

rank #	Contig	Putative identity (annotation based on the five best hits by BLAST search in GenBank)	log2 (test/control); Average 90_92(L)	log2 (test/control); Average 90_92(R)	log2 (test/control); Average 95_91(L)	log2 (test/control); Average 95_91(R)	Median log2 (test/control)	Fold Change*	up- or down-regulation**
1	C601646.1	gb AAW24491.1 unknown [Schistosoma japonicum]; gb AAW27052.1 unknown [Schistosoma japonicum]; gb AAP05892.1 hypothetical protein [Schistosoma japonicum]; gb ACE06850.1 unknown [Schistosoma japonicum];	-1,911635991	-1,916860881	-2,539131732	-2,483400315	-2,200130598	4,6	DOWN
2	C609462.1	gb AAW27174.1 SJCHGC06407 protein [Schistosoma japonicum]; gb AAW25739.1 SJCHGC02535 protein [Schistosoma japonicum]; gb AAW27568.1 SJCHGC02279 protein [Schistosoma japonicum]; gb ACE06927.1 unknown [Schistosoma japonicum];	-1,688135128	-1,796641657	-1,76949007	-1,664122819	-1,728812599	3,3	DOWN
3	C612169.1	No match	-1,464504037	-1,437284429	-1,957083948	-1,972765517	-1,710793993	3,3	DOWN
4	C608060.1	emb CAG02932.1 unnamed protein product [Tetraodon nigroviridis]; gb AAI16544.1 Thoc2 protein [Danio rerio]; ref NP_001003847.1 Tho2 [Danio rerio] gb AAT68136.1 Tho2 [Danio rerio]; gb AAH93105.1 Thoc2 protein [Danio rerio];	-1,872416457	-1,896338176	-1,420751516	-1,307612643	-1,646583987	3,1	DOWN
5	C601379.1	No match	-1,89162378	-1,933031415	-1,367269277	-0,883171054	-1,629446529	3,1	DOWN
6	C607243.1	gb ABW08111.1 alkaline phosphatase [Schistosoma mansoni]; ref XP_606676.3 PREDICTED: similar to intestinal alkaline phosphatase III; IAP III [Bos taurus]; gb AAG39908.1 tissue-nonspecific alkaline phosphatase [Mus musculus]; sp P08289 PPBT_RAT Alkaline phosphatase, tissue-nonspecific isozyme precursor (AP-TNAP) (TNSALP) (Alkaline phosphatase liver/bone/kidney isozyme) emb CAA34160.1 alkaline phosphatase [Rattus norvegicus] gb AAH88399.1 Alkaline phosphatase, liver/bone/kidney [Rattus norvegicus] gb EDL80848.1 alkaline phosphatase, tissue-nonspecific, isoform CRA_a [Rattus norvegicus] gb EDL80849.1 alkaline phosphatase, tissue-nonspecific, isoform CRA_a [Rattus norvegicus] gb EDL80850.1 alkaline phosphatase, tissue-nonspecific, isoform CRA_a [Rattus norvegicus];	-1,234545141	-1,192710413	-2,028417714	-1,999880152	-1,617212647	3,1	DOWN
7	C601146.1	gb AAW24964.1 SJCHGC03760 protein [Schistosoma japonicum]; gb AAW24762.1 SJCHGC04453 protein [Schistosoma japonicum]; gb AAW26349.1 SJCHGC03072 protein [Schistosoma japonicum]; gb AAM53938.1 AF514300_1 IB1 protein [Schistosoma japonicum];	-1,341485213	-1,408984609	-1,689633984	-1,627427217	-1,518205913	2,9	DOWN
8	C606709.1	gb AAX28327.2 SJCHGC05589 protein [Schistosoma japonicum]; ref XP_001175610.1 PREDICTED: similar to Synaptophysin (Major synaptic vesicle protein p38) [Strongylocentrotus purpuratus]; ref NP_989081.1 synaptophysin-like 1 [Xenopus tropicalis] gb AAH62512.1 Synaptophysin-like 1 [Xenopus tropicalis] emb CAJ81619.1 synaptophysin-like 1 [Xenopus tropicalis]; gb EDV29003.1 hypothetical protein TRIADDRAFT_52445 [Trichoplax adhaerens];	-1,261818992	-1,372273074	-1,644519908	-1,741013975	-1,508396491	2,8	DOWN
9	C611037.1	gb AAW27737.1 SJCHGC04773 protein [Schistosoma japonicum];	-1,50033629	-1,563610982	-1,434024306	-1,46215157	-1,48124393	2,8	DOWN
10	C609059.1	tpe CAJ00234.1 TPA: hypothetical protein [Schistosoma mansoni];	-1,322380687	-1,473296649	-1,461626265	-1,438219799	-1,449923032	2,7	DOWN

11	C608810.1	ref XP_001369707.1 PREDICTED: similar to rhoGAP protein [Monodelphis domestica]; gb EDL04450.1 mCG141063, isoform CRA_b [Mus musculus]; gb AAH10306.2 3110043J09Rik protein [Mus musculus]; sp Q9CXP4.3 RHG08_MOUSE Rho GTPase-activating protein 8 (Rho-type GTPase-activating protein 8) gb AAH05563.1 RIKEN cDNA 3110043J09 gene [Mus musculus] dbj BAC39750.1 unnamed protein product [Mus musculus];	-1,625317595	-1,658782319	-1,264853485	-1,243484259	-1,44508554	2,7	DOWN
12	C707839.1	ref XP_001110803.1 PREDICTED: HtrA serine peptidase 2 isoform 2 [Macaca mulatta]; dbj BAF84666.1 unnamed protein product [Homo sapiens]; ref XP_001500096.1 PREDICTED: similar to HtrA serine peptidase 2 isoform 1 [Equus caballus]; ref XP_001500119.1 PREDICTED: hypothetical protein isoform 2 [Equus caballus];	-1,412230832	-1,443759851	-1,468326964	-1,354259715	-1,427995342	2,7	DOWN
13	C603200.1	No match	-1,206112282	-1,422392002	-1,386728941	-1,468875708	-1,404560472	2,6	DOWN
14	C612148.1	gb EDW79485.1 GK20386 [Drosophila willistoni]; gb EDW18112.1 GI13050 [Drosophila mojavensis]; gb EDV39506.1 GF24451 [Drosophila ananassae]; gb EDW33061.1 GL16175 [Drosophila persimilis];	-1,41005322	-1,557144886	-1,394107429	-1,334247789	-1,402080325	2,6	DOWN
15	C609450.1	ref XP_580486.2 PREDICTED: similar to DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae) [Bos taurus]; ref XP_001926894.1 PREDICTED: similar to DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae) [Sus scrofa]; ref NP_061301.2 DNA cross-link repair 1A, PSO2 homolog [Mus musculus] gb EDL01762.1 DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae), isoform CRA_b [Mus musculus]; dbj BAD90139.1 mKIAA0086 protein [Mus musculus];	-1,378589405	-1,406377436	-1,735158412	-1,218460932	-1,392483421	2,6	DOWN
16	C600211.1	No match	-1,362917849	-1,4854718	-1,421016031	-1,152952641	-1,39196694	2,6	DOWN
17	C604312.1	gb AAW25986.1 SJCHGC02396 protein [Schistosoma japonicum]; gb AAP06073.1 similar to NM_022756 hypothetical protein FLJ11730 in Homo sapiens; hypothetical protein FLJ11730 in Homo sapiens [Schistosoma japonicum]; gb AAW25871.1 SJCHGC00146 protein [Schistosoma japonicum]; gb AAW25057.1 unknown [Schistosoma japonicum];	-1,45929147	-1,352518024	-1,398289729	-1,039995326	-1,375403877	2,6	DOWN
18	C600324.1	No match	-1,536961606	-1,566819379	-1,094790921	-1,196275042	-1,366618324	2,6	DOWN
19	C609525.1	gb EDV23243.1 hypothetical protein TRIADDRAFT_27759 [Trichoplax adhaerens]; ref NP_001007877.1 MGC89709 protein [Xenopus tropicalis] sp Q68EQ9 TMM49_XENTR Transmembrane protein 49 gb AAH80142.1 MGC89709 protein [Xenopus tropicalis]; ref XP_415880.1 PREDICTED: hypothetical protein [Gallus gallus]; ref NP_996943.1 transmembrane protein 49 [Danio rerio] sp Q6NYY9 TMM49_BRARE Transmembrane protein 49 gb AAH66412.1 Transmembrane protein 49 [Danio rerio];	-1,235777614	-1,273833154	-1,429465759	-1,480930785	-1,351649457	2,6	DOWN
20	C602031.1	gb AAW25516.1 SJCHGC02507 protein [Schistosoma japonicum]; ref XP_001504303.1 PREDICTED: similar to golgi SNAP receptor complex member 1 isoform 1 [Equus caballus]; ref XP_001504305.1 PREDICTED: similar to golgi SNAP receptor complex member 1 isoform 2 [Equus caballus]; ref NP_001006222.1 golgi SNAP receptor complex member 1 [Gallus gallus] emb CAG31892.1 hypothetical protein [Gallus gallus];	-1,176546662	-1,234038948	-1,393808984	-1,435480802	-1,313923966	2,5	DOWN

21	C606451.1	No match	-1,068172875	-1,307823795	-1,37421799	-1,317624708	-1,312724252	2,5	DOWN
22	C600569.1	gb AAW25266.1 SJCHGC09427 protein [Schistosoma japonicum]; ref XP_001950428.1 PREDICTED: similar to Splicing factor 3A subunit 3 (Spliceosome-associated protein 61) (SAP 61) (SF3a60) [Acyrtosiphon pisum]; ref XP_001606271.1 PREDICTED: hypothetical protein [Nasonia vitripennis]; ref XP_785281.2 PREDICTED: hypothetical protein, partial [Strongylocentrotus purpuratus] ref XP_001182994.1 PREDICTED: hypothetical protein, partial [Strongylocentrotus purpuratus];	-1,113628406	-1,149337064	-1,574393487	-1,388075559	-1,268706312	2,4	DOWN
23	C600192.1	ref XP_419506.2 PREDICTED: similar to ATP-binding cassette, sub-family C, member 10 [Gallus gallus]; ref XP_585169.3 PREDICTED: similar to FLJ00002 protein [Bos taurus]; dbj BAA92227.1 FLJ00002 protein [Homo sapiens]; sp Q5T3U5 MRP7_HUMAN Multidrug resistance-associated protein 7 (ATP-binding cassette sub-family C member 10) emb CAI23217.1 ATP-binding cassette, sub-family C (CFTR/MRP), member 10 [Homo sapiens] gb EAX04181.1 ATP-binding cassette, sub-family C (CFTR/MRP), member 10, isoform CRA_b [Homo sapiens] gb EAX04182.1 ATP-binding cassette, sub-family C (CFTR/MRP), member 10, isoform CRA_b [Homo sapiens] dbj BAG10267.1 ATP-binding cassette, sub-family C member 10 [synthetic construct];	-1,337450303	-1,336983978	-1,190939057	-1,079621314	-1,263961518	2,4	DOWN
24	C606289.1	No match	-1,877981365	-0,37944501	-1,23903302	-1,288679617	-1,263856319	2,4	DOWN
25	C601991.1	gb AAW26256.1 SJCHGC06423 protein [Schistosoma japonicum]; ref XP_001635718.1 predicted protein [Nematostella vectensis] gb EDO43655.1 predicted protein [Nematostella vectensis]; ref NP_001016075.1 ORM1-like 1 [Xenopus tropicalis]; emb CAG03979.1 unnamed protein product [Tetraodon nigroviridis];	-0,839263785	-0,894380521	-1,622558713	-1,599613379	-1,24699695	2,4	DOWN
26	C607394.1	gb AAX24553.2 SJCHGC06523 protein [Schistosoma japonicum];	-1,283216941	-1,345699685	-1,177916928	-1,207814791	-1,245515866	2,4	DOWN
27	C602913.1	gb AAW25145.1 SJCHGC02192 protein [Schistosoma japonicum]; ref XP_001604182.1 PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis]; ref XP_967379.1 PREDICTED: similar to CG11964 CG11964-PA [Tribolium castaneum]; gb EDX13697.1 GD20833 [Drosophila simulans];	-0,925637164	-1,045381276	-1,503341567	-1,442646034	-1,244013655	2,4	DOWN
28	C604210.1	No match	-1,152875767	-1,121537306	-1,388943686	-1,30846746	-1,230671614	2,3	DOWN
29	C601385.1	emb CAM34681.1 INSIG protein [Schistosoma mansoni]; ref NP_956163.1 insulin induced gene 1 [Danio rerio] ref XP_001922160.1 PREDICTED: similar to insulin induced gene 1 [Danio rerio] sp Q8AV61 INSI1_BRARE Insulin-induced gene 1 protein (INSIG-1) gb AAN28327.1 INSIG-1 membrane protein [Danio rerio] gb AAH45341.1 Insulin induced gene 1 [Danio rerio] gb AAI65115.1 Insig1 protein [synthetic construct]; ref XP_001249364.1 PREDICTED: hypothetical protein LOC511899 isoform 1 [Bos taurus]; ref NP_001091219.1 hypothetical protein LOC100036994 [Xenopus laevis] gb AAI30075.1 LOC100036994 protein [Xenopus laevis];	-1,408537827	-1,287211021	-1,168369095	-0,871718322	-1,227790058	2,3	DOWN
30	C608987.1	No match	-1,432652068	-1,427696738	-1,018936296	-0,946580762	-1,223316517	2,3	DOWN

31	C602990.1	gb AAW27619.1 SJCHGC06261 protein [Schistosoma japonicum]; ref NP_505261.2 B0507.2 [Caenorhabditis elegans] sp Q22885.2 BROX_CAEL BRO1 domain-containing protein BROX homolog gb AAB04821.2 Hypothetical protein B0507.2 [Caenorhabditis elegans]; ref XP_419397.1 PREDICTED: similar to RIKEN cDNA 0610010K06 gene [Gallus gallus]; emb CAG12984.1 unnamed protein product [Tetraodon nigroviridis];	-1,199861305	-1,295025785	-1,166821143	-1,243795651	-1,221828478	2,3	DOWN
32	C607921.1	ref XP_969961.1 PREDICTED: similar to syntaxin 18 [Tribolium castaneum]; ref NP_001019596.1 hypothetical protein LOC554130 [Danio rerio] sp Q4VBI7 STX18_BRARE Syntaxin-18 gb AAH95763.1 Zgc:112326 [Danio rerio]; gb AAH73006.1 LOC443606 protein [Xenopus laevis]; gb AAH92152.1 Unknown (protein for IMAGE:6949850) [Xenopus laevis];	-1,447576779	-1,425206619	-0,999483108	-0,731493256	-1,212344864	2,3	DOWN
33	C715533.1	gb AAX24320.2 SJCHGC03143 protein [Schistosoma japonicum]; gb EDL05030.1 autophagy-related 5 (yeast) [Mus musculus]; ref NP_444299.1 autophagy-related 5-like [Mus musculus] sp Q99J83 ATG5_MOUSE Autophagy protein 5 (APG5-like) gb AAH02166.1 Autophagy-related 5 (yeast) [Mus musculus] dbj BAB33383.1 mApp5 [Mus musculus] dbj BAC25874.1 unnamed protein product [Mus musculus]; ref XP_001503989.1 PREDICTED: similar to Autophagy protein 5 (APG5-like) (Apoptosis-specific protein) isoform 2 [Equus caballus] ref XP_001503988.1 PREDICTED: similar to Autophagy protein 5 (APG5-like) (Apoptosis-specific protein) isoform 1 [Equus caballus];	-1,03479893	-1,150219358	-1,242173615	-1,307037386	-1,196196487	2,3	DOWN
34	C611698.1	gb EDL24096.1 eukaryotic translation initiation factor 3, subunit 12, isoform CRA_a [Mus musculus]; gb AAH89069.1 Eif3s12-prov protein [Xenopus tropicalis]; emb CAJ83157.1 eukaryotic translation initiation factor 3, subunit 12 [Xenopus tropicalis] gb AAI57543.1 Unknown (protein for MGC:180700) [Xenopus tropicalis]; ref NP_082935.1 eukaryotic translation initiation factor 3, subunit K [Mus musculus] sp Q9DBZ5.1 EIF3K_MOUSE Eukaryotic translation initiation factor 3 subunit K (eIF3k) (Eukaryotic translation initiation factor 3 subunit 12) (eIF-3 p25) dbj BAB23454.1 unnamed protein product [Mus musculus] gb AAH91749.1 Eukaryotic translation initiation factor 3, subunit K [Mus musculus];	-1,041671509	-1,151302084	-1,300764075	-1,234192867	-1,192747476	2,3	DOWN
35	C602061.1	No match	-1,427963928	-1,360236587	-0,99528509	-0,777538931	-1,177760839	2,3	DOWN

