor b-like	480	1E-65	61.90%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF28 (PANTHER)
129	isotig00422_gene_isogroup00213_length_1413_numContigs_1_4	213	52	carboxypeptidase b	471	2E-119	63.00%	P:proteolysis; F:metallocarboxypeptidase activity; F:carboxypeptidase activity; F:zinc ion binding	4	IPR000834; IPR003146; IPR009020; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF53187 (SUPERFAMILY)
130	isotig00423_gene_isogroup00214_length_1403_numContigs_1_3	214	16	isoform c	468	2.9E-34	59.60%	-	0	IPR002172; IPR023415; PTHR10529 (PANTHER), tmhmm (TMHMM)
131	isotig00426_gene_isogroup00217_length_1405_numContigs_1_2	217	3658	transmembrane protease serine 6	468	9.1E-43	49.40%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR001314; IPR002172; IPR009003; IPR018114; IPR023415; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
132	isotig00439_gene_isogroup00230_length_1333_numContigs_1_2	230	25	prepro-ion transport peptide	444	1.1E-29	77.80%	-	0	IPR000346; IPR001166; IPR018251; tmhmm (TMHMM)
133	isotig00447_gene_isogroup00238_length_1310_numContigs_1_0	238	12	ferritin 1-like protein a	437	4.5E-46	64.80%	P:oxidation-reduction process; P:cellular iron ion homeostasis; F:oxidoreductase activity; F:transition metal ion binding; F:ferric iron binding; P:iron ion transport	6	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; PTHR11431:SF5 (PANTHER), tmhmm (TMHMM)

134	isotig00450_gene_isogroup00241_length_1289_numContigs_1_2	241	41	ferritin	429	1.6E-83	84.70%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; IPR014034; tmhmm (TMHMM)
135	isotig00454_gene_isogroup00245_length_1279_numContigs_1_4	245	78	granulin- partial	426	6.4E-35	50.10%	C:mitochondrion; P:embryo implantation; P:blastocyst hatching; P:positive regulation of epithelial cell proliferation	4	IPR000118; PTHR12274 (PANTHER), PTHR12274:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF57277 (SUPERFAMILY)
136	isotig00456_gene_isogroup00247_length_1251_numContigs_1_0	247	9	---NA---	417			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
137	isotig00457_gene_isogroup00248_length_1241_numContigs_1_5	248	109	tandem repeat galectin	413	5.5E-50	52.10%	F:carbohydrate binding	1	IPR001079; IPR008985; IPR013320; PTHR11346 (PANTHER)
138	isotig00462_gene_isogroup00253_length_1229_numContigs_1_4	253	42	thioredoxin peroxidase	410	4E-137	87.00%	P:metabolic process; F:antioxidant activity; F:catalytic activity	3	IPR000866; IPR012336; IPR019479; PTHR10681 (PANTHER), PTHR10681:SF46 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
139	isotig00466_gene_isogroup00257_length_1208_numContigs_1_5	257	674	chymotrypsinogen 2-like	402	4E-46	56.60%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24258 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
140	isotig00468_gene_isogroup00259_length_1197_numContigs_1_5	259	38	plasma kallikrein-like	399	2.1E-40	52.70%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER), SignalP-NN(euk) (SIGNALP)
141	isotig00471_gene_isogroup00262_length_1192_numContigs_1_3	262	561	proclotting enzyme	398	1.1E-48	54.80%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
142	isotig00473_gene_isogroup00264_length_1188_numContigs_1_4	264	44	plasma kallikrein	396	2.3E-40	53.50%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24258 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
143	isotig00474_gene_isogroup00265_length_1183_numContigs_1_4	265	775	serine protease	394	3.1E-40	52.60%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), tmhmm (TMHMM)
144	isotig00475_gene_isogroup00266_length_1178_numContigs_1_1	266	1037	transmembrane protease serine 4	393	3.8E-37	51.00%	P:proteolysis; F:serine-type endopeptidase activity; F:scavenger receptor activity; C:integral to membrane; C:membrane; F:catalytic activity	6	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24258 (PANTHER), SignalP-NN(euk) (SIGNALP)
145	isotig00477_gene_isogroup00268_length_1175_numContigs_1_3	268	25	steroid dehydrogenase	392	3E-115	69.20%	P:oxidation-reduction process; F:oxidoreductase activity; P:metabolic process; F:nucleotide binding; F:estradiol 17-beta-dehydrogenase activity	5	IPR002198; IPR002347; IPR016040; PTHR24316 (PANTHER), PTHR24316:SF68 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF51735 (SUPERFAMILY)
146	isotig00478_gene_isogroup00269_length_1173_numContigs_1_3	269	21	serine protease	391	5.1E-30	48.10%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
147	isotig00480_gene_isogroup00271_length_1162_numContigs_1_3	271	21	hemocyanin subunit type 1 precursor	388	0	75.00%	-	0	IPR002227; IPR005203; IPR008922; IPR013788; IPR014756; tmhmm (TMHMM)
148	isotig00483_gene_isogroup00274_length_1137_numContigs_1_2	274	11	annulin-like isoform 2	379	9E-120	74.50%	-	0	IPR002931; IPR008958; IPR013783; IPR023608; PTHR11590:SF16 (PANTHER), SSF54001 (SUPERFAMILY)
149	isotig00487_gene_isogroup00278_length_1128_numContigs_1_5	278	171	plasminogen activator spa	376	9.7E-45	56.30%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24258 (PANTHER)
150	isotig00488_gene_isogroup00279_length_1127_numContigs_1_4	279	83	plasma kallikrein-like	376	9.8E-41	53.80%	P:biological_process; P:response to external stimulus; P:response to stress; F:catalytic activity	4	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

151	isotig00492_gene_isogroup00283_length_1124_numContigs_1_5	283	17	projectin short variant	374	9E-122	73.60%	-	0	IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; SSF48726 (SUPERFAMILY)
152	isotig00496_gene_isogroup00287_length_1112_numContigs_1_3	287	759	transmembrane serine protease	371	4.8E-45	53.70%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
153	isotig00497_gene_isogroup00288_length_1110_numContigs_1_3	288	11	glrx3_xentr ame: full=glutaredoxin-3 ame: full=thioredoxin-like protein 2	370	1E-142	77.20%	P:cellular homeostasis; P:regulation of biological process; C:cytoplasm; F:electron carrier activity; F:catalytic activity	5	IPR002109; IPR004480; IPR012336; IPR013766; PTHR10293:SF17 (PANTHER)
154	isotig00500_gene_isogroup00291_length_1107_numContigs_1_0	291	13	thioredoxin peroxidase	369	9.3E-59	88.20%	-	0	IPR000866; IPR012336; IPR019479; PTHR10681 (PANTHER), PTHR10681:SF44 (PANTHER)
155	isotig00504_gene_isogroup00295_length_1103_numContigs_1_1	295	6	beta 1-like 2	368	4E-113	66.40%	F:hydrolase activity	1	IPR001944; IPR013781; IPR017853; IPR019801; PTHR23421:SF14 (PANTHER)
156	isotig00513_gene_isogroup00304_length_1078_numContigs_1_5	304	8	serine protease 56-like	359	2.7E-10	48.60%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24261 (PANTHER), PTHR24261:SF9 (PANTHER)
157	isotig00515_gene_isogroup00306_length_1073_numContigs_1_5	306	196	ves g 5 allergen	357	7.6E-39	49.50%	C:extracellular region	1	IPR001283; IPR002413; IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
158	isotig00521_gene_isogroup00312_length_1051_numContigs_1_1	312	12	predicted protein	350	2.6E-07	46.00%	P:neuropeptide signaling pathway	1	no IPS match
159	isotig00531_gene_isogroup00322_length_1039_numContigs_1_4	322	23	selenium-dependent glutathione peroxidase	346	3.7E-87	78.60%	-	0	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
160	isotig00538_gene_isogroup00329_length_1025_numContigs_1_0	329	507	ves g 5 allergen	342	1.5E-43	51.60%	C:extracellular region	1	IPR001283; IPR002413; IPR014044; IPR018244; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
161	isotig00539_gene_isogroup00330_length_1022_numContigs_1_4	330	27	virulence metalloprotease	341	6.3E-15	53.90%	F:metal ion binding; P:proteolysis; F:metallopeptidase activity; F:hydrolase activity; F:peptidase activity; F:metalloendopeptidase activity	6	IPR025711; tmhmm (TMHMM)
162	isotig00543_gene_isogroup00334_length_1012_numContigs_1_5	334	15	acyl- -binding domain-containing protein 6	337	2.7E-69	63.70%	F:fatty-acyl-CoA binding; F:lipid binding; C:cytoplasm; P:proteolysis; F:aspartic-type endopeptidase activity	5	IPR000582; IPR002110; IPR014352; IPR020683; PTHR24119 (PANTHER), PTHR24119:SF0 (PANTHER)
163	isotig00553_gene_isogroup00344_length_986_numContigs_1_3	344	14	chitinase 1	329	1.7E-56	56.70%	F:catalytic activity	1	IPR001223; IPR002557; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SSF54556 (SUPERFAMILY)
164	isotig00554_gene_isogroup00345_length_984_numContigs_1_5	345	177	anti-lipopolysaccharide factor	328	1.3E-32	73.40%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
165	isotig00557_gene_isogroup00348_length_978_numContigs_1_3	348	8	upf0670 protein cg4666-like isoform 1	326	4.4E-26	57.60%	-	0	G3DSA:3.10.129.10 (GENE3D), PTHR12475 (PANTHER), PF13279 (PFAM), tmhmm (TMHMM), SSF54637 (SUPERFAMILY)
166	isotig00565_gene_isogroup00356_length_954_numContigs_1_1	356	8	inactive hydroxysteroid dehydrogenase-like protein 1	318	3E-102	69.90%	-	0	IPR002198; IPR002347; IPR016040; IPR020904; PTHR24316 (PANTHER), PTHR24316:SF68 (PANTHER), SSF51735 (SUPERFAMILY)
167	isotig00577_gene_isogroup00368_length_931_numContigs_1_3	368	15	si:dkey- protein	311	6.5E-42	59.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
168	isotig00586_gene_isogroup00377_length_911_numContigs_1_5	377	11	long form-like	303	1.1E-69	88.00%	C:cytoskeleton; C:protein complex; F:motor activity	3	IPR002928; IPR007999; PTHR13140 (PANTHER), PTHR13140:SF11 (PANTHER)
169	isotig00592_gene_isogroup00383_length_899_numContigs_1_0	383	30	proclotting enzyme-like	300	4.2E-43	56.60%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER)
170	isotig00599_gene_isogroup00390_length_869_numContigs_1_1	390	13	ubiquitin c	290	1.9E-94	94.60%	-	0	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)

171	isotig00649_gene_isogroup00440_length_794_numContigs_1_0	440	17	ubiquitin c	265	8E-75	99.80%	P:cell cycle; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:cellular protein modification process; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:transport	27	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), tmhmm (TMHMM), SSF54236 (SUPERFAMILY)
172	isotig00655_gene_isogroup00446_length_782_numContigs_1_1	446	54	protein cpg-2	261	8.9E-13	47.20%	P:biological_process	1	IPR002557; PTHR23301 (PANTHER), PTHR23301:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
173	isotig00661_gene_isogroup00452_length_753_numContigs_1_5	452	11	dermatopontin 2	251	2.1E-40	60.40%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
174	isotig00744_gene_isogroup00535_length_668_numContigs_1_4	535	26	alkaline serine exoprotease a	223	1.3E-21	64.40%	F:peptidase activity	1	IPR007280; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
175	isotig00753_gene_isogroup00544_length_661_numContigs_1_4	544	8	cytosolic non-specific dipeptidase	220	3E-105	79.00%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR002933; IPR011650; G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF15 (PANTHER), SSF53187 (SUPERFAMILY)
176	isotig00761_gene_isogroup00552_length_647_numContigs_1_3	552	7	mast cell protease 6	216	1E-86	72.80%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF68 (PANTHER)
177	isotig00764_gene_isogroup00555_length_644_numContigs_1_1	555	7	cyclin a	215	6.8E-27	61.30%	P:cell cycle	1	IPR006671; IPR013763; IPR014400; PTHR10177 (PANTHER)
178	isotig00811_gene_isogroup00602_length_590_numContigs_1_1	602	6	aldehyde dehydrogenase family 1 member mitochondrial	197	7.9E-89	93.70%	C:cytoplasm; F:catalytic activity; P:biosynthetic process; F:transferase activity; P:metabolic process; P:catabolic process; F:binding	7	IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER), SignalP-NN(euk) (SIGNALP)
179	isotig00832_gene_isogroup00623_length_563_numContigs_1_5	623	26	serine protease precursor	187	5.7E-18	60.40%	P:proteolysis; F:serine-type endopeptidase activity; P:negative regulation of catalytic activity; F:identical protein binding	4	IPR007280; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
180	isotig00836_gene_isogroup00627_length_562_numContigs_1_3	627	23	ubiquitin ribosomal protein s27a fusion protein	188	6.1E-78	97.50%	C:nucleoplasm; P:signal transduction; P:response to stress; P:DNA metabolic process; P:translation; F:binding; P:metabolic process; F:structural molecule activity; C:endosome; C:ribosome; C:cytosol	11	IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)

181	isotig00856_gene_isogroup00647_length_546_numContigs_1_3	647	50	ribosomal protein ubq l40e	182	8.4E-86	98.90%	C:cytoskeleton; C:protein complex; F:structural molecule activity; C:lipid particle; P:cellular protein modification process; P:protein metabolic process; P:catabolic process; C:ribosome; C:cytosol; P:translation	10	IPR000626; IPR001975; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
182	isotig00863_gene_isogroup00654_length_535_numContigs_1_5	654	22	low-density lipoprotein receptor-related protein 8	178	9.1E-26	63.40%	P:multicellular organismal development; F:protein binding	2	IPR002172; IPR023415; PR00261 (PRINTS), PTHR10529 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
183	isotig00882_gene_isogroup00673_length_518_numContigs_1_5	673	6	transmembrane protease	172	4.1E-32	58.30%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity; C:integral to membrane; F:peptidase activity	5	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER)
184	isotig00901_gene_isogroup00692_length_491_numContigs_1_0	692	9	chitinase 10 precursor	164	1.3E-36	70.50%	F:hydrolase activity; F:binding; P:carbohydrate metabolic process	3	IPR001223; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
185	isotig00921_gene_isogroup00712_length_473_numContigs_1_3	712	11	suppressor of tumorigenicity 14 protein	158	2.8E-17	47.90%	-	0	IPR002172; IPR009003; IPR023415; PR00261 (PRINTS), PTHR10529 (PANTHER)
186	isotig00965_gene_isogroup00756_length_430_numContigs_1_1	756	9	short-chain dehydrogenase	143	4.6E-38	71.60%	P:oxidation-reduction process; F:oxidoreductase activity; P:metabolic process; F:nucleotide binding	4	IPR002198; IPR016040; PTHR24322 (PANTHER), PTHR24322:SF57 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF51735 (SUPERFAMILY)
187	isotig00971_gene_isogroup00762_length_408_numContigs_1_2	762	6	serine protease hepsin	136	2.3E-11	61.50%	P:anatomical structure morphogenesis; P:regulation of biological process; F:peptidase activity; P:multicellular organismal development; P:cellular component organization; P:primary metabolic process; C:intracellular; P:biological_process; P:metabolic process; C:cell	10	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
188	isotig00991_gene_isogroup00782_length_328_numContigs_1_1	782	20	low-density lipoprotein receptor-related protein 2	109	9E-19	65.90%	C:cell	1	IPR002172; IPR023415; PR00261 (PRINTS), PTHR10529 (PANTHER)
189	isotig00996_gene_isogroup00787_length_306_numContigs_1_1	787	15	hemocyanin subunit type 1 precursor	102	1.3E-55	67.80%	-	0	IPR005204; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
190	isotig01022_gene_isogroup00813_length_204_numContigs_1_0	813	8	serine protease	68	2.6E-07	52.50%	F:catalytic activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER)
191	isotig01025_gene_isogroup00816_length_186_numContigs_1_2	816	14	low-density lipoprotein receptor-related protein partial	62	1.6E-08	65.70%	P:multicellular organismal development; F:protein binding; C:cell	3	IPR002172; IPR023415; PTHR10529 (PANTHER)

Supplementary Table 2 | All 2400 hit sequences for secreted proteins of complete specimen's tissue (BVgT) cDNA library. For each transcript the contig name, sequence description based o nthe results using BLAST nr is given including sequence length, e-value, and mean similarity. BLAST2GO results are shown including Gene ontology terms (GO's) and the InterProScan results (green background highlightspositive SignalP results) to identify signalpeptides. Additionally external SignalP search was condcuted to identify signal peptides (positive hits are highlighted in blue font color).

Nr	Contig sequence name	Sequence description (BLAST nr, E-value= > 0.0001)	Length (aa pos.)	E-Value	mean Similarity	Gene ontology terms and annotation (GO's)	Nr. of GO's	Interpro scan results (BLAST2GO) | - Green background = SignalP hit in BLAST2GO - SIgnalP 4.0 results with SignalP 3.1 sensitivity settings (externally identified siganl peptides)
1	DMPC15149382_Speleonectes_tulumensis_2	manganese superoxide dismutase	91	2.34E-12	73.70%	P:metabolic process; F:catalytic activity	2	IPR001189; IPR019831; PTHR11404:SF5 (PANTHER)
2	DMPC15149384_Speleonectes_tulumensis_4	dual oxidase 1	144	1.99E-41	80.70%	P:signal transduction; F:catalytic activity; P:response to stress; F:binding; F:calcium ion binding; F:antioxidant activity; P:multicellular organismal development; C:cell; P:biological_process; P:metabolic process	10	IPR002007; IPR010255; PTHR11972 (PANTHER), PTHR11972:SF6 (PANTHER), tmhmm (TMHMM)
3	DMPC15149548_Speleonectes_tulumensis_2	c4b-binding protein beta chain	123	7.99E-15	70.10%	F:peptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	3	IPR000436; G3DSA:2.10.70.10 (GENE3D), PTHR19325 (PANTHER), PTHR19325:SF74 (PANTHER), tmhmm (TMHMM)
4	DMPC15149677_Speleonectes_tulumensis_1	retinal dehydrogenase 1	283	7.92E-128	80.30%	C:cytoplasm; F:catalytic activity; P:lipid metabolic process; P:secondary metabolic process; P:metabolic process	5	IPR015590; IPR016160; IPR016161; IPR016162; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
5	DMPC15149734_Speleonectes_tulumensis_0	---NA---	171			-	0	IPR000668; IPR013128; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
6	DMPC15149760_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	154	3.98E-32	61.30%	-	0	IPR026645
7	DMPC15149791_Speleonectes_tulumensis_1	annulin-like isoform 2	358	4.94E-42	66.80%	-	0	IPR008958; IPR013783; IPR023608; PTHR11590:SF16 (PANTHER), tmhmm (TMHMM)
8	DMPC15149805_Speleonectes_tulumensis_0	78 kda glucose-regulated protein	286	3.08E-78	93.80%	C:cytoskeleton; C:protein complex; P:cytoskeleton organization; P:cell cycle; C:extracellular space; P:response to stress; P:response to abiotic stimulus; F:nucleotide binding; F:hydrolase activity; C:lipid particle; C:endoplasmic reticulum; P:regulation of gene expression, epigenetic; P:behavior	13	IPR013126; IPR018181; G3DSA:3.30.420.40 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), SSF53067 (SUPERFAMILY)
9	DMPC15149833_Speleonectes_tulumensis_0	na(+) h(+) exchange regulatory cofactor nhe-rf2-like	114	5.56E-37	84.90%	-	0	IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR14191 (PANTHER)
10	DMPC15149905_Speleonectes_tulumensis_0	---NA---	138			-	0	IPR026645; tmhmm (TMHMM)
11	DMPC15149948_Speleonectes_tulumensis_0	cathepsin l1-like	104	8.26E-13	59.40%	P:proteolysis; F:peptidase activity; C:cellular_component	3	IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
12	DMPC15149951_Speleonectes_tulumensis_2	---NA---	91			-	0	PTHR12274 (PANTHER), PTHR12274:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
13	DMPC15149989_Speleonectes_tulumensis_2	chymotrypsin-like elastase family member 2a-like	152	4.21E-21	62.30%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER), SignalP-NN(euk) (SIGNALP)
14	DMPC15150167_Speleonectes_tulumensis_1	ame: full=histone h2a	127	7.79E-43	96.00%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)

15	DMPC15150175_Speleonectes_tulumensis_2	serine protease 137 precursor	89	3.28E-12	66.90%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
16	DMPC15150291_Speleonectes_tulumensis_0	von willebrand factor a domain-containing protein 8	155	1.50E-62	79.50%	-	0	PTHR21610 (PANTHER), PTHR21610:SF6 (PANTHER), tmhmm (TMHMM)
17	DMPC15150330_Speleonectes_tulumensis_0	enolase 1 alpha 2	89	3.39E-28	96.80%	C:cytosol; C:protein complex; F:catalytic activity; F:binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process	7	IPR000941; IPR020810; G3DSA:3.20.20.120 (GENE3D), SSF51604 (SUPERFAMILY)
18	DMPC15150337_Speleonectes_tulumensis_2	ferritin 3-like protein	155	2.25E-22	81.70%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
19	DMPC15150343_Speleonectes_tulumensis_0	---NA---	100			-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21418 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF100895 (SUPERFAMILY)
20	DMPC15150374_Speleonectes_tulumensis_0	gamma-interferon-inducible lysosomal thiol reductase	163	1.18E-14	49.70%	-	0	IPR004911; tmhmm (TMHMM)
21	DMPC15150477_Speleonectes_tulumensis_3	---NA---	214			-	0	no IPS match
22	DMPC15150518_Speleonectes_tulumensis_0	dermatopontin 3	123	4.62E-15	59.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
23	DMPC15150685_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	132	8.28E-68	69.50%	-	0	IPR005203; IPR013788; IPR014756
24	DMPC15150691_Speleonectes_tulumensis_0	diuretic hormone class 2-like	176	1.18E-22	72.10%	-	0	tmhmm (TMHMM)
25	DMPC15150736_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor-like	117	8.84E-12	61.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
26	DMPC15150760_Speleonectes_tulumensis_0	perlucin 5	146	7.46E-12	49.60%	F:binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
27	DMPC15150816_Speleonectes_tulumensis_2	thioredoxin peroxidase	71	1.59E-18	77.40%	P:metabolic process; F:catalytic activity; F:antioxidant activity	3	PTHR10681 (PANTHER), PTHR10681:SF46 (PANTHER), SignalP-NN(euk) (SIGNALP)
28	DMPC15150881_Speleonectes_tulumensis_2	kazal-type protease inhibitor	140	5.81E-22	53.80%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SSF100895 (SUPERFAMILY)
29	DMPC15150990_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor-like	134	1.27E-20	66.50%	-	0	IPR026645
30	DMPC15151023_Speleonectes_tulumensis_2	nidogen 1	107	3.43E-08	70.75%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER)
31	DMPC15151084_Speleonectes_tulumensis_1	chymotrypsinogen b-like	133	2.44E-17	56.70%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24250 (PANTHER), SignalP-NN(euk) (SIGNALP)
32	DMPC15151230_Speleonectes_tulumensis_0	thioredoxin peroxidase	226	1.60E-118	88.10%	-	0	IPR000866; IPR012336; IPR019479; IPR024706; PTHR10681 (PANTHER), PTHR10681:SF44 (PANTHER)
33	DMPC15151331_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor	144	2.35E-28	65.50%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
34	DMPC15151344_Speleonectes_tulumensis_2	pancreatic lipase-related protein 1	148	6.51E-14	54.80%	F:calcium ion binding; F:hydrolase activity	2	IPR000734; IPR002331; IPR013818; G3DSA:3.40.50.1820 (GENE3D), SignalP-NN(euk) (SIGNALP)
35	DMPC15151400_Speleonectes_tulumensis_2	plasminogen activator spa	99	1.94E-07	73.00%	-	0	IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24252 (PANTHER)
36	DMPC15151417_Speleonectes_tulumensis_2	oocyte protease inhibitor-1 precursor	113	7.77E-11	63.60%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)

37	DMPC15151440_Speleonectes_tulumensis_1	trypsinogen h2_1a	193	7.45E-22	54.20%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
38	DMPC15151465_Speleonectes_tulumensis_1	alkyl hydroperoxide reductase thiol specific antioxidant mal allergen	123	6.19E-32	68.40%	F:catalytic activity	1	IPR000866; IPR012336; PTHR10681 (PANTHER), SignalP-NN(euk) (SIGNALP)
39	DMPC15151474_Speleonectes_tulumensis_0	kazal-type serine proteinase inhibitor 4	120	9.27E-26	58.60%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), SSF100895 (SUPERFAMILY)
40	DMPC15151526_Speleonectes_tulumensis_1	---NA---	127			-	0	IPR001747; IPR011030
41	DMPC15151533_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	133	1.92E-18	56.90%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
42	DMPC15151551_Speleonectes_tulumensis_0	aldehyde dehydrogenase mitochondrial-like	128	1.71E-64	86.20%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
43	DMPC15151645_Speleonectes_tulumensis_2	hypothetical protein DAPPUDRAFT_300066	121	6.50E-08	58.00%	-	0	IPR001134; IPR018933; SignalP-NN(euk) (SIGNALP)
44	DMPC15151760_Speleonectes_tulumensis_2	probable chitinase 1	412	2.21E-62	55.40%	-	0	IPR001223; IPR002557; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SSF54556 (SUPERFAMILY)
45	DMPC15151804_Speleonectes_tulumensis_0	purple acid	540	1.78E-28	67.00%	F:metal ion binding; F:hydrolase activity; F:acid phosphatase activity	3	IPR008963; IPR015914; PTHR22953 (PANTHER), PTHR22953:SF0 (PANTHER)
46	DMPC15151804_Speleonectes_tulumensis_1	iron zinc purple acid phosphatase-like	540	6.27E-147	77.50%	F:hydrolase activity	1	IPR004843; IPR025733; G3DSA:3.60.21.10 (GENE3D), PTHR22953 (PANTHER), PTHR22953:SF0 (PANTHER), tmhmm (TMHMM), SSF56300 (SUPERFAMILY)
47	DMPC15151883_Speleonectes_tulumensis_1	trypsin-like serine proteinase 1	123	4.35E-25	65.30%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
48	DMPC15151902_Speleonectes_tulumensis_0	trypsin-like serine proteinase 1	111	2.17E-13	52.60%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
49	DMPC15151907_Speleonectes_tulumensis_2	clotting factor b-like	140	1.58E-30	63.30%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF28 (PANTHER)
50	DMPC15152039_Speleonectes_tulumensis_0	ferritin-1 heavy chain	107	2.15E-22	88.80%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
51	DMPC15152053_Speleonectes_tulumensis_0	glyceraldehyde-3-phosphate dehydrogenase	158	4.37E-28	93.60%	F:catalytic activity; P:metabolic process	2	IPR020829; IPR020831; G3DSA:3.30.360.10 (GENE3D), tmhmm (TMHMM), SSF55347 (SUPERFAMILY)
52	DMPC15152055_Speleonectes_tulumensis_1	aldo-keto partial	119	7.35E-19	71.80%	F:catalytic activity; P:multicellular organismal development	2	IPR001395; IPR018170; IPR023210; PTHR11732:SF34 (PANTHER), SignalP-NN(euk) (SIGNALP)
53	DMPC15152138_Speleonectes_tulumensis_1	glyceraldehyde-3-phosphate dehydrogenase	153	8.59E-16	88.40%	F:catalytic activity; P:metabolic process; F:nucleotide binding	3	IPR016040; IPR020828; IPR020831; SSF51735 (SUPERFAMILY)
54	DMPC15152188_Speleonectes_tulumensis_1	calreticulin	125	4.28E-29	80.00%	-	0	IPR001580; IPR008985; IPR013320; PTHR11073:SF2 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
55	DMPC15152342_Speleonectes_tulumensis_2	aldehyde mitochondrial-like isoform 1	246	1.75E-126	84.50%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016160; IPR016161; IPR016162; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
56	DMPC15152349_Speleonectes_tulumensis_2	dehydrogenase reductase sdr family member 11-like	206	1.04E-13	81.90%	F:binding; F:catalytic activity; P:metabolic process; F:nucleotide binding	4	IPR002198; IPR016040; PTHR24322 (PANTHER), PTHR24322:SF7 (PANTHER), SSF51735 (SUPERFAMILY)
57	DMPC15152357_Speleonectes_tulumensis_1	epididymal secretory protein e1 isoform 1	142	1.23E-21	57.80%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
58	DMPC15152416_Speleonectes_tulumensis_0	vitellogenin 2	147	3.76E-12	50.40%	P:lipid transport; F:lipid transporter activity	2	IPR001747; IPR015816; IPR015819; PTHR23345 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

59	DMPC15152501_Speleonectes _tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	138	2.97E-21	51.80%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
60	DMPC15152503_Speleonectes _tulumensis_0	stress-induced-phosphoprotein 1	128	3.95E-45	79.60%	-	0	IPR001440; IPR011990; IPR013026; IPR019734; PTHR22904 (PANTHER), PTHR22904:SF14 (PANTHER), PF13414 (PFAM), SSF48452 (SUPERFAMILY)
61	DMPC15152511_Speleonectes _tulumensis_1	soma ferritin	120	6.65E-36	87.00%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
62	DMPC15152776_Speleonectes _tulumensis_0	glucose dehydrogenase	139	3.81E-46	72.20%	P:metabolic process; F:catalytic activity	2	IPR000172; G3DSA:3.30.560.10 (GENE3D), G3DSA:3.50.50.60 (GENE3D), PTHR11552 (PANTHER), PTHR11552:SF10 (PANTHER), SSF51905 (SUPERFAMILY)
63	DMPC15152874_Speleonectes _tulumensis_0	hemocyanin subunit 2 precursor	127	1.46E-18	84.67%	-	0	IPR005203; IPR013788; IPR014756
64	DMPC15152892_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor	136	1.83E-13	56.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
65	DMPC15152895_Speleonectes _tulumensis_1	cathepsin l-like	147	5.18E-81	85.80%	-	0	IPR000169; IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
66	DMPC15152898_Speleonectes _tulumensis_0	hypothetical protein CAPTEDRAFT_171631	148	9.84E-09	62.00%	-	0	PTHR12630 (PANTHER)
67	DMPC15152963_Speleonectes _tulumensis_1	32 kda beta-galactoside-binding lectin (galectin-1)	131	1.34E-18	61.50%	F:carbohydrate binding	1	IPR001079; IPR008985; IPR013320; PTHR11346 (PANTHER)
68	DMPC15152996_Speleonectes _tulumensis_0	---NA---	153			-	0	IPR008197; PTHR19441 (PANTHER)
69	DMPC15153009_Speleonectes _tulumensis_2	dermatopontin 2	127	2.29E-14	59.60%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
70	DMPC15153037_Speleonectes _tulumensis_0	---NA---	150			-	0	IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
71	DMPC15153070_Speleonectes _tulumensis_2	vitellogenin 2	496	6.97E-53	48.70%	-	0	IPR001747; IPR015816; IPR015819; PTHR23345 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
72	DMPC15153082_Speleonectes _tulumensis_0	hyaluronidase-3 isoform 1	208	1.62E-07	66.00%	-	0	IPR013785; IPR017853; IPR018155
73	DMPC15153089_Speleonectes _tulumensis_0	plasminogen activator spa	135	1.59E-18	65.20%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24257 (PANTHER)
74	DMPC15153117_Speleonectes _tulumensis_2	arylsulfatase b	250	1.12E-07	62.83%	P:metabolic process; F:catalytic activity; F:sulfuric ester hydrolase activity	3	G3DSA:3.30.1120.10 (GENE3D), tmhmm (TMHMM)
75	DMPC15153155_Speleonectes _tulumensis_2	si:dkey- protein	105	4.93E-09	61.44%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
76	DMPC15153204_Speleonectes _tulumensis_1	suppressor of tumorigenicity protein 14	350	1.12E-45	51.80%	-	0	IPR001254; IPR001314; IPR002172; IPR009003; IPR018114; IPR023415; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
77	DMPC15153227_Speleonectes _tulumensis_0	---NA---	149			-	0	IPR008197; PTHR19441 (PANTHER)
78	DMPC15153251_Speleonectes _tulumensis_2	serine protease 56-like	204	2.02E-10	50.80%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24261 (PANTHER), PTHR24261:SF9 (PANTHER), SignalP-NN(euk) (SIGNALP)
79	DMPC15153289_Speleonectes _tulumensis_2	y-box factor-like protein	145	5.24E-29	67.10%	P:regulation of transcription, DNA-dependent; F:nucleic acid binding; F:DNA binding	3	IPR002059; IPR011129; IPR012340; IPR019844; PTHR11544 (PANTHER), PTHR11544:SF14 (PANTHER)
80	DMPC15153444_Speleonectes _tulumensis_2	chain tachylectin 5a from tachypleus tridentatus (japanese horseshoe crab)	292	2.35E-60	63.30%	-	0	IPR002181; IPR014715; IPR014716; IPR020837; PTHR19143 (PANTHER)

81	DMPC15153462_Speleonectes _tulumensis_0	mgc52890 protein	148	2.95E-24	60.00%	C:extracellular space; P:multicellular organismal development; F:hydrolase activity; P:response to endogenous stimulus; F:protein binding	5	IPR000734; IPR002331; IPR013818; G3DSA:3.40.50.1820 (GENE3D), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53474 (SUPERFAMILY)
82	DMPC15153496_Speleonectes _tulumensis_1	glutathione peroxidase 7	100	1.18E-16	78.00%	C:extracellular region; F:catalytic activity; F:antioxidant activity; P:response to stress; P:metabolic process	5	IPR000889; IPR012336; SignalP-NN(euk) (SIGNALP)
83	DMPC15153572_Speleonectes _tulumensis_2	3-hydroxybutyrate dehydrogenase type 2-like	251	5.91E-122	80.40%	F:nucleotide binding; C:mitochondrion; F:catalytic activity; P:biological_process; P:catabolic process; P:lipid metabolic process; P:biosynthetic process; P:metabolic process	8	IPR002198; IPR002347; IPR016040; IPR020904; PTHR24321 (PANTHER), PTHR24321:SF0 (PANTHER), PF13561 (PFAM), SSF51735 (SUPERFAMILY)
84	DMPC15153590_Speleonectes _tulumensis_2	nk-tumor recognition protein	225	7.06E-69	89.20%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF130 (PANTHER)
85	DMPC15153641_Speleonectes _tulumensis_1	glyceraldehyde-3-phosphate dehydrogenase	149	3.32E-57	85.80%	F:nucleotide binding; P:carbohydrate metabolic process; F:catalytic activity; P:metabolic process	4	IPR016040; IPR020828; IPR020831; SSF51735 (SUPERFAMILY)
86	DMPC15153712_Speleonectes _tulumensis_0	ame: full=hemagglutinin amebocyte aggregation factor ame: full=18k-laf flags: precursor	101	7.60E-07	65.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
87	DMPC15153713_Speleonectes _tulumensis_1	aael012452- partial	186	1.38E-11	42.50%	-	0	IPR000436; G3DSA:2.10.70.10 (GENE3D), PTHR19325 (PANTHER)
88	DMPC15153745_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor-like	142	2.66E-10	59.20%	-	0	IPR026645; tmhmm (TMHMM)
89	DMPC15153843_Speleonectes _tulumensis_2	ferritin gfl	106	3.24E-24	88.30%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
90	DMPC15153890_Speleonectes _tulumensis_1	---NA---	122			-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), PTHR24275:SF2 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
91	DMPC15153910_Speleonectes _tulumensis_2	epidermal retinol dehydrogenase 2	177	1.78E-32	70.10%	F:catalytic activity	1	IPR002198; IPR016040; PTHR24316 (PANTHER), PTHR24316:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF51735 (SUPERFAMILY)
92	DMPC15153976_Speleonectes _tulumensis_2	trypsin	113	3.96E-45	77.30%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER)
93	DMPC15154034_Speleonectes _tulumensis_2	dermatopontin 2	104	1.41E-07	63.17%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
94	DMPC15154185_Speleonectes _tulumensis_2	PREDICTED: nidogen-1	146	9.15E-08	59.00%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339
95	DMPC15154392_Speleonectes _tulumensis_2	mast cell protease 6	272	1.13E-92	72.60%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF68 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
96	DMPC15154421_Speleonectes _tulumensis_2	PREDICTED: chymotrypsin-C-like	106	7.52E-08	53.00%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), PTHR24275:SF2 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

97	DMPC15154435_Speleonectes _tulumensis_0	ubiquitin-40s ribosomal protein s27a	148	1.98E-58	97.10%	P:cell cycle; P:metabolic process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:cellular protein modification process; P:transport	27	IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
98	DMPC15154482_Speleonectes _tulumensis_2	---NA---	143			-	0	no IPS match
99	DMPC15154520_Speleonectes _tulumensis_0	hypothetical protein DAPPUDRAFT_189509	115	1.92E-44	79.00%	F:calcium ion binding	1	IPR002048; IPR011992; IPR018247; IPR027241; PTHR10827 (PANTHER), SSF47473 (SUPERFAMILY)
100	DMPC15154565_Speleonectes _tulumensis_1	lipase 3	72	5.24E-25	81.80%	P:catabolic process; P:lipid metabolic process; F:hydrolase activity	3	G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER), SSF53474 (SUPERFAMILY)
101	DMPC15154637_Speleonectes _tulumensis_1	epididymal secretory protein e1-like	140	3.64E-11	63.50%	P:transport; F:binding; C:intracellular	3	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
102	DMPC15154645_Speleonectes _tulumensis_2	hypothetical protein DAPPUDRAFT_194525	201	1.45E-27	61.50%	F:catalytic activity	1	IPR002557; IPR013781; IPR017853; PTHR11177 (PANTHER)
103	DMPC15154703_Speleonectes _tulumensis_2	mdl2	151	9.92E-11	52.30%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
104	DMPC15154704_Speleonectes _tulumensis_1	ves g 5 allergen	376	4.95E-39	52.50%	C:extracellular region	1	IPR001283; IPR002413; IPR014044; IPR018244; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
105	DMPC15154765_Speleonectes _tulumensis_2	vitelline membrane outer layer protein 1 homolog	136	4.96E-13	53.40%	-	0	IPR005515; PTHR18841:SF0 (PANTHER)
106	DMPC15154809_Speleonectes _tulumensis_0	heavy polypeptide 1	110	1.88E-21	87.20%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
107	DMPC15154820_Speleonectes _tulumensis_2	zinc finger protein glis2-like	230	2.46E-37	65.20%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR19818 (PANTHER), PTHR19818:SF11 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
108	DMPC15154843_Speleonectes _tulumensis_2	hemolectin cg7002-pa	545	6.42E-51	53.40%	P:cell adhesion; F:chitin binding; P:chitin metabolic process; C:extracellular region	4	IPR006207; IPR006208; PTHR11339 (PANTHER), PTHR11339:SF25 (PANTHER), SSF57603 (SUPERFAMILY)
109	DMPC15154971_Speleonectes _tulumensis_1	neutral protease precursor	147	1.48E-12	67.40%	F:peptidase activity	1	IPR007280; SignalP-NN(euk) (SIGNALP)
110	DMPC15155046_Speleonectes _tulumensis_2	hemocyanin subunit type 1 precursor	140	2.59E-49	67.90%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
111	DMPC15155140_Speleonectes _tulumensis_0	serine protease precursor	149	3.23E-17	59.50%	P:proteolysis; F:serine-type endopeptidase activity; P:negative regulation of catalytic activity; F:identical protein binding	4	IPR007280; SignalP-NN(euk) (SIGNALP)
112	DMPC15155284_Speleonectes _tulumensis_1	histone 2b	374	3.16E-60	98.20%	C:chromosome; F:DNA binding; C:nucleoplasm; C:protein complex; P:organelle organization; C:lipid particle	6	IPR000558; IPR007125; IPR009072
113	DMPC15155302_Speleonectes _tulumensis_1	upf0364 protein c6orf211 homolog	150	3.74E-42	73.00%	-	0	IPR002791; PTHR12260 (PANTHER)
114	DMPC15155309_Speleonectes _tulumensis_1	female reproductive tract protease gleanr_2574	156	4.10E-12	60.50%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER)

115	DMPC15155311_Speleonectes _tulumensis_0	hyaluronidase-1 isoform 4	102	1.75E-14	64.30%	P:response to biotic stimulus; P:regulation of biological process; P:cell growth; P:cell cycle; P:biosynthetic process; P:carbohydrate metabolic process; P:biological_process; P:anatomical structure morphogenesis; P:multicellular organismal development; C:extracellular space; C:lysosome; P:response to stress; P:catabolic process; P:response to abiotic stimulus; F:hydrolase activity; F:receptor activity; C:organelle; C:cytoplasm; F:transferase activity; P:response to external stimulus; P:cell proliferation; F:protein binding	22	IPR013785; IPR017853; IPR018155
116	DMPC15155327_Speleonectes _tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	130	1.14E-14	50.20%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
117	DMPC15155428_Speleonectes _tulumensis_1	heat shock cognate 70 kda protein	304	6.82E-176	97.70%	F:nucleotide binding; P:response to stress	2	IPR013126; IPR018181; G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375 (PANTHER), SSF100920 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
118	DMPC15155487_Speleonectes _tulumensis_2	pancreatic lipase-related protein 1	217	5.30E-30	65.00%	F:catalytic activity	1	IPR000734; IPR013818; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
119	DMPC15155611_Speleonectes _tulumensis_2	oocyte protease inhibitor-1 precursor	123	1.08E-10	65.60%	P:proteolysis; F:peptidase activity	2	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP)
120	DMPC15155906_Speleonectes _tulumensis_2	protein	145	5.92E-17	49.90%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER)
121	DMPC15155912_Speleonectes _tulumensis_2	histone h2a	161	4.74E-57	85.30%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)
122	DMPC15155918_Speleonectes _tulumensis_2	gamma-glutamyl hydrolase-like	144	2.70E-08	63.40%	F:hydrolase activity; P:glutamine metabolic process; F:catalytic activity; F:omega peptidase activity	4	IPR015527; PTHR11315:SF0 (PANTHER)
123	DMPC15155953_Speleonectes _tulumensis_1	cd74 major histocompatibility class ii invariant chain a	123	4.84E-08	67.67%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
124	DMPC15156060_Speleonectes _tulumensis_0	thioredoxin peroxidase	114	4.47E-68	90.70%	-	0	IPR000866; IPR012336; IPR019479; PTHR10681 (PANTHER), PTHR10681:SF44 (PANTHER)
125	DMPC15156104_Speleonectes _tulumensis_0	a chain crystal spectroscopic and catalytic properties of cobalt copper nickel and mercury derivatives of the zinc endopeptidase a correlation of structure and proteolytic activity	85	1.24E-12	64.10%	F:peptidase activity; P:reproduction; P:protein metabolic process; C:cytoplasm	4	IPR001506; IPR024079; PTHR10127 (PANTHER), SSF55486 (SUPERFAMILY)
126	DMPC15156112_Speleonectes _tulumensis_1	dlg-interacting metalloprotease	198	1.35E-24	49.60%	P:proteolysis; F:metallopeptidase activity; F:hydrolase activity; F:peptidase activity; F:metalloendopeptidase activity	5	IPR006586; IPR024079; PTHR13723 (PANTHER), PF13574 (PFAM), SSF55486 (SUPERFAMILY)
127	DMPC15156162_Speleonectes _tulumensis_0	plasminogen activator spa	150	4.22E-20	65.30%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

128	DMPC15156454_Speleonectes_tulumensis_2	serine protease hepsin	133	9.87E-12	57.90%	P:anatomical structure morphogenesis; P:regulation of biological process; F:peptidase activity; P:embryo development; P:cellular component organization; P:response to external stimulus; P:response to abiotic stimulus; C:plasma membrane; C:cell; F:ion channel activity; C:intracellular; P:metabolic process	12	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
129	DMPC15156478_Speleonectes_tulumensis_2	calponin transgelin	179	9.79E-76	88.40%	F:actin binding; P:cytoskeleton organization	2	IPR001715; IPR001997; IPR003096; PTHR18959 (PANTHER), PTHR18959:SF3 (PANTHER)
130	DMPC15156485_Speleonectes_tulumensis_0	---NA---	337			-	0	IPR014853
131	DMPC15156513_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	110	3.36E-22	61.20%	-	0	IPR026645
132	DMPC15156534_Speleonectes_tulumensis_2	kazal-type protease inhibitor	107	3.12E-13	55.60%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SSF100895 (SUPERFAMILY)
133	DMPC15156566_Speleonectes_tulumensis_0	phosphoglucose isomerase	69	8.78E-21	78.00%	P:carbohydrate metabolic process; F:catalytic activity	2	IPR001672; G3DSA:3.40.50.10490 (GENE3D), PTHR11469:SF0 (PANTHER), SSF53697 (SUPERFAMILY)
134	DMPC15156577_Speleonectes_tulumensis_0	chitinase chit1 precursor	213	4.03E-10	59.30%	F:chitin binding; P:chitin metabolic process; C:extracellular region	3	IPR002557; PTHR23301 (PANTHER)
135	DMPC15156635_Speleonectes_tulumensis_0	phospholipase a2	132	3.76E-15	68.10%	F:calcium ion binding; F:hydrolase activity; P:lipid metabolic process; P:catabolic process	4	IPR001211; IPR016090
136	DMPC15156697_Speleonectes_tulumensis_3	syntaxin 1a	138	3.59E-14	95.20%	C:cell; F:protein binding; C:intracellular; P:transport; P:protein transport	5	IPR000727; IPR010989; G3DSA:1.20.5.110 (GENE3D), PTHR19957 (PANTHER), PTHR19957:SF33 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
137	DMPC15156708_Speleonectes_tulumensis_1	membrane metallo-endopeptidase-like 1-like	306	2.32E-66	68.50%	P:proteolysis; F:metallopeptidase activity; F:metalloendopeptidase activity	3	IPR000718; IPR018497; IPR024079; PTHR11733:SF26 (PANTHER), SSF55486 (SUPERFAMILY)
138	DMPC15156777_Speleonectes_tulumensis_1	soma ferritin	123	4.74E-27	88.40%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
139	DMPC15156807_Speleonectes_tulumensis_2	hemocyanin subunit type 2 precursor	80	4.00E-31	72.70%	-	0	IPR005203; IPR014756
140	DMPC15156826_Speleonectes_tulumensis_0	si:dkey- protein	106	3.27E-08	63.29%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
141	DMPC15156876_Speleonectes_tulumensis_0	peptidase m4 thermolysin	120	2.55E-07	59.83%	P:proteolysis; F:hydrolase activity; F:metalloendopeptidase activity	3	SignalP-NN(euk) (SIGNALP)
142	DMPC15156906_Speleonectes_tulumensis_2	isoform e	120	2.53E-11	67.30%	F:calcium ion binding; C:integral to membrane; C:membrane	3	IPR002172; IPR023415; PTHR10529 (PANTHER), tmhmm (TMHMM)
143	DMPC15156935_Speleonectes_tulumensis_1	hatching enzyme	185	3.38E-30	56.00%	F:hydrolase activity	1	IPR001506; IPR006026; IPR024079; PTHR24543 (PANTHER), PTHR24543:SF85 (PANTHER), SSF55486 (SUPERFAMILY)
144	DMPC15156938_Speleonectes_tulumensis_1	---NA---	175			-	0	no IPS match
145	DMPC15156956_Speleonectes_tulumensis_1	thioredoxin peroxidase 2	188	2.67E-20	89.00%	P:metabolic process; F:catalytic activity; F:antioxidant activity	3	IPR012336; IPR019479; PTHR10681 (PANTHER)
146	DMPC15156958_Speleonectes_tulumensis_1	succinate semialdehyde	211	7.94E-93	77.80%	P:metabolic process; F:catalytic activity	2	IPR015590; IPR016160; IPR016161; IPR016162; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF49 (PANTHER)
147	DMPC15157009_Speleonectes_tulumensis_1	thioredoxin-like protein	121	1.64E-24	82.00%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; SignalP-NN(euk) (SIGNALP)
148	DMPC15157030_Speleonectes_tulumensis_1	peroxidasin homolog	287	1.08E-14	63.80%	P:oxidation-reduction process; F:heme binding; F:oxidoreductase activity; P:response to oxidative stress; F:peroxidase activity	5	IPR002007; IPR010255; PTHR11475 (PANTHER), tmhmm (TMHMM)

149	DMPC15157083_Speleonectes _tulumensis_1	interferon-related developmental regulator 1-like	330	4.84E-27	49.50%	-	0	IPR009832; PTHR20997 (PANTHER), PTHR20997:SF0 (PANTHER), tmhmm (TMHMM)
150	DMPC15157124_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor	107	3.52E-22	56.30%	-	0	IPR026645
151	DMPC15157129_Speleonectes _tulumensis_1	dermatopontin 2	135	4.11E-09	63.75%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
152	DMPC15157190_Speleonectes _tulumensis_1	crisp3: cysteine-rich secretory	129	6.38E-11	51.40%	C:extracellular region	1	IPR001283; IPR014044; IPR018244
153	DMPC15157220_Speleonectes _tulumensis_1	phospholipase a2-like	154	5.78E-17	61.30%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; C:extracellular region	5	IPR001211; IPR013090; IPR016090; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
154	DMPC15157247_Speleonectes _tulumensis_2	manganese superoxide dismutase	96	7.05E-17	83.90%	F:binding; P:metabolic process; F:catalytic activity	3	IPR001189; IPR019831; PTHR11404:SF5 (PANTHER)
155	DMPC15157302_Speleonectes _tulumensis_1	chain crystallographic structure of thioredoxin from litopenaeus vannamei	104	3.37E-21	77.20%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; IPR017937; PTHR10438:SF17 (PANTHER), SignalP-NN(euk) (SIGNALP)
156	DMPC15157334_Speleonectes _tulumensis_2	peptidoglycan recognition protein 2 short class	105	1.57E-17	64.80%	F:zinc ion binding; P:peptidoglycan catabolic process; F:N-acetylmuramoyl-L-alanine amidase activity	3	IPR002502; IPR006619; IPR015510; SignalP-NN(euk) (SIGNALP)
157	DMPC15157398_Speleonectes _tulumensis_1	26kda protease	133	2.40E-16	62.90%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
158	DMPC15157497_Speleonectes _tulumensis_2	carbohydrate sulfotransferase 11-like	232	8.39E-28	63.60%	-	0	IPR005331; IPR018011; PTHR12137:SF1 (PANTHER)
159	DMPC15157535_Speleonectes _tulumensis_1	hypothetical protein DAPPUDRAFT_308200	144	3.06E-09	51.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
160	DMPC15157545_Speleonectes _tulumensis_1	phosphoglycerate kinase	122	1.28E-38	86.70%	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; P:metabolic process; F:kinase activity	5	IPR001576; IPR015824; IPR015911
161	DMPC15157553_Speleonectes _tulumensis_0	gonadotropin inducible transcription	161	6.04E-32	69.90%	F:binding	1	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
162	DMPC15157662_Speleonectes _tulumensis_2	soma ferritin	110	1.46E-32	89.50%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
163	DMPC15157667_Speleonectes _tulumensis_0	plasminogen activator spa	394	1.05E-60	64.40%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
164	DMPC15157696_Speleonectes _tulumensis_2	cathepsin l	150	8.61E-68	78.80%	-	0	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
165	DMPC15157704_Speleonectes _tulumensis_0	lysozyme precursor	117	7.95E-08	61.00%	-	0	IPR001916; IPR023346; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER), PTHR11407:SF2 (PANTHER)
166	DMPC15157711_Speleonectes _tulumensis_1	serine protease inhibitor kazal-type 6-like	119	5.41E-08	66.50%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SSF100895 (SUPERFAMILY)
167	DMPC15157773_Speleonectes _tulumensis_1	soma ferritin	126	4.24E-39	85.30%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
168	DMPC15157797_Speleonectes _tulumensis_2	female neotenic-specific protein 3	152	8.88E-11	57.75%	-	0	no IPS match
169	DMPC15157812_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor	107	5.03E-20	63.10%	-	0	IPR026645
170	DMPC15157831_Speleonectes _tulumensis_0	cg3556 cg3556-pa	224	1.51E-21	57.90%	P:cobalamin transport; F:cobalamin binding	2	IPR002157

171	DMPC15157857_Speleonectes_tulumensis_2	aldehyde dehydrogenase family 1 member mitochondrial	137	4.21E-68	94.70%	C:cytoplasm; F:catalytic activity; P:biosynthetic process; F:transferase activity; P:metabolic process; P:catabolic process; F:binding	7	IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
172	DMPC15157876_Speleonectes_tulumensis_1	soma ferritin	114	4.96E-33	88.50%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
173	DMPC15157895_Speleonectes_tulumensis_2	cyclophilin a	498	7.99E-58	90.10%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), tmhmm (TMHMM)
174	DMPC15157900_Speleonectes_tulumensis_2	protein disulfide isoform a	150	2.68E-53	83.80%	C:extracellular space; P:protein metabolic process; C:cell; C:endoplasmic reticulum; C:cytoplasm; C:lipid particle; F:electron carrier activity; P:cellular homeostasis; P:regulation of biological process; P:metabolic process; C:nuclear envelope; C:organelle; C:intracellular; F:catalytic activity	14	IPR005746; IPR005788; IPR012336; IPR013766; IPR017937; PTHR18929 (PANTHER), PTHR18929:SF32 (PANTHER), SignalP-NN(euk) (SIGNALP)
175	DMPC15158036_Speleonectes_tulumensis_2	---NA---	100			-	0	PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
176	DMPC15158091_Speleonectes_tulumensis_1	lipase 3-like	171	5.08E-22	66.60%	F:hydrolase activity; P:lipid metabolic process	2	G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER), tmhmm (TMHMM)
177	DMPC15158127_Speleonectes_tulumensis_1	ferritin h subunit	118	6.56E-20	91.50%	P:cellular homeostasis; F:binding; P:regulation of biological process; P:cell proliferation; F:catalytic activity; P:ion transport; C:mitochondrion; P:metabolic process	8	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
178	DMPC15158128_Speleonectes_tulumensis_2	syntaxin-1a-like isoform 2	306	3.67E-14	76.60%	-	0	no IPS match
179	DMPC15158185_Speleonectes_tulumensis_2	carboxypeptidase a1-like	160	3.32E-29	71.20%	-	0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
180	DMPC15158213_Speleonectes_tulumensis_1	ferritin-1 heavy chain	106	1.74E-20	90.40%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
181	DMPC15158229_Speleonectes_tulumensis_1	trypsin	126	3.94E-13	60.30%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
182	DMPC15158249_Speleonectes_tulumensis_2	plasma alpha-l-fucosidase	243	4.76E-74	68.80%	P:metabolic process; F:hydrolase activity	2	IPR000933; IPR013781; IPR016286; IPR017853; PTHR10030:SF3 (PANTHER), tmhmm (TMHMM)
183	DMPC15158291_Speleonectes_tulumensis_0	ferritin subunit	146	1.53E-39	76.60%	F:binding	1	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
184	DMPC15158475_Speleonectes_tulumensis_0	sh3 domain-containing ring finger protein 3-like isoform 2	270	1.01E-18	67.10%	F:binding	1	IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR10661 (PANTHER), PTHR10661:SF7 (PANTHER), tmhmm (TMHMM)
185	DMPC15158487_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	145	4.24E-29	68.20%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
186	DMPC15158533_Speleonectes_tulumensis_0	cysteine string	137	9.04E-63	94.80%	P:protein metabolic process; F:protein binding	2	IPR001623; IPR018253; PTHR24078 (PANTHER), PTHR24078:SF7 (PANTHER), SignalP-NN(euk) (SIGNALP)
187	DMPC15158632_Speleonectes_tulumensis_2	dermatopontin 3	98	3.72E-08	69.20%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
188	DMPC15158662_Speleonectes_tulumensis_1	glucose-6-phosphate isomerase	78	5.19E-22	72.90%	P:carbohydrate metabolic process; F:catalytic activity	2	IPR001672; G3DSA:3.40.50.10490 (GENE3D), PTHR11469:SF0 (PANTHER), SSF53697 (SUPERFAMILY)
189	DMPC15158690_Speleonectes_tulumensis_1	thioredoxin 1	144	1.68E-42	85.20%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; IPR017937; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
190	DMPC15158700_Speleonectes_tulumensis_1	lachesin	90	1.28E-20	71.90%	-	0	IPR003598; IPR007110; IPR013098; IPR013783; PTHR19831 (PANTHER), PTHR19831:SF16 (PANTHER), SSF48726 (SUPERFAMILY)

191	DMPC15158773_Speleonectes_tulumensis_2	hypothetical protein DAPPUDRAFT_308544	132	5.33E-07	66.00%	-	0	IPR004911
192	DMPC15158883_Speleonectes_tulumensis_2	tpa_inf: hypothetical secreted protein 469	190	6.69E-09	47.75%	-	0	IPR020234
193	DMPC15158914_Speleonectes_tulumensis_1	galectin partial	196	5.98E-25	59.90%	F:carbohydrate binding	1	IPR001079; IPR008985; IPR013320; PTHR11346 (PANTHER)
194	DMPC15159017_Speleonectes_tulumensis_2	phospholipase a2-like	132	9.38E-08	59.67%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; C:extracellular region	5	IPR001211; IPR016090; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
195	DMPC15159052_Speleonectes_tulumensis_0	galactose-specific c-type lectin	230	8.33E-13	48.30%	F:carbohydrate binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER)
196	DMPC15159087_Speleonectes_tulumensis_0	tissue factor pathway inhibitor-like	253	3.35E-16	51.50%	F:peptidase inhibitor activity; P:blood coagulation; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	5	IPR002223; IPR020901; PTHR10083 (PANTHER)
197	DMPC15159129_Speleonectes_tulumensis_0	superoxide dismutase	246	4.46E-22	52.00%	P:cell differentiation; P:reproduction; F:antioxidant activity; P:biological_process; F:binding; P:cellular homeostasis; P:cell communication; P:DNA metabolic process; F:catalytic activity; P:multicellular organismal development; C:organelle; C:intracellular; P:metabolic process; P:regulation of biological process; P:biosynthetic process; F:protein binding; P:response to stress; P:cell death; C:cytoplasm; P:transport	20	IPR001424; IPR024134
198	DMPC15159211_Speleonectes_tulumensis_1	epididymal secretory protein e1	149	5.64E-19	60.50%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
199	DMPC15159236_Speleonectes_tulumensis_0	dermatopontin 2	121	4.24E-12	59.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
200	DMPC15159243_Speleonectes_tulumensis_0	trypsinogen 2	193	1.37E-34	64.80%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP)
201	DMPC15159284_Speleonectes_tulumensis_1	peptidyl-prolyl cis-trans isomerase-like 3	155	6.74E-53	93.30%	P:protein metabolic process; P:nucleobase-containing compound metabolic process; F:catalytic activity; C:nucleus	4	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER)
202	DMPC15159307_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor isoform 7	128	8.15E-17	61.20%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
203	DMPC15159397_Speleonectes_tulumensis_0	ferritin gfl	136	3.09E-27	88.70%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
204	DMPC15159471_Speleonectes_tulumensis_1	macrophage migration inhibitory factor	91	4.52E-08	66.70%	F:catalytic activity; P:signal transduction; P:regulation of biological process; P:cell death; P:cellular protein modification process; P:behavior; P:response to external stimulus; F:receptor binding; P:cell cycle; P:metabolic process; P:protein transport; P:response to stress; C:extracellular region; C:cell; P:biosynthetic process; P:lipid metabolic process; F:binding; F:molecular_function; P:cell proliferation; P:cellular component organization	20	IPR001398; G3DSA:3.30.429.10 (GENE3D), PTHR11954:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP)
205	DMPC15159481_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_308200	281	5.26E-18	49.00%	-	0	IPR020234

206	DMPC15159489_Speleonectes_tulumensis_1	gamma-interferon-inducible lysosomal thiol reductase	143	1.29E-26	58.80%	-	0	IPR004911; SignalP-NN(euk) (SIGNALP)
207	DMPC15159532_Speleonectes_tulumensis_0	upf0378 protein kiaa0100-like	106	9.17E-34	83.20%	-	0	IPR019443; PTHR15678 (PANTHER)
208	DMPC15159533_Speleonectes_tulumensis_1	clotting factor b-like	166	1.91E-26	59.50%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER)
209	DMPC15159662_Speleonectes_tulumensis_1	heat shock protein 70	149	5.13E-56	92.30%	F:protein binding; F:lipid binding; P:organelle organization; P:cell cycle; P:metabolic process; P:regulation of biological process; C:cell; C:nuclear chromosome; P:reproduction; P:cell differentiation; C:nucleus; P:response to stress; P:response to abiotic stimulus; F:nucleotide binding; C:mitochondrion	15	IPR013126; G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), PTHR19375 (PANTHER), SSF53067 (SUPERFAMILY)
210	DMPC15159824_Speleonectes_tulumensis_1	soma ferritin	126	9.28E-42	77.20%	F:binding	1	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
211	DMPC15159848_Speleonectes_tulumensis_2	dermatopontin 3	89	3.16E-07	66.33%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
212	DMPC15159898_Speleonectes_tulumensis_1	thioredoxin peroxidase	140	4.77E-71	88.10%	P:metabolic process; F:antioxidant activity; F:catalytic activity	3	IPR000866; IPR012336; IPR024706; PTHR10681 (PANTHER), PTHR10681:SF44 (PANTHER)
213	DMPC15159904_Speleonectes_tulumensis_2	ovarian cysteine protease inhibitor	112	1.36E-10	55.50%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
214	DMPC15159972_Speleonectes_tulumensis_0	dysferlin-interacting protein 1	155	3.38E-53	68.20%	P:negative regulation of phosphatase activity; F:phosphatase binding	2	IPR002110; IPR020683; PTHR24179 (PANTHER), PTHR24179:SF2 (PANTHER)
215	DMPC15160077_Speleonectes_tulumensis_2	---NA---	145			-	0	IPR002591; IPR017849; IPR017850; IPR024873
216	DMPC15160097_Speleonectes_tulumensis_0	nidogen and related basement membrane protein	172	6.61E-12	47.20%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP)
217	DMPC15160132_Speleonectes_tulumensis_1	---NA---	106			-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
218	DMPC15160149_Speleonectes_tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	147	2.15E-21	51.80%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:cell-matrix adhesion; F:calcium ion binding	6	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
219	DMPC15160166_Speleonectes_tulumensis_1	epididymal secretory protein e1	149	7.47E-19	60.50%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
220	DMPC15160180_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	151	1.61E-85	68.70%	-	0	IPR005203; IPR013788; IPR014756
221	DMPC15160259_Speleonectes_tulumensis_2	hypothetical protein TcasGA2_TC013968	190	5.05E-11	46.17%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP)
222	DMPC15160261_Speleonectes_tulumensis_2	adam 19	195	1.01E-10	71.57%	F:hydrolase activity	1	IPR013032; PTHR11905 (PANTHER), PTHR11905:SF15 (PANTHER), tmhmm (TMHMM)
223	DMPC15160281_Speleonectes_tulumensis_0	serine protease 137 precursor	86	4.52E-12	65.60%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
224	DMPC15160325_Speleonectes_tulumensis_2	hypothetical protein DAPPUDRAFT_332702	272	4.97E-80	67.00%	-	0	IPR001747; IPR011030; IPR015817; PTHR23345 (PANTHER)
225	DMPC15160326_Speleonectes_tulumensis_1	---NA---	127			-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)