36	C606486.1	sp Q9UHV7.2 MED13_HUMAN Mediator of RNA polymerase II transcription subunit 13 (Mediator complex subunit 13) (Thyroid hormone receptor-associated protein complex 240 kDa component) (Trap240) (Thyroid hormone receptor-associated protein 1) (Vitamin D3 receptor-interacting protein complex component DRIP250) (DRIP 250) (Activator-recruited cofactor 250 kDa component) (ARC250); ref NP_005112.2 mediator complex subunit 13 [Homo sapiens] gb EAW51438.1 thyroid hormone receptor associated protein 1, isoform CRA_b [Homo sapiens] gb EAW51439.1 thyroid hormone receptor associated protein 1, isoform CRA_b [Homo sapiens] gb AAI40892.1 Mediator complex subunit 13 [Homo sapiens]; dbj BAA25519.2 KIAA0593 protein [Homo sapiens]; gb AAD22032.1 thyroid hormone receptor-associated protein complex component TRAP240 [Homo sapiens];	-1,093591134	-0,988696567	-1,25809344	-1,240242489	-1,166916812	2,2	DOWN
37	C604197.1	gb AAW26476.1 SJCHGC01111 protein [Schistosoma japonicum]; ref XP_001638494.1 predicted protein [Nematostella vectensis] gb EDO46431.1 predicted protein [Nematostella vectensis]; gb AAW25407.1 SJCHGC02502 protein [Schistosoma japonicum]; gb EDW49160.1 GM23254 [Drosophila sechellia];	-1,179856567	-1,14651979	-1,260115199	-1,129145371	-1,163188179	2,2	DOWN
38	C603237.1	gb EDV52205.1 GG15951 [Drosophila erecta]; ref XP_392451.3 PREDICTED: similar to Transcription initiation factor TFIID subunit 4 (Transcription initiation factor TFIID 110 kDa subunit) (p110) (TAFII-110) (110 kDa TBP-associated factor) [Apis mellifera]; gb EDV40044.1 GF24156 [Drosophila ananassae]; ref XP_966532.1 PREDICTED: similar to transcription initiation factor [Tribolium castaneum];	-1,195153819	-1,200985984	-1,122228905	-0,910708589	-1,158691362	2,2	DOWN
39	C611641.1	ref NP_476908.1 Vacuolar H ⁺ -ATPase 55kD B subunit CG17369-PB, isoform B [Drosophila melanogaster] ref NP_731726.1 Vacuolar H ⁺ -ATPase 55kD B subunit CG17369-PA, isoform A [Drosophila melanogaster] sp P31409 VATB_DROME Vacuolar ATP synthase subunit B (V-ATPase subunit B) (Vacuolar proton pump subunit B) (V-ATPase 55 kDa subunit) emb CAA48034.1 vacuolar ATPase B subunit [Drosophila melanogaster] gb AAF54836.1 CG17369-PA, isoform A [Drosophila melanogaster] gb AAF54837.1 CG17369-PB, isoform B [Drosophila melanogaster] gb AAK93047.1 GH27148p [Drosophila melanogaster] gb AAN71057.1 AT12604p [Drosophila melanogaster] gb EDV30327.1 GF23001 [Drosophila ananassae] gb EDV49337.1 GG17111 [Drosophila erecta] gb EDW15311.1 G124752 [Drosophila mojavensis] gb EDW83646.1 GK13566 [Drosophila willistoni] gb EDW97128.1 GE24501 [Drosophila yakuba]; ref XP_001357789.1 GA14484-PA [Drosophila pseudoobscura] gb EAL26924.1 GA14484-PA [Drosophila pseudoobscura] gb EDW39130.1 GL13570 [Drosophila persimilis]; gb EDW42428.1 GM25995 [Drosophila sechellia] gb EDX13185.1 GD20555 [Drosophila simulans]; sp P31401 VATB	-1,256884225	-1,21431755	-1,004946098	-1,098672701	-1,156495126	2,2	DOWN
40	C608241.1	gb AAW24763.1 SJCHGC05980 protein [Schistosoma japonicum]; gb AAP06091.1 hypothetical protein [Schistosoma japonicum];	-0,851798823	-0,94544227	-1,36265391	-1,521643952	-1,15404809	2,2	DOWN
41	C603939.1	No match	-1,152120674	-1,152588876	-1,147362555	-0,932952437	-1,149741615	2,2	DOWN

42	C611360.1	gb AAX27020.1 unknown [Schistosoma japonicum]; gb AAX27010.1 unknown [Schistosoma japonicum]; gb AAX30131.1 SJCHGC00333 protein [Schistosoma japonicum]; gb AAX27546.2 SJCHGC02390 protein [Schistosoma japonicum];	-0,891469404	-1,016190071	-1,316108353	-1,279418056	-1,147804064	2,2	DOWN
43	C600203.1	gb AAX24848.2 SJCHGC09620 protein [Schistosoma japonicum];	-1,135086038	-1,054739593	-1,197689191	-1,141656171	-1,138371105	2,2	DOWN
44	C605209.1	gb AAO59420.2 lactate dehydrogenase-like protein [Schistosoma japonicum]; gb AAW25909.1 SJCHGC02274 protein [Schistosoma japonicum]; gb AAP06144.1 similar to GenBank Accession Number AF070998 lactate dehydrogenase A in Ambystoma mexicanum [Schistosoma japonicum]; gb AAV80238.1 lactate dehydrogenase [Clonorchis sinensis];	-1,030978064	-1,106018587	-1,17181833	-1,149102922	-1,127560755	2,2	DOWN
45	C606417.1	gb AAW25054.1 SJCHGC05912 protein [Schistosoma japonicum]; gb AAP06438.1 similar to NM_005731 actin related protein 2/3 complex, subunit 2 (34 kD) in Homo sapiens [Schistosoma japonicum]; ref XP_001915183.1 PREDICTED: similar to actin related protein 2/3 complex subunit 2 [Equus caballus]; ref XP_001925034.1 PREDICTED: similar to actin related protein 2/3 complex subunit 2 [Sus scrofa];	-1,051114724	0,290335283	-1,286142675	-1,201478285	-1,126296505	2,2	DOWN
46	C609140.1	gb AAW26075.1 SJCHGC05150 protein [Schistosoma japonicum];	-1,038911567	-0,93138094	-1,275095676	-1,19562424	-1,117267904	2,2	DOWN
47	C604803.1	gb AAW26542.1 SJCHGC05854 protein [Schistosoma japonicum];	-0,852963283	-0,930573288	-1,423037902	-1,296941893	-1,113757591	2,2	DOWN
48	C604360.1	gb AAW27458.1 SJCHGC06870 protein [Schistosoma japonicum]; ref XP_973073.1 PREDICTED: similar to putative GABA-A receptor associated protein [Tribolium castaneum]; gb ABD98773.1 putative GABA-A receptor associated protein [Graphocephala atropunctata]; ref XP_001844428.1 conserved hypothetical protein [Culex pipiens quinquefasciatus]; gb EDS36925.1 conserved hypothetical protein [Culex quinquefasciatus];	-1,126630311	-1,295304674	-1,100214006	-0,87694941	-1,113422159	2,2	DOWN
49	C610331.1	No match	-1,034379174	-1,008598461	-1,186859453	-1,236342126	-1,110619314	2,2	DOWN
50	C608397.1	No match	-1,004613078	-0,719512903	-1,210204951	-1,232828269	-1,107409015	2,2	DOWN
51	C611326.1	tpe CAJ00239.1 TPA: hypothetical protein [Schistosoma mansoni]; tpe CAJ00241.1 TPA: hypothetical protein [Schistosoma mansoni]; tpe CAJ00234.1 TPA: hypothetical protein [Schistosoma mansoni];	-1,063129506	-1,137064824	-1,202929945	-0,93871013	-1,100097165	2,1	DOWN
52	C610848.1	sp P25320 FRIH2_SCHMA Ferritin-2 heavy chain gb AAA29881.1 ferritin light chain; gb AAW26332.1 SJCHGC06812 protein [Schistosoma japonicum]; gb AAS92978.1 ferritin [Clonorchis sinensis]; gb ABD75379.1 ferritin H [Bufo gargarizans];	-0,390065036	-0,565615937	-1,631665709	-1,785583211	-1,098640823	2,1	DOWN
53	C611493.1	No match	-0,850715805	-1,018348902	-1,202836749	-1,147263888	-1,082806395	2,1	DOWN
54	C604310.1	No match	-1,157134047	-1,164018133	-0,997781542	-0,925962871	-1,077457795	2,1	DOWN
55	C708663.1	gb AAW24733.1 SJCHGC06204 protein [Schistosoma japonicum]; gb EDW94314.1 GE20110 [Drosophila yakuba]; gb EDW78772.1 GK12617 [Drosophila willistoni]; gb EDW70509.1 GJ13811 [Drosophila virilis];	-1,529115581	-1,378682528	-0,769698248	-0,672076028	-1,074190388	2,1	DOWN
56	C610760.1	No match	-0,826926921	-0,95540418	-1,192191891	-1,248999443	-1,073798036	2,1	DOWN

57	C606116.1	gb AAW26990.1 SJCHGC05537 protein [Schistosoma japonicum]; gb AAS90835.1 G protein beta subunit [Pinctada fucata]; sp P23232 GBB_LOLFO Guanine nucleotide-binding protein subunit beta emb CAA40077.1 GTP-binding protein beta subunit [Loligo forbesi] prf 1705183A GTP binding protein; gb AAQ90156.1 visual G-protein beta subunit [Loligo pealei];	-0,789967769	-1,264298677	-1,050198002	-1,088311455	-1,069254729	2,1	DOWN
58	C606703.1	gb AAW26108.1 SJCHGC05178 protein [Schistosoma japonicum]; ref NP_082588.1 coiled-coil domain containing 12 [Mus musculus] dbj BAB28353.1 unnamed protein product [Mus musculus]; sp Q8R344 CCD12_MOUSE Coiled-coil domain-containing protein 12 gb EDL09006.1 coiled-coil domain containing 12 [Mus musculus]; ref NP_001102253.1 coiled-coil domain containing 12 [Rattus norvegicus] gb EDL77064.1 coiled-coil domain containing 12 (predicted), isoform CRA_a [Rattus norvegicus];	-0,987741383	-0,998254939	-1,158129123	-1,137015205	-1,067635072	2,1	DOWN
59	C604859.1	gb AAW25677.1 SJCHGC01656 protein [Schistosoma japonicum]; ref XP_001896774.1 UPF0279 protein C14orf129 homolog [Brugia malayi] gb EDP34381.1 UPF0279 protein C14orf129 homolog, putative [Brugia malayi]; ref XP_001367855.1 PREDICTED: similar to Chromosome 14 open reading frame 129 [Monodelphis domestica]; gb EDV41299.1 GF23488 [Drosophila ananassae];	-0,616091889	-0,664292342	-1,466499461	-1,508303365	-1,065395902	2,1	DOWN
60	C605987.1	gb EDV43759.1 GF16361 [Drosophila ananassae]; gb EDV92742.1 GH18927 [Drosophila grimshawi]; gb AAD39600.1 AC007858_14 10A191.3 [Oryza sativa (japonica cultivar-group)]; ref NP_001056416.1 Os05g0579000 [Oryza sativa (japonica cultivar-group)] gb AAU10692.1 putative sugar transporter [Oryza sativa (japonica cultivar-group)] dbj BAF18330.1 Os05g0579000 [Oryza sativa (japonica cultivar-group)];	-1,024202408	-0,856317488	-1,136497056	-1,104028481	-1,064115445	2,1	DOWN
61	C609884.1	gb AAX24837.2 SJCHGC02515 protein [Schistosoma japonicum];	-1,196869826	-1,161990072	-0,964217854	-0,902551366	-1,063103963	2,1	DOWN
62	C604379.1	No match	-1,152521304	-1,084490637	-1,01756126	-1,041607049	-1,063048843	2,1	DOWN
63	C601898.1	gb EDW77741.1 GK24389 [Drosophila willistoni]; gb EDV30846.1 GF15062 [Drosophila ananassae]; gb EDW90296.1 GE13195 [Drosophila yakuba]; gb EDV54773.1 GG21122 [Drosophila erecta];	-0,703664993	-0,791624053	-1,421332845	-1,329367768	-1,060495911	2,1	DOWN
64	C606373.1	gb AAP06363.1 hypothetical protein [Schistosoma japonicum]; gb ACE06787.1 unknown [Schistosoma japonicum];	-1,278084033	-1,249687011	-0,863691577	-0,822719011	-1,056689294	2,1	DOWN
65	C602181.1	sp P49965 SRP72_SCHMA Signal recognition particle 72 kDa protein (SRP72) gb AAA69689.1 signal recognition particle 72 kDa subunit; gb AAW27494.1 unknown [Schistosoma japonicum];	-1,014181874	-1,008980481	-1,094446841	-1,108778576	-1,054314358	2,1	DOWN
66	C611543.1	gb AAW25713.1 SJCHGC00391 protein [Schistosoma japonicum]; gb AAW26336.1 unknown [Schistosoma japonicum]; ref NP_998068.1 eukaryotic translation initiation factor 2B, subunit 2 beta [Danio rerio] gb AAH67147.1 Eukaryotic translation initiation factor 2B, subunit 2 beta [Danio rerio] emb CAH69026.1 novel protein (zgc:77512) [Danio rerio]; dbj BAC36248.1 unnamed protein product [Mus musculus];	-1,081834815	-1,041044508	-0,990217201	-1,056064965	-1,048554737	2,1	DOWN
67	C600688.1	gb AAX25206.2 SJCHGC02554 protein [Schistosoma japonicum];	-0,72622152	-1,051284523	-1,041515998	-1,041759708	-1,041637853	2,1	DOWN

68	C607201.1	gb AAX28601.2 SJCHGC08387 protein [Schistosoma japonicum]; gb AAG01032.1 Stat3-interacting protein [Mus musculus]; dbj BAE39871.1 unnamed protein product [Mus musculus]; dbj BAE39766.1 unnamed protein product [Mus musculus];	-1,02707029	-0,901615664	-1,055437831	-1,181268215	-1,041254061	2,1	DOWN
69	C607961.1	gb ACE06868.1 unknown [Schistosoma japonicum]; gb AAC69992.1 tetraspanin TE736 [Schistosoma japonicum]; gb AAW24656.1 unknown [Schistosoma japonicum]; gb AAW27678.1 unknown [Schistosoma japonicum];	-0,849241796	-0,937858865	-1,151337883	-1,139441123	-1,038649994	2,1	DOWN
70	C612131.1	No match	-1,131611412	-1,171233445	-0,94033123	-0,852997818	-1,035971321	2,1	DOWN
71	C606800.1	No match	-0,72473017	-0,952395236	-1,2114256	-1,114903974	-1,033649605	2,0	DOWN
72	C608727.1	gb AAX27988.2 SJCHGC05935 protein [Schistosoma japonicum]; gb AAW27057.1 SJCHGC05282 protein [Schistosoma japonicum]; emb CAF99798.1 unnamed protein product [Tetraodon nigroviridis]; ref XP_416562.2 PREDICTED: similar to MGC69357 protein [Gallus gallus];	-1,272229836	-1,1518321	-0,915246485	-0,889046859	-1,033539293	2,0	DOWN
73	C608278.1	No match	-1,10177231	-1,057965446	-0,973328313	-1,008603844	-1,033284645	2,0	DOWN
74	C606420.1	gb AAX30499.2 SJCHGC04165 protein [Schistosoma japonicum]; ref XP_001120146.1 PREDICTED: similar to CG8320-PA [Apis mellifera]; ref NP_001040235.1 hypothetical protein LOC692928 [Bombyx mori]; gb ABD36286.1 unknown [Bombyx mori]; gb ABI52781.1 DUF788 membrane protein [Argas monolakensis];	-1,107635192	-1,099179469	-0,966176558	-0,964157567	-1,032678014	2,0	DOWN
75	C606543.1	tpe CAJ00236.1 TPA: endonuclease-reverse transcriptase [Schistosoma mansoni]; gb AAY56755.1 reverse transcriptase SR3-left [Schistosoma mansoni]; gb AAY56756.1 reverse transcriptase SR3-right [Schistosoma mansoni];	-1,067551847	-1,186203072	-0,926614506	-0,997295526	-1,032423687	2,0	DOWN
76	C605045.1	gb AAP05921.1 similar to NM_024231 zinc finger like protein 1 [Schistosoma japonicum]; gb ACE06939.1 unknown [Schistosoma japonicum];	-1,224384889	-1,033846607	-1,030250226	-0,877254526	-1,032048417	2,0	DOWN
77	C608792.1	ref NP_001026008.1 ribonucleoside-diphosphate reductase M1 chain [Gallus gallus]; emb CAG31174.1 hypothetical protein [Gallus gallus]; ref XP_001746543.1 predicted protein [Monosiga brevicollis MX1]; gb EDQ88439.1 predicted protein [Monosiga brevicollis MX1]; ref XP_001505371.1 PREDICTED: similar to M1 subunit of ribonucleotide reductase [Ornithorhynchus anatinus]; ref XP_968671.1 PREDICTED: similar to AGAP010198-PA [Tribolium castaneum];	-1,154538565	-1,199279308	-0,905183622	-0,759418163	-1,029861094	2,0	DOWN
78	C602575.1	gb ABL86191.1 unknown [Schistosoma japonicum]; gb AAW27089.1 unknown [Schistosoma japonicum]; gb AAW26412.1 SJCHGC00398 protein [Schistosoma japonicum]; gb AAW27337.1 unknown [Schistosoma japonicum];	-1,14107812	-1,030892638	-1,020795895	-1,015031104	-1,025844267	2,0	DOWN
79	C605938.1	gb AAW27043.1 SJCHGC08900 protein [Schistosoma japonicum];	-0,707866714	-0,724822329	-1,3751306	-1,321814106	-1,023318218	2,0	DOWN
80	C608377.1	No match	-0,778100556	-0,936269349	-1,145380355	-1,109646592	-1,022957971	2,0	DOWN
81	C608749.1	gb AAW26930.1 SJCHGC02342 protein [Schistosoma japonicum];	-0,856406365	-0,94412924	-1,206142181	-1,101518477	-1,022823859	2,0	DOWN