226	DMPC15160512_Speleonectes_tulumensis_1	kazal-type serine proteinase inhibitor 4	131	4.58E-12	56.67%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
227	DMPC15160527_Speleonectes_tulumensis_1	zinc proteinase mpc1	149	9.14E-18	52.40%	F:hydrolase activity	1	IPR001506; IPR006026; IPR024079; PTHR24543 (PANTHER), PTHR24543:SF85 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF55486 (SUPERFAMILY)
228	DMPC15160584_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor-like	102	8.30E-18	64.50%	-	0	IPR026645
229	DMPC15160591_Speleonectes_tulumensis_2	dnaj homolog subfamily c member 9	119	3.74E-38	83.30%	P:protein metabolic process; F:protein binding	2	IPR001623; IPR018253; PTHR24078 (PANTHER), PTHR24078:SF16 (PANTHER)
230	DMPC15160712_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor isoform 7	108	1.31E-16	64.60%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
231	DMPC15160776_Speleonectes_tulumensis_1	phospholipase a2	135	1.25E-18	63.70%	F:hydrolase activity; P:lipid metabolic process	2	IPR001211; IPR013090; IPR016090; SignalP-NN(euk) (SIGNALP)
232	DMPC15160878_Speleonectes_tulumensis_2	hyaluronidase precursor	159	7.90E-28	61.40%	P:defense response; P:carbohydrate metabolic process; F:hyalurononglucosaminidase activity; F:catalytic activity	4	IPR013785; IPR017853; IPR018155; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
233	DMPC15160904_Speleonectes_tulumensis_1	---NA---	145			-	0	IPR016186; IPR016187; PTHR22803 (PANTHER), SignalP-NN(euk) (SIGNALP)
234	DMPC15160908_Speleonectes_tulumensis_1	zinc metalloprotease	145	5.10E-36	68.50%	F:peptidase activity	1	IPR001570; G3DSA:1.10.390.10 (GENE3D), SSF55486 (SUPERFAMILY)
235	DMPC15160971_Speleonectes_tulumensis_2	plasma glutamate carboxypeptidase	145	7.43E-22	71.50%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	G3DSA:3.40.630.10 (GENE3D), PTHR12053 (PANTHER), PTHR12053:SF2 (PANTHER)
236	DMPC15160990_Speleonectes_tulumensis_2	perlucin 5	147	1.01E-11	49.20%	F:protein binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP)
237	DMPC15161062_Speleonectes_tulumensis_0	female neotenic-specific protein 3	139	2.91E-09	54.75%	-	0	no IPS match
238	DMPC15161106_Speleonectes_tulumensis_0	epidermal retinal dehydrogenase 2	121	2.18E-35	72.40%	P:metabolic process; F:catalytic activity	2	IPR016040; PTHR24316 (PANTHER), PTHR24316:SF1 (PANTHER), SSF51735 (SUPERFAMILY)
239	DMPC15161143_Speleonectes_tulumensis_1	trypsinogen 2	121	1.16E-25	67.70%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
240	DMPC15161155_Speleonectes_tulumensis_2	gamma-interferon-inducible lysosomal thiol reductase	155	4.08E-34	59.20%	-	0	IPR004911; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
241	DMPC15161195_Speleonectes_tulumensis_2	pacifastin-related precursor 4t	122	9.43E-08	48.00%	-	0	IPR008037; IPR020862; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
242	DMPC15161200_Speleonectes_tulumensis_1	isoform a	285	6.94E-34	51.20%	P:proteolysis; P:cell proliferation; F:metalloendopeptidase activity; C:cellular_component	4	IPR001590; IPR024079; PTHR11905 (PANTHER), PF13574 (PFAM), SSF55486 (SUPERFAMILY)
243	DMPC15161352_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	153	2.94E-16	58.10%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
244	DMPC15161373_Speleonectes_tulumensis_2	protein disulfide isomerase	246	1.04E-110	87.30%	F:electron carrier activity; P:cellular homeostasis; P:regulation of biological process; P:metabolic process; F:catalytic activity; F:transferase activity; C:endoplasmic reticulum	7	IPR005746; IPR005788; IPR012336; IPR013766; IPR017937; PTHR18929 (PANTHER), PTHR18929:SF32 (PANTHER), PF13848 (PFAM)
245	DMPC15161381_Speleonectes_tulumensis_1	dermatopontin 2	204	1.33E-31	60.80%	-	0	IPR026645; tmhmm (TMHMM)
246	DMPC15161438_Speleonectes_tulumensis_0	hypothetical protein DAPPUDRAFT_308200	159	2.84E-09	50.00%	-	0	IPR020234

247	DMPC15161626_Speleonectes_tulumensis_1	serine protease inhibitor kazal-type 6-like	157	1.24E-08	67.67%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
248	DMPC15161633_Speleonectes_tulumensis_2	torsin a	98	8.09E-33	79.60%	-	0	IPR010448; G3DSA:3.40.50.300 (GENE3D), PTHR10760:SF2 (PANTHER)
249	DMPC15161672_Speleonectes_tulumensis_2	hypothetical protein TcasGA2_TC030735	93	3.81E-07	70.00%	-	0	IPR002172; IPR023415; PTHR10529 (PANTHER), PTHR10529:SF113 (PANTHER), SignalP-NN(euk) (SIGNALP)
250	DMPC15161739_Speleonectes_tulumensis_0	ame: full=hemagglutinin amebocyte aggregation factor ame: full=18k-laf flags: precursor	111	6.46E-08	57.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
251	DMPC15161946_Speleonectes_tulumensis_0	dermatopontin 3	92	1.85E-07	62.50%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
252	DMPC15162008_Speleonectes_tulumensis_0	protein yellow	166	9.43E-27	62.30%	-	0	IPR003534; IPR011042; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
253	DMPC15162069_Speleonectes_tulumensis_0	vitellogenin 2	297	8.13E-29	52.00%	P:lipid transport; F:lipid transporter activity	2	IPR001747; IPR015816; IPR015819; PTHR23345 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
254	DMPC15162299_Speleonectes_tulumensis_2	trypsin	135	2.32E-31	62.10%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER)
255	DMPC15162331_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_300066	144	1.57E-10	51.00%	-	0	IPR015526
256	DMPC15162449_Speleonectes_tulumensis_2	hypothetical protein DAPPUDRAFT_332702	155	9.34E-15	56.86%	-	0	IPR001747; IPR015816; IPR015819; PTHR13769 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
257	DMPC15162470_Speleonectes_tulumensis_2	ecdysteroid-regulated protein	153	5.97E-25	56.50%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
258	DMPC15162604_Speleonectes_tulumensis_1	ferritin-1 heavy chain	111	8.26E-22	89.40%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
259	DMPC15162711_Speleonectes_tulumensis_0	proclotting enzyme-like	309	6.50E-48	56.60%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
260	DMPC15162780_Speleonectes_tulumensis_0	glyceraldehyde-3-phosphate partial	66	8.54E-12	79.60%	F:catalytic activity; P:metabolic process; F:nucleotide binding	3	IPR020829; IPR020831; G3DSA:3.30.360.10 (GENE3D), SignalP-NN(euk) (SIGNALP), SSF55347 (SUPERFAMILY)
261	DMPC15162825_Speleonectes_tulumensis_2	kazal-type serine proteinase inhibitor 4	127	8.82E-17	53.80%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
262	DMPC15162848_Speleonectes_tulumensis_1	masquerade-like protein	244	1.88E-14	43.30%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), PTHR24260:SF3 (PANTHER)
263	DMPC15162864_Speleonectes_tulumensis_0	hemocyanin subunit type 2 precursor	184	1.50E-26	77.40%	-	0	IPR005203; IPR013788; IPR014756
264	DMPC15162912_Speleonectes_tulumensis_0	---NA---	105			-	0	IPR003959; G3DSA:3.40.50.300 (GENE3D), SignalP-NN(euk) (SIGNALP)
265	DMPC15162993_Speleonectes_tulumensis_2	dermatopontin 2	97	4.68E-08	70.00%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
266	DMPC15163042_Speleonectes_tulumensis_2	heavy polypeptide 1	111	2.36E-22	89.20%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
267	DMPC15163048_Speleonectes_tulumensis_2	hepatopancreas partial	157	7.73E-36	73.30%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
268	DMPC15163133_Speleonectes_tulumensis_0	dermatopontin 2	135	2.64E-09	60.60%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
269	DMPC15163197_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor	153	5.92E-29	65.80%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
270	DMPC15163235_Speleonectes_tulumensis_2	glyceraldehyde 3-phosphate dehydrogenase	177	3.57E-35	92.30%	F:nucleotide binding; P:carbohydrate metabolic process; F:catalytic activity; P:metabolic process	4	IPR020829; IPR020831; G3DSA:3.30.360.10 (GENE3D), tmhmm (TMHMM), SSF55347 (SUPERFAMILY)

271	DMPC15163246_Speleonectes _tulumensis_2	zinc proteinase mpc1	133	7.29E-07	45.00%	-	0	IPR001506; IPR024079; PTHR10127 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF55486 (SUPERFAMILY)
272	DMPC15163255_Speleonectes _tulumensis_0	anti-lipopolysaccharide factor	152	3.40E-29	68.50%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
273	DMPC15163300_Speleonectes _tulumensis_1	46 kda fk506-binding nuclear protein	360	2.62E-45	77.10%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR001179; IPR023566; G3DSA:3.10.50.40 (GENE3D), PTHR10516:SF125 (PANTHER), SSF54534 (SUPERFAMILY)
274	DMPC15163335_Speleonectes _tulumensis_0	c-type lectin 3	150	5.24E-10	47.57%	F:carbohydrate binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF5 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
275	DMPC15163351_Speleonectes _tulumensis_0	platelet-activating factor acetylhydrolase	257	1.81E-25	55.50%	P:low-density lipoprotein particle remodeling; F:hydrolase activity; P:lipid catabolic process; C:extracellular region; P:plasma lipoprotein particle oxidation; F:calcium-independent phospholipase A2 activity; P:lipid oxidation; C:low-density lipoprotein particle; P:positive regulation of monocyte chemotaxis; F:1-alkyl-2-acetylglycerophosphocholine esterase activity; F:phospholipid binding; C:extracellular space	12	IPR005065; G3DSA:3.40.50.1820 (GENE3D), PTHR10272:SF2 (PANTHER)
276	DMPC15163411_Speleonectes _tulumensis_1	mite allergen tyr p 7	227	4.30E-14	46.70%	-	0	IPR020234
277	DMPC15163445_Speleonectes _tulumensis_0	hypothetical protein AaeL_AAEL012633	146	5.50E-32	76.80%	-	0	IPR002172; IPR023415; PTHR10529 (PANTHER), PTHR10529:SF83 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
278	DMPC15163588_Speleonectes _tulumensis_1	60s ribosomal protein l40	126	3.24E-47	97.50%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
279	DMPC15163692_Speleonectes _tulumensis_0	ferritin	161	2.12E-51	87.20%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; IPR014034; SignalP-NN(euk) (SIGNALP)
280	DMPC15163724_Speleonectes _tulumensis_2	---NA---	139			-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
281	DMPC15163947_Speleonectes _tulumensis_2	---NA---	152			-	0	IPR008197; PTHR19441 (PANTHER), PTHR19441:SF8 (PANTHER)
282	DMPC15163956_Speleonectes _tulumensis_1	serine protease	283	7.56E-20	72.20%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF68 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
283	DMPC15164029_Speleonectes _tulumensis_0	ecdysteroid-regulated protein	143	6.97E-23	58.60%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER)
284	DMPC15164047_Speleonectes _tulumensis_0	secreted salivary gland	443	7.16E-20	50.30%	C:extracellular region; P:pathogenesis	2	IPR004991; IPR023307; tmhmm (TMHMM), SSF56973 (SUPERFAMILY)
285	DMPC15164219_Speleonectes _tulumensis_2	hemocyanin subunit type 1 precursor	195	1.07E-61	75.70%	-	0	IPR005203; IPR013788; IPR014756
286	DMPC15164292_Speleonectes _tulumensis_2	cathepsin l-like	124	1.46E-27	87.60%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
287	DMPC15164410_Speleonectes _tulumensis_0	polyubiquitin with 3 ub domains	155	2.08E-57	96.80%	-	0	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
288	DMPC15164580_Speleonectes _tulumensis_0	kazal-type protease inhibitor	245	2.09E-24	51.70%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
289	DMPC15164651_Speleonectes _tulumensis_0	neuroendocrine convertase	136	1.04E-68	84.20%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR002884; IPR008979; IPR015500; PTHR10795:SF11 (PANTHER), SignalP-NN(euk) (SIGNALP)

290	DMPC15164762_Speleonectes_tulumensis_1	kazal-type protease inhibitor	131	1.74E-21	54.80%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
291	DMPC15164788_Speleonectes_tulumensis_2	c-type lectin 1	159	9.18E-11	63.30%	F:carbohydrate binding	1	IPR001304; IPR016186; IPR016187; IPR018378; PTHR22802 (PANTHER)
292	DMPC15164808_Speleonectes_tulumensis_3	---NA---	163			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
293	DMPC15164814_Speleonectes_tulumensis_1	beta 1-like 2	288	3.34E-67	57.30%	F:hydrolase activity	1	IPR001944; IPR008979; PTHR23421:SF14 (PANTHER)
294	DMPC15164848_Speleonectes_tulumensis_1	enolase	133	3.52E-25	86.30%	C:cytosol; C:protein complex; F:catalytic activity; F:binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process	7	IPR000941; IPR020811; G3DSA:3.30.390.10 (GENE3D), SSF54826 (SUPERFAMILY)
295	DMPC15164897_Speleonectes_tulumensis_2	membrane glycoprotein lig-	366	8.38E-11	45.60%	F:hydrolase activity; F:phosphoprotein phosphatase activity; C:integral to membrane	3	IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR24367 (PANTHER), PF13855 (PFAM), SignalP-NN(euk) (SIGNALP), SSF52058 (SUPERFAMILY)
296	DMPC15164938_Speleonectes_tulumensis_2	zinc finger	134	1.44E-22	54.20%	F:nucleic acid binding; F:zinc ion binding; C:intracellular; F:ATP binding; F:protein kinase activity; P:protein phosphorylation; F:transferase activity, transferring phosphorus-containing groups	7	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PF13465 (PFAM), PF13894 (PFAM), SSF57667 (SUPERFAMILY)
297	DMPC15164950_Speleonectes_tulumensis_2	lipase 3-like	214	9.95E-47	69.10%	P:lipid metabolic process; F:hydrolase activity, acting on ester bonds; F:hydrolase activity; P:lipid catabolic process	4	G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER), tmhmm (TMHMM), SSF53474 (SUPERFAMILY)
298	DMPC15165031_Speleonectes_tulumensis_0	protein lethal giant larvae-like isoform 2	171	9.09E-45	67.30%	P:multicellular organismal development	1	IPR000664; IPR001680; IPR015943; IPR019775; PTHR10241 (PANTHER), PTHR10241:SF21 (PANTHER)
299	DMPC15165128_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor-like	133	2.75E-12	57.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
300	DMPC15165178_Speleonectes_tulumensis_2	dermatopontin 2	96	3.71E-09	68.14%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
301	DMPC15165218_Speleonectes_tulumensis_2	c4b-binding protein beta	130	1.37E-34	65.70%	F:hydrolase activity	1	IPR000436; G3DSA:2.10.70.10 (GENE3D), PTHR19325 (PANTHER)
302	DMPC15165229_Speleonectes_tulumensis_2	---NA---	123			-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), tmhmm (TMHMM)
303	DMPC15165243_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor isoform 7	149	1.91E-26	67.00%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
304	DMPC15165288_Speleonectes_tulumensis_1	soma ferritin	122	5.28E-36	86.70%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
305	DMPC15165290_Speleonectes_tulumensis_1	dipeptidyl peptidase 9	130	5.73E-40	92.50%	-	0	IPR001375; G3DSA:3.40.50.1820 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF9 (PANTHER), SSF53474 (SUPERFAMILY)
306	DMPC15165322_Speleonectes_tulumensis_1	puromycin-sensitive partial	147	6.08E-86	90.20%	F:peptidase activity; P:protein metabolic process; P:catabolic process; F:binding	4	IPR001930; IPR014782; IPR015568; G3DSA:1.10.390.10 (GENE3D), SSF55486 (SUPERFAMILY)
307	DMPC15165330_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	131	6.15E-11	57.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
308	DMPC15165391_Speleonectes_tulumensis_0	carboxypeptidase b-like	210	6.68E-64	68.40%	-	0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
309	DMPC15165423_Speleonectes_tulumensis_2	pancreatic lipase-related protein 2	188	1.53E-32	52.80%	P:lipid metabolic process; F:hydrolase activity; F:catalytic activity; F:triglyceride lipase activity; C:extracellular region	5	IPR000734; IPR001024; IPR002331; IPR008976; IPR013818; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
310	DMPC15165503_Speleonectes_tulumensis_2	---NA---	148			-	0	IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

311	DMPC15165548_Speleonectes _tulumensis_2	grn protein	114	1.37E-14	59.50%	-	0	IPR000118; PTHR12274 (PANTHER), PTHR12274:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
312	DMPC15165570_Speleonectes _tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	119	1.70E-13	55.70%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:proteolysis; F:peptidase activity	6	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
313	DMPC15165662_Speleonectes _tulumensis_1	upf0670 protein cg4666-like	140	9.41E-10	54.30%	-	0	PTHR12475 (PANTHER), tmhmm (TMHMM)
314	DMPC15165700_Speleonectes _tulumensis_2	anti-lipopolysaccharide factor isoform 7	138	2.97E-31	67.90%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
315	DMPC15165742_Speleonectes _tulumensis_2	ribosomal protein s27a	145	5.43E-47	99.40%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
316	DMPC15165751_Speleonectes _tulumensis_2	serine protease inhibitor kazal-type 6-like	140	8.22E-07	71.00%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
317	DMPC15165770_Speleonectes _tulumensis_2	loc496089 protein	242	9.66E-61	94.10%	P:metabolic process; F:antioxidant activity; F:catalytic activity	3	IPR000866; IPR012336; IPR019479; PTHR10681 (PANTHER), PTHR10681:SF46 (PANTHER)
318	DMPC15165819_Speleonectes _tulumensis_2	cathepsin l	94	9.05E-44	82.70%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
319	DMPC15165851_Speleonectes _tulumensis_2	protein twisted gastrulation	77	2.90E-32	80.70%	-	0	IPR006761; PTHR12312:SF4 (PANTHER)
320	DMPC15165898_Speleonectes _tulumensis_1	ubiquitin-40s ribosomal protein s27a	151	1.72E-65	97.00%	P:cell cycle; P:metabolic process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:cellular protein modification process; P:transport	27	IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
321	DMPC15165914_Speleonectes _tulumensis_2	mantle protein 9	152	1.51E-08	67.75%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
322	DMPC15165962_Speleonectes _tulumensis_0	protein	130	1.63E-18	52.30%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
323	DMPC15166091_Speleonectes _tulumensis_0	ale o 1 allergen	113	9.27E-14	90.10%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
324	DMPC15166109_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor	140	3.22E-30	67.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
325	DMPC15166131_Speleonectes _tulumensis_1	copa partial	225	1.55E-82	82.30%	F:protein kinase activity; P:transport; P:protein transport; C:Golgi apparatus; C:protein complex; C:cytoplasmic membrane-bounded vesicle; F:structural molecule activity	7	IPR010714; PTHR19876 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

326	DMPC15166149_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	131	7.93E-19	62.20%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
327	DMPC15166154_Speleonectes_tulumensis_2	heat shock 70 kda protein cognate 4	285	1.77E-122	95.80%	-	0	IPR013126; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), PTHR19375 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY)
328	DMPC15166174_Speleonectes_tulumensis_0	zinc finger protein interacting with k protein 1	154	1.18E-19	60.80%	F:binding	1	IPR007087; IPR013087; IPR015880; PTHR24402 (PANTHER), PTHR24402:SF3 (PANTHER), PF13465 (PFAM), PF13894 (PFAM), SSF57667 (SUPERFAMILY)
329	DMPC15166340_Speleonectes_tulumensis_2	hypothetical protein DAPPUDRAFT_308200	142	5.43E-10	50.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
330	DMPC15166364_Speleonectes_tulumensis_0	plasminogen activator spa	105	1.80E-17	67.90%	P:metabolic process; F:catalytic activity	2	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)
331	DMPC15166391_Speleonectes_tulumensis_1	---NA---	105			-	0	IPR001254; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER)
332	DMPC15166468_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	152	2.37E-59	70.20%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
333	DMPC15166472_Speleonectes_tulumensis_0	---NA---	153			-	0	IPR001211; IPR013090; IPR016090
334	DMPC15166497_Speleonectes_tulumensis_2	isoform a	131	5.50E-19	56.60%	P:proteolysis; F:metallopeptidase activity; F:hydrolase activity; F:peptidase activity; F:metalloendopeptidase activity; P:cell proliferation; C:cellular_component	7	IPR001590; IPR024079; PTHR13723 (PANTHER), PF13574 (PFAM), SSF55486 (SUPERFAMILY)
335	DMPC15166553_Speleonectes_tulumensis_0	retinol dehydrogenase 14-like	163	1.40E-11	68.40%	P:oxidation-reduction process; F:oxidoreductase activity; P:metabolic process; F:nucleotide binding	4	IPR016040; PTHR24320 (PANTHER), PTHR24320:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF51735 (SUPERFAMILY)
336	DMPC15166686_Speleonectes_tulumensis_1	5 ecto-like	122	2.23E-11	67.10%	F:hydrolase activity; F:binding; P:nucleobase-containing compound metabolic process; P:catabolic process; F:nucleotide binding	5	IPR006146; IPR006179; G3DSA:3.60.21.10 (GENE3D), tmhmm (TMHMM), SSF56300 (SUPERFAMILY)
337	DMPC15166755_Speleonectes_tulumensis_2	heat shock cognate 70	195	7.04E-44	92.10%	-	0	IPR013126; G3DSA:1.20.1270.10 (GENE3D), PTHR19375 (PANTHER), tmhmm (TMHMM), SSF100934 (SUPERFAMILY)
338	DMPC15166855_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_308200	140	4.48E-09	51.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
339	DMPC15166875_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor	152	9.20E-30	68.40%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
340	DMPC15166980_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	139	1.86E-13	57.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
341	DMPC15166982_Speleonectes_tulumensis_1	hemocyanin subunit type 2 precursor	103	4.79E-50	72.60%	-	0	IPR005203; IPR013788; IPR014756
342	DMPC15167041_Speleonectes_tulumensis_0	zinc finger protein	127	5.34E-15	54.60%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR24401 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
343	DMPC15167091_Speleonectes_tulumensis_2	zinc metalloprotease	112	1.97E-23	71.80%	F:peptidase activity	1	IPR001570; G3DSA:1.10.390.10 (GENE3D), tmhmm (TMHMM), SSF55486 (SUPERFAMILY)
344	DMPC15167134_Speleonectes_tulumensis_0	chitinase partial	175	3.31E-67	70.10%	-	0	IPR001223; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SSF54556 (SUPERFAMILY)
345	DMPC15167141_Speleonectes_tulumensis_1	adp-ribosylation factor-like protein 1-like	331	1.73E-119	96.10%	C:intracellular; F:nucleotide binding; P:signal transduction	3	IPR003579; IPR005225; IPR006687; IPR006689; IPR024156; IPR027417; G3DSA:3.40.50.300 (GENE3D), PTHR11711 (PANTHER), PTHR11711:SF41 (PANTHER)

346	DMPC15167290_Speleonectes_tulumensis_1	vitellogenin 1	98	6.16E-16	61.38%	-	0	IPR001846
347	DMPC15167314_Speleonectes_tulumensis_1	hemocyanin subunit type 2 precursor	120	8.59E-25	79.80%	-	0	IPR000896; IPR008922; IPR013788
348	DMPC15167326_Speleonectes_tulumensis_2	hypothetical protein TcasGA2_TC013968	150	4.92E-07	55.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
349	DMPC15167369_Speleonectes_tulumensis_2	dermatopontin 2	104	5.36E-08	68.22%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
350	DMPC15167372_Speleonectes_tulumensis_1	glutathione peroxidase	112	6.57E-11	59.70%	F:catalytic activity	1	IPR000889; IPR012336; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
351	DMPC15167423_Speleonectes_tulumensis_1	serine protease	126	8.96E-16	60.30%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
352	DMPC15167475_Speleonectes_tulumensis_1	proclotting enzyme-like	143	2.90E-17	67.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER)
353	DMPC15167504_Speleonectes_tulumensis_1	myosin heavy muscle	411	2.05E-94	90.60%	C:cytoskeleton; C:protein complex; F:motor activity	3	IPR002928; PTHR13140 (PANTHER), PTHR13140:SF106 (PANTHER), tmhmm (TMHMM)
354	DMPC15167609_Speleonectes_tulumensis_1	limbic system-associated membrane protein	112	4.10E-13	54.50%	-	0	IPR007110; IPR013098; IPR013783; PTHR10489 (PANTHER), PF13895 (PFAM), SignalP-NN(euk) (SIGNALP), SSF48726 (SUPERFAMILY)
355	DMPC15167624_Speleonectes_tulumensis_2	sjchgc02838 protein	322	3.67E-50	53.40%	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process; F:cation binding; F:catalytic activity	4	IPR013781
356	DMPC15167630_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor-like	141	7.06E-21	59.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
357	DMPC15167633_Speleonectes_tulumensis_0	pancreatic lipase-related protein 1	228	4.76E-22	50.80%	F:hydrolase activity	1	IPR000734; IPR001024; IPR002331; IPR008976; IPR013818; G3DSA:3.40.50.1820 (GENE3D)
358	DMPC15167700_Speleonectes_tulumensis_0	ga22152	359	1.03E-10	71.60%	F:kinase activity; P:metabolic process	2	IPR001576; IPR015824
359	DMPC15167700_Speleonectes_tulumensis_1	phosphoglycerate kinase	358	4.45E-112	86.80%	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; P:metabolic process; F:kinase activity	5	IPR001576; IPR015901
360	DMPC15167787_Speleonectes_tulumensis_2	---NA---	134			-	0	IPR026645
361	DMPC15167844_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor	140	5.67E-31	68.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
362	DMPC15167887_Speleonectes_tulumensis_2	chymotrypsin-like elastase family member 2a-like	101	2.10E-13	76.30%	C:cell; P:protein metabolic process; P:catabolic process; F:peptidase activity	4	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
363	DMPC15167984_Speleonectes_tulumensis_2	thioredoxin-like protein	102	2.79E-25	82.00%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; SignalP-NN(euk) (SIGNALP)
364	DMPC15168025_Speleonectes_tulumensis_1	transmembrane serine protease	263	2.12E-33	52.20%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
365	DMPC15168027_Speleonectes_tulumensis_0	xanthine dehydrogenase oxidase	94	8.50E-09	76.67%	-	0	PTHR11908 (PANTHER), PTHR11908:SF9 (PANTHER)
366	DMPC15168034_Speleonectes_tulumensis_1	hypothetical protein TcasGA2_TC013968	147	1.72E-07	55.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
367	DMPC15168140_Speleonectes_tulumensis_0	nidogen 1	141	8.90E-11	67.50%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
368	DMPC15168200_Speleonectes_tulumensis_0	carbonic anhydrase 1	169	4.19E-52	70.50%	F:binding; F:catalytic activity	2	IPR001148; IPR018338; IPR018436; IPR023561

369	DMPC15168236_Speleonectes_tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	135	2.15E-21	52.70%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
370	DMPC15168296_Speleonectes_tulumensis_1	alkaline serine exoprotease a	160	3.79E-22	66.40%	F:peptidase activity	1	IPR007280; SignalP-NN(euk) (SIGNALP)
371	DMPC15168327_Speleonectes_tulumensis_2	pacifastin-related serine protease inhibitor precursor	156	1.52E-16	51.10%	F:peptidase inhibitor activity; P:negative regulation of peptidase activity	2	IPR008037; IPR016307; IPR020862; SignalP-NN(euk) (SIGNALP)
372	DMPC15168354_Speleonectes_tulumensis_1	dopamine beta hydroxylase	233	2.57E-37	56.90%	F:catalytic activity	1	IPR000945; IPR005018; IPR008960; IPR015920; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
373	DMPC15168377_Speleonectes_tulumensis_2	coiled-coil domain-containing protein 134	106	1.03E-28	67.90%	-	0	IPR026321; PTHR14735:SF0 (PANTHER)
374	DMPC15168444_Speleonectes_tulumensis_0	membrane metallo-endopeptidase-like 1-like	124	1.87E-24	85.00%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000718; IPR018497; IPR024079; PTHR11733:SF48 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF55486 (SUPERFAMILY)
375	DMPC15168472_Speleonectes_tulumensis_0	macrophage migration inhibitory factor	270	4.13E-15	71.00%	-	0	IPR001398; IPR014347; G3DSA:3.30.429.10 (GENE3D), PTHR11954:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP)
376	DMPC15168489_Speleonectes_tulumensis_1	trypsin	151	3.54E-37	71.60%	F:catalytic activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER)
377	DMPC15168501_Speleonectes_tulumensis_1	isoamyl acetate-hydrolyzing esterase 1 homolog	174	2.61E-38	64.50%	F:hydrolase activity; P:lipid metabolic process; F:hydrolase activity, acting on ester bonds	3	IPR001087; IPR013831; PTHR14209 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF52266 (SUPERFAMILY)
378	DMPC15168555_Speleonectes_tulumensis_0	---NA---	146			-	0	IPR000566; IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
379	DMPC15168566_Speleonectes_tulumensis_1	glutaredoxin 3	98	2.55E-17	66.60%	P:biological_process; F:protein binding; P:regulation of biological process	3	IPR004480; IPR012336; IPR013766; PTHR10293:SF17 (PANTHER)
380	DMPC15168600_Speleonectes_tulumensis_0	---NA---	78			-	0	no IPS match
381	DMPC15168608_Speleonectes_tulumensis_1	sifa preprohormone	138	9.78E-18	74.50%	-	0	tmhmm (TMHMM)
382	DMPC15168627_Speleonectes_tulumensis_0	hemocyanin subunit type 1 precursor	154	5.75E-87	67.70%	-	0	IPR005204; IPR013788; PTHR11511:SF20 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
383	DMPC15168765_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	140	8.85E-17	51.20%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
384	DMPC15168767_Speleonectes_tulumensis_0	gamma-glutamyl hydrolase-like	155	3.33E-15	65.00%	F:hydrolase activity	1	IPR011697; IPR015527; G3DSA:3.40.50.880 (GENE3D), PTHR11315:SF0 (PANTHER)
385	DMPC15168773_Speleonectes_tulumensis_1	dnaj homolog subfamily b member 5-partial	89	2.95E-13	90.00%	P:protein metabolic process; F:protein binding	2	IPR001623; PTHR24077 (PANTHER), PTHR24077:SF6 (PANTHER)
386	DMPC15168816_Speleonectes_tulumensis_0	soma ferritin	104	4.38E-24	87.00%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
387	DMPC15168834_Speleonectes_tulumensis_0	cd74 major histocompatibility class ii invariant chain a	135	7.00E-08	67.67%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
388	DMPC15168909_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor	109	7.78E-08	61.71%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
389	DMPC15168933_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor-like	142	3.62E-11	62.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
390	DMPC15168951_Speleonectes_tulumensis_0	perlucin 5	149	6.18E-11	49.90%	F:protein binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
391	DMPC15169038_Speleonectes_tulumensis_2	loc100145034 protein	183	1.10E-11	49.30%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; C:extracellular region	5	IPR001211; IPR016090; PTHR12253:SF5 (PANTHER)

392	DMPC15169043_Speleonectes_tulumensis_2	kazal-type serine proteinase inhibitor 4	104	1.48E-11	66.00%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR25189 (PANTHER), PTHR25189:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
393	DMPC15169049_Speleonectes_tulumensis_2	glutathione peroxidase 1	119	1.24E-55	80.20%	P:response to external stimulus; P:anatomical structure morphogenesis; P:multicellular organismal development; P:response to stress; P:response to abiotic stimulus; P:cell proliferation; P:catabolic process; P:regulation of biological process; P:cell death; P:cell differentiation; P:biological_process; P:cellular protein modification process; P:nucleobase-containing compound metabolic process; C:cytosol; F:catalytic activity; F:antioxidant activity; P:growth; P:cellular homeostasis; ; P:lipid metabolic process; F:enzyme regulator activity; P:mitochondrion organization; F:protein binding; P:regulation of gene expression, epigenetic; P:signal transduction; C:mitochondrion	26	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
394	DMPC15169200_Speleonectes_tulumensis_0	cathepsin l-like	183	2.02E-19	86.30%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
395	DMPC15169261_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	109	5.89E-14	63.20%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
396	DMPC15169274_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	126	1.23E-18	63.40%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
397	DMPC15169350_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	145	9.96E-24	58.10%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
398	DMPC15169420_Speleonectes_tulumensis_0	soma ferritin	123	1.31E-30	88.10%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
399	DMPC15169439_Speleonectes_tulumensis_1	ferritin subunit	105	6.88E-22	89.20%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
400	DMPC15169593_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor-like	144	5.76E-22	59.10%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
401	DMPC15169648_Speleonectes_tulumensis_1	ferritin h subunit	107	1.34E-19	88.80%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
402	DMPC15169696_Speleonectes_tulumensis_2	epididymal secretory protein e1 isoform 1	145	1.20E-23	56.30%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
403	DMPC15169704_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	123	8.36E-11	60.20%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
404	DMPC15169724_Speleonectes_tulumensis_0	dermatopontin 3	130	2.67E-16	60.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
405	DMPC15169738_Speleonectes_tulumensis_2	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphex133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein	128	3.54E-16	60.60%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PF13894 (PFAM), SSF57667 (SUPERFAMILY)
406	DMPC15169774_Speleonectes_tulumensis_0	dermatopontin 3	95	3.51E-08	67.50%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
407	DMPC15169802_Speleonectes_tulumensis_5	glutathione peroxidase 1	125	3.60E-21	82.60%	-	0	IPR000889; IPR012336; tmhmm (TMHMM)

408	DMPC15169828_Speleonectes_tulumensis_1	zgc:66168 partial	120	1.08E-42	99.40%	-	0	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
409	DMPC15169838_Speleonectes_tulumensis_1	cysteine-rich motor neuron 1 protein	130	1.12E-25	69.40%	C:extracellular region; F:protein binding; P:regulation of biological process; P:cell growth	4	IPR000867; IPR011390; PTHR14186:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
410	DMPC15169873_Speleonectes_tulumensis_0	phospholipase major isoenzyme-like	142	1.78E-13	68.70%	P:biosynthetic process; P:lipid metabolic process; C:cytoplasmic membrane-bounded vesicle; P:response to endogenous stimulus; F:hydrolase activity; F:calcium ion binding; P:regulation of biological process; P:DNA metabolic process; P:catabolic process; ; C:extracellular space; P:transport; F:receptor binding; F:binding	14	IPR001211; IPR016090; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
411	DMPC15169895_Speleonectes_tulumensis_0	protein 60a-like	108	1.57E-14	55.80%	-	0	IPR001839; IPR015615; PTHR11848:SF55 (PANTHER)
412	DMPC15169921_Speleonectes_tulumensis_2	lectin b isoform 2	144	5.55E-10	54.70%	F:carbohydrate binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
413	DMPC15170017_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	140	3.74E-19	53.10%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
414	DMPC15170112_Speleonectes_tulumensis_0	---NA---	117			-	0	IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
415	DMPC15170184_Speleonectes_tulumensis_1	upf0670 protein cg4666-like	84	3.69E-10	65.00%	F:molecular_function; P:biological_process; C:cellular_component	3	PTHR12475 (PANTHER), PTHR12475:SF3 (PANTHER), tmhmm (TMHMM)
416	DMPC15170221_Speleonectes_tulumensis_2	aminoacylase-1-like isoform 1	283	3.54E-91	73.30%	P:primary metabolic process; F:hydrolase activity	2	IPR001261; IPR002933; IPR011650; G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF53187 (SUPERFAMILY)
417	DMPC15170228_Speleonectes_tulumensis_2	trypsin partial	130	1.04E-11	57.90%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
418	DMPC15170269_Speleonectes_tulumensis_1	kallikrein isoform cra_b	122	3.47E-10	55.80%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER)
419	DMPC15170341_Speleonectes_tulumensis_0	ecdysteroid-regulated protein	142	4.13E-20	61.50%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER)
420	DMPC15170355_Speleonectes_tulumensis_1	zinc finger protein 300-like	82	7.95E-13	59.30%	F:nucleic acid binding; F:zinc ion binding; C:intracellular; C:nucleus	4	IPR007087; IPR013087; IPR015880; PTHR24402 (PANTHER), PTHR24402:SF3 (PANTHER), PF13894 (PFAM), SSF57667 (SUPERFAMILY)
421	DMPC15170413_Speleonectes_tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	148	3.32E-22	52.90%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:cell-matrix adhesion; F:calcium ion binding	6	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
422	DMPC15170422_Speleonectes_tulumensis_2	---NA---	128			-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
423	DMPC15170455_Speleonectes_tulumensis_0	serine protease 14	94	1.63E-13	71.00%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
424	DMPC15170506_Speleonectes_tulumensis_1	zinc metalloprotease	160	3.59E-15	58.80%	F:peptidase activity	1	IPR007280
425	DMPC15170510_Speleonectes_tulumensis_1	epididymal secretory protein e1 isoform 1	148	4.52E-24	57.70%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

426	DMPC15170537_Speleonectes _tulumensis_1	partial	117	1.21E-40	73.40%	P:oxidation-reduction process; F:heme binding; P:response to oxidative stress; F:peroxidase activity	4	IPR002007; IPR010255; IPR019791; PTHR11475 (PANTHER)
427	DMPC15170590_Speleonectes _tulumensis_0	trypsin-like serine proteinase 1	133	4.47E-22	63.40%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
428	DMPC15170691_Speleonectes _tulumensis_0	maltase- intestinal-like	156	1.13E-17	64.70%	F:catalytic activity	1	IPR000322
429	DMPC15170704_Speleonectes _tulumensis_0	techylectin-5b isoform	313	1.05E-53	66.20%	-	0	IPR002181; IPR014715; IPR014716; IPR020837; PTHR19143 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
430	DMPC15170788_Speleonectes _tulumensis_1	cathepsin l	304	6.02E-109	72.40%	-	0	IPR000169; IPR000668; IPR013128; IPR013201; IPR025660; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
431	DMPC15170859_Speleonectes _tulumensis_2	tyrosine--trna cytoplasmic-like	225	7.10E-80	74.60%	F:catalytic activity; P:translation; P:nucleobase-containing compound metabolic process; ; F:nucleotide binding	5	IPR002547; IPR012340; IPR023617; PTHR11946 (PANTHER)
432	DMPC15170921_Speleonectes _tulumensis_0	trypsin 3	163	2.81E-56	76.40%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER)
433	DMPC15170987_Speleonectes _tulumensis_2	tpa_inf: fibrinogen-related protein 2	114	1.91E-24	68.40%	F:receptor binding; C:extracellular space; P:signal transduction	3	IPR002181; IPR014715; IPR020837; PTHR19143 (PANTHER)
434	DMPC15171035_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor-like	136	3.23E-10	61.20%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
435	DMPC15171043_Speleonectes _tulumensis_2	dermatopontin 3	100	5.26E-09	63.13%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
436	DMPC15171055_Speleonectes _tulumensis_0	kazal-type protease inhibitor	112	3.18E-14	56.50%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
437	DMPC15171060_Speleonectes _tulumensis_1	peptidase s8 and sedolisin	193	2.94E-22	68.30%	F:peptidase activity	1	IPR007280
438	DMPC15171081_Speleonectes _tulumensis_1	dermatopontin 3	150	9.98E-20	60.60%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
439	DMPC15171218_Speleonectes _tulumensis_1	h-2 class ii histocompatibility antigen gamma chain	110	1.64E-08	66.00%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
440	DMPC15171224_Speleonectes _tulumensis_0	nas-15 protein	217	1.32E-25	60.90%	F:hydrolase activity	1	IPR001506; IPR024079; PTHR24543 (PANTHER), PTHR24543:SF85 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF55486 (SUPERFAMILY)
441	DMPC15171239_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor	155	2.08E-29	67.50%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
442	DMPC15171253_Speleonectes _tulumensis_0	thioredoxin 1	165	1.48E-51	83.80%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; IPR017937; SignalP-NN(euk) (SIGNALP)
443	DMPC15171262_Speleonectes _tulumensis_2	aldehyde dehydrogenase mitochondrial-like	213	2.98E-45	85.50%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER), tmhmm (TMHMM)
444	DMPC15171342_Speleonectes _tulumensis_2	aspartic proteinase	130	4.59E-34	65.70%	C:cytoplasmic membrane-bounded vesicle	1	IPR001461; IPR001969; IPR021109; PTHR13683:SF84 (PANTHER), SignalP-NN(euk) (SIGNALP)
445	DMPC15171360_Speleonectes _tulumensis_2	---NA---	151			-	0	IPR000566; IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
446	DMPC15171417_Speleonectes _tulumensis_1	oocyte protease inhibitor-1 precursor	133	1.04E-09	68.10%	P:metabolic process	1	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
447	DMPC15171448_Speleonectes _tulumensis_2	---NA---	46			-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), SSF100895 (SUPERFAMILY)

448	DMPC15171476_Speleonectes_tulumensis_0	saxiphilin precursor	126	7.17E-11	65.20%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
449	DMPC15171503_Speleonectes_tulumensis_1	hemocyanin subunit type 1 precursor	128	1.24E-58	75.30%	-	0	IPR005203; IPR013788; IPR014756
450	DMPC15171706_Speleonectes_tulumensis_1	retinal dehydrogenase 1	169	3.77E-63	81.30%	C:cytoplasm; F:catalytic activity; P:lipid metabolic process; P:secondary metabolic process; P:metabolic process	5	IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
451	DMPC15171725_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	145	4.08E-53	68.20%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
452	DMPC15171826_Speleonectes_tulumensis_0	kazal-type serine proteinase inhibitor 4	126	9.63E-16	54.60%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
453	DMPC15171827_Speleonectes_tulumensis_1	plasminogen activator spa	89	3.80E-08	56.80%	F:catalytic activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER), PTHR24272:SF11 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
454	DMPC15171832_Speleonectes_tulumensis_2	chondroitin sulfate synthase 1	120	8.21E-25	68.30%	C:Golgi cisterna membrane; F:transferase activity, transferring hexosyl groups	2	IPR008428; G3DSA:3.90.550.10 (GENE3D), PTHR12369:SF5 (PANTHER), SignalP-NN(euk) (SIGNALP)
455	DMPC15171842_Speleonectes_tulumensis_2	---NA---	297			-	0	IPR001283; IPR014044; IPR018244; tmhmm (TMHMM)
456	DMPC15171843_Speleonectes_tulumensis_1	chloride channel calcium activated 2-like	553	5.30E-21	55.20%	-	0	IPR003961; IPR013783; PTHR10579 (PANTHER), PTHR10579:SF8 (PANTHER), tmhmm (TMHMM)
457	DMPC15171847_Speleonectes_tulumensis_1	---NA---	141			-	0	IPR000562; IPR013806; PTHR22803 (PANTHER), PTHR22803:SF17 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
458	DMPC15171946_Speleonectes_tulumensis_0	ecdysteroid-regulated 16 kda protein	229	2.52E-16	54.30%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER)
459	DMPC15171986_Speleonectes_tulumensis_0	er-type hsp70	149	1.13E-43	75.40%	P:signal transduction; F:protein binding; C:endoplasmic reticulum; C:cell; P:regulation of biological process; P:cellular protein modification process; P:response to stress; C:protein complex; P:multicellular organismal development; F:nucleotide binding	10	IPR013126; G3DSA:2.60.34.10 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY)
460	DMPC15172053_Speleonectes_tulumensis_1	---NA---	145			-	0	IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
461	DMPC15172056_Speleonectes_tulumensis_1	trypsin-like serine proteinase 2	265	2.19E-40	54.10%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)
462	DMPC15172075_Speleonectes_tulumensis_2	mannose-binding protein a-like	120	6.60E-14	54.50%	F:carbohydrate binding	1	IPR001304; IPR016186; IPR016187; IPR018378; PTHR22802 (PANTHER)
463	DMPC15172107_Speleonectes_tulumensis_1	dermatopontin 2	141	3.39E-10	59.30%	-	0	IPR026645; tmhmm (TMHMM)
464	DMPC15172136_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	136	3.50E-16	57.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
465	DMPC15172207_Speleonectes_tulumensis_0	chymotrypsin-like elastase family member 2a	226	1.15E-19	56.90%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
466	DMPC15172211_Speleonectes_tulumensis_0	glycosyl-phosphatidylinositol-linked carbonic anhydrase	116	2.56E-13	55.50%	F:carbonate dehydratase activity	1	IPR001148; IPR023561; SignalP-NN(euk) (SIGNALP)
467	DMPC15172216_Speleonectes_tulumensis_2	epididymal secretory protein e1 precursor	153	1.03E-26	55.80%	C:extracellular region	1	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

468	DMPC15172265_Speleonectes_tulumensis_1	ubiquitin-40s ribosomal protein s27a	153	2.07E-56	96.70%	P:cell cycle; P:metabolic process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:cellular protein modification process; P:transport	27	IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
469	DMPC15172267_Speleonectes_tulumensis_2	serine proteinase stubble-like	123	8.30E-19	53.40%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER)
470	DMPC15172357_Speleonectes_tulumensis_1	kazal-type serine proteinase inhibitor 4	134	1.03E-12	64.00%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR25189 (PANTHER), PTHR25189:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
471	DMPC15172383_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor	280	3.38E-12	65.30%	-	0	tmhmm (TMHMM)
472	DMPC15172398_Speleonectes_tulumensis_0	inactive hydroxysteroid dehydrogenase-like protein 1	194	3.44E-57	72.00%	-	0	IPR002198; IPR002347; IPR016040; PTHR24316 (PANTHER), PTHR24316:SF68 (PANTHER), SSF51735 (SUPERFAMILY)
473	DMPC15172464_Speleonectes_tulumensis_2	protein	146	5.17E-21	53.50%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:cell-matrix adhesion; F:calcium ion binding	6	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
474	DMPC15172474_Speleonectes_tulumensis_5	stretchin- isoform s	151	5.52E-42	86.70%	F:structural molecule activity; F:protein kinase activity; C:cytoskeleton; C:protein complex; P:cellular protein modification process; F:nucleotide binding	6	IPR007110; IPR013783; IPR020675; IPR020682; PF13895 (PFAM), SSF48726 (SUPERFAMILY)
475	DMPC15172502_Speleonectes_tulumensis_1	ferritin gf1	112	9.52E-23	86.70%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
476	DMPC15172555_Speleonectes_tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	196	1.60E-19	50.80%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), tmhmm (TMHMM)
477	DMPC15172601_Speleonectes_tulumensis_1	cathepsin l	129	9.23E-59	78.40%	-	0	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
478	DMPC15172629_Speleonectes_tulumensis_2	---NA---	100			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
479	DMPC15172654_Speleonectes_tulumensis_2	sifa preprohormone	131	1.27E-17	74.50%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
480	DMPC15172754_Speleonectes_tulumensis_1	ame: full=trypsin-1 ame: full=trypsin i	143	6.99E-31	72.40%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
481	DMPC15172841_Speleonectes_tulumensis_0	sjchgc02838 protein	214	2.73E-42	59.30%	F:catalytic activity	1	IPR001547; IPR013781; IPR017853
482	DMPC15172931_Speleonectes_tulumensis_1	sulfakinin-like peptide	238	1.76E-16	62.50%	C:extracellular region	1	IPR013152; tmhmm (TMHMM)
483	DMPC15172948_Speleonectes_tulumensis_1	chitinase domain-containing protein 1	139	3.01E-34	59.70%	F:hydrolase activity	1	IPR013781; IPR017853; PTHR11177 (PANTHER)

484	DMPC15173039_Speleonectes_tulumensis_0	nidogen and related basement membrane protein	284	3.90E-12	47.60%	-	0	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
485	DMPC15173062_Speleonectes_tulumensis_1	astakine variant 1	212	9.17E-20	62.00%	-	0	G3DSA:2.10.80.10 (GENE3D)
486	DMPC15173080_Speleonectes_tulumensis_1	carcinolectin 5b partial	141	3.39E-38	67.90%	F:receptor binding; C:extracellular space; P:signal transduction	3	IPR002181; IPR014715; IPR014716; IPR020837; PTHR19143 (PANTHER)
487	DMPC15173109_Speleonectes_tulumensis_2	dimethylaniline monooxygenase	289	7.50E-35	57.70%	P:oxidation-reduction process; F:oxidoreductase activity; F:N,N-dimethylaniline monooxygenase activity; F:monooxygenase activity; F:NADP binding; F:flavin adenine dinucleotide binding; F:nucleotide binding	7	IPR020946; G3DSA:3.50.50.60 (GENE3D), PTHR23023 (PANTHER), SSF51905 (SUPERFAMILY)
488	DMPC15173121_Speleonectes_tulumensis_2	trypsin	143	1.05E-51	72.00%	F:catalytic activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER)
489	DMPC15173162_Speleonectes_tulumensis_1	pancreatic lipase-related protein 3-like	255	3.94E-45	51.00%	P:lipid metabolic process; F:hydrolase activity; F:catalytic activity; F:triglyceride lipase activity; C:extracellular region; F:retinyl-palmitate esterase activity	6	IPR000734; IPR001024; IPR002331; IPR008976; IPR013818; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
490	DMPC15173169_Speleonectes_tulumensis_0	vitelline membrane outer layer protein 1-like	179	3.28E-25	53.40%	-	0	IPR005515; PTHR18841:SF0 (PANTHER)
491	DMPC15173264_Speleonectes_tulumensis_1	---NA---	224			-	0	IPR000566; IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
492	DMPC15173276_Speleonectes_tulumensis_2	histone -like	145	3.56E-64	98.00%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR000558; IPR007125; IPR009072
493	DMPC15173346_Speleonectes_tulumensis_2	trypsin 3	154	2.13E-58	78.00%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
494	DMPC15173520_Speleonectes_tulumensis_0	dermatopontin 2	105	1.62E-08	64.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
495	DMPC15173527_Speleonectes_tulumensis_1	trypsin-like serine proteinase 1	158	1.49E-27	74.00%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
496	DMPC15173564_Speleonectes_tulumensis_1	trypsin-like serine proteinase 1	111	1.21E-21	65.70%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
497	DMPC15173573_Speleonectes_tulumensis_0	hemocyanin subunit type 2	134	9.04E-77	67.10%	-	0	IPR005203; IPR013788; IPR014756
498	DMPC15173661_Speleonectes_tulumensis_2	plasminogen activator spa	293	7.08E-59	57.80%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
499	DMPC15173662_Speleonectes_tulumensis_5	---NA---	159			-	0	IPR002172; PTHR24652 (PANTHER), tmhmm (TMHMM)
500	DMPC15173673_Speleonectes_tulumensis_1	cathepsin l-like	230	5.37E-47	87.00%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
501	DMPC15173689_Speleonectes_tulumensis_0	thioredoxin-dependent peroxide mitochondrial-like	78	5.92E-13	78.40%	F:catalytic activity	1	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF44 (PANTHER)
502	DMPC15173699_Speleonectes_tulumensis_0	kazal-type serine proteinase inhibitor 4	146	8.14E-15	57.50%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
503	DMPC15173707_Speleonectes_tulumensis_2	plasma kallikrein-like	365	2.92E-48	55.80%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

504	DMPC15173711_Speleonectes_tulumensis_0	pacifastin-related serine protease inhibitor precursor	139	2.16E-09	53.14%	F:peptidase inhibitor activity; P:negative regulation of peptidase activity	2	IPR008037; IPR020862; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
505	DMPC15173721_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	157	6.40E-16	56.80%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
506	DMPC15173811_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	137	1.75E-27	67.80%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
507	DMPC15173886_Speleonectes_tulumensis_0	dermatopontin 2	103	1.31E-08	61.86%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
508	DMPC15174029_Speleonectes_tulumensis_3	---NA---	147			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
509	DMPC15174081_Speleonectes_tulumensis_2	serine protease 56-like	263	5.61E-10	54.50%	F:catalytic activity	1	IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24261 (PANTHER), PTHR24261:SF9 (PANTHER)
510	DMPC15174195_Speleonectes_tulumensis_0	secreted salivary gland	364	4.91E-26	47.10%	-	0	IPR004991; IPR023307; SignalP-NN(euk) (SIGNALP), SSF56973 (SUPERFAMILY)
511	DMPC15174233_Speleonectes_tulumensis_1	soma ferritin	113	9.03E-28	88.90%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
512	DMPC15174318_Speleonectes_tulumensis_1	---NA---	143			-	0	IPR000566; IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
513	DMPC15174320_Speleonectes_tulumensis_2	serine protease homolog 93 precursor	110	8.20E-13	66.50%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
514	DMPC15174405_Speleonectes_tulumensis_2	tyrosine-protein kinase dnt	70	5.84E-33	89.00%	F:protein kinase activity; F:receptor activity; P:cellular protein modification process; F:nucleotide binding	4	IPR000719; IPR001245; IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR24416 (PANTHER), PTHR24416:SF85 (PANTHER), SignalP-NN(euk) (SIGNALP)
515	DMPC15174483_Speleonectes_tulumensis_2	torsin family protein	206	3.93E-25	67.50%	F:ATP binding; P:chaperone mediated protein folding requiring cofactor	2	IPR009724; IPR010448; PTHR10760:SF2 (PANTHER), tmhmm (TMHMM)
516	DMPC15174484_Speleonectes_tulumensis_0	serine protease	134	3.23E-20	68.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
517	DMPC15174512_Speleonectes_tulumensis_2	cre-nas-15 protein	273	9.52E-64	56.70%	F:metal ion binding; P:proteolysis; F:metallopeptidase activity; F:hydrolase activity; F:zinc ion binding; F:peptidase activity; F:metalloendopeptidase activity	7	IPR001506; IPR006026; IPR024079; PTHR10127 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF55486 (SUPERFAMILY)
518	DMPC15174535_Speleonectes_tulumensis_0	neutral protease precursor	149	5.58E-12	67.40%	F:peptidase activity	1	SignalP-NN(euk) (SIGNALP)
519	DMPC15174542_Speleonectes_tulumensis_1	kazal-type serine proteinase inhibitor 4	197	5.39E-25	56.70%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
520	DMPC15174656_Speleonectes_tulumensis_0	trypsinogen 2	165	3.16E-50	69.40%	-	0	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER)
521	DMPC15174677_Speleonectes_tulumensis_1	serine protease	99	1.89E-15	61.40%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP)
522	DMPC15174718_Speleonectes_tulumensis_1	alpha-amylase 1	189	2.76E-37	56.40%	P:carbohydrate metabolic process; F:cation binding; F:catalytic activity; F:hydrolase activity; P:metabolic process; F:hydrolase activity, acting on glycosyl bonds	6	IPR006048; IPR013780; IPR015902; PTHR10357:SF26 (PANTHER), SSF51011 (SUPERFAMILY)
523	DMPC15174739_Speleonectes_tulumensis_0	trypsin partial	154	8.90E-12	63.40%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
524	DMPC15174744_Speleonectes_tulumensis_2	PREDICTED: peroxiredoxin-4-like	73	1.05E-15	93.00%	P:metabolic process; F:antioxidant activity; F:catalytic activity	3	IPR012336; IPR019479; PTHR10681 (PANTHER), PTHR10681:SF46 (PANTHER)

525	DMPC15174854_Speleonectes _tulumensis_2	zinc finger protein draculin	67	1.26E-11	65.10%	F:nucleic acid binding; F:zinc ion binding; C:intracellular; P:biological_process	4	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PF13894 (PFAM), SSF57667 (SUPERFAMILY)
526	DMPC15174899_Speleonectes _tulumensis_2	latrophilin 2-like	189	1.14E-13	59.70%	F:transmembrane signaling receptor activity; F:receptor activity; C:integral to membrane; F:G-protein coupled receptor activity; C:membrane; P:cell surface receptor signaling pathway; P:G-protein coupled receptor signaling pathway	7	IPR000832; PTHR12011 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
527	DMPC15174987_Speleonectes _tulumensis_0	lysosomal alphamannosidase	170	1.15E-36	70.50%	P:carbohydrate metabolic process; F:binding; F:hydrolase activity	3	IPR000602; IPR011330; IPR027291; PTHR11607 (PANTHER), PTHR11607:SF3 (PANTHER), SignalP-NN(euk) (SIGNALP)
528	DMPC15175024_Speleonectes _tulumensis_2	ame: full=annulin ame: full=protein-glutamine gamma-glutamyltransferase ame: full=transglutaminase	141	5.97E-37	69.90%	-	0	IPR008958; IPR013783; IPR023608; PTHR11590:SF16 (PANTHER)
529	DMPC15175062_Speleonectes _tulumensis_1	vitellogenin 1	146	6.41E-17	51.80%	-	0	IPR001846; PTHR11339 (PANTHER)
530	DMPC15175068_Speleonectes _tulumensis_0	aldehyde dehydrogenase mitochondrial-like	146	1.45E-61	87.30%	C:cytoplasm; F:catalytic activity; P:lipid metabolic process; P:secondary metabolic process; P:metabolic process	5	IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
531	DMPC15175105_Speleonectes _tulumensis_2	loc558601 protein	126	8.83E-29	79.70%	P:metabolic process; F:catalytic activity	2	IPR006076; G3DSA:3.50.50.60 (GENE3D), PTHR10961 (PANTHER), PTHR10961:SF7 (PANTHER), SSF51905 (SUPERFAMILY)
532	DMPC15175179_Speleonectes _tulumensis_0	ubiquitin-40s ribosomal protein s27a-like	141	1.66E-51	90.10%	C:nucleoplasm; P:signal transduction; P:response to stress; P:DNA metabolic process; P:translation; F:binding; P:metabolic process; F:structural molecule activity; C:endosome; C:ribosome; C:cytosol	11	IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
533	DMPC15175303_Speleonectes _tulumensis_0	selenium-dependent glutathione peroxidase	113	1.61E-33	78.40%	-	0	IPR000889; IPR012336
534	DMPC15175317_Speleonectes _tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	130	3.50E-20	52.30%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP)
535	DMPC15175323_Speleonectes _tulumensis_2	soma ferritin	112	1.90E-32	88.50%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
536	DMPC15175381_Speleonectes _tulumensis_1	aminoacyl-trna synthetase auxiliary	198	9.60E-65	82.80%	F:catalytic activity; F:RNA binding	2	IPR002547; IPR012340; PTHR11946 (PANTHER), PTHR11946:SF3 (PANTHER)
537	DMPC15175587_Speleonectes _tulumensis_0	---NA---	139			-	0	IPR004911
538	DMPC15175643_Speleonectes _tulumensis_2	thioredoxin 1	134	1.32E-26	82.60%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; SignalP-NN(euk) (SIGNALP)
539	DMPC15175735_Speleonectes _tulumensis_2	ame: full=hemagglutinin amebocyte aggregation factor ame: full=18k-laf flags: precursor	128	4.99E-09	55.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
540	DMPC15175737_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor	118	1.40E-10	60.10%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
541	DMPC15175782_Speleonectes _tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	131	4.96E-21	53.30%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
542	DMPC15175794_Speleonectes _tulumensis_0	hemocyanin subunit type 1 precursor	174	1.26E-109	73.80%	-	0	IPR005203; IPR013788; IPR014756
543	DMPC15175831_Speleonectes _tulumensis_1	elastase	164	1.40E-28	56.90%	F:hydrolase activity	1	IPR013856; IPR023612; SSF55486 (SUPERFAMILY)