82	C612252.1	gb AAW24984.1 SJCHGC06626 protein [Schistosoma japonicum]; emb CAG06397.1 unnamed protein product [Tetraodon nigroviridis]; ref NP_001007769.1 phenylalanine-tRNA synthetase-like [Danio rerio] gb AAH85625.1 Phenylalanine-tRNA synthetase-like [Danio rerio]; ref XP_864045.1 PREDICTED: similar to Phenylalanyl-tRNA synthetase beta chain (Phenylalanine-tRNA ligase beta chain) (PheRS) isoform 3 [Canis familiaris];	-0,675204497	-0,891144162	-1,137404483	-1,185982905	-1,014274323	2,0	DOWN
83	C607022.1	No match	-0,971549725	-1,033877217	-1,122351716	-0,990222423	-1,01204982	2,0	DOWN
84	C606084.1	tpg DAA04500.1 TPA_exp: pol polyprotein [Schistosoma mansoni]; tpg DAA04502.1 TPA_exp: ORF3 [Schistosoma mansoni];	-1,005217173	-0,853512339	-1,13796554	-1,015142466	-1,01017982	2,0	DOWN
85	C601007.1	ref XP_001896274.1 UDP-sugar transporter-like protein [Brugia malayi] gb EDP34887.1 UDP-sugar transporter-like protein [Brugia malayi]; ref XP_395030.3 PREDICTED: similar to fringe connection CG3874-PA [Apis mellifera]; ref XP_001637195.1 predicted protein [Nematostella vectensis] gb EDO45132.1 predicted protein [Nematostella vectensis];	-0,721963963	-0,651245717	-1,403196664	-1,298080402	-1,010022183	2,0	DOWN
86	C610237.1	tpe CAJ00235.1 TPA: endonuclease-reverse transcriptase [Schistosoma mansoni]; tpe CAJ00242.1 TPA: endonuclease-reverse transcriptase [Schistosoma mansoni]; tpe CAJ00240.1 TPA: endonuclease-reverse transcriptase [Schistosoma mansoni];	-0,834999256	-0,914959042	-1,137436533	-1,105064557	-1,0100118	2,0	DOWN
87	C610832.1	gb AAX26272.2 SJCHGC07577 protein [Schistosoma japonicum]; ref XP_320556.4 AGAP011975-PA [Anopheles gambiae str. PEST] gb EAA00315.4 AGAP011975-PA [Anopheles gambiae str. PEST]; ref XP_001651941.1 hypothetical protein AaeL_AAEL006337 [Aedes aegypti] gb EAT42101.1 conserved hypothetical protein [Aedes aegypti]; ref XP_001602901.1 PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis];	-1,030450519	-1,128743129	-0,913115359	-0,987735809	-1,009093164	2,0	DOWN
88	C609365.1	gb AAW27442.1 SJCHGC02482 protein [Schistosoma japonicum]; gb AAW27607.1 SJCHGC02483 protein [Schistosoma japonicum]; ref XP_001490497.2 PREDICTED: similar to MIT, microtubule interacting and transport, domain containing 1 [Equus caballus]; ref XP_001368545.1 PREDICTED: hypothetical protein [Monodelphis domestica];	-0,861492541	-0,869590884	-1,192971497	-1,142907842	-1,006249363	2,0	DOWN
89	C602638.1	ref XP_974460.1 PREDICTED: similar to CG9752 CG9752-PA [Tribolium castaneum]; ref XP_394550.2 PREDICTED: similar to CG9752-PA [Apis mellifera]; gb EDW74027.1 GK21592 [Drosophila willistoni]; ref XP_001604967.1 PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis];	-0,969128821	-1,071383009	-1,043014461	-0,91395858	-1,006071641	2,0	DOWN
90	C602560.1	ref XP_972549.2 PREDICTED: similar to RNA (guanine-9-)-methyltransferase domain-containing protein 1 homolog, mitochondrial [Tribolium castaneum]; gb EDW08762.1 GI20132 [Drosophila mojavensis]; gb EDW02745.1 GH19713 [Drosophila grimshawi]; gb EDW85720.1 GK23002 [Drosophila willistoni];	-0,958552418	-1,041765786	-1,344150694	-0,948003993	-1,000159102	2,0	DOWN

91	C604190.1	ref XP_535891.2 PREDICTED: similar to NAD-dependent deacetylase sirtuin-5 (SIR2-like protein 5) [Canis familiaris]; ref XP_001915269.1 PREDICTED: similar to sirtuin [Equus caballus]; gb ABY65335.1 sirtuin 5 [Sus scrofa]; ref NP_849179.1 sirtuin 5 (silent mating type information regulation 2 homolog) 5 [Mus musculus] sp Q8K2C6 SIRT5_MOUSE NAD-dependent deacetylase sirtuin-5 (SIR2-like protein 5) gb AAH31770.1 Sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae) [Mus musculus] gb EDL40991.1 sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae) [Mus musculus];	-0,968060322	-1,031921667	-1,342327491	-0,95264541	-0,999990995	2,0	DOWN
92	C610421.1	gb AAX25786.2 SJCHGC06308 protein [Schistosoma japonicum]; ref XP_001950180.1 PREDICTED: similar to FCH domain only 2 [Acyrtosiphon pisum]; ref XP_972256.2 PREDICTED: similar to FCH domain only 2 [Tribolium castaneum]; gb EDW15768.1 GI10156 [Drosophila mojavensis];	-0,922180884	-0,898209352	-1,073895162	-1,087906993	-0,998038023	2,0	DOWN
93	C603786.1	gb AAW26600.1 SJCHGC06283 protein [Schistosoma japonicum]; ref XP_001640523.1 predicted protein [Nematostella vectensis] gb EDO48460.1 predicted protein [Nematostella vectensis]; gb EDW43046.1 GM23722 [Drosophila sechellia]; gb EDV43144.1 GF18341 [Drosophila ananassae] gb EDV49939.1 GG24917 [Drosophila erecta] gb EDV91406.1 GH14195 [Drosophila grimshawi] gb EDW15501.1 GI24868 [Drosophila mojavensis] gb EDW68059.1 GJ24512 [Drosophila virilis] gb EDW96503.1 GE25867 [Drosophila yakuba];	-1,030509833	-1,20051242	-0,931672781	-0,963255727	-0,99688278	2,0	DOWN
94	C602475.1	gb AAW27690.1 SJCHGC04924 protein [Schistosoma japonicum]; emb CAD21532.1 hypothetical protein [Taenia solium];	-0,990726052	-1,131634861	-1,000342966	-0,980379837	-0,995534509	2,0	DOWN
95	C609066.1	gb AAX27215.2 SJCHGC03451 protein [Schistosoma japonicum]; ref XP_001518734.1 PREDICTED: hypothetical protein, partial [Ornithorhynchus anatinus]; sp Q8VDQ9.2 KRI1_MOUSE Protein KRI1 homolog; ref NP_663391.2 KRI1 homolog [Mus musculus] gb EDL25175.1 cDNA sequence BC021438 [Mus musculus];	-0,971781897	-0,248839233	-1,063145379	-1,018806191	-0,995294044	2,0	DOWN
96	C602228.1	No match	-1,07668	-1,046097829	-0,944316846	-0,94142386	-0,995207338	2,0	DOWN
97	C612384.1	gb AAW27684.1 SJCHGC08954 protein [Schistosoma japonicum]; ref NP_001033227.1 PRELI domain containing 1 [Bos taurus] sp Q32KN9 PRLD1_BOVIN PRELI domain-containing protein 1, mitochondrial precursor gb AAI10002.1 PRELI domain containing 1 [Bos taurus]; dbj BAE29582.1 unnamed protein product [Mus musculus]; ref XP_001169493.1 PREDICTED: similar to CGI-106 protein isoform 3 [Pan troglodytes];	-1,049279841	-1,28004941	-0,936855288	-0,836302429	-0,993067565	2,0	DOWN
98	C609895.1	gb AAZ57334.1 CREB-binding protein [Schistosoma mansoni]; gb AAX24597.2 SJCHGC08730 protein [Schistosoma japonicum];	-0,710461744	-0,87854555	-1,193726101	-1,10289025	-0,9907179	2,0	DOWN

99	C603418.1	gb AAW27439.2 SJCHGC02252 protein [Schistosoma japonicum]; gb AAX27473.2 SJCHGC02253 protein [Schistosoma japonicum]; ref XP_308251.4 AGAP007620-PA [Anopheles gambiae str. PEST]; gb EAA04505.4 AGAP007620-PA [Anopheles gambiae str. PEST]; sp Q03751 CSP_DROME Cysteine string protein gb AAA28432.1 csp32;	-0,968860177	-1,15092698	-0,949378104	-1,012201635	-0,990530906	2,0	DOWN
100	C601295.1	sp P19331 IM23_SCHMA 23 kDa integral membrane protein (Sm23) gb AAA29900.1 integral membrane protein; gb AAA73525.1 integral membrane protein 23; sp Q26499 IM23_SCHHA 23 kDa integral membrane protein (Sh23) gb AAC46959.1 Sh23 [Schistosoma haematobium]; gb ABS19440.1 multivalent antigen sjTPI-23 [synthetic construct];	-0,787545563	-1,063120634	-0,967351467	-1,012688869	-0,990020168	2,0	DOWN
101	C711036.1	ref XP_001380141.1 PREDICTED: hypothetical protein [Monodelphis domestica]; ref XP_001625397.1 predicted protein [Nematostella vectensis] gb EDO33297.1 predicted protein [Nematostella vectensis]; gb AAM18868.1 AF391288_4 unknown [Branchiostoma floridae]; ref XP_001599787.1 PREDICTED: similar to wd-repeat protein [Nasonia vitripennis];	-1,186096365	-1,082508927	-0,823428615	-0,895804972	-0,98915695	2,0	DOWN
102	C604966.1	gb AAI28795.1 Aars protein [Danio rerio]; ref NP_001037775.1 alanyl-tRNA synthetase [Danio rerio]; emb CAK04586.1 alanyl-tRNA synthetase [Danio rerio]; emb CAQ13590.1 novel protein similar to vertebrate alanyl-tRNA synthetase (AARS) [Danio rerio]; emb CAK04587.1 alanyl-tRNA synthetase [Danio rerio];	-0,943924193	-0,980214538	-1,045364207	-0,995415199	-0,987814869	2,0	DOWN
103	C605577.1	ref XP_973990.1 PREDICTED: similar to O-fucosyltransferase, putative [Tribolium castaneum]; ref NP_001037061.2 protein-O-fucosyltransferase 1 [Bombyx mori] gb ABA29467.1 protein O-fucosyltransferase 1 [Bombyx mori]; emb CAH40835.1 protein-O-fucosyltransferase 1 [Bombyx mori]; gb ABA29465.1 protein O-fucosyltransferase 1 [Aedes aegypti];	-0,9372823	-0,781778951	-1,088789111	-1,026198006	-0,981740153	2,0	DOWN
104	C610121.1	gb AAC79802.3 annexin [Schistosoma mansoni]; gb ACC78610.1 annexin [Schistosoma bovis]; gb AAW25344.1 SJCHGC06760 protein [Schistosoma japonicum]; gb AAD34598.1 AF147955_1 antigen cC1 [Taenia solium];	-0,740030497	-0,573915943	-1,355218849	-1,216652165	-0,978341331	2,0	DOWN
105	C612596.1	No match	-0,966164515	-0,988132163	-0,808007658	-1,048173202	-0,977148339	2,0	DOWN
106	C610195.1	No match	-0,756372033	-0,841899356	-1,223602458	-1,112078898	-0,976989127	2,0	DOWN
107	C603901.1	gb AAW26656.1 SJCHGC09074 protein [Schistosoma japonicum];	-0,964147385	-0,978198318	-1,032387582	-0,915050753	-0,971172852	2,0	DOWN
108	C607341.1	No match	-0,818688682	-0,978015355	-1,035372581	-0,96119463	-0,969604993	2,0	DOWN
109	C605188.1	gb AAW27105.1 SJCHGC03317 protein [Schistosoma japonicum]; gb EDW06752.1 G115232 [Drosophila mojavensis]; gb EDW65808.1 GJ18691 [Drosophila virilis]; gb EDW86514.1 GK14620 [Drosophila willistoni];	-0,653151803	-0,74977649	-1,18494236	-1,220570914	-0,967359425	2,0	DOWN
110	C608724.1	No match	-0,881475989	-1,00306577	-1,061835204	-0,930719949	-0,96689286	2,0	DOWN
111	C612307.1	tpe CAJ00236.1 TPA: endonuclease-reverse transcriptase [Schistosoma mansoni]; gb AAX26802.2 SJCHGC02939 protein [Schistosoma japonicum];	-0,700550993	-0,752097738	-1,267305406	-1,180321581	-0,96620966	2,0	DOWN

112	C603749.1	gb AAP06016.2 SJCHGC01960 protein [Schistosoma japonicum]; gb AAW26587.1 SJCHGC09469 protein [Schistosoma japonicum]; emb CAG02594.1 unnamed protein product [Tetraodon nigroviridis]; ref NP_001006882.1 heat shock 10kDa protein 1 [Xenopus tropicalis] gb AAH77653.1 Heat shock 10kDa protein 1 (chaperonin 10) [Xenopus tropicalis] emb CAJ81476.1 heat shock 10kDa protein 1 (chaperonin 10) [Xenopus tropicalis];	-1,251656914	-1,244720404	-0,687070375	-0,646771551	-0,96589539	2,0	DOWN
113	C611581.1	gb AAW26671.1 SJCHGC02427 protein [Schistosoma japonicum]; gb AAX28339.1 unknown [Schistosoma japonicum]; sp Q8AXS6 S35B1_XENTR Solute carrier family 35 member B1 emb CAJ82891.1 solute carrier family 35, member B1 [Xenopus tropicalis]; ref NP_989418.1 endoplasmic reticulum nucleotide sugar transporter [Xenopus tropicalis] emb CAD54627.1 endoplasmic reticulum nucleotide sugar transporter [Xenopus tropicalis];	-1,00977753	-1,01422161	-0,901342094	-0,917697548	-0,963737539	2,0	DOWN
114	C605890.1	ref XP_001494366.1 PREDICTED: ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 [Equus caballus]; ref NP_777263.1 ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 [Bos taurus] sp Q29449 AT8A1_BOVIN Probable phospholipid-transporting ATPase IA (Chromaffin granule ATPase II) (ATPase class I type 8A member 1) gb AAD03352.1 chromaffin granule ATPase II [Bos taurus]; ref XP_420729.2 PREDICTED: similar to ATPase II [Gallus gallus]; ref XP_001337058.2 PREDICTED: similar to ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1, partial [Danio rerio];	-0,798676287	-0,924774514	-0,99805464	-1,028031378	-0,961414577	1,9	DOWN
115	C610316.1	gb AAX24987.2 SJCHGC04429 protein [Schistosoma japonicum];	-0,811426295	-0,890323644	-1,030898612	-1,110034045	-0,960611128	1,9	DOWN
116	C602195.1	gb AAX26785.2 SJCHGC05057 protein [Schistosoma japonicum]; ref XP_001478203.1 PREDICTED: similar to Inosine 5-phosphate dehydrogenase 2 [Mus musculus]; gb AAA39311.1 IMP dehydrogenase (EC 1.2.1.14); ref NP_035960.2 inosine 5'-phosphate dehydrogenase 2 [Mus musculus] sp P24547 IMDH2_MOUSE Inosine-5'-monophosphate dehydrogenase 2 (IMP dehydrogenase 2) (IMPDH-II) (IMPD 2) gb AAH10314.1 Inosine 5'-phosphate dehydrogenase 2 [Mus musculus] gb AAH52671.1 Inosine 5'-phosphate dehydrogenase 2 [Mus musculus] dbj BAE35879.1 unnamed protein product [Mus musculus] dbj BAE40908.1 unnamed protein product [Mus musculus] dbj BAE41367.1 unnamed protein product [Mus musculus] dbj BAE38929.1 unnamed protein product [Mus musculus] dbj BAE29791.1 unnamed protein product [Mus musculus] dbj BAE30225.1 unnamed protein product [Mus musculus] dbj BAE35402.1 unnamed protein product [Mus musculus] dbj BAE31422.1 unnamed protein product [Mus musculus] gb EDL21302.1 inosine 5'-phosphate dehydrogenase 2 [Mus musculus];	-1,01472003	-0,931928806	-0,980234353	-0,940565324	-0,960399839	1,9	DOWN