544	DMPC15175843_Speleonectes _tulumensis_1	trypsin-like serine proteinase 1	114	9.59E-12	52.70%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
545	DMPC15175844_Speleonectes _tulumensis_2	glyceraldehyde-3-phosphate dehydrogenase	129	2.06E-09	84.63%	F:nucleotide binding; P:carbohydrate metabolic process; F:catalytic activity; P:metabolic process	4	IPR020831
546	DMPC15175944_Speleonectes _tulumensis_1	selenium-dependent glutathione peroxidase	131	2.25E-46	77.10%	-	0	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
547	DMPC15175960_Speleonectes _tulumensis_1	duf563 domain protein	135	1.55E-41	61.80%	F:transferase activity	1	IPR007657; PTHR20961 (PANTHER), PTHR20961:SF0 (PANTHER)
548	DMPC15176054_Speleonectes _tulumensis_0	aael015320- partial	175	3.57E-88	85.80%	F:protein kinase activity	1	IPR001680; IPR015943; IPR017986; IPR019775; PTHR15653 (PANTHER), PTHR15653:SF0 (PANTHER)
549	DMPC15176085_Speleonectes _tulumensis_0	14-3-3 zeta	151	1.68E-90	94.60%	C:cytoplasm; F:protein binding	2	IPR000308; IPR023409; IPR023410; PTHR18860:SF0 (PANTHER)
550	DMPC15176139_Speleonectes _tulumensis_0	superoxide dismutase	289	1.95E-27	52.30%	F:metal ion binding; P:oxidation-reduction process; F:oxidoreductase activity; F:antioxidant activity; P:superoxide metabolic process; F:superoxide dismutase activity	6	IPR001424; IPR018152; IPR024134
551	DMPC15176193_Speleonectes _tulumensis_0	hypothetical protein DAPPUDRAFT_332702	147	6.37E-14	58.17%	-	0	IPR001747; IPR015816; IPR015819; PTHR13769 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
552	DMPC15176214_Speleonectes _tulumensis_2	ame: full=hemagglutinin amebocyte aggregation factor ame: full=18k-laf flags: precursor	116	9.82E-08	57.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
553	DMPC15176330_Speleonectes _tulumensis_0	anti-lipopolysaccharide factor	144	1.22E-30	68.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
554	DMPC15176386_Speleonectes _tulumensis_2	si:dkey- protein	99	8.56E-09	68.89%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
555	DMPC15176409_Speleonectes _tulumensis_1	hemocyanin subunit type 1 precursor	134	6.08E-65	76.90%	-	0	IPR005203; IPR013788; IPR014756
556	DMPC15176424_Speleonectes _tulumensis_1	mitochondrial manganese superoxide dismutase	222	3.69E-77	85.00%	-	0	IPR001189; IPR019831; IPR019832; IPR019833; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER), tmhmm (TMHMM)
557	DMPC15176425_Speleonectes _tulumensis_2	plasminogen activator spa	322	6.82E-69	57.70%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
558	DMPC15176426_Speleonectes _tulumensis_2	soma ferritin	121	6.82E-36	84.80%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
559	DMPC15176430_Speleonectes _tulumensis_0	ferritin peptide	250	1.66E-37	88.00%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; IPR014034
560	DMPC15176491_Speleonectes _tulumensis_0	ferritin 3 heavy chain protein copy c	146	1.75E-39	78.20%	F:binding	1	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
561	DMPC15176494_Speleonectes _tulumensis_1	60s ribosomal protein l40	148	4.06E-47	97.90%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
562	DMPC15176527_Speleonectes _tulumensis_2	pvf3 cg34378-pd	204	2.77E-09	58.60%	F:growth factor activity; C:membrane	2	IPR000072; G3DSA:2.10.90.10 (GENE3D), PTHR21719 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF57501 (SUPERFAMILY)
563	DMPC15176545_Speleonectes _tulumensis_0	pyrroline-5-carboxylate dehydrogenase	354	1.26E-129	82.50%	F:catalytic activity; C:mitochondrion; P:biosynthetic process; ; P:metabolic process	5	IPR015590; IPR016160; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF52 (PANTHER)
564	DMPC15176630_Speleonectes _tulumensis_1	chymotrypsin-like elastase family member 2a	144	3.66E-13	60.30%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), PTHR24275:SF2 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

565	DMPC15176654_Speleonectes_tulumensis_0	isoform cra_b	152	5.80E-45	96.60%	-	0	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
566	DMPC15176703_Speleonectes_tulumensis_0	---NA---	142			-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER)
567	DMPC15176747_Speleonectes_tulumensis_1	cg7872 cg7872-pa	148	3.24E-49	81.00%	P:protein metabolic process; F:protein binding	2	IPR001623; IPR018253; PTHR24078 (PANTHER), PTHR24078:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
568	DMPC15176794_Speleonectes_tulumensis_1	egf-like repeat and discoidin i-like domain-containing protein 3-like	136	5.22E-16	63.80%	P:cell adhesion	1	IPR000421; IPR008979; IPR027060; PTHR10127 (PANTHER)
569	DMPC15176820_Speleonectes_tulumensis_2	cathepsin l	194	1.21E-45	87.20%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
570	DMPC15176869_Speleonectes_tulumensis_0	kazal-type serine proteinase inhibitor 2	90	1.54E-12	57.80%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
571	DMPC15176949_Speleonectes_tulumensis_1	serine-type enodpeptidase	78	5.42E-12	61.70%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)
572	DMPC15177022_Speleonectes_tulumensis_1	fras1-related extracellular matrix protein 1-like	146	2.56E-14	52.20%	-	0	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
573	DMPC15177077_Speleonectes_tulumensis_0	chitinase domain-containing protein 1	165	7.37E-14	61.20%	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process; F:cation binding; F:catalytic activity; P:chitin catabolic process; F:chitinase activity	6	PTHR11177 (PANTHER)
574	DMPC15177078_Speleonectes_tulumensis_0	proclotting enzyme	236	4.15E-39	73.50%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF28 (PANTHER)
575	DMPC15177087_Speleonectes_tulumensis_1	chitinase partial	198	2.56E-78	70.60%	-	0	IPR001223; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SSF54556 (SUPERFAMILY)
576	DMPC15177108_Speleonectes_tulumensis_2	serine protease inhibitor kazal-type 6-like	150	1.80E-07	67.75%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
577	DMPC15177133_Speleonectes_tulumensis_1	kazal-type serine proteinase inhibitor 4	117	1.50E-09	52.20%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
578	DMPC15177191_Speleonectes_tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	130	1.12E-16	52.10%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP)
579	DMPC15177307_Speleonectes_tulumensis_1	soma ferritin	111	6.88E-30	86.00%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
580	DMPC15177395_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor-like	118	1.24E-12	62.60%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
581	DMPC15177435_Speleonectes_tulumensis_2	lipase 3-like	268	1.51E-41	71.90%	F:hydrolase activity; P:lipid metabolic process	2	G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER), SSF53474 (SUPERFAMILY)
582	DMPC15177483_Speleonectes_tulumensis_0	low quality protein: titin-like	225	3.31E-54	85.00%	-	0	IPR003599; IPR007110; IPR013098; IPR013783; IPR020675; PTHR22964:SF3 (PANTHER), SSF48726 (SUPERFAMILY)
583	DMPC15177513_Speleonectes_tulumensis_1	epididymal secretory protein e1	146	7.79E-19	60.50%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
584	DMPC15177529_Speleonectes_tulumensis_1	prophenoloxidase-activating enzyme 2	123	7.85E-08	64.78%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER)
585	DMPC15177545_Speleonectes_tulumensis_1	14-3-3 protein	97	6.47E-24	76.30%	F:protein binding	1	IPR000308; IPR023410; PTHR18860:SF0 (PANTHER)

586	DMPC15177768_Speleonectes_tulumensis_2	sifa preprohormone	153	1.81E-17	74.50%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
587	DMPC15177818_Speleonectes_tulumensis_1	---NA---	202			-	0	IPR000566; IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
588	DMPC15177855_Speleonectes_tulumensis_1	multicopper oxidase	143	1.08E-19	61.80%	P:oxidation-reduction process; F:oxidoreductase activity; F:copper ion binding; F:metal ion binding	4	IPR008972; IPR011706; PTHR11709 (PANTHER), PTHR11709:SF8 (PANTHER)
589	DMPC15177908_Speleonectes_tulumensis_0	---NA---	104			-	0	PTHR22897 (PANTHER)
590	DMPC15177957_Speleonectes_tulumensis_0	simila to cg9796	157	3.33E-21	62.90%	-	0	IPR004911; SignalP-NN(euk) (SIGNALP)
591	DMPC15178012_Speleonectes_tulumensis_0	---NA---	244			-	0	IPR008160; PTHR24023 (PANTHER)
592	DMPC15178020_Speleonectes_tulumensis_0	---NA---	80			-	0	IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24252 (PANTHER)
593	DMPC15178098_Speleonectes_tulumensis_2	---NA---	121			-	0	IPR001283; IPR014044
594	DMPC15178135_Speleonectes_tulumensis_2	aldo-keto partial	122	9.62E-24	74.50%	F:catalytic activity; P:multicellular organismal development	2	IPR001395; IPR023210; PTHR11732:SF34 (PANTHER), SignalP-NN(euk) (SIGNALP)
595	DMPC15178312_Speleonectes_tulumensis_2	PREDICTED: mucin-5B	403	5.91E-08	42.67%	-	0	IPR001007; PTHR11339 (PANTHER), PTHR11339:SF42 (PANTHER), tmhmm (TMHMM), SSF57603 (SUPERFAMILY)
596	DMPC15178316_Speleonectes_tulumensis_2	hemocyte protein-glutamine gamma-glutamyltransferase	290	3.70E-38	72.10%	F:metal ion binding; P:peptide cross-linking; F:protein-glutamine gamma-glutamyltransferase activity	3	IPR008958; IPR013783; IPR023608; PTHR11590:SF17 (PANTHER)
597	DMPC15178340_Speleonectes_tulumensis_2	dysferlin-interacting protein 1	163	3.54E-52	68.60%	P:negative regulation of phosphatase activity; F:phosphatase binding	2	IPR002110; IPR020683; PTHR24179 (PANTHER), PTHR24179:SF2 (PANTHER)
598	DMPC15178358_Speleonectes_tulumensis_1	trypsinogen 2	380	4.30E-62	59.00%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
599	DMPC15178381_Speleonectes_tulumensis_1	kallikrein-2 isoform 1	117	1.39E-14	54.20%	P:proteolysis; P:extracellular matrix disassembly; F:serine-type endopeptidase activity; P:extracellular matrix organization; C:extracellular region	5	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP)
600	DMPC15178394_Speleonectes_tulumensis_5	protein	435	1.21E-24	70.20%	-	0	SignalP-NN(euk) (SIGNALP)
601	DMPC15178467_Speleonectes_tulumensis_0	cathepsin l-like	131	5.57E-59	80.80%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
602	DMPC15178469_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	153	2.22E-16	61.90%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
603	DMPC15178631_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	151	3.40E-30	66.90%	-	0	IPR024509; IPR024716
604	DMPC15178647_Speleonectes_tulumensis_2	zinc finger protein 670	129	2.14E-17	54.90%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PTHR11389:SF382 (PANTHER), PF12874 (PFAM), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
605	DMPC15178648_Speleonectes_tulumensis_1	neutral ceramidase	180	1.02E-52	62.30%	-	0	IPR006823
606	DMPC15178654_Speleonectes_tulumensis_1	hypothetical protein YQE_03041, partial	183	1.14E-55	86.50%	-	0	IPR004878; PTHR21522:SF20 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
607	DMPC15178662_Speleonectes_tulumensis_1	cathepsin l	154	7.70E-49	76.60%	F:peptidase activity	1	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)

608	DMPC15178672_Speleonectes_tulumensis_2	serine protease	126	1.03E-13	67.30%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
609	DMPC15178727_Speleonectes_tulumensis_2	chitinase	126	4.33E-07	60.00%	-	0	IPR001223; IPR013781; IPR017853; G3DSA:2.40.10.10 (GENE3D), PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
610	DMPC15178741_Speleonectes_tulumensis_2	serine protease inhibitor serpin-4	165	2.26E-21	52.40%	F:serine-type endopeptidase inhibitor activity; P:proteolysis; F:peptidase activity	3	IPR000215; IPR023796; G3DSA:2.30.39.10 (GENE3D), G3DSA:3.30.497.10 (GENE3D)
611	DMPC15178775_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	132	5.30E-16	64.70%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
612	DMPC15178827_Speleonectes_tulumensis_5	---NA---	51			-	0	IPR001881; G3DSA:2.10.25.10 (GENE3D), PTHR24040 (PANTHER), SSF57196 (SUPERFAMILY)
613	DMPC15178833_Speleonectes_tulumensis_2	clipd1 protein	151	9.66E-14	59.40%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF28 (PANTHER)
614	DMPC15178836_Speleonectes_tulumensis_2	---NA---	107			-	0	no IPS match
615	DMPC15178844_Speleonectes_tulumensis_2	trypsin	130	4.04E-25	61.10%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER)
616	DMPC15178966_Speleonectes_tulumensis_2	wd40 repeat-containing protein smu1	283	3.47E-139	92.10%	C:nucleus; C:cytoplasm	2	IPR001680; IPR015943; IPR017986; IPR019775; PTHR22848 (PANTHER)
617	DMPC15179033_Speleonectes_tulumensis_2	dbh-like monooxygenase protein 1 homolog	156	4.84E-12	65.20%	F:transferase activity; F:binding; F:catalytic activity; P:nucleobase-containing compound metabolic process	4	IPR000945; IPR008977; IPR014784; PF03712 (PFAM)
618	DMPC15179042_Speleonectes_tulumensis_0	clotting factor b-like	451	7.16E-45	64.60%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), tmhmm (TMHMM)
619	DMPC15179092_Speleonectes_tulumensis_2	histone h1	284	4.31E-33	87.40%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR005818; IPR005819; IPR011991; PTHR11467 (PANTHER), PTHR11467:SF0 (PANTHER), SSF46785 (SUPERFAMILY)
620	DMPC15179137_Speleonectes_tulumensis_0	peroxiredoxin 1-like	100	4.45E-20	61.40%	P:oxidation-reduction process; F:oxidoreductase activity; F:antioxidant activity; F:peroxiredoxin activity	4	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF45 (PANTHER)
621	DMPC15179156_Speleonectes_tulumensis_1	3-oxoacyl-acyl-carrier-protein reductase-like	176	1.55E-64	82.60%	F:catalytic activity; P:metabolic process; F:nucleotide binding	3	IPR002198; IPR002347; IPR016040; IPR020904; PTHR24322 (PANTHER), PTHR24322:SF0 (PANTHER), PF13561 (PFAM), SSF51735 (SUPERFAMILY)
622	DMPC15179209_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor	137	1.27E-29	69.80%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
623	DMPC15179211_Speleonectes_tulumensis_0	ferritin h subunit	94	5.14E-16	79.70%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; PTHR11431:SF14 (PANTHER)
624	DMPC15179255_Speleonectes_tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	146	1.33E-21	51.60%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
625	DMPC15179318_Speleonectes_tulumensis_1	soma ferritin	114	1.32E-27	88.30%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
626	DMPC15179374_Speleonectes_tulumensis_0	serine protease	338	1.90E-28	56.80%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity; F:peptidase activity	4	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), tmhmm (TMHMM)

627	DMPC15179402_Speleonectes_tulumensis_0	ubiquitin-40s ribosomal protein s27a	150	1.08E-59	96.20%	P:cell cycle; P:metabolic process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:cellular protein modification process; P:transport	27	IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
628	DMPC15179423_Speleonectes_tulumensis_2	ame: full=hemagglutinin amebocyte aggregation factor ame: full=18k-laf flags: precursor	138	8.13E-08	57.00%	-	0	IPR026645
629	DMPC15179428_Speleonectes_tulumensis_0	---NA---	301			-	0	IPR003961; IPR013783; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
630	DMPC15179436_Speleonectes_tulumensis_0	---NA---	91			-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF100895 (SUPERFAMILY)
631	DMPC15179574_Speleonectes_tulumensis_0	---NA---	75			-	0	IPR001424; IPR024134
632	DMPC15179683_Speleonectes_tulumensis_3	protein	132	8.58E-16	67.30%	P:oxidation-reduction process; F:oxidoreductase activity; P:metabolic process; F:nucleotide binding	4	IPR016040; PTHR24322 (PANTHER), PTHR24322:SF57 (PANTHER), SSF51735 (SUPERFAMILY)
633	DMPC15179705_Speleonectes_tulumensis_1	carcinolectin 5a isoform	155	1.10E-17	69.30%	F:receptor binding; C:extracellular space; P:signal transduction	3	IPR002181; IPR014715; IPR020837; PTHR19143 (PANTHER)
634	DMPC15179718_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	136	6.90E-28	67.60%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
635	DMPC15179722_Speleonectes_tulumensis_1	thioredoxin 1	100	1.11E-20	79.30%	P:cell redox homeostasis; F:electron carrier activity; P:glycerol ether metabolic process; F:protein disulfide oxidoreductase activity	4	IPR005746; IPR012336; IPR013766; SignalP-NN(euk) (SIGNALP)
636	DMPC15179750_Speleonectes_tulumensis_1	matrix metalloproteinase-17	115	7.44E-21	70.60%	P:proteolysis; P:metabolic process; C:extracellular matrix; F:zinc ion binding; F:metalloendopeptidase activity	5	IPR002477; PTHR10201 (PANTHER)
637	DMPC15179764_Speleonectes_tulumensis_1	clip-domain serine family d	129	2.46E-15	67.70%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
638	DMPC15179777_Speleonectes_tulumensis_2	dermatopontin 2	141	4.56E-20	61.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
639	DMPC15179780_Speleonectes_tulumensis_1	lipase 3-like	142	5.00E-39	70.10%	F:hydrolase activity; P:lipid metabolic process	2	G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER), tmhmm (TMHMM), SSF53474 (SUPERFAMILY)
640	DMPC15179782_Speleonectes_tulumensis_2	platelet-activating factor acetylhydrolase-like	71	1.18E-09	55.70%	P:low-density lipoprotein particle remodeling; P:lipid catabolic process; P:plasma lipoprotein particle oxidation; P:lipid oxidation; F:calcium-independent phospholipase A2 activity; C:low-density lipoprotein particle; F:1-alkyl-2-acetylglycerophosphocholine esterase activity; F:phospholipid binding; P:positive regulation of monocyte chemotaxis; C:extracellular space	10	IPR005065

641	DMPC15179801_Speleonectes _tulumensis_0	---NA---	107			-	0	IPR000562; IPR001254; IPR009003; IPR013806; G3DSA:2.40.10.10 (GENE3D), PTHR22918 (PANTHER), PTHR22918:SF0 (PANTHER)
642	DMPC15179899_Speleonectes _tulumensis_0	thioredoxin peroxidase	148	5.88E-39	89.20%	-	0	IPR012336; IPR019479; PTHR10681 (PANTHER), PTHR10681:SF44 (PANTHER)
643	DMPC15179972_Speleonectes _tulumensis_2	galactose-specific c-type	349	9.14E-19	54.30%	F:protein binding	1	IPR001304; IPR016186; IPR016187; IPR018378; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
644	DMPC15179980_Speleonectes _tulumensis_0	plasminogen activator spa	103	2.32E-20	63.30%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24257 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
645	DMPC15179994_Speleonectes _tulumensis_1	ras-responsive element-binding protein 1	158	4.52E-19	63.10%	F:nucleic acid binding; F:zinc ion binding; C:nucleus; C:intracellular	4	IPR007087; IPR013087; IPR015880; PTHR24403 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
646	DMPC15180008_Speleonectes _tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	130	4.48E-11	58.60%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
647	DMPC15180065_Speleonectes _tulumensis_1	kazal-type serine proteinase inhibitor 4	119	7.90E-14	56.70%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SSF100895 (SUPERFAMILY)
648	DMPC15180086_Speleonectes _tulumensis_1	---NA---	123			-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
649	DMPC15180122_Speleonectes _tulumensis_2	cyclophilin ovcyp-2	135	2.71E-34	85.00%	P:protein metabolic process; P:biological_process; C:plasma membrane; F:protein binding; C:plastid; P:cellular protein modification process; C:extracellular region; F:catalytic activity	8	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), tmhmm (TMHMM)
650	DMPC15180126_Speleonectes _tulumensis_2	kazal-type serine proteinase inhibitor 4	126	9.83E-11	74.00%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR25189 (PANTHER), PTHR25189:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
651	DMPC15180129_Speleonectes _tulumensis_2	hemocyanin subunit 2 precursor	141	4.45E-14	70.00%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
652	DMPC15180158_Speleonectes _tulumensis_1	ribosome biogenesis protein bop1 homolog	221	1.35E-99	79.40%	C:nucleolus; C:nucleoplasm; P:regulation of biological process; P:cell cycle; F:binding; P:nucleobase-containing compound metabolic process; P:cell differentiation; P:multicellular organismal development	8	IPR001680; IPR015943; IPR017986; PTHR17605 (PANTHER)
653	DMPC15180165_Speleonectes _tulumensis_2	transmembrane protease serine 2	109	4.22E-18	71.60%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
654	DMPC15180173_Speleonectes _tulumensis_2	hemocyanin subunit type 2 precursor	121	3.91E-41	71.30%	-	0	IPR005203; IPR013788; IPR014756
655	DMPC15180243_Speleonectes _tulumensis_0	anti-lipopolysaccharide factor isoform 7	128	1.34E-10	72.60%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
656	DMPC15180273_Speleonectes _tulumensis_1	fertilization envelope outer layer protein	145	3.40E-15	54.10%	-	0	IPR005515; PTHR18841:SF0 (PANTHER)
657	DMPC15180312_Speleonectes _tulumensis_1	trypsin	165	2.57E-25	62.50%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER)
658	DMPC15180331_Speleonectes _tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	140	1.42E-18	52.30%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
659	DMPC15180360_Speleonectes _tulumensis_2	GF16338	231	3.95E-60	65.70%	P:oxidation-reduction process; F:oxidoreductase activity; P:metabolic process; F:nucleotide binding	4	IPR002198; IPR002347; IPR016040; IPR020904; PTHR24322 (PANTHER), PTHR24322:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF51735 (SUPERFAMILY)

660	DMPC15180428_Speleonectes _tulumensis_0	predicted protein	159	2.25E-07	50.00%	-	0	no IPS match
661	DMPC15180464_Speleonectes _tulumensis_1	dermatopontin 2	138	8.68E-13	61.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
662	DMPC15180501_Speleonectes _tulumensis_2	peptidylprolyl isomerase a	158	4.31E-43	71.60%	P:protein metabolic process; F:catalytic activity	2	IPR002130; IPR020892; IPR024936; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER)
663	DMPC15180524_Speleonectes _tulumensis_0	neprilysin isoform b	113	1.28E-25	66.10%	F:peptidase activity; C:extracellular space; P:protein metabolic process; P:catabolic process; C:cell	5	IPR000718; IPR018497; IPR024079; PTHR11733:SF26 (PANTHER), tmhmm (TMHMM), SSF55486 (SUPERFAMILY)
664	DMPC15180582_Speleonectes _tulumensis_2	plasminogen activator spa	120	1.12E-17	67.40%	P:metabolic process; F:catalytic activity	2	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)
665	DMPC15180671_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor-like	114	1.88E-09	61.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
666	DMPC15180685_Speleonectes _tulumensis_1	si:dkey- protein	140	3.40E-22	61.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
667	DMPC15180734_Speleonectes _tulumensis_0	60s ribosomal protein l40	131	1.18E-47	98.50%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
668	DMPC15180835_Speleonectes _tulumensis_2	soma ferritin	111	1.69E-30	86.30%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
669	DMPC15180855_Speleonectes _tulumensis_1	multiple inositol polyphosphate phosphatase 1	315	6.65E-72	61.80%	F:hydrolase activity	1	IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR20963 (PANTHER), PTHR20963:SF8 (PANTHER), SSF53254 (SUPERFAMILY)
670	DMPC15181005_Speleonectes _tulumensis_1	ubiquitin c	166	4.63E-113	100.00%	P:cell cycle; P:signal transduction; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; C:cytosol; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; C:plasma membrane; C:mitochondrion; ; C:endosome; P:cellular component organization; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; P:cellular protein modification process; P:transport	23	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
671	DMPC15181030_Speleonectes _tulumensis_1	---NA---	127			-	0	IPR002413; IPR014044
672	DMPC15181058_Speleonectes _tulumensis_2	carboxypeptidase a	121	9.14E-24	66.60%	F:hydrolase activity	1	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
673	DMPC15181204_Speleonectes _tulumensis_0	chh xo- variant 4	173	3.67E-27	70.10%	F:neuropeptide hormone activity; C:extracellular region	2	IPR000346; IPR001166
674	DMPC15181210_Speleonectes _tulumensis_0	glyceraldehyde-3-phosphate dehydrogenase	142	3.83E-27	60.40%	P:oxidation-reduction process; P:glucose metabolic process; F:oxidoreductase activity; F:oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor; F:nucleotide binding; F:glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity; F:NAD binding; F:NADP binding	8	IPR016040; IPR020828; IPR020831; SSF51735 (SUPERFAMILY)

675	DMPC15181244_Speleonectes_tulumensis_1	dermatopontin 3	94	3.80E-08	61.17%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
676	DMPC15181357_Speleonectes_tulumensis_4	purple acid	132	9.16E-39	74.00%	F:binding; F:hydrolase activity	2	G3DSA:3.60.21.10 (GENE3D), PTHR22953 (PANTHER), PTHR22953:SF0 (PANTHER)
677	DMPC15181553_Speleonectes_tulumensis_1	oocyte protease inhibitor-1 precursor	139	3.63E-11	58.20%	P:proteolysis; F:peptidase activity; F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	6	IPR000716; PTHR12352 (PANTHER)
678	DMPC15181586_Speleonectes_tulumensis_2	trypsin	138	2.56E-25	62.60%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
679	DMPC15181659_Speleonectes_tulumensis_2	trypsin partial	110	1.61E-10	54.20%	F:catalytic activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER), SignalP-NN(euk) (SIGNALP)
680	DMPC15181665_Speleonectes_tulumensis_2	pacifastin light chain	366	1.13E-15	51.60%	F:peptidase inhibitor activity; P:negative regulation of peptidase activity	2	IPR008037; IPR020862; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
681	DMPC15181725_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor-like	148	2.91E-14	61.50%	-	0	IPR026645
682	DMPC15181762_Speleonectes_tulumensis_2	hyaluronidase precursor	161	1.04E-27	61.40%	P:defense response; P:carbohydrate metabolic process; F:hyalurononglucosaminidase activity; F:catalytic activity	4	IPR013785; IPR017853; IPR018155; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
683	DMPC15181777_Speleonectes_tulumensis_0	hypothetical protein DAPPUDRAFT_308200	146	2.92E-09	50.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
684	DMPC15181792_Speleonectes_tulumensis_2	lipase 3	124	3.41E-34	66.20%	P:lipid metabolic process; F:hydrolase activity, acting on ester bonds; F:hydrolase activity; P:lipid catabolic process	4	IPR000073; G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER), tmhmm (TMHMM), SSF53474 (SUPERFAMILY)
685	DMPC15181862_Speleonectes_tulumensis_2	testicular serine protease 3	121	4.60E-11	63.80%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
686	DMPC15181868_Speleonectes_tulumensis_2	saxiphilin precursor	127	1.59E-10	63.00%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
687	DMPC15181880_Speleonectes_tulumensis_0	hatching enzyme	130	6.82E-30	61.80%	F:hydrolase activity	1	IPR001506; IPR006026; IPR024079; PTHR10127 (PANTHER), SSF55486 (SUPERFAMILY)
688	DMPC15181945_Speleonectes_tulumensis_0	soma ferritin	119	1.39E-32	90.10%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
689	DMPC15181983_Speleonectes_tulumensis_0	GJ13839	498	7.36E-27	46.10%	F:chitin binding; P:chitin metabolic process; P:cell adhesion; C:extracellular region; F:receptor binding; P:signal transduction	6	IPR001846; IPR002919; IPR014853; G3DSA:2.10.25.10 (GENE3D), PTHR11339 (PANTHER), PTHR11339:SF26 (PANTHER)
690	DMPC15182132_Speleonectes_tulumensis_1	---NA---	132			-	0	IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
691	DMPC15182179_Speleonectes_tulumensis_0	membrane metallo-endopeptidase-like 1-like	176	6.66E-61	81.30%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000718; IPR018497; IPR024079; PTHR11733:SF48 (PANTHER), tmhmm (TMHMM), SSF55486 (SUPERFAMILY)
692	DMPC15182383_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_332702	239	2.68E-56	55.30%	P:lipid transport; F:lipid transporter activity	2	IPR001747; IPR011030; PTHR23345 (PANTHER)
693	DMPC15182392_Speleonectes_tulumensis_2	cathepsin l-like	174	2.45E-22	87.40%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
694	DMPC15182417_Speleonectes_tulumensis_0	isoform a	187	2.87E-12	44.30%	P:proteolysis; P:cell proliferation; F:metalloendopeptidase activity; C:cellular_component	4	IPR006586; IPR024079; SSF55486 (SUPERFAMILY)
695	DMPC15182504_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	154	1.59E-29	67.40%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)

696	DMPC15182585_Speleonectes _tulumensis_1	epididymal secretory protein e1	126	4.81E-15	59.50%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
697	DMPC15182634_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor	144	1.02E-29	67.60%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
698	DMPC15182678_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor	131	1.67E-27	67.20%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
699	DMPC15182725_Speleonectes _tulumensis_0	zinc finger protein 836	99	9.95E-25	61.90%	P:regulation of transcription, DNA-dependent; P:transcription, DNA-dependent; F:zinc ion binding; C:nucleus; F:DNA binding	5	IPR007087; IPR013087; IPR015880; PTHR24377 (PANTHER), PTHR24377:SF0 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
700	DMPC15182735_Speleonectes _tulumensis_0	oocyte zinc finger protein 20	79	2.21E-12	62.10%	F:nucleic acid binding; F:zinc ion binding; C:nucleus; C:intracellular	4	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PTHR11389:SF381 (PANTHER), PF13465 (PFAM), PF13912 (PFAM), SSF57667 (SUPERFAMILY)
701	DMPC15182831_Speleonectes _tulumensis_2	---NA---	163			-	0	IPR004169; SSF57059 (SUPERFAMILY)
702	DMPC15182852_Speleonectes _tulumensis_1	isoform a	273	1.31E-17	43.80%	P:cell adhesion; F:chitin binding; P:chitin metabolic process; C:extracellular region	4	IPR001007; IPR006207; PTHR11339 (PANTHER), PTHR11339:SF42 (PANTHER), SSF57603 (SUPERFAMILY)
703	DMPC15182853_Speleonectes _tulumensis_2	amine oxidase	228	1.44E-23	58.70%	-	0	IPR002937; IPR011032; PR00419 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF22 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF51905 (SUPERFAMILY)
704	DMPC15182855_Speleonectes _tulumensis_2	beta-galactosidase bga35a	306	1.27E-25	61.70%	F:hydrolase activity	1	IPR001944; IPR008979; PTHR23421:SF14 (PANTHER)
705	DMPC15182859_Speleonectes _tulumensis_2	epididymal secretory protein e1	137	2.12E-20	58.10%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
706	DMPC15182897_Speleonectes _tulumensis_2	female neotenic-specific protein 3	143	9.96E-13	55.00%	-	0	tmhmm (TMHMM)
707	DMPC15182935_Speleonectes _tulumensis_1	mhc class ii-associated invariant chain	118	1.79E-07	66.67%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
708	DMPC15183026_Speleonectes _tulumensis_0	tfpia protein	199	2.49E-10	62.30%	F:serine-type endopeptidase inhibitor activity; F:peptidase inhibitor activity; P:negative regulation of endopeptidase activity; P:blood coagulation; C:extracellular region; P:negative regulation of peptidase activity	6	IPR002223; IPR020901; PTHR10083 (PANTHER), SignalP-NN(euk) (SIGNALP)
709	DMPC15183058_Speleonectes _tulumensis_1	phosphoglycerate kinase	102	9.65E-40	81.10%	C:cytoplasm; F:kinase activity; P:metabolic process; F:nucleotide binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process	7	IPR001576; IPR015824; IPR015901
710	DMPC15183094_Speleonectes _tulumensis_0	zinc finger protein	79	2.12E-10	65.70%	C:intracellular; F:binding	2	IPR007087; IPR013087; IPR015880; PTHR24387 (PANTHER), SSF57667 (SUPERFAMILY)

711	DMPC15183168_Speleonectes_tulumensis_0	ubiquitin-40s ribosomal protein s27a	146	5.38E-52	97.00%	P:cell cycle; P:metabolic process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:cellular protein modification process; P:transport	27	IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
712	DMPC15183212_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	135	4.28E-26	67.50%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
713	DMPC15183323_Speleonectes_tulumensis_0	isoform a	127	1.29E-16	76.20%	F:hydrolase activity	1	IPR025733; G3DSA:3.60.21.10 (GENE3D), PTHR22953 (PANTHER), PTHR22953:SF0 (PANTHER)
714	DMPC15183344_Speleonectes_tulumensis_0	---NA---	144			-	0	IPR011038; IPR012674; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
715	DMPC15183350_Speleonectes_tulumensis_0	saxiphilin precursor	111	9.28E-11	65.10%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
716	DMPC15183355_Speleonectes_tulumensis_1	isoamyl acetate-hydrolyzing esterase 1 homolog	126	6.31E-25	76.30%	F:hydrolase activity	1	IPR001087; IPR013831; PTHR14209 (PANTHER), SSF52266 (SUPERFAMILY)
717	DMPC15183389_Speleonectes_tulumensis_2	cathepsin l	194	5.78E-31	85.40%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
718	DMPC15183401_Speleonectes_tulumensis_1	epididymal secretory protein e1	145	4.13E-16	58.80%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
719	DMPC15183410_Speleonectes_tulumensis_2	ubiquitin c	172	2.74E-68	99.60%	P:cell cycle; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:cellular protein modification process; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:transport	27	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
720	DMPC15183487_Speleonectes_tulumensis_2	ame: full=hemagglutinin amebocyte aggregation factor ame: full=18k-laf flags: precursor	107	2.85E-07	58.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
721	DMPC15183490_Speleonectes_tulumensis_0	plasminogen activator spa	121	2.48E-17	69.30%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24252 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
722	DMPC15183553_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor	151	6.89E-30	67.70%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

723	DMPC15183558_Speleonectes _tulumensis_0	stereocilin	229	1.67E-15	50.00%	-	0	IPR026061; IPR026664
724	DMPC15183577_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor	106	5.68E-22	65.20%	-	0	IPR026645
725	DMPC15183616_Speleonectes _tulumensis_2	anti-lipopolysaccharide factor	222	1.09E-33	73.60%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
726	DMPC15183652_Speleonectes _tulumensis_1	hemocyanin subunit type 2 precursor	170	1.63E-108	74.60%	-	0	IPR000896; IPR002227; IPR005203; IPR008922; IPR013788; IPR014756; PTHR11511:SF4 (PANTHER)
727	DMPC15183694_Speleonectes _tulumensis_2	female neotenic-specific protein 3	136	5.66E-10	57.00%	-	0	no IPS match
728	DMPC15183791_Speleonectes _tulumensis_1	kazal-type serine proteinase inhibitor 4	111	2.98E-11	66.00%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR25189 (PANTHER), PTHR25189:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
729	DMPC15183820_Speleonectes _tulumensis_0	hypothetical protein CAPTEDRAFT_177616	131	5.28E-07	69.00%	-	0	IPR005065
730	DMPC15183878_Speleonectes _tulumensis_0	cell adhesion	103	1.23E-09	92.83%	F:calcium ion binding	1	PTHR10913 (PANTHER), PTHR10913:SF18 (PANTHER)
731	DMPC15183940_Speleonectes _tulumensis_1	peroxiredoxin 1 isoform 1	114	1.36E-12	55.50%	-	0	PTHR10681 (PANTHER), PTHR10681:SF46 (PANTHER)
732	DMPC15184040_Speleonectes _tulumensis_0	ankyrin repeat domain-containing	124	9.16E-33	91.70%	F:hydrolase activity	1	IPR002110; IPR020683; PTHR24123 (PANTHER), PTHR24123:SF0 (PANTHER), tmhmm (TMHMM)
733	DMPC15184045_Speleonectes _tulumensis_2	proclotting enzyme	115	2.82E-25	78.20%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF28 (PANTHER)
734	DMPC15184210_Speleonectes _tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	148	6.49E-15	49.40%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:proteolysis; F:peptidase activity	6	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
735	DMPC15184317_Speleonectes _tulumensis_2	nidogen 1	92	5.03E-11	64.60%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
736	DMPC15184372_Speleonectes _tulumensis_2	multiple epidermal growth factor-like domains protein 10-like	106	4.19E-32	66.50%	-	0	IPR000742; IPR002049; IPR013032; PR00011 (PRINTS), G3DSA:2.170.300.10 (GENE3D), PTHR24035 (PANTHER), PTHR24035:SF3 (PANTHER), SSF57196 (SUPERFAMILY)
737	DMPC15184411_Speleonectes _tulumensis_2	ame: full=conoporin-cn1 flags: precursor	132	1.01E-09	56.00%	-	0	IPR015926
738	DMPC15184494_Speleonectes _tulumensis_2	---NA---	155			-	0	no IPS match
739	DMPC15184523_Speleonectes _tulumensis_2	GJ10839	190	3.76E-23	74.70%	P:metabolic process; F:catalytic activity	2	IPR002198; IPR016040; PTHR24320 (PANTHER), PTHR24320:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF51735 (SUPERFAMILY)
740	DMPC15184550_Speleonectes _tulumensis_0	zinc finger protein 187	157	4.28E-15	58.70%	P:regulation of transcription, DNA-dependent; F:nucleic acid binding; P:transcription, DNA-dependent; P:viral reproduction; F:zinc ion binding; C:nucleus; F:sequence-specific DNA binding transcription factor activity	7	IPR007087; IPR013087; IPR015880; PTHR24382 (PANTHER), PTHR24382:SF0 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
741	DMPC15184584_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor	137	1.24E-27	66.90%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
742	DMPC15184598_Speleonectes _tulumensis_1	der p 3 allergen	121	8.36E-10	52.20%	P:proteolysis; F:serine-type endopeptidase activity; F:serine-type peptidase activity; F:hydrolase activity; F:catalytic activity; F:peptidase activity	6	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER)

743	DMPC15184635_Speleonectes _tulumensis_1	trypsin 4	145	2.58E-16	61.70%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER)
744	DMPC15184665_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor	135	3.38E-13	62.10%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
745	DMPC15184675_Speleonectes _tulumensis_2	lipase 3-like	125	5.04E-18	73.50%	F:hydrolase activity; P:lipid metabolic process	2	G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER)
746	DMPC15184682_Speleonectes _tulumensis_1	cathepsin l-like	157	1.55E-12	90.30%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
747	DMPC15184691_Speleonectes _tulumensis_1	soma ferritin	119	1.06E-34	86.50%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
748	DMPC15184708_Speleonectes _tulumensis_1	multiple epidermal growth factor-like domains protein 8-like	78	4.32E-24	72.20%	C:cell	1	IPR002165; PTHR10574 (PANTHER), PTHR10574:SF11 (PANTHER)
749	DMPC15184749_Speleonectes _tulumensis_1	isoform c	131	1.95E-51	90.80%	P:cellular homeostasis; P:regulation of biological process; F:catalytic activity	3	IPR012336; IPR013766; PTHR18929 (PANTHER), tmhmm (TMHMM)
750	DMPC15184813_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor	128	2.49E-10	55.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
751	DMPC15184864_Speleonectes _tulumensis_2	---NA---	138			-	0	IPR008197; PTHR19441 (PANTHER)
752	DMPC15184913_Speleonectes _tulumensis_0	ubiquitin-60s ribosomal protein l40-like	112	3.82E-37	95.20%	F:peptidase activity; P:cell cycle; F:protein binding; P:cellular protein modification process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; F:catalytic activity; P:protein transport; ; C:endosome; F:nucleotide binding; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:transport	30	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
753	DMPC15184925_Speleonectes _tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	130	1.35E-20	52.90%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
754	DMPC15185027_Speleonectes _tulumensis_0	ves g 5 allergen	375	2.96E-41	53.20%	C:extracellular region	1	IPR001283; IPR002413; IPR014044; IPR018244; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
755	DMPC15185077_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor-like	119	5.21E-26	64.70%	-	0	IPR026645
756	DMPC15185080_Speleonectes _tulumensis_1	vitellogenin fused with superoxide dismutase	809	4.01E-42	43.60%	P:lipid transport; F:lipid transporter activity	2	IPR001846; IPR015255; IPR015818; IPR015819
757	DMPC15185083_Speleonectes _tulumensis_2	peptidase thermolysin	154	3.97E-07	64.00%	P:proteolysis; F:hydrolase activity; F:metalloendopeptidase activity	3	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
758	DMPC15185099_Speleonectes _tulumensis_2	hemocyanin subunit type 2 precursor	152	1.83E-17	81.67%	-	0	IPR005203; IPR013788; IPR014756; tmhmm (TMHMM)
759	DMPC15185230_Speleonectes _tulumensis_0	thioredoxin- isoform a	129	2.73E-21	83.70%	P:response to stress; F:electron carrier activity; P:cellular homeostasis; P:regulation of biological process; P:metabolic process; P:multicellular organismal development; C:nucleus; F:catalytic activity	8	IPR005746; IPR012336; IPR013766; SignalP-NN(euk) (SIGNALP)

760	DMPC15185245_Speleonectes_tulumensis_0	serine protease precursor	152	1.25E-17	59.40%	P:proteolysis; F:serine-type endopeptidase activity; P:negative regulation of catalytic activity; F:identical protein binding	4	IPR007280; SignalP-NN(euk) (SIGNALP)
761	DMPC15185259_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor	145	1.33E-28	67.40%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
762	DMPC15185326_Speleonectes_tulumensis_1	trypsin 2	175	5.12E-27	78.90%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
763	DMPC15185358_Speleonectes_tulumensis_0	glutathione peroxidase 7-like	137	1.65E-27	68.70%	F:catalytic activity	1	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER), tmhmm (TMHMM)
764	DMPC15185383_Speleonectes_tulumensis_0	neuropeptide precursor protein	234	7.93E-17	75.40%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
765	DMPC15185390_Speleonectes_tulumensis_0	astakine variant 1	118	6.00E-08	72.25%	-	0	G3DSA:2.10.80.10 (GENE3D)
766	DMPC15185474_Speleonectes_tulumensis_0	triglyceride lipase	281	9.25E-45	51.60%	P:lipid metabolic process; F:hydrolase activity; F:catalytic activity; F:triglyceride lipase activity; C:extracellular region; P:lipid catabolic process; F:retinyl-palmitate esterase activity	7	IPR000734; IPR001024; IPR002331; IPR008976; IPR013818; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
767	DMPC15185483_Speleonectes_tulumensis_1	epididymal secretory protein e1	136	1.26E-15	61.60%	P:transport	1	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
768	DMPC15185529_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor	140	1.21E-14	59.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
769	DMPC15185620_Speleonectes_tulumensis_2	ferritin h subunit	87	4.36E-19	96.80%	P:cellular homeostasis; F:binding; P:regulation of biological process; P:cell proliferation; F:catalytic activity; P:ion transport; C:mitochondrion; P:metabolic process	8	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
770	DMPC15185677_Speleonectes_tulumensis_1	lipase 3	138	2.57E-21	66.20%	P:lipid metabolic process; F:hydrolase activity, acting on ester bonds; F:hydrolase activity; P:lipid catabolic process	4	G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER)
771	DMPC15185831_Speleonectes_tulumensis_0	female neotenic-specific protein 3	129	5.73E-10	58.75%	-	0	no IPS match
772	DMPC15185840_Speleonectes_tulumensis_1	soma ferritin	107	5.67E-23	86.70%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
773	DMPC15185865_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor-like	111	5.59E-13	64.20%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
774	DMPC15185887_Speleonectes_tulumensis_0	dehydrogenase reductase sdr family member 11-like	111	6.99E-37	72.20%	-	0	IPR002198; IPR016040; PTHR24322 (PANTHER), PTHR24322:SF7 (PANTHER), SSF51735 (SUPERFAMILY)
775	DMPC15185900_Speleonectes_tulumensis_1	epididymal secretory protein e1	142	5.66E-19	60.50%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
776	DMPC15185995_Speleonectes_tulumensis_0	epididymal secretory protein e1 isoform 1	147	2.07E-23	56.20%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
777	DMPC15186050_Speleonectes_tulumensis_2	zinc finger protein 271-like	134	2.72E-31	63.70%	-	0	IPR007087; IPR013087; IPR015880; PTHR24382 (PANTHER), PTHR24382:SF0 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
778	DMPC15186163_Speleonectes_tulumensis_0	hypothetical protein DAPPUDRAFT_308544	113	5.64E-07	72.00%	-	0	IPR004911
779	DMPC15186166_Speleonectes_tulumensis_2	zinc finger protein 25	130	1.29E-25	60.80%	F:nucleic acid binding; F:zinc ion binding; C:intracellular; P:biological_process	4	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
780	DMPC15186255_Speleonectes_tulumensis_0	kazal-type serine proteinase inhibitor 4	130	3.49E-17	57.90%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)

781	DMPC15186271_Speleonectes_tulumensis_2	glycosyl-phosphatidylinositol-linked carbonic anhydrase	314	1.43E-86	60.50%	-	0	IPR001148; IPR018338; IPR023561; SignalP-NN(euk) (SIGNALP)
782	DMPC15186299_Speleonectes_tulumensis_0	superoxide dismutase	127	1.45E-22	82.50%	P:regulation of biological process; P:cell death; P:biological_process; ; P:cellular component organization; C:mitochondrion; P:response to stress; F:binding; P:multicellular organismal development; P:metabolic process; P:cell differentiation; F:catalytic activity; P:cell proliferation; P:mitochondrion organization	14	IPR001189; IPR019831; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER)
783	DMPC15186441_Speleonectes_tulumensis_0	fibronectin type iii domain protein	217	6.79E-12	48.10%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; F:calcium ion binding	5	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
784	DMPC15186462_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_332703	178	2.30E-61	56.10%	P:lipid transport; F:lipid transporter activity	2	IPR001846; IPR014853; PTHR11339 (PANTHER)
785	DMPC15186489_Speleonectes_tulumensis_1	---NA---	88			-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), SSF100895 (SUPERFAMILY)
786	DMPC15186493_Speleonectes_tulumensis_1	ferritin h subunit	97	3.30E-20	92.40%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
787	DMPC15186517_Speleonectes_tulumensis_1	ferritin gf1	115	1.52E-33	87.60%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
788	DMPC15186521_Speleonectes_tulumensis_1	ectonucleotide pyrophosphatase phosphodiesterase family member 6	122	9.93E-16	63.70%	C:cytoplasm; F:catalytic activity	2	IPR017850; IPR024873; tmhmm (TMHMM)
789	DMPC15186546_Speleonectes_tulumensis_0	dermatopontin 2	363	2.71E-39	59.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
790	DMPC15186552_Speleonectes_tulumensis_1	cathepsin l	150	8.93E-72	79.40%	-	0	IPR000668; IPR013128; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
791	DMPC15186754_Speleonectes_tulumensis_1	si:dkey- protein	106	7.77E-10	60.60%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
792	DMPC15186817_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	134	2.68E-19	52.40%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
793	DMPC15186867_Speleonectes_tulumensis_2	chymotrypsin a	159	3.39E-35	59.40%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER)
794	DMPC15186869_Speleonectes_tulumensis_2	leucine rich repeat protein	338	1.31E-19	53.20%	-	0	IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR24367 (PANTHER), PF13504 (PFAM), PF13855 (PFAM), SM00364 (SMART), SSF52058 (SUPERFAMILY)
795	DMPC15186873_Speleonectes_tulumensis_1	plasminogen activator spa	103	6.14E-08	62.67%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), tmhmm (TMHMM)
796	DMPC15186896_Speleonectes_tulumensis_2	---NA---	112			-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
797	DMPC15187018_Speleonectes_tulumensis_1	---NA---	163			-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
798	DMPC15187119_Speleonectes_tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	141	1.32E-17	51.50%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
799	DMPC15187182_Speleonectes_tulumensis_1	epididymal secretory protein e1 isoform 1	126	2.77E-18	59.60%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

800	DMPC15187262_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	160	5.44E-23	52.90%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:cell-matrix adhesion; F:calcium ion binding	6	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
801	DMPC15187365_Speleonectes_tulumensis_1	serine-threonine kinase receptor-associated protein	72	6.63E-13	86.40%	F:receptor activity; F:kinase activity; P:metabolic process	3	PTHR19877 (PANTHER)
802	DMPC15187382_Speleonectes_tulumensis_0	vitelline membrane outer layer protein 1 homolog precursor	131	4.34E-09	55.33%	P:vitelline membrane formation	1	IPR005515; PTHR18841:SF0 (PANTHER)
803	DMPC15187384_Speleonectes_tulumensis_2	chitinase 1 precursor	266	1.02E-46	55.80%	-	0	IPR001223; IPR002557; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), PTHR11177:SF30 (PANTHER), SSF54556 (SUPERFAMILY)
804	DMPC15187398_Speleonectes_tulumensis_2	plasminogen activator spa	96	4.11E-12	63.80%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24257 (PANTHER), SignalP-NN(euk) (SIGNALP)
805	DMPC15187455_Speleonectes_tulumensis_2	brasiliensin precursor	160	8.49E-24	53.10%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SSF100895 (SUPERFAMILY)
806	DMPC15187538_Speleonectes_tulumensis_1	peptidase thermolysin	164	4.48E-07	64.00%	P:proteolysis; F:hydrolase activity; F:metalloendopeptidase activity	3	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
807	DMPC15187652_Speleonectes_tulumensis_0	---NA---	144			-	0	IPR011038; IPR012674; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
808	DMPC15187711_Speleonectes_tulumensis_0	glutaminyl-peptide cyclotransferase	163	2.28E-13	58.00%	P:proteolysis; F:transferase activity; F:peptidase activity	3	PTHR12283 (PANTHER), PTHR12283:SF0 (PANTHER), tmhmm (TMHMM)
809	DMPC15187713_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	140	4.24E-31	68.20%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
810	DMPC15187740_Speleonectes_tulumensis_2	trypsin	202	9.52E-23	54.30%	F:catalytic activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
811	DMPC15187763_Speleonectes_tulumensis_2	dermatopontin 2	107	3.20E-09	62.40%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
812	DMPC15187818_Speleonectes_tulumensis_1	peptidyl-prolyl cis-trans isomerase 5	124	1.19E-36	90.90%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF63 (PANTHER), SignalP-NN(euk) (SIGNALP)
813	DMPC15187840_Speleonectes_tulumensis_0	venom allergen 3	152	5.60E-21	51.20%	C:extracellular region	1	IPR001283; IPR002413; IPR014044
814	DMPC15187852_Speleonectes_tulumensis_2	glucan pattern-recognition lipoprotein	283	2.76E-16	46.50%	P:lipid transport; F:lipid transporter activity	2	no IPS match
815	DMPC15187972_Speleonectes_tulumensis_1	alpha-galactosidase alpha-n-acetylgalactosaminidase	135	3.95E-56	83.70%	P:carbohydrate metabolic process; F:hydrolase activity; F:binding	3	IPR000111; IPR002241; IPR013785; IPR017853; PTHR11452 (PANTHER)
816	DMPC15188029_Speleonectes_tulumensis_0	intestinal trypsin 4 precursor	114	1.63E-17	81.10%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
817	DMPC15188077_Speleonectes_tulumensis_1	plasminogen activator spa	150	9.16E-21	59.80%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
818	DMPC15188215_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	143	1.88E-15	57.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
819	DMPC15188223_Speleonectes_tulumensis_2	ame: full=carboxypeptidase b	249	5.24E-97	69.10%	-	0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
820	DMPC15188266_Speleonectes_tulumensis_1	aldh9a1a protein	140	5.02E-60	77.10%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016161; IPR016162; PTHR11699 (PANTHER), PTHR11699:SF47 (PANTHER)

821	DMPC15188433_Speleonectes_tulumensis_1	female neotenic-specific protein 3	152	4.22E-10	60.00%	-	0	no IPS match
822	DMPC15188464_Speleonectes_tulumensis_1	glyceraldehyde-3-phosphate dehydrogenase	241	5.90E-47	90.80%	C:cytoplasm; F:nucleotide binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:catalytic activity; P:metabolic process	7	IPR020829; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF55347 (SUPERFAMILY)
823	DMPC15188569_Speleonectes_tulumensis_1	chymotrypsin a	150	1.16E-23	65.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER)
824	DMPC15188634_Speleonectes_tulumensis_3	---NA---	281			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
825	DMPC15188726_Speleonectes_tulumensis_2	---NA---	137			-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), SignalP-NN(euk) (SIGNALP), SSF100895 (SUPERFAMILY)
826	DMPC15188811_Speleonectes_tulumensis_2	hyaluronan-binding protein 2-like	126	1.07E-10	57.10%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER), SignalP-NN(euk) (SIGNALP)
827	DMPC15188821_Speleonectes_tulumensis_1	cd74 major histocompatibility class ii invariant chain a	134	4.30E-08	67.67%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP)
828	DMPC15188883_Speleonectes_tulumensis_2	GL15638	234	1.49E-56	75.40%	P:metabolic process; F:peptidase activity	2	IPR002933; G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF15 (PANTHER), SSF53187 (SUPERFAMILY)
829	DMPC15189038_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor-like	137	1.80E-22	61.10%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
830	DMPC15189192_Speleonectes_tulumensis_1	ame: full=venom protein 302 flags: precursor	143	1.23E-10	65.00%	P:regulation of cell growth; F:insulin-like growth factor binding; C:extracellular region	3	IPR000867; IPR011390; PS51257 (PROFILE), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
831	DMPC15189221_Speleonectes_tulumensis_0	cd74 major histocompatibility class ii invariant chain a	106	1.95E-07	65.67%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
832	DMPC15189251_Speleonectes_tulumensis_3	neuroglian-like isoform 2	113	1.97E-33	80.70%	-	0	IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF132 (PANTHER), SSF48726 (SUPERFAMILY)
833	DMPC15189384_Speleonectes_tulumensis_0	thioredoxin peroxidase	109	1.31E-27	81.70%	-	0	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF50 (PANTHER)
834	DMPC15189399_Speleonectes_tulumensis_0	chymotrypsin-like protease ctrl- partial	128	1.67E-17	56.10%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
835	DMPC15189486_Speleonectes_tulumensis_0	gamma-glutamyl hydrolase	265	1.11E-68	65.50%	F:peptidase activity; P:metabolic process	2	IPR011697; IPR015527; G3DSA:3.40.50.880 (GENE3D), PTHR11315:SF0 (PANTHER), tmhmm (TMHMM), SSF52317 (SUPERFAMILY)
836	DMPC15189497_Speleonectes_tulumensis_2	mite allergen tyr p 7	409	2.28E-18	47.90%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP)
837	DMPC15189508_Speleonectes_tulumensis_1	epoxide hydrolase 4	485	7.88E-97	60.50%	F:catalytic activity	1	IPR000639; G3DSA:3.40.50.1820 (GENE3D), PTHR10992 (PANTHER), PTHR10992:SF98 (PANTHER), PF12697 (PFAM), tmhmm (TMHMM), SSF53474 (SUPERFAMILY)
838	DMPC15189516_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	148	2.29E-19	49.50%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
839	DMPC15189591_Speleonectes_tulumensis_0	carboxypeptidase b-like	98	3.96E-30	72.70%	-	0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
840	DMPC15189592_Speleonectes_tulumensis_2	cysteine string	122	4.00E-31	95.20%	P:protein metabolic process; F:protein binding	2	IPR001623; IPR018253; PTHR24078 (PANTHER), PTHR24078:SF7 (PANTHER), tmhmm (TMHMM)
841	DMPC15189606_Speleonectes_tulumensis_1	-like protein subfamily c member 11	94	2.61E-30	89.20%	P:protein metabolic process; F:protein binding	2	IPR001623; PTHR24078 (PANTHER), PTHR24078:SF6 (PANTHER)
842	DMPC15189639_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	119	6.31E-12	60.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

843	DMPC15189681_Speleonectes _tulumensis_0	hemocyanin subunit 1	89	3.42E-15	81.33%	-	0	IPR005203; IPR013788; IPR014756; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
844	DMPC15189698_Speleonectes _tulumensis_2	cg3556 cg3556-pa	242	1.60E-23	52.80%	P:cobalamin transport; F:cobalamin binding	2	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
845	DMPC15189705_Speleonectes _tulumensis_0	ubiquitin-40s ribosomal protein s27a-like	141	1.09E-50	97.40%	-	0	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
846	DMPC15189727_Speleonectes _tulumensis_0	---NA---	88			-	0	IPR002181; IPR014715; PTHR19143 (PANTHER), PTHR19143:SF46 (PANTHER)
847	DMPC15189728_Speleonectes _tulumensis_0	lipase 3	130	1.82E-36	67.10%	P:lipid metabolic process; F:hydrolase activity, acting on ester bonds; F:hydrolase activity; P:lipid catabolic process	4	G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER), tmhmm (TMHMM)
848	DMPC15189914_Speleonectes _tulumensis_0	peptidyl-prolyl cis-trans isomerase e	384	4.58E-92	90.20%	P:protein metabolic process; P:cellular protein modification process; F:RNA binding; F:catalytic activity; F:nucleotide binding	5	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER)
849	DMPC15189943_Speleonectes _tulumensis_2	anti-lipopolysaccharide factor	133	5.72E-29	69.60%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
850	DMPC15189976_Speleonectes _tulumensis_1	membrane metallo-endopeptidase (neutral cd10) isoform cra_a	265	4.21E-12	59.00%	P:biological_process; F:binding; C:cell; P:response to abiotic stimulus; F:peptidase activity; P:protein metabolic process; P:catabolic process; ; F:protein binding; P:multicellular organismal development; C:cytoplasm; C:plasma membrane	12	IPR000718; IPR018497; IPR024079; SSF55486 (SUPERFAMILY)
851	DMPC15189996_Speleonectes _tulumensis_0	apolipoprotein d-like isoform 2	154	8.63E-21	61.60%	F:lipid binding; P:transport; F:transporter activity	3	IPR011038; IPR012674; IPR022272; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP)
852	DMPC15190084_Speleonectes _tulumensis_0	cytosolic non-specific dipeptidase-like	207	2.36E-98	78.90%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR002933; IPR011650; G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF15 (PANTHER), SSF53187 (SUPERFAMILY)
853	DMPC15190145_Speleonectes _tulumensis_2	hypothetical protein DAPPUDRAFT_305141	117	6.24E-14	58.00%	F:carboxylic ester hydrolase activity	1	IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559 (PANTHER), SSF53474 (SUPERFAMILY)
854	DMPC15190216_Speleonectes _tulumensis_0	u8-agatoxin-ao1a-like isoform 1	152	2.20E-32	75.00%	-	0	IPR004169; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF57059 (SUPERFAMILY)
855	DMPC15190273_Speleonectes _tulumensis_0	nucleolar protein 5	118	6.58E-58	87.40%	-	0	IPR002687; PTHR10894 (PANTHER), SSF89124 (SUPERFAMILY)
856	DMPC15190292_Speleonectes _tulumensis_0	saxiphilin precursor	148	4.50E-11	62.20%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
857	DMPC15190293_Speleonectes _tulumensis_2	isoform a	273	7.10E-38	49.00%	P:proteolysis; P:cell proliferation; F:metalloendopeptidase activity; C:cellular_component	4	IPR001590; IPR006586; IPR024079; PTHR11905 (PANTHER), PF13574 (PFAM), SSF55486 (SUPERFAMILY)
858	DMPC15190352_Speleonectes _tulumensis_2	---NA---	146			-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF100895 (SUPERFAMILY)
859	DMPC15190383_Speleonectes _tulumensis_1	plasminogen activator spa	153	1.95E-21	55.40%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
860	DMPC15190401_Speleonectes _tulumensis_0	---NA---	149			-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF30 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
861	DMPC15190466_Speleonectes _tulumensis_1	cysteine protease family	183	1.68E-16	91.10%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)

862	DMPC15190494_Speleonectes_tulumensis_1	phosphatidylethanolamine-binding protein homolog -like	146	1.63E-16	68.40%	-	0	IPR008914; PTHR11362 (PANTHER), PTHR11362:SF0 (PANTHER)
863	DMPC15190604_Speleonectes_tulumensis_0	extracellular alkaline serine protease	161	6.22E-20	64.60%	F:peptidase activity	1	IPR007280; SignalP-NN(euk) (SIGNALP)
864	DMPC15190612_Speleonectes_tulumensis_1	serine protease	175	6.78E-09	55.20%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), PTHR24260:SF33 (PANTHER), SignalP-NN(euk) (SIGNALP)
865	DMPC15190697_Speleonectes_tulumensis_0	ferritin 3-like protein	125	9.44E-22	73.80%	F:binding	1	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
866	DMPC15190737_Speleonectes_tulumensis_2	histone h2a	183	2.03E-60	97.00%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)
867	DMPC15190750_Speleonectes_tulumensis_0	dermatopontin 2	147	7.63E-19	59.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
868	DMPC15190781_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	188	1.92E-82	69.70%	-	0	IPR005203; IPR013788; IPR014756
869	DMPC15190783_Speleonectes_tulumensis_3	female reproductive tract protease gleanr_896	146	4.96E-20	70.30%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
870	DMPC15190802_Speleonectes_tulumensis_0	granulins precursor	179	2.69E-15	55.50%	-	0	IPR000118; PTHR12274 (PANTHER), PTHR12274:SF0 (PANTHER), tmhmm (TMHMM)
871	DMPC15190943_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor	150	6.31E-31	67.20%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
872	DMPC15190956_Speleonectes_tulumensis_2	Otogelin, partial	261	3.56E-09	48.33%	-	0	no IPS match
873	DMPC15190968_Speleonectes_tulumensis_0	ferritin	282	3.94E-20	84.00%	-	0	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; IPR014034; tmhmm (TMHMM)
874	DMPC15191122_Speleonectes_tulumensis_1	uncharacterized aarf domain-containing protein kinase 1	193	6.33E-27	68.50%	F:transferase activity, transferring phosphorus-containing groups; F:ATP binding; F:protein kinase activity; P:protein phosphorylation	4	PTHR10566 (PANTHER), PTHR10566:SF24 (PANTHER), tmhmm (TMHMM)
875	DMPC15191135_Speleonectes_tulumensis_2	cytochrome b5-like heme steroid binding domain containing protein	140	4.85E-20	66.90%	F:heme binding; F:molecular_function; P:biological_process; C:extracellular region; C:cellular_component	5	IPR001199; PTHR10281 (PANTHER), PTHR10281:SF4 (PANTHER)
876	DMPC15191189_Speleonectes_tulumensis_0	adp-ribosylation factor-like protein 1-like	123	5.21E-51	84.50%	C:intracellular; F:nucleotide binding; P:signal transduction	3	IPR006689; IPR024156; IPR027417; G3DSA:3.40.50.300 (GENE3D), PTHR11711 (PANTHER), PTHR11711:SF41 (PANTHER)
877	DMPC15191194_Speleonectes_tulumensis_0	pancreatic lipase-related protein 1	355	1.45E-30	56.90%	P:lipid metabolic process; F:hydrolase activity; F:catalytic activity; F:triglyceride lipase activity; C:extracellular region; F:retinyl-palmitate esterase activity	6	IPR000734; IPR013818; G3DSA:3.40.50.1820 (GENE3D), PTHR11610:SF32 (PANTHER), SSF53474 (SUPERFAMILY)
878	DMPC15191217_Speleonectes_tulumensis_1	serine protease	160	5.54E-17	63.30%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER)
879	DMPC15191264_Speleonectes_tulumensis_2	soma ferritin	117	2.38E-22	86.50%	-	0	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
880	DMPC15191291_Speleonectes_tulumensis_0	copper chaperone for superoxide dismutase	204	3.37E-33	72.00%	-	0	IPR001424; IPR024134; IPR024142
881	DMPC15191349_Speleonectes_tulumensis_2	histone -like	196	6.97E-65	99.60%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)
882	DMPC15191354_Speleonectes_tulumensis_2	lysozyme precursor	197	1.12E-47	64.60%	F:lysozyme activity; P:cell wall macromolecule catabolic process	2	IPR000974; IPR001916; IPR019799; IPR023346; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER), SignalP-NN(euk) (SIGNALP)