117	C603420.1	gb AAX26129.2 SJCHGC06300 protein [Schistosoma japonicum]; ref XP_001602516.1 PREDICTED: similar to MGC53562 protein [Nasonia vitripennis]; ref NP_001079679.1 hypothetical protein LOC379366 [Xenopus laevis] sp Q7ZWN0.1 LMF2_XENLA Lipase maturation factor 2 gb AAH46869.1 Lmf2 protein [Xenopus laevis]; ref NP_001072170.1 hypothetical protein LOC594899 [Xenopus tropicalis] sp Q0P4Y8.1 LMF2_XENTR Lipase maturation factor 2 gb AAI21840.1 Lipase maturation factor 2 [Xenopus tropicalis];	#DIV/0!	-0,04390379	-0,959593214	-1,024477707	-0,959593214	1,9	DOWN
118	C602495.1	gb AAW25367.1 unknown [Schistosoma japonicum]; gb AAW24629.1 SJCHGC01322 protein [Schistosoma japonicum]; gb AAK15271.1 AF308144_1 Sj-Ts4 protein [Schistosoma japonicum]; gb AAX25898.2 SJCHGC07013 protein [Schistosoma japonicum];	-0,648175843	-0,828497035	-1,251488703	-1,090413804	-0,95945542	1,9	DOWN
119	C602650.1	No match	-1,073461763	-1,078416108	-0,838445712	-0,775430871	-0,955953738	1,9	DOWN
120	C607625.1	No match	-0,494637862	-0,72796806	-1,18354495	-1,411303326	-0,955756505	1,9	DOWN
121	C608302.1	gb AAX25184.2 SJCHGC08832 protein [Schistosoma japonicum];	-0,664897261	-0,749908118	-1,159865564	-1,177403561	-0,954886841	1,9	DOWN
122	C610520.1	gb AAX27136.2 SJCHGC07961 protein [Schistosoma japonicum]; ref XP_001942990.1 PREDICTED: similar to SEC63 protein, putative [Acyrtosiphon pisum]; ref XP_001638715.1 predicted protein [Nematostella vectensis] gb EDO46652.1 predicted protein [Nematostella vectensis]; gb EDX09557.1 GD14009 [Drosophila simulans];	-0,962060597	-0,978601378	-0,915869311	-0,940996852	-0,951528725	1,9	DOWN
123	C609184.1	No match	-0,965157527	-0,729974837	-0,936388243	-0,966737549	-0,950772885	1,9	DOWN
124	C609423.1	gb AAW27625.1 SJCHGC01869 protein [Schistosoma japonicum];	-1,098154078	-0,864516793	-1,026912182	-0,848812828	-0,945714488	1,9	DOWN
125	C610194.1	No match	-0,836088557	-0,774540783	-1,097643125	-1,054711148	-0,945399853	1,9	DOWN
126	C611344.1	gb AAP06286.1 SJCHGC00554 protein [Schistosoma japonicum]; gb AAX27560.2 SJCHGC02038 protein [Schistosoma japonicum]; ref XP_793449.2 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus] ref XP_001178548.1 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]; ref NP_001090309.1 hypothetical protein LOC779218 [Xenopus laevis] gb AAI23144.1 MGC154331 protein [Xenopus laevis];	-0,861361953	-0,77086676	-1,022244254	-1,025744743	-0,941803104	1,9	DOWN
127	C601552.1	No match	-0,772803102	-0,6454877	-1,108961294	-1,106975939	-0,939889521	1,9	DOWN
128	C603352.1	gb AAW27868.1 SJCHGC06337 protein [Schistosoma japonicum]; gb AAW27771.1 SJCHGC01525 protein [Schistosoma japonicum]; gb AAW25162.1 unknown [Schistosoma japonicum]; dbj BAD08526.1 17-beta hydroxysteroid dehydrogenase [Ciona intestinalis];	-1,215205718	-1,053562543	-0,817642804	-0,722569299	-0,935602674	1,9	DOWN
129	C612230.1	gb AAX27733.2 SJCHGC06480 protein [Schistosoma japonicum]; ref XP_395702.2 PREDICTED: similar to Xeroderma pigmentosum group A-like CG6358-PA [Apis mellifera]; dbj BAA06690.1 Dxpa protein [Drosophila melanogaster]; ref NP_476866.1 Xeroderma pigmentosum group A-like CG6358-PA [Drosophila melanogaster] sp P28518 XPA_DROME DNA-repair protein complementing XP-A cells homolog (Xeroderma pigmentosum group A-complementing protein homolog) emb CAA21834.1 EG:EG0007.8 [Drosophila melanogaster] gb AAF45917.1 CG6358-PA [Drosophila melanogaster];	-0,946429437	-1,031890244	-0,923002075	-0,911969384	-0,934715756	1,9	DOWN

130	C606835.1	No match	-0,713709284	-0,77484006	-1,207541709	-1,088284164	-0,931562112	1,9	DOWN
131	C607154.1	gb AAW27297.1 SJCHGC01783 protein [Schistosoma japonicum]; gb EDV25878.1 expressed hypothetical protein [Trichoplax adhaerens]; emb CAB46230.1 rab GDP-dissociation inhibitor [Branchiostoma floridae]; ref XP_623197.2 PREDICTED: similar to GDP dissociation inhibitor CG4422-PA [Apis mellifera];	-0,734614123	-0,900583657	-1,00265488	-0,961765872	-0,931174765	1,9	DOWN
132	C607081.1	gb AAX30490.2 SJCHGC04027 protein [Schistosoma japonicum]; gb EDV25795.1 hypothetical protein TRIADDRAFT_23475 [Trichoplax adhaerens];	-0,826901307	-0,795324085	-1,032337024	-1,119710872	-0,929619166	1,9	DOWN
133	C714068.1	gb AAX30649.1 SJCHGC06493 protein [Schistosoma japonicum]; ref XP_001120892.1 PREDICTED: similar to CG14214-PA [Apis mellifera]; gb EDV20899.1 conserved hypothetical protein [Trichoplax adhaerens]; ref NP_001037674.1 transport protein Sec61 gamma subunit [Bombyx mori] gb ABF51395.1 transport protein SEC61 [Bombyx mori] gb ABF85697.1 transport protein Sec61 gamma subunit [Bombyx mori];	-0,496983746	-0,483967769	-1,36375159	-1,355571711	-0,926277729	1,9	DOWN
134	C600001.1	gb AAX26813.2 SJCHGC05893 protein [Schistosoma japonicum]; ref XP_780071.2 PREDICTED: similar to Chimerin (chimaerin) 1 [Strongylocentrotus purpuratus] ref XP_001195747.1 PREDICTED: similar to Chimerin (chimaerin) 1 [Strongylocentrotus purpuratus]; ref NP_497323.3 BE0003N10.2 [Caenorhabditis elegans]; gb AAK73856.2 AC092690_2 Hypothetical protein BE0003N10.2 [Caenorhabditis elegans];	-0,872167559	-1,063087353	-0,950485725	-0,893912197	-0,922198961	1,9	DOWN
135	C611836.1	No match	-0,912079809	-1,001683527	-0,789738982	-0,929092382	-0,920586096	1,9	DOWN
136	C609023.1	gb AAX27464.2 SJCHGC08006 protein [Schistosoma japonicum]; gb AAP06311.1 hypothetical protein [Schistosoma japonicum];	-0,693691374	-0,707218199	-1,251670436	-1,130341686	-0,918779943	1,9	DOWN
137	C611483.1	No match	-0,850153466	-0,742348696	-1,063103345	-0,985924511	-0,918038989	1,9	DOWN
138	C609782.1	gb AAG52888.1 AF333765_1 DAD-1-like protein [Schistosoma japonicum] gb ACE06891.1 unknown [Schistosoma japonicum]; ref XP_001123277.1 PREDICTED: similar to CG13393-PA [Apis mellifera]; gb ABM55607.1 dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1-like protein [Maconellicoccus hirsutus]; ref XP_966764.1 PREDICTED: similar to CG13393 CG13393-PA [Tribolium castaneum];	-0,936751902	-0,898705249	-0,982194022	-0,778800347	-0,917728576	1,9	DOWN
139	C601649.1	gb AAX30160.2 SJCHGC01212 protein [Schistosoma japonicum]; ref YP_873485.1 beta-lactamase domain protein [Acidothermus cellulolyticus 11B] gb ABK53499.1 beta-lactamase domain protein [Acidothermus cellulolyticus 11B]; ref XP_001949112.1 PREDICTED: similar to CG9117 CG9117-PA [Acyrtosiphon pisum]; ref XP_692640.2 PREDICTED: similar to CG9117 CG9117-PA [Danio rerio];	-0,880709302	-0,936223645	-0,936314327	-0,899158874	-0,91769126	1,9	DOWN
140	C612154.1	gb AAW27619.1 SJCHGC06261 protein [Schistosoma japonicum]; ref XP_001915357.1 PREDICTED: similar to BRO1 domain-containing protein BROX [Equus caballus]; ref XP_600599.3 PREDICTED: hypothetical protein [Bos taurus]; dbj BAB71331.1 unnamed protein product [Homo sapiens] dbj BAF56045.1 Bro1-domain-containing protein [Homo sapiens];	-0,882510863	-1,291703903	-0,869186866	-0,950765079	-0,916637971	1,9	DOWN

141	C603400.1	gb AAW25867.1 SJCHGC02436 protein [Schistosoma japonicum]; ref XP_001604174.1 PREDICTED: similar to HDC19127 [Nasonia vitripennis]; ref NP_001018527.1 hypothetical protein LOC553720 [Danio rerio] gb AAH95784.1 Zgc:112365 [Danio rerio] gb AAI64762.1 Zgc:112365 [synthetic construct]; ref NP_001096035.1 alkB, alkylation repair homolog 1 [Mus musculus];	-1,166996569	-0,90720598	-0,912362186	-0,910402101	-0,911382144	1,9	DOWN
142	C603357.1	No match	-1,061824895	-1,003819201	-0,735631435	-0,812668227	-0,908243714	1,9	DOWN
143	C608968.1	No match	-0,635287775	-0,651283872	-1,205872403	-1,157578249	-0,904431061	1,9	DOWN
144	C611828.1	gb AAW24999.2 SJCHGC04012 protein [Schistosoma japonicum];	-1,083314683	-1,073619832	-0,726643063	-0,667324661	-0,900131448	1,9	DOWN
145	C611706.1	gb AAW25843.1 unknown [Schistosoma japonicum]; gb AAW24972.1 SJCHGC01067 protein [Schistosoma japonicum]; gb EDV57554.1 GG24473 [Drosophila erecta]; ref XP_001201855.1 PREDICTED: hypothetical protein, partial [Strongylocentrotus purpuratus] ref XP_796678.2 PREDICTED: hypothetical protein, partial [Strongylocentrotus purpuratus];	-0,780310572	-0,868088416	-1,037301328	-0,926779355	-0,897433886	1,9	DOWN
146	C605248.1	gb AAW24880.1 SJCHGC06172 protein [Schistosoma japonicum]; gb ABY56687.1 Ts3 protein [Taenia solium]; ref XP_001362363.1 PREDICTED: similar to ribosomal protein L18a [Monodelphis domestica]; gb AAH42256.1 RPL18A protein [Xenopus laevis];	-0,648077044	-0,668725565	-1,122897732	-1,198689532	-0,895811649	1,9	DOWN
147	C601166.1	No match	-1,074784113	-1,217694422	-0,710196788	-0,710483909	-0,892634011	1,9	DOWN
148	C602909.1	No match	-0,523106523	-0,554337974	-1,230233748	-1,246708312	-0,892285861	1,9	DOWN
149	C610721.1	gb AAW27711.1 SJCHGC02387 protein [Schistosoma japonicum]; gb AAW25706.1 SJCHGC02386 protein [Schistosoma japonicum];	-0,877516761	-0,744188818	-0,903497332	-1,006015995	-0,890507047	1,9	DOWN
150	C607539.1	gb AAW26809.2 SJCHGC06221 protein [Schistosoma japonicum];	-0,784386476	-0,788845002	-0,983086455	-1,004182934	-0,885965729	1,8	DOWN
151	C604842.1	No match	-0,73190702	-0,799371717	-1,031486469	-0,970823778	-0,885097748	1,8	DOWN
152	C602617.1	No match	-0,885093633	-0,819398995	-0,905731569	-0,880661047	-0,88287734	1,8	DOWN
153	C713563.1	gb AAW27569.1 SJCHGC03345 protein [Schistosoma japonicum]; gb ABO77964.1 nanos-like protein [Schmidtea mediterranea]; gb ABO52809.1 nanos-like protein [Schmidtea mediterranea]; dbj BAD88623.1 nanos-related protein [Dugesia japonica];	-0,826040095	-0,884872613	-0,878705308	-0,948456483	-0,881788961	1,8	DOWN
154	C605824.1	gb AAW25423.1 SJCHGC06005 protein [Schistosoma japonicum];	-0,782308052	-0,882669684	-0,879707325	-1,277692888	-0,881188505	1,8	DOWN
155	C603972.1	gb AAA29882.1 fimbrin; gb AAX24922.2 SJCHGC01985 protein [Schistosoma japonicum]; gb EDW05622.1 G111134 [Drosophila mojavensis]; gb EDV46485.1 GG18187 [Drosophila erecta];	-0,879935851	-0,879877699	-0,933398464	-0,852243172	-0,879906775	1,8	DOWN
156	C603408.1	No match	-1,099889263	-1,120736647	-0,656798853	-0,586580765	-0,878344058	1,8	DOWN
157	C603897.1	gb AAV49163.1 polo-like kinase [Schistosoma mansoni]; ref XP_001915939.1 PREDICTED: similar to Serine/threonine-protein kinase PLK1 (Polo-like kinase 1) (PLK-1) (Serine/threonine-protein kinase 13) (STPK13) [Equus caballus]; ref XP_547091.2 PREDICTED: similar to Serine/threonine-protein kinase PLK1 (Polo-like kinase 1) (PLK-1) (Serine/threonine-protein kinase 13) (STPK13) [Canis familiaris]; dbj BAG36038.1 unnamed protein product [Homo sapiens];	-0,552743924	-0,824852894	-0,915968268	-1,032814777	-0,870410581	1,8	DOWN

158	C606776.1	gb AAW24796.1 SJCHGC06638 protein [Schistosoma japonicum]; gb AAW25340.1 SJCHGC09559 protein [Schistosoma japonicum]; ref XP_788872.1 PREDICTED: similar to Adenine phosphoribosyl transferase [Strongylocentrotus purpuratus] ref XP_001202862.1 PREDICTED: similar to Adenine phosphoribosyl transferase [Strongylocentrotus purpuratus]; ref ZP_01741785.1 adenine phosphoribosyltransferase [Rhodobacterales bacterium HTCC2150] gb EBA04238.1 adenine phosphoribosyltransferase [Rhodobacterales bacterium HTCC2150];	-0,872835139	-0,867431426	-0,868412925	-0,795201581	-0,867922176	1,8	DOWN
159	C606907.1	gb AAV65745.2 insulin receptor tyrosine kinase [Schistosoma mansoni]; emb CAD30260.1 putative insulin receptor [Echinococcus multilocularis]; ref XP_972770.2 PREDICTED: similar to insulin receptor, partial [Tribolium castaneum]; ref XP_001377572.1 PREDICTED: similar to insulin receptor [Monodelphis domestica];	-0,882218928	-0,853316367	-0,684421136	-1,184136939	-0,867767648	1,8	DOWN
160	C608771.1	gb AAD52698.1 AF091537_1 very low density lipoprotein binding protein precursor [Schistosoma japonicum] gb ACE06889.1 unknown [Schistosoma japonicum];	-0,865999646	-0,699591727	-1,036084899	-0,866689835	-0,866344741	1,8	DOWN
161	C611764.1	gb AAX25077.2 SJCHGC03771 protein [Schistosoma japonicum]; gb AAX26627.2 SJCHGC07255 protein [Schistosoma japonicum];	-0,920491589	-1,032852461	-0,748989203	-0,807975504	-0,864233547	1,8	DOWN
162	C605909.1	No match	-0,557973858	-0,652265494	-1,058304557	-1,067984364	-0,855285026	1,8	DOWN
163	C606347.1	gb AAW25679.1 SJCHGC01491 protein [Schistosoma japonicum]; gb AAP05894.1 similar to GenBank Accession Number AF183413 dolichyl-phosphate beta-glucosyltransferase in Homo sapiens [Schistosoma japonicum]; ref XP_417093.2 PREDICTED: similar to dolichyl-phosphate beta-glucosyltransferase [Gallus gallus]; ref XP_001496408.2 PREDICTED: similar to Dolichyl-phosphate beta-glucosyltransferase (DoLP-glucosyltransferase) (Asparagine-linked glycosylation protein 5) [Equus caballus];	-0,958663426	-0,949340541	-0,758881104	-0,662591204	-0,854110823	1,8	DOWN
164	C714516.1	gb AAW25130.1 SJCHGC02831 protein [Schistosoma japonicum]; gb AAY32924.1 TGF-beta receptor interacting protein 1 [Clonorchis sinensis]; ref NP_001087664.1 eukaryotic translation initiation factor 3, subunit 2 beta [Xenopus laevis] gb AAH81058.1 Eif3s2 protein [Xenopus laevis]; gb AAI27353.1 Eif3s2 protein [Xenopus tropicalis];	-0,578253504	-0,64018225	-1,091136156	-1,067195847	-0,853689049	1,8	DOWN
165	C601947.1	gb AAX26526.2 SJCHGC09040 protein [Schistosoma japonicum]; gb AAF64527.1 AF254148_1 PUR-alpha-like protein [Schistosoma mansoni]; gb AAW26889.1 SJCHGC06753 protein [Schistosoma japonicum]; gb EDW50911.1 GM26800 [Drosophila sechellia];	-0,658073909	-0,80505112	-0,90112043	-1,009823433	-0,853085775	1,8	DOWN
166	C606089.1	No match	-0,860645166	-0,980944742	-0,84506953	-0,811201329	-0,852857348	1,8	DOWN
167	C602647.1	No match	-0,782837078	-0,538068725	-1,031210498	-0,91983169	-0,851334384	1,8	DOWN