883	DMPC15191361_Speleonectes _tulumensis_1	dermatopontin 3	106	3.73E-08	60.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
884	DMPC15191374_Speleonectes _tulumensis_2	glutathione peroxidase 6	143	1.11E-15	72.20%	F:catalytic activity; F:antioxidant activity; P:response to stress; P:metabolic process	4	IPR000889; IPR012336
885	DMPC15191529_Speleonectes _tulumensis_2	adp-ribosylation factor 4	155	1.60E-54	92.10%	F:nucleotide binding; C:Golgi apparatus; P:transport; P:signal transduction; P:protein transport	5	IPR005225; IPR006689; IPR024156; IPR027417; G3DSA:3.40.50.300 (GENE3D), PTHR11711 (PANTHER)
886	DMPC15191563_Speleonectes _tulumensis_0	epididymal secretory protein e1 isoform 1	138	1.14E-19	60.10%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
887	DMPC15191603_Speleonectes _tulumensis_0	chitinase partial	125	5.60E-41	81.60%	F:hydrolase activity; F:binding; P:carbohydrate metabolic process; P:catabolic process	4	IPR001223; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
888	DMPC15191667_Speleonectes _tulumensis_2	neutral ceramidase b	225	5.18E-69	68.40%	-	0	IPR006823
889	DMPC15191690_Speleonectes _tulumensis_2	trypsin	145	6.29E-57	77.00%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER)
890	DMPC15191691_Speleonectes _tulumensis_2	venom allergen 5-like	198	1.86E-09	58.80%	C:extracellular region	1	IPR001283; IPR002172; IPR014044; IPR023415
891	DMPC15191869_Speleonectes _tulumensis_1	thioredoxin 1	147	2.54E-52	83.30%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; IPR017937; SignalP-NN(euk) (SIGNALP)
892	DMPC15191872_Speleonectes _tulumensis_1	---NA---	134			-	0	IPR000742; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR24838 (PANTHER), tmhmm (TMHMM), SSF57196 (SUPERFAMILY)
893	DMPC15191886_Speleonectes _tulumensis_0	purple acid	105	9.11E-45	83.30%	F:binding; F:hydrolase activity	2	IPR004843; G3DSA:3.60.21.10 (GENE3D), PTHR22953 (PANTHER), PTHR22953:SF0 (PANTHER), SSF56300 (SUPERFAMILY)
894	DMPC15191896_Speleonectes _tulumensis_2	protein bv8	104	2.89E-11	61.60%	-	0	G3DSA:2.10.80.10 (GENE3D)
895	DMPC15191924_Speleonectes _tulumensis_2	ecdysteroid-regulated protein	151	1.30E-13	50.40%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
896	DMPC15191941_Speleonectes _tulumensis_0	proclotting enzyme	135	1.58E-26	61.90%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF28 (PANTHER), SignalP-NN(euk) (SIGNALP)
897	DMPC15191960_Speleonectes _tulumensis_1	peptidyl-prolyl cis-trans cyclophilin-type family	159	6.15E-21	83.40%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER)
898	DMPC15192006_Speleonectes _tulumensis_0	---NA---	93			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
899	DMPC15192027_Speleonectes _tulumensis_1	protein shifted-like	239	3.71E-41	76.20%	-	0	IPR000742; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR24838 (PANTHER), SSF57196 (SUPERFAMILY)
900	DMPC15192073_Speleonectes _tulumensis_1	mast cell protease 6	198	1.03E-58	73.60%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF68 (PANTHER)
901	DMPC15192078_Speleonectes _tulumensis_2	cathepsin l precursor	154	1.27E-13	90.10%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
902	DMPC15192185_Speleonectes _tulumensis_0	dermatopontin 3	106	1.50E-12	64.10%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
903	DMPC15192231_Speleonectes _tulumensis_0	trypsin partial	124	2.04E-11	64.90%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

904	DMPC15192327_Speleonectes _tulumensis_1	soma ferritin	123	1.16E-27	88.90%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
905	DMPC15192413_Speleonectes _tulumensis_1	---NA---	107			-	0	IPR024509
906	DMPC15192472_Speleonectes _tulumensis_5	salivary hyaluronidase	167	6.61E-11	60.90%	F:catalytic activity	1	IPR013785; IPR017853; IPR018155; tmhmm (TMHMM)
907	DMPC15192530_Speleonectes _tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	130	2.80E-13	48.90%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP)
908	DMPC15192596_Speleonectes _tulumensis_2	gamma-interferon-inducible lysosomal thiol reductase	127	2.50E-10	66.10%	-	0	IPR004911
909	DMPC15192602_Speleonectes _tulumensis_0	ensangp00000031746-like protein	107	3.84E-57	88.20%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF41 (PANTHER)
910	DMPC15192615_Speleonectes _tulumensis_1	kazal-type protease inhibitor	99	6.20E-13	57.30%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
911	DMPC15192695_Speleonectes _tulumensis_2	serpin peptidase clade b member 6	151	5.75E-19	70.00%	F:protein metabolic process; P:regulation of biological process; P:catabolic process; F:enzyme regulator activity; P:biological process	5	IPR000215; IPR023796; G3DSA:3.30.497.10 (GENE3D)
912	DMPC15192737_Speleonectes _tulumensis_0	coiled-coil domain-containing protein 75	159	1.57E-31	66.00%	F:nucleic acid binding	1	IPR000467; PTHR21032 (PANTHER)
913	DMPC15192764_Speleonectes _tulumensis_0	serine protease homolog 93 precursor	94	7.84E-09	71.00%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
914	DMPC15192901_Speleonectes _tulumensis_2	lysine--trna ligase-like	140	1.42E-55	93.30%	-	0	IPR002313; IPR004364; IPR006195; IPR018150; G3DSA:3.30.930.10 (GENE3D), SSF55681 (SUPERFAMILY)
915	DMPC15192903_Speleonectes _tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	133	3.18E-21	53.40%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
916	DMPC15193007_Speleonectes _tulumensis_0	enolase	231	3.85E-44	78.60%	F:catalytic activity	1	IPR000941; IPR020810; G3DSA:3.20.20.120 (GENE3D), SSF51604 (SUPERFAMILY)
917	DMPC15193097_Speleonectes _tulumensis_2	ame: full=zinc metalloproteinase disintegrin contains: ame: full=snake venom metalloproteinase short=svmp contains: ame: full=disintegrin flavoridin flags: precursor	188	2.59E-09	54.80%	-	0	IPR002870; PTHR11905 (PANTHER), tmhmm (TMHMM)
918	DMPC15193112_Speleonectes _tulumensis_0	serine protease inhibitor	174	6.78E-18	57.30%	P:proteolysis; F:peptidase activity; F:serine-type endopeptidase inhibitor activity	3	IPR000215; IPR023796; G3DSA:2.30.39.10 (GENE3D), G3DSA:3.30.497.10 (GENE3D), PTHR11461:SF71 (PANTHER)
919	DMPC15193211_Speleonectes _tulumensis_2	pdz domain-containing protein 2	288	5.27E-38	76.60%	-	0	IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR19964 (PANTHER), PTHR19964:SF22 (PANTHER)
920	DMPC15193231_Speleonectes _tulumensis_0	si:dkey- protein	151	6.67E-24	61.80%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
921	DMPC15193238_Speleonectes _tulumensis_2	serine protease inhibitor	199	2.81E-13	63.80%	F:serine-type endopeptidase inhibitor activity; P:proteolysis; F:peptidase activity	3	IPR000215; IPR023795; IPR023796; G3DSA:2.30.39.10 (GENE3D)
922	DMPC15193337_Speleonectes _tulumensis_2	dermatopontin 3	131	4.64E-11	59.80%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
923	DMPC15193368_Speleonectes _tulumensis_1	histone 1	386	2.92E-26	81.80%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR005818; IPR005819; IPR011991; PTHR11467 (PANTHER), PTHR11467:SF0 (PANTHER), SSF46785 (SUPERFAMILY)
924	DMPC15193412_Speleonectes _tulumensis_2	27 kda hemolymph protein	125	2.98E-14	54.40%	C:extracellular region	1	IPR009832; PTHR20997 (PANTHER), PTHR20997:SF0 (PANTHER)
925	DMPC15193474_Speleonectes _tulumensis_0	soma ferritin	118	3.87E-31	89.40%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347

926	DMPC15193478_Speleonectes _tulumensis_2	sel1l protein	348	1.54E-91	81.40%	F:hydrolase activity	1	IPR006597; IPR011990; PTHR11102 (PANTHER), PTHR11102:SF26 (PANTHER), tmhmm (TMHMM), SSF81901 (SUPERFAMILY)
927	DMPC15193480_Speleonectes _tulumensis_0	leucine-rich repeat-containing protein 47-like	160	4.15E-21	65.10%	F:RNA binding; F:phenylalanine-tRNA ligase activity; F:aminoacyl-tRNA ligase activity	3	IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PF13855 (PFAM), SM00364 (SMART), SSF52058 (SUPERFAMILY)
928	DMPC15193570_Speleonectes _tulumensis_0	serine protease	100	5.31E-09	64.10%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), PTHR24260:SF3 (PANTHER)
929	DMPC15193608_Speleonectes _tulumensis_1	cationic trypsin-3-like	238	7.92E-17	60.60%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
930	DMPC15193629_Speleonectes _tulumensis_0	phosphoglycerate kinase	187	4.25E-94	86.40%	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; P:metabolic process; F:kinase activity	5	IPR001576; IPR015901
931	DMPC15193639_Speleonectes _tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	132	1.90E-21	53.00%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:cell-matrix adhesion; F:calcium ion binding	6	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
932	DMPC15193718_Speleonectes _tulumensis_2	trypsin-like serine protease	439	1.39E-17	53.70%	F:catalytic activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER)
933	DMPC15193759_Speleonectes _tulumensis_2	membrane metallo-endopeptidase-like 1-like	103	8.49E-24	59.60%	P:proteolysis; F:metallopeptidase activity; F:hydrolase activity; F:metalloendopeptidase activity	4	IPR000718; IPR018497; IPR024079; SSF55486 (SUPERFAMILY)
934	DMPC15193794_Speleonectes _tulumensis_2	zinc finger protein 502-like	127	4.90E-09	63.70%	C:intracellular; F:binding	2	IPR007087; IPR013087; IPR015880; PTHR24382 (PANTHER), PTHR24382:SF0 (PANTHER), SSF57667 (SUPERFAMILY)
935	DMPC15193839_Speleonectes _tulumensis_1	dehydrogenase reductase sdr family member 4	403	8.79E-108	75.00%	P:metabolic process	1	IPR002198; IPR002347; IPR016040; IPR020904; IPR027052; PTHR24322 (PANTHER), PF13561 (PFAM), tmhmm (TMHMM), SSF51735 (SUPERFAMILY)
936	DMPC15193840_Speleonectes _tulumensis_2	serine protease p127	122	2.70E-15	58.80%	F:catalytic activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER)
937	DMPC15193844_Speleonectes _tulumensis_0	peptidylprolyl isomerase-like 1-like isoform 1	97	2.43E-18	90.60%	P:cellular protein modification process; C:nucleus; P:protein metabolic process; P:reproduction; P:behavior; P:regulation of biological process; F:catalytic activity; P:nucleobase-containing compound metabolic process	8	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF41 (PANTHER)
938	DMPC15193982_Speleonectes _tulumensis_0	anti-lipopolysaccharide factor isoform 7	136	1.57E-26	63.70%	-	0	IPR024509; IPR024716
939	DMPC15194027_Speleonectes _tulumensis_1	lissencephaly-1 homolog	216	3.03E-49	91.40%	C:cytoplasm; P:organelle organization; P:cell cycle; P:transport; F:hydrolase activity; P:biological_process; C:cytoskeleton; C:protein complex	8	IPR001680; IPR015943; IPR017252; IPR017986; IPR019775; PTHR22847 (PANTHER), tmhmm (TMHMM)
940	DMPC15194040_Speleonectes _tulumensis_0	hemocyanin subunit type 2 precursor	83	3.02E-33	72.00%	-	0	IPR005203; IPR013788; IPR014756
941	DMPC15194104_Speleonectes _tulumensis_2	calponin transgelin	184	2.13E-63	90.20%	F:actin binding; P:cytoskeleton organization	2	IPR001715; IPR001997; IPR003096; PTHR18959 (PANTHER), PTHR18959:SF3 (PANTHER), SignalP-NN(euk) (SIGNALP)
942	DMPC15194122_Speleonectes _tulumensis_2	C-factor	136	1.23E-19	67.60%	P:metabolic process	1	IPR016040; PTHR24322 (PANTHER), PTHR24322:SF57 (PANTHER), SSF51735 (SUPERFAMILY)
943	DMPC15194177_Speleonectes _tulumensis_2	soma ferritin	116	8.28E-24	88.40%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347

944	DMPC15194181_Speleonectes _tulumensis_1	mantle protein 9	134	1.03E-08	67.75%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
945	DMPC15194194_Speleonectes _tulumensis_1	prosalusin-like isoform 1	157	1.42E-14	61.70%	F:ATP binding; P:chaperone mediated protein folding requiring cofactor	2	IPR010448; PTHR10760:SF2 (PANTHER), tmhmm (TMHMM)
946	DMPC15194201_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor isoform 7	250	6.69E-29	68.30%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
947	DMPC15194252_Speleonectes _tulumensis_0	---NA---	130			-	0	IPR008160; PTHR24023 (PANTHER), PTHR24023:SF164 (PANTHER), SignalP-NN(euk) (SIGNALP)
948	DMPC15194259_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor-like	152	2.26E-24	63.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
949	DMPC15194304_Speleonectes _tulumensis_1	female reproductive tract protease gleanr_898	147	6.04E-21	57.60%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
950	DMPC15194309_Speleonectes _tulumensis_1	alkyl hydroperoxide reductase thiol specific antioxidant mal allergen	159	1.46E-55	66.80%	F:catalytic activity	1	IPR000866; IPR012336; IPR019479; IPR024706; PTHR10681 (PANTHER), PTHR10681:SF51 (PANTHER)
951	DMPC15194310_Speleonectes _tulumensis_1	thioredoxin 1	121	1.94E-22	83.00%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; SignalP-NN(euk) (SIGNALP)
952	DMPC15194321_Speleonectes _tulumensis_0	discoidin domain-containing receptor 2-like	109	9.06E-10	63.40%	-	0	IPR001245; IPR011009; G3DSA:3.30.200.20 (GENE3D), PTHR24416 (PANTHER), PTHR24416:SF84 (PANTHER)
953	DMPC15194385_Speleonectes _tulumensis_2	protoporphyrinogen oxidase-like	131	3.51E-11	73.60%	P:metabolic process; F:catalytic activity	2	G3DSA:3.50.50.60 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF16 (PANTHER), PF13450 (PFAM), tmhmm (TMHMM), SSF51905 (SUPERFAMILY)
954	DMPC15194457_Speleonectes _tulumensis_1	kazal-type protease inhibitor	185	5.62E-15	54.60%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
955	DMPC15194466_Speleonectes _tulumensis_0	l-xylulose reductase-like	126	6.13E-42	72.80%	P:carbohydrate metabolic process; F:catalytic activity; C:cell	3	IPR002198; IPR002347; IPR016040; PTHR24311 (PANTHER), PTHR24311:SF0 (PANTHER), SSF51735 (SUPERFAMILY)
956	DMPC15194549_Speleonectes _tulumensis_0	female neotenic-specific protein 3	153	5.53E-11	57.00%	-	0	tmhmm (TMHMM)
957	DMPC15194578_Speleonectes _tulumensis_5	hypothetical protein DAPPUDRAFT_303360	131	2.40E-08	64.00%	-	0	IPR024079; PTHR13723 (PANTHER), PTHR13723:SF38 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
958	DMPC15194582_Speleonectes _tulumensis_0	oocyte protease inhibitor-1 precursor	123	3.63E-09	64.40%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), PTHR12352:SF3 (PANTHER), SignalP-NN(euk) (SIGNALP)
959	DMPC15194588_Speleonectes _tulumensis_2	projectin short variant	239	9.40E-22	52.70%	P:biological_process; F:transferase activity; P:anatomical structure morphogenesis; F:structural molecule activity; C:cytoplasm	5	IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; PTHR10489 (PANTHER), SSF48726 (SUPERFAMILY)
960	DMPC15194625_Speleonectes _tulumensis_1	eclosion hormone-like	276	2.47E-15	62.70%	P:ecdysis, chitin-based cuticle; P:neuropeptide signaling pathway; F:ecdysis-triggering hormone activity	3	IPR006825; tmhmm (TMHMM)
961	DMPC15194681_Speleonectes _tulumensis_2	40s ribosomal protein s15a	150	1.20E-12	75.10%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000630; IPR008037; IPR020862; G3DSA:3.30.1490.10 (GENE3D), SignalP-NN(euk) (SIGNALP)
962	DMPC15194733_Speleonectes _tulumensis_0	protein	139	3.62E-17	52.00%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
963	DMPC15194764_Speleonectes _tulumensis_0	protein	130	1.90E-12	51.90%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:proteolysis; F:peptidase activity	6	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)

964	DMPC15194800_Speleonectes_tulumensis_0	matrix metalloproteinase-9	360	5.79E-16	52.10%	F:carbohydrate binding; P:extracellular matrix organization; P:positive regulation of apoptotic process; P:positive regulation of keratinocyte migration; F:metalloendopeptidase activity; P:skeletal system development; F:zinc ion binding; P:embryo implantation; C:proteinaceous extracellular matrix; C:extracellular matrix; P:proteolysis; P:collagen catabolic process; C:extracellular space	13	IPR000562; IPR013806; PTHR22918 (PANTHER), PTHR22918:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
965	DMPC15194809_Speleonectes_tulumensis_2	trypsin	151	2.96E-25	65.20%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)
966	DMPC15194921_Speleonectes_tulumensis_0	ferritin subunit	106	3.44E-21	80.50%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
967	DMPC15194972_Speleonectes_tulumensis_0	peroxidase-like isoform 2	284	1.52E-85	63.30%	-	0	IPR002007; IPR010255; IPR019791; PTHR11475 (PANTHER)
968	DMPC15195045_Speleonectes_tulumensis_1	fat tumor suppressor-like protein partial	155	6.43E-27	63.50%	C:cell	1	IPR002126; IPR015919; IPR020894; PTHR24027 (PANTHER), tmhmm (TMHMM)
969	DMPC15195111_Speleonectes_tulumensis_0	14-3-3 zeta	249	2.31E-86	75.20%	F:protein domain specific binding	1	IPR000308; IPR023409; IPR023410; PTHR18860:SF0 (PANTHER)
970	DMPC15195138_Speleonectes_tulumensis_0	serine protease 19	111	3.44E-08	65.14%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER)
971	DMPC15195179_Speleonectes_tulumensis_3	terribly reduced optic isoform ad	131	2.10E-25	64.00%	P:anatomical structure morphogenesis; P:cellular component organization; C:lipid particle; C:proteinaceous extracellular matrix	4	IPR002172; PTHR10529 (PANTHER), SignalP-NN(euk) (SIGNALP)
972	DMPC15195219_Speleonectes_tulumensis_2	tripsin i-p1	160	1.03E-25	48.80%	P:proteolysis; F:serine-type endopeptidase activity; F:hydrolase activity; F:catalytic activity	4	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER)
973	DMPC15195412_Speleonectes_tulumensis_1	kazal-type serine protease inhibitor 1 serpin	122	2.95E-09	66.60%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
974	DMPC15195421_Speleonectes_tulumensis_1	proclotting enzyme	201	1.51E-65	69.00%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF28 (PANTHER)
975	DMPC15195423_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	165	3.87E-79	62.20%	-	0	IPR005203; IPR013788; IPR014756
976	DMPC15195455_Speleonectes_tulumensis_3	ensangp00000031746-like protein	69	2.21E-17	99.40%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF41 (PANTHER), tmhmm (TMHMM)
977	DMPC15195470_Speleonectes_tulumensis_0	hemocyanin subunit type 1 precursor	147	5.04E-91	70.10%	-	0	IPR005203; IPR013788; IPR014756; PTHR11511:SF4 (PANTHER)
978	DMPC15195516_Speleonectes_tulumensis_1	ligand of numb protein x 2-like	377	1.89E-66	62.80%	F:metal ion binding; F:zinc ion binding	2	IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR19964 (PANTHER)
979	DMPC15195608_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor	144	1.42E-30	67.60%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
980	DMPC15195633_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor	145	6.70E-31	68.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
981	DMPC15195645_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_308200	144	2.22E-09	49.50%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
982	DMPC15195652_Speleonectes_tulumensis_2	cationic trypsin-3-like	118	3.11E-14	53.40%	P:proteolysis; P:extracellular matrix disassembly; F:serine-type endopeptidase activity; P:extracellular matrix organization; C:extracellular region	5	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24250 (PANTHER), SignalP-NN(euk) (SIGNALP)

983	DMPC15195693_Speleonectes_tulumensis_0	lysozyme precursor	149	2.15E-45	67.20%	F:lysozyme activity; P:cell wall macromolecule catabolic process	2	IPR000974; IPR001916; IPR019799; IPR023346; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER)
984	DMPC15195712_Speleonectes_tulumensis_1	ferritin 3-like protein	128	4.00E-25	80.50%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
985	DMPC15195872_Speleonectes_tulumensis_2	ame: full=serine protease inhibitor dipetalogastin short=dipetalin flags: precursor	126	4.57E-11	59.70%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF100895 (SUPERFAMILY)
986	DMPC15195938_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	154	5.72E-69	69.10%	-	0	IPR005203; IPR013788; IPR014756
987	DMPC15195947_Speleonectes_tulumensis_0	multiple inositol polyphosphate phosphatase 1-like	275	1.71E-41	60.00%	F:hydrolase activity	1	IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR20963 (PANTHER), PTHR20963:SF8 (PANTHER), tmhmm (TMHMM), SSF53254 (SUPERFAMILY)
988	DMPC15195948_Speleonectes_tulumensis_2	---NA---	68			-	0	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)
989	DMPC15195966_Speleonectes_tulumensis_2	glutathione peroxidase 1	203	3.97E-37	82.10%	F:catalytic activity; F:antioxidant activity; C:cytoplasm; P:response to stress	4	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
990	DMPC15195978_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor isoform 7	154	1.18E-16	60.50%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
991	DMPC15196033_Speleonectes_tulumensis_0	laminin a	211	6.88E-57	63.50%	P:biological_process; P:regulation of biological process	2	IPR001791; IPR008985; IPR013320; PTHR10574 (PANTHER), PTHR10574:SF56 (PANTHER)
992	DMPC15196035_Speleonectes_tulumensis_0	peptidyl-prolyl cis-trans isomerase fkbp14-like	197	3.68E-63	72.80%	P:protein metabolic process; F:calcium ion binding	2	IPR001179; IPR002048; IPR018247; IPR023566; G3DSA:3.10.50.40 (GENE3D), PTHR10516:SF20 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54534 (SUPERFAMILY)
993	DMPC15196063_Speleonectes_tulumensis_0	von willebrand factor type egf and pentraxin domain-containing protein 1	153	4.10E-12	54.60%	F:carbohydrate binding; F:hydrolase activity	2	IPR000436; G3DSA:2.10.70.10 (GENE3D), PTHR19325 (PANTHER), PTHR19325:SF43 (PANTHER), tmhmm (TMHMM)
994	DMPC15196080_Speleonectes_tulumensis_2	chymotrypsin a	149	9.92E-21	67.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), tmhmm (TMHMM)
995	DMPC15196086_Speleonectes_tulumensis_2	astakine variant 2	148	2.96E-11	61.60%	-	0	G3DSA:2.10.80.10 (GENE3D)
996	DMPC15196111_Speleonectes_tulumensis_1	lipase 3-like	135	3.99E-33	69.80%	F:hydrolase activity; P:lipid metabolic process	2	G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER), SSF53474 (SUPERFAMILY)
997	DMPC15196130_Speleonectes_tulumensis_1	a chain crystal spectroscopic and catalytic properties of cobalt copper nickel and mercury derivatives of the zinc endopeptidase a correlation of structure and proteolytic activity	147	4.27E-09	69.60%	C:cell; C:protein complex; P:reproduction; P:regulation of biological process; F:peptidase activity; F:binding; C:cytoplasmic membrane-bounded vesicle; P:biological_process; P:protein metabolic process; C:plasma membrane	10	IPR001506; IPR024079; PTHR24543 (PANTHER), PTHR24543:SF85 (PANTHER), SSF55486 (SUPERFAMILY)
998	DMPC15196177_Speleonectes_tulumensis_1	ferritin	109	8.80E-40	77.80%	-	0	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
999	DMPC15196180_Speleonectes_tulumensis_1	si:dkey- protein	117	1.30E-09	60.20%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1000	DMPC15196208_Speleonectes_tulumensis_0	cg4147	108	9.00E-41	94.00%	F:nucleotide binding	1	IPR013126; G3DSA:2.60.34.10 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF100920 (SUPERFAMILY)
1001	DMPC15196224_Speleonectes_tulumensis_2	chh xo- variant 4	145	1.91E-22	74.10%	F:neuropeptide hormone activity; C:extracellular region	2	IPR001166
1002	DMPC15196317_Speleonectes_tulumensis_2	ecdysteroid-regulated protein	149	2.05E-08	58.40%	F:cholesterol binding; P:cholesterol homeostasis; C:lysosome; F:enzyme binding; P:cholesterol efflux; P:response to virus; P:intracellular cholesterol transport; C:extracellular region	8	IPR003172; IPR014756; PTHR11306 (PANTHER)

1003	DMPC15196408_Speleonectes_tulumensis_1	female neotenic-specific protein 3	140	4.61E-10	58.50%	-	0	tmhmm (TMHMM)
1004	DMPC15196428_Speleonectes_tulumensis_1	ancylostoma secreted	123	6.57E-07	51.00%	-	0	IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1005	DMPC15196459_Speleonectes_tulumensis_2	kelch-like protein 18-like	359	4.90E-73	80.40%	-	0	IPR006652; IPR015915; PR00501 (PRINTS), PTHR24414 (PANTHER), PTHR24414:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF117281 (SUPERFAMILY)
1006	DMPC15196531_Speleonectes_tulumensis_2	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphex133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein	119	1.75E-23	64.10%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PTHR11389:SF381 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
1007	DMPC15196562_Speleonectes_tulumensis_0	oocyte protease inhibitor-1 precursor	116	7.61E-11	65.40%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1008	DMPC15196615_Speleonectes_tulumensis_2	thioredoxin peroxidase	126	1.19E-62	69.00%	-	0	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF44 (PANTHER)
1009	DMPC15196698_Speleonectes_tulumensis_2	trypsin-like serine proteinase 2	133	1.56E-11	58.80%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), tmhmm (TMHMM)
1010	DMPC15196769_Speleonectes_tulumensis_2	perlucin 5	138	8.80E-12	49.70%	F:protein binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1011	DMPC15196778_Speleonectes_tulumensis_1	core 1 glycoprotein-n-acetylgalactosamine 3-beta- 1-like	93	2.58E-07	74.00%	C:Golgi cisterna membrane; C:membrane; F:transferase activity, transferring hexosyl groups; F:transferase activity, transferring glycosyl groups	4	IPR008428
1012	DMPC15196802_Speleonectes_tulumensis_2	ame: full=conoporin-cn1 flags: precursor	229	5.28E-27	52.20%	-	0	IPR009104; IPR015926
1013	DMPC15196842_Speleonectes_tulumensis_1	---NA---	128			-	0	no IPS match
1014	DMPC15196855_Speleonectes_tulumensis_1	membrane metallo-endopeptidase-like 1-like	143	1.27E-54	75.20%	-	0	IPR000718; IPR018497; IPR024079; PTHR11733:SF24 (PANTHER), tmhmm (TMHMM), SSF55486 (SUPERFAMILY)
1015	DMPC15196889_Speleonectes_tulumensis_2	trypsin 7	128	3.57E-35	72.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP)
1016	DMPC15196906_Speleonectes_tulumensis_1	lysozyme precursor	127	1.19E-09	80.00%	-	0	IPR001916; IPR023346; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER), PTHR11407:SF2 (PANTHER), tmhmm (TMHMM)
1017	DMPC15196910_Speleonectes_tulumensis_0	ubiquitin-60s ribosomal protein l40-like	125	9.15E-43	98.80%	F:peptidase activity; P:cell cycle; F:protein binding; P:cellular protein modification process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; F:catalytic activity; P:protein transport; ; C:endosome; F:nucleotide binding; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:transport	30	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)

1018	DMPC15197036_Speleonectes_tulumensis_2	serine protease inhibitor dipetalogastin precursor	157	7.35E-15	51.60%	P:proteolysis; F:peptidase activity	2	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1019	DMPC15197049_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor-like	130	1.16E-25	64.10%	-	0	IPR026645
1020	DMPC15197164_Speleonectes_tulumensis_0	hemocyanin subunit type 2 precursor	129	1.92E-70	68.60%	-	0	IPR005203; IPR013788; IPR014756
1021	DMPC15197211_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor-like	138	1.23E-13	57.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1022	DMPC15197217_Speleonectes_tulumensis_2	dermatopontin 3	103	9.50E-08	59.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1023	DMPC15197246_Speleonectes_tulumensis_0	nucleolar protein 56-like	370	2.76E-125	90.80%	-	0	IPR002687; IPR012976; PTHR10894 (PANTHER), SSF89124 (SUPERFAMILY)
1024	DMPC15197339_Speleonectes_tulumensis_0	---NA---	105			-	0	IPR002047; IPR010475; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1025	DMPC15197414_Speleonectes_tulumensis_1	trypsin 3	129	2.04E-40	80.60%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1026	DMPC15197448_Speleonectes_tulumensis_1	---NA---	155			-	0	IPR011038; IPR012674; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER)
1027	DMPC15197465_Speleonectes_tulumensis_0	dermatopontin 3	102	5.75E-08	65.29%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1028	DMPC15197503_Speleonectes_tulumensis_0	oocyte zinc finger protein 6-like	280	3.85E-28	58.90%	F:nucleic acid binding; P:biological_process; F:zinc ion binding; C:intracellular	4	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
1029	DMPC15197505_Speleonectes_tulumensis_0	---NA---	216			-	0	no IPS match
1030	DMPC15197516_Speleonectes_tulumensis_2	pacifastin light chain	130	5.10E-07	53.00%	F:peptidase inhibitor activity; P:negative regulation of peptidase activity	2	IPR008037; IPR020862; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1031	DMPC15197531_Speleonectes_tulumensis_0	ferritin subunit	104	1.98E-20	87.10%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1032	DMPC15197540_Speleonectes_tulumensis_0	protein	145	6.45E-17	58.60%	C:extracellular region	1	IPR001283; IPR014044
1033	DMPC15197605_Speleonectes_tulumensis_2	female neotenic-specific protein 3	125	6.24E-12	53.80%	-	0	no IPS match
1034	DMPC15197655_Speleonectes_tulumensis_1	superoxide dismutase mitochondrial	163	1.65E-20	79.50%	F:binding; P:metabolic process; F:catalytic activity; P:biological_process	4	IPR001189; IPR019831; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER)
1035	DMPC15197739_Speleonectes_tulumensis_0	hemocyanin subunit type 1 precursor	109	6.20E-53	69.50%	-	0	IPR005203; IPR013788; IPR014756
1036	DMPC15197740_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor	134	3.32E-12	73.80%	-	0	IPR024509; IPR024716
1037	DMPC15197932_Speleonectes_tulumensis_0	cathepsin b	273	1.86E-98	82.40%	P:protein metabolic process; P:catabolic process; P:biological_process; F:peptidase activity	4	IPR000668; IPR013128; IPR015643; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
1038	DMPC15198045_Speleonectes_tulumensis_2	hypothetical protein BRAFLDRAFT_123613	168	1.11E-26	65.80%	F:catalytic activity; P:metabolic process; P:primary metabolic process	3	IPR000945; IPR005018; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1039	DMPC15198058_Speleonectes_tulumensis_0	low quality protein: calreticulin-like	127	1.19E-46	85.40%	-	0	IPR001580; IPR008985; IPR009033; PTHR11073:SF2 (PANTHER)
1040	DMPC15198119_Speleonectes_tulumensis_0	serine 27 precursor	141	2.45E-12	63.10%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER)
1041	DMPC15198204_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	92	8.16E-51	71.00%	-	0	IPR005203; IPR013788; IPR014756
1042	DMPC15198256_Speleonectes_tulumensis_0	bone morphogenetic protein 7	116	5.62E-10	54.30%	F:growth factor activity; P:growth; C:extracellular region	3	IPR015615; PTHR11848:SF55 (PANTHER)

1043	DMPC15198322_Speleonectes_tulumensis_1	serine protease inhibitor kazal-type 6-like	106	1.35E-08	63.75%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1044	DMPC15198418_Speleonectes_tulumensis_2	kazal-type serine proteinase inhibitor 4	132	1.44E-16	56.20%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1045	DMPC15198621_Speleonectes_tulumensis_2	chitinase partial	191	5.12E-42	67.00%	-	0	IPR001223; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SSF54556 (SUPERFAMILY)
1046	DMPC15198663_Speleonectes_tulumensis_1	nidogen 1	122	4.81E-09	64.10%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1047	DMPC15198677_Speleonectes_tulumensis_2	secreted ferritin g subunit	210	5.10E-17	57.80%	P:oxidation-reduction process; P:cellular iron ion homeostasis; F:oxidoreductase activity; F:transition metal ion binding; F:ferric iron binding; P:iron ion transport	6	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; PTHR11431:SF2 (PANTHER), tmhmm (TMHMM)
1048	DMPC15198683_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor-like	137	3.21E-09	52.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1049	DMPC15198702_Speleonectes_tulumensis_2	fasciclin ii transmembrane isoform	269	7.22E-08	52.25%	-	0	IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; PTHR19831 (PANTHER), tmhmm (TMHMM), SSF48726 (SUPERFAMILY)
1050	DMPC15198730_Speleonectes_tulumensis_2	gamma-interferon-inducible lysosomal thiol reductase	158	1.94E-32	60.10%	-	0	IPR004911; PTHR13234:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP)
1051	DMPC15198749_Speleonectes_tulumensis_1	vitellogenin 1	110	6.72E-17	56.50%	-	0	IPR001846; PTHR11339 (PANTHER)
1052	DMPC15198771_Speleonectes_tulumensis_0	ame: full=carboxypeptidase b	160	1.04E-20	52.60%	P:proteolysis; F:metallocarboxypeptidase activity; F:carboxypeptidase activity; F:zinc ion binding	4	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
1053	DMPC15198800_Speleonectes_tulumensis_1	folate receptor alpha precursor	118	8.56E-17	81.80%	F:receptor activity	1	IPR004269; IPR018143; PTHR10517:SF3 (PANTHER)
1054	DMPC15198880_Speleonectes_tulumensis_1	n-acetylglucosamine-1-phosphotransferase subunit gamma precursor	113	1.67E-15	68.80%	F:transferase activity	1	PTHR12630 (PANTHER), PTHR12630:SF2 (PANTHER), PF13015 (PFAM)
1055	DMPC15198883_Speleonectes_tulumensis_1	---NA---	124			-	0	IPR008037; IPR020862; SignalP-NN(euk) (SIGNALP)
1056	DMPC15198932_Speleonectes_tulumensis_4	trypsin	157	4.91E-11	72.90%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)
1057	DMPC15199040_Speleonectes_tulumensis_1	serine protease	149	7.82E-15	62.90%	P:proteolysis; F:peptidase activity; F:metalloendopeptidase activity; F:serine-type endopeptidase activity; P:negative regulation of catalytic activity; F:identical protein binding	6	IPR007280; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1058	DMPC15199144_Speleonectes_tulumensis_0	prolyl 3-hydroxylase 2-like	132	1.11E-19	82.30%	F:binding; F:catalytic activity; P:metabolic process	3	PTHR14049 (PANTHER), PTHR14049:SF1 (PANTHER)
1059	DMPC15199174_Speleonectes_tulumensis_1	loc495415 protein	180	9.64E-56	69.60%	C:extracellular region	1	IPR001283; IPR014044; IPR018244
1060	DMPC15199238_Speleonectes_tulumensis_0	trypsin	171	3.76E-29	62.00%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)

1061	DMPC15199255_Speleonectes_tulumensis_0	60s ribosomal protein l40	149	5.49E-46	97.30%	F:peptidase activity; P:cell cycle; F:protein binding; P:cellular protein modification process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; F:catalytic activity; P:protein transport; ; C:endosome; F:nucleotide binding; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:transport	30	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1062	DMPC15199256_Speleonectes_tulumensis_2	iron zinc purple acid phosphatase-like	208	4.53E-101	81.50%	F:binding; F:hydrolase activity	2	IPR004843; IPR025733; G3DSA:3.60.21.10 (GENE3D), PTHR22953 (PANTHER), PTHR22953:SF0 (PANTHER), SSF56300 (SUPERFAMILY)
1063	DMPC15199287_Speleonectes_tulumensis_1	---NA---	148			-	0	IPR008197; PTHR19441 (PANTHER)
1064	DMPC15199438_Speleonectes_tulumensis_1	apolipophorin, putative	368	1.37E-24	50.80%	P:lipid transport; F:lipid transporter activity	2	tmhmm (TMHMM)
1065	DMPC15199471_Speleonectes_tulumensis_0	peptidyl-prolyl cis-trans isomerase e	212	1.39E-10	81.70%	-	0	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF72 (PANTHER)
1066	DMPC15199540_Speleonectes_tulumensis_0	niemann-pick type c2	130	2.68E-14	59.50%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1067	DMPC15199544_Speleonectes_tulumensis_1	muscle-specific protein 20	137	3.77E-48	75.60%	-	0	IPR001715; IPR001997; IPR003096; PTHR18959 (PANTHER)
1068	DMPC15199585_Speleonectes_tulumensis_0	---NA---	128			-	0	IPR002119; IPR009072; PTHR23430 (PANTHER), tmhmm (TMHMM)
1069	DMPC15199620_Speleonectes_tulumensis_2	chymotrypsin-like protease ctrl- partial	126	4.32E-17	57.50%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
1070	DMPC15199725_Speleonectes_tulumensis_1	seminal fluid protein isoform a	154	9.86E-13	50.60%	F:carbohydrate binding; P:multicellular organism reproduction; C:extracellular space	3	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1071	DMPC15199750_Speleonectes_tulumensis_2	ankyrin repeat domain-containing	119	6.52E-38	74.00%	F:hydrolase activity	1	IPR002110; IPR020683; PTHR24123 (PANTHER)
1072	DMPC15199758_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor	156	3.66E-30	67.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1073	DMPC15199796_Speleonectes_tulumensis_1	---NA---	487			-	0	IPR006207; tmhmm (TMHMM)
1074	DMPC15199926_Speleonectes_tulumensis_0	coatomer alpha	169	2.43E-35	76.40%	P:transport; C:Golgi apparatus; C:protein complex; C:cytoplasmic membrane-bounded vesicle; F:protein kinase activity; P:cellular protein modification process; P:organelle organization; F:transferase activity; P:protein transport; F:structural molecule activity	10	IPR010714; PTHR19876 (PANTHER)
1075	DMPC15199948_Speleonectes_tulumensis_2	deformed epidermal autoregulatory factor 1-like	148	2.33E-19	54.20%	F:DNA binding	1	IPR000770; IPR010919; IPR024119; PTHR10237:SF0 (PANTHER)
1076	DMPC15199961_Speleonectes_tulumensis_1	---NA---	124			-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

1077	DMPC15199980_Speleonectes_tulumensis_1	wingless-type mmtv integration site member 8 precursor	142	4.42E-17	63.10%	F:receptor binding; P:multicellular organismal development; P:Wnt receptor signaling pathway; C:proteinaceous extracellular matrix; C:extracellular region	5	IPR005817; tmhmm (TMHMM)
1078	DMPC15199993_Speleonectes_tulumensis_1	trypsinogen 2	209	1.61E-40	65.70%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER)
1079	DMPC15200012_Speleonectes_tulumensis_0	beta lysosomal variant	300	3.18E-45	58.30%	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process; F:cation binding; F:catalytic activity	4	IPR013781; IPR017853; PTHR10066 (PANTHER), PTHR10066:SF12 (PANTHER)
1080	DMPC15200146_Speleonectes_tulumensis_1	dermatopontin 3	101	3.01E-07	58.00%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1081	DMPC15200173_Speleonectes_tulumensis_0	low affinity immunoglobulin epsilon fc receptor	134	3.40E-14	52.80%	-	0	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER)
1082	DMPC15200280_Speleonectes_tulumensis_1	si:dkey- protein	124	4.73E-10	60.10%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1083	DMPC15200367_Speleonectes_tulumensis_0	myosin heavy chain	517	2.38E-161	91.10%	C:cytoskeleton; C:protein complex; F:motor activity	3	IPR002928; IPR009053; PTHR13140 (PANTHER), PTHR13140:SF106 (PANTHER), SignalP-NN(euk) (SIGNALP)
1084	DMPC15200438_Speleonectes_tulumensis_0	anopheles stephensi ubiquitin	133	1.82E-60	98.20%	C:cytoskeleton; C:protein complex; F:structural molecule activity; C:lipid particle; P:cellular protein modification process; P:protein metabolic process; P:catabolic process; C:ribosome; C:cytosol; P:translation	10	IPR000626; IPR001975; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1085	DMPC15200513_Speleonectes_tulumensis_0	metalloprotease	155	1.15E-07	58.22%	P:proteolysis; F:metallopeptidase activity; F:peptidase activity; F:metalloendopeptidase activity	4	no IPS match
1086	DMPC15200625_Speleonectes_tulumensis_1	PREDICTED: hypothetical protein LOC100122506	125	9.98E-21	63.10%	-	0	IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR11324 (PANTHER)
1087	DMPC15200723_Speleonectes_tulumensis_2	cysteine proteinase inhibitor precursor	115	7.62E-32	87.50%	F:enzyme regulator activity; P:protein metabolic process; P:catabolic process; F:peptidase activity	4	IPR000668; IPR013128; IPR025660; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF43 (PANTHER), SSF54001 (SUPERFAMILY)
1088	DMPC15200833_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor-like	126	2.74E-13	58.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1089	DMPC15200856_Speleonectes_tulumensis_1	plasma kallikrein	174	6.77E-19	58.40%	F:catalytic activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER)
1090	DMPC15200858_Speleonectes_tulumensis_1	26s proteasome non-atpase regulatory subunit 10 isoform 2	119	4.56E-34	69.30%	P:viral reproduction; P:cell cycle; P:metabolic process; P:regulation of biological process; C:protein complex; C:intracellular; P:biological_process; P:signal transduction; P:cell death; P:mitochondrion organization; C:cytoskeleton; ; P:response to stress; C:cytosol; C:nucleoplasm; F:protein binding; P:protein metabolic process; P:catabolic process; ; P:cell growth; P:cellular component organization; P:nucleobase-containing compound metabolic process; P:protein transport; P:cellular protein modification process	24	IPR002110; IPR020683; PTHR24199 (PANTHER), PTHR24199:SF0 (PANTHER)
1091	DMPC15200914_Speleonectes_tulumensis_2	upf0670 protein cg4666-like	222	5.20E-31	54.60%	-	0	G3DSA:3.10.129.10 (GENE3D), PTHR12475 (PANTHER), PF13279 (PFAM), tmhmm (TMHMM), SSF54637 (SUPERFAMILY)
1092	DMPC15200952_Speleonectes_tulumensis_0	serine protease	161	1.85E-12	68.30%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER)

1093	DMPC15200961_Speleonectes _tulumensis_1	chitinase 2	151	1.75E-20	66.70%	P:carbohydrate metabolic process; F:hydrolase activity	2	IPR001223; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1094	DMPC15200995_Speleonectes _tulumensis_1	immunoglobulin i-set domain containing protein	146	8.45E-11	56.30%	F:hydrolase activity	1	IPR007110; IPR013098; IPR013783; IPR020675; SSF48726 (SUPERFAMILY)
1095	DMPC15201008_Speleonectes _tulumensis_2	hemocyanin subunit type 1 precursor	142	9.21E-35	72.00%	-	0	IPR005203; IPR013788; IPR014756; SignalP-NN(euk) (SIGNALP)
1096	DMPC15201018_Speleonectes _tulumensis_2	hemocyanin subunit type 1 precursor	116	2.04E-39	70.20%	-	0	IPR005203; IPR013788; IPR014756; PTHR11511:SF4 (PANTHER)
1097	DMPC15201047_Speleonectes _tulumensis_2	---NA---	189			-	0	IPR000998; IPR008985; PTHR23282 (PANTHER)
1098	DMPC15201073_Speleonectes _tulumensis_2	heat shock 70 kda protein	402	6.42E-126	92.80%	P:protein metabolic process; F:catalytic activity; F:protein binding; F:nucleotide binding; P:response to stress; P:metabolic process	6	IPR013126; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), tmhmm (TMHMM), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY)
1099	DMPC15201214_Speleonectes _tulumensis_1	oocyte protease inhibitor-1 precursor	86	5.14E-11	65.30%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), PTHR12352:SF3 (PANTHER), SignalP-NN(euk) (SIGNALP)
1100	DMPC15201287_Speleonectes _tulumensis_1	thioredoxin peroxidase	221	1.50E-41	95.10%	P:metabolic process; F:antioxidant activity; F:catalytic activity	3	IPR012336; IPR019479; G3DSA:3.30.1020.10 (GENE3D), PTHR10681 (PANTHER), PTHR10681:SF46 (PANTHER)
1101	DMPC15201385_Speleonectes _tulumensis_0	sifa preprohormone	116	1.14E-17	74.50%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1102	DMPC15201393_Speleonectes _tulumensis_1	vitellogenin 1	95	4.11E-16	57.78%	-	0	IPR001846
1103	DMPC15201401_Speleonectes _tulumensis_1	ferritin	117	8.18E-39	78.30%	-	0	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1104	DMPC15201422_Speleonectes _tulumensis_1	group iii secreted phospholipase	301	4.31E-34	47.70%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; F:hydrolase activity	5	IPR001211; IPR016090
1105	DMPC15201518_Speleonectes _tulumensis_0	saposin-related protein	191	3.75E-60	78.50%	C:lysosome; P:lipid metabolic process	2	IPR003119; IPR007856; IPR008138; IPR008139; IPR008373; IPR011001; PTHR11480 (PANTHER), PTHR11480:SF3 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1106	DMPC15201627_Speleonectes _tulumensis_2	ankyrin isoform x	214	4.49E-72	91.00%	F:cytoskeletal protein binding; P:anatomical structure morphogenesis; P:cellular component organization; P:cell differentiation; P:multicellular organismal development; P:cytoskeleton organization; C:cell; C:cellular_component; P:signal transduction; P:cellular homeostasis; F:structural molecule activity; C:plasma membrane	12	IPR002110; IPR020683; PTHR24123 (PANTHER), PTHR24123:SF0 (PANTHER), PF13637 (PFAM)
1107	DMPC15201637_Speleonectes _tulumensis_0	apolipoprotein d	277	1.39E-32	56.30%	F:lipid binding; P:transport; F:transporter activity	3	IPR000566; IPR003057; IPR011038; IPR012674; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER)
1108	DMPC15201786_Speleonectes _tulumensis_1	cysteine-rich with egf-like domain protein 1	96	1.01E-25	66.40%	F:calcium ion binding	1	IPR006212; IPR009030; G3DSA:2.10.220.10 (GENE3D), PTHR24838 (PANTHER), PTHR24838:SF29 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1109	DMPC15201820_Speleonectes _tulumensis_1	protein	139	1.41E-19	52.90%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1110	DMPC15201842_Speleonectes _tulumensis_2	protein disulfide isomerase	231	6.62E-44	57.60%	F:catalytic activity	1	IPR012336; IPR013766; PTHR18929 (PANTHER), PTHR18929:SF32 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

1111	DMPC15201883_Speleonectes_tulumensis_0	dermatopontin 3	216	2.42E-38	59.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1112	DMPC15202148_Speleonectes_tulumensis_2	trypsin 3	230	1.56E-80	73.30%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
1113	DMPC15202254_Speleonectes_tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	128	9.84E-08	46.67%	-	0	IPR000716; IPR022339; PTHR14093:SF3 (PANTHER)
1114	DMPC15202321_Speleonectes_tulumensis_2	cathepsin l	269	3.52E-83	69.10%	P:proteolysis; F:cysteine-type peptidase activity	2	IPR000169; IPR000668; IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
1115	DMPC15202335_Speleonectes_tulumensis_0	group 3 secretory phospholipase a2	189	2.44E-54	64.00%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process	3	IPR001211; IPR016090; PTHR12253:SF5 (PANTHER)
1116	DMPC15202409_Speleonectes_tulumensis_0	isoform a	169	6.74E-20	53.10%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER)
1117	DMPC15202471_Speleonectes_tulumensis_1	pacifastin-related peptide precursor	131	7.04E-07	61.00%	-	0	IPR008037; IPR020862; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1118	DMPC15202579_Speleonectes_tulumensis_0	fertilization envelope outer layer protein	252	1.24E-14	55.00%	-	0	IPR000152; IPR000742; IPR005515; IPR013032; IPR020864; IPR023413; IPR024731; PTHR18841:SF0 (PANTHER), SSF57196 (SUPERFAMILY)
1119	DMPC15202674_Speleonectes_tulumensis_2	thioredoxin domain-containing protein 1	420	3.06E-54	83.40%	C:cytoplasm; P:anatomical structure morphogenesis; P:regulation of biological process; P:growth; P:behavior; P:reproduction; P:cellular homeostasis; P:cellular protein modification process; P:biological_process; F:catalytic activity; C:cell	11	IPR012336; IPR013766; IPR017937; PTHR18929 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1120	DMPC15202735_Speleonectes_tulumensis_1	mitochondrial manganese superoxide dismutase	109	3.17E-13	81.70%	-	0	IPR001189; IPR019831; PTHR11404:SF5 (PANTHER)
1121	DMPC15202765_Speleonectes_tulumensis_0	venom allergen 5	107	8.06E-14	66.00%	-	0	IPR001283; IPR014044
1122	DMPC15202791_Speleonectes_tulumensis_2	dnak protein	244	5.59E-99	83.60%	F:nucleotide binding; P:response to stress	2	IPR013126; G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
1123	DMPC15202815_Speleonectes_tulumensis_1	peritrophic membrane protein 2	171	1.51E-10	57.50%	P:metabolic process; F:catalytic activity	2	IPR002557; PTHR23301 (PANTHER)
1124	DMPC15202850_Speleonectes_tulumensis_0	early growth response	374	3.94E-89	65.30%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR10042 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
1125	DMPC15202861_Speleonectes_tulumensis_0	calreticulin	125	1.03E-59	91.10%	P:protein metabolic process; C:endoplasmic reticulum; F:carbohydrate binding; F:calcium ion binding; F:protein binding	5	IPR001580; IPR008985; IPR013320; IPR018124
1126	DMPC15202868_Speleonectes_tulumensis_0	h-2 class ii histocompatibility antigen gamma chain	103	3.56E-08	65.80%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER)
1127	DMPC15202906_Speleonectes_tulumensis_2	apolipoprotein o-like	325	3.05E-18	55.20%	-	0	IPR019166; PTHR14564 (PANTHER), PTHR14564:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1128	DMPC15202917_Speleonectes_tulumensis_1	pacifastin light chain	394	1.73E-15	50.50%	F:peptidase inhibitor activity; P:negative regulation of peptidase activity	2	IPR008037; IPR020862; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1129	DMPC15202972_Speleonectes_tulumensis_0	chymotrypsin-like protease ctrl- partial	116	1.20E-14	59.40%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
1130	DMPC15203130_Speleonectes_tulumensis_4	prophenol oxidase a1	99	2.94E-17	80.70%	F:catalytic activity; P:metabolic process	2	IPR000896; IPR008922; IPR013788; PTHR11511:SF4 (PANTHER)

1131	DMPC15203147_Speleonectes _tulumensis_0	predicted protein	363	2.76E-07	44.00%	P:proteolysis; F:serine-type endopeptidase activity; F:serine-type peptidase activity; F:hydrolase activity; F:catalytic activity; F:peptidase activity	6	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D)
1132	DMPC15203182_Speleonectes _tulumensis_2	secreted frizzled-related protein 4	168	2.47E-21	53.80%	P:metabolic process; P:multicellular organismal development; P:transport; P:regulation of biological process; P:signal transduction; C:extracellular region; C:intracellular; P:cellular component organization; P:cell differentiation; P:response to endogenous stimulus	10	IPR015526; IPR020067; IPR026556
1133	DMPC15203191_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor-like	138	1.89E-22	61.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1134	DMPC15203197_Speleonectes _tulumensis_1	mam-containing astacin-like metalloprotease	130	6.98E-07	48.00%	-	0	IPR001506; IPR024079; PTHR10127 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF55486 (SUPERFAMILY)
1135	DMPC15203234_Speleonectes _tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	136	8.75E-11	60.00%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1136	DMPC15203259_Speleonectes _tulumensis_1	serine protease	129	1.08E-19	68.90%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24252 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1137	DMPC15203296_Speleonectes _tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	112	1.29E-10	56.50%	P:proteolysis; F:peptidase activity; F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	6	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1138	DMPC15203384_Speleonectes _tulumensis_1	---NA---	144			-	0	IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1139	DMPC15203398_Speleonectes _tulumensis_0	chorion peroxidase	121	6.08E-20	63.90%	P:oxidation-reduction process; F:heme binding; F:oxidoreductase activity; P:response to oxidative stress; F:peroxidase activity	5	IPR002007; IPR010255; PTHR11475 (PANTHER)
1140	DMPC15203413_Speleonectes _tulumensis_2	phospholipase a2	132	9.65E-20	64.50%	F:hydrolase activity; P:lipid metabolic process	2	IPR001211; IPR013090; IPR016090; SignalP-NN(euk) (SIGNALP)
1141	DMPC15203568_Speleonectes _tulumensis_1	60s ribosomal protein l40	132	1.03E-42	94.40%	P:cell cycle; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:cellular protein modification process; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:transport	27	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
1142	DMPC15203595_Speleonectes _tulumensis_1	isoform c	97	2.69E-49	96.60%	P:protein metabolic process; P:catabolic process; F:peptidase activity; C:plasma membrane	4	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24258 (PANTHER), PTHR24258:SF3 (PANTHER)
1143	DMPC15203661_Speleonectes _tulumensis_1	anopheles stephensi ubiquitin	134	2.97E-80	96.50%	C:cytoskeleton; C:protein complex; F:structural molecule activity; C:lipid particle; P:cellular protein modification process; P:protein metabolic process; P:catabolic process; C:ribosome; C:cytosol; P:translation	10	IPR000626; IPR001975; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)

1144	DMPC15203713_Speleonectes_tulumensis_1	cyclophilin 1	132	1.20E-38	85.80%	C:cytosol; C:cytoskeleton; C:protein complex; P:cellular protein modification process; P:protein metabolic process; F:enzyme regulator activity; P:anatomical structure morphogenesis; P:multicellular organismal development; P:cell death; C:nucleus; F:catalytic activity; C:nucleoplasm	12	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), SignalP-NN(euk) (SIGNALP)
1145	DMPC15203722_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_315125	153	4.28E-09	50.50%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1146	DMPC15203781_Speleonectes_tulumensis_1	lectin e	152	1.15E-08	59.00%	-	0	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER)
1147	DMPC15203812_Speleonectes_tulumensis_2	isoform a	198	1.22E-25	57.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER)
1148	DMPC15203872_Speleonectes_tulumensis_0	trypsinogen 2	104	1.58E-24	67.60%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24257 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1149	DMPC15204079_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	107	3.96E-08	59.40%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1150	DMPC15204127_Speleonectes_tulumensis_1	dermatopontin 2	139	7.64E-18	60.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1151	DMPC15204163_Speleonectes_tulumensis_1	peptidase s8 and sedolisin	170	1.54E-22	68.50%	F:peptidase activity	1	IPR007280; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1152	DMPC15204200_Speleonectes_tulumensis_0	zinc finger	119	1.09E-19	64.60%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PF13465 (PFAM), PF13894 (PFAM), SSF57667 (SUPERFAMILY)
1153	DMPC15204207_Speleonectes_tulumensis_2	glutaminyl-peptide cyclotransferase	118	4.79E-35	71.00%	P:proteolysis; F:peptidase activity	2	IPR007484; G3DSA:3.40.630.10 (GENE3D), PTHR12283 (PANTHER), PTHR12283:SF0 (PANTHER), SSF53187 (SUPERFAMILY)
1154	DMPC15204375_Speleonectes_tulumensis_2	protein lec- isoform b	306	9.58E-31	52.00%	F:binding	1	IPR001079; IPR008985; IPR013320; PTHR11346 (PANTHER)
1155	DMPC15204408_Speleonectes_tulumensis_1	subfamily member 9	142	8.61E-42	80.70%	P:protein metabolic process; F:protein binding	2	IPR001623; IPR018253; PTHR24078 (PANTHER), PTHR24078:SF16 (PANTHER)
1156	DMPC15204492_Speleonectes_tulumensis_0	pancreatic triacylglycerol lipase-like	260	1.81E-59	59.70%	P:lipid metabolic process; F:hydrolase activity; F:catalytic activity; F:triglyceride lipase activity; C:extracellular region	5	IPR000734; IPR013818; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
1157	DMPC15204499_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	144	1.34E-21	67.60%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1158	DMPC15204519_Speleonectes_tulumensis_2	nucleobindin 1	171	2.77E-35	67.40%	-	0	PTHR19237 (PANTHER), SignalP-NN(euk) (SIGNALP)
1159	DMPC15204534_Speleonectes_tulumensis_1	ecdysteroid-regulated protein	153	2.58E-26	58.10%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
1160	DMPC15204565_Speleonectes_tulumensis_2	dnak protein	188	9.53E-17	84.50%	P:protein metabolic process; F:protein binding; F:nucleotide binding	3	IPR013126; IPR018181; G3DSA:3.30.420.40 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53067 (SUPERFAMILY)
1161	DMPC15204578_Speleonectes_tulumensis_2	g-protein coupled receptor mth2-like	283	6.63E-41	58.20%	F:transmembrane signaling receptor activity; F:receptor activity; C:integral to membrane; F:G-protein coupled receptor activity; C:membrane; P:cell surface receptor signaling pathway; P:G-protein coupled receptor signaling pathway	7	IPR000832; IPR017981; PTHR12011 (PANTHER), PTHR12011:SF12 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1162	DMPC15204727_Speleonectes_tulumensis_2	annexin x	158	3.36E-25	80.80%	F:calcium ion binding; F:lipid binding	2	IPR001464; IPR018252; IPR018502; tmhmm (TMHMM)