168	C602253.1	gb AAW26219.1 SJCHGC02185 protein [Schistosoma japonicum]; gb AAP06082.1 similar to XM_040577 CGI-12 protein in Homo sapiens [Schistosoma japonicum]; ref XP_001951989.1 PREDICTED: similar to CG5047 CG5047-PA [Acyrtosiphon pisum]; ref NP_001002615.1 MTERF domain containing 1 [Danio rerio] gb AAH75975.1 MTERF domain containing 1 [Danio rerio];	-0,89554423	-0,852454534	-0,777423973	-0,844495646	-0,84847509	1,8	DOWN
169	C601216.1	No match	-0,996591184	-0,8432526	-0,840867176	-0,84998355	-0,846618075	1,8	DOWN
170	C608615.1	tpe CAJ00235.1 TPA: endonuclease-reverse transcriptase [Schistosoma mansoni];	-0,72111761	0,211029298	-0,966389971	-1,175164237	-0,843753791	1,8	DOWN
171	C601960.1	gb AAW26659.1 SJCHGC01731 protein [Schistosoma japonicum]; gb EDW27311.1 GL21220 [Drosophila persimilis]; gb EDW13480.1 GI18231 [Drosophila mojavensis]; ref XP_001356252.1 GA20298-PA [Drosophila pseudoobscura] gb EAL33315.1 GA20298-PA [Drosophila pseudoobscura];	-0,839927769	-0,757668827	-0,839364833	-0,894513514	-0,839646301	1,8	DOWN
172	C610618.1	No match	-0,317768923	-0,447728424	-1,423058994	-1,220634631	-0,834181528	1,8	DOWN
173	C609011.1	gb AAP06411.1 SJCHGC06675 protein [Schistosoma japonicum]; gb ABS45569.1 QM protein [Marsupenaeus japonicus]; gb ABU41039.1 putative QM protein [Lepeophtheirus salmonis]; gb ABY61391.1 QM protein [Polyrhachis vicina];	-0,816637617	-0,77524753	-0,905174126	-0,848830014	-0,832733816	1,8	DOWN
174	C605584.1	ref XP_001380983.1 PREDICTED: similar to PIG-A protein [Monodelphis domestica]; ref XP_001138368.1 PREDICTED: phosphatidylinositol N-acetylglucosaminyltransferase subunit A isoform 2 [Pan troglodytes]; ref XP_520945.2 PREDICTED: phosphatidylinositol N-acetylglucosaminyltransferase subunit A isoform 6 [Pan troglodytes]; dbj BAG37537.1 unnamed protein product [Homo sapiens];	-0,692307254	-0,709185289	-1,01394869	-0,945697792	-0,827441541	1,8	DOWN
175	C604320.1	No match	-0,77632374	-0,770488883	-0,888400923	-0,876530672	-0,826427206	1,8	DOWN
176	C601338.1	No match	-0,84377598	-0,80638567	-0,70012312	-0,858694278	-0,825080825	1,8	DOWN
177	C610092.1	gb AAW27429.1 SJCHGC02676 protein [Schistosoma japonicum];	-0,778886204	-0,771250954	-0,950312752	-0,871163133	-0,825024669	1,8	DOWN
178	C603197.1	ref NP_031888.2 discs large homolog 1 [Mus musculus] ref XP_001479222.1 PREDICTED: similar to Discs, large homolog 1 (Drosophila) isoform 2 [Mus musculus] gb AAH57118.1 Discs, large homolog 1 (Drosophila) [Mus musculus] gb EDK97752.1 discs, large homolog 1 (Drosophila), isoform CRA_a [Mus musculus]; ref XP_001500922.1 PREDICTED: discs, large homolog 1 (Drosophila) [Equus caballus]; gb EDM11461.1 discs, large homolog 1 (Drosophila), isoform CRA_e [Rattus norvegicus]; gb EDM11460.1 discs, large homolog 1 (Drosophila), isoform CRA_d [Rattus norvegicus];	-0,757837551	-0,66753714	-0,889984981	-1,181235368	-0,823911266	1,8	DOWN
179	C612334.1	No match	-0,965379167	-0,831712429	-0,813830635	-0,728685345	-0,822771532	1,8	DOWN
180	C603446.1	No match	-0,909316419	-1,041414795	-0,734912801	-0,470899793	-0,82211461	1,8	DOWN
181	C612595.1	No match	-0,727654773	-0,732236981	-0,966693704	-0,909826736	-0,821031859	1,8	DOWN
182	C604281.1	gb AAW25623.1 SJCHGC01247 protein [Schistosoma japonicum]; ref NP_001123800.1 hypothetical protein LOC100170551 [Xenopus (Silurana) tropicalis] gb AAI67594.1 Unknown (protein for MGC:184902) [Xenopus tropicalis]; gb EDW17245.1 GI16794 [Drosophila mojavensis]; gb EDV38789.1 GF24975 [Drosophila ananassae];	-0,776176835	-0,68186374	-0,862130524	-0,86311472	-0,81915368	1,8	DOWN
183	C611102.1	No match	-0,838579458	-0,864883997	-0,798589639	-0,355500651	-0,818584549	1,8	DOWN

184	C608994.1	gb AAX30391.1 SJCHGC03240 protein [Schistosoma japonicum];	-0,88597884	-1,043504616	-0,691833551	-0,750125357	-0,818052099	1,8	DOWN
185	C608093.1	ref NP_001106670.1 nascent polypeptide-associated complex alpha subunit isoform a [Mus musculus]; gb EDL24536.1 mCG17022, isoform CRA_a [Mus musculus]; sp P70670 NACAM_MOUSE Nascent polypeptide-associated complex subunit alpha, muscle-specific form (Alpha-NAC, muscle-specific form) gb AAB18732.1 alpha-NAC, muscle-specific form gp220 gb AAB18734.1 alpha-NAC, muscle-specific form gp220 [Mus musculus]; ref XP_001115411.1 PREDICTED: similar to Nascent polypeptide-associated complex alpha subunit, muscle-specific form (Alpha-NAC, muscle-specific form) [Macaca mulatta];	-0,261623737	-0,787636519	-0,870716555	-0,84603105	-0,816833785	1,8	DOWN
186	C611222.1	gb AAI57611.1 Unknown (protein for IMAGE:8857551) [Xenopus tropicalis]; gb AAI54786.1 Zgc:64155 [Danio rerio]; gb AAI52670.1 Zgc:64155 protein [Danio rerio]; ref NP_956343.2 zinc finger, DHHC domain containing 4 [Danio rerio];	-0,845125075	-0,819579631	-0,813420013	-0,769800764	-0,816499822	1,8	DOWN
187	C610843.1	No match	-0,542332694	-0,747242544	-0,882841918	-1,104451171	-0,815042231	1,8	DOWN
188	C609637.1	gb AAW27050.1 SJCHGC05369 protein [Schistosoma japonicum];	-0,842698546	-0,931944845	-0,786777828	-0,726319631	-0,814738187	1,8	DOWN
189	C610204.1	No match	-0,637120811	-0,722665889	-0,934705164	-0,89747376	-0,810069825	1,8	DOWN
190	C603465.1	No match	-0,783159065	-0,535842059	-0,83973335	-0,835866162	-0,809512614	1,8	DOWN
191	C609020.1	gb AAX24535.2 SJCHGC07456 protein [Schistosoma japonicum];	-0,716612808	-0,923095116	-0,801609055	-0,817081901	-0,809345478	1,8	DOWN
192	C605069.1	gb AAW25441.1 SJCHGC06472 protein [Schistosoma japonicum]; ref XP_553715.3 AGAP009835-PA [Anopheles gambiae str. PEST] gb EAL39215.3 AGAP009835-PA [Anopheles gambiae str. PEST]; gb EDW77669.1 GK24436 [Drosophila willistoni]; ref XP_001355895.1 GA19445-PA [Drosophila pseudoobscura] gb EAL32954.1 GA19445-PA [Drosophila pseudoobscura];	-0,815194722	-0,67350664	-0,801463483	-0,826936061	-0,808329103	1,8	DOWN
193	C611089.1	gb AAW26023.1 SJCHGC09218 protein [Schistosoma japonicum];	-0,774177282	-0,868619134	-0,788991913	-0,815454476	-0,802223195	1,7	DOWN
194	C607480.1	gb AAW25563.1 SJCHGC04928 protein [Schistosoma japonicum];	-0,849169983	-0,821471523	-0,756257802	-0,781632119	-0,801551821	1,7	DOWN
195	C607654.1	gb AAX27329.2 SJCHGC00542 protein [Schistosoma japonicum]; gb AAP06056.1 hypothetical protein [Schistosoma japonicum];	-0,708210437	-0,815522272	-0,834752181	-0,7872582	-0,801390236	1,7	DOWN
196	C607067.1	gb AAW27124.1 SJCHGC03490 protein [Schistosoma japonicum]; gb AAX25376.2 SJCHGC08502 protein [Schistosoma japonicum];	-0,75197777	-0,909864352	-0,84866551	-0,752361623	-0,800513567	1,7	DOWN
197	C610245.1	No match	-0,638100089	-0,687000126	-1,034358487	-0,907854303	-0,797427215	1,7	DOWN
198	C711918.1	gb AAX26453.2 SJCHGC06422 protein [Schistosoma japonicum]; gb AAX26480.2 SJCHGC07601 protein [Schistosoma japonicum]; ref XP_792209.2 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus] ref XP_001195941.1 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]; ref NP_001026408.1 acyl-CoA synthetase long-chain family member 5 [Gallus gallus] emb CAG32476.1 hypothetical protein [Gallus gallus];	-0,738388638	-0,026191026	-0,851801746	-0,858173356	-0,795095192	1,7	DOWN

199	C608103.1	gb AAW25842.1 SJCHGC09285 protein [Schistosoma japonicum]; ref NP_001086484.1 ribosomal protein L19 [Xenopus laevis] gb AAH75206.1 Rpl19-prov protein [Xenopus laevis]; gb ABN14900.1 ribosomal protein L19 [Taenia asiatica]; emb CAD91441.1 ribosomal protein L19 [Crassostrea gigas];	-0,603753059	-0,728481123	-0,964098701	-0,859624361	-0,794052742	1,7	DOWN
200	C605075.1	No match	-0,860879907	-0,66184195	-0,912075216	-0,726455654	-0,793667781	1,7	DOWN
201	C608919.1	No match	-0,834442641	-1,00138371	-0,751520498	-0,463861182	-0,79298157	1,7	DOWN
202	C612498.1	gb AAX27118.2 SJCHGC07833 protein [Schistosoma japonicum];	-1,057517366	-0,995591019	-0,589710526	-0,354863342	-0,792650773	1,7	DOWN
203	C717897.1	ref XP_556087.3 AGAP005449-PA [Anopheles gambiae str. PEST] gb EAL39826.3 AGAP005449-PA [Anopheles gambiae str. PEST]; ref NP_001006802.1 Cas-Br-M (murine) ecotropic retroviral transforming sequence b [Xenopus tropicalis] sp Q6DFR2 CBLB_XENTR E3 ubiquitin-protein ligase CBL-B (Signal transduction protein CBL-B) (SH3-binding protein CBL-B) gb AAH76671.1 Cas-Br-M (murine) ecotropic retroviral transforming sequence b [Xenopus tropicalis]; ref XP_556088.3 AGAP005449-PB [Anopheles gambiae str. PEST] gb EAL39827.3 AGAP005449-PB [Anopheles gambiae str. PEST]; ref NP_001084790.1 hypothetical protein LOC431829 [Xenopus laevis] sp Q6NRE7 CBLBB_XENLA E3 ubiquitin-protein ligase CBL-B-B (Signal transduction protein CBL-B-B) (SH3-binding protein CBL-B-B) gb AAH70806.1 MGC83879 protein [Xenopus laevis];	-0,510337189	-0,503928543	-1,190459387	-1,072349258	-0,791343224	1,7	DOWN
204	C603037.1	gb AAX25383.2 SJCHGC05029 protein [Schistosoma japonicum];	-0,504740954	-0,47458321	-1,076775187	-1,13567746	-0,790758071	1,7	DOWN
205	C601160.1	No match	-0,638987112	-0,655827375	-1,056395931	-0,924794419	-0,790310897	1,7	DOWN
206	C606357.1	ref XP_643550.1 hypothetical protein DDBDRAFT_0167213 [Dictyostelium discoideum AX4] gb AAO53180.1 hypothetical protein [Dictyostelium discoideum] gb EAL69515.1 hypothetical protein DDBDRAFT_0167213 [Dictyostelium discoideum AX4];	-0,70967841	-0,660618964	-1,146623724	-0,870381902	-0,790030156	1,7	DOWN
207	C600716.1	gb ABB51559.1 CD36-like class B scavenger receptor [Schistosoma mansoni]; gb AAW26454.1 SJCHGC06304 protein [Schistosoma japonicum]; ref NP_001095623.1 scavenger receptor class B, member 2 [Bos taurus] gb AAI49936.1 SCARB2 protein [Bos taurus]; ref XP_001376794.1 PREDICTED: hypothetical protein [Monodelphis domestica];	-0,952223138	-0,853703638	-0,602883501	-0,726231966	-0,789967802	1,7	DOWN
208	C601151.1	gb AAX27845.2 SJCHGC05385 protein [Schistosoma japonicum]; ref XP_001337123.1 PREDICTED: similar to Abcf2 protein [Danio rerio]; gb AAH66505.1 Abcf2 protein [Danio rerio]; ref NP_958472.1 ATP-binding cassette, sub-family F (GCN20), member 2 [Danio rerio] gb AAH47181.1 ATP-binding cassette, sub-family F (GCN20), member 2 [Danio rerio] gb AAI65771.1 Abcf2 protein [synthetic construct];	-0,858423924	-0,65485496	-0,750406179	-0,828666012	-0,789536096	1,7	DOWN
209	C610602.1	No match	-0,732482444	-0,748617449	-0,826503279	-1,008863343	-0,787560364	1,7	DOWN

210	C609479.1	ref XP_001378737.1 PREDICTED: similar to protein phosphatase 2A 65 kDa regulatory subunit, alpha [Monodelphis domestica]; ref NP_001080135.1 protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform [Xenopus laevis]; gb AAH46723.1 Ppp2r1a-prov protein [Xenopus laevis]; ref NP_989405.1 hypothetical protein LOC395042 [Xenopus tropicalis] gb AAH64863.1 Hypothetical protein MGC76072 [Xenopus tropicalis] emb CAJ81356.1 protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform [Xenopus tropicalis]; dbj BAF83282.1 unnamed protein product [Homo sapiens];	-0,846092041	-0,833071399	-0,739006652	-0,680539917	-0,786039026	1,7	DOWN
211	C609859.1	gb AAW25614.1 SJCHGC07048 protein [Schistosoma japonicum]; ref XP_001657058.1 neurobeachin [Aedes aegypti]; gb EAT45124.1 neurobeachin [Aedes aegypti]; ref XP_001649459.1 neurobeachin [Aedes aegypti]; gb EAT33014.1 neurobeachin [Aedes aegypti]; ref XP_311142.4 AGAP000017-PA [Anopheles gambiae str. PEST]; gb EAA06488.4 AGAP000017-PA [Anopheles gambiae str. PEST];	-0,946178343	-0,779680644	-0,754771759	-0,788188633	-0,783934639	1,7	DOWN
212	C602080.1	gb AAW28101.2 SJCHGC06578 protein [Schistosoma japonicum]; gb AAP06171.1 hypothetical protein [Schistosoma japonicum]; gb ACE06837.1 unknown [Schistosoma japonicum];	-0,649687901	-0,651525672	-0,935093673	-0,91040697	-0,780966321	1,7	DOWN
213	C608256.1	No match	-0,69528818	-0,831749464	-0,728911639	-0,863652392	-0,780330552	1,7	DOWN
214	C600229.1	gb AAA96714.1 ATPase; gb ABS19816.1 sarco/endoplasmic reticulum calcium ATPase isoform B [Pinctada fucata]; gb ABS19817.1 sarco/endoplasmic reticulum calcium ATPase isoform C [Pinctada fucata]; gb ABS19815.1 sarco/endoplasmic reticulum calcium ATPase isoform A [Pinctada fucata];	-0,649961984	-0,680315025	-1,039461292	-0,879807606	-0,780061316	1,7	DOWN
215	C604563.1	gb AAW24708.1 SJCHGC01209 protein [Schistosoma japonicum]; gb AAW27547.1 SJCHGC06637 protein [Schistosoma japonicum]; gb AAW25408.1 SJCHGC02061 protein [Schistosoma japonicum]; gb ACE06868.1 unknown [Schistosoma japonicum];	-0,640172599	-0,676035392	-1,013598003	-0,881356281	-0,778695837	1,7	DOWN
216	C601272.1	No match	-0,849517234	-0,740802585	-0,816310466	-0,695177704	-0,778556526	1,7	DOWN
217	C602198.1	No match	-0,934200577	-0,869648271	-0,686792303	-0,619563739	-0,778220287	1,7	DOWN
218	C603876.1	emb CAK26791.1 PrA2 protein [Schistosoma mansoni]; emb CAK26789.1 PrB [Schistosoma mansoni];	-0,568862768	-0,573020265	-1,141322578	-0,982719759	-0,777870012	1,7	DOWN
219	C607463.1	gb AAW27114.1 SJCHGC06129 protein [Schistosoma japonicum];	-0,69951889	-0,695868738	-0,902467956	-0,849380299	-0,774449595	1,7	DOWN
220	C606724.1	No match	-0,648531755	-0,714910306	-0,832464012	-0,874113638	-0,773687159	1,7	DOWN

221	C602476.1	gb AAW26315.1 SJCHGC05429 protein [Schistosoma japonicum]; ref NP_001006327.1 mediator complex subunit 20 [Gallus gallus] sp Q5ZKY9.1 MED20_CHICK Mediator of RNA polymerase II transcription subunit 20 (Mediator complex subunit 20) (TRF-proximal protein homolog) emb CAG31604.1 hypothetical protein [Gallus gallus]; ref NP_001096763.1 mediator complex subunit 20 [Bos taurus] gb AAI46259.1 MED20 protein [Bos taurus]; ref NP_001013196.1 mediator complex subunit 20 [Rattus norvegicus] sp Q5XIE9.1 MED20_RAT Mediator of RNA polymerase II transcription subunit 20 (Mediator complex subunit 20) (TRF-proximal protein homolog) gb AAH83734.1 Mediator complex subunit 20 [Rattus norvegicus] gb EDM18891.1 rCG43485, isoform CRA_b [Rattus norvegicus];	-0,782719552	-0,829813669	-0,753065834	-0,759275026	-0,770997289	1,7	DOWN
222	C610914.1	gb AAX27546.2 SJCHGC02390 protein [Schistosoma japonicum]; gb AAP06359.1 hypothetical protein [Schistosoma japonicum]; gb AAX27010.1 unknown [Schistosoma japonicum]; gb AAX30131.1 SJCHGC00333 protein [Schistosoma japonicum]; gb AAX27020.1 unknown [Schistosoma japonicum];	-1,064281434	-0,835009792	-0,676009745	-0,703181225	-0,769095509	1,7	DOWN
223	C608351.1	sp P42637 TPM1_SCHMA Tropomyosin-1 (TMI) (Polypeptide 49) gb AAA03011.1 tropomyosin; sp Q26503 TPM_SCHHA Tropomyosin gb AAA88530.1 'Schistosoma haematobium tropomyosin'; gb AAS66088.1 tropomyosin [Orientobilharzia turkestanicum]; gb ACE06925.1 unknown [Schistosoma japonicum];	-0,573756086	-0,574112294	-0,99721354	-0,961491611	-0,767801953	1,7	DOWN
224	C605114.1	dbj BAE40671.1 unnamed protein product [Mus musculus]; ref NP_081086.1 MutL protein homolog 1 [Mus musculus] gb AAH21815.1 MutL homolog 1 (E. coli) [Mus musculus]; sp Q9JK91 MLH1_MOUSE DNA mismatch repair protein Mlh1 (MutL protein homolog 1) gb AAF64514.1 AF250844_1 MutL homolog 1 protein [Mus musculus]; ref XP_859198.1 PREDICTED: similar to MutL protein homolog 1 isoform 3 [Canis familiaris];	-1,039184231	-0,877318359	-0,653143083	-0,648201383	-0,765230721	1,7	DOWN
225	C603116.1	gb AAP06391.1 similar to NM_001414 eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kD) in Homo sapiens [Schistosoma japonicum]; gb AAW26067.1 SJCHGC06103 protein [Schistosoma japonicum]; ref XP_001927637.1 PREDICTED: similar to Translation initiation factor eIF-2B subunit alpha (eIF-2B GDP-GTP exchange factor subunit alpha) [Sus scrofa]; ref NP_001405.1 eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa [Homo sapiens] ref XP_522583.2 PREDICTED: eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa [Pan troglodytes] sp Q5RAR0.2 EI2BA_PONAB Translation initiation factor eIF-2B subunit alpha (eIF-2B GDP-GTP exchange factor subunit alpha) sp Q14232 EI2BA_HUMAN Translation initiation factor eIF-2B subunit alpha (eIF-2B GDP-GTP exchange factor subunit alpha) emb CAA64950.1 eIF-2B [Homo sapiens] emb CAG33112.1 EIF2B1 [Homo sapiens] gb AAI03764.1 Eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa [Homo sapiens] gb AAI04189.1 Eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa [Homo sapiens] gb AAI04190.1 Eukaryotic translation	-0,787811455	-0,812882243	-0,742389903	-0,718730012	-0,765100679	1,7	DOWN

226	C602958.1	gb AAC36355.1 apoferritin-2 [Schistosoma japonicum]; gb ACE06912.1 unknown [Schistosoma japonicum]; gb ABU49726.1 ferritin [Solanum tuberosum]; emb CAH05075.1 ferritin [Conyza canadensis];	-0,658754457	-0,721122253	-0,809017003	-0,840189267	-0,765069628	1,7	DOWN
227	C600599.1	gb AAW27499.1 SJCHGC06360 protein [Schistosoma japonicum]; ref XP_309798.4 AGAP010894-PA [Anopheles gambiae str. PEST] gb EAA05506.5 AGAP010894-PA [Anopheles gambiae str. PEST]; ref XP_001599499.1 PREDICTED: similar to signal recognition particle receptor alpha subunit [Nasonia vitripennis]; ref XP_395013.2 PREDICTED: similar to GTP-binding protein CG2522-PA isoform 1 [Apis mellifera];	-0,783119406	-0,859301392	-0,742051614	-0,637529616	-0,76258551	1,7	DOWN
228	C606929.1	No match	-0,669365766	-0,682582125	-0,863784252	-0,830888975	-0,75673555	1,7	DOWN
229	C603551.1	gb AAW27453.1 SJCHGC09200 protein [Schistosoma japonicum]; gb AAW24780.1 SJCHGC06442 protein [Schistosoma japonicum]; gb AAX26772.2 SJCHGC09234 protein [Schistosoma japonicum]; gb AAW27224.1 SJCHGC06580 protein [Schistosoma japonicum];	-0,417969054	-0,430441656	-1,081686037	-1,109633298	-0,756063847	1,7	DOWN
230	C605350.1	gb AAW26983.1 SJCHGC09421 protein [Schistosoma japonicum]; ref XP_001369190.1 PREDICTED: similar to Signal recognition particle 68 kDa protein (SRP68) [Monodelphis domestica]; ref NP_001120316.1 hypothetical protein LOC100145378 [Xenopus tropicalis] ref XP_001922310.1 PREDICTED: signal recognition particle 68 [Danio rerio] gb AAI52636.1 Srp68 protein [Danio rerio] gb AAI60941.1 Unknown (protein for MGC:180907) [Xenopus tropicalis]; gb AAT68165.1 68kDa signal recognition particle [Danio rerio];	-0,719225751	-0,712130999	-0,791756354	-1,163837713	-0,755491053	1,7	DOWN
231	C603060.1	No match	-0,602475662	-0,648307297	-0,895837295	-0,861870581	-0,755088939	1,7	DOWN
232	C607110.1	ref XP_001637772.1 predicted protein [Nematostella vectensis] gb EDO45709.1 predicted protein [Nematostella vectensis]; ref NP_061377.2 phosphatidylinositol glycan anchor biosynthesis, class B [Mus musculus] sp Q9JJQ0 PIGB_MOUSE GPI mannosyltransferase 3 (GPI mannosyltransferase III) (GPI-MT-III) (Phosphatidylinositol-glycan biosynthesis class B protein) (PIG-B) dbj BAE32195.1 unnamed protein product [Mus musculus]; dbj BAA94827.1 Pig-b [Mus musculus] gb EDL26282.1 phosphatidylinositol glycan anchor biosynthesis, class B, isoform CRA_b [Mus musculus]; gb AAH52658.1 Pigb protein [Mus musculus];	-1,010944181	-1,059363301	-0,497356682	-0,44646123	-0,754150432	1,7	DOWN
233	C602218.1	gb AAX25391.2 SJCHGC07955 protein [Schistosoma japonicum];	-0,821300428	-0,815211718	-0,657874375	-0,691406953	-0,753309336	1,7	DOWN

234	C606706.1	gb AAW24618.1 SJCHGC07079 protein [Schistosoma japonicum]; ref NP_001017874.1 hypothetical protein LOC550572 [Danio rerio] sp Q561X0.1 TM188_DANRE Transmembrane protein 188 gb AAH92973.1 Zgc:110674 [Danio rerio]; ref NP_001099643.1 transmembrane protein 188 [Rattus norvegicus] gb EDL87521.1 similar to CG8009-PA (predicted), isoform CRA_b [Rattus norvegicus]; ref NP_001011315.1 hypothetical protein LOC496772 [Xenopus tropicalis] sp Q5M8F7.1 TM188_XENTR Transmembrane protein 188 gb AAH88044.1 Hypothetical LOC496772 [Xenopus tropicalis] emb CAJ81789.1 novel protein [Xenopus tropicalis];	-0,894860769	-0,782930967	-0,720195944	-0,714535498	-0,751563456	1,7	DOWN
235	C611835.1	No match	-0,765399409	-0,814503376	-0,735604298	-0,65931614	-0,750501854	1,7	DOWN
236	C609457.1	No match	-0,363860839	-0,573340944	-0,999053683	-0,927451752	-0,750396348	1,7	DOWN
237	C611442.1	gb AAW24724.1 SJCHGC03621 protein [Schistosoma japonicum]; ref NP_001107356.1 hypothetical protein LOC100135181 [Xenopus tropicalis] gb AAI57204.1 Unknown (protein for MGC:135899) [Xenopus tropicalis]; gb EDV27133.1 hypothetical protein TRIADDRAFT_54778 [Trichoplax adhaerens]; ref NP_001079638.1 hypothetical protein LOC379325 [Xenopus laevis] sp Q7ZWY2.1 PIHD1_XENLA PIH1 domain-containing protein 1 gb AAH46655.1 MGC52879 protein [Xenopus laevis] gb AAI06294.1 MGC52879 protein [Xenopus laevis];	-0,753814824	-0,744574756	-0,911191895	-0,715907294	-0,74919479	1,7	DOWN
238	C601416.1	gb ABA40919.1 SJCHGC09844 protein [Schistosoma japonicum]; gb AAX30374.1 SJCHGC03136 protein [Schistosoma japonicum]; gb AAX31002.2 SJCHGC09704 protein [Schistosoma japonicum];	-0,626914544	-0,64508488	-0,874621038	-0,850191552	-0,747638216	1,7	DOWN
239	C603360.1	gb AAW26296.1 SJCHGC05033 protein [Schistosoma japonicum]; ref NP_001025681.1 MGC97807 protein [Xenopus tropicalis] gb AAH93470.1 MGC97807 protein [Xenopus tropicalis]; ref NP_957030.1 hypothetical protein LOC393709 [Danio rerio] gb AAH59520.1 Chromosome 20 open reading frame 20 (H. sapiens) [Danio rerio]; gb AAQ97748.1 chromosome 20 open reading frame 20 [Danio rerio];	-0,662581005	-0,801439701	-0,774689296	-0,719835585	-0,747262441	1,7	DOWN
240	C606707.1	gb AAP06324.1 similar to NM_016539 sir2-related protein type 6 in Homo sapiens [Schistosoma japonicum]; ref NP_989353.1 sirtuin (silent mating type information regulation 2 homolog) 6 [Xenopus (Silurana) tropicalis] gb AAH64193.1 Sirtuin (silent mating type information regulation 2 homolog) 6 [Xenopus tropicalis]; emb CAG33481.1 SIRT6 [Homo sapiens]; ref XP_001624617.1 predicted protein [Nematostella vectensis] gb EDO32517.1 predicted protein [Nematostella vectensis];	-0,990459417	-0,889597397	-0,604521901	-0,601046431	-0,747059649	1,7	DOWN
241	C610981.1	No match	-0,89832866	-0,864982803	-0,629122787	-0,542288831	-0,747052795	1,7	DOWN
242	C610259.1	No match	-0,664381911	-0,69415158	-0,96743182	-0,799393029	-0,746772305	1,7	DOWN
243	C603229.1	gb AAX25526.2 SJCHGC06794 protein [Schistosoma japonicum];	-0,661691161	-0,720287983	-0,820339508	-0,773228845	-0,746758414	1,7	DOWN
244	C605936.1	No match	-0,80155867	-0,752924723	-0,740388368	-0,683612438	-0,746656546	1,7	DOWN

245	C711705.1	ref NP_001085191.1 hypothetical protein LOC432280 [Xenopus laevis] gb AAH72276.1 MGC82410 protein [Xenopus laevis]; emb CAG02724.1 unnamed protein product [Tetraodon nigroviridis]; ref XP_001372829.1 PREDICTED: hypothetical protein [Monodelphis domestica];	-0,838852317	-0,724423108	-0,766484151	-0,715908107	-0,74545363	1,7	DOWN
246	C609950.1	No match	-0,559447253	-0,693964304	-0,808110152	-0,791691994	-0,742828149	1,7	DOWN
247	C608473.1	gb AAX24393.2 SJCHGC08648 protein [Schistosoma japonicum];	-0,906132779	-0,835515475	-0,649778283	-0,642614975	-0,742646879	1,7	DOWN
248	C610954.1	gb ACE06921.1 unknown [Schistosoma japonicum]; gb AAG40801.1 MF2 protein [Schistosoma japonicum]; gb AAX30252.1 SJCHGC02425 protein [Schistosoma japonicum];	-0,453452143	-0,620446859	-0,864831078	-0,883406342	-0,742638969	1,7	DOWN
249	C612177.1	gb AAX24517.2 SJCHGC05069 protein [Schistosoma japonicum]; gb AAX24756.2 SJCHGC07014 protein [Schistosoma japonicum];	-0,724796428	-0,71267254	-0,760368574	-0,865025662	-0,742582501	1,7	DOWN
250	C603980.1	gb AAX27122.2 SJCHGC07140 protein [Schistosoma japonicum]; ref NP_808446.1 armadillo repeat containing 7 [Mus musculus] sp Q3UJZ3.2 ARMC7_MOUSE Armadillo repeat-containing protein 7 gb AAH23126.1 Armadillo repeat containing 7 [Mus musculus] dbj BAC31232.1 unnamed protein product [Mus musculus] emb CAM23019.1 novel protein [Mus musculus] gb EDL34497.1 armadillo repeat containing 7, isoform CRA_c [Mus musculus]; dbj BAE27011.1 unnamed protein product [Mus musculus]; ref XP_001138859.1 PREDICTED: hypothetical protein [Pan troglodytes];	-0,838042392	-0,896791459	-0,646657732	-0,523219549	-0,742350062	1,7	DOWN
251	C604782.1	No match	-0,853540183	-1,05220495	-0,626871919	-0,605703187	-0,740206051	1,7	DOWN
252	C600304.1	emb CAE51198.1 src tyrosine kinase [Schistosoma mansoni];	-0,604860846	-0,618620327	-0,95985719	-0,860149062	-0,739384695	1,7	DOWN
253	C603401.1	No match	-0,705646466	-0,774783366	-0,769988599	-0,664365464	-0,737817533	1,7	DOWN
254	C605174.1	gb EDW07154.1 G115022 [Drosophila mojavensis]; ref XP_001866846.1 histidyl-tRNA synthetase [Culex pipiens quinquefasciatus] gb EDS43994.1 histidyl-tRNA synthetase [Culex quinquefasciatus]; gb EDW04530.1 GH23584 [Drosophila grimshawi]; gb EDV46605.1 GG19169 [Drosophila erecta];	-0,724928045	-0,606349925	-0,781139544	-0,748849921	-0,736888983	1,7	DOWN
255	C609178.1	No match	-0,565497238	-0,5721339	-0,899883724	-0,955383707	-0,736008812	1,7	DOWN
256	C607906.1	gb EDV22419.1 hypothetical protein TRIADDRAFT_59005 [Trichoplax adhaerens]; ref XP_001648295.1 flotillin-2 [Aedes aegypti] gb EAT44635.1 flotillin-2 [Aedes aegypti]; ref XP_001601913.1 PREDICTED: similar to CG32593-PB [Nasonia vitripennis]; ref XP_001121998.1 PREDICTED: similar to flotillin 2 CG32593-PB, isoform B [Apis mellifera];	-0,974862667	-0,824502919	-0,532761572	-0,646137794	-0,735320357	1,7	DOWN
257	C601025.1	gb AAR89512.1 ankyrin-like protein [Schistosoma mansoni]; ref XP_001055725.1 PREDICTED: similar to ankyrin repeat domain 15 [Rattus norvegicus]; ref XP_001080106.1 PREDICTED: similar to ankyrin repeat domain 15 [Rattus norvegicus]; ref NP_852069.4 KN motif and ankyrin repeat domains 1 [Mus musculus];	-0,84801001	-0,769111608	-0,655548562	-0,698791811	-0,73395171	1,7	DOWN
258	C605465.1	No match	-0,814918276	-0,705698174	-0,734789444	-0,730580864	-0,732685154	1,7	DOWN