1163	DMPC15204768_Speleonectes_tulumensis_2	carboxypeptidase b-like	169	1.46E-45	64.50%	-	0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
1164	DMPC15204769_Speleonectes_tulumensis_1	ame: full=conoporin-cn1 flags: precursor	127	6.18E-14	56.00%	-	0	IPR015926
1165	DMPC15204845_Speleonectes_tulumensis_0	ferritin-1 heavy chain	91	1.02E-19	91.00%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1166	DMPC15204917_Speleonectes_tulumensis_0	ubiquitin ribosomal protein s27a fusion protein	157	2.71E-70	96.90%	-	0	IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1167	DMPC15205076_Speleonectes_tulumensis_0	hemocyanin subunit type 2 precursor	180	5.49E-121	71.00%	-	0	IPR005203; IPR013788; IPR014756
1168	DMPC15205089_Speleonectes_tulumensis_2	niemann-pick type c2	122	2.45E-25	57.60%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER)
1169	DMPC15205307_Speleonectes_tulumensis_1	si:dkey- protein	120	1.78E-13	57.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1170	DMPC15205316_Speleonectes_tulumensis_2	hemocyanin subunit 1	155	2.02E-38	68.80%	-	0	IPR005203; IPR013788; IPR014756
1171	DMPC15205361_Speleonectes_tulumensis_4	apolipoprotein a-i-binding	98	1.55E-30	76.20%	F:binding; F:catalytic activity; F:nucleotide binding	3	IPR004443; PTHR13232 (PANTHER)
1172	DMPC15205374_Speleonectes_tulumensis_2	protein disulfide-isomerase a6-like	153	6.04E-48	81.00%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR005788; IPR012336; IPR013766; IPR017937; PTHR18929 (PANTHER)
1173	DMPC15205380_Speleonectes_tulumensis_0	glutathione peroxidase 4 (phospholipid hydroperoxidase)	378	2.81E-33	82.50%	P:response to stress; P:lipid metabolic process; P:multicellular organismal development; F:catalytic activity; F:antioxidant activity; C:mitochondrion; P:metabolic process	7	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
1174	DMPC15205622_Speleonectes_tulumensis_1	plasminogen activator spa	137	1.54E-18	56.50%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24250 (PANTHER), SignalP-NN(euk) (SIGNALP)
1175	DMPC15205653_Speleonectes_tulumensis_1	kazal-type serine proteinase inhibitor 4	113	2.77E-12	55.60%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR25189 (PANTHER), PTHR25189:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1176	DMPC15205673_Speleonectes_tulumensis_2	angiotensin-converting enzyme-like	231	1.39E-41	68.90%	-	0	IPR001548; IPR002000; PTHR10514:SF16 (PANTHER), tmhmm (TMHMM), SSF55486 (SUPERFAMILY)
1177	DMPC15205704_Speleonectes_tulumensis_1	mhc class ii-associated invariant chain	116	3.64E-08	67.00%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1178	DMPC15205735_Speleonectes_tulumensis_2	angiotensin converting enzyme	130	6.59E-45	76.70%	-	0	IPR001548; PTHR10514:SF16 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF55486 (SUPERFAMILY)
1179	DMPC15205911_Speleonectes_tulumensis_1	serine protease 56-like	252	7.14E-10	50.50%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24261 (PANTHER), PTHR24261:SF9 (PANTHER)
1180	DMPC15205922_Speleonectes_tulumensis_0	pancreatic triacylglycerol lipase-like	141	1.85E-10	58.10%	P:lipid metabolic process; F:hydrolase activity; F:catalytic activity; C:extracellular region	4	IPR000734; IPR013818; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
1181	DMPC15205978_Speleonectes_tulumensis_5	---NA---	270			-	0	no IPS match
1182	DMPC15205989_Speleonectes_tulumensis_0	sifa preprohormone	154	2.10E-17	74.50%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1183	DMPC15205992_Speleonectes_tulumensis_2	urokinase-type plasminogen activator precursor	150	1.46E-07	68.50%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
1184	DMPC15205994_Speleonectes_tulumensis_1	---NA---	128			-	0	IPR000010; G3DSA:3.10.450.10 (GENE3D), SignalP-NN(euk) (SIGNALP), SSF54403 (SUPERFAMILY)

1185	DMPC15206045_Speleonectes _tulumensis_1	60s ribosomal protein l40	122	5.02E-42	96.70%	P:cell cycle; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; C:cytosol; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; C:plasma membrane; ; C:endosome; P:cellular component organization; C:ribosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; P:cellular protein modification process; P:translation; P:transport	25	IPR000626; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1186	DMPC15206124_Speleonectes _tulumensis_1	glyceraldhyde-3-phosphate dehydrogenase	124	4.59E-38	93.20%	-	0	IPR016040; IPR020828; IPR020829; IPR020830; IPR020831; G3DSA:3.30.360.10 (GENE3D), tmhmm (TMHMM), SSF51735 (SUPERFAMILY)
1187	DMPC15206248_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor isoform 7	136	5.62E-18	65.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1188	DMPC15206289_Speleonectes _tulumensis_1	fibrinolytic enzyme	125	2.02E-16	59.20%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
1189	DMPC15206304_Speleonectes _tulumensis_1	soma ferritin	106	6.98E-23	87.30%	-	0	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1190	DMPC15206313_Speleonectes _tulumensis_2	glutathione peroxidase	150	2.41E-18	86.60%	-	0	IPR000889; IPR012336; tmhmm (TMHMM)
1191	DMPC15206345_Speleonectes _tulumensis_1	suppressor of tumorigenicity protein 14	302	5.94E-39	51.80%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), G3DSA:4.10.1220.10 (GENE3D), PTHR24265 (PANTHER)
1192	DMPC15206400_Speleonectes _tulumensis_1	copper chaperone for superoxide dismutase	138	5.31E-55	79.20%	-	0	IPR001424; IPR018152; IPR024134
1193	DMPC15206401_Speleonectes _tulumensis_0	selenium-dependent glutathione peroxidase	131	6.36E-27	62.50%	-	0	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
1194	DMPC15206420_Speleonectes _tulumensis_0	hypothetical protein DAPPUDRAFT_332702	199	1.20E-49	64.80%	-	0	IPR015255; IPR015817; IPR015819; PTHR13769 (PANTHER)
1195	DMPC15206429_Speleonectes _tulumensis_2	trypsin 3	125	2.38E-35	75.90%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1196	DMPC15206441_Speleonectes _tulumensis_1	peptidyl-glycine alpha-amidating monooxygenase	230	8.09E-17	61.20%	F:peptidylglycine monooxygenase activity; P:oxidation-reduction process; P:peptide metabolic process; F:copper ion binding; C:membrane; F:monooxygenase activity	6	IPR011042; PTHR10680 (PANTHER), PTHR10680:SF11 (PANTHER)
1197	DMPC15206443_Speleonectes _tulumensis_2	dermatopontin 3	135	2.18E-09	63.78%	-	0	IPR026645; tmhmm (TMHMM)
1198	DMPC15206479_Speleonectes _tulumensis_0	nidogen 1	78	1.40E-10	65.90%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1199	DMPC15206554_Speleonectes _tulumensis_1	carboxypeptidase b-like	159	5.51E-39	78.60%	-	0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
1200	DMPC15206585_Speleonectes _tulumensis_1	hypothetical protein DAPPUDRAFT_312473	151	2.36E-08	68.67%	-	0	IPR014044; tmhmm (TMHMM)
1201	DMPC15206658_Speleonectes _tulumensis_2	ferritin 3-like protein	145	2.27E-22	77.60%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1202	DMPC15206695_Speleonectes _tulumensis_1	soma ferritin	115	4.38E-33	87.50%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347

1203	DMPC15206773_Speleonectes _tulumensis_3	vitellogenin 1	302	1.04E-41	53.10%	-	0	IPR001747; IPR011030; PTHR23345 (PANTHER)
1204	DMPC15206871_Speleonectes _tulumensis_0	thioredoxin peroxidase	131	9.30E-36	80.10%	P:metabolic process; F:catalytic activity; F:antioxidant activity	3	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF46 (PANTHER), SignalP-NN(euk) (SIGNALP)
1205	DMPC15206884_Speleonectes _tulumensis_3	dipeptidyl peptidase 4	195	4.70E-31	75.80%	-	0	G3DSA:2.140.10.30 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF23 (PANTHER), tmhmm (TMHMM)
1206	DMPC15206979_Speleonectes _tulumensis_1	endoglycoceramidase-like protein	156	2.04E-22	64.40%	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process; F:cation binding; F:catalytic activity	4	IPR001547; IPR013781; IPR017853; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1207	DMPC15207021_Speleonectes _tulumensis_2	si:dkey- protein	97	4.91E-08	64.80%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
1208	DMPC15207092_Speleonectes _tulumensis_0	serine protease precursor	149	4.80E-16	58.80%	P:proteolysis; F:serine-type endopeptidase activity; P:negative regulation of catalytic activity; F:identical protein binding	4	IPR007280; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1209	DMPC15207161_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor	178	7.36E-30	60.50%	-	0	IPR026645
1210	DMPC15207163_Speleonectes _tulumensis_2	aldo-keto reductase	114	1.94E-21	76.70%	P:oxidation-reduction process; F:oxidoreductase activity; C:cellular_component	3	IPR001395; IPR023210; PTHR11732:SF34 (PANTHER)
1211	DMPC15207250_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor-like	141	2.01E-22	59.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
1212	DMPC15207398_Speleonectes _tulumensis_1	low quality protein: hemicentin-2	96	7.68E-08	55.20%	-	0	IPR007110; IPR013098; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF25 (PANTHER), SSF48726 (SUPERFAMILY)
1213	DMPC15207466_Speleonectes _tulumensis_0	oocyte protease inhibitor-2 precursor	125	7.17E-14	48.90%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1214	DMPC15207498_Speleonectes _tulumensis_2	peptidyl-prolyl cis-trans isomerase cyp20-3	141	1.34E-35	63.40%	P:regulation of biological process; P:ion transport; P:generation of precursor metabolites and energy; P:response to abiotic stimulus; C:plastid; C:extracellular region; P:biological_process; F:protein binding; P:biosynthetic process; P:protein transport; P:lipid metabolic process; C:ribosome; C:organelle; C:thylakoid; P:carbohydrate metabolic process; P:metabolic process; P:response to stress; P:catabolic process; ; P:secondary metabolic process; P:response to biotic stimulus; P:anatomical structure morphogenesis; P:multicellular organismal development; P:cell differentiation; F:catalytic activity; P:response to endogenous stimulus; ; P:cellular protein modification process; P:nucleobase-containing compound metabolic process	29	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER)
1215	DMPC15207540_Speleonectes _tulumensis_0	apolipoprotein d	119	7.26E-16	61.30%	-	0	IPR011038; IPR012674; IPR022272; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1216	DMPC15207574_Speleonectes _tulumensis_0	blastula protease 10	152	2.61E-08	58.40%	-	0	IPR001506; IPR024079; PTHR24543 (PANTHER), PTHR24543:SF85 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF55486 (SUPERFAMILY)
1217	DMPC15207606_Speleonectes _tulumensis_2	---NA---	108			-	0	SignalP-NN(euk) (SIGNALP)

1218	DMPC15207643_Speleonectes_tulumensis_0	serine carboxypeptidase family protein	194	7.90E-56	64.70%	F:hydrolase activity	1	IPR001563; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF6 (PANTHER), SSF53474 (SUPERFAMILY)
1219	DMPC15207671_Speleonectes_tulumensis_2	apolipoprotein d-like isoform 1	155	1.82E-41	63.30%	F:lipid binding; P:transport; F:transporter activity	3	IPR011038; IPR012674; IPR022272; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP)
1220	DMPC15207731_Speleonectes_tulumensis_0	glutathione peroxidase 6	113	3.32E-09	71.33%	F:catalytic activity; F:antioxidant activity	2	IPR000889; IPR012336
1221	DMPC15207750_Speleonectes_tulumensis_1	saxiphilin precursor	112	7.90E-11	66.20%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1222	DMPC15207755_Speleonectes_tulumensis_2	serine proteinase stubble-like	144	8.10E-21	63.60%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER)
1223	DMPC15207759_Speleonectes_tulumensis_1	egf-like domain-containing	147	5.94E-30	65.30%	F:catalytic activity	1	IPR000742; IPR013032; G3DSA:2.170.300.10 (GENE3D), PTHR24035 (PANTHER), PTHR24035:SF3 (PANTHER)
1224	DMPC15207788_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor-like	137	2.58E-15	56.60%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1225	DMPC15207925_Speleonectes_tulumensis_0	zinc finger protein 235	136	1.47E-12	54.40%	F:metal ion binding; P:regulation of transcription, DNA-dependent; F:nucleic acid binding; P:biological_process; F:zinc ion binding; C:intracellular	6	IPR007087; IPR015880; PTHR11389 (PANTHER), PTHR11389:SF378 (PANTHER), PF13465 (PFAM), PF13894 (PFAM), SSF57667 (SUPERFAMILY)
1226	DMPC15207991_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	126	4.91E-15	50.20%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1227	DMPC15208111_Speleonectes_tulumensis_0	---NA---	145			-	0	IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1228	DMPC15208150_Speleonectes_tulumensis_1	pancreatic lipase related protein 1	200	2.47E-47	63.50%	C:extracellular space; F:binding; P:multicellular organismal development; F:hydrolase activity; P:response to endogenous stimulus; F:protein binding; P:metabolic process	7	IPR000734; IPR002331; IPR013818; G3DSA:3.40.50.1820 (GENE3D), SignalP-NN(euk) (SIGNALP), SSF53474 (SUPERFAMILY)
1229	DMPC15208190_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor-like	112	8.13E-09	62.90%	-	0	IPR026645
1230	DMPC15208192_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	108	1.58E-07	58.00%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1231	DMPC15208217_Speleonectes_tulumensis_2	PREDICTED: uncharacterized protein LOC100175254	524	4.91E-10	40.00%	-	0	IPR000436; G3DSA:2.10.70.10 (GENE3D), PTHR19325 (PANTHER), tmhmm (TMHMM)
1232	DMPC15208247_Speleonectes_tulumensis_1	ferritin 3-like protein	122	1.00E-23	76.40%	F:binding	1	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1233	DMPC15208329_Speleonectes_tulumensis_0	peroxisomal trans-2-enoyl- reductase-like	190	1.93E-57	74.20%	P:metabolic process; F:catalytic activity	2	IPR002198; IPR002347; IPR016040; PTHR24317 (PANTHER), PTHR24317:SF0 (PANTHER), SSF51735 (SUPERFAMILY)
1234	DMPC15208350_Speleonectes_tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	148	1.31E-21	53.30%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1235	DMPC15208430_Speleonectes_tulumensis_2	serine protease	161	2.45E-11	69.90%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
1236	DMPC15208434_Speleonectes_tulumensis_2	parkinson disease 7 domain-containing	108	6.04E-35	74.00%	C:extracellular region	1	G3DSA:3.40.50.880 (GENE3D), PTHR31141 (PANTHER)
1237	DMPC15208443_Speleonectes_tulumensis_2	---NA---	42			-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER)
1238	DMPC15208449_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor isoform 7	149	1.13E-25	71.90%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1239	DMPC15208616_Speleonectes_tulumensis_1	kazal-type serine proteinase inhibitor 4	95	5.23E-10	55.70%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
1240	DMPC15208690_Speleonectes_tulumensis_2	14-3-3 zeta	114	3.21E-16	81.70%	-	0	IPR000308; IPR023410; PTHR18860:SF0 (PANTHER)

1241	DMPC15208693_Speleonectes_tulumensis_0	hla class ii histocompatibility antigen gamma chain-like isoform 2	161	2.78E-10	63.50%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER)
1242	DMPC15208702_Speleonectes_tulumensis_2	pdgf- and vegf-related factor 1-like precursor	197	1.66E-37	56.90%	F:growth factor activity; P:positive regulation of cell division; C:membrane	3	IPR000072; G3DSA:2.10.90.10 (GENE3D), PTHR11633 (PANTHER), PTHR11633:SF4 (PANTHER), SSF57501 (SUPERFAMILY)
1243	DMPC15208731_Speleonectes_tulumensis_1	dermatopontin 2	125	7.01E-13	57.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1244	DMPC15208778_Speleonectes_tulumensis_2	---NA---	144			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1245	DMPC15208783_Speleonectes_tulumensis_2	mitochondrial import inner membrane translocase subunit	118	2.62E-43	84.50%	F:binding; P:mitochondrion organization; P:protein transport; C:mitochondrion; C:protein complex	5	IPR004217; PTHR19338 (PANTHER)
1246	DMPC15208879_Speleonectes_tulumensis_1	epidermal retinol dehydrogenase 2	109	1.74E-17	76.70%	P:metabolic process; F:catalytic activity; F:nucleotide binding	3	IPR016040; PTHR24316 (PANTHER), PTHR24316:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF51735 (SUPERFAMILY)
1247	DMPC15208930_Speleonectes_tulumensis_1	ale o 1 allergen	154	4.07E-74	80.40%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1248	DMPC15208956_Speleonectes_tulumensis_0	5 -nucleotidase-like	115	8.29E-37	73.00%	-	0	IPR006179; IPR008334; PTHR11575:SF7 (PANTHER)
1249	DMPC15208958_Speleonectes_tulumensis_1	neutral alpha-glucosidase ab	148	3.88E-27	74.30%	F:carbohydrate binding; P:carbohydrate metabolic process; F:hydrolase activity	3	IPR000322; PTHR22762:SF7 (PANTHER), SSF51011 (SUPERFAMILY)
1250	DMPC15208986_Speleonectes_tulumensis_1	serine protease inhibitor kazal-type 6-like	135	6.97E-09	67.33%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF100895 (SUPERFAMILY)
1251	DMPC15209000_Speleonectes_tulumensis_0	fibroblast growth factor receptor 3-iiic	114	2.44E-13	70.10%	P:anatomical structure morphogenesis; P:cellular component organization; P:cell differentiation; P:multicellular organismal development; P:signal transduction; P:response to endogenous stimulus; C:extracellular region; C:intracellular; P:biological_process; P:cellular protein modification process; P:embryo development; F:carbohydrate binding; P:regulation of biological process; P:cell proliferation; P:metabolic process; F:receptor activity; F:protein kinase activity; F:protein binding; C:plasma membrane	19	IPR013783; PTHR24416 (PANTHER), PTHR24416:SF131 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF48726 (SUPERFAMILY)
1252	DMPC15209010_Speleonectes_tulumensis_1	epididymal secretory protein e1	155	1.86E-11	65.00%	P:transport; F:binding; C:intracellular	3	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1253	DMPC15209033_Speleonectes_tulumensis_1	epididymal secretory protein e1	128	4.30E-19	60.50%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
1254	DMPC15209059_Speleonectes_tulumensis_5	glutathione peroxidase 1	131	1.25E-19	83.00%	-	0	IPR000889; IPR012336; tmhmm (TMHMM)
1255	DMPC15209130_Speleonectes_tulumensis_2	sulfakinin-like peptide	186	4.21E-13	65.80%	C:extracellular region	1	IPR013152
1256	DMPC15209181_Speleonectes_tulumensis_1	histone h2a	258	1.22E-74	92.70%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)
1257	DMPC15209224_Speleonectes_tulumensis_1	clotting factor b-like	258	5.37E-18	55.00%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
1258	DMPC15209238_Speleonectes_tulumensis_1	prophenoloxidase activating factor	122	3.86E-42	72.40%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF68 (PANTHER)

1259	DMPC15209294_Speleonectes_tulumensis_1	enolase	173	2.20E-105	90.60%	C:cytosol; C:protein complex; F:catalytic activity; F:binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process	7	IPR000941; IPR020809; IPR020810; G3DSA:3.20.20.120 (GENE3D), SSF51604 (SUPERFAMILY)
1260	DMPC15209303_Speleonectes_tulumensis_1	protein creg2-like	189	1.33E-15	71.60%	P:oxidation-reduction process; F:oxidoreductase activity; F:FMN binding; C:cellular_component	4	IPR012349; PTHR13343 (PANTHER), PTHR13343:SF4 (PANTHER), PF13883 (PFAM)
1261	DMPC15209322_Speleonectes_tulumensis_0	serine proteinase	122	5.69E-13	53.60%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
1262	DMPC15209372_Speleonectes_tulumensis_2	epididymal secretory protein e1 precursor	149	2.80E-17	58.00%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
1263	DMPC15209398_Speleonectes_tulumensis_2	sortilin-related receptor	154	2.32E-13	46.40%	F:low-density lipoprotein particle binding; C:integral to membrane; C:membrane; P:lipid metabolic process; P:lipid transport; P:endocytosis; P:transport; C:perinuclear region of cytoplasm; P:multicellular organismal development; C:low-density lipoprotein particle; F:receptor activity; F:protein binding; P:cholesterol metabolic process; P:steroid metabolic process	14	IPR002172; IPR023415; PR00261 (PRINTS), PTHR12106 (PANTHER), PTHR12106:SF7 (PANTHER)
1264	DMPC15209399_Speleonectes_tulumensis_1	si:dkey- protein	106	2.25E-09	61.33%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1265	DMPC15209466_Speleonectes_tulumensis_1	seminal fluid protein isoform a	147	3.25E-12	49.80%	F:carbohydrate binding; P:multicellular organism reproduction; C:extracellular space	3	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1266	DMPC15209478_Speleonectes_tulumensis_0	carboxypeptidase a	118	4.07E-17	65.50%	C:extracellular region; F:peptidase activity	2	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
1267	DMPC15209524_Speleonectes_tulumensis_2	ubiquitin-40s ribosomal protein s27a-like	119	4.35E-42	95.00%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1268	DMPC15209537_Speleonectes_tulumensis_0	alpha-carbonic anhydrase	177	4.99E-37	64.80%	-	0	IPR001148; IPR023561
1269	DMPC15209538_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor	258	2.32E-23	67.30%	-	0	IPR026645
1270	DMPC15209581_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	155	7.20E-82	69.10%	-	0	IPR005203; IPR013788; IPR014756
1271	DMPC15209670_Speleonectes_tulumensis_2	molecular chaperone	172	3.10E-60	84.90%	P:protein metabolic process; F:protein binding; F:nucleotide binding; P:response to stress	4	IPR013126; G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
1272	DMPC15209688_Speleonectes_tulumensis_2	serine protease	119	4.53E-10	61.00%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP)
1273	DMPC15209708_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	135	7.50E-14	60.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1274	DMPC15209756_Speleonectes_tulumensis_0	clotting factor b-like	340	7.59E-47	53.90%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
1275	DMPC15209768_Speleonectes_tulumensis_0	low-density lipoprotein receptor-related protein 2-like	287	7.82E-09	64.20%	F:calcium ion binding; C:integral to membrane; C:membrane	3	IPR002172; IPR023415; PTHR10529 (PANTHER), PTHR10529:SF151 (PANTHER), tmhmm (TMHMM)

1276	DMPC15209776_Speleonectes _tulumensis_1	late trypsin	319	6.16E-39	57.80%	F:catalytic activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP)
1277	DMPC15209896_Speleonectes _tulumensis_2	fasciclin-like protein precursor	155	4.04E-19	57.33%	-	0	IPR000782; PTHR10900 (PANTHER)
1278	DMPC15209971_Speleonectes _tulumensis_0	cd74 antigen (invariant polypeptide of major histocompatibility class ii antigen-associated) isoform cra_d	124	4.57E-10	72.40%	P:cellular component organization; P:regulation of biological process; P:cell proliferation; C:endosome; F:protein binding; C:lysosome; P:cell death; P:signal transduction; F:receptor binding; C:endoplasmic reticulum; P:cell differentiation; P:multicellular organismal development; P:response to stress; P:protein metabolic process; P:biological_process; P:cellular protein modification process; P:biosynthetic process; P:lipid metabolic process; F:receptor activity; C:cell; P:protein transport; C:Golgi apparatus; C:plasma membrane; P:behavior; P:response to external stimulus; C:protein complex; P:transport; F:enzyme regulator activity	28	IPR000716; IPR022339
1279	DMPC15210070_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor	137	5.41E-16	60.20%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1280	DMPC15210130_Speleonectes _tulumensis_0	PREDICTED: similar to harmonin	226	2.75E-37	70.50%	-	0	IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR23116 (PANTHER), PTHR23116:SF12 (PANTHER)
1281	DMPC15210193_Speleonectes _tulumensis_2	cathepsin l	141	1.02E-66	79.60%	-	0	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1282	DMPC15210220_Speleonectes _tulumensis_0	---NA---	87			-	0	G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1283	DMPC15210247_Speleonectes _tulumensis_0	cytosolic non-specific dipeptidase	145	1.33E-60	82.20%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR011650; G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF15 (PANTHER)
1284	DMPC15210250_Speleonectes _tulumensis_2	clotting factor g beta subunit precursor	215	9.06E-17	60.50%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
1285	DMPC15210290_Speleonectes _tulumensis_1	ecdysteroid-regulated protein	191	4.87E-30	59.50%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
1286	DMPC15210322_Speleonectes _tulumensis_0	26kda protease	263	5.66E-45	58.80%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER)
1287	DMPC15210394_Speleonectes _tulumensis_0	adhesive plaque matrix protein	163	7.04E-17	55.00%	-	0	SignalP-NN(euk) (SIGNALP)
1288	DMPC15210450_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor	137	8.83E-11	55.40%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1289	DMPC15210489_Speleonectes _tulumensis_1	protein disulfide isomerase	278	7.78E-39	87.00%	F:electron carrier activity; P:cellular homeostasis; P:regulation of biological process; P:metabolic process; F:catalytic activity; F:transferase activity; C:endoplasmic reticulum	7	IPR005746; IPR005788; IPR012336; IPR013766; IPR017937; PTHR18929 (PANTHER), PTHR18929:SF32 (PANTHER)
1290	DMPC15210503_Speleonectes _tulumensis_0	myosin heavy chain	124	6.04E-38	89.00%	-	0	IPR002928; PTHR13140 (PANTHER), PTHR13140:SF106 (PANTHER)
1291	DMPC15210620_Speleonectes _tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	133	1.43E-16	53.20%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1292	DMPC15210733_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor isoform 7	146	3.03E-20	63.70%	-	0	IPR024509; IPR024716

1293	DMPC15210821_Speleonectes_tulumensis_0	adp-ribosylation factor-like protein 1-like	128	9.45E-65	99.10%	C:intracellular; F:nucleotide binding; P:signal transduction	3	IPR005225; IPR006689; IPR024156; IPR027417; G3DSA:3.40.50.300 (GENE3D), PTHR11711 (PANTHER), PTHR11711:SF41 (PANTHER)
1294	DMPC15210925_Speleonectes_tulumensis_1	cathepsin l	608	6.08E-129	71.90%	-	0	IPR000169; IPR000668; IPR013128; IPR013201; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
1295	DMPC15210948_Speleonectes_tulumensis_1	female neotenic-specific protein 3	144	6.48E-11	55.14%	-	0	no IPS match
1296	DMPC15211036_Speleonectes_tulumensis_0	neutral ceramidase	307	4.56E-25	61.20%	-	0	IPR006823
1297	DMPC15211084_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor-like	113	4.06E-11	61.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1298	DMPC15211093_Speleonectes_tulumensis_1	dehydrogenase reductase sdr family member 11-like	159	7.79E-30	76.10%	P:metabolic process	1	IPR002347; IPR016040; PTHR24322 (PANTHER), PTHR24322:SF7 (PANTHER), SSF51735 (SUPERFAMILY)
1299	DMPC15211133_Speleonectes_tulumensis_1	serine protease	129	1.75E-20	65.10%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1300	DMPC15211354_Speleonectes_tulumensis_2	kallikrein-2 isoform 1	125	1.60E-13	54.90%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER), SignalP-NN(euk) (SIGNALP)
1301	DMPC15211502_Speleonectes_tulumensis_2	hyaluronan-binding protein 2-like	115	4.42E-12	53.80%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1302	DMPC15211617_Speleonectes_tulumensis_2	---NA---	427			-	0	IPR001304; IPR016186; IPR016187; IPR018378; PTHR22802 (PANTHER), tmhmm (TMHMM)
1303	DMPC15211627_Speleonectes_tulumensis_0	prepronuropeptide f i	128	3.95E-18	65.00%	-	0	IPR001955; IPR020392; tmhmm (TMHMM)
1304	DMPC15211739_Speleonectes_tulumensis_0	soma ferritin	108	8.44E-30	88.40%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1305	DMPC15211791_Speleonectes_tulumensis_2	frizzled-related protein 2	122	2.38E-27	77.30%	C:extracellular region; P:multicellular organismal development; P:signal transduction	3	IPR015526; IPR020067; IPR026559; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1306	DMPC15211793_Speleonectes_tulumensis_2	trypsin 7	157	7.18E-30	75.80%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1307	DMPC15211927_Speleonectes_tulumensis_1	hyaluronidase precursor	158	1.07E-22	59.20%	F:catalytic activity	1	IPR013785; IPR017853; IPR018155; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1308	DMPC15211978_Speleonectes_tulumensis_2	soma ferritin	111	3.07E-31	88.40%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1309	DMPC15212018_Speleonectes_tulumensis_1	plasminogen activator spa	328	7.17E-69	57.70%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1310	DMPC15212051_Speleonectes_tulumensis_2	phospholipase a2-like	141	6.01E-15	62.80%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; C:extracellular region	5	IPR001211; IPR013090; IPR016090; SignalP-NN(euk) (SIGNALP)
1311	DMPC15212065_Speleonectes_tulumensis_2	plasminogen activator spa	216	8.28E-32	57.10%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1312	DMPC15212135_Speleonectes_tulumensis_0	glyceraldehyde-3-phosphate dehydrogenase	284	2.01E-130	84.60%	C:cytoplasm; F:nucleotide binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:catalytic activity; P:metabolic process	7	IPR016040; IPR020828; IPR020829; IPR020830; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF51735 (SUPERFAMILY), SSF55347 (SUPERFAMILY)

1313	DMPC15212183_Speleonectes_tulumensis_0	placental protein 11	137	5.57E-29	68.50%	F:hydrolase activity, acting on ester bonds	1	IPR018998; PTHR12439 (PANTHER), PTHR12439:SF6 (PANTHER), SSF142877 (SUPERFAMILY)
1314	DMPC15212221_Speleonectes_tulumensis_2	epididymal secretory protein e1 precursor	152	7.78E-26	56.80%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1315	DMPC15212227_Speleonectes_tulumensis_1	---NA---	310			-	0	no IPS match
1316	DMPC15212275_Speleonectes_tulumensis_1	dnaj homolog subfamily c member 9	124	1.17E-37	83.00%	P:protein metabolic process; F:protein binding	2	IPR001623; IPR018253; PTHR24078 (PANTHER), PTHR24078:SF16 (PANTHER)
1317	DMPC15212379_Speleonectes_tulumensis_1	isoform f	162	1.59E-09	42.00%	P:proteolysis; P:cell proliferation; F:metalloendopeptidase activity; C:cellular_component	4	IPR006586; IPR024079
1318	DMPC15212425_Speleonectes_tulumensis_0	---NA---	124			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1319	DMPC15212439_Speleonectes_tulumensis_1	phospholipase a2-like	155	5.01E-17	58.80%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; C:extracellular region	5	IPR001211; IPR013090; IPR016090; SignalP-NN(euk) (SIGNALP)
1320	DMPC15212613_Speleonectes_tulumensis_1	---NA---	333			-	0	no IPS match
1321	DMPC15212626_Speleonectes_tulumensis_0	low quality protein: neuferricin-like	285	4.10E-62	61.70%	F:heme binding	1	IPR001199; PTHR10281 (PANTHER), PTHR10281:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1322	DMPC15212733_Speleonectes_tulumensis_2	chitinase domain-containing protein 1-like	122	5.12E-17	63.10%	P:chitin catabolic process; F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process; F:cation binding; F:catalytic activity; F:chitinase activity	6	PTHR11177 (PANTHER), tmhmm (TMHMM)
1323	DMPC15212774_Speleonectes_tulumensis_2	selenium-dependent glutathione peroxidase	134	8.37E-49	78.80%	-	0	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
1324	DMPC15212875_Speleonectes_tulumensis_1	mantle protein 9	148	1.42E-08	64.75%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1325	DMPC15212935_Speleonectes_tulumensis_0	14-3-3 protein	248	3.20E-97	79.20%	F:protein binding	1	IPR000308; IPR023410; PTHR18860:SF0 (PANTHER)
1326	DMPC15212943_Speleonectes_tulumensis_0	---NA---	86			-	0	IPR000867; IPR011390
1327	DMPC15212961_Speleonectes_tulumensis_2	kazal-type protease inhibitor	100	1.62E-12	57.20%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
1328	DMPC15213014_Speleonectes_tulumensis_0	aldehyde dehydrogenase mitochondrial-like	129	3.55E-64	85.70%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
1329	DMPC15213046_Speleonectes_tulumensis_0	---NA---	129			-	0	IPR026645
1330	DMPC15213182_Speleonectes_tulumensis_2	group 3 secretory phospholipase a2-like	147	5.57E-44	60.00%	-	0	IPR001211; IPR013090; IPR016090; PTHR12253:SF7 (PANTHER)
1331	DMPC15213186_Speleonectes_tulumensis_1	cathepsin l	106	8.88E-29	72.60%	-	0	IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
1332	DMPC15213236_Speleonectes_tulumensis_2	heat shock cognate 70	145	3.89E-39	91.80%	-	0	IPR013126; G3DSA:1.20.1270.10 (GENE3D), PTHR19375 (PANTHER), SSF100934 (SUPERFAMILY)
1333	DMPC15213304_Speleonectes_tulumensis_1	isoamyl acetate-hydrolyzing esterase 1 homolog	147	5.78E-26	68.30%	-	0	IPR001087; IPR013831; PTHR14209 (PANTHER), SSF52266 (SUPERFAMILY)

1334	DMPC15213349_Speleonectes _tulumensis_2	hemocyanin subunit type 1 precursor	138	8.84E-48	69.10%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1335	DMPC15213391_Speleonectes _tulumensis_1	hypothetical protein, partial	336	5.29E-08	47.50%	-	0	no IPS match
1336	DMPC15213470_Speleonectes _tulumensis_2	---NA---	79			-	0	IPR000941; IPR020810; G3DSA:3.20.20.120 (GENE3D), SSF51604 (SUPERFAMILY)
1337	DMPC15213495_Speleonectes _tulumensis_0	ubiquitin-40s ribosomal protein s27a	136	6.55E-47	97.50%	P:cell cycle; P:metabolic process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:cellular protein modification process; P:transport	27	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1338	DMPC15213553_Speleonectes _tulumensis_1	upf0364 protein c6orf211 homolog	128	4.29E-22	61.30%	F:molecular_function; P:biological_process; C:cellular_component	3	IPR002791; PTHR12260 (PANTHER)
1339	DMPC15213629_Speleonectes _tulumensis_0	abhydrolase domain-containing protein 9	65	5.77E-15	90.10%	P:metabolic process; F:hydrolase activity	2	G3DSA:3.40.50.1820 (GENE3D), PTHR10992 (PANTHER), PTHR10992:SF98 (PANTHER), SSF53474 (SUPERFAMILY)
1340	DMPC15213669_Speleonectes _tulumensis_2	cathepsin l-like	122	6.13E-20	86.00%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1341	DMPC15213729_Speleonectes _tulumensis_2	soma ferritin	119	5.22E-26	77.30%	F:binding	1	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1342	DMPC15213733_Speleonectes _tulumensis_2	grn protein	149	4.18E-08	46.89%	P:axon extension	1	IPR000118; PTHR12274 (PANTHER), PTHR12274:SF0 (PANTHER)
1343	DMPC15213742_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor	135	6.67E-12	72.40%	-	0	IPR024509; IPR024716
1344	DMPC15213758_Speleonectes _tulumensis_0	dermatopontin 2	271	3.70E-27	57.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1345	DMPC15213872_Speleonectes _tulumensis_0	soma ferritin	124	4.90E-32	87.10%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1346	DMPC15213911_Speleonectes _tulumensis_2	myotrophin-like isoform 2	143	4.80E-52	81.80%	-	0	IPR002110; IPR020683; PTHR24152 (PANTHER), PTHR24152:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
1347	DMPC15213957_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor precursor	147	3.14E-26	62.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1348	DMPC15213986_Speleonectes _tulumensis_0	aldehyde dehydrogenase 3-1 variant b	292	5.42E-74	72.30%	F:catalytic activity; P:metabolic process	2	IPR012394; IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), tmhmm (TMHMM)
1349	DMPC15214186_Speleonectes _tulumensis_1	isoform cra_b	121	1.21E-46	97.70%	-	0	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
1350	DMPC15214207_Speleonectes _tulumensis_0	transcription factor sp5	286	1.50E-32	83.40%	-	0	IPR007087; IPR013087; IPR015880; PTHR23223 (PANTHER), PTHR23223:SF14 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
1351	DMPC15214232_Speleonectes _tulumensis_2	d-dopachrome decarboxylase-a	197	1.07E-16	57.10%	-	0	IPR001398; IPR014347; G3DSA:3.30.429.10 (GENE3D)

1352	DMPC15214342_Speleonectes_tulumensis_1	---NA---	152			-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24250 (PANTHER), PTHR24250:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
1353	DMPC15214367_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor	133	1.14E-25	68.90%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1354	DMPC15214380_Speleonectes_tulumensis_0	phospholipase a2	145	1.40E-18	65.60%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; F:hydrolase activity; C:extracellular region	6	IPR001211; IPR013090; IPR016090
1355	DMPC15214455_Speleonectes_tulumensis_2	cathepsin l-like	161	2.11E-22	87.40%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
1356	DMPC15214488_Speleonectes_tulumensis_5	protein	140	8.57E-09	72.33%	-	0	no IPS match
1357	DMPC15214497_Speleonectes_tulumensis_2	trypsin-like serine proteinase 1	128	1.45E-27	64.90%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP)
1358	DMPC15214500_Speleonectes_tulumensis_1	kazal-type proteinase inhibitor	146	1.55E-15	56.40%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
1359	DMPC15214546_Speleonectes_tulumensis_1	ame: full=hemagglutinin amebocyte aggregation factor ame: full=18k-laf flags: precursor	167	3.19E-11	69.80%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1360	DMPC15214569_Speleonectes_tulumensis_0	i-type lysozyme	270	1.28E-36	64.10%	F:lysozyme activity	1	IPR008597; IPR018247
1361	DMPC15214614_Speleonectes_tulumensis_2	dermatopontin 2	225	6.33E-40	59.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1362	DMPC15214630_Speleonectes_tulumensis_0	chitinase 1	176	1.99E-30	52.00%	-	0	IPR001223; IPR002557; IPR013781; IPR017853; PTHR11177 (PANTHER)
1363	DMPC15214659_Speleonectes_tulumensis_0	protein	134	2.10E-18	51.80%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1364	DMPC15214698_Speleonectes_tulumensis_2	protein	145	4.05E-19	52.70%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER)
1365	DMPC15214721_Speleonectes_tulumensis_0	vitellogenin 2	431	1.70E-40	46.30%	P:lipid transport; F:lipid transporter activity	2	IPR001747; IPR011030; IPR015816; IPR015819; PTHR23345 (PANTHER)
1366	DMPC15214932_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	149	3.54E-69	68.50%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1367	DMPC15215020_Speleonectes_tulumensis_0	#NAME?	211	2.65E-25	52.80%	F:unfolded protein binding; P:protein folding; F:heat shock protein binding; F:molecular_function; C:membrane; P:biological_process; P:spermatogenesis; C:cellular_component	8	IPR001623; PTHR24078 (PANTHER), PTHR24078:SF22 (PANTHER), tmhmm (TMHMM)
1368	DMPC15215075_Speleonectes_tulumensis_0	annexin x	223	6.28E-50	72.40%	F:actin binding; F:calcium ion binding; F:lipid binding	3	IPR001464; IPR018252; IPR018502; PTHR10502:SF23 (PANTHER), tmhmm (TMHMM)
1369	DMPC15215188_Speleonectes_tulumensis_0	proclotting enzyme	202	1.28E-27	60.50%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER)
1370	DMPC15215273_Speleonectes_tulumensis_2	neutral alpha-glucosidase ab-like	349	1.25E-33	66.20%	F:hydrolase activity, hydrolyzing O-glycosyl compounds; F:carbohydrate binding; P:carbohydrate metabolic process; F:catalytic activity	4	IPR000322; PTHR22762:SF7 (PANTHER)
1371	DMPC15215274_Speleonectes_tulumensis_1	dermatopontin 2	114	1.32E-09	58.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

1372	DMPC15215323_Speleonectes _tulumensis_2	ame: full=prohormone-1 contains: ame: full=brain peptide lrnqldigdlq contains: ame: full=brain peptide lrnqldigdl contains: ame: full=brain peptide sywkqcafnavscf-amide flags: precursor	118	1.21E-24	73.80%	-	0	tmhmm (TMHMM)
1373	DMPC15215329_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor	176	1.59E-32	61.00%	-	0	IPR026645
1374	DMPC15215334_Speleonectes _tulumensis_1	hyaluronidase precursor	225	1.15E-49	56.80%	P:defense response; F:hydrolase activity; P:metabolic process; P:carbohydrate metabolic process; F:hyalurononglucosaminidase activity; F:hydrolase activity, acting on glycosyl bonds; F:catalytic activity; C:extracellular region	8	IPR013785; IPR017853; IPR018155; PTHR11769:SF8 (PANTHER)
1375	DMPC15215401_Speleonectes _tulumensis_0	---NA---	120			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1376	DMPC15215491_Speleonectes _tulumensis_0	glycosyl-phosphatidylinositol-linked carbonic anhydrase	238	2.06E-26	65.60%	-	0	IPR001148; IPR023561; SignalP-NN(euk) (SIGNALP)
1377	DMPC15215574_Speleonectes _tulumensis_0	nad-dependent glyceraldehyde-3-phosphate dehydrogenase	124	1.55E-19	89.60%	F:catalytic activity; P:metabolic process	2	IPR020829; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF55347 (SUPERFAMILY)
1378	DMPC15215587_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor	104	1.27E-22	61.30%	-	0	IPR026645
1379	DMPC15215662_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor-like	143	9.36E-22	62.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1380	DMPC15215671_Speleonectes _tulumensis_2	epididymal secretory protein e1 isoform 1	137	4.59E-22	59.30%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1381	DMPC15215701_Speleonectes _tulumensis_0	dermatopontin 3	101	3.53E-09	63.43%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1382	DMPC15215784_Speleonectes _tulumensis_2	plasminogen activator spa	132	2.62E-22	63.00%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1383	DMPC15215790_Speleonectes _tulumensis_0	lipophorin receptor	94	1.41E-12	70.40%	F:receptor activity; F:transferase activity; P:transport; P:cellular component organization; C:cell	5	IPR002172; IPR023415; PTHR10529 (PANTHER), SignalP-NN(euk) (SIGNALP)
1384	DMPC15215840_Speleonectes _tulumensis_2	dermatopontin	223	3.07E-08	64.00%	-	0	no IPS match
1385	DMPC15215858_Speleonectes _tulumensis_2	trypsin 3	120	4.11E-17	59.30%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1386	DMPC15215904_Speleonectes _tulumensis_2	prophenoloxidase activating factor	129	2.78E-27	65.40%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF68 (PANTHER)
1387	DMPC15216196_Speleonectes _tulumensis_0	hemocyanin subunit type 2 precursor	95	3.82E-27	89.90%	-	0	IPR000896; IPR008922; IPR013788; PTHR11511:SF20 (PANTHER)

1388	DMPC15216380_Speleonectes _tulumensis_0	ubiquitin-40s ribosomal protein s27a	150	1.09E-57	97.20%	P:cell cycle; P:metabolic process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:cellular protein modification process; P:transport	27	IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
1389	DMPC15216412_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor	145	1.80E-29	67.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1390	DMPC15216438_Speleonectes _tulumensis_0	trypsin-like serine proteinase 1	115	2.67E-12	56.90%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1391	DMPC15216449_Speleonectes _tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	143	7.75E-20	52.20%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP)
1392	DMPC15216542_Speleonectes _tulumensis_1	glucose dehydrogenase	194	2.36E-26	72.60%	-	0	IPR000172; G3DSA:3.50.50.60 (GENE3D), PTHR11552 (PANTHER), PTHR11552:SF10 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF51905 (SUPERFAMILY)
1393	DMPC15216595_Speleonectes _tulumensis_2	PREDICTED: hypothetical protein	97	3.55E-09	78.00%	-	0	tmhmm (TMHMM)
1394	DMPC15216626_Speleonectes _tulumensis_2	ferritin mitochondrial	88	1.66E-18	87.80%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; tmhmm (TMHMM)
1395	DMPC15216726_Speleonectes _tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	234	5.05E-12	57.10%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:proteolysis; F:peptidase activity	6	IPR000716; PTHR12352 (PANTHER)
1396	DMPC15216782_Speleonectes _tulumensis_0	chorion peroxidase	209	2.24E-42	63.20%	P:oxidation-reduction process; F:heme binding; F:oxidoreductase activity; P:response to oxidative stress; F:peroxidase activity; F:carbohydrate binding; P:cell adhesion	7	IPR002007; IPR010255; PTHR11475 (PANTHER), tmhmm (TMHMM)
1397	DMPC15216812_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor	130	1.34E-13	55.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1398	DMPC15216827_Speleonectes _tulumensis_2	glutathione peroxidase	303	1.89E-37	63.40%	F:catalytic activity	1	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
1399	DMPC15216873_Speleonectes _tulumensis_0	trypsinogen 2	162	2.82E-29	64.10%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER)
1400	DMPC15216878_Speleonectes _tulumensis_0	hemocyanin subunit type 1 precursor	135	2.73E-84	68.80%	-	0	IPR005203; IPR013788; IPR014756
1401	DMPC15216891_Speleonectes _tulumensis_0	60s ribosomal protein l40	98	5.37E-47	97.00%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1402	DMPC15216908_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor	105	2.29E-14	57.20%	-	0	IPR026645
1403	DMPC15216941_Speleonectes _tulumensis_2	ferritin-1 heavy chain	92	3.88E-22	90.60%	P:cellular homeostasis; F:binding; F:catalytic activity; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347

1404	DMPC15216956_Speleonectes_tulumensis_2	galactosamine (n-acetyl)-6-sulfate sulfatase	120	4.47E-23	94.40%	C:lysosome; F:binding; P:metabolic process; F:hydrolase activity	4	IPR000917; IPR017849; IPR017850; PTHR10342 (PANTHER), PTHR10342:SF27 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1405	DMPC15216958_Speleonectes_tulumensis_0	dermatopontin 3	182	7.85E-15	61.20%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1406	DMPC15216966_Speleonectes_tulumensis_0	dermatopontin 2	134	7.34E-12	54.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1407	DMPC15216983_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	133	1.45E-24	68.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1408	DMPC15217041_Speleonectes_tulumensis_0	oocyte protease inhibitor-1 precursor	106	8.01E-11	66.90%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1409	DMPC15217219_Speleonectes_tulumensis_1	protein	94	3.10E-11	80.40%	C:extracellular region; F:calcium ion binding	2	IPR000152; IPR000742; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR24048 (PANTHER), PTHR24048:SF15 (PANTHER), SSF57196 (SUPERFAMILY)
1410	DMPC15217236_Speleonectes_tulumensis_2	nidogen 1	76	2.15E-10	67.60%	P:proteolysis; F:peptidase activity	2	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP)
1411	DMPC15217300_Speleonectes_tulumensis_2	metalloprotease	139	4.57E-07	57.40%	P:proteolysis; F:peptidase activity; F:metalloendopeptidase activity; F:metallopeptidase activity	4	SignalP-NN(euk) (SIGNALP)
1412	DMPC15217341_Speleonectes_tulumensis_0	ferritin 3-like protein	134	1.37E-25	76.80%	F:binding	1	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1413	DMPC15217465_Speleonectes_tulumensis_0	carcinolectin5b-4	216	1.53E-50	66.90%	-	0	IPR002181; IPR014715; IPR014716; IPR020837; PTHR19143 (PANTHER)
1414	DMPC15217472_Speleonectes_tulumensis_1	wnt inhibitory factor 1 precursor	111	7.73E-49	83.90%	-	0	IPR000742; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR24838 (PANTHER), PTHR24838:SF30 (PANTHER), SSF57196 (SUPERFAMILY)
1415	DMPC15217495_Speleonectes_tulumensis_0	probable reductase	122	6.10E-16	74.60%	P:oxidation-reduction process; F:oxidoreductase activity; C:cellular_component	3	IPR001395; IPR023210; PTHR11732:SF34 (PANTHER)
1416	DMPC15217524_Speleonectes_tulumensis_2	dehydrogenase reductase sdr family member 7	312	1.70E-33	71.70%	P:metabolic process	1	IPR002198; IPR002347; IPR016040; PTHR24322 (PANTHER), PTHR24322:SF27 (PANTHER), tmhmm (TMHMM), SSF51735 (SUPERFAMILY)
1417	DMPC15217525_Speleonectes_tulumensis_0	aael013299- partial	139	1.57E-22	60.30%	F:catalytic activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP)
1418	DMPC15217645_Speleonectes_tulumensis_1	transmembrane protease serine 6- partial	141	1.52E-12	50.75%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER), SignalP-NN(euk) (SIGNALP)
1419	DMPC15217661_Speleonectes_tulumensis_1	zinc finger protein 248-like	80	3.08E-16	64.00%	-	0	IPR007087; IPR013087; IPR015880; PTHR24382 (PANTHER), PTHR24382:SF0 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
1420	DMPC15217756_Speleonectes_tulumensis_1	epididymal secretory protein e1 precursor	147	1.01E-23	59.00%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER)
1421	DMPC15217764_Speleonectes_tulumensis_0	carcinolectin 5a partial	162	1.34E-32	59.40%	-	0	IPR002181; IPR014716; PTHR19143 (PANTHER)
1422	DMPC15218054_Speleonectes_tulumensis_2	subfamily member 9	124	7.42E-38	82.40%	P:protein metabolic process; P:behavior; F:protein binding	3	IPR001623; IPR018253; PTHR24078 (PANTHER), PTHR24078:SF16 (PANTHER)
1423	DMPC15218111_Speleonectes_tulumensis_0	peptidase m4 thermolysin	119	2.32E-07	62.63%	P:proteolysis; F:hydrolase activity; F:metalloendopeptidase activity	3	no IPS match
1424	DMPC15218195_Speleonectes_tulumensis_0	protein lethal giant larvae-like	165	8.96E-48	84.70%	-	0	IPR001680; IPR015943; IPR017986; IPR019775; PTHR10241 (PANTHER), PTHR10241:SF10 (PANTHER)

1425	DMPC15218226_Speleonectes _tulumensis_1	---NA---	88			-	0	IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER)
1426	DMPC15218227_Speleonectes _tulumensis_2	hemocyanin subunit type 1 precursor	150	4.47E-56	72.20%	-	0	IPR005203; IPR013788; IPR014756; SignalP-NN(euk) (SIGNALP)
1427	DMPC15218313_Speleonectes _tulumensis_0	calmodulin	199	5.84E-101	100.00%	P:biological_process; P:regulation of biological process; P:protein transport; P:cytoskeleton organization; P:cell cycle; P:transport; P:cellular component organization; P:cell-cell signaling; C:cell; P:response to external stimulus; P:signal transduction; P:response to abiotic stimulus; F:cytoskeletal protein binding; P:reproduction; P:behavior; P:organelle organization; P:ion transport; P:growth; C:cytoskeleton; C:protein complex; C:microtubule organizing center; P:cell death; C:plasma membrane; P:anatomical structure morphogenesis; F:protein kinase activity; P:embryo development; C:cellular_component; F:nucleotide binding; P:cell differentiation; P:multicellular organismal development; F:protein binding; C:intracellular; F:calcium ion binding; P:cellular protein modification process	34	IPR002048; IPR011992; IPR018247; PTHR23050 (PANTHER), SSF47473 (SUPERFAMILY)
1428	DMPC15218369_Speleonectes _tulumensis_0	hypothetical protein DAPPUDRAFT_332702	312	5.30E-73	62.00%	P:lipid transport; F:lipid transporter activity	2	IPR001747; IPR015816; IPR015819; PTHR23345 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1429	DMPC15218411_Speleonectes _tulumensis_1	hemocyanin subunit type 1 precursor	143	6.49E-58	69.70%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER)
1430	DMPC15218415_Speleonectes _tulumensis_2	gamma-interferon-inducible lysosomal thiol reductase	135	2.64E-11	55.80%	-	0	IPR004911; PTHR13234:SF7 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1431	DMPC15218443_Speleonectes _tulumensis_0	dermatopontin 2	104	2.77E-08	62.14%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1432	DMPC15218559_Speleonectes _tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	127	1.67E-15	50.30%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1433	DMPC15218611_Speleonectes _tulumensis_0	-like protein subfamily c member 1	97	6.63E-15	84.40%	P:regulation of biological process; P:protein transport; F:protein binding; P:protein metabolic process; C:nuclear envelope; C:cell; C:endoplasmic reticulum; P:catabolic process; F:enzyme regulator activity; F:DNA binding; P:translation; P:biological_process	12	IPR001623; PTHR24078 (PANTHER), PTHR24078:SF10 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1434	DMPC15218665_Speleonectes _tulumensis_1	lysozyme precursor	116	2.32E-12	60.60%	F:lysozyme activity; P:cell wall macromolecule catabolic process	2	IPR001916; IPR023346; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER), PTHR11407:SF2 (PANTHER)
1435	DMPC15218669_Speleonectes _tulumensis_0	perlucin 5	153	1.22E-12	50.30%	F:protein binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1436	DMPC15218694_Speleonectes _tulumensis_2	allergen 5	155	1.35E-18	53.60%	-	0	IPR001283; IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1437	DMPC15218695_Speleonectes _tulumensis_0	perlucin 5	152	3.64E-11	47.20%	F:carbohydrate binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1438	DMPC15218813_Speleonectes _tulumensis_2	soma ferritin	117	8.70E-36	89.00%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1439	DMPC15218848_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor-like	149	1.93E-11	62.40%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

1440	DMPC15218869_Speleonectes_tulumensis_0	---NA---	247			-	0	IPR008197; PTHR19441 (PANTHER)
1441	DMPC15218879_Speleonectes_tulumensis_0	alkyl hydroperoxide reductase thiol specific antioxidant mal allergen	154	3.41E-59	81.00%	P:metabolic process; F:catalytic activity; F:antioxidant activity	3	IPR000866; IPR012336; IPR024706; PTHR10681 (PANTHER), PTHR10681:SF51 (PANTHER)
1442	DMPC15218880_Speleonectes_tulumensis_2	protein phosphatase 1 regulatory subunit 7-like	128	1.45E-26	87.30%	-	0	IPR001611; IPR003591; IPR025875; G3DSA:3.80.10.10 (GENE3D), PTHR10588 (PANTHER), PTHR10588:SF96 (PANTHER), SM00365 (SMART), SSF52058 (SUPERFAMILY)
1443	DMPC15218930_Speleonectes_tulumensis_2	pc3-like endoprotease variant a-like	460	4.45E-98	61.20%	F:hydrolase activity	1	IPR000209; IPR002884; IPR008979; IPR015500; IPR023828; PTHR10795:SF155 (PANTHER)
1444	DMPC15219005_Speleonectes_tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	133	3.45E-09	58.60%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:proteolysis; F:peptidase activity	6	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1445	DMPC15219012_Speleonectes_tulumensis_0	---NA---	177			-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER), PTHR24259:SF33 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1446	DMPC15219026_Speleonectes_tulumensis_2	i-type lysozyme partial	240	8.91E-21	66.90%	F:lysozyme activity	1	IPR008597; PTHR11195:SF12 (PANTHER)
1447	DMPC15219030_Speleonectes_tulumensis_2	apolipoprotein d	182	1.46E-38	61.70%	F:lipid binding; P:transport; F:transporter activity	3	IPR000566; IPR011038; IPR012674; IPR022272; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP)
1448	DMPC15219033_Speleonectes_tulumensis_1	trypsinogen 3	155	2.25E-23	55.50%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP)
1449	DMPC15219114_Speleonectes_tulumensis_2	gamma-interferon-inducible lysosomal thiol reductase	166	1.27E-34	54.60%	-	0	IPR004911
1450	DMPC15219163_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	128	1.95E-23	67.00%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1451	DMPC15219203_Speleonectes_tulumensis_1	low quality protein: zinc finger protein 233	178	4.13E-40	76.90%	F:nucleic acid binding; C:nucleoplasm; C:protein complex; C:nucleolus; F:protein binding; P:regulation of biological process;	7	IPR007087; IPR013087; IPR015880; PTHR24402 (PANTHER), PTHR24402:SF42 (PANTHER), PF13465 (PFAM), tmhmm (TMHMM), SSF57667 (SUPERFAMILY)
1452	DMPC15219212_Speleonectes_tulumensis_2	---NA---	140			-	0	IPR002110; IPR020683; PTHR24125 (PANTHER)
1453	DMPC15219215_Speleonectes_tulumensis_2	PREDICTED: hypothetical protein LOC100645147	158	1.28E-07	61.33%	-	0	SSF57501 (SUPERFAMILY)
1454	DMPC15219374_Speleonectes_tulumensis_2	trypsinogen 2	157	6.95E-42	66.40%	-	0	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER)
1455	DMPC15219420_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	155	2.05E-29	67.90%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1456	DMPC15219436_Speleonectes_tulumensis_1	trypsinogens 1	161	1.21E-23	57.50%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1457	DMPC15219493_Speleonectes_tulumensis_0	protein	139	6.03E-18	51.90%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1458	DMPC15219511_Speleonectes_tulumensis_0	---NA---	95			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1459	DMPC15219585_Speleonectes_tulumensis_2	dehydrogenase reductase sdr family member 11-like	130	9.58E-37	77.10%	P:metabolic process	1	IPR002198; IPR016040; PTHR24322 (PANTHER), PTHR24322:SF7 (PANTHER), SSF51735 (SUPERFAMILY)

1460	DMPC15219631_Speleonectes _tulumensis_2	---NA---	137			-	0	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP)
1461	DMPC15219730_Speleonectes _tulumensis_1	bola-like protein 3	141	1.68E-10	79.80%	C:extracellular region	1	PTHR12735 (PANTHER), PTHR12735:SF1 (PANTHER)
1462	DMPC15219755_Speleonectes _tulumensis_2	ame: full=venom allergen 5 ame: full=antigen 5 ame: full=cysteine-rich venom protein short=crvp ame: allergen=pac c 3	160	3.58E-07	65.00%	-	0	IPR001283; IPR014044
1463	DMPC15220102_Speleonectes _tulumensis_1	hypothetical protein DAPPUDRAFT_332703	549	1.12E-22	43.00%	P:lipid transport; F:lipid transporter activity	2	no IPS match
1464	DMPC15220114_Speleonectes _tulumensis_2	nucleobindin 1	169	2.92E-31	67.70%	-	0	PTHR19237 (PANTHER), SignalP-NN(euk) (SIGNALP)
1465	DMPC15220129_Speleonectes _tulumensis_1	coiled-coil domain-containing	203	2.27E-07	72.00%	-	0	IPR026321; PTHR14735:SF0 (PANTHER), tmhmm (TMHMM)
1466	DMPC15220173_Speleonectes _tulumensis_1	niemann-pick type c2	123	5.47E-16	58.60%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1467	DMPC15220419_Speleonectes _tulumensis_2	anti-lipopolysaccharide factor	143	2.14E-13	71.60%	-	0	IPR024509; IPR024716
1468	DMPC15220459_Speleonectes _tulumensis_2	pacifastin light chain	157	4.84E-09	52.86%	F:peptidase inhibitor activity; P:negative regulation of peptidase activity	2	IPR008037; IPR020862
1469	DMPC15220495_Speleonectes _tulumensis_2	carboxypeptidase b-like	134	1.18E-19	68.30%	P:proteolysis; F:metallocarboxypeptidase activity; F:carboxypeptidase activity; F:zinc ion	4	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
1470	DMPC15220535_Speleonectes _tulumensis_2	epididymal secretory protein e1	139	3.57E-11	63.50%	P:transport; F:binding; C:intracellular	3	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1471	DMPC15220552_Speleonectes _tulumensis_0	ubiquitin-40s ribosomal protein s27a-like protein	144	2.65E-52	90.90%	C:nucleoplasm; P:signal transduction; P:response to stress; P:DNA metabolic process; P:translation; F:binding; P:metabolic process; F:structural molecule activity; C:endosome; C:ribosome; C:cytosol	11	IPR000626; IPR002906; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1472	DMPC15220657_Speleonectes _tulumensis_1	ubiquitin-40s ribosomal protein s27a	152	9.32E-56	97.00%	P:cell cycle; P:metabolic process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:cellular protein modification process; P:transport	27	IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1473	DMPC15220671_Speleonectes _tulumensis_0	chymotrypsin-like elastase family member 2a-like	136	2.92E-09	61.80%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER)
1474	DMPC15220740_Speleonectes _tulumensis_2	chymotrypsin 1	130	2.72E-15	65.90%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
1475	DMPC15220830_Speleonectes _tulumensis_0	trypsinogen 2	121	1.41E-12	72.00%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24250 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

1476	DMPC15220872_Speleonectes _tulumensis_1	soma ferritin	119	4.12E-35	87.50%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1477	DMPC15220935_Speleonectes _tulumensis_2	ves g 5 allergen	154	2.64E-21	53.20%	C:extracellular region	1	IPR001283; IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1478	DMPC15220965_Speleonectes _tulumensis_2	adp ribosylation factor isoform a	131	3.94E-24	95.10%	F:signal transducer activity; F:signal transduction; C:intracellular; P:cellular protein modification process; P:transport; P:cell-cell signaling; F:hydrolase activity; F:transferase activity; P:multicellular organismal development; P:cellular component organization; P:protein transport; F:nucleotide binding	12	IPR006689; IPR027417; G3DSA:3.40.50.300 (GENE3D), PTHR11711 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1479	DMPC15221082_Speleonectes _tulumensis_1	isoform a	153	1.89E-20	82.20%	F:molecular_function; P:biological_process; C:cellular_component	3	tmhmm (TMHMM)
1480	DMPC15221090_Speleonectes _tulumensis_0	epididymal secretory protein e1 isoform 1	150	2.74E-22	57.30%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1481	DMPC15221140_Speleonectes _tulumensis_2	---NA---	119			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1482	DMPC15221142_Speleonectes _tulumensis_0	anti-lipopolysaccharide factor isoform 7	136	2.28E-21	72.00%	-	0	IPR024509; IPR024716
1483	DMPC15221158_Speleonectes _tulumensis_2	soma ferritin	121	2.46E-36	85.60%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1484	DMPC15221288_Speleonectes _tulumensis_1	leg5_rat ame: full=galectin-5 short=gal-5 ame: full=rl-18	128	3.95E-27	58.40%	F:carbohydrate binding	1	IPR001079; IPR008985; IPR013320; PTHR11346 (PANTHER)
1485	DMPC15221359_Speleonectes _tulumensis_1	hypothetical protein DAPPUDRAFT_196945	333	5.77E-57	68.70%	-	0	IPR002007; IPR010255; PTHR11475 (PANTHER), tmhmm (TMHMM)
1486	DMPC15221387_Speleonectes _tulumensis_2	---NA---	152			-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1487	DMPC15221530_Speleonectes _tulumensis_2	prolyl 3-hydroxylase 2	195	8.10E-62	69.80%	-	0	PTHR13986 (PANTHER)
1488	DMPC15221604_Speleonectes _tulumensis_2	trypsinogen 2	314	2.42E-36	76.10%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), tmhmm (TMHMM)
1489	DMPC15221645_Speleonectes _tulumensis_1	ame: full=annulin ame: full=protein-glutamine gamma-glutamyltransferase ame: full=transglutaminase	337	1.36E-47	71.80%	-	0	IPR002931; IPR008958; IPR013783; IPR023608; PTHR11590:SF16 (PANTHER), SSF54001 (SUPERFAMILY)
1490	DMPC15221773_Speleonectes _tulumensis_2	ves g 5 allergen	228	1.88E-22	55.70%	C:extracellular region	1	IPR001283; IPR014044; IPR018244
1491	DMPC15221997_Speleonectes _tulumensis_2	female neotenic-specific protein 3	158	3.91E-12	54.00%	-	0	tmhmm (TMHMM)
1492	DMPC15222030_Speleonectes _tulumensis_2	hypothetical protein DAPPUDRAFT_241333	199	1.38E-07	45.33%	-	0	IPR001073; IPR008983; PTHR22923 (PANTHER), PTHR22923:SF1 (PANTHER)
1493	DMPC15222035_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor-like	131	2.89E-13	63.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1494	DMPC15222087_Speleonectes _tulumensis_2	nidogen-related basement membrane protein	237	8.97E-08	45.00%	-	0	IPR000716; IPR009168; tmhmm (TMHMM)
1495	DMPC15222121_Speleonectes _tulumensis_1	---NA---	111			-	0	IPR003172; PTHR11306 (PANTHER)
1496	DMPC15222220_Speleonectes _tulumensis_1	collagen alpha type	323	1.23E-65	62.80%	P:anatomical structure morphogenesis; P:cellular component organization; P:cell differentiation; P:multicellular organismal development; C:nucleus; C:mitochondrion	6	IPR010515; IPR016186; IPR016187; PTHR24637 (PANTHER), PTHR24637:SF88 (PANTHER)

1497	DMPC15222233_Speleonectes_tulumensis_1	carboxypeptidase a1-like	141	1.03E-25	71.90%	P:proteolysis; F:metallocarboxypeptidase activity; F:zinc ion binding	3	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
1498	DMPC15222256_Speleonectes_tulumensis_1	trypsin-like serine proteinase 1	83	1.73E-09	65.70%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24257 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1499	DMPC15222305_Speleonectes_tulumensis_2	exostosin-2	127	2.41E-73	93.00%	F:transferase activity; C:endoplasmic reticulum	2	IPR015338; G3DSA:3.90.550.10 (GENE3D), PTHR11062 (PANTHER), PTHR11062:SF6 (PANTHER), SSF53448 (SUPERFAMILY)
1500	DMPC15222396_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	153	7.82E-29	67.20%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1501	DMPC15222547_Speleonectes_tulumensis_2	trypsin-1 precursor	85	8.84E-09	55.40%	P:proteolysis; F:serine-type endopeptidase activity; C:extracellular region	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)
1502	DMPC15222555_Speleonectes_tulumensis_1	serine protease 52-like	121	6.55E-17	63.00%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1503	DMPC15222682_Speleonectes_tulumensis_1	ubiquitin-40s ribosomal protein s27a-like	113	2.38E-50	96.40%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1504	DMPC15222702_Speleonectes_tulumensis_0	chitinase partial	56	2.71E-14	64.90%	-	0	IPR001223; G3DSA:3.10.50.10 (GENE3D), PTHR24833 (PANTHER), PTHR24833:SF3 (PANTHER), SSF54556 (SUPERFAMILY)
1505	DMPC15222734_Speleonectes_tulumensis_1	si:dkey- protein	115	3.49E-08	61.60%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1506	DMPC15222763_Speleonectes_tulumensis_1	aael007448- partial	258	1.69E-57	71.60%	P:proteolysis; F:serine-type peptidase activity; C:membrane	3	IPR001375; G3DSA:3.40.50.1820 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF23 (PANTHER), SSF53474 (SUPERFAMILY)
1507	DMPC15222805_Speleonectes_tulumensis_2	epidermal retinol dehydrogenase 2-like	216	4.20E-37	69.50%	P:oxidation-reduction process; F:oxidoreductase activity; P:metabolic process; F:nucleotide binding	4	IPR016040; PTHR24316 (PANTHER), PTHR24316:SF1 (PANTHER), SSF51735 (SUPERFAMILY)
1508	DMPC15222836_Speleonectes_tulumensis_1	---NA---	133			-	0	IPR024276; tmhmm (TMHMM)
1509	DMPC15222875_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	95	8.27E-47	76.30%	-	0	IPR005203; IPR013788; IPR014756
1510	DMPC15222902_Speleonectes_tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	126	1.19E-20	50.20%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER)
1511	DMPC15222930_Speleonectes_tulumensis_1	dermatopontin 3	125	6.18E-10	56.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1512	DMPC15222937_Speleonectes_tulumensis_0	si:dkey- protein	107	2.82E-09	61.17%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1513	DMPC15222993_Speleonectes_tulumensis_0	kazal-type serine proteinase inhibitor 4	100	6.17E-14	66.00%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), SSF100895 (SUPERFAMILY)
1514	DMPC15223001_Speleonectes_tulumensis_2	apolipoprotein d-like isoform 2	154	2.64E-16	61.20%	F:lipid binding; P:transport; F:transporter activity	3	IPR011038; IPR012674; IPR022272; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP)
1515	DMPC15223049_Speleonectes_tulumensis_1	carboxypeptidase b	202	2.17E-57	67.30%	P:proteolysis; F:metallocarboxypeptidase activity; F:carboxypeptidase activity; F:zinc ion	4	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
1516	DMPC15223133_Speleonectes_tulumensis_0	female neotenic-specific protein 3	149	5.18E-09	58.67%	-	0	tmhmm (TMHMM)
1517	DMPC15223134_Speleonectes_tulumensis_2	sulfakinin-like peptide	217	1.38E-15	63.33%	-	0	IPR013152; tmhmm (TMHMM)

1518	DMPC15223138_Speleonectes_tulumensis_1	proclotting enzyme	318	1.46E-32	52.00%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
1519	DMPC15223148_Speleonectes_tulumensis_0	apolipoprotein d	372	2.83E-08	45.30%	P:response to external stimulus; P:response to stress; P:biological_process; P:regulation of biological process; C:cytoplasm	5	IPR011038; IPR012674; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER)
1520	DMPC15223202_Speleonectes_tulumensis_1	group 3 secretory phospholipase a2	182	4.84E-52	72.30%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process	3	IPR001211; IPR016090; PTHR12253:SF5 (PANTHER)
1521	DMPC15223275_Speleonectes_tulumensis_0	sifa preprohormone	105	8.74E-18	73.80%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1522	DMPC15223276_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	142	2.69E-63	68.00%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1523	DMPC15223328_Speleonectes_tulumensis_2	---NA---	200			-	0	IPR016179; tmhmm (TMHMM)
1524	DMPC15223336_Speleonectes_tulumensis_1	kazal-type protease inhibitor	107	1.15E-13	55.90%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
1525	DMPC15223371_Speleonectes_tulumensis_0	histone -like	130	8.66E-66	97.40%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR000558; IPR007125; IPR009072
1526	DMPC15223495_Speleonectes_tulumensis_1	trypsinogen 2	140	1.50E-26	66.00%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER)
1527	DMPC15223514_Speleonectes_tulumensis_2	dermatopontin 3	95	4.14E-08	66.50%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1528	DMPC15223519_Speleonectes_tulumensis_2	cathepsin l	216	1.65E-33	85.60%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1529	DMPC15223546_Speleonectes_tulumensis_1	trypsin	121	1.53E-29	62.00%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER)
1530	DMPC15223554_Speleonectes_tulumensis_1	epididymal secretory protein e1	214	3.22E-19	59.90%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER)
1531	DMPC15223655_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	144	2.61E-22	60.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1532	DMPC15223668_Speleonectes_tulumensis_0	dopamine beta hydroxylase	161	4.46E-35	60.20%	F:catalytic activity	1	IPR000323; IPR000945; IPR008977; IPR014784; PF03712 (PFAM)
1533	DMPC15223674_Speleonectes_tulumensis_2	plasminogen activator spa	111	8.84E-23	64.80%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24257 (PANTHER), SignalP-NN(euk) (SIGNALP)
1534	DMPC15223688_Speleonectes_tulumensis_0	adp ribosylation factor isoform a	161	2.27E-57	92.40%	F:signal transducer activity; F:signal transduction; C:intracellular; P:cellular protein modification process; P:transport; P:cell-cell signaling; F:hydrolase activity; F:transferase activity; P:multicellular organismal development; P:cellular component organization; P:protein transport; F:nucleotide binding	12	IPR005225; IPR006689; IPR024156; IPR027417; G3DSA:3.40.50.300 (GENE3D), PTHR11711 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1535	DMPC15223743_Speleonectes_tulumensis_1	insulin-like growth factor binding protein 7-like protein	216	7.07E-07	57.00%	-	0	IPR000867; IPR011390; SignalP-NN(euk) (SIGNALP)
1536	DMPC15223786_Speleonectes_tulumensis_3	lysosomal acid	133	1.15E-12	64.10%	F:hydrolase activity; P:transport; P:cellular component organization	3	IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53254 (SUPERFAMILY)
1537	DMPC15223789_Speleonectes_tulumensis_2	enolase	166	1.58E-65	95.00%	C:cytosol; C:protein complex; F:catalytic activity; F:binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process	7	IPR000941; IPR020809; IPR020810; G3DSA:3.20.20.120 (GENE3D), SSF51604 (SUPERFAMILY)

1538	DMPC15223816_Speleonectes _tulumensis_2	ame: full=techylectin-5a flags: precursor	305	7.02E-58	67.50%	-	0	IPR002181; IPR014715; IPR014716; IPR020837; PTHR19143 (PANTHER)
1539	DMPC15223859_Speleonectes _tulumensis_1	ensangp00000031746-like protein	112	9.81E-65	91.90%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF41 (PANTHER)
1540	DMPC15223871_Speleonectes _tulumensis_0	iron zinc purple acid phosphatase-like	207	4.14E-23	78.00%	F:binding; F:hydrolase activity	2	IPR025733; G3DSA:3.60.21.10 (GENE3D), PTHR22953 (PANTHER), PTHR22953:SF0 (PANTHER), tmhmm (TMHMM), SSF56300 (SUPERFAMILY)
1541	DMPC15223916_Speleonectes _tulumensis_0	bola-like protein 2-like	136	2.27E-35	81.00%	-	0	IPR002634; PTHR12735 (PANTHER)
1542	DMPC15223944_Speleonectes _tulumensis_2	---NA---	115			-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
1543	DMPC15223983_Speleonectes _tulumensis_2	lysyl-trna synthetase-like isoform 2	228	4.77E-35	78.20%	C:cytoplasm; F:nucleic acid binding; F:catalytic activity; P:nucleobase-containing compound metabolic process; P:translation; ; F:nucleotide binding	7	IPR002313; IPR004365; IPR012340; IPR018150
1544	DMPC15223985_Speleonectes _tulumensis_2	phosphoglucose isomerase	66	8.50E-19	76.80%	P:carbohydrate metabolic process; F:catalytic activity	2	IPR001672; G3DSA:3.40.50.10490 (GENE3D), PTHR11469:SF0 (PANTHER), SSF53697 (SUPERFAMILY)
1545	DMPC15224008_Speleonectes _tulumensis_2	---NA---	161			-	0	IPR012336; IPR019479; PTHR10681 (PANTHER), tmhmm (TMHMM)
1546	DMPC15224066_Speleonectes _tulumensis_0	trypsin-like serine proteinase 1	131	3.77E-12	53.20%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1547	DMPC15224083_Speleonectes _tulumensis_2	60s ribosomal protein l40	140	8.33E-43	97.40%	P:cell cycle; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; C:cytosol; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; C:plasma membrane; ; C:endosome; P:cellular component organization; C:ribosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; P:cellular protein modification process; P:translation; P:transport	25	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1548	DMPC15224105_Speleonectes _tulumensis_0	cathepsin l2	154	5.81E-31	85.10%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1549	DMPC15224202_Speleonectes _tulumensis_2	anti-lipopolysaccharide factor	142	9.02E-31	68.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1550	DMPC15224246_Speleonectes _tulumensis_2	vitellogenin 2	128	4.77E-15	58.50%	-	0	IPR001747; IPR011030; PTHR23345 (PANTHER)
1551	DMPC15224257_Speleonectes _tulumensis_1	mantle protein 9	159	2.16E-08	66.33%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1552	DMPC15224269_Speleonectes _tulumensis_1	glyceraldehyde-3-phosphate dehydrogenase	137	3.49E-35	65.10%	F:catalytic activity; F:nucleotide binding	2	IPR020829; IPR020831; G3DSA:3.30.360.10 (GENE3D), PTHR10836:SF4 (PANTHER), SSF55347 (SUPERFAMILY)
1553	DMPC15224283_Speleonectes _tulumensis_2	lipophorin receptor isoform e	245	2.04E-10	58.30%	C:plasma membrane	1	IPR002172; IPR023415; PR00261 (PRINTS), PTHR24652 (PANTHER), PTHR24652:SF0 (PANTHER)

1554	DMPC15224328_Speleonectes_tulumensis_2	mantle protein 9	150	1.21E-08	66.75%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1555	DMPC15224428_Speleonectes_tulumensis_0	---NA---	128			-	0	SignalP-NN(euk) (SIGNALP)
1556	DMPC15224448_Speleonectes_tulumensis_2	tissue factor pathway inhibitor 2	95	4.77E-26	63.40%	F:serine-type endopeptidase inhibitor activity; C:extracellular space; P:blood coagulation	3	IPR002223; IPR020901; PTHR10083 (PANTHER)
1557	DMPC15224478_Speleonectes_tulumensis_1	carboxypeptidase b-like	228	5.11E-52	68.70%	-	0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
1558	DMPC15224496_Speleonectes_tulumensis_0	thioredoxin-like protein	189	2.72E-28	84.10%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; tmhmm (TMHMM)
1559	DMPC15224500_Speleonectes_tulumensis_0	lysozyme precursor	103	1.61E-25	64.80%	F:lysozyme activity; P:cell wall macromolecule catabolic process	2	IPR001916; IPR023346; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER), SignalP-NN(euk) (SIGNALP)
1560	DMPC15224526_Speleonectes_tulumensis_2	proactivator polypeptide	135	1.18E-20	55.10%	P:lipid metabolic process; P:sphingolipid metabolic process; C:lysosome	3	IPR007856; IPR008138; IPR008139; IPR011001; PTHR11480 (PANTHER), PTHR11480:SF3 (PANTHER)
1561	DMPC15224561_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_308200	147	1.01E-07	52.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1562	DMPC15224610_Speleonectes_tulumensis_0	---NA---	112			-	0	IPR007233; tmhmm (TMHMM)
1563	DMPC15224619_Speleonectes_tulumensis_2	lysozyme c precursor	138	4.76E-12	73.20%	F:hydrolase activity; P:metabolic process	2	IPR001916; IPR019799; IPR023346; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER)
1564	DMPC15224696_Speleonectes_tulumensis_1	trypsin-like serine proteinase 1	154	1.74E-22	66.40%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1565	DMPC15224730_Speleonectes_tulumensis_0	60s ribosomal protein l40	115	1.64E-41	96.90%	P:cell cycle; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; C:cytosol; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; C:plasma membrane; ; C:endosome; P:cellular component organization; C:ribosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; P:cellular protein modification process; P:translation; P:transport	25	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
1566	DMPC15224747_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor	252	5.78E-26	61.50%	-	0	IPR026645
1567	DMPC15224762_Speleonectes_tulumensis_3	vitellogenin 2	231	9.01E-27	53.00%	-	0	IPR001747; IPR011030
1568	DMPC15224786_Speleonectes_tulumensis_1	isoform h	380	3.70E-29	68.50%	F:hydrolase activity; P:carbohydrate metabolic process	2	IPR001223; IPR002557; IPR013781; IPR017853; PTHR11177 (PANTHER), tmhmm (TMHMM)
1569	DMPC15224814_Speleonectes_tulumensis_0	oxidase peroxidase	195	2.47E-53	66.10%	-	0	IPR002007; IPR010255; PTHR11475 (PANTHER)
1570	DMPC15224852_Speleonectes_tulumensis_0	hemocyanin subunit type 2 precursor	181	2.37E-19	82.00%	-	0	IPR005203; IPR013788; IPR014756
1571	DMPC15224867_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor	204	1.09E-19	66.50%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)

1572	DMPC15224898_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	150	5.50E-20	50.80%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1573	DMPC15224945_Speleonectes_tulumensis_1	ecdysteroid-regulated 16 kda protein	186	5.85E-17	54.50%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
1574	DMPC15224971_Speleonectes_tulumensis_2	perlucin 5	155	1.91E-11	49.30%	F:carbohydrate binding; P:cell adhesion	2	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP)
1575	DMPC15224981_Speleonectes_tulumensis_0	h-2 class ii histocompatibility antigen gamma chain	145	1.30E-08	67.60%	-	0	IPR000716; IPR022339
1576	DMPC15224994_Speleonectes_tulumensis_1	alkaline serine exoprotease a	152	4.50E-13	62.50%	F:peptidase activity	1	IPR007280; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1577	DMPC15225135_Speleonectes_tulumensis_2	carboxypeptidase b-like	155	7.56E-26	69.10%	F:peptidase activity	1	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
1578	DMPC15225140_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	157	1.65E-63	70.10%	-	0	IPR005203; IPR013788; IPR014756
1579	DMPC15225186_Speleonectes_tulumensis_1	diuretic hormone class 2-like	124	2.27E-10	63.00%	-	0	tmhmm (TMHMM)
1580	DMPC15225195_Speleonectes_tulumensis_2	thioredoxin 1	133	3.22E-42	84.00%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; IPR017937; SignalP-NN(euk) (SIGNALP)
1581	DMPC15225216_Speleonectes_tulumensis_1	glutathione peroxidase	374	2.41E-58	64.20%	F:catalytic activity	1	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1582	DMPC15225286_Speleonectes_tulumensis_2	phospholipase a2-like	227	1.02E-25	50.30%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; C:extracellular region; F:hydrolase activity	6	IPR001211; IPR013090; IPR016090; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1583	DMPC15225298_Speleonectes_tulumensis_1	fmrfamide-related neuropeptides-like	148	2.43E-16	75.90%	-	0	tmhmm (TMHMM)
1584	DMPC15225306_Speleonectes_tulumensis_0	trypsinogen 2	229	1.07E-78	70.50%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
1585	DMPC15225308_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	152	9.71E-25	78.20%	-	0	IPR005204; IPR013788; PTHR11511:SF19 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1586	DMPC15225483_Speleonectes_tulumensis_0	epididymal secretory protein e1 precursor	139	1.11E-17	59.80%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1587	DMPC15225519_Speleonectes_tulumensis_1	flavin-dependent monooxygenase fmo3b	100	1.99E-26	70.20%	F:catalytic activity; F:binding; F:nucleotide binding	3	IPR020946; G3DSA:3.50.50.60 (GENE3D), PTHR23023 (PANTHER), PTHR23023:SF4 (PANTHER), SSF51905 (SUPERFAMILY)
1588	DMPC15225581_Speleonectes_tulumensis_1	ectonucleotide pyrophosphatase phosphodiesterase family member 6	114	3.57E-23	51.40%	P:metabolic process; F:catalytic activity; C:integral to membrane; F:hydrolase activity; C:membrane; P:lipid catabolic process; C:plasma membrane	7	IPR002591; IPR017849; IPR017850; IPR024873
1589	DMPC15225607_Speleonectes_tulumensis_0	ves g 5 allergen	239	2.45E-24	50.90%	C:extracellular region	1	IPR001283; IPR002413; IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1590	DMPC15225642_Speleonectes_tulumensis_0	a chain crystal spectroscopic and catalytic properties of cobalt copper nickel and mercury derivatives of the zinc endopeptidase a correlation of structure and proteolytic activity	149	9.39E-19	53.40%	F:peptidase activity	1	IPR001506; IPR006026; IPR024079; PTHR24543 (PANTHER), PTHR24543:SF85 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF55486 (SUPERFAMILY)

1591	DMPC15225643_Speleonectes _tulumensis_1	netrin- partial	150	8.20E-13	78.90%	P:anatomical structure morphogenesis; P:cellular component organization; P:cell differentiation; P:multicellular organismal development; F:receptor binding; C:proteinaceous extracellular matrix; P:regulation of biological process; P:biological_process; C:Golgi apparatus; P:cell proliferation	10	IPR008993; IPR018933; G3DSA:2.40.50.120 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF44 (PANTHER)
1592	DMPC15225649_Speleonectes _tulumensis_2	26kda protease	122	9.66E-16	60.40%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
1593	DMPC15225693_Speleonectes _tulumensis_0	ecdysteroid-regulated 16 kda protein	146	3.05E-13	55.60%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
1594	DMPC15225706_Speleonectes _tulumensis_1	serine protease 82 precursor	118	1.41E-11	59.75%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
1595	DMPC15225810_Speleonectes _tulumensis_1	cathepsin d	134	6.36E-45	78.50%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR001461; IPR001969; IPR012848; IPR021109; PTHR13683:SF84 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1596	DMPC15225814_Speleonectes _tulumensis_1	peptidyl-prolyl cis-trans rhodopsin-specific isozyme-like	121	8.96E-33	73.90%	F:peptidyl-prolyl cis-trans isomerase activity; P:protein folding; P:protein peptidyl-prolyl isomerization; F:isomerase activity	4	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF168 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1597	DMPC15225821_Speleonectes _tulumensis_2	aminoacyl trna synthase complex-interacting multifunctional protein 1	141	3.97E-10	66.80%	P:biological_process; F:binding; C:organelle; C:intracellular; P:primary metabolic process; C:cytoplasm	6	no IPS match
1598	DMPC15225971_Speleonectes _tulumensis_1	amine oxidase	408	2.10E-41	65.10%	C:mitochondrion; F:oxidoreductase activity; P:dopamine catabolic process	3	IPR001613; IPR002937; G3DSA:3.50.50.60 (GENE3D), G3DSA:3.90.660.10 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF5 (PANTHER), tmhmm (TMHMM), SSF51905 (SUPERFAMILY), SSF54373 (SUPERFAMILY)
1599	DMPC15225978_Speleonectes _tulumensis_1	cathepsin l precursor	142	1.03E-22	87.20%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1600	DMPC15226006_Speleonectes _tulumensis_2	ectonucleotide pyrophosphatase phosphodiesterase family member 5	121	1.62E-25	56.80%	P:metabolic process; F:catalytic activity	2	IPR002591; IPR017850; IPR024873
1601	DMPC15226057_Speleonectes _tulumensis_2	trypsin-like serine proteinase 1	129	4.53E-13	52.50%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
1602	DMPC15226078_Speleonectes _tulumensis_2	serine protease precursor	156	2.45E-18	59.90%	P:proteolysis; F:serine-type endopeptidase activity; P:negative regulation of catalytic activity; F:identical protein binding	4	IPR007280; SignalP-NN(euk) (SIGNALP)
1603	DMPC15226183_Speleonectes _tulumensis_2	endothelin-converting enzyme	190	3.80E-86	83.40%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000718; IPR018497; IPR024079; PTHR11733:SF31 (PANTHER), SSF55486 (SUPERFAMILY)
1604	DMPC15226214_Speleonectes _tulumensis_0	GM15238	131	6.73E-12	59.90%	P:oxidation-reduction process; F:heme binding; P:response to oxidative stress; F:peroxidase activity	4	IPR002007; IPR010255; PTHR11475 (PANTHER), PTHR11475:SF7 (PANTHER), tmhmm (TMHMM)
1605	DMPC15226362_Speleonectes _tulumensis_1	cd74 major histocompatibility class ii invariant chain a	126	1.37E-07	67.67%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP)
1606	DMPC15226378_Speleonectes _tulumensis_2	chitinase partial	112	6.79E-19	87.00%	F:hydrolase activity; F:binding; P:carbohydrate metabolic process; P:catabolic process	4	IPR001223; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1607	DMPC15226407_Speleonectes _tulumensis_0	---NA---	150			-	0	IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1608	DMPC15226433_Speleonectes _tulumensis_2	epididymal secretory protein e1 isoform 1	143	1.90E-23	57.90%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

1609	DMPC15226450_Speleonectes_tulumensis_1	---NA---	107			-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
1610	DMPC15226533_Speleonectes_tulumensis_0	---NA---	136			-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21179 (PANTHER), PTHR21179:SF0 (PANTHER), SSF100895 (SUPERFAMILY)
1611	DMPC15226567_Speleonectes_tulumensis_0	glutathione peroxidase 7	115	8.38E-33	77.60%	C:extracellular region; F:catalytic activity; F:antioxidant activity; P:response to stress; P:metabolic process	5	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
1612	DMPC15226625_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_308200	146	1.20E-08	50.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1613	DMPC15226639_Speleonectes_tulumensis_1	cathepsin l	160	4.10E-39	85.50%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1614	DMPC15226707_Speleonectes_tulumensis_1	epididymal secretory protein e1 precursor	153	1.86E-26	58.10%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
1615	DMPC15226713_Speleonectes_tulumensis_2	cathepsin l	36	6.27E-13	87.10%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1616	DMPC15226772_Speleonectes_tulumensis_0	dermatopontin 3	105	3.58E-07	58.60%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1617	DMPC15226781_Speleonectes_tulumensis_1	membrane metallo-endopeptidase-like 1-like	112	5.47E-20	71.10%	P:proteolysis; F:hydrolase activity; F:metalloendopeptidase activity	3	IPR000718; IPR018497; IPR024079; PTHR11733:SF31 (PANTHER), SSF55486 (SUPERFAMILY)
1618	DMPC15226810_Speleonectes_tulumensis_1	perlucin 5	146	1.05E-11	50.00%	F:binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1619	DMPC15226861_Speleonectes_tulumensis_0	dermatopontin 2	111	2.24E-08	61.25%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1620	DMPC15226905_Speleonectes_tulumensis_2	---NA---	140			-	0	IPR001283; IPR014044
1621	DMPC15227056_Speleonectes_tulumensis_2	muscle-specific protein 20	141	2.14E-46	74.40%	-	0	IPR001715; IPR001997; IPR003096; PTHR18959 (PANTHER)
1622	DMPC15227064_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	354	1.29E-38	60.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1623	DMPC15227175_Speleonectes_tulumensis_0	epididymal secretory protein e1	153	4.54E-11	63.80%	P:transport; F:binding; C:intracellular	3	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1624	DMPC15227215_Speleonectes_tulumensis_2	thioredoxin 2	123	1.67E-24	70.70%	P:cell redox homeostasis; F:electron carrier activity; P:glycerol ether metabolic process; F:protein disulfide oxidoreductase activity	4	IPR005746; IPR012336; IPR013766; PTHR10438:SF13 (PANTHER)
1625	DMPC15227279_Speleonectes_tulumensis_1	cathepsin l	151	3.49E-14	59.50%	-	0	IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
1626	DMPC15227325_Speleonectes_tulumensis_0	glutathione peroxidase 1	108	3.09E-34	79.60%	F:catalytic activity; F:antioxidant activity; P:response to stress; P:metabolic process	4	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
1627	DMPC15227360_Speleonectes_tulumensis_1	ankyrin repeat and sam domain-containing protein 1a-like	162	3.87E-56	89.90%	-	0	IPR002110; IPR020683; PTHR24178 (PANTHER), PTHR24178:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP)
1628	DMPC15227404_Speleonectes_tulumensis_0	trypsin 3	174	5.13E-41	74.50%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1629	DMPC15227415_Speleonectes_tulumensis_1	microfibrillar-associated protein 1-like	197	7.26E-16	79.00%	-	0	IPR009730; PTHR15327:SF0 (PANTHER)
1630	DMPC15227418_Speleonectes_tulumensis_1	serine proteinase stubble-like	196	3.03E-45	55.70%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)

1631	DMPC15227420_Speleonectes_tulumensis_1	ame: full=isotocin-neurophysin it 1 contains: ame: full=isotocin short=it contains: ame: full=neurophysin it 1 flags: precursor	149	7.87E-10	64.50%	F:neurohypophyseal hormone activity; C:extracellular region	2	IPR000981; PTHR11681:SF0 (PANTHER), tmhmm (TMHMM)
1632	DMPC15227429_Speleonectes_tulumensis_2	---NA---	50			-	0	IPR001672; G3DSA:3.40.50.10490 (GENE3D), PTHR11469:SF0 (PANTHER)
1633	DMPC15227486_Speleonectes_tulumensis_2	pkhd domain-containing transmembrane protein c17orf101 homolog	130	1.71E-68	84.60%	-	0	IPR005123; PTHR14650 (PANTHER), PTHR14650:SF0 (PANTHER)
1634	DMPC15227555_Speleonectes_tulumensis_1	60s ribosomal protein l40	124	5.21E-43	96.20%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)
1635	DMPC15227565_Speleonectes_tulumensis_1	secreted protein, putative	253	2.16E-43	82.80%	F:cytoskeletal protein binding; C:cell	2	IPR001050; IPR003585; PTHR10915:SF1 (PANTHER), tmhmm (TMHMM)
1636	DMPC15227586_Speleonectes_tulumensis_5	hemocyanin subunit type 1 precursor	146	2.42E-44	84.50%	-	0	IPR000896; IPR008922; IPR013788; PTHR11511:SF20 (PANTHER)
1637	DMPC15227808_Speleonectes_tulumensis_1	zinc proteinase mpc1	152	6.26E-10	48.50%	-	0	IPR001506; IPR024079; PTHR10127 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF55486 (SUPERFAMILY)
1638	DMPC15227891_Speleonectes_tulumensis_2	short isoform c	125	1.77E-18	61.50%	P:signal transduction; P:anatomical structure morphogenesis; P:multicellular organismal development; P:embryo development; P:reproduction; P:cell differentiation	6	IPR010895
1639	DMPC15227961_Speleonectes_tulumensis_0	projectin short variant	244	8.13E-83	75.30%	-	0	IPR003599; IPR007110; IPR013098; IPR013783; IPR020675; SSF48726 (SUPERFAMILY)
1640	DMPC15227988_Speleonectes_tulumensis_2	phospholipase a2	146	6.09E-17	66.20%	F:hydrolase activity; P:lipid metabolic process	2	IPR001211; IPR016090
1641	DMPC15228058_Speleonectes_tulumensis_2	cytochrome b5 domain-containing protein 2	152	1.11E-12	62.70%	F:heme binding	1	IPR001199; PTHR10281 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1642	DMPC15228135_Speleonectes_tulumensis_1	ale o 1 allergen	157	4.95E-63	78.90%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1643	DMPC15228196_Speleonectes_tulumensis_0	glyceraldehyde 3-phosphate dehydrogenase	144	1.19E-70	93.30%	C:cytoplasm; F:nucleotide binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:catalytic activity; P:metabolic process	7	IPR020829; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF55347 (SUPERFAMILY)
1644	DMPC15228211_Speleonectes_tulumensis_0	arylsulfatase b	157	5.46E-42	74.20%	F:catalytic activity	1	IPR000917; IPR017849; IPR017850; IPR024607; PTHR10342 (PANTHER), PTHR10342:SF19 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1645	DMPC15228215_Speleonectes_tulumensis_0	heat shock protein 70	387	5.85E-132	93.90%	F:nucleotide binding	1	IPR013126; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), PTHR19375 (PANTHER), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY)
1646	DMPC15228230_Speleonectes_tulumensis_2	cathepsin l	109	1.44E-33	83.30%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1647	DMPC15228248_Speleonectes_tulumensis_0	---NA---	150			-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER)
1648	DMPC15228276_Speleonectes_tulumensis_1	trypsin 2	158	4.20E-24	57.20%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1649	DMPC15228343_Speleonectes_tulumensis_0	endothelin-converting enzyme 1	209	1.50E-68	72.80%	-	0	IPR000718; IPR018497; IPR024079; PTHR11733:SF26 (PANTHER), SSF55486 (SUPERFAMILY)

1650	DMPC15228357_Speleonectes _tulumensis_0	protein disulfide-isomerase a4-like	373	1.72E-102	73.20%	P:cell redox homeostasis	1	IPR012336; IPR013766; PTHR18929 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1651	DMPC15228360_Speleonectes _tulumensis_1	stromal cell-derived factor 2-like protein 1-like isoform 1	110	5.63E-28	74.80%	C:cell; F:transferase activity	2	IPR016093; IPR027005; G3DSA:2.80.10.50 (GENE3D), SignalP-NN(euk) (SIGNALP)
1652	DMPC15228378_Speleonectes _tulumensis_1	trypsin	102	2.86E-17	66.90%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24257 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1653	DMPC15228380_Speleonectes _tulumensis_1	glyceraldehyde-3-phosphate dehydrogenase	160	2.29E-27	89.10%	-	0	IPR020829; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF55347 (SUPERFAMILY)
1654	DMPC15228449_Speleonectes _tulumensis_1	glutaredoxin-3	100	2.17E-13	60.80%	P:cell redox homeostasis; F:electron carrier activity; F:protein disulfide oxidoreductase activity	3	IPR004480; IPR012336; IPR013766; PTHR10293:SF17 (PANTHER)
1655	DMPC15228482_Speleonectes _tulumensis_2	cathepsin l	108	3.18E-21	62.10%	P:proteolysis; F:hydrolase activity; F:cysteine-type peptidase activity; F:peptidase activity	4	IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1656	DMPC15228492_Speleonectes _tulumensis_0	protein	148	3.15E-20	50.20%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1657	DMPC15228527_Speleonectes _tulumensis_1	cd74 major histocompatibility class ii invariant chain a	145	7.67E-08	67.00%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1658	DMPC15228541_Speleonectes _tulumensis_1	galectin partial	205	6.73E-27	60.70%	F:carbohydrate binding	1	IPR001079; IPR008985; IPR013320; PTHR11346 (PANTHER)
1659	DMPC15228667_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor-like	113	5.05E-11	62.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1660	DMPC15228681_Speleonectes _tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	133	4.17E-19	52.30%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12036 (PANTHER), PTHR12036:SF5 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1661	DMPC15228686_Speleonectes _tulumensis_2	carcinolectin 5a partial	188	1.28E-12	66.50%	-	0	IPR002181; IPR014716; PTHR19143 (PANTHER), PTHR19143:SF47 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1662	DMPC15228714_Speleonectes _tulumensis_2	60s ribosomal protein l40	131	1.11E-46	98.10%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1663	DMPC15228770_Speleonectes _tulumensis_2	oocyte protease inhibitor-1 precursor	120	2.16E-08	63.40%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1664	DMPC15228834_Speleonectes _tulumensis_1	60s ribosomal protein l40	129	3.47E-42	95.30%	P:cell cycle; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; C:cytosol; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; C:plasma membrane; ; C:endosome; P:cellular component organization; C:ribosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; P:cellular protein modification process; P:translation; P:transport	25	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1665	DMPC15228985_Speleonectes _tulumensis_1	cathepsin l	123	1.28E-13	63.80%	-	0	IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
1666	DMPC15229048_Speleonectes _tulumensis_0	variable lymphocyte receptor	143	5.71E-07	49.50%	-	0	IPR001611; G3DSA:3.80.10.10 (GENE3D), PTHR24365 (PANTHER), SSF52058 (SUPERFAMILY)

1667	DMPC15229080_Speleonectes_tulumensis_2	beta- -	127	1.29E-20	71.70%	F:transferase activity	1	IPR003859; G3DSA:3.90.550.10 (GENE3D), PTHR19300:SF5 (PANTHER), PF13733 (PFAM), SSF53448 (SUPERFAMILY)
1668	DMPC15229116_Speleonectes_tulumensis_2	histone h2a	124	3.09E-47	90.20%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)
1669	DMPC15229132_Speleonectes_tulumensis_1	orcokinin precursor	127	3.73E-20	76.40%	-	0	PTHR22283 (PANTHER)
1670	DMPC15229218_Speleonectes_tulumensis_0	oocyte protease inhibitor-1 precursor	117	1.10E-10	63.90%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1671	DMPC15229316_Speleonectes_tulumensis_0	---NA---	113			-	0	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1672	DMPC15229369_Speleonectes_tulumensis_1	cd74 major histocompatibility class ii invariant chain a	133	4.00E-08	67.67%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP)
1673	DMPC15229487_Speleonectes_tulumensis_2	isoform cra_b	149	6.17E-49	93.20%	C:nucleoplasm; P:signal transduction; P:response to stress; P:DNA metabolic process; P:translation; F:binding; P:metabolic process; F:structural molecule activity; C:endosome; C:ribosome; C:cytosol	11	IPR000626; IPR002906; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1674	DMPC15229530_Speleonectes_tulumensis_0	virulence metalloprotease	286	9.63E-10	48.60%	P:proteolysis; F:metallopeptidase activity; F:hydrolase activity; F:peptidase activity; F:metalloendopeptidase activity	5	IPR025711; tmhmm (TMHMM)
1675	DMPC15229628_Speleonectes_tulumensis_2	hypothetical protein Phum_PHUM596260	148	7.30E-08	73.00%	-	0	SSF57501 (SUPERFAMILY)
1676	DMPC15229668_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	135	3.85E-09	58.30%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1677	DMPC15229686_Speleonectes_tulumensis_1	peroxiredoxin 1-like	101	9.74E-36	87.70%	P:metabolic process; F:antioxidant activity; F:catalytic activity	3	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF50 (PANTHER)
1678	DMPC15229763_Speleonectes_tulumensis_2	prophenoloxidase activating factor	135	3.33E-09	57.60%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
1679	DMPC15229917_Speleonectes_tulumensis_2	thioredoxin 1	86	1.15E-20	83.10%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; PTHR10438:SF127 (PANTHER), SignalP-NN(euk) (SIGNALP)
1680	DMPC15229945_Speleonectes_tulumensis_0	nas-15 protein	145	1.63E-23	60.60%	F:hydrolase activity	1	IPR001506; IPR024079; PTHR24543 (PANTHER), PTHR24543:SF85 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF55486 (SUPERFAMILY)
1681	DMPC15229970_Speleonectes_tulumensis_1	cathepsin l	167	1.58E-56	78.60%	F:peptidase activity	1	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1682	DMPC15229990_Speleonectes_tulumensis_2	beta 1-like 2	178	6.63E-26	61.10%	F:hydrolase activity	1	IPR001944; PTHR23421:SF14 (PANTHER)
1683	DMPC15230023_Speleonectes_tulumensis_1	ferritin	121	8.00E-23	88.50%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1684	DMPC15230087_Speleonectes_tulumensis_2	grn protein	132	2.24E-13	57.40%	-	0	IPR000118; PTHR12274 (PANTHER), PTHR12274:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1685	DMPC15230089_Speleonectes_tulumensis_0	uncharacterized aarf domain-containing protein kinase 1-like isoform 2	121	1.19E-26	72.30%	F:transferase activity	1	PTHR10566 (PANTHER), PTHR10566:SF24 (PANTHER)
1686	DMPC15230150_Speleonectes_tulumensis_0	trypsin	126	3.34E-20	54.00%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER)
1687	DMPC15230166_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor-like	114	9.70E-12	63.60%	-	0	IPR026645
1688	DMPC15230255_Speleonectes_tulumensis_1	proclotting enzyme-like	256	1.06E-46	55.90%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER)

1689	DMPC15230263_Speleonectes_tulumensis_1	epididymal secretory protein e1 isoform 1	146	2.31E-17	55.40%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER)
1690	DMPC15230359_Speleonectes_tulumensis_1	hemocyanin subunit type 1 precursor	153	1.47E-37	72.90%	-	0	IPR005203; IPR013788; IPR014756
1691	DMPC15230408_Speleonectes_tulumensis_1	chymotrypsin a	204	1.74E-26	60.10%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), tmhmm (TMHMM)
1692	DMPC15230431_Speleonectes_tulumensis_2	superoxide dismutase mitochondrial	92	1.32E-19	77.10%	F:binding; P:metabolic process; F:catalytic activity; P:biological_process	4	IPR001189; IPR019831; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER)
1693	DMPC15230517_Speleonectes_tulumensis_2	serine-threonine kinase receptor-associated	132	3.01E-42	86.70%	-	0	IPR001680; IPR015943; IPR017986; IPR019775; PTHR19877 (PANTHER), SSF82171 (SUPERFAMILY)
1694	DMPC15230547_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor-like	107	7.71E-14	64.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1695	DMPC15230567_Speleonectes_tulumensis_0	thioredoxin 1	151	1.39E-52	83.30%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; IPR017937; SignalP-NN(euk) (SIGNALP)
1696	DMPC15230596_Speleonectes_tulumensis_1	soma ferritin	105	3.27E-24	88.00%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1697	DMPC15230637_Speleonectes_tulumensis_0	cathepsin d	218	1.03E-62	82.10%	C:lysosome; P:protein metabolic process; P:catabolic process; F:peptidase activity	4	IPR001461; IPR001969; IPR021109; PTHR13683:SF84 (PANTHER), tmhmm (TMHMM)
1698	DMPC15230646_Speleonectes_tulumensis_1	dermatopontin 2	133	3.17E-14	57.60%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1699	DMPC15230722_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	140	2.55E-13	56.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
1700	DMPC15230764_Speleonectes_tulumensis_0	glutathione peroxidase 1	124	1.75E-25	77.40%	-	0	IPR000889; IPR012336
1701	DMPC15230777_Speleonectes_tulumensis_1	dermatopontin 2	250	1.43E-35	59.80%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1702	DMPC15230822_Speleonectes_tulumensis_1	vitellogenin 1	89	1.24E-11	61.57%	-	0	IPR001846
1703	DMPC15230839_Speleonectes_tulumensis_1	hemocyanin subunit type 1 precursor	147	1.23E-55	68.60%	-	0	IPR005204; IPR013788; PTHR11511:SF20 (PANTHER), SignalP-NN(euk) (SIGNALP)
1704	DMPC15230852_Speleonectes_tulumensis_0	kazal-type serine proteinase inhibitor 4	125	3.38E-13	59.50%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR25189 (PANTHER), PTHR25189:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1705	DMPC15230901_Speleonectes_tulumensis_2	si:dkey- protein	108	3.88E-10	59.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1706	DMPC15230935_Speleonectes_tulumensis_1	arylsulfatase b-like	118	4.63E-18	89.90%	P:metabolic process; F:hydrolase activity	2	IPR000917; IPR017849; IPR017850; PTHR10342 (PANTHER), PTHR10342:SF19 (PANTHER)
1707	DMPC15231009_Speleonectes_tulumensis_1	secretory phospholipase partial	140	3.96E-19	62.30%	F:phospholipase A2 activity; F:calcium ion binding; F:hydrolase activity; P:lipid catabolic process	4	IPR001211; IPR016090; PTHR12253:SF1 (PANTHER)
1708	DMPC15231017_Speleonectes_tulumensis_1	cathepsin l	145	5.75E-67	78.00%	-	0	IPR000668; IPR013128; IPR025660; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1709	DMPC15231066_Speleonectes_tulumensis_2	nk-tumor recognition protein	162	5.92E-63	88.60%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; IPR020892; IPR024936; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF130 (PANTHER)
1710	DMPC15231099_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	130	1.91E-27	68.50%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1711	DMPC15231216_Speleonectes_tulumensis_0	hepatopancreas partial	177	4.15E-37	73.90%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)

1712	DMPC15231220_Speleonectes_tulumensis_2	ame: full=hemagglutinin amebocyte aggregation factor ame: full=18k-laf flags: precursor	96	2.79E-07	67.00%	-	0	no IPS match
1713	DMPC15231353_Speleonectes_tulumensis_0	ectonucleotide pyrophosphatase phosphodiesterase family member 6	138	1.43E-25	54.80%	P:metabolic process; F:catalytic activity	2	IPR002591; IPR017849; IPR017850; IPR024873; PTHR10151:SF15 (PANTHER)
1714	DMPC15231475_Speleonectes_tulumensis_1	transmembrane protease serine 4	281	1.59E-27	49.60%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24258 (PANTHER), SignalP-NN(euk) (SIGNALP)
1715	DMPC15231483_Speleonectes_tulumensis_1	selenium-dependent glutathione peroxidase	113	3.16E-33	78.90%	-	0	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
1716	DMPC15231495_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	146	3.52E-23	59.10%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1717	DMPC15231519_Speleonectes_tulumensis_2	dermatopontin 3	104	4.19E-08	64.29%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1718	DMPC15231572_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor	155	1.59E-30	68.10%	-	0	IPR024509; IPR024716
1719	DMPC15231607_Speleonectes_tulumensis_2	histone h1	123	1.49E-27	82.50%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR005818; IPR005819; IPR011991; PTHR11467 (PANTHER), PTHR11467:SF0 (PANTHER), SSF46785 (SUPERFAMILY)
1720	DMPC15231700_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	109	6.11E-08	59.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1721	DMPC15231715_Speleonectes_tulumensis_0	lipase 1 precursor	255	4.26E-60	65.60%	P:lipid metabolic process; F:hydrolase activity, acting on ester bonds; F:hydrolase activity; P:lipid catabolic process	4	IPR000073; IPR006693; G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53474 (SUPERFAMILY)
1722	DMPC15231766_Speleonectes_tulumensis_1	si:dkey- protein	140	2.01E-10	54.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
1723	DMPC15231837_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor-like	138	2.61E-13	63.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1724	DMPC15231940_Speleonectes_tulumensis_0	thioredoxin 2	165	1.49E-30	69.80%	P:cell redox homeostasis; F:electron carrier activity; P:glycerol ether metabolic process; F:protein disulfide oxidoreductase activity	4	IPR005746; IPR012336; IPR013766; PTHR10438:SF13 (PANTHER)
1725	DMPC15231975_Speleonectes_tulumensis_1	plasma glutamate carboxypeptidase-like	195	1.31E-46	70.80%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	G3DSA:3.40.630.10 (GENE3D), PTHR12053 (PANTHER), PTHR12053:SF2 (PANTHER), SignalP-NN(euk) (SIGNALP)
1726	DMPC15231985_Speleonectes_tulumensis_1	von willebrand factor d and egf domain-containing protein	112	2.33E-24	59.30%	F:calcium ion binding	1	IPR000742; IPR013032; G3DSA:2.170.300.10 (GENE3D), PTHR24044 (PANTHER), SSF57196 (SUPERFAMILY)
1727	DMPC15232110_Speleonectes_tulumensis_0	membrane glycoprotein lig-	235	6.94E-08	48.00%	F:hydrolase activity; F:phosphoprotein phosphatase activity	2	IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR24369 (PANTHER), SSF52058 (SUPERFAMILY)
1728	DMPC15232178_Speleonectes_tulumensis_1	multiple coagulation factor deficiency protein 2 homolog	289	1.05E-21	65.00%	-	0	IPR011992; IPR018247; PTHR23104 (PANTHER), PTHR23104:SF0 (PANTHER), SSF47473 (SUPERFAMILY)
1729	DMPC15232232_Speleonectes_tulumensis_1	dermatopontin 3	103	4.29E-08	59.13%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1730	DMPC15232237_Speleonectes_tulumensis_2	dermatopontin 2	104	1.51E-08	65.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1731	DMPC15232241_Speleonectes_tulumensis_1	serine protease precursor	149	5.34E-16	59.30%	P:proteolysis; F:serine-type endopeptidase activity; P:negative regulation of catalytic activity; F:identical protein binding	4	IPR007280; SignalP-NN(euk) (SIGNALP)
1732	DMPC15232248_Speleonectes_tulumensis_2	60s ribosomal protein l40	151	5.48E-42	96.00%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF54236 (SUPERFAMILY)

1733	DMPC15232279_Speleonectes_tulumensis_2	ame: full=venom allergen 5 ame: full=allergen ves s v ame: full=antigen 5 short=ag5 ame: full=cysteine-rich venom protein short=crvp ame: allergen=ves s 5	192	7.30E-18	61.50%	-	0	IPR001283; IPR002413; IPR014044; SignalP-NN(euk) (SIGNALP)
1734	DMPC15232341_Speleonectes_tulumensis_1	chymotrypsin-like elastase family member 2a-like	138	1.35E-10	60.10%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
1735	DMPC15232358_Speleonectes_tulumensis_2	dnaj homolog subfamily c member 24	120	3.59E-14	64.20%	F:binding	1	IPR001623; PTHR24078 (PANTHER)
1736	DMPC15232430_Speleonectes_tulumensis_0	mantle protein 9	138	1.30E-08	67.00%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF100895 (SUPERFAMILY)
1737	DMPC15232478_Speleonectes_tulumensis_0	hyaluronidase precursor	271	2.83E-67	62.60%	P:defense response; P:carbohydrate metabolic process; F:hyalurononglucosaminidase activity; F:catalytic activity	4	IPR001329; IPR013785; IPR017853; IPR018155; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1738	DMPC15232500_Speleonectes_tulumensis_1	hemocyanin subunit type 2 precursor	159	1.09E-27	77.80%	-	0	IPR005203; IPR013788; IPR014756; tmhmm (TMHMM)
1739	DMPC15232506_Speleonectes_tulumensis_2	dermatopontin 2	124	4.00E-08	59.38%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1740	DMPC15232564_Speleonectes_tulumensis_0	oxidase peroxidase	172	1.36E-51	63.90%	-	0	IPR002007; IPR010255; PTHR11475 (PANTHER)
1741	DMPC15232588_Speleonectes_tulumensis_2	venom allergen 5	150	2.09E-20	54.40%	-	0	IPR001283; IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1742	DMPC15232590_Speleonectes_tulumensis_1	zinc finger	154	8.71E-20	56.30%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR24402 (PANTHER), PTHR24402:SF54 (PANTHER), PF13894 (PFAM), SSF57667 (SUPERFAMILY)
1743	DMPC15232692_Speleonectes_tulumensis_0	clipb6 protein	116	8.63E-12	62.00%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
1744	DMPC15232731_Speleonectes_tulumensis_2	oocyte protease inhibitor-1 precursor	88	1.43E-10	66.90%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1745	DMPC15232755_Speleonectes_tulumensis_2	iron zinc purple acid phosphatase-like	118	2.88E-12	60.30%	F:metal ion binding; F:hydrolase activity; F:acid phosphatase activity	3	IPR008963; IPR015914; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1746	DMPC15232757_Speleonectes_tulumensis_1	soma ferritin	115	6.46E-34	87.40%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1747	DMPC15232764_Speleonectes_tulumensis_1	retinal dehydrogenase 1	125	2.94E-51	81.30%	C:cytoplasm; F:catalytic activity; P:lipid metabolic process; P:secondary metabolic process; P:metabolic process	5	IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
1748	DMPC15232765_Speleonectes_tulumensis_2	nas-15 protein	272	4.63E-44	54.00%	F:metal ion binding; P:proteolysis; F:metallopeptidase activity; F:hydrolase activity; F:zinc ion binding; F:peptidase activity; F:metalloendopeptidase activity	7	IPR001506; IPR006026; IPR024079; PTHR10127 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF55486 (SUPERFAMILY)
1749	DMPC15232859_Speleonectes_tulumensis_1	female neotenic-specific protein 3	116	1.80E-08	66.50%	-	0	no IPS match
1750	DMPC15232922_Speleonectes_tulumensis_2	hypothetical protein DAPPUDRAFT_57749	129	9.02E-45	75.30%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), PTHR24260:SF33 (PANTHER)
1751	DMPC15232926_Speleonectes_tulumensis_2	l-xylulose reductase	169	8.88E-54	69.20%	P:oxidation-reduction process; F:oxidoreductase activity; P:metabolic process; F:nucleotide binding; C:cellular_component	5	IPR002198; IPR002347; IPR016040; PTHR24311 (PANTHER), PTHR24311:SF0 (PANTHER), SSF51735 (SUPERFAMILY)
1752	DMPC15232937_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor	109	2.12E-08	60.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

1753	DMPC15233031_Speleonectes _tulumensis_2	predicted protein	103	5.07E-07	61.50%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
1754	DMPC15233076_Speleonectes _tulumensis_1	beta actin	132	6.91E-23	93.90%	F:nucleotide binding	1	IPR001916; IPR004000; IPR023346; G3DSA:1.10.530.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), PTHR11937:SF93 (PANTHER), SSF53067 (SUPERFAMILY)
1755	DMPC15233085_Speleonectes _tulumensis_0	hypothetical protein BRAFLDRAFT_77844	239	3.26E-35	51.40%	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process; F:cation binding; F:catalytic activity	4	IPR013781
1756	DMPC15233111_Speleonectes _tulumensis_0	sphingomyelin phosphodiesterase	262	1.64E-75	68.20%	F:sphingomyelin phosphodiesterase activity; F:hydrolase activity; P:sphingomyelin catabolic process	3	IPR004843; G3DSA:3.60.21.10 (GENE3D), PTHR10340 (PANTHER), PTHR10340:SF13 (PANTHER), SSF56300 (SUPERFAMILY)
1757	DMPC15233182_Speleonectes _tulumensis_0	er degradation-enhancing alpha-mannosidase-like 1	148	1.13E-25	86.50%	C:cell; P:metabolic process; F:hydrolase activity; F:calcium ion binding	4	IPR001382; PTHR11742:SF11 (PANTHER)
1758	DMPC15233192_Speleonectes _tulumensis_2	zinc finger protein 271-like	140	7.07E-47	68.30%	-	0	IPR007087; IPR013087; IPR015880; PTHR24402 (PANTHER), PTHR24402:SF42 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
1759	DMPC15233202_Speleonectes _tulumensis_2	grn protein	165	6.65E-11	49.00%	C:mitochondrion; P:embryo implantation; P:blastocyst hatching; P:positive regulation of epithelial cell proliferation	4	IPR000118; PTHR12274 (PANTHER), PTHR12274:SF0 (PANTHER)
1760	DMPC15233258_Speleonectes _tulumensis_1	cathepsin l2	140	1.86E-29	82.10%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1761	DMPC15233334_Speleonectes _tulumensis_0	thioredoxin-like protein 1-like	127	5.59E-42	88.10%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; IPR017937; PTHR10438:SF19 (PANTHER)
1762	DMPC15233422_Speleonectes _tulumensis_1	ferritin h subunit	115	1.79E-19	89.80%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1763	DMPC15233477_Speleonectes _tulumensis_0	glyceraldehyde-3-phosphate dehydrogenase	138	1.36E-12	84.90%	F:catalytic activity; P:metabolic process	2	IPR020829; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF55347 (SUPERFAMILY)
1764	DMPC15233480_Speleonectes _tulumensis_2	cathepsin partial	134	2.26E-47	69.80%	F:hydrolase activity	1	IPR000169; IPR000668; IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1765	DMPC15233504_Speleonectes _tulumensis_2	canopy homolog 2 precursor	258	7.22E-42	71.80%	-	0	IPR021852; PTHR13341 (PANTHER), PTHR13341:SF3 (PANTHER), tmhmm (TMHMM)
1766	DMPC15233564_Speleonectes _tulumensis_0	plasminogen activator spa	123	1.05E-21	63.80%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
1767	DMPC15233600_Speleonectes _tulumensis_2	acyl- -binding protein	152	6.55E-40	81.20%	F:lipid binding	1	IPR000582; IPR014352; IPR022408; PTHR23310 (PANTHER)
1768	DMPC15233659_Speleonectes _tulumensis_0	pr domain zinc finger protein 16-like	103	1.76E-16	67.00%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
1769	DMPC15233727_Speleonectes _tulumensis_0	soma ferritin	115	4.57E-24	88.30%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1770	DMPC15233826_Speleonectes _tulumensis_2	hyaluronidase ph-20-like	81	4.58E-10	55.30%	-	0	IPR013785; IPR017853; IPR018155; PTHR11769:SF8 (PANTHER)
1771	DMPC15233890_Speleonectes _tulumensis_1	lysozyme c-like	102	7.77E-07	63.00%	-	0	IPR001916; IPR023346; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER), PTHR11407:SF2 (PANTHER)
1772	DMPC15233917_Speleonectes _tulumensis_1	a chain carbonic anhydrase ii complexed with 4- -n-	337	4.03E-37	59.20%	P:biological_process; F:binding; C:cytoplasm; C:cell	4	IPR001148; IPR018338; IPR023561; SignalP-NN(euk) (SIGNALP)
1773	DMPC15233952_Speleonectes _tulumensis_1	calreticulin	69	2.80E-08	76.00%	-	0	IPR001580; IPR013320; PTHR11073:SF2 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

1774	DMPC15233955_Speleonectes _tulumensis_2	dermatopontin 3	103	4.06E-08	59.13%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1775	DMPC15233957_Speleonectes _tulumensis_0	serine protease	181	3.91E-15	61.30%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1776	DMPC15233990_Speleonectes _tulumensis_0	peptidoglycan recognition protein 3 short class	324	6.05E-56	63.40%	F:zinc ion binding; P:peptidoglycan catabolic process; F:N-acetylmuramoyl-L-alanine amidase activity	3	IPR002502; IPR006619; IPR015510; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1777	DMPC15234069_Speleonectes _tulumensis_2	peptidase s1 and s6 chymotrypsin hap	144	8.24E-11	66.40%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
1778	DMPC15234204_Speleonectes _tulumensis_0	peptidyl-prolyl cis-trans	300	2.29E-57	70.70%	P:protein metabolic process; F:binding; F:catalytic activity	3	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF22 (PANTHER)
1779	DMPC15234258_Speleonectes _tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	147	8.97E-20	51.50%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12036 (PANTHER), PTHR12036:SF5 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1780	DMPC15234310_Speleonectes _tulumensis_2	anti-lipopolysaccharide factor	144	5.47E-21	65.60%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1781	DMPC15234337_Speleonectes _tulumensis_2	epididymal secretory protein e1	145	1.74E-12	57.60%	P:transport	1	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
1782	DMPC15234450_Speleonectes _tulumensis_2	60s ribosomal protein l40	125	8.55E-47	96.10%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1783	DMPC15234487_Speleonectes _tulumensis_1	---NA---	92			-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1784	DMPC15234511_Speleonectes _tulumensis_1	calponin transgelin	153	1.13E-54	91.40%	F:actin binding; P:cytoskeleton organization	2	IPR001715; IPR001997; IPR003096; PTHR18959 (PANTHER), PTHR18959:SF3 (PANTHER), SignalP-NN(euk) (SIGNALP)
1785	DMPC15234517_Speleonectes _tulumensis_2	low affinity immunoglobulin epsilon fc receptor	197	3.51E-17	50.10%	F:carbohydrate binding	1	IPR001304; IPR016186; IPR016187; IPR018378; PTHR22802 (PANTHER)
1786	DMPC15234535_Speleonectes _tulumensis_2	matrix metalloproteinase-9	104	8.41E-09	54.00%	-	0	IPR000562; IPR013806; PTHR22918 (PANTHER), PTHR22918:SF0 (PANTHER)
1787	DMPC15234597_Speleonectes _tulumensis_1	selenium-dependent glutathione peroxidase	129	1.82E-44	78.60%	-	0	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
1788	DMPC15234647_Speleonectes _tulumensis_2	cathepsin l	158	1.94E-75	79.70%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1789	DMPC15234692_Speleonectes _tulumensis_1	chain crystal structure of engineered northeast structural genomics consortium target	159	6.29E-32	67.00%	F:catalytic activity	1	IPR002110; IPR020683; PTHR24188 (PANTHER), PF13637 (PFAM)
1790	DMPC15234696_Speleonectes _tulumensis_2	zinc finger protein 251-like	118	1.66E-12	64.90%	-	0	IPR007087; IPR013087; IPR015880; PTHR24382 (PANTHER), PTHR24382:SF0 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
1791	DMPC15234706_Speleonectes _tulumensis_1	cathepsin l	109	3.38E-17	78.30%	-	0	IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1792	DMPC15234712_Speleonectes _tulumensis_1	---NA---	177			-	0	IPR008197; PTHR19441 (PANTHER)
1793	DMPC15234752_Speleonectes _tulumensis_2	cathepsin l-like	150	1.51E-22	87.40%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
1794	DMPC15234810_Speleonectes _tulumensis_1	beta-ig-h3 fasciclin	87	1.06E-12	56.20%	-	0	IPR000782; PTHR10900 (PANTHER)