259	C604714.1	ref XP_001655563.1 paxillin, putative [Aedes aegypti] gb EAT48671.1 paxillin, putative [Aedes aegypti]; ref XP_001845508.1 paxillin [Culex pipiens quinquefasciatus]; gb EDS40541.1 paxillin [Culex quinquefasciatus]; ref XP_316909.4 AGAP008532-PA [Anopheles gambiae str. PEST] gb EAA12524.5 AGAP008532-PA [Anopheles gambiae str. PEST]; gb EDW90406.1 GE12653 [Drosophila yakuba];	-0,982141172	-0,740881061	-0,69038629	-0,720560111	-0,730720586	1,7	DOWN
260	C611441.1	No match	-0,046832709	-0,487355414	-1,051355402	-0,972086096	-0,729720755	1,7	DOWN
261	C606274.1	ref XP_001197710.1 PREDICTED: similar to KIAA0268 [Strongylocentrotus purpuratus] ref XP_001192525.1 PREDICTED: similar to KIAA0268 [Strongylocentrotus purpuratus]; ref XP_317566.4 AGAP007919-PA [Anopheles gambiae str. PEST] gb EAA12907.4 AGAP007919-PA [Anopheles gambiae str. PEST]; ref XP_968468.2 PREDICTED: similar to Transport and Golgi organization 1 CG11098-PA [Tribolium castaneum]; ref XP_001376049.1 PREDICTED: similar to C219-reactive peptide (FLJ39207) [Monodelphis domestica];	-0,734876244	-0,724498054	-0,760233264	-0,67147708	-0,729687149	1,7	DOWN
262	C607204.1	ref NP_989228.1 thyroid hormone receptor interactor 13 [Xenopus tropicalis] gb AAH63217.1 Thyroid hormone receptor interactor 13 [Xenopus tropicalis]; ref XP_785120.1 PREDICTED: similar to Thyroid hormone receptor interactor 13 isoform 1 [Strongylocentrotus purpuratus] ref XP_001185736.1 PREDICTED: similar to Thyroid hormone receptor interactor 13 [Strongylocentrotus purpuratus]; ref XP_418892.2 PREDICTED: similar to HPV16 E1 protein binding protein [Gallus gallus]; ref XP_001203908.1 PREDICTED: similar to Thyroid hormone receptor interactor 13, partial [Strongylocentrotus purpuratus] ref XP_795235.2 PREDICTED: similar to Thyroid hormone receptor interactor 13, partial [Strongylocentrotus purpuratus];	-1,199056783	-0,895957032	-0,562149156	-0,453184516	-0,729053094	1,7	DOWN
263	C601420.1	gb AAW27593.1 SJCHGC09090 protein [Schistosoma japonicum]; ref XP_001626060.1 predicted protein [Nematostella vectensis] gb EDO33960.1 predicted protein [Nematostella vectensis]; gb AAX43326.1 ribosomal protein S13 [synthetic construct]; ref NP_001008.1 ribosomal protein S13 [Homo sapiens] ref NP_080809.1 ribosomal protein S13 [Mus musculus] ref NP_569116.1 ribosomal protein S13 [Rattus norvegicus] ref NP_001001783.1 ribosomal protein S13 [Gallus gallus] ref NP_001020513.1 ribosomal protein S13 [Bos taurus] ref XP_508306.1 PREDICTED: hypothetical protein [Pan troglodytes] ref XP_852037.1 PREDICTED: similar to ribosomal protein S13 isoform 1 [Canis familiaris] ref XP_864902.1 PREDICTED: similar to ribosomal protein S13 isoform 2 [Canis familiaris] ref XP_894950.1 PREDICTED: hypothetical protein [Mus musculus] ref XP_913564.1 PREDICTED: hypothetical protein [Mus musculus] ref XP_001086088.1 PREDICTED: similar to ribosomal protein S13 [Macaca mulatta] ref XP_001053043.1 PREDICTED: similar to ribosomal protein S13 [Rattus norvegicus] ref XP_001479810.1 PREDICTED: hypothetical protein [Mus musc	-0,584408147	-0,556984404	-0,890227194	-0,87143531	-0,727921729	1,7	DOWN
264	C606928.1	No match	-0,63011682	-0,560872979	-0,825421933	-0,852168191	-0,727769377	1,7	DOWN
265	C610100.1	No match	-0,43808925	-0,389809875	-1,017361655	-1,339640273	-0,727725453	1,7	DOWN

266	C607572.1	gb AAAX26584.2 SJCHGC03347 protein [Schistosoma japonicum]; ref XP_001398362.1 hypothetical protein An17g01330 [Aspergillus niger] emb CAK43029.1 unnamed protein product [Aspergillus niger]; emb CAB40376.1 adenosine kinase [Zea mays]; gb ABR25519.1 adenosine kinase 2 [Oryza sativa (indica cultivar-group)];	-0,709144491	-0,71735682	-0,737428071	-0,753154637	-0,727392446	1,7	DOWN
267	C602981.1	gb AAW25159.1 SJCHGC05901 protein [Schistosoma japonicum]; gb AAI58932.1 Unknown (protein for IMAGE:7534917) [Xenopus tropicalis]; ref NP_001016176.1 hypothetical protein LOC548930 [Xenopus tropicalis] emb CAJ82567.1 Novel protein containing CRAL/TRIO domain [Xenopus tropicalis]; ref NP_001026025.1 chromosome 20 open reading frame 121 [Gallus gallus] emb CAH65429.1 hypothetical protein [Gallus gallus];	-0,77982841	-0,87232879	-0,669439268	-0,636407509	-0,724633839	1,7	DOWN
268	C612311.1	gb AAAX25647.2 SJCHGC05300 protein [Schistosoma japonicum];	-0,589946851	-0,453624073	-0,859210248	-0,947659255	-0,72457855	1,7	DOWN
269	C605879.1	No match	-0,563219081	-0,647808062	-0,899035369	-0,801337709	-0,724572886	1,7	DOWN
270	C604622.1	No match	-0,53671302	-0,551942799	-0,896369227	-1,10999212	-0,724156013	1,7	DOWN
271	C600901.1	No match	-0,717943008	-0,779184578	-0,727807337	-0,528492703	-0,722875173	1,7	DOWN
272	C612459.1	gb AAAX30386.1 SJCHGC03195 protein [Schistosoma japonicum]; dbj BAD22612.1 Immt-Es [Meriones unguiculatus]; dbj BAD22611.1 Immt-Er [Meriones unguiculatus]; gb EDK98954.1 inner membrane protein, mitochondrial, isoform CRA_a [Mus musculus];	-0,837831303	-0,756620548	-0,684133218	-0,685752407	-0,721186478	1,6	DOWN
273	C602449.1	No match	-0,229812829	-0,41142566	-1,029156948	-1,062846999	-0,720291304	1,6	DOWN
274	C611219.1	gb AAA99798.1 Pro-His-rich protein;	-0,668769522	-0,842577957	-0,771773304	-0,582748417	-0,720271413	1,6	DOWN
275	C602251.1	No match	-0,617402544	-0,698537179	-0,74168698	-0,787856656	-0,72011208	1,6	DOWN
276	C605523.1	gb AAW27171.1 SJCHGC09312 protein [Schistosoma japonicum]; ref XP_001602921.1 PREDICTED: similar to retinoblastoma-binding protein 4 (rbbp4) [Nasonia vitripennis]; ref XP_973479.1 PREDICTED: similar to retinoblastoma-binding protein 4 (rbbp4) [Tribolium castaneum]; ref XP_624580.1 PREDICTED: similar to Chromatin assembly factor 1 subunit CG4236-PA [Apis mellifera];	-1,046637945	-0,931854087	-0,507724755	-0,364217745	-0,719789421	1,6	DOWN
277	C604536.1	No match	-0,664700553	-0,519232747	-0,926751985	-0,774272231	-0,719486392	1,6	DOWN
278	C606129.1	gb AAW26537.1 SJCHGC05331 protein [Schistosoma japonicum]; gb EDM02368.1 SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae), isoform CRA_c [Rattus norvegicus]; gb EDM02366.1 SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae), isoform CRA_a [Rattus norvegicus]; ref XP_214242.2 PREDICTED: similar to SGT1, suppressor of G2 allele of SKP1 [Rattus norvegicus] ref XP_001073449.1 PREDICTED: similar to SGT1, suppressor of G2 allele of SKP1 [Rattus norvegicus] sp B0BN85.1 SUGT1_RAT Suppressor of G2 allele of SKP1 homolog gb EDM02367.1 SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae), isoform CRA_b [Rattus norvegicus] gb AAI58725.1 Sugt1 protein [Rattus norvegicus];	-0,533231982	-0,489956777	-0,903135429	-0,948921984	-0,718183706	1,6	DOWN
279	C607076.1	gb AAAX25389.2 SJCHGC05691 protein [Schistosoma japonicum];	-0,632023231	-0,786881103	-0,64763071	-1,087498906	-0,717255907	1,6	DOWN
280	C602153.1	gb AAW25030.1 SJCHGC06604 protein [Schistosoma japonicum];	-0,818451603	-0,802970133	-0,631341733	-0,434762404	-0,717155933	1,6	DOWN

281	C610101.1	gb AAW26064.1 SJCHGC06192 protein [Schistosoma japonicum]; ref XP_001199439.1 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]; ref XP_396596.1 PREDICTED: similar to CG9769-PA [Apis mellifera]; ref XP_001659715.1 eukaryotic translation initiation factor 3f, eif3f [Aedes aegypti] gb ABF18280.1 eukaryotic translation initiation factor 3 subunit 5 epsilon-like protein [Aedes aegypti] gb EAT39069.1 eukaryotic translation initiation factor 3f, eif3f [Aedes aegypti];	-0,472645917	-0,522997741	-0,980822719	-0,910403175	-0,716700458	1,6	DOWN
282	C611337.1	No match	-0,393848196	-0,487555479	-1,012724212	-0,942770202	-0,715162841	1,6	DOWN
283	C610659.1	gb AAX26112.2 SJCHGC03668 protein [Schistosoma japonicum]; ref XP_001640751.1 predicted protein [Nematostella vectensis]; gb EDO48688.1 predicted protein [Nematostella vectensis]; ref XP_001371170.1 PREDICTED: hypothetical protein [Monodelphis domestica]; gb EDM04317.1 nucleolar protein family A, member 2 (predicted), isoform CRA_c [Rattus norvegicus] gb AAI62010.1 Nola2 protein [Rattus norvegicus];	-0,301634961	-0,574004839	-0,853735794	-1,111418888	-0,713870317	1,6	DOWN
284	C603770.1	No match	-0,636526561	-0,689663238	-0,74630028	-0,736926105	-0,713294672	1,6	DOWN
285	C609856.1	No match	-0,771705609	-0,801279554	-0,65334683	-0,63045739	-0,71252622	1,6	DOWN
286	C608869.1	No match	-0,626777704	-0,177817293	-0,796465925	-0,83348933	-0,711621815	1,6	DOWN
287	C611909.1	No match	-0,835891082	-0,86741178	-0,587226232	-0,434691322	-0,711558657	1,6	DOWN
288	C600917.1	No match	-0,613752472	-0,588554171	-0,906085449	-0,807651461	-0,710701967	1,6	DOWN
289	C603382.1	No match	-0,784835136	-0,790313735	-0,634209348	-0,572949443	-0,709522242	1,6	DOWN
290	C606958.1	No match	-0,845998879	-0,68577134	-0,659650677	-0,732741389	-0,709256365	1,6	DOWN
291	C610841.1	No match	-0,488958488	-0,555846712	-0,893163095	-0,859331403	-0,707589058	1,6	DOWN
292	C612451.1	ref NP_001085639.1 MGC82703 protein [Xenopus laevis] sp Q6GPP7.1 TM209_XENLA Transmembrane protein 209 gb AAH73065.1 MGC82703 protein [Xenopus laevis]; ref XP_682843.3 PREDICTED: similar to transmembrane protein 209 [Danio rerio]; ref NP_001086561.1 MGC83764 protein [Xenopus laevis] gb AAH76809.1 MGC83764 protein [Xenopus laevis]; ref XP_780705.1 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus] ref XP_001193783.1 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus];	-0,765592677	-0,658113916	-0,645838216	-0,755321212	-0,706717564	1,6	DOWN
293	C608370.1	gb AAW26144.1 SJCHGC02223 protein [Schistosoma japonicum]; gb AAF73250.1 AF153977_1 eukaryotic translation initiation factor 5 [Schistosoma mansoni]; gb EDV24103.1 hypothetical protein TRIADDRAFT_50382 [Trichoplax adhaerens]; ref NP_955885.1 eukaryotic translation initiation factor 5 [Danio rerio] gb AAH49502.1 Eukaryotic translation initiation factor 5 [Danio rerio] gb AAH66614.1 Eukaryotic translation initiation factor 5 [Danio rerio] gb AAS92648.1 eukaryotic translation initiation factor 5 [Danio rerio] emb CAI21349.1 novel protein (zgc:77026) [Danio rerio];	-0,308841383	-0,338395654	-1,073657356	-1,086691705	-0,706026505	1,6	DOWN

294	C605237.1	sp Q86QS6 AN32_SCHMA Acidic leucine-rich nuclear phosphoprotein 32-related protein (ANP32/acidic nuclear phosphoprotein-like protein) gb AAO21365.1 leucine-rich protein [Schistosoma mansoni]; gb AAW25017.1 SJCHGC00366 protein [Schistosoma japonicum] gb ABA40386.2 SJCHGC02024 protein [Schistosoma japonicum]; gb AAW24968.1 unknown [Schistosoma japonicum]; gb AAW24920.1 unknown [Schistosoma japonicum];	-0,508863356	-0,536249204	-0,968210492	-0,874930088	-0,705589646	1,6	DOWN
295	C603706.1	gb ACE06846.1 unknown [Schistosoma japonicum]; gb ABG21812.1 60S ribosomal protein L15-like protein [Schistosoma mansoni]; gb AAP06105.1 similar to GenBank Accession Number X78167 ribosomal protein L15 in Rattus norvegicus [Schistosoma japonicum]; ref XP_932648.1 PREDICTED: hypothetical protein isoform 1 [Homo sapiens] ref XP_949197.1 PREDICTED: hypothetical protein isoform 4 [Homo sapiens] ref XP_001725140.1 PREDICTED: hypothetical protein [Homo sapiens];	-0,873721955	-0,871843167	-0,537203866	-0,310260326	-0,704523517	1,6	DOWN
296	C606337.1	gb AAW27674.1 SJCHGC04249 protein [Schistosoma japonicum]; gb ABW23219.1 ribosomal protein rpl13a [Eurythoe complanata]; gb ABX75375.1 60S ribosomal protein L13A [Lycosa singoriensis]; gb ABZ04228.1 ribosomal protein rpl13a [Lineus viridis];	-0,324751489	-0,425272922	-1,007997354	-0,983419993	-0,704346458	1,6	DOWN
297	C611150.1	No match	-0,522660654	-0,360421018	-0,884171294	-0,90567964	-0,703415974	1,6	DOWN
298	C608712.1	gb AAX26800.2 SJCHGC06570 protein [Schistosoma japonicum];	-0,743445726	-0,780182656	-0,663313708	-0,639127407	-0,703379717	1,6	DOWN
299	C609829.1	ref XP_855370.1 PREDICTED: similar to Delta-aminolevulinic acid dehydratase (Porphobilinogen synthase) (ALADH) [Canis familiaris]; ref XP_001101487.1 PREDICTED: similar to delta-aminolevulinic acid dehydratase isoform a isoform 2 [Macaca mulatta]; ref XP_001101392.1 PREDICTED: similar to delta-aminolevulinic acid dehydratase isoform a isoform 1 [Macaca mulatta]; ref XP_001101576.1 PREDICTED: similar to delta-aminolevulinic acid dehydratase isoform b isoform 3 [Macaca mulatta] dbj BAE02020.1 unnamed protein product [Macaca fascicularis];	-0,800016276	-0,932101987	-0,606436244	-0,18524033	-0,70322626	1,6	DOWN
300	C602959.1	No match	-0,463931324	-0,543286672	-0,862108541	-0,917536963	-0,702697607	1,6	DOWN
301	C611397.1	gb AAX27308.2 SJCHGC04233 protein [Schistosoma japonicum]; ref XP_968299.1 PREDICTED: similar to N-glycosylase/DNA lyase [Tribolium castaneum]; ref XP_001619921.1 hypothetical protein NEMVEDRAFT_v1g149802 [Nematostella vectensis]; gb EDO27821.1 predicted protein [Nematostella vectensis]; ref XP_001375382.1 PREDICTED: similar to 8-oxoguanine DNA glycosylase [Monodelphis domestica];	-0,626500245	-0,898273118	-0,686444174	-0,718379777	-0,702411976	1,6	DOWN
302	C601498.1	gb AAW26397.1 SJCHGC09094 protein [Schistosoma japonicum];	-0,723032251	-0,620019037	-0,72723921	-0,678789803	-0,700911027	1,6	DOWN
303	C609300.1	No match	-0,596499744	-0,683849615	-0,803881273	-0,716572524	-0,70021107	1,6	DOWN
304	C610858.1	No match	-0,593914772	-0,645075295	-0,849540735	-0,749499218	-0,697287257	1,6	DOWN