1795	DMPC15234852_Speleonectes_tulumensis_1	chitinase partial	178	4.07E-36	60.10%	P:chitin catabolic process; F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process; F:cation binding; F:catalytic activity; F:chitinase activity	6	IPR001223; IPR011583; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SSF54556 (SUPERFAMILY)
1796	DMPC15234877_Speleonectes_tulumensis_1	serine protease like protein	153	4.64E-15	60.40%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER)
1797	DMPC15234887_Speleonectes_tulumensis_1	dermatopontin 2	138	2.34E-17	58.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1798	DMPC15234903_Speleonectes_tulumensis_1	---NA---	211			-	0	IPR002172; IPR023415; PTHR24652 (PANTHER), PTHR24652:SF0 (PANTHER)
1799	DMPC15234913_Speleonectes_tulumensis_1	serine protease 52-like	126	8.44E-19	63.30%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1800	DMPC15234944_Speleonectes_tulumensis_2	female neotenic-specific protein 3	137	4.22E-10	54.14%	-	0	tmhmm (TMHMM)
1801	DMPC15235027_Speleonectes_tulumensis_1	serine protease inhibitor kazal-type 6-like	285	3.24E-09	63.75%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1802	DMPC15235164_Speleonectes_tulumensis_2	phosphoglucose isomerase	244	1.13E-68	78.40%	-	0	IPR001672; IPR023096; G3DSA:3.40.50.10490 (GENE3D), PTHR11469:SF0 (PANTHER), SSF53697 (SUPERFAMILY)
1803	DMPC15235190_Speleonectes_tulumensis_0	abhydrolase domain-containing protein 13-like	207	1.12E-77	75.10%	-	0	G3DSA:3.40.50.1820 (GENE3D), PTHR12277 (PANTHER), PF12695 (PFAM), SSF53474 (SUPERFAMILY)
1804	DMPC15235221_Speleonectes_tulumensis_0	trypsin 3	161	7.19E-56	76.80%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1805	DMPC15235315_Speleonectes_tulumensis_2	macrophage migration inhibitory factor	228	1.92E-39	68.40%	-	0	IPR001398; IPR014347; G3DSA:3.30.429.10 (GENE3D), PTHR11954:SF4 (PANTHER)
1806	DMPC15235331_Speleonectes_tulumensis_2	protein flightless-1	96	1.81E-32	89.00%	F:actin binding	1	IPR007122; PTHR11977:SF6 (PANTHER), SSF55753 (SUPERFAMILY)
1807	DMPC15235336_Speleonectes_tulumensis_1	trypsinogen 1	140	3.52E-30	71.60%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1808	DMPC15235342_Speleonectes_tulumensis_2	ferritin-1 heavy chain	114	5.85E-21	88.90%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1809	DMPC15235346_Speleonectes_tulumensis_2	glutamate carboxypeptidase	142	1.44E-12	74.50%	C:cytoplasm; F:peptidase activity	2	no IPS match
1810	DMPC15235532_Speleonectes_tulumensis_2	heat shock cognate 70 protein	101	3.60E-42	95.10%	-	0	IPR013126; G3DSA:3.90.640.10 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), SSF53067 (SUPERFAMILY)
1811	DMPC15235609_Speleonectes_tulumensis_0	hyaluronan-binding protein 2	96	7.00E-11	55.70%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)
1812	DMPC15235619_Speleonectes_tulumensis_2	myosin light chain smooth muscle	121	5.54E-30	68.10%	-	0	IPR003599; IPR007110; IPR013098; IPR013783; PTHR25963 (PANTHER), SSF48726 (SUPERFAMILY)
1813	DMPC15235621_Speleonectes_tulumensis_1	phosphoglycerate kinase 2	148	2.67E-31	88.50%	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; P:metabolic process; F:kinase activity	5	IPR001576; IPR015901; PTHR11406:SF1 (PANTHER)
1814	DMPC15235626_Speleonectes_tulumensis_2	n-acetylglucosamine-1-phosphotransferase subunit gamma	88	7.96E-22	69.60%	F:transferase activity; C:Golgi apparatus; C:extracellular region	3	PTHR12630 (PANTHER), PTHR12630:SF2 (PANTHER)
1815	DMPC15235685_Speleonectes_tulumensis_0	protein lethal giant larvae-like isoform 1	294	4.94E-82	75.10%	-	0	PTHR10241 (PANTHER), PTHR10241:SF10 (PANTHER)
1816	DMPC15235800_Speleonectes_tulumensis_0	perlucin 5	155	2.20E-12	48.70%	F:carbohydrate binding	1	IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1817	DMPC15235840_Speleonectes_tulumensis_0	carboxypeptidase b-like	369	6.89E-118	65.30%	-	0	IPR000834; IPR003146; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)

1818	DMPC15235857_Speleonectes _tulumensis_2	isoform e	152	1.81E-18	50.70%	-	0	IPR004911; PTHR13234:SF7 (PANTHER), SignalP-NN(euk) (SIGNALP)
1819	DMPC15235904_Speleonectes _tulumensis_2	soma ferritin	116	2.17E-36	89.00%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1820	DMPC15236058_Speleonectes _tulumensis_1	trypsin	156	1.81E-28	63.50%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER)
1821	DMPC15236072_Speleonectes _tulumensis_1	soma ferritin	114	1.36E-34	87.50%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1822	DMPC15236124_Speleonectes _tulumensis_0	grn protein	97	9.99E-09	62.00%	-	0	IPR000118; PTHR12274 (PANTHER), PTHR12274:SF0 (PANTHER)
1823	DMPC15236158_Speleonectes _tulumensis_2	protein mother of ft and tf 1-like	172	1.64E-16	55.00%	P:response to abscisic acid stimulus; P:positive regulation of seed germination; C:nucleus	3	IPR001858; IPR008914; PTHR11362 (PANTHER), PTHR11362:SF2 (PANTHER), tmhmm (TMHMM)
1824	DMPC15236167_Speleonectes _tulumensis_1	kallikrein-11 isoform 2	175	9.87E-21	64.80%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), tmhmm (TMHMM)
1825	DMPC15236225_Speleonectes _tulumensis_1	histone partial	126	2.07E-32	95.70%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)
1826	DMPC15236246_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor	140	2.98E-08	56.83%	-	0	IPR026645
1827	DMPC15236505_Speleonectes _tulumensis_1	---NA---	111			-	0	IPR000716; PTHR12352 (PANTHER)
1828	DMPC15236515_Speleonectes _tulumensis_2	epididymal secretory protein e1 precursor	200	2.60E-30	57.40%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER)
1829	DMPC15236524_Speleonectes _tulumensis_1	hemocyanin subunit type 1 precursor	138	5.34E-49	69.50%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1830	DMPC15236584_Speleonectes _tulumensis_1	female neotenic-specific protein 3	152	9.68E-12	53.78%	-	0	no IPS match
1831	DMPC15236605_Speleonectes _tulumensis_2	SP14D1	160	7.74E-07	65.00%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1832	DMPC15236713_Speleonectes _tulumensis_0	tsa family	166	1.35E-37	71.30%	F:catalytic activity; F:antioxidant activity	2	IPR000866; IPR012336; PTHR10681 (PANTHER)
1833	DMPC15236737_Speleonectes _tulumensis_2	ferritin gf1	111	8.78E-32	89.20%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1834	DMPC15236912_Speleonectes _tulumensis_1	ferritin-1 heavy chain	107	1.23E-18	92.20%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1835	DMPC15236991_Speleonectes _tulumensis_1	zinc carboxypeptidase a 1-like	145	3.73E-11	52.25%	-	0	IPR003146; IPR009020; PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1836	DMPC15237028_Speleonectes _tulumensis_0	carboxypeptidase b-like	178	8.65E-64	71.50%	-	0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
1837	DMPC15237041_Speleonectes _tulumensis_0	ferritin 3-like protein	125	1.98E-26	75.00%	F:binding	1	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1838	DMPC15237064_Speleonectes _tulumensis_2	u8-agatoxin-ao1a-like isoform 2	149	5.33E-33	75.60%	P:hormone-mediated signaling pathway; C:extracellular region	2	IPR004169; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF57059 (SUPERFAMILY)
1839	DMPC15237147_Speleonectes _tulumensis_2	catalase	316	1.05E-105	82.30%	P:response to stress; P:catabolic process; F:binding; F:antioxidant activity; F:catalytic activity; P:metabolic process	6	IPR002226; IPR010582; IPR011614; IPR018028; IPR020835; PTHR11465:SF0 (PANTHER)
1840	DMPC15237189_Speleonectes _tulumensis_1	heat shock 70 kda protein 14	132	2.39E-44	73.80%	-	0	IPR013126; IPR018181; G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF81 (PANTHER), SSF53067 (SUPERFAMILY)
1841	DMPC15237229_Speleonectes _tulumensis_1	testicular serine protease 3	129	1.91E-10	63.10%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER), tmhmm (TMHMM)

1842	DMPC15237478_Speleonectes_tulumensis_2	arylsulfatase b	232	3.50E-54	59.70%	P:metabolic process; F:catalytic activity; F:sulfuric ester hydrolase activity	3	IPR000917; IPR017849; IPR017850; G3DSA:3.30.1120.10 (GENE3D), PTHR10342 (PANTHER), PTHR10342:SF19 (PANTHER)
1843	DMPC15237631_Speleonectes_tulumensis_0	soma ferritin	107	1.92E-28	89.20%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1844	DMPC15237690_Speleonectes_tulumensis_1	hemocyanin subunit type 2 precursor	95	4.47E-31	71.60%	-	0	IPR005203; IPR013788; IPR014756
1845	DMPC15237709_Speleonectes_tulumensis_1	lysosomal pro-x carboxypeptidase-like	151	1.52E-54	75.80%	F:peptidase activity	1	IPR008758; PTHR11010:SF9 (PANTHER)
1846	DMPC15237717_Speleonectes_tulumensis_2	glucan pattern-recognition lipoprotein	650	2.39E-17	46.67%	-	0	no IPS match
1847	DMPC15237750_Speleonectes_tulumensis_0	oocyte protease inhibitor-1 precursor	88	2.66E-08	65.50%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12036 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1848	DMPC15237793_Speleonectes_tulumensis_2	fk506-binding protein 2	119	4.94E-33	78.50%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR001179; IPR023566; G3DSA:3.10.50.40 (GENE3D), PTHR10516:SF134 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54534 (SUPERFAMILY)
1849	DMPC15237825_Speleonectes_tulumensis_2	39s ribosomal protein mitochondrial-like	307	2.26E-61	62.80%	C:ribosome	1	IPR008914; PTHR11362 (PANTHER), PTHR11362:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP)
1850	DMPC15237902_Speleonectes_tulumensis_1	serine protease mitochondrial	208	1.43E-14	68.80%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR22939 (PANTHER), PTHR22939:SF12 (PANTHER), SignalP-NN(euk) (SIGNALP)
1851	DMPC15238013_Speleonectes_tulumensis_2	mitochondrial manganese superoxide dismutase	199	5.59E-65	84.00%	P:biological_process; F:binding; P:metabolic process; F:catalytic activity	4	IPR001189; IPR019831; IPR019832; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER)
1852	DMPC15238015_Speleonectes_tulumensis_0	hemocyanin subunit type 1 precursor	141	8.09E-76	76.00%	-	0	IPR005203; IPR013788; IPR014756
1853	DMPC15238109_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	145	1.52E-13	59.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1854	DMPC15238147_Speleonectes_tulumensis_2	peroxiredoxin-4	138	6.88E-40	97.00%	P:metabolic process; F:antioxidant activity; F:catalytic activity	3	IPR012336; IPR019479; G3DSA:3.30.1020.10 (GENE3D), PTHR10681 (PANTHER), PTHR10681:SF46 (PANTHER), SignalP-NN(euk) (SIGNALP)
1855	DMPC15238173_Speleonectes_tulumensis_1	trypsin 3	131	2.12E-47	78.80%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1856	DMPC15238222_Speleonectes_tulumensis_0	---NA---	203			-	0	IPR007947; PTHR11337 (PANTHER), tmhmm (TMHMM)
1857	DMPC15238268_Speleonectes_tulumensis_0	carbonic anhydrase 1	338	3.27E-34	67.10%	F:zinc ion binding; P:one-carbon metabolic process; F:carbonate dehydratase activity; F:metal ion binding	4	IPR001148; IPR018436; IPR023561
1858	DMPC15238313_Speleonectes_tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	119	7.77E-15	54.20%	P:metabolic process	1	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1859	DMPC15238328_Speleonectes_tulumensis_1	---NA---	81			-	0	IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1860	DMPC15238345_Speleonectes_tulumensis_2	epididymal secretory protein e1 isoform 1	142	1.47E-21	59.10%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1861	DMPC15238407_Speleonectes_tulumensis_2	pacifastin light chain	166	1.79E-08	53.50%	F:peptidase inhibitor activity; P:negative regulation of peptidase activity	2	IPR008037; IPR020862; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1862	DMPC15238448_Speleonectes_tulumensis_0	pacifastin light chain	128	2.08E-08	53.33%	F:peptidase inhibitor activity; P:negative regulation of peptidase activity	2	IPR008037; IPR020862; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1863	DMPC15238620_Speleonectes_tulumensis_1	tpa_inf: fibrinogen-related protein 2	154	1.63E-24	68.70%	F:receptor binding; C:extracellular space; P:signal transduction	3	IPR002181; IPR014715; IPR020837; PTHR19143 (PANTHER)

1864	DMPC15238625_Speleonectes _tulumensis_2	diuretic hormone class 2-like	215	1.09E-21	86.40%	-	0	no IPS match
1865	DMPC15238735_Speleonectes _tulumensis_2	pancreatic alpha-amylase-like isoform 1	79	1.08E-18	75.60%	F:hydrolase activity; P:metabolic process	2	IPR013781; IPR015902; IPR017853; PTHR10357:SF26 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1866	DMPC15238776_Speleonectes _tulumensis_1	transmembrane protease serine 12-like	325	1.47E-07	75.00%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
1867	DMPC15238829_Speleonectes _tulumensis_2	phospholipase a2-like	154	5.24E-16	62.50%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; C:extracellular region	5	IPR001211; IPR013090; IPR016090; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1868	DMPC15238885_Speleonectes _tulumensis_4	---NA---	153			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1869	DMPC15238894_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor-like	104	4.03E-09	60.60%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1870	DMPC15238907_Speleonectes _tulumensis_0	anti-lipopolysaccharide factor isoform 7	143	1.04E-29	67.40%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1871	DMPC15238912_Speleonectes _tulumensis_2	ferritin 3-like protein	136	1.08E-25	79.80%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1872	DMPC15238974_Speleonectes _tulumensis_0	von willebrand factor type egf and pentraxin domain-containing protein 1	438	1.44E-10	42.30%	-	0	IPR000436; G3DSA:2.10.70.10 (GENE3D), PTHR19325 (PANTHER)
1873	DMPC15239085_Speleonectes _tulumensis_1	protein	158	4.09E-29	62.30%	-	0	IPR026645
1874	DMPC15239103_Speleonectes _tulumensis_2	serine protease 52-like	124	8.09E-19	63.10%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1875	DMPC15239163_Speleonectes _tulumensis_2	mitochondrial manganese superoxide dismutase	119	1.55E-27	87.50%	F:binding; P:metabolic process; F:catalytic activity	3	IPR001189; IPR019831; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER)
1876	DMPC15239173_Speleonectes _tulumensis_2	chymotrypsinogen b-like	181	7.64E-29	59.00%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER)
1877	DMPC15239272_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor-like	145	2.39E-22	60.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1878	DMPC15239285_Speleonectes _tulumensis_2	si:dkey- protein	108	4.03E-10	59.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1879	DMPC15239332_Speleonectes _tulumensis_0	probable er retained protein	111	3.19E-27	73.40%	C:membrane	1	IPR016093; IPR027005; G3DSA:2.80.10.50 (GENE3D), SignalP-NN(euk) (SIGNALP)
1880	DMPC15239374_Speleonectes _tulumensis_0	peroxiredoxin 1-like	118	2.79E-17	47.50%	P:oxidation-reduction process; F:oxidoreductase activity; F:antioxidant activity; F:peroxiredoxin activity	4	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF44 (PANTHER)
1881	DMPC15239390_Speleonectes _tulumensis_5	glutathione peroxidase 1	152	1.16E-22	84.00%	-	0	IPR000889; IPR012336; tmhmm (TMHMM)
1882	DMPC15239533_Speleonectes _tulumensis_0	cysteine protease	127	1.07E-09	66.80%	P:proteolysis; F:peptidase activity; F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	6	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1883	DMPC15239549_Speleonectes _tulumensis_2	serine protease nudel	170	1.12E-19	51.50%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001190; IPR002172; IPR017448; IPR023415; PR00261 (PRINTS), G3DSA:3.10.250.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF113 (PANTHER)
1884	DMPC15239570_Speleonectes _tulumensis_1	n-acetylgalactosamine-6-sulfatase- partial	314	2.86E-61	71.20%	P:metabolic process; F:catalytic activity; F:sulfuric ester hydrolase activity; C:cellular_component	4	IPR017850; G3DSA:3.30.1120.10 (GENE3D), PTHR10342 (PANTHER), PTHR10342:SF27 (PANTHER), tmhmm (TMHMM)
1885	DMPC15239699_Speleonectes _tulumensis_0	ferritin-1 heavy chain	96	5.19E-22	91.80%	P:cellular homeostasis; F:binding; F:catalytic activity; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347

1886	DMPC15239719_Speleonectes_tulumensis_0	inactive hydroxysteroid dehydrogenase-like protein 1	225	6.93E-79	75.40%	P:metabolic process	1	IPR002198; IPR002347; IPR016040; IPR020904; PTHR24316 (PANTHER), PTHR24316:SF68 (PANTHER), SSF51735 (SUPERFAMILY)
1887	DMPC15239744_Speleonectes_tulumensis_2	trypsin	143	8.65E-24	62.60%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER)
1888	DMPC15239797_Speleonectes_tulumensis_0	serine carboxypeptidase family protein	109	1.55E-16	73.40%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR001563; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
1889	DMPC15239899_Speleonectes_tulumensis_2	kazal-type protease inhibitor	133	3.22E-11	51.88%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
1890	DMPC15239973_Speleonectes_tulumensis_2	cytosolic non-specific dipeptidase	203	7.57E-74	79.20%	P:metabolic process; F:peptidase activity	2	IPR011650; PTHR11014 (PANTHER), PTHR11014:SF15 (PANTHER)
1891	DMPC15239989_Speleonectes_tulumensis_1	mitochondrial cardiolipin hydrolase-like	160	6.26E-47	72.20%	F:binding; P:metabolic process; C:cell; F:catalytic activity; C:mitochondrion	5	IPR001736; IPR025202; G3DSA:3.30.870.10 (GENE3D), PTHR21248 (PANTHER), PTHR21248:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF56024 (SUPERFAMILY)
1892	DMPC15240030_Speleonectes_tulumensis_1	kazal-type protease inhibitor	118	2.82E-15	57.80%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
1893	DMPC15240080_Speleonectes_tulumensis_2	gamma-interferon-inducible lysosomal thiol reductase	461	2.11E-37	54.40%	-	0	IPR004911; tmhmm (TMHMM)
1894	DMPC15240126_Speleonectes_tulumensis_0	cathepsin c	167	2.10E-73	80.30%	C:lysosome; F:peptidase activity; F:protein binding; F:binding; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:biological_process; C:endoplasmic reticulum; C:Golgi apparatus	11	IPR000169; IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF17 (PANTHER), SSF54001 (SUPERFAMILY)
1895	DMPC15240130_Speleonectes_tulumensis_1	aminoacylase-1-like isoform 2	167	8.49E-71	77.60%	C:cytoplasm; ; F:peptidase activity; P:protein metabolic process; P:catabolic process; F:hydrolase activity	6	IPR001261; IPR002933; G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF8 (PANTHER), SSF53187 (SUPERFAMILY)
1896	DMPC15240164_Speleonectes_tulumensis_1	trypsin 3	120	2.79E-37	76.40%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1897	DMPC15240270_Speleonectes_tulumensis_2	trypsin partial	162	8.32E-10	70.60%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1898	DMPC15240281_Speleonectes_tulumensis_1	---NA---	141			-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF30 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1899	DMPC15240312_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	125	3.44E-17	51.50%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1900	DMPC15240368_Speleonectes_tulumensis_0	long form-like	613	8.03E-167	86.90%	C:cytoskeleton; C:protein complex; F:motor activity	3	IPR002928; PTHR13140 (PANTHER), PTHR13140:SF11 (PANTHER)
1901	DMPC15240374_Speleonectes_tulumensis_1	fibrinogen c domain-containing protein 1-a-like	257	2.00E-31	67.80%	F:receptor binding; C:extracellular space; P:signal transduction	3	IPR002181; IPR014715; IPR014716; IPR020837; PTHR19143 (PANTHER), tmhmm (TMHMM)
1902	DMPC15240428_Speleonectes_tulumensis_0	ovarian cysteine protease inhibitor	89	1.89E-10	64.20%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
1903	DMPC15240473_Speleonectes_tulumensis_1	trypsin 3	128	1.16E-22	58.00%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1904	DMPC15240512_Speleonectes_tulumensis_1	trypsinogen 2	126	8.20E-37	75.30%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1905	DMPC15240522_Speleonectes_tulumensis_0	hemocyanin subunit type 1 precursor	123	1.67E-75	69.50%	-	0	IPR005203; IPR013788; IPR014756

1906	DMPC15240533_Speleonectes_tulumensis_0	zinc c2h2 type family protein	92	5.29E-16	66.40%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PF13465 (PFAM), PF13894 (PFAM), PF13912 (PFAM), SSF57667 (SUPERFAMILY)
1907	DMPC15240583_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	127	2.34E-18	59.20%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
1908	DMPC15240589_Speleonectes_tulumensis_4	down syndrome cell adhesion molecule-like protein cg42256-like	113	4.49E-24	64.80%	-	0	IPR013098; IPR013783; PTHR10489 (PANTHER), SSF48726 (SUPERFAMILY)
1909	DMPC15240880_Speleonectes_tulumensis_0	oocyte protease inhibitor-1 precursor	75	2.99E-08	69.80%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12036 (PANTHER), SignalP-NN(euk) (SIGNALP)
1910	DMPC15240973_Speleonectes_tulumensis_0	anopheles stephensi ubiquitin	141	5.34E-64	98.90%	C:cytoskeleton; C:protein complex; F:structural molecule activity; C:lipid particle; P:cellular protein modification process; P:protein metabolic process; P:catabolic process; C:ribosome; C:cytosol; P:translation	10	IPR000626; IPR001975; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1911	DMPC15240975_Speleonectes_tulumensis_1	mantle protein 9	146	3.60E-08	67.67%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1912	DMPC15241030_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor precursor	251	1.43E-25	59.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1913	DMPC15241107_Speleonectes_tulumensis_2	cationic trypsin-3-like	143	3.91E-19	62.80%	P:proteolysis; F:serine-type peptidase activity; F:hydrolase activity; F:peptidase activity	4	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER)
1914	DMPC15241239_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	145	2.04E-30	66.60%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1915	DMPC15241250_Speleonectes_tulumensis_0	thioredoxin 1	108	1.31E-20	74.50%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; SignalP-NN(euk) (SIGNALP)
1916	DMPC15241319_Speleonectes_tulumensis_1	isoform cra_b	130	4.24E-38	98.00%	-	0	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1917	DMPC15241391_Speleonectes_tulumensis_1	trypsin 3	157	1.94E-36	73.30%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1918	DMPC15241401_Speleonectes_tulumensis_1	insulin-degrading enzyme	127	1.65E-24	76.00%	F:binding; F:catalytic activity	2	IPR011237; IPR011249; PTHR11851 (PANTHER), PTHR11851:SF64 (PANTHER)
1919	DMPC15241410_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor-like	121	3.86E-13	58.40%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1920	DMPC15241438_Speleonectes_tulumensis_2	estradiol 17-beta-dehydrogenase 8	199	1.61E-57	69.80%	P:oxidation-reduction process; F:oxidoreductase activity; P:metabolic process; F:nucleotide binding	4	IPR002198; IPR002347; IPR016040; IPR020842; IPR020904; PTHR24316 (PANTHER), PTHR24316:SF3 (PANTHER), SSF51735 (SUPERFAMILY)
1921	DMPC15241557_Speleonectes_tulumensis_1	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphex133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein	122	5.04E-16	63.80%	F:nucleic acid binding; F:zinc ion binding; C:intracellular	3	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
1922	DMPC15241600_Speleonectes_tulumensis_2	ame: full=saxiphilin short=sax flags: precursor	147	6.80E-22	52.20%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1923	DMPC15241696_Speleonectes_tulumensis_1	---NA---	142			-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)

1924	DMPC15241722_Speleonectes_tulumensis_0	serine protease precursor	147	3.80E-16	58.80%	P:proteolysis; F:serine-type endopeptidase activity; P:negative regulation of catalytic activity; F:identical protein binding	4	IPR007280; SignalP-NN(euk) (SIGNALP)
1925	DMPC15241800_Speleonectes_tulumensis_1	ecdysteroid-regulated protein	153	1.07E-25	58.70%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP)
1926	DMPC15241912_Speleonectes_tulumensis_0	peptidyl-prolyl cis-trans isomerase h	123	2.27E-56	93.80%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF58 (PANTHER)
1927	DMPC15241977_Speleonectes_tulumensis_0	serine protease	269	6.08E-23	55.80%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP)
1928	DMPC15241998_Speleonectes_tulumensis_0	tachykinin precursor	110	1.12E-09	64.33%	-	0	SignalP-NN(euk) (SIGNALP)
1929	DMPC15242008_Speleonectes_tulumensis_0	atrial natriuretic peptide-converting enzyme	102	7.63E-35	81.30%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF63 (PANTHER)
1930	DMPC15242053_Speleonectes_tulumensis_1	dermatopontin 3	97	6.79E-08	67.20%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1931	DMPC15242154_Speleonectes_tulumensis_0	a disintegrin and metalloproteinase with thrombospondin motifs 18-like	126	5.21E-24	59.20%	F:hydrolase activity	1	IPR001590; IPR024079; PTHR13723 (PANTHER), SSF55486 (SUPERFAMILY)
1932	DMPC15242187_Speleonectes_tulumensis_0	cationic trypsin-3-like	150	3.77E-34	63.00%	-	0	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER)
1933	DMPC15242339_Speleonectes_tulumensis_5	cg41536 cg41536- partial	179	1.22E-10	75.30%	-	0	no IPS match
1934	DMPC15242436_Speleonectes_tulumensis_0	ame: full=hemagglutinin amebocyte aggregation factor ame: full=18k-laf flags: precursor	70	8.04E-10	65.30%	-	0	no IPS match
1935	DMPC15242520_Speleonectes_tulumensis_0	hemocyanin subunit 1	155	2.43E-48	68.20%	-	0	IPR005203; IPR013788; IPR014756
1936	DMPC15242549_Speleonectes_tulumensis_0	dentin matrix protein 4-like	107	3.34E-53	85.20%	-	0	IPR009581; IPR024869; PTHR12450:SF8 (PANTHER)
1937	DMPC15242596_Speleonectes_tulumensis_1	dnaj homolog subfamily c member 8-like	161	4.81E-69	89.40%	-	0	IPR001623; PTHR15606 (PANTHER)
1938	DMPC15242618_Speleonectes_tulumensis_1	prolyl 3-hydroxylase 2-like	218	2.31E-51	70.90%	F:catalytic activity	1	PTHR14049 (PANTHER)
1939	DMPC15242622_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	131	1.90E-20	53.50%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12036 (PANTHER), PTHR12036:SF5 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1940	DMPC15242690_Speleonectes_tulumensis_1	chorion peroxidase	177	2.91E-47	61.60%	P:oxidation-reduction process; F:heme binding; F:oxidoreductase activity; P:response to oxidative stress; F:peroxidase activity	5	IPR002007; IPR010255; PTHR11475 (PANTHER)
1941	DMPC15242780_Speleonectes_tulumensis_0	trypsin	160	4.90E-26	55.20%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)

1942	DMPC15242832_Speleonectes_tulumensis_0	ubiquitin c	142	7.67E-82	99.00%	P:cell cycle; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:cellular protein modification process; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:transport	27	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
1943	DMPC15242904_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	144	4.19E-30	68.30%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
1944	DMPC15242923_Speleonectes_tulumensis_1	chitinase 2	168	9.69E-26	67.30%	P:carbohydrate metabolic process; F:hydrolase activity	2	IPR001223; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1945	DMPC15242938_Speleonectes_tulumensis_2	ankyrin repeat domain-containing protein 49-like	199	6.63E-30	66.90%	-	0	IPR002110; IPR020683; PTHR24193 (PANTHER)
1946	DMPC15242961_Speleonectes_tulumensis_2	---NA---	97			-	0	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1947	DMPC15243063_Speleonectes_tulumensis_0	gamma-interferon-inducible lysosomal thiol reductase	164	5.95E-39	58.30%	-	0	IPR004911; SignalP-NN(euk) (SIGNALP)
1948	DMPC15243072_Speleonectes_tulumensis_1	---NA---	136			-	0	IPR003172; PTHR11306 (PANTHER)
1949	DMPC15243078_Speleonectes_tulumensis_4	vitellogenin 2	139	1.89E-12	47.80%	P:lipid transport; F:lipid transporter activity	2	IPR015255; IPR015819
1950	DMPC15243110_Speleonectes_tulumensis_2	15-hydroxyprostaglandin dehydrogenase	170	4.27E-30	64.50%	P:lipid metabolic process; F:receptor activity; C:nucleolus; F:catalytic activity; P:reproduction; F:nucleotide binding; P:signal transduction; F:protein binding; P:regulation of biological process; P:cell cycle; C:cytoplasm	11	IPR002198; IPR002347; IPR016040; PTHR24310 (PANTHER), PTHR24310:SF0 (PANTHER), SSF51735 (SUPERFAMILY)
1951	DMPC15243161_Speleonectes_tulumensis_2	dnaj homolog subfamily c member 4-like	107	4.55E-16	70.10%	F:protein binding	1	IPR001623; PTHR24078 (PANTHER), PTHR24078:SF22 (PANTHER)
1952	DMPC15243169_Speleonectes_tulumensis_0	dehydrogenase reductase sdr family member 11-like	164	1.27E-45	75.40%	P:metabolic process	1	IPR002198; IPR016040; PTHR24322 (PANTHER), PTHR24322:SF7 (PANTHER), SSF51735 (SUPERFAMILY)
1953	DMPC15243180_Speleonectes_tulumensis_2	dnaj homolog subfamily b member 6-like	329	4.72E-62	63.80%	F:unfolded protein binding; P:protein folding; F:heat shock protein binding	3	IPR001623; IPR018253; PTHR24077 (PANTHER), PTHR24077:SF24 (PANTHER)
1954	DMPC15243195_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	141	1.63E-13	56.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1955	DMPC15243206_Speleonectes_tulumensis_2	iron zinc purple acid phosphatase-like	138	2.41E-31	67.40%	F:metal ion binding; F:hydrolase activity; F:acid phosphatase activity	3	IPR003961; IPR008963; IPR015914; PTHR22953 (PANTHER), PTHR22953:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1956	DMPC15243251_Speleonectes_tulumensis_0	epidermal retinol dehydrogenase 2	295	5.58E-94	75.60%	P:metabolic process	1	IPR002198; IPR002347; IPR016040; PTHR24316 (PANTHER), PTHR24316:SF1 (PANTHER), SSF51735 (SUPERFAMILY)
1957	DMPC15243308_Speleonectes_tulumensis_1	trypsinogen 2	125	2.31E-32	67.90%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP)
1958	DMPC15243343_Speleonectes_tulumensis_0	carboxypeptidase b-like	139	2.69E-13	76.10%	-	0	G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)

1959	DMPC15243390_Speleonectes_tulumensis_2	---NA---	129			-	0	no IPS match
1960	DMPC15243394_Speleonectes_tulumensis_2	calreticulin	296	1.10E-22	80.10%	-	0	IPR001580; IPR008985; PTHR11073:SF2 (PANTHER), tmhmm (TMHMM)
1961	DMPC15243474_Speleonectes_tulumensis_2	ves g 5 allergen	158	1.57E-19	57.10%	C:extracellular region	1	IPR001283; IPR002413; IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1962	DMPC15243508_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	139	4.51E-14	61.80%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1963	DMPC15243631_Speleonectes_tulumensis_0	orcokinin precursor	348	2.81E-21	71.50%	-	0	PTHR22283 (PANTHER), tmhmm (TMHMM)
1964	DMPC15243653_Speleonectes_tulumensis_1	c1q and tumor necrosis factor-related protein 2	304	2.39E-09	46.80%	-	0	IPR001073; IPR008983; PTHR22923 (PANTHER), PTHR22923:SF1 (PANTHER), tmhmm (TMHMM)
1965	DMPC15243674_Speleonectes_tulumensis_0	glucose dehydrogenase	115	4.28E-15	85.70%	P:metabolic process; F:nucleotide binding; P:reproduction; P:carbohydrate metabolic process; P:multicellular organismal development; F:catalytic activity; C:extracellular region	7	IPR000172; G3DSA:3.50.50.60 (GENE3D), PTHR11552 (PANTHER), PTHR11552:SF10 (PANTHER), tmhmm (TMHMM), SSF51905 (SUPERFAMILY)
1966	DMPC15243697_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	155	2.89E-22	62.40%	-	0	IPR026645
1967	DMPC15243737_Speleonectes_tulumensis_1	---NA---	87			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1968	DMPC15243747_Speleonectes_tulumensis_1	granulin	163	9.09E-16	54.90%	-	0	IPR000118; PTHR12274 (PANTHER), PTHR12274:SF0 (PANTHER)
1969	DMPC15243755_Speleonectes_tulumensis_2	inactive hydroxysteroid dehydrogenase-like protein 1	210	8.82E-70	71.40%	-	0	IPR002198; IPR002347; IPR016040; PTHR24316 (PANTHER), PTHR24316:SF68 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF51735 (SUPERFAMILY)
1970	DMPC15243805_Speleonectes_tulumensis_2	cathepsin l	138	1.18E-64	79.60%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
1971	DMPC15243810_Speleonectes_tulumensis_1	heavy polypeptide 1	106	1.30E-20	90.70%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
1972	DMPC15243830_Speleonectes_tulumensis_2	equistatin precursor	116	8.01E-11	60.60%	P:proteolysis; F:peptidase activity	2	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP)
1973	DMPC15243868_Speleonectes_tulumensis_0	epoxide hydrolase	122	8.05E-28	83.10%	P:metabolic process; F:hydrolase activity	2	G3DSA:3.40.50.1820 (GENE3D), PTHR10992 (PANTHER), PTHR10992:SF98 (PANTHER), PF12697 (PFAM), SSF53474 (SUPERFAMILY)
1974	DMPC15243921_Speleonectes_tulumensis_2	serine protease	143	1.83E-30	66.10%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
1975	DMPC15243928_Speleonectes_tulumensis_1	proclotting enzyme-like	216	7.80E-17	61.30%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER)
1976	DMPC15243995_Speleonectes_tulumensis_0	mhc class ii-associated invariant chain	93	9.15E-08	64.67%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1977	DMPC15244002_Speleonectes_tulumensis_0	sans isoform a	189	2.34E-62	80.20%	C:endosome	1	IPR002110; IPR020683; PTHR24161 (PANTHER), PTHR24161:SF6 (PANTHER)
1978	DMPC15244014_Speleonectes_tulumensis_2	carbonyl isoform b	115	2.98E-22	62.40%	F:catalytic activity	1	IPR002347; IPR016040; PTHR24316 (PANTHER), PTHR24316:SF44 (PANTHER), SSF51735 (SUPERFAMILY)
1979	DMPC15244039_Speleonectes_tulumensis_1	chorion peroxidase-like	385	5.46E-69	70.10%	-	0	IPR002007; IPR010255; PTHR11475 (PANTHER)
1980	DMPC15244094_Speleonectes_tulumensis_2	thioredoxin peroxidase	121	1.87E-23	84.00%	-	0	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF50 (PANTHER)
1981	DMPC15244154_Speleonectes_tulumensis_0	14.03.03	78	4.39E-12	82.60%	F:protein binding	1	IPR000308; IPR023410; PTHR18860:SF0 (PANTHER)

1982	DMPC15244274_Speleonectes _tulumensis_2	epididymal secretory protein e1	114	6.54E-12	65.00%	P:transport; F:binding; C:intracellular	3	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1983	DMPC15244339_Speleonectes _tulumensis_1	mitochondrial import inner membrane translocase subunit tim8 a	145	7.27E-33	80.40%	-	0	IPR004217; PTHR21535 (PANTHER), SignalP-NN(euk) (SIGNALP)
1984	DMPC15244422_Speleonectes _tulumensis_1	carcinolectin 5b partial	282	8.49E-34	69.10%	F:receptor binding; C:extracellular space; P:signal transduction	3	IPR002181; IPR014715; IPR014716; IPR020837; PTHR19143 (PANTHER), tmhmm (TMHMM)
1985	DMPC15244426_Speleonectes _tulumensis_2	kazal-type serine proteinase inhibitor 4	128	3.69E-08	72.00%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR25189 (PANTHER), PTHR25189:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1986	DMPC15244479_Speleonectes _tulumensis_2	chitinase 1 precursor	201	6.94E-72	81.90%	F:hydrolase activity; P:carbohydrate metabolic process; P:catabolic process; F:binding; F:carbohydrate binding; C:extracellular region	6	IPR001223; IPR011583; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF30 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1987	DMPC15244524_Speleonectes _tulumensis_1	thioredoxin peroxidase	166	1.40E-100	89.30%	-	0	IPR000866; IPR012336; IPR019479; IPR024706; PTHR10681 (PANTHER), PTHR10681:SF44 (PANTHER)
1988	DMPC15244538_Speleonectes _tulumensis_2	venom allergen 5-like	246	4.77E-18	49.80%	C:extracellular region	1	IPR001283; IPR014044; IPR018244
1989	DMPC15244563_Speleonectes _tulumensis_2	ferritin 1-like protein a	619	5.79E-45	64.80%	P:oxidation-reduction process; P:cellular iron ion homeostasis; F:oxidoreductase activity; F:transition metal ion binding; F:ferric iron binding; P:iron ion transport	6	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; PTHR11431:SF5 (PANTHER)
1990	DMPC15244577_Speleonectes _tulumensis_2	peroxidasin-like protein	149	1.28E-27	62.60%	P:oxidation-reduction process; F:heme binding; P:response to oxidative stress; F:peroxidase activity; F:oxidoreductase activity; F:catalytic activity; F:FMN binding	7	IPR002007; IPR010255; PTHR11475 (PANTHER)
1991	DMPC15244598_Speleonectes _tulumensis_2	extracellular alkaline serine protease	149	4.54E-18	64.80%	F:peptidase activity	1	IPR007280; SignalP-NN(euk) (SIGNALP)
1992	DMPC15244654_Speleonectes _tulumensis_2	zinc finger protein 43-like	66	1.79E-17	73.40%	-	0	IPR007087; IPR013087; IPR015880; PTHR24382 (PANTHER), PTHR24382:SF0 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
1993	DMPC15244754_Speleonectes _tulumensis_2	gamma-glutamyl hydrolase-like	213	2.01E-21	69.40%	F:catalytic activity	1	IPR015527; G3DSA:3.40.50.880 (GENE3D), PTHR11315:SF0 (PANTHER), SSF52317 (SUPERFAMILY)
1994	DMPC15244811_Speleonectes _tulumensis_2	trypsin	140	4.28E-57	77.70%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER)
1995	DMPC15244865_Speleonectes _tulumensis_1	heat shock protein partial	175	2.12E-93	95.30%	F:nucleotide binding	1	IPR013126; G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), PTHR19375 (PANTHER), SSF100920 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
1996	DMPC15244955_Speleonectes _tulumensis_1	vitellogenic-like precursor	163	2.54E-30	70.90%	F:peptidase activity	1	IPR001563; G3DSA:3.40.50.1820 (GENE3D), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53474 (SUPERFAMILY)
1997	DMPC15244975_Speleonectes _tulumensis_2	hypothetical protein DAPPUDRAFT_308200	149	9.83E-09	50.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
1998	DMPC15244977_Speleonectes _tulumensis_1	mantle protein 9	144	1.31E-08	67.67%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
1999	DMPC15244979_Speleonectes _tulumensis_2	peptidyl-prolyl cis-trans isomerase h-like	101	3.40E-21	85.00%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF58 (PANTHER)
2000	DMPC15245035_Speleonectes _tulumensis_1	retinal dehydrogenase 1-like	157	1.23E-63	82.80%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016160; IPR016161; IPR016162; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER), SignalP-NN(euk) (SIGNALP)
2001	DMPC15245040_Speleonectes _tulumensis_2	h-2 class ii histocompatibility antigen gamma chain	89	5.05E-08	65.17%	P:multicellular organismal development	1	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

2002	DMPC15245053_Speleonectes _tulumensis_0	thioredoxin 1	108	4.03E-26	79.50%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; PTHR10438:SF17 (PANTHER), SignalP-NN(euk) (SIGNALP)
2003	DMPC15245069_Speleonectes _tulumensis_0	chitinase partial	100	5.63E-21	82.50%	F:hydrolase activity; F:binding; P:carbohydrate metabolic process; P:catabolic process	4	IPR001223; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2004	DMPC15245086_Speleonectes _tulumensis_0	ame: full=conoporin-cn1 flags: precursor	361	8.91E-22	51.10%	-	0	IPR009104; IPR015926; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2005	DMPC15245112_Speleonectes _tulumensis_0	glyceraldehyde-3-phosphate dehydrogenase	173	2.22E-14	90.20%	F:nucleotide binding; P:carbohydrate metabolic process; F:catalytic activity; P:metabolic process	4	IPR020831; tmhmm (TMHMM)
2006	DMPC15245133_Speleonectes _tulumensis_2	epididymal secretory protein e1 precursor	255	1.15E-09	58.00%	P:transport	1	IPR003172; IPR014756; PTHR11306 (PANTHER)
2007	DMPC15245138_Speleonectes _tulumensis_1	saxiphilin precursor	136	1.68E-10	68.30%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
2008	DMPC15245230_Speleonectes _tulumensis_2	cathepsin l	123	4.47E-26	87.50%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2009	DMPC15245286_Speleonectes _tulumensis_2	PREDICTED: hypothetical protein LOC100121115	100	5.28E-07	65.00%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF100895 (SUPERFAMILY)
2010	DMPC15245310_Speleonectes _tulumensis_0	histone h2a	208	4.48E-59	94.90%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)
2011	DMPC15245378_Speleonectes _tulumensis_2	serine protease	135	4.76E-20	60.00%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), PTHR24260:SF27 (PANTHER)
2012	DMPC15245379_Speleonectes _tulumensis_2	protein	137	6.07E-18	51.50%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; PTHR12036 (PANTHER), PTHR12036:SF5 (PANTHER), SignalP-NN(euk) (SIGNALP)
2013	DMPC15245522_Speleonectes _tulumensis_1	vitellogenin 2	157	2.73E-11	49.70%	P:lipid transport; F:lipid transporter activity	2	IPR001747; IPR015816; IPR015819; PTHR23345 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2014	DMPC15245604_Speleonectes _tulumensis_0	peroxiredoxin 4	272	1.60E-61	88.80%	P:metabolic process; F:antioxidant activity; F:catalytic activity	3	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF46 (PANTHER), tmhmm (TMHMM)
2015	DMPC15245618_Speleonectes _tulumensis_1	cathepsin l	153	8.02E-42	84.20%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2016	DMPC15245647_Speleonectes _tulumensis_1	epidermal retinol dehydrogenase 2	152	2.29E-39	72.10%	P:metabolic process	1	IPR002198; IPR002347; IPR016040; PTHR24316 (PANTHER), PTHR24316:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF51735 (SUPERFAMILY)
2017	DMPC15245749_Speleonectes _tulumensis_1	---NA---	147			-	0	IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2018	DMPC15245800_Speleonectes _tulumensis_1	hemocyanin subunit type 2 precursor	176	1.82E-16	85.00%	-	0	IPR005203; IPR013788; IPR014756; tmhmm (TMHMM)
2019	DMPC15245833_Speleonectes _tulumensis_0	protein	169	1.27E-17	75.00%	F:receptor binding; C:extracellular space; P:signal transduction	3	IPR002181; IPR014715; IPR020837; PTHR19143 (PANTHER)
2020	DMPC15245901_Speleonectes _tulumensis_2	anti-lipopolysaccharide factor isoform 7	126	7.41E-27	62.90%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2021	DMPC15245937_Speleonectes _tulumensis_0	trypsin	162	8.58E-24	58.30%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER)
2022	DMPC15245988_Speleonectes _tulumensis_0	fibrinolytic enzyme	110	1.60E-15	60.20%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)

2023	DMPC15246049_Speleonectes_tulumensis_2	serine proteinase stubble-like	207	5.67E-32	55.80%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity; F:hydrolase activity	4	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER)
2024	DMPC15246058_Speleonectes_tulumensis_0	protein spaetzle	198	1.01E-09	56.83%	-	0	SSF57501 (SUPERFAMILY)
2025	DMPC15246085_Speleonectes_tulumensis_0	---NA---	119			-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24259 (PANTHER)
2026	DMPC15246086_Speleonectes_tulumensis_1	glutathione peroxidase 1	188	9.47E-59	79.50%	P:response to external stimulus; P:anatomical structure morphogenesis; P:multicellular organismal development; P:response to stress; P:response to abiotic stimulus; P:cell proliferation; P:catabolic process; P:regulation of biological process; P:cell death; P:cell differentiation; P:biological_process; P:cellular protein modification process; P:nucleobase-containing compound metabolic process; C:cytosol; F:catalytic activity; F:antioxidant activity; P:growth; P:cellular homeostasis; ; P:lipid metabolic process; F:enzyme regulator activity; P:mitochondrion organization; F:protein binding; P:regulation of gene expression, epigenetic; P:signal transduction; C:mitochondrion	26	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
2027	DMPC15246112_Speleonectes_tulumensis_2	cathepsin l	210	3.99E-78	79.80%	-	0	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2028	DMPC15246180_Speleonectes_tulumensis_2	cre-nas-8 protein	212	2.59E-11	60.60%	F:hydrolase activity	1	IPR001506; IPR024079; PTHR10127 (PANTHER), SSF55486 (SUPERFAMILY)
2029	DMPC15246223_Speleonectes_tulumensis_1	plasminogen activator spa	135	6.76E-27	59.80%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
2030	DMPC15246237_Speleonectes_tulumensis_2	carboxypeptidase b-like	147	3.29E-42	59.10%	-	0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF53187 (SUPERFAMILY)
2031	DMPC15246251_Speleonectes_tulumensis_2	protein disulfide-isomerase a3-like	353	1.11E-71	82.90%	F:electron carrier activity; P:cellular homeostasis; P:regulation of biological process; P:metabolic process; F:catalytic activity; F:transferase activity; C:endoplasmic reticulum	7	IPR005746; IPR005788; IPR012336; IPR013766; IPR017937; PTHR18929 (PANTHER), PTHR18929:SF32 (PANTHER)
2032	DMPC15246322_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor	102	4.56E-14	63.90%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2033	DMPC15246336_Speleonectes_tulumensis_0	saxiphilin precursor	148	1.54E-10	63.70%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
2034	DMPC15246347_Speleonectes_tulumensis_1	calponin transgelin	184	9.74E-78	86.60%	F:actin binding; P:cytoskeleton organization	2	IPR001715; IPR001997; IPR003096; PTHR18959 (PANTHER), PTHR18959:SF3 (PANTHER)
2035	DMPC15246370_Speleonectes_tulumensis_0	ferritin	134	1.70E-31	80.60%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; SignalP-NN(euk) (SIGNALP)
2036	DMPC15246381_Speleonectes_tulumensis_0	trypsinogen 2	116	4.14E-36	77.40%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
2037	DMPC15246386_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor-like	136	2.41E-15	56.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

2038	DMPC15246387_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	136	7.75E-12	57.40%	P:proteolysis; F:peptidase activity; F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	6	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
2039	DMPC15246415_Speleonectes_tulumensis_2	cathepsin l	151	5.25E-69	79.20%	-	0	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2040	DMPC15246499_Speleonectes_tulumensis_0	soma ferritin	112	3.98E-33	89.40%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2041	DMPC15246513_Speleonectes_tulumensis_2	mhc class ii-associated invariant chain	169	1.59E-07	67.00%	P:multicellular organismal development	1	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2042	DMPC15246594_Speleonectes_tulumensis_1	soma ferritin	149	4.89E-39	83.70%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2043	DMPC15246670_Speleonectes_tulumensis_2	cathepsin q-like	93	2.20E-08	69.00%	-	0	IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
2044	DMPC15246747_Speleonectes_tulumensis_2	26kda protease	306	3.35E-47	56.00%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2045	DMPC15246748_Speleonectes_tulumensis_2	heat shock protein 70	130	2.57E-32	88.90%	P:protein metabolic process; F:protein binding; F:nucleotide binding	3	IPR013126; IPR018181; G3DSA:3.30.420.40 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF53067 (SUPERFAMILY)
2046	DMPC15246760_Speleonectes_tulumensis_3	interstitial collagenase	155	1.63E-11	74.00%	F:binding; P:metabolic process; F:peptidase activity	3	IPR000585; IPR018487; PTHR10201 (PANTHER), PTHR10201:SF96 (PANTHER), tmhmm (TMHMM)
2047	DMPC15246808_Speleonectes_tulumensis_0	#NAME?	162	2.63E-63	79.80%	F:transferase activity; F:hydrolase activity; P:biosynthetic process; P:carbohydrate metabolic process	4	IPR001830; G3DSA:3.40.50.2000 (GENE3D), PTHR10788 (PANTHER), PTHR10788:SF6 (PANTHER), SSF53756 (SUPERFAMILY)
2048	DMPC15246863_Speleonectes_tulumensis_2	ankyrin repeat protein partial	110	5.33E-14	61.50%	F:transferase activity	1	IPR002110; IPR020683; PTHR24198 (PANTHER)
2049	DMPC15246899_Speleonectes_tulumensis_2	kazal-type serine proteinase inhibitor 4	114	3.95E-11	56.80%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR25189 (PANTHER), PTHR25189:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
2050	DMPC15247051_Speleonectes_tulumensis_2	trypsin-like serine proteinase 2	192	1.40E-31	60.40%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER)
2051	DMPC15247136_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor	148	1.22E-34	73.80%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2052	DMPC15247169_Speleonectes_tulumensis_1	alpha amylase	57	1.22E-11	81.20%	-	0	IPR015902; PTHR10357:SF26 (PANTHER)
2053	DMPC15247217_Speleonectes_tulumensis_1	cathepsin l-like	137	1.40E-50	83.80%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2054	DMPC15247254_Speleonectes_tulumensis_0	lysozyme precursor	103	1.79E-08	63.00%	-	0	IPR001916; IPR023346; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER), PTHR11407:SF2 (PANTHER)
2055	DMPC15247271_Speleonectes_tulumensis_2	serine protease 137 precursor	98	5.65E-16	62.80%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
2056	DMPC15247311_Speleonectes_tulumensis_0	orcokinin precursor	206	2.56E-19	51.38%	-	0	no IPS match

2057	DMPC15247361_Speleonectes_tulumensis_0	ribosomal protein ubq l40e	174	8.98E-86	98.90%	C:cytoskeleton; C:protein complex; F:structural molecule activity; C:lipid particle; P:cellular protein modification process; P:protein metabolic process; P:catabolic process; C:ribosome; C:cytosol; P:translation	10	IPR000626; IPR001975; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
2058	DMPC15247373_Speleonectes_tulumensis_1	chitinase 1 precursor	162	5.41E-67	72.90%	P:carbohydrate metabolic process; F:hydrolase activity	2	IPR001223; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), PTHR11177:SF30 (PANTHER), SSF54556 (SUPERFAMILY)
2059	DMPC15247375_Speleonectes_tulumensis_0	epididymal secretory protein e1	107	1.05E-15	61.40%	F:cholesterol binding; P:cholesterol homeostasis; C:lysosome; F:enzyme binding; P:cholesterol efflux; P:response to virus; P:intracellular cholesterol transport; C:extracellular region	8	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2060	DMPC15247419_Speleonectes_tulumensis_2	kazal-type serine proteinase inhibitor 1	178	7.34E-23	52.90%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SSF100895 (SUPERFAMILY)
2061	DMPC15247508_Speleonectes_tulumensis_2	trypsinogen 2	105	2.71E-24	68.00%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
2062	DMPC15247509_Speleonectes_tulumensis_1	soma ferritin	111	4.97E-27	88.90%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2063	DMPC15247576_Speleonectes_tulumensis_2	---NA---	107			-	0	SignalP-NN(euk) (SIGNALP)
2064	DMPC15247592_Speleonectes_tulumensis_0	epidermal retinol dehydrogenase 2-like	203	1.50E-62	74.30%	P:metabolic process	1	IPR002198; IPR002347; IPR016040; PTHR24316 (PANTHER), PTHR24316:SF1 (PANTHER), SSF51735 (SUPERFAMILY)
2065	DMPC15247614_Speleonectes_tulumensis_2	cathepsin l precursor	156	2.15E-51	80.70%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2066	DMPC15247822_Speleonectes_tulumensis_2	stress-70 mitochondrial	120	2.89E-25	91.10%	P:protein metabolic process; F:protein binding; F:nucleotide binding	3	IPR013126; IPR018181; G3DSA:3.30.420.40 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), SSF53067 (SUPERFAMILY)
2067	DMPC15247886_Speleonectes_tulumensis_0	collagen and calcium-binding egf domain-containing protein 1-like	155	5.96E-43	64.60%	F:binding; C:intracellular; P:protein metabolic process	3	G3DSA:2.10.25.10 (GENE3D), PTHR24023 (PANTHER), PTHR24023:SF13 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2068	DMPC15247966_Speleonectes_tulumensis_0	epididymal secretory protein e1 isoform 1	141	2.21E-20	58.20%	P:biological_process; C:lysosome; P:transport; F:protein binding; P:response to biotic stimulus; F:lipid binding	6	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2069	DMPC15248074_Speleonectes_tulumensis_2	hatching enzyme	257	8.47E-41	64.00%	F:peptidase activity	1	IPR001506; IPR006026; IPR024079; PTHR10127 (PANTHER), SSF55486 (SUPERFAMILY)
2070	DMPC15248190_Speleonectes_tulumensis_2	sphingomyelin phosphodiesterase	197	7.29E-60	66.70%	C:organelle; C:intracellular; P:metabolic process; P:regulation of biological process; P:lipid metabolic process; F:hydrolase activity; P:signal transduction; C:cytoplasm; P:cellular protein modification process	9	IPR004843; G3DSA:3.60.21.10 (GENE3D), PTHR10340 (PANTHER), PTHR10340:SF13 (PANTHER), SSF56300 (SUPERFAMILY)
2071	DMPC15248228_Speleonectes_tulumensis_1	trypsin partial	104	8.27E-09	58.80%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP)
2072	DMPC15248259_Speleonectes_tulumensis_1	protein vit-4	171	9.57E-15	54.70%	P:embryo development; P:behavior; P:reproduction; P:regulation of biological process; P:growth; P:multicellular organismal development	6	IPR001846
2073	DMPC15248310_Speleonectes_tulumensis_0	---NA---	292			-	0	IPR006207; tmhmm (TMHMM)

2074	DMPC15248324_Speleonectes_tulumensis_1	serine protease 52-like	124	1.06E-18	63.10%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
2075	DMPC15248388_Speleonectes_tulumensis_1	cysteine protease family	134	1.51E-16	85.00%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2076	DMPC15248403_Speleonectes_tulumensis_0	chitinase domain-containing protein 1	197	1.74E-42	67.40%	F:catalytic activity	1	IPR017853; PTHR11177 (PANTHER), SignalP-NN(euk) (SIGNALP)
2077	DMPC15248435_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_311761	428	5.26E-95	62.20%	-	0	IPR003128; IPR007122; IPR007123; IPR015627; G3DSA:3.40.20.10 (GENE3D), SSF55753 (SUPERFAMILY)
2078	DMPC15248446_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	132	2.49E-11	59.10%	P:proteolysis; F:peptidase activity; F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	6	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
2079	DMPC15248498_Speleonectes_tulumensis_1	dehydrogenase reductase sdr family member 11-like	166	1.71E-40	78.70%	F:catalytic activity; P:metabolic process; F:nucleotide binding	3	IPR002198; IPR002347; IPR016040; PTHR24322 (PANTHER), PTHR24322:SF7 (PANTHER), SSF51735 (SUPERFAMILY)
2080	DMPC15248562_Speleonectes_tulumensis_0	manganese superoxide dismutase	98	7.33E-20	85.80%	F:binding; P:metabolic process; F:catalytic activity	3	IPR001189; IPR019831; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER)
2081	DMPC15248571_Speleonectes_tulumensis_0	protein giant-lens-like	145	1.82E-73	78.80%	-	0	IPR021633
2082	DMPC15248593_Speleonectes_tulumensis_2	tissue factor pathway inhibitor 2 precursor	259	5.84E-28	57.90%	F:serine-type endopeptidase inhibitor activity	1	IPR002223; IPR020901; PTHR10083 (PANTHER)
2083	DMPC15248746_Speleonectes_tulumensis_0	glycosyl-phosphatidylinositol-linked carbonic anhydrase	121	4.92E-14	55.00%	F:carbonate dehydratase activity	1	IPR001148; IPR023561; SignalP-NN(euk) (SIGNALP)
2084	DMPC15248819_Speleonectes_tulumensis_1	ame: full= cytoplasmic ame: full=actin-depolymerizing factor short=adf	154	1.75E-53	69.80%	F:actin binding	1	IPR007122; IPR007123; G3DSA:3.40.20.10 (GENE3D), PTHR11977:SF11 (PANTHER), SSF55753 (SUPERFAMILY)
2085	DMPC15248890_Speleonectes_tulumensis_0	PREDICTED: zonadhesin-like	316	8.55E-10	50.00%	-	0	no IPS match
2086	DMPC15249053_Speleonectes_tulumensis_1	probable carboxypeptidase pm20d1-like	220	5.73E-47	70.30%	F:hydrolase activity; P:metabolic process; F:carboxypeptidase activity	3	G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF9 (PANTHER), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
2087	DMPC15249071_Speleonectes_tulumensis_0	cathepsin l	142	1.27E-57	81.90%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000169; IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2088	DMPC15249098_Speleonectes_tulumensis_1	dermatopontin 2	197	1.19E-35	59.20%	-	0	IPR026645
2089	DMPC15249127_Speleonectes_tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	146	3.62E-22	52.90%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2090	DMPC15249131_Speleonectes_tulumensis_1	trypsinogen 2	265	4.49E-53	60.30%	-	0	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER)
2091	DMPC15249237_Speleonectes_tulumensis_0	apolipoprotein d	145	4.63E-09	47.25%	F:pigment binding; F:lipid binding; C:extracellular region; P:transport; F:transporter activity	5	IPR000566; IPR011038; IPR012674; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP)
2092	DMPC15249255_Speleonectes_tulumensis_0	manganese superoxide dismutase	116	1.06E-20	85.60%	-	0	IPR001189; IPR019831; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER)
2093	DMPC15249295_Speleonectes_tulumensis_1	ferritin gfl	110	2.05E-30	88.70%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2094	DMPC15249377_Speleonectes_tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	148	1.84E-21	52.00%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

2095	DMPC15249380_Speleonectes_tulumensis_2	serine protease inhibitor	153	8.43E-18	55.90%	-	0	IPR000215; IPR023796; G3DSA:2.30.39.10 (GENE3D), G3DSA:3.30.497.10 (GENE3D)
2096	DMPC15249433_Speleonectes_tulumensis_1	histone partial	124	4.24E-32	98.00%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)
2097	DMPC15249436_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor	115	5.68E-09	63.90%	-	0	IPR026645
2098	DMPC15249440_Speleonectes_tulumensis_1	neuferricin-like isoform 3	279	3.75E-19	78.00%	P:nervous system development; F:heme binding; C:extracellular region	3	PTHR10281 (PANTHER)
2099	DMPC15249512_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor isoform 7	135	4.88E-29	68.80%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2100	DMPC15249596_Speleonectes_tulumensis_2	dermatopontin 3	101	3.34E-08	57.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2101	DMPC15249758_Speleonectes_tulumensis_2	---NA---	146			-	0	IPR011038; IPR012674; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2102	DMPC15249853_Speleonectes_tulumensis_0	ferritin h subunit	110	7.17E-20	91.60%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2103	DMPC15249916_Speleonectes_tulumensis_0	sortilin-related receptor-like	98	1.55E-07	76.00%	-	0	IPR002172; IPR023415; PTHR10529 (PANTHER), PTHR10529:SF116 (PANTHER)
2104	DMPC15250033_Speleonectes_tulumensis_2	down syndrome cell adhesion molecule	137	1.81E-12	77.20%	F:nucleic acid binding	1	IPR003961; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF165 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2105	DMPC15250034_Speleonectes_tulumensis_1	annexin isoform a	433	9.12E-62	70.30%	F:actin binding; F:calcium ion binding; F:lipid binding	3	IPR001464; IPR018252; IPR018502; SignalP-NN(euk) (SIGNALP)
2106	DMPC15250064_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor-like	96	1.04E-08	64.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2107	DMPC15250099_Speleonectes_tulumensis_1	hemocyanin subunit type 1 precursor	437	0	77.20%	-	0	IPR000896; IPR002227; IPR005203; IPR008922; IPR013788; IPR014756
2108	DMPC15250350_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor	144	8.29E-31	68.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2109	DMPC15250392_Speleonectes_tulumensis_0	trypsin 7	152	8.15E-31	77.40%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
2110	DMPC15250400_Speleonectes_tulumensis_1	metalloprotease ii	151	3.78E-18	58.80%	P:proteolysis; F:serine-type endopeptidase activity; P:negative regulation of catalytic activity; F:identical protein binding	4	IPR007280; SignalP-NN(euk) (SIGNALP)
2111	DMPC15250428_Speleonectes_tulumensis_2	anti-lipopolysaccharide factor isoform 7	100	1.02E-08	56.30%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2112	DMPC15250526_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor	148	5.99E-29	66.80%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2113	DMPC15250536_Speleonectes_tulumensis_2	proclotting enzyme	292	2.00E-60	57.90%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER)
2114	DMPC15250556_Speleonectes_tulumensis_2	ankyrin unc44	160	1.75E-38	87.70%	P:signal transduction; F:hydrolase activity	2	IPR002110; IPR020683; PTHR24123 (PANTHER), PTHR24123:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2115	DMPC15250604_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	98	2.68E-12	61.80%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2116	DMPC15250649_Speleonectes_tulumensis_2	enolase	80	7.07E-21	92.20%	C:cytosol; C:protein complex; F:catalytic activity; F:binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process	7	IPR000941; IPR020810; G3DSA:3.20.20.120 (GENE3D), SSF51604 (SUPERFAMILY)
2117	DMPC15250684_Speleonectes_tulumensis_2	histone h2 z	79	1.78E-21	95.00%	C:chromosome; F:DNA binding; P:organelle organization; C:nucleus	4	IPR002119; IPR007125; IPR009072; PTHR23430 (PANTHER)

2118	DMPC15250705_Speleonectes _tulumensis_1	zgc:101788 protein	149	6.11E-29	60.10%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2119	DMPC15250730_Speleonectes _tulumensis_0	guanine nucleotide-binding protein subunit beta-like protein	231	9.43E-152	94.30%	F:receptor activity; F:kinase activity; P:metabolic process	3	IPR001680; IPR015943; IPR017986; IPR019775; IPR020472; PTHR19868 (PANTHER), PTHR19868:SF0 (PANTHER)
2120	DMPC15250770_Speleonectes _tulumensis_0	---NA---	123			-	0	no IPS match
2121	DMPC15250787_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor	122	3.66E-13	61.60%	-	0	IPR026645
2122	DMPC15250845_Speleonectes _tulumensis_1	semaphorin-2a-like isoform 1	103	1.48E-58	95.70%	-	0	IPR001627; IPR015943; IPR027231; PTHR11036:SF6 (PANTHER)
2123	DMPC15250852_Speleonectes _tulumensis_0	leucine-rich repeat and calponin homology domain-containing protein 1-like	209	1.04E-55	77.50%	-	0	IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF10 (PANTHER), PF13855 (PFAM), SSF52058 (SUPERFAMILY)
2124	DMPC15250907_Speleonectes _tulumensis_2	gamma-interferon-inducible lysosomal thiol reductase	146	2.18E-29	60.70%	-	0	IPR004911; SignalP-NN(euk) (SIGNALP)
2125	DMPC15250939_Speleonectes _tulumensis_2	kazal-type serine proteinase inhibitor 4	114	2.93E-14	55.30%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
2126	DMPC15250951_Speleonectes _tulumensis_0	vitellogenin 2	240	3.96E-32	50.50%	-	0	IPR001846
2127	DMPC15251109_Speleonectes _tulumensis_0	anti-lipopolysaccharide factor	152	5.73E-31	67.20%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2128	DMPC15251163_Speleonectes _tulumensis_1	follistatin-related protein	115	4.14E-24	68.50%	P:signal transduction; C:extracellular region; P:cell differentiation; P:embryo development	4	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF13 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
2129	DMPC15251304_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor	135	1.15E-13	61.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2130	DMPC15251343_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor	145	2.28E-30	68.50%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2131	DMPC15251416_Speleonectes _tulumensis_0	basement membrane-specific heparan sulfate proteoglycan core	97	3.14E-15	71.40%	-	0	IPR007110; IPR013783; PF13895 (PFAM), SSF48726 (SUPERFAMILY)
2132	DMPC15251442_Speleonectes _tulumensis_2	glucose dehydrogenase	383	3.07E-17	80.30%	F:nucleotide binding; P:metabolic process; F:catalytic activity	3	IPR007867; G3DSA:3.50.50.60 (GENE3D), PTHR11552 (PANTHER), PTHR11552:SF10 (PANTHER), tmhmm (TMHMM), SSF51905 (SUPERFAMILY)
2133	DMPC15251467_Speleonectes _tulumensis_0	probable serine carboxypeptidase cpvl precursor	97	2.63E-23	65.60%	P:proteolysis; F:carboxypeptidase activity; F:serine-type carboxypeptidase activity	3	no IPS match
2134	DMPC15251484_Speleonectes _tulumensis_0	---NA---	129			-	0	IPR000941; IPR020810; G3DSA:3.20.20.120 (GENE3D), tmhmm (TMHMM)
2135	DMPC15251602_Speleonectes _tulumensis_1	cathepsin l-like	127	5.93E-25	85.80%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2136	DMPC15251610_Speleonectes _tulumensis_0	leucine-rich repeat-containing protein 49	148	1.49E-54	78.90%	-	0	IPR001611; IPR003591; IPR025875; G3DSA:3.80.10.10 (GENE3D), PTHR10588 (PANTHER), PTHR10588:SF5 (PANTHER), SM00365 (SMART), SSF52058 (SUPERFAMILY)
2137	DMPC15251666_Speleonectes _tulumensis_1	---NA---	108			-	0	IPR003172; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2138	DMPC15251709_Speleonectes _tulumensis_1	mitochondrial aldehyde dehydrogenase	121	1.43E-48	81.30%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016160; IPR016161; IPR016162; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER), SignalP-NN(euk) (SIGNALP)
2139	DMPC15251730_Speleonectes _tulumensis_1	ecdysteroid-regulated 16 kda protein	150	2.81E-12	55.10%	-	0	IPR003172; IPR014756; PTHR11306 (PANTHER)

2140	DMPC15251797_Speleonectes _tulumensis_2	hmct_bommo ame: full=hemocytin ame: full=humoral lectin flags: precursor	177	1.76E-18	50.60%	F:nucleic acid binding; F:carbohydrate binding; P:cell adhesion; F:zinc ion binding; F:chitin binding; P:chitin metabolic process; C:extracellular region	7	IPR001846; G3DSA:2.10.25.10 (GENE3D), PTHR11339 (PANTHER)
2141	DMPC15251878_Speleonectes _tulumensis_2	---NA---	280			-	0	IPR007947; PTHR11337 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2142	DMPC15251950_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor	120	7.56E-11	61.60%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
2143	DMPC15251973_Speleonectes _tulumensis_0	ubiquitin family protein	201	3.42E-44	98.00%	P:cell cycle; P:signal transduction; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; C:cytosol; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; C:plasma membrane; ; C:endosome; P:cellular component organization; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; P:cellular protein modification process; P:transport	22	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), tmhmm (TMHMM), SSF54236 (SUPERFAMILY)
2144	DMPC15251990_Speleonectes _tulumensis_1	---NA---	200			-	0	IPR008197; PTHR14131 (PANTHER), PTHR14131:SF0 (PANTHER)
2145	DMPC15252013_Speleonectes _tulumensis_1	angiotensin-converting enzyme	186	1.01E-34	79.30%	C:cell; F:peptidase activity; P:protein metabolic process; P:catabolic process	4	IPR001548; tmhmm (TMHMM), SSF55486 (SUPERFAMILY)
2146	DMPC15252040_Speleonectes _tulumensis_2	phospholipase a2	247	1.09E-38	62.50%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; C:extracellular region	5	IPR001211; IPR013090; IPR016090; SignalP-NN(euk) (SIGNALP)
2147	DMPC15252109_Speleonectes _tulumensis_0	ame: full=prohormone-1 contains: ame: full=brain peptide lrnqldigdlq contains: ame: full=brain peptide lrnqldigdl contains: ame: full=brain peptide sywkqcafnavscf-amide flags: precursor	162	1.25E-32	76.90%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2148	DMPC15252162_Speleonectes _tulumensis_0	chloride channel accessory 2-like	156	1.09E-24	53.30%	-	0	IPR013642; PTHR10579 (PANTHER), PTHR10579:SF7 (PANTHER)
2149	DMPC15252180_Speleonectes _tulumensis_1	chh xo- variant 4	146	6.44E-09	68.78%	F:neuropeptide hormone activity; C:extracellular region	2	IPR001166; tmhmm (TMHMM)
2150	DMPC15252185_Speleonectes _tulumensis_1	vascular endothelial growth factor receptor 1-like	138	2.80E-13	46.50%	F:ATP binding; F:protein kinase activity; P:protein phosphorylation	3	IPR013783; SSF48726 (SUPERFAMILY)
2151	DMPC15252219_Speleonectes _tulumensis_5	cg1504	159	3.51E-66	78.60%	-	0	IPR001611; IPR003591; IPR026906; G3DSA:3.80.10.10 (GENE3D), PTHR24367 (PANTHER), SM00365 (SMART), SSF52058 (SUPERFAMILY)
2152	DMPC15252400_Speleonectes _tulumensis_0	na(+) h(+) exchange regulatory cofactor nhe-rf2-like	210	2.87E-49	79.60%	-	0	IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR14191 (PANTHER), PTHR14191:SF0 (PANTHER)

2153	DMPC15252542_Speleonectes _tulumensis_0	beta- -galactosyltransferase 1	72	2.87E-10	81.60%	P:response to external stimulus; P:anatomical structure morphogenesis; P:multicellular organismal development; P:response to stress; P:transport; P:reproduction; P:regulation of biological process; P:biological_process; C:external encapsulating structure; P:biosynthetic process; P:carbohydrate metabolic process; C:plasma membrane; P:cellular component organization; F:transferase activity; C:cell; P:cell proliferation; C:extracellular region; F:binding; F:cytoskeletal protein binding; P:cell recognition; P:cellular protein modification process; C:Golgi apparatus; F:protein binding; P:cell differentiation; P:cell death	25	IPR003859; G3DSA:3.90.550.10 (GENE3D), PTHR19300:SF5 (PANTHER), PF13733 (PFAM)
2154	DMPC15252543_Speleonectes _tulumensis_2	low quality protein: reticulocalbin-2-like	64	5.41E-17	85.60%	F:calcium ion binding	1	PTHR10827 (PANTHER), PTHR10827:SF38 (PANTHER)
2155	DMPC15252546_Speleonectes _tulumensis_1	arylsulfatase i-like	104	9.61E-18	64.40%	P:metabolic process; F:catalytic activity; F:sulfuric ester hydrolase activity	3	IPR000917; IPR017849; IPR017850; PTHR10342 (PANTHER), PTHR10342:SF19 (PANTHER)
2156	DMPC15252556_Speleonectes _tulumensis_2	cationic trypsin-3-like	120	4.44E-15	55.10%	F:catalytic activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)
2157	DMPC15252622_Speleonectes _tulumensis_1	sphingomyelin phosphodiesterase	113	4.31E-13	62.20%	F:hydrolase activity; F:sphingomyelin phosphodiesterase activity; P:sphingomyelin catabolic process	3	G3DSA:3.60.21.10 (GENE3D), PTHR10340 (PANTHER), PTHR10340:SF13 (PANTHER)
2158	DMPC15252648_Speleonectes _tulumensis_1	peptidase inhibitor partial	333	3.85E-15	57.40%	C:extracellular region	1	IPR001283; IPR002172; IPR014044; IPR018244; IPR023415; PTHR10334:SF25 (PANTHER)
2159	DMPC15252706_Speleonectes _tulumensis_2	extracellular cyanophycinase	172	2.04E-14	49.67%	-	0	SignalP-NN(euk) (SIGNALP)
2160	DMPC15252762_Speleonectes _tulumensis_0	si:dkey- protein	103	3.85E-09	64.29%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2161	DMPC15252792_Speleonectes _tulumensis_2	plasminogen activator spa	98	6.86E-15	62.10%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24276 (PANTHER), SignalP-NN(euk) (SIGNALP)
2162	DMPC15252812_Speleonectes _tulumensis_2	---NA---	157			-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF100895 (SUPERFAMILY)
2163	DMPC15252844_Speleonectes _tulumensis_0	ubiquitin-40s ribosomal protein s27a	132	1.11E-48	97.30%	P:cell cycle; P:metabolic process; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; P:translation; F:binding; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; P:cellular component organization; C:plasma membrane; P:protein transport; ; C:endosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; C:ribosome; C:cytosol; P:cellular protein modification process; P:transport	27	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)

2164	DMPC15252914_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	131	9.29E-22	52.20%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:cell-matrix adhesion; F:calcium ion binding	6	IPR000716; IPR022339
2165	DMPC15252917_Speleonectes_tulumensis_2	selenium-dependent glutathione peroxidase	135	2.17E-37	80.20%	-	0	IPR000889; IPR012336; PTHR11592:SF0 (PANTHER)
2166	DMPC15252978_Speleonectes_tulumensis_2	soma ferritin	104	2.49E-22	84.10%	-	0	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2167	DMPC15253042_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	108	1.83E-08	57.10%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2168	DMPC15253088_Speleonectes_tulumensis_1	dnaj homolog subfamily b member 11-like	138	1.30E-35	88.40%	P:protein metabolic process; F:protein binding	2	IPR001623; IPR018253; PTHR24077 (PANTHER), PTHR24077:SF14 (PANTHER), SignalP-NN(euk) (SIGNALP)
2169	DMPC15253091_Speleonectes_tulumensis_2	---NA---	157			-	0	IPR001199; PTHR10281 (PANTHER), PTHR10281:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2170	DMPC15253135_Speleonectes_tulumensis_1	iron zinc purple acid phosphatase-like	235	6.53E-58	79.40%	F:binding; F:hydrolase activity	2	IPR025733; G3DSA:3.60.21.10 (GENE3D), PTHR22953 (PANTHER), PTHR22953:SF0 (PANTHER), tmhmm (TMHMM), SSF56300 (SUPERFAMILY)
2171	DMPC15253146_Speleonectes_tulumensis_0	kazal-type serine proteinase inhibitor 4	142	5.47E-17	58.80%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR10913 (PANTHER), PTHR10913:SF21 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
2172	DMPC15253150_Speleonectes_tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	149	3.71E-21	51.70%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity; P:cell-matrix adhesion; F:calcium ion binding	6	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2173	DMPC15253159_Speleonectes_tulumensis_0	enolase	218	1.26E-19	95.80%	C:cytosol; C:protein complex; F:catalytic activity; F:binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process	7	IPR000941; IPR020810; G3DSA:3.20.20.120 (GENE3D), tmhmm (TMHMM), SSF51604 (SUPERFAMILY)
2174	DMPC15253218_Speleonectes_tulumensis_2	thioredoxin peroxidase	115	3.39E-35	86.60%	-	0	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF50 (PANTHER)
2175	DMPC15253238_Speleonectes_tulumensis_2	hemocyte protein-glutamine gamma-glutamyltransferase-like	261	1.05E-64	72.50%	-	0	IPR008958; IPR013783; IPR023608; PTHR11590:SF17 (PANTHER)
2176	DMPC15253376_Speleonectes_tulumensis_1	protein lethal giant larvae-like	188	7.53E-71	80.00%	-	0	IPR000664; PTHR10241 (PANTHER), PTHR10241:SF10 (PANTHER)
2177	DMPC15253406_Speleonectes_tulumensis_1	lipophorin receptor	240	3.10E-14	62.40%	F:calcium ion binding; C:integral to membrane; C:membrane; F:receptor activity	4	IPR002172; IPR023415; PR00261 (PRINTS), PTHR10529 (PANTHER), tmhmm (TMHMM)
2178	DMPC15253421_Speleonectes_tulumensis_0	trypsin	183	3.48E-35	78.30%	F:catalytic activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER)
2179	DMPC15253425_Speleonectes_tulumensis_5	low quality protein: protein dachsous-like	78	1.28E-21	71.90%	C:cell; P:biological_process	2	IPR002126; IPR015919; IPR020894; PTHR24027 (PANTHER), PTHR24027:SF53 (PANTHER)
2180	DMPC15253445_Speleonectes_tulumensis_2	isoform a	95	9.06E-15	61.90%	F:calcium ion binding; C:integral to membrane; C:membrane	3	IPR002172; PR00261 (PRINTS), PTHR10529 (PANTHER)
2181	DMPC15253469_Speleonectes_tulumensis_0	superoxide dismutase	449	6.84E-43	82.70%	F:binding; P:metabolic process; F:catalytic activity	3	IPR001424; IPR024134; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2182	DMPC15253488_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	145	4.62E-46	68.80%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2183	DMPC15253537_Speleonectes_tulumensis_0	---NA---	52			-	0	no IPS match

2184	DMPC15253556_Speleonectes_tulumensis_2	epidermal retinol dehydrogenase 2 isoform 2	109	2.91E-09	70.40%	P:lipid metabolic process; P:secondary metabolic process; F:catalytic activity; P:cell proliferation; C:endoplasmic reticulum	5	IPR002198; IPR016040; PTHR24316 (PANTHER), PTHR24316:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF51735 (SUPERFAMILY)
2185	DMPC15253563_Speleonectes_tulumensis_2	trypsin 2	158	3.69E-21	57.00%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2186	DMPC15253609_Speleonectes_tulumensis_1	anti-lipopolysaccharide factor isoform 7	125	5.47E-12	57.30%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2187	DMPC15253682_Speleonectes_tulumensis_2	plasminogen activator spa	116	5.39E-11	55.60%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
2188	DMPC15253734_Speleonectes_tulumensis_0	hypothetical protein DAPPUDRAFT_308200	131	4.24E-08	52.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP)
2189	DMPC15253927_Speleonectes_tulumensis_0	protein lethal giant larvae-like isoform 2	131	1.89E-41	75.80%	P:multicellular organismal development	1	IPR000664; IPR001680; IPR015943; IPR019775; PTHR10241 (PANTHER), PTHR10241:SF21 (PANTHER)
2190	DMPC15253954_Speleonectes_tulumensis_1	secreted salivary gland	338	3.57E-42	54.90%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
2191	DMPC15253959_Speleonectes_tulumensis_0	60s ribosomal protein l40	119	1.63E-45	96.50%	C:ribosome; F:structural molecule activity; P:translation	3	IPR000626; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
2192	DMPC15254006_Speleonectes_tulumensis_1	midgut glutamate specific carboxypeptidase	117	3.25E-15	59.80%	P:proteolysis; F:metallocarboxypeptidase activity; F:carboxypeptidase activity; F:zinc ion binding	4	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
2193	DMPC15254035_Speleonectes_tulumensis_2	---NA---	122			-	0	IPR000716; IPR022339; PTHR14093:SF3 (PANTHER)
2194	DMPC15254245_Speleonectes_tulumensis_1	trypsin 3	155	3.84E-28	63.90%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER), SignalP-NN(euk) (SIGNALP)
2195	DMPC15254250_Speleonectes_tulumensis_0	26s proteasome non-atpase regulatory subunit 10	135	7.75E-42	67.10%	P:biological_process	1	IPR002110; IPR020683; PTHR24199 (PANTHER), PTHR24199:SF0 (PANTHER)
2196	DMPC15254329_Speleonectes_tulumensis_0	---NA---	225			-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2197	DMPC15254361_Speleonectes_tulumensis_1	aldehyde mitochondrial	301	5.90E-126	85.40%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016160; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
2198	DMPC15254374_Speleonectes_tulumensis_2	heat shock related 70kda protein (hsp 70 family)	166	3.05E-38	61.70%	F:ATP binding; F:nucleotide binding; P:response to stress; C:cytoplasm	4	IPR013126; G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), PTHR19375 (PANTHER), PTHR19375:SF1 (PANTHER), SSF53067 (SUPERFAMILY)
2199	DMPC15254375_Speleonectes_tulumensis_0	26s proteasome non-atpase regulatory subunit 10	123	8.22E-36	69.90%	P:metabolic process; P:regulation of biological process; P:cell cycle; C:protein complex; C:intracellular; P:signal transduction; P:cell death; P:mitochondrion organization; C:cytoskeleton; ; F:protein binding; P:cellular protein modification process; P:response to stress; C:cytoplasm; P:cell growth; P:cellular component organization; P:protein metabolic process; P:catabolic process; P:protein transport; C:nucleus	20	IPR002110; IPR020683; PTHR24199 (PANTHER), PTHR24199:SF0 (PANTHER)
2200	DMPC15254391_Speleonectes_tulumensis_0	peptidyl-prolyl cis-trans isomerase-like 3-like	257	3.17E-46	62.50%	F:peptidyl-prolyl cis-trans isomerase activity; P:protein folding; P:protein peptidyl-prolyl isomerization; F:isomerase activity	4	IPR002130; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER)

2201	DMPC15254409_Speleonectes_tulumensis_1	soma ferritin	112	7.98E-29	88.80%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2202	DMPC15254461_Speleonectes_tulumensis_1	collagen and calcium binding egf domains 1	208	4.73E-65	63.50%	F:binding	1	IPR000742; IPR001881; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR24023 (PANTHER), PTHR24023:SF13 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF57196 (SUPERFAMILY)
2203	DMPC15254503_Speleonectes_tulumensis_2	glucan pattern-recognition lipoprotein	574	1.45E-31	41.75%	P:lipid transport; F:lipid transporter activity	2	IPR020292
2204	DMPC15254595_Speleonectes_tulumensis_2	armet-like protein	161	2.01E-37	79.30%	-	0	IPR011001; IPR019345; PTHR12990 (PANTHER), PTHR12990:SF2 (PANTHER), tmhmm (TMHMM)
2205	DMPC15254634_Speleonectes_tulumensis_1	short-chain dehydrogenease reductase	97	9.64E-16	79.30%	F:catalytic activity; P:metabolic process; F:nucleotide binding	3	IPR002198; IPR016040; PTHR24322 (PANTHER), PTHR24322:SF0 (PANTHER), tmhmm (TMHMM), SSF51735 (SUPERFAMILY)
2206	DMPC15254663_Speleonectes_tulumensis_2	chitinase partial	74	2.71E-23	67.00%	-	0	IPR001223; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER), SSF54556 (SUPERFAMILY)
2207	DMPC15254666_Speleonectes_tulumensis_2	hypothetical protein DAPPUDRAFT_248374	155	8.98E-28	82.80%	F:calcium ion binding	1	PTHR19237 (PANTHER)
2208	DMPC15254789_Speleonectes_tulumensis_2	protein wnt-8b	174	2.10E-58	68.50%	P:anatomical structure morphogenesis; P:embryo development; P:regulation of biological process; ; P:signal transduction; P:multicellular organismal development	6	IPR005817; IPR013301; IPR018161
2209	DMPC15254790_Speleonectes_tulumensis_2	ame: full=annexin-b12 ame: full=annexin xii ame: full=annexin-12	236	3.67E-15	78.30%	F:binding	1	IPR001464; IPR018252; IPR018502
2210	DMPC15254805_Speleonectes_tulumensis_1	carboxypeptidase d-like	149	7.23E-47	75.20%	-	0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11532 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
2211	DMPC15254862_Speleonectes_tulumensis_4	n-acetylglucosamine-1-phosphotransferase subunit gamma-like	91	4.51E-16	64.80%	F:transferase activity; C:Golgi apparatus; C:extracellular region	3	IPR009011; PTHR12630 (PANTHER), PF13015 (PFAM), SignalP-NN(euk) (SIGNALP)
2212	DMPC15254892_Speleonectes_tulumensis_0	hemagglutinin amebocyte aggregation factor-like	113	1.19E-11	63.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2213	DMPC15254984_Speleonectes_tulumensis_0	anti-lipopolysaccharide factor	152	1.79E-29	68.50%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2214	DMPC15254992_Speleonectes_tulumensis_0	chymotrypsin a	129	1.13E-08	73.75%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2215	DMPC15254994_Speleonectes_tulumensis_4	pacifastin-related peptide precursor	131	1.02E-16	49.90%	F:peptidase inhibitor activity; P:negative regulation of peptidase activity	2	IPR006552; IPR008037; IPR016307; IPR020862
2216	DMPC15255062_Speleonectes_tulumensis_2	---NA---	100			-	0	IPR000716; IPR022339; PTHR14093:SF6 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2217	DMPC15255167_Speleonectes_tulumensis_1	prophenoloxidase subunit 2	292	2.45E-22	72.10%	P:biosynthetic process; ; P:secondary metabolic process; P:response to stress; F:catalytic activity; C:extracellular region	6	IPR005203; IPR013788; IPR014756; PTHR11511:SF4 (PANTHER)
2218	DMPC15255169_Speleonectes_tulumensis_2	serine protease hepsin	139	2.27E-09	55.40%	F:peptidase activity; P:cellular component organization; P:anatomical structure morphogenesis; P:embryo development; P:response to external stimulus; P:response to abiotic stimulus; C:plasma membrane; F:ion channel activity; P:metabolic process; P:regulation of biological process; C:cell	11	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

2219	DMPC15255247_Speleonectes_tulumensis_1	chymotrypsin-like protease ctrl- partial	155	5.66E-18	57.60%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2220	DMPC15255285_Speleonectes_tulumensis_0	myosin heavy chain	124	6.04E-38	89.00%	-	0	IPR002928; PTHR13140 (PANTHER), PTHR13140:SF106 (PANTHER)
2221	DMPC15255293_Speleonectes_tulumensis_0	dermatopontin 3	102	2.97E-08	60.50%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2222	DMPC15255305_Speleonectes_tulumensis_1	selenium-dependent glutathione peroxidase	108	4.03E-27	78.30%	-	0	IPR000889; IPR012336
2223	DMPC15255400_Speleonectes_tulumensis_1	hemocyanin subunit type 1 precursor	144	4.96E-46	67.90%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP)
2224	DMPC15255417_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor	106	5.01E-08	57.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2225	DMPC15255534_Speleonectes_tulumensis_2	ame: full=trypsin-1 ame: full=trypsin i	128	1.81E-22	78.40%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
2226	DMPC15255627_Speleonectes_tulumensis_0	maltase- intestinal-like	179	6.85E-50	67.00%	-	0	IPR000322; IPR017853; SSF51011 (SUPERFAMILY)
2227	DMPC15255667_Speleonectes_tulumensis_1	60s ribosomal protein l40	149	4.84E-42	98.70%	P:cell cycle; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; C:cytosol; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; C:plasma membrane; ; C:endosome; P:cellular component organization; C:ribosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; P:cellular protein modification process; P:translation; P:transport	25	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
2228	DMPC15255685_Speleonectes_tulumensis_1	gelsolin-like allergen der f 16	231	2.22E-51	66.60%	F:actin binding; P:cytoskeleton organization	2	IPR007122; IPR007123; G3DSA:3.40.20.10 (GENE3D), SSF55753 (SUPERFAMILY)
2229	DMPC15255746_Speleonectes_tulumensis_1	alpha-aminoadipic semialdehyde dehydrogenase-like	371	0	84.80%	F:catalytic activity; P:metabolic process; F:nucleotide binding	3	IPR015590; IPR016160; IPR016161; IPR016162; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF26 (PANTHER), tmhmm (TMHMM)
2230	DMPC15255822_Speleonectes_tulumensis_1	proclotting enzyme	346	1.76E-30	59.10%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24272 (PANTHER), SignalP-NN(euk) (SIGNALP)
2231	DMPC15255883_Speleonectes_tulumensis_2	allergen 5	137	2.24E-19	56.70%	-	0	IPR001283; IPR014044; SignalP-NN(euk) (SIGNALP)
2232	DMPC15255887_Speleonectes_tulumensis_1	dipeptidyl peptidase 9	171	4.65E-78	85.80%	F:peptidase activity; C:cell; P:protein metabolic process; P:catabolic process	4	IPR001375; G3DSA:3.40.50.1820 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF9 (PANTHER), SSF53474 (SUPERFAMILY)
2233	DMPC15255935_Speleonectes_tulumensis_2	hemocyanin subunit type 2 precursor	141	8.08E-32	73.80%	-	0	IPR005203; IPR013788; IPR014756
2234	DMPC15256044_Speleonectes_tulumensis_2	calponin homology domain- chdc lrch	85	7.61E-21	76.80%	F:hydrolase activity	1	IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF10 (PANTHER), SSF52058 (SUPERFAMILY)
2235	DMPC15256085_Speleonectes_tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	144	7.65E-20	50.70%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

2236	DMPC15256110_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_57749	169	1.46E-40	77.50%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), PTHR24260:SF33 (PANTHER), tmhmm (TMHMM)
2237	DMPC15256113_Speleonectes_tulumensis_0	serine protease	193	6.02E-08	42.60%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2238	DMPC15256314_Speleonectes_tulumensis_2	serine proteinase stubble-like	238	4.67E-74	67.30%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity	3	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), PTHR24260:SF33 (PANTHER)
2239	DMPC15256357_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_308200	180	8.09E-12	46.30%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP)
2240	DMPC15256439_Speleonectes_tulumensis_0	allergen 5	161	3.45E-17	69.30%	-	0	IPR001283; IPR002413; IPR014044
2241	DMPC15256549_Speleonectes_tulumensis_2	glycosyl-phosphatidylinositol-linked carbonic anhydrase	131	1.10E-15	54.00%	-	0	IPR001148; IPR023561
2242	DMPC15256564_Speleonectes_tulumensis_1	neutral ceramidase-like	128	7.05E-25	71.00%	-	0	IPR006823; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2243	DMPC15256596_Speleonectes_tulumensis_2	phosphoglucose isomerase	140	5.97E-37	94.30%	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; C:cytoplasm; F:catalytic activity; P:biosynthetic process	6	IPR001672; IPR018189; IPR023096; G3DSA:3.40.50.10490 (GENE3D), PTHR11469:SF0 (PANTHER), SSF53697 (SUPERFAMILY)
2244	DMPC15256597_Speleonectes_tulumensis_2	low affinity immunoglobulin epsilon fc receptor	302	5.75E-19	52.60%	P:positive regulation of killing of cells of other organism; F:carbohydrate binding; P:positive regulation of humoral immune response mediated by circulating immunoglobulin; P:positive regulation of nitric-oxide synthase biosynthetic process; P:positive regulation of nitric-oxide synthase activity; C:external side of plasma membrane	6	IPR001304; IPR016186; IPR016187; IPR018378; PTHR22802 (PANTHER), SignalP-NN(euk) (SIGNALP)
2245	DMPC15256655_Speleonectes_tulumensis_0	chymotrypsin-like elastase family member 2a-like	174	7.83E-11	59.80%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
2246	DMPC15256680_Speleonectes_tulumensis_2	serine protease	126	2.57E-27	59.40%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity; F:peptidase activity	4	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), PTHR24260:SF33 (PANTHER)
2247	DMPC15256690_Speleonectes_tulumensis_2	trypsin 7	135	4.09E-20	74.60%	F:hydrolase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
2248	DMPC15256696_Speleonectes_tulumensis_1	leucine-rich repeat and calponin homology domain-containing protein 1-like	213	1.05E-72	68.20%	F:hydrolase activity	1	IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF10 (PANTHER), PF13504 (PFAM), SM00364 (SMART), SSF52058 (SUPERFAMILY)
2249	DMPC15256710_Speleonectes_tulumensis_2	lim and sh3 domain protein lasp-like	197	3.74E-27	86.20%	F:binding	1	IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR11039 (PANTHER)
2250	DMPC15256819_Speleonectes_tulumensis_1	dermatopontin 2	331	2.30E-37	59.20%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2251	DMPC15256863_Speleonectes_tulumensis_2	serine protease 82 precursor	115	2.17E-16	59.50%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
2252	DMPC15256868_Speleonectes_tulumensis_2	neurogenic locus notch protein	119	1.92E-47	78.90%	F:enzyme regulator activity	1	IPR000152; IPR000742; IPR001881; IPR013032; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR24047 (PANTHER), PTHR24047:SF0 (PANTHER), SSF57196 (SUPERFAMILY)
2253	DMPC15256935_Speleonectes_tulumensis_0	hypothetical protein DAPPUDRAFT_308200	151	1.03E-08	50.25%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

2254	DMPC15256957_Speleonectes_tulumensis_1	mitochondrial manganese superoxide dismutase	121	2.21E-18	85.50%	-	0	IPR001189; IPR019831; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER)
2255	DMPC15256998_Speleonectes_tulumensis_2	ame: full=plasminogen contains: ame: full=plasmin heavy chain a contains: ame: full=activation peptide contains: ame: full=plasmin heavy chain short form contains: ame: full=plasmin light chain b flags: precursor	106	2.82E-09	73.10%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER)
2256	DMPC15257007_Speleonectes_tulumensis_1	---NA---	110			-	0	IPR008197; PTHR19441 (PANTHER), SignalP-NN(euk) (SIGNALP)
2257	DMPC15257126_Speleonectes_tulumensis_0	techylectin-5b isoform	225	6.79E-55	65.70%	-	0	IPR002181; IPR014715; IPR014716; IPR020837; PTHR19143 (PANTHER)
2258	DMPC15257137_Speleonectes_tulumensis_2	hemocyanin 2	149	1.06E-21	85.60%	-	0	IPR000896; IPR008922; IPR013788; PTHR11511:SF20 (PANTHER), tmhmm (TMHMM)
2259	DMPC15257225_Speleonectes_tulumensis_0	guanine nucleotide-binding protein subunit beta-like	315	5.68E-134	94.20%	F:receptor activity; F:kinase activity; P:metabolic process	3	IPR001680; IPR015943; IPR017986; IPR019775; IPR020472; PTHR19868 (PANTHER), PTHR19868:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP)
2260	DMPC15257411_Speleonectes_tulumensis_2	serine threonine-protein kinase mos	131	4.01E-18	57.20%	F:kinase activity	1	IPR000719; IPR008271; IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR23257 (PANTHER)
2261	DMPC15257460_Speleonectes_tulumensis_0	heavy polypeptide 1	117	2.64E-22	89.20%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2262	DMPC15257519_Speleonectes_tulumensis_1	gastric mucin	277	8.65E-18	43.90%	P:cell adhesion	1	IPR001007; IPR006207; PTHR11339 (PANTHER), PTHR11339:SF25 (PANTHER)
2263	DMPC15257529_Speleonectes_tulumensis_0	cathepsin l	176	8.21E-40	75.10%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
2264	DMPC15257613_Speleonectes_tulumensis_1	kazal-type protease inhibitor	126	4.08E-16	51.70%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
2265	DMPC15257683_Speleonectes_tulumensis_0	hemocyanin subunit type 1 precursor	191	1.09E-103	70.40%	-	0	IPR005203; IPR013788; IPR014756
2266	DMPC15257695_Speleonectes_tulumensis_1	glyceraldehyde-3-phosphate dehydrogenase	133	1.67E-31	85.50%	F:nucleotide binding; P:carbohydrate metabolic process; F:catalytic activity; P:metabolic process	4	IPR016040; IPR020828; IPR020831; SignalP-NN(euk) (SIGNALP), SSF51735 (SUPERFAMILY)
2267	DMPC15257723_Speleonectes_tulumensis_0	aldehyde dehydrogenase mitochondrial-like	154	1.01E-54	85.00%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
2268	DMPC15257812_Speleonectes_tulumensis_2	tpa_exp: ubiquitin	121	1.53E-78	100.00%	-	0	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
2269	DMPC15257835_Speleonectes_tulumensis_0	boophilin-like protein	120	2.90E-09	58.30%	F:hydrolase activity	1	IPR002223; IPR020901; PTHR10083 (PANTHER)
2270	DMPC15257863_Speleonectes_tulumensis_2	hemagglutinin amebocyte aggregation factor-like	136	1.29E-12	63.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2271	DMPC15257890_Speleonectes_tulumensis_0	ankyrin repeat and socs box protein 13-like	177	4.49E-30	68.60%	F:protein binding	1	IPR002110; IPR020683; PTHR24196 (PANTHER), PTHR24196:SF3 (PANTHER)
2272	DMPC15257974_Speleonectes_tulumensis_2	cathepsin l	152	5.61E-71	78.10%	-	0	IPR000668; IPR013128; IPR025660; IPR025661; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2273	DMPC15257996_Speleonectes_tulumensis_2	chymotrypsinogen b-like	128	1.46E-15	53.50%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)

2274	DMPC15258022_Speleonectes_tulumensis_1	carboxypeptidase b-like	208	2.21E-49	68.30%	P:proteolysis; F:metallocarboxypeptidase activity; F:carboxypeptidase activity; F:zinc ion binding	4	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
2275	DMPC15258027_Speleonectes_tulumensis_0	chitinase partial	285	1.08E-58	67.20%	-	0	IPR001223; IPR002557; IPR013781; IPR017853; G3DSA:3.10.50.10 (GENE3D), PTHR11177 (PANTHER), SSF54556 (SUPERFAMILY)
2276	DMPC15258133_Speleonectes_tulumensis_0	trypsin	144	2.97E-22	66.70%	-	0	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
2277	DMPC15258154_Speleonectes_tulumensis_1	trypsin 3	227	4.04E-31	51.50%	-	0	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
2278	DMPC15258162_Speleonectes_tulumensis_1	lipase 3-like	118	7.08E-30	71.50%	F:hydrolase activity; P:lipid metabolic process	2	G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), PTHR11005:SF0 (PANTHER), SSF53474 (SUPERFAMILY)
2279	DMPC15258219_Speleonectes_tulumensis_2	lysozyme precursor	180	1.97E-45	64.80%	F:lysozyme activity; P:cell wall macromolecule catabolic process	2	IPR000974; IPR001916; IPR019799; IPR023346; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER)
2280	DMPC15258291_Speleonectes_tulumensis_1	GF20025	138	8.36E-08	68.00%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
2281	DMPC15258299_Speleonectes_tulumensis_2	---NA---	140			-	0	IPR001283; IPR014044
2282	DMPC15258487_Speleonectes_tulumensis_0	pdz domain-containing protein 11	72	2.13E-09	73.80%	F:protein binding; C:cytosol; C:plasma membrane	3	PTHR14063 (PANTHER)
2283	DMPC15258580_Speleonectes_tulumensis_0	cathepsin l	128	1.32E-25	67.20%	-	0	IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2284	DMPC15258587_Speleonectes_tulumensis_2	kazal-type protease inhibitor	249	2.30E-24	51.40%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
2285	DMPC15258601_Speleonectes_tulumensis_0	ferritin gfl	102	4.63E-25	86.60%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2286	DMPC15258620_Speleonectes_tulumensis_2	hemocyanin subunit type 1 precursor	150	1.38E-62	68.00%	-	0	IPR005204; IPR013788; PTHR11511:SF23 (PANTHER), SignalP-NN(euk) (SIGNALP)
2287	DMPC15258631_Speleonectes_tulumensis_2	Trypsin-1	107	8.54E-07	56.00%	-	0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
2288	DMPC15258664_Speleonectes_tulumensis_1	ame: full=trypsin-1 ame: full=trypsin i	184	3.36E-20	75.10%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24256 (PANTHER)
2289	DMPC15258704_Speleonectes_tulumensis_2	serine protease	150	4.75E-22	57.90%	F:peptidase activity	1	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
2290	DMPC15258732_Speleonectes_tulumensis_1	soma ferritin	98	7.40E-23	87.40%	-	0	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2291	DMPC15258810_Speleonectes_tulumensis_1	hypothetical protein DAPPUDRAFT_315125	161	4.69E-09	50.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2292	DMPC15258864_Speleonectes_tulumensis_2	aldehyde dehydrogenase mitochondrial-like	210	1.43E-69	83.00%	F:catalytic activity; P:metabolic process	2	IPR015590; IPR016161; IPR016163; PTHR11699 (PANTHER), PTHR11699:SF46 (PANTHER)
2293	DMPC15258914_Speleonectes_tulumensis_2	female neotenic-specific protein 3	155	2.67E-11	53.67%	-	0	no IPS match
2294	DMPC15258940_Speleonectes_tulumensis_1	soma ferritin	122	5.43E-24	88.00%	-	0	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2295	DMPC15259028_Speleonectes_tulumensis_1	cytosolic non-specific dipeptidase-like	111	1.72E-28	75.30%	P:metabolic process; F:peptidase activity	2	G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF15 (PANTHER), SSF53187 (SUPERFAMILY)

2296	DMPC15259044_Speleonectes_tulumensis_1	cathepsin l	142	7.84E-14	62.80%	-	0	IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
2297	DMPC15259105_Speleonectes_tulumensis_0	hyaluronan-binding protein 2-like	96	3.79E-12	55.60%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), SignalP-NN(euk) (SIGNALP)
2298	DMPC15259127_Speleonectes_tulumensis_2	trypsinogen 3	122	5.47E-13	44.80%	-	0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP)
2299	DMPC15259237_Speleonectes_tulumensis_0	hemocyanin subunit type 2 precursor	125	2.17E-21	75.20%	-	0	IPR005203; IPR013788; IPR014756
2300	DMPC15259324_Speleonectes_tulumensis_4	hemocyanin subunit type 1 precursor	150	1.12E-59	67.80%	-	0	IPR005204; IPR013788; PTHR11511:SF20 (PANTHER)
2301	DMPC15259358_Speleonectes_tulumensis_1	---NA---	101			-	0	IPR013785; IPR017853; IPR018155; SignalP-NN(euk) (SIGNALP)
2302	DMPC15259374_Speleonectes_tulumensis_1	cathepsin l-like	185	1.59E-19	86.90%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025661; G3DSA:2.40.50.170 (GENE3D), PTHR12411:SF149 (PANTHER), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
2303	DMPC15259391_Speleonectes_tulumensis_1	retinol dehydrogenase 10-b-like	87	3.94E-09	75.60%	-	0	PTHR24316 (PANTHER), PTHR24316:SF1 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2304	DMPC15259424_Speleonectes_tulumensis_0	subfamily member 9	158	7.90E-43	81.20%	P:protein metabolic process; F:protein binding	2	IPR001623; IPR018253; PTHR24078 (PANTHER), PTHR24078:SF16 (PANTHER)
2305	DMPC15259429_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor-like	134	3.62E-11	60.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2306	DMPC15259441_Speleonectes_tulumensis_0	hemocyanin subunit type 1 precursor	96	2.70E-25	73.40%	-	0	IPR005203; IPR013788; IPR014756; PTHR11511:SF18 (PANTHER)
2307	DMPC15259461_Speleonectes_tulumensis_2	serine protease p127	323	1.04E-26	55.80%	F:catalytic activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER)
2308	DMPC15259510_Speleonectes_tulumensis_1	ame: full=hyaluronidase short=hya ame: full=hyaluronoglucosaminidase	164	6.59E-27	60.50%	F:catalytic activity	1	IPR013785; IPR017853; IPR018155
2309	DMPC15259513_Speleonectes_tulumensis_1	mitochondrial manganese superoxide dismutase	108	1.95E-26	87.70%	F:binding; P:metabolic process; F:catalytic activity	3	IPR001189; IPR019831; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER)
2310	DMPC15259530_Speleonectes_tulumensis_2	ferritin h subunit	91	3.54E-20	92.60%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2311	DMPC15259534_Speleonectes_tulumensis_2	transcriptional repressor ctcfl-like	135	1.06E-82	95.10%	F:binding; C:intracellular; F:DNA binding	3	IPR007087; IPR013087; IPR015880; PTHR24375 (PANTHER), PTHR24375:SF1 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
2312	DMPC15259620_Speleonectes_tulumensis_1	protein shifted-like isoform 2	118	9.44E-49	85.10%	-	0	IPR003306
2313	DMPC15259732_Speleonectes_tulumensis_0	dermatopontin 3	98	2.07E-09	68.50%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2314	DMPC15259738_Speleonectes_tulumensis_2	mantle protein 9	148	1.36E-08	67.75%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
2315	DMPC15259797_Speleonectes_tulumensis_1	peptidase s8 s53 subtilisin kexin sedolisin	148	1.37E-13	58.80%	F:hydrolase activity	1	IPR007280; SignalP-NN(euk) (SIGNALP)
2316	DMPC15259923_Speleonectes_tulumensis_0	linear gramicidin synthetase subunit d	121	2.24E-51	80.70%	F:binding; F:catalytic activity; P:metabolic process; F:nucleotide binding	4	IPR002198; IPR002347; IPR016040; IPR020904; PTHR24322 (PANTHER), SSF51735 (SUPERFAMILY)
2317	DMPC15259970_Speleonectes_tulumensis_0	trypsin-like serine proteinase 1	90	1.43E-09	67.60%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), SignalP-NN(euk) (SIGNALP)
2318	DMPC15259995_Speleonectes_tulumensis_0	dysferlin-interacting protein 1	150	3.72E-49	69.80%	P:negative regulation of phosphatase activity; F:phosphatase binding	2	IPR002110; IPR020683; PTHR24179 (PANTHER), PTHR24179:SF2 (PANTHER)

2319	DMPC15260028_Speleonectes _tulumensis_0	equistatin precursor	107	6.76E-08	65.57%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase	4	IPR000716; IPR022339; tmhmm (TMHMM)
2320	DMPC15260242_Speleonectes _tulumensis_0	ame: full=venom allergen 5 ame: full=allergen ves vi v ame: full=antigen 5 short=ag5 ame: full=cysteine-rich venom protein short=crvp ame: allergen=ves vi 5	111	5.82E-10	63.20%	-	0	IPR002413; IPR014044; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2321	DMPC15260263_Speleonectes _tulumensis_0	upf0764 protein c16orf89 homolog	250	5.34E-09	62.78%	-	0	no IPS match
2322	DMPC15260371_Speleonectes _tulumensis_0	low density lipoprotein receptor-1	137	7.78E-18	61.00%	C:integral to membrane; C:membrane; P:lipid metabolic process; P:lipid transport; P:endocytosis; P:transport; C:low-density lipoprotein particle; F:receptor activity; P:cholesterol metabolic process; P:steroid metabolic process; F:calcium ion binding; C:coated pit	12	IPR002172; PR00261 (PRINTS), PTHR10529 (PANTHER), tmhmm (TMHMM)
2323	DMPC15260470_Speleonectes _tulumensis_1	hemocyanin subunit 6	145	3.40E-23	67.60%	-	0	IPR005203; IPR013788; IPR014756; PTHR11511:SF4 (PANTHER)
2324	DMPC15260549_Speleonectes _tulumensis_1	anti-lipopolysaccharide factor isoform 7	264	1.34E-19	72.00%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2325	DMPC15260651_Speleonectes _tulumensis_1	serine protease	120	1.70E-23	74.70%	F:peptidase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF68 (PANTHER)
2326	DMPC15260658_Speleonectes _tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	147	2.46E-20	50.30%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase	4	IPR000716; PTHR12036 (PANTHER), PTHR12036:SF5 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2327	DMPC15260736_Speleonectes _tulumensis_2	dermatopontin 3	106	3.04E-08	57.38%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2328	DMPC15260842_Speleonectes _tulumensis_0	trypsin	150	1.58E-59	76.70%	F:catalytic activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER)
2329	DMPC15260922_Speleonectes _tulumensis_2	chymotrypsin a	147	1.06E-23	65.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER)
2330	DMPC15261051_Speleonectes _tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	138	2.53E-12	55.10%	P:proteolysis; F:peptidase activity	2	IPR000716; PTHR12352 (PANTHER), SignalP-NN(euk) (SIGNALP)
2331	DMPC15261136_Speleonectes _tulumensis_3	protein isoform a	123	5.13E-08	74.14%	P:embryo development	1	IPR002172; IPR023415; PTHR12106 (PANTHER), PTHR12106:SF7 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2332	DMPC15261152_Speleonectes _tulumensis_1	isoform a	175	9.70E-26	60.00%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF28 (PANTHER)
2333	DMPC15261154_Speleonectes _tulumensis_1	chymotrypsin a	152	1.19E-23	65.20%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24275 (PANTHER), tmhmm (TMHMM)
2334	DMPC15261258_Speleonectes _tulumensis_0	dermatopontin 2	110	7.05E-09	58.30%	-	0	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2335	DMPC15261373_Speleonectes _tulumensis_1	ribosomal protein ubq l40e	139	1.22E-84	98.40%	C:cytoskeleton; C:protein complex; F:structural molecule activity; C:lipid particle; P:cellular protein modification process; P:protein metabolic process; P:catabolic process; C:ribosome; C:cytosol; P:translation	10	IPR000626; IPR001975; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)

2336	DMPC15261449_Speleonectes _tulumensis_0	epidermal growth factor receptor	146	2.88E-42	88.60%	F:protein kinase activity; F:receptor activity; P:cellular protein modification process; F:nucleotide binding; C:cell; P:signal transduction	6	IPR000719; IPR001245; IPR008266; IPR011009; IPR020635; G3DSA:1.10.510.10 (GENE3D), PTHR24416 (PANTHER), PTHR24416:SF95 (PANTHER)
2337	DMPC15261587_Speleonectes _tulumensis_0	mhc class ii antigen-associated invariant chain	87	3.49E-11	63.60%	P:proteolysis; F:peptidase activity	2	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP)
2338	DMPC15261608_Speleonectes _tulumensis_2	kazal-type serine proteinase inhibitor 4	137	2.37E-13	66.00%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR25189 (PANTHER), PTHR25189:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)
2339	DMPC15261615_Speleonectes _tulumensis_0	ame: full=saxiphilin short=sax flags: precursor	140	1.58E-21	52.60%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2340	DMPC15261654_Speleonectes _tulumensis_2	ankyrin repeat and kh domain-containing protein 1	322	0	92.70%	-	0	IPR002110; IPR020683; PTHR24139 (PANTHER), PTHR24139:SF7 (PANTHER)
2341	DMPC15261690_Speleonectes _tulumensis_0	lysosomal acid phosphatase	197	3.38E-59	68.90%	F:acid phosphatase activity	1	IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF26 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF53254 (SUPERFAMILY)
2342	DMPC15261706_Speleonectes _tulumensis_2	cathepsin l	143	1.62E-35	84.70%	F:peptidase activity; P:protein metabolic process; P:catabolic process	3	IPR000668; IPR013128; IPR025660; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SSF54001 (SUPERFAMILY)
2343	DMPC15261726_Speleonectes _tulumensis_0	apolipoprotein d-like isoform 2	102	4.89E-13	68.10%	F:lipid binding; P:transport; F:transporter activity	3	IPR011038; IPR012674; IPR022272; PTHR10612 (PANTHER), PTHR10612:SF4 (PANTHER), SignalP-NN(euk) (SIGNALP)
2344	DMPC15261778_Speleonectes _tulumensis_1	salivary fat body serine carboxypeptidase	209	7.12E-33	63.90%	F:hydrolase activity	1	IPR001563; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
2345	DMPC15261798_Speleonectes _tulumensis_1	cbpa1_drops ame: full=zinc carboxypeptidase a 1 flags: precursor	129	8.02E-27	67.40%	C:extracellular region; F:peptidase activity	2	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF53187 (SUPERFAMILY)
2346	DMPC15261900_Speleonectes _tulumensis_0	armet-like protein	128	3.03E-29	77.60%	-	0	IPR011001; IPR019345; PTHR12990 (PANTHER), PTHR12990:SF2 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2347	DMPC15261973_Speleonectes _tulumensis_0	---NA---	140			-	0	SignalP-NN(euk) (SIGNALP)
2348	DMPC15262033_Speleonectes _tulumensis_1	soma ferritin	113	9.46E-33	88.60%	P:cellular homeostasis; F:catalytic activity; F:binding; P:ion transport; P:metabolic process	5	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2349	DMPC15262039_Speleonectes _tulumensis_1	thioredoxin peroxidase	255	3.68E-73	88.00%	-	0	IPR000866; IPR012336; IPR019479; PTHR10681 (PANTHER), PTHR10681:SF44 (PANTHER)
2350	DMPC15262235_Speleonectes _tulumensis_0	hemocyanin subunit type 2 precursor	161	5.99E-16	83.00%	-	0	IPR005203; IPR013788; IPR014756; tmhmm (TMHMM)
2351	DMPC15262292_Speleonectes _tulumensis_2	serine protease inhibitor kazal-type 6-like	157	1.39E-08	67.00%	-	0	IPR001239; IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21312 (PANTHER), PTHR21312:SF8 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF100895 (SUPERFAMILY)

2352	DMPC15262378_Speleonectes _tulumensis_1	60s ribosomal protein l40	143	2.00E-42	97.80%	P:cell cycle; P:signal transduction; F:structural molecule activity; P:biological_process; P:response to stress; P:DNA metabolic process; P:reproduction; P:viral reproduction; C:cytosol; C:nucleoplasm; P:protein metabolic process; P:catabolic process; P:regulation of biological process; P:cell death; F:protein binding; C:plasma membrane; ; C:endosome; P:cellular component organization; C:ribosome; C:cytoplasmic membrane-bounded vesicle; P:nucleobase-containing compound metabolic process; P:cellular protein modification process; P:translation; P:transport	25	IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF54236 (SUPERFAMILY)
2353	DMPC15262423_Speleonectes _tulumensis_0	ame: full= cytoplasmic ame: full=actin-depolymerizing factor short=adf	119	6.12E-22	72.00%	F:actin binding; P:response to abscisic acid stimulus; P:cytoskeleton organization	3	IPR007122; IPR007123; G3DSA:3.40.20.10 (GENE3D), SignalP-NN(euk) (SIGNALP), SSF55753 (SUPERFAMILY)
2354	DMPC15262533_Speleonectes _tulumensis_0	kazal-type protease inhibitor	128	8.09E-15	53.20%	-	0	IPR002350; G3DSA:3.30.60.30 (GENE3D), PTHR21131 (PANTHER), SSF100895 (SUPERFAMILY)
2355	DMPC15262546_Speleonectes _tulumensis_0	superoxide dismutase soluble	127	3.51E-11	74.80%	P:metabolic process; F:catalytic activity; F:antioxidant activity	3	IPR001424; IPR024134; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2356	DMPC15262633_Speleonectes _tulumensis_1	ensangp00000031746-like protein	259	1.06E-94	92.20%	P:protein metabolic process; P:cellular protein modification process; F:catalytic activity	3	IPR002130; IPR020892; G3DSA:2.40.100.10 (GENE3D), PTHR11071 (PANTHER), PTHR11071:SF41 (PANTHER)
2357	DMPC15262640_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor-like	134	2.06E-22	61.70%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)
2358	DMPC15262646_Speleonectes _tulumensis_0	extracellular cyanophycinase	382	4.09E-73	49.10%	-	0	IPR005320; G3DSA:3.40.50.880 (GENE3D), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF52317 (SUPERFAMILY)
2359	DMPC15262650_Speleonectes _tulumensis_1	---NA---	152			-	0	no IPS match
2360	DMPC15262656_Speleonectes _tulumensis_2	thioredoxin 1	96	9.64E-18	81.80%	P:cellular homeostasis; P:regulation of biological process; F:electron carrier activity; F:catalytic activity; P:metabolic process	5	IPR005746; IPR012336; IPR013766; IPR017937; PTHR10438:SF17 (PANTHER), SignalP-NN(euk) (SIGNALP)
2361	DMPC15262678_Speleonectes _tulumensis_1	phospholipase a2-like	146	4.68E-16	62.80%	F:phospholipase A2 activity; F:calcium ion binding; P:lipid catabolic process; P:phospholipid metabolic process; C:extracellular region	5	IPR001211; IPR013090; IPR016090; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2362	DMPC15262786_Speleonectes _tulumensis_2	alkaline serine protease	153	8.08E-13	65.80%	F:peptidase activity	1	IPR007280; SignalP-NN(euk) (SIGNALP)
2363	DMPC15262800_Speleonectes _tulumensis_0	hemagglutinin amebocyte aggregation factor	190	5.48E-37	57.40%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2364	DMPC15262855_Speleonectes _tulumensis_1	mitochondrial manganese superoxide dismutase	104	1.85E-25	84.60%	F:binding; P:metabolic process; F:catalytic activity	3	IPR001189; IPR019831; G3DSA:1.10.287.990 (GENE3D), PTHR11404:SF5 (PANTHER)
2365	DMPC15262872_Speleonectes _tulumensis_2	hemocyanin subunit type 1	147	6.53E-71	75.70%	-	0	IPR005203; IPR013788; IPR014756
2366	DMPC15262923_Speleonectes _tulumensis_0	anti-lipopolysaccharide factor	128	1.98E-19	61.50%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP)
2367	DMPC15262928_Speleonectes _tulumensis_2	---NA---	157			-	0	IPR007233; SignalP-NN(euk) (SIGNALP)
2368	DMPC15262988_Speleonectes _tulumensis_0	group 10 secretory phospholipase a2	215	9.39E-08	49.57%	F:phospholipase A2 activity; F:calcium ion binding; F:hydrolase activity; P:lipid catabolic process; P:phospholipid metabolic process; C:extracellular region	6	IPR001211; IPR013090; IPR016090; PTHR11716:SF2 (PANTHER)
2369	DMPC15263032_Speleonectes _tulumensis_1	hemagglutinin amebocyte aggregation factor	139	1.86E-13	57.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP)

2370	DMPC15263049_Speleonectes _tulumensis_2	anti-lipopolysaccharide factor	142	6.33E-31	68.10%	-	0	IPR024509; IPR024716; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2371	DMPC15263172_Speleonectes _tulumensis_1	ame: full= heavy subunit short=ferritin h	122	4.79E-41	77.20%	-	0	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347
2372	DMPC15263241_Speleonectes _tulumensis_2	ace-paralogous acetylcholinesterase	155	2.44E-45	74.90%	F:hydrolase activity	1	IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559 (PANTHER), PTHR11559:SF33 (PANTHER), SSF53474 (SUPERFAMILY)
2373	DMPC15263264_Speleonectes _tulumensis_1	plasminogen activator spa	123	3.24E-20	60.30%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER)
2374	DMPC15263282_Speleonectes _tulumensis_1	---NA---	104			-	0	IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF149 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF54001 (SUPERFAMILY)
2375	DMPC15263332_Speleonectes _tulumensis_1	epididymal secretory protein e1	119	6.68E-16	59.50%	P:transport	1	IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2376	DMPC15263457_Speleonectes _tulumensis_2	unnamed protein product	148	3.23E-07	61.00%	-	0	IPR001506; IPR024079; PTHR24543 (PANTHER), PTHR24543:SF85 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF55486 (SUPERFAMILY)
2377	DMPC15263470_Speleonectes _tulumensis_1	ame: full=techylectin-5a flags: precursor	273	4.08E-47	60.40%	F:receptor binding; C:extracellular space; P:signal transduction	3	IPR002181; IPR014715; IPR014716; IPR020837; PTHR19143 (PANTHER)
2378	DMPC15263476_Speleonectes _tulumensis_2	isoform g	452	2.73E-26	60.50%	C:proteinaceous extracellular matrix; F:structural molecule activity; F:hydrolase activity; P:cellular component organization; C:nucleus	5	IPR002223; IPR020901; PTHR10083 (PANTHER), tmhmm (TMHMM)
2379	DMPC15263514_Speleonectes _tulumensis_1	glyceraldehyde-3-phosphate dehydrogenase	138	9.86E-35	90.30%	C:cytoplasm; F:nucleotide binding; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:catalytic activity; P:metabolic process	7	IPR020829; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF55347 (SUPERFAMILY)
2380	DMPC15263533_Speleonectes _tulumensis_2	hypothetical protein DAPPUDRAFT_308200	153	2.82E-08	52.00%	-	0	IPR020234; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2381	DMPC15263538_Speleonectes _tulumensis_1	dermatopontin 2	148	2.75E-09	59.40%	-	0	IPR026645; tmhmm (TMHMM)
2382	DMPC15263596_Speleonectes _tulumensis_0	trypsinogens 1	136	2.96E-18	56.70%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
2383	DMPC15263605_Speleonectes _tulumensis_0	mannosyl-oligosaccharide -alpha-mannosidase ib	104	2.31E-26	78.80%	F:hydrolase activity; F:calcium ion binding; C:cell	3	IPR001382; PTHR11742:SF10 (PANTHER)
2384	DMPC15263659_Speleonectes _tulumensis_2	thioredoxin peroxidase	130	3.89E-23	59.30%	P:oxidation-reduction process; F:oxidoreductase activity; F:antioxidant activity; F:peroxiredoxin activity; F:peroxidase activity	5	IPR000866; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF51 (PANTHER)
2385	DMPC15263697_Speleonectes _tulumensis_1	ame: full=saxiphilin short=sax flags: precursor	128	1.53E-18	51.50%	F:peptidase inhibitor activity; F:serine-type endopeptidase inhibitor activity; C:extracellular region; P:negative regulation of peptidase activity	4	IPR000716; IPR022339; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2386	DMPC15263754_Speleonectes _tulumensis_0	zinc metalloproteinase nas-8	113	1.54E-12	57.80%	F:hydrolase activity	1	IPR001506; IPR024079; PTHR10127 (PANTHER), SSF55486 (SUPERFAMILY)
2387	DMPC15263757_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor-like	116	2.71E-12	63.30%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2388	DMPC15263818_Speleonectes _tulumensis_1	fatty acid binding protein	171	5.43E-48	79.20%	P:transport; F:lipid binding; F:transporter activity	3	IPR000463; IPR000566; IPR011038; IPR012674; PTHR11955 (PANTHER)
2389	DMPC15263820_Speleonectes _tulumensis_2	hemagglutinin amebocyte aggregation factor	137	1.93E-13	60.00%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2390	DMPC15263824_Speleonectes _tulumensis_1	growth differentiation factor 8	172	7.42E-25	57.70%	F:growth factor activity; P:growth; C:extracellular region	3	IPR001111; IPR015615; PTHR11848:SF15 (PANTHER)

2391	DMPC15263860_Speleonectes_tulumensis_2	factor d-like protein	340	5.44E-74	61.10%	P:proteolysis; F:serine-type endopeptidase activity; F:catalytic activity; F:peptidase activity	4	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24268 (PANTHER), PTHR24268:SF68 (PANTHER)
2392	DMPC15263939_Speleonectes_tulumensis_1	serine protease 82 precursor	115	2.81E-16	59.80%	F:hydrolase activity	1	IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24265 (PANTHER), SignalP-NN(euk) (SIGNALP)
2393	DMPC15263965_Speleonectes_tulumensis_1	projectin short variant	274	5.81E-94	72.30%	-	0	IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; SSF48726 (SUPERFAMILY)
2394	DMPC15264029_Speleonectes_tulumensis_1	zinc c2h2 type family protein	117	3.37E-15	60.70%	F:nucleic acid binding; F:zinc ion binding; C:intracellular; P:biological_process	4	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), PTHR11389:SF381 (PANTHER), PF13465 (PFAM), SSF57667 (SUPERFAMILY)
2395	DMPC15264050_Speleonectes_tulumensis_1	hypothetical protein BRAFLDRAFT_120123	96	1.60E-07	66.00%	F:peptidase activity	1	IPR002172; IPR023415; PTHR10529 (PANTHER), SignalP-NN(euk) (SIGNALP)
2396	DMPC15264085_Speleonectes_tulumensis_1	hemagglutinin amebocyte aggregation factor-like	108	3.90E-09	60.90%	-	0	IPR026645; SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2397	DMPC15264186_Speleonectes_tulumensis_0	trypsin partial	165	1.78E-15	60.70%	F:hydrolase activity	1	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR24264 (PANTHER), PTHR24264:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2398	DMPC15264249_Speleonectes_tulumensis_2	zinc metalloproteinase nas-4-like isoform 1	118	6.48E-13	56.20%	F:metal ion binding; P:proteolysis; F:metallopeptidase activity; F:hydrolase activity; F:zinc ion binding; F:peptidase activity; F:metalloendopeptidase activity	7	IPR001506; IPR024079; PTHR10127 (PANTHER), SSF55486 (SUPERFAMILY)
2399	DMPC15264257_Speleonectes_tulumensis_0	plasminogen activator spa	132	1.59E-22	60.80%	F:peptidase activity	1	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR24260 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
2400	DMPC15264362_Speleonectes_tulumensis_0	3-oxoacyl-acyl-carrier-protein reductase-like	232	1.28E-50	83.40%	F:catalytic activity; P:metabolic process; F:nucleotide binding	3	IPR002198; IPR002347; IPR016040; IPR020904; PTHR24322 (PANTHER), PTHR24322:SF0 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF51735 (SUPERFAMILY)