305	C603255.1	gb AAW24485.1 SJCHGC06694 protein [Schistosoma japonicum]; gb EDV21550.1 hypothetical protein TRIADDRAFT_59660 [Trichoplax adhaerens]; ref NP_997968.1 eukaryotic translation initiation factor 4E binding protein 2 [Danio rerio] gb AAH66546.1 Eukaryotic translation initiation factor 4E binding protein 2 [Danio rerio]; ref NP_001028241.1 eukaryotic translation initiation factor 4E binding protein 2 [Rattus norvegicus] gb AAI00639.1 Eukaryotic translation initiation factor 4E binding protein 2 [Rattus norvegicus] gb EDL93024.1 eukaryotic translation initiation factor 4E binding protein 2, isoform CRA_b [Rattus norvegicus];	-0,683957941	-0,62570637	-0,72605246	-0,706759933	-0,695358937	1,6	DOWN
306	C608005.1	gb EDV20694.1 hypothetical protein TRIADDRAFT_31577 [Trichoplax adhaerens]; gb AAG60622.1 AF294916_1 phosphoinositide-dependent protein kinase I [Aplysia californica]; emb CAG04372.1 unnamed protein product [Tetraodon nigroviridis]; ref XP_786576.2 PREDICTED: similar to phosphoinositide dependent kinase-1 [Strongylocentrotus purpuratus] ref XP_001189048.1 PREDICTED: similar to phosphoinositide dependent kinase-1 [Strongylocentrotus purpuratus];	-0,851657231	-1,219246167	-0,535862834	-0,479986656	-0,693760033	1,6	DOWN
307	C606376.1	gb ABQ15152.1 nuclear coactivator 1 [Schistosoma mansoni]; emb CAI59265.1 ski interacting protein [Echinococcus multilocularis]; ref NP_001017145.1 SKI interacting protein [Xenopus tropicalis] emb CAJ83628.1 SKI interacting protein [Xenopus tropicalis]; ref NP_001002864.1 SNW domain containing 1 [Danio rerio] gb AAT68034.1 ski-interacting protein [Danio rerio];	-0,652583479	-0,730036457	-0,735290866	-0,604064522	-0,691309968	1,6	DOWN
308	C605630.1	gb AAX30712.2 SJCHGC07106 protein [Schistosoma japonicum];	-0,650478272	-0,790614323	-0,702215296	-0,67870379	-0,690459543	1,6	DOWN
309	C602841.1	No match	-0,397170657	-0,489879899	-0,950741548	-0,890614415	-0,690247157	1,6	DOWN
310	C608753.1	gb AAX26899.2 SJCHGC03553 protein [Schistosoma japonicum];	-0,636756755	-0,510984288	-0,984669572	-0,743551366	-0,690154061	1,6	DOWN
311	C602787.1	tpe CAJ00244.1 TPA: endonuclease-reverse transcriptase [Schistosoma mansoni];	-0,576099168	-0,542763447	-0,836036942	-0,803681975	-0,689890572	1,6	DOWN
312	C607827.1	gb AAW26207.1 SJCHGC02796 protein [Schistosoma japonicum];	-0,931042224	-0,759750019	-0,619546993	-0,514956992	-0,689648506	1,6	DOWN
313	C603861.1	No match	-0,577624372	-0,694674628	-0,870573443	-0,680680273	-0,687677451	1,6	DOWN
314	C603772.1	ref XP_624814.2 PREDICTED: similar to CG31717-PA, partial [Apis mellifera];	-0,807021369	-0,594576364	-0,780626999	-0,594035142	-0,687601682	1,6	DOWN
315	C606086.1	No match	-0,270300967	-0,797484976	-0,577661962	-1,089132358	-0,687573469	1,6	DOWN
316	C610127.1	No match	-0,651620426	-0,589177641	-0,733809493	-0,718372332	-0,684996379	1,6	DOWN
317	C606115.1	gb AAW24653.1 SJCHGC09419 protein [Schistosoma japonicum];	-0,86178136	-0,774099179	-0,576175843	-0,595717809	-0,684908494	1,6	DOWN
318	C605917.1	No match	-0,958684866	-0,75972997	-0,564674083	-0,605796568	-0,682763269	1,6	DOWN
319	C608120.1	gb AAX24759.2 SJCHGC04711 protein [Schistosoma japonicum];	-0,727790806	-0,711304548	-0,626138449	-0,635233488	-0,673269018	1,6	DOWN
320	C607128.1	ref XP_001599458.1 PREDICTED: similar to CG32156-PC [Nasonia vitripennis];	-0,445589965	-0,513875141	-0,92937341	-0,831017604	-0,672446373	1,6	DOWN
321	C601174.1	No match	-0,534847548	-0,708149275	-0,743034083	-0,635169316	-0,671659296	1,6	DOWN
322	C612014.1	gb AAW27065.1 SJCHGC05775 protein [Schistosoma japonicum];	-0,936998812	-0,762502308	-0,57584278	-0,313020462	-0,669172544	1,6	DOWN
323	C611710.1	No match	-0,79145199	-0,750096664	-0,534436704	-0,587371071	-0,668733868	1,6	DOWN

324	C608609.1	gb AAP06199.1 similar to porin 31HM in human, skeletal muscle membranes [Schistosoma japonicum]; gb AAI35546.1 Vdac1 protein [Xenopus tropicalis]; ref NP_001016492.1 voltage-dependent anion channel 1 [Xenopus tropicalis] emb CAJ83146.1 voltage-dependent anion channel 1 [Xenopus tropicalis] gb AAI27349.1 Voltage-dependent anion channel 1 [Xenopus tropicalis]; ref XP_780266.1 PREDICTED: similar to voltage-dependent anion channel 2 isoform 1 [Strongylocentrotus purpuratus] ref XP_001177783.1 PREDICTED: similar to voltage-dependent anion channel 2 [Strongylocentrotus purpuratus];	-0,633414051	-0,635702992	-0,813047313	-0,701410458	-0,668556725	1,6	DOWN
325	C600948.1	gb AAP06073.1 similar to NM_022756 hypothetical protein FLJ11730 in Homo sapiens; hypothetical protein FLJ11730 in Homo sapiens [Schistosoma japonicum]; gb AAW25861.1 unknown [Schistosoma japonicum]; gb AAW25871.1 SJCHGC00146 protein [Schistosoma japonicum]; gb AAW25057.1 unknown [Schistosoma japonicum];	-0,874436554	-0,778277641	-0,493159849	-0,558794983	-0,668536312	1,6	DOWN
326	C606432.1	gb AAW26531.1 unknown [Schistosoma japonicum]; gb AAW25871.1 SJCHGC00146 protein [Schistosoma japonicum]; gb AAW25213.1 unknown [Schistosoma japonicum]; gb AAW27485.1 SJCHGC01610 protein [Schistosoma japonicum];	-0,376790577	-0,47313811	-0,87518738	-0,862179311	-0,667658711	1,6	DOWN
327	C603837.1	No match	-0,594139763	-0,616601024	-0,883348932	-0,714139527	-0,665370276	1,6	DOWN
328	C609703.1	gb AAW25973.1 SJCHGC09415 protein [Schistosoma japonicum]; gb EDX15624.1 GD15199 [Drosophila simulans]; gb EDL84806.1 within bgn homolog (Drosophila) (predicted), isoform CRA_a [Rattus norvegicus]; gb AAI61580.1 Hypothetical protein LOC549028 [Xenopus tropicalis];	-0,604736865	-0,575415149	-0,725951027	-0,761558589	-0,665343946	1,6	DOWN
329	C607489.1	gb AAW26907.1 SJCHGC09493 protein [Schistosoma japonicum]; gb AAV97787.1 inhibitor of apoptosis protein [Schistosoma japonicum]; gb ABZ82033.1 inhibitor of apoptosis protein [Clonorchis sinensis];	-0,573886758	-0,641180279	-0,759848251	-0,685379409	-0,663279844	1,6	DOWN
330	C607349.1	No match	-0,078431333	-0,419575431	-0,905719172	-0,918796108	-0,662647302	1,6	DOWN
331	C606245.1	No match	-0,320147211	-0,524349265	-0,818836219	-0,797683178	-0,661016222	1,6	DOWN
332	C607552.1	ref XP_001812886.1 PREDICTED: similar to gmp synthase [Tribolium castaneum]; ref XP_393336.2 PREDICTED: similar to GMP synthase [glutamine-hydrolyzing] (Glutamine amidotransferase) (GMP synthetase) [Apis mellifera]; ref NP_001006556.1 guanine monophosphate synthetase [Gallus gallus] emb CAG32582.1 hypothetical protein [Gallus gallus]; ref XP_001512299.1 PREDICTED: similar to guanosine 5-monophosphate synthetase, partial [Ornithorhynchus anatinus];	-0,815821227	-0,788558387	-0,532933398	-0,529498142	-0,660745893	1,6	DOWN
333	C611310.1	No match	-0,724667236	-0,754664454	-0,430468702	-0,596770469	-0,660718853	1,6	DOWN
334	C607884.1	gb AAW26173.1 SJCHGC06268 protein [Schistosoma japonicum]; gb ABA40291.1 SJCHGC03923 protein [Schistosoma japonicum];	-0,709086505	-0,704758264	-0,616140603	-0,555201721	-0,660449434	1,6	DOWN
335	C601632.1	No match	-0,536789526	-0,47385286	-0,829994043	-0,781934968	-0,659362247	1,6	DOWN

336	C610640.1	ref XP_001178408.1 PREDICTED: similar to translation initiation factor 2 gamma subunit [Strongylocentrotus purpuratus]; ref XP_787081.2 PREDICTED: similar to translation initiation factor 2 gamma subunit [Strongylocentrotus purpuratus]; ref XP_001607783.1 PREDICTED: similar to eukaryotic translation initiation factor 2 gamma [Nasonia vitripennis]; emb CAG29663.1 translation initiation factor 2 gamma subunit [Lithobius forficatus]; emb CAG29668.1 translation initiation factor 2 gamma subunit [Lepismachilis sp. VK-2004];	-0.64121094	-0.674713459	-0.715847697	-0.643179358	-0.658946409	1,6	DOWN
337	C610615.1	gb AAW26828.1 SJCHGC09446 protein [Schistosoma japonicum];	-0.73328078	-0.766812953	-0.584105742	-0.578510221	-0.658693261	1,6	DOWN
338	C604546.1	No match	-0.594511405	-0.46745921	-0.752253302	-0.722484381	-0.658497893	1,6	DOWN
339	C612582.1	gb AAW25491.1 unknown [Schistosoma japonicum]; gb ABN14902.1 60S ribosomal protein L10a [Taenia asiatica]; ref XP_001891868.1 60S ribosomal protein L10a [Brugia malayi]; gb EDP39318.1 60S ribosomal protein L10a, putative [Brugia malayi]; ref NP_001120029.1 hypothetical protein LOC100144995 [Xenopus tropicalis] gb AAI58336.1 Unknown (protein for MGC:185542) [Xenopus tropicalis];	-0.573944492	-0.471048957	-0.742388621	-0.901152193	-0.658166557	1,6	DOWN
340	C609005.1	No match	-0.632123236	-0.731908617	-0.664961468	-0.649981672	-0.65747157	1,6	DOWN
341	C605552.1	gb AAX27943.2 SJCHGC05670 protein [Schistosoma japonicum];	-0.387863948	-0.606964198	-0.706323359	-0.793814357	-0.656643779	1,6	DOWN
342	C611119.1	gb AAX24328.2 SJCHGC05542 protein [Schistosoma japonicum];	-0.633093413	-0.736771771	-0.680076905	-0.626601514	-0.656585159	1,6	DOWN
343	C605103.1	gb AAW25211.1 SJCHGC02533 protein [Schistosoma japonicum]; ref XP_001599894.1 PREDICTED: similar to past-1 [Nasonia vitripennis]; ref XP_001674306.1 Hypothetical protein CBG18887 [Caenorhabditis briggsae AF16] emb CAP36229.1 C. briggsae CBR-RME-1 protein [Caenorhabditis briggsae]; ref XP_396463.2 PREDICTED: similar to Putative Achaete Scute Target 1 CG6148-PB, isoform B [Apis mellifera];	-1.070189129	-0.882764321	-0.429741143	-0.333911241	-0.656252732	1,6	DOWN
344	C610123.1	gb AAW27501.1 SJCHGC01083 protein [Schistosoma japonicum]; gb AAR16282.1 capping protein (actin filament) muscle Z-line, alpha 2 [Takifugu rubripes]; sp P25229.1 CAZA1_XENLA F-actin-capping protein subunit alpha 1 (Actin-binding protein chain A) (ABP-A) emb CAA35948.1 nuclear actin-binding protein chain a [Xenopus laevis] prf 1602248A nuclear actin binding protein; gb ABJ08879.1 capping protein (actin filament) muscle Z-line, alpha 2 [Ginglymostoma cirratum];	-0.519477361	-0.502649032	-0.797875545	-0.792212763	-0.655845062	1,6	DOWN
345	C611942.1	No match	-0.961287005	-0.239409836	-0.697601298	-0.611561422	-0.65458136	1,6	DOWN
346	C604799.1	No match	-0.699128257	-0.654301788	-0.259975556	-0.653695684	-0.653998736	1,6	DOWN
347	C601080.1	gb AAW26780.1 SJCHGC02748 protein [Schistosoma japonicum];	-0.604572945	-0.801730841	-0.70026364	-0.512840558	-0.652418293	1,6	DOWN
348	C600648.1	gb AAX30655.1 SJCHGC06537 protein [Schistosoma japonicum]; gb ABW23211.1 ribosomal protein rps21 [Eurythoe complanata]; gb ABK32077.1 ribosomal protein S21 [Branchiostoma belcheri]; sp Q86CT3 RS21_BRABE 40S ribosomal protein S21 gb AAP21828.1 ribosomal protein S21 [Branchiostoma belcheri tsingtaunese];	-0.167584648	-0.274040117	-1.100838128	-1.030572641	-0.652306379	1,6	DOWN
349	C612121.1	No match	-0.616324254	-0.643962358	-0.708755568	-0.660063734	-0.652013046	1,6	DOWN

350	C607061.1	gb AAX26988.2 SJCHGC08857 protein [Schistosoma japonicum];	-0,795869646	-0,73502389	-0,506261497	-0,568047839	-0,651535865	1,6	DOWN
351	C605483.1	No match	-0,46217891	-0,643581582	-0,712506892	-0,658808358	-0,65119497	1,6	DOWN
352	C603801.1	No match	-0,809466094	-0,883565048	-0,463774844	-0,492113471	-0,650789783	1,6	DOWN
353	C611076.1	No match	-0,663857314	-0,641417711	-0,658740195	-0,632280032	-0,650078953	1,6	DOWN
354	C607705.1	gb AAX25542.2 SJCHGC07903 protein [Schistosoma japonicum];	-0,643353947	-0,656718279	-0,614818761	-0,664250547	-0,650036113	1,6	DOWN
355	C611926.1	No match	-0,81829595	-0,7867082	-0,462181312	-0,511247793	-0,648977997	1,6	DOWN
356	C610202.1	ref XP_001497523.2 PREDICTED: similar to serine/threonine kinase receptor associated protein [Equus caballus]; ref XP_001159216.1 PREDICTED: serine/threonine kinase receptor associated protein [Pan troglodytes]; ref XP_001159067.1 PREDICTED: serine/threonine kinase receptor associated protein [Pan troglodytes]; ref XP_001159167.1 PREDICTED: serine/threonine kinase receptor associated protein [Pan troglodytes];	-0,596262182	-0,700574508	-0,526111483	-0,843607528	-0,648418345	1,6	DOWN
357	C602929.1	gb AAW25379.1 SJCHGC09123 protein [Schistosoma japonicum]; gb AAW26667.1 SJCHGC09411 protein [Schistosoma japonicum];	-0,398687602	-0,446501401	-0,878469137	-0,850045112	-0,648273257	1,6	DOWN
358	C612081.1	ref XP_784978.2 PREDICTED: similar to mKIAA1219 protein [Strongylocentrotus purpuratus] ref XP_001179040.1 PREDICTED: similar to mKIAA1219 protein [Strongylocentrotus purpuratus]; gb EDW71187.1 GJ16196 [Drosophila virilis]; ref NP_001096938.1 CG34408 CG34408-PB, isoform B [Drosophila melanogaster] gb AAN09629.2 CG34408-PB, isoform B [Drosophila melanogaster]; gb EDX16334.1 GD24698 [Drosophila simulans];	-0,49658552	-0,715435393	-0,669441844	-0,625632615	-0,64753723	1,6	DOWN
359	C600628.1	gb AAF98445.1 Sj-Ts1 [Schistosoma japonicum]; gb ACE06845.1 unknown [Schistosoma japonicum];	-0,060440999	-0,223966501	-1,065902177	-1,093566502	-0,644934339	1,6	DOWN
360	C612476.1	gb ABC69927.1 STIP [Tetraodon nigroviridis]; emb CAG08558.1 unnamed protein product [Tetraodon nigroviridis]; ref NP_001073674.1 Sip1/TFIP11 interacting protein [Apis mellifera] gb ABC69933.1 STIP [Apis mellifera]; gb AAH17682.1 Tuftelin interacting protein 11 [Mus musculus];	-0,783898874	-0,727719457	-0,5613534	-0,272788287	-0,644536429	1,6	DOWN
361	C609825.1	gb ABG21823.1 ribosomal protein L4-like protein [Schistosoma mansoni]; gb AAW25794.1 SJCHGC06667 protein [Schistosoma japonicum]; gb ABN14894.1 ribosomal protein L4 [Taenia asiatica]; gb AAH63811.1 Ribosomal protein L4 [Rattus norvegicus] gb AAH81801.1 Ribosomal protein L4 [Rattus norvegicus] gb EDL95788.1 rCG58071, isoform CRA_a [Rattus norvegicus];	-0,255174852	-0,454944396	-0,833661141	-0,872183083	-0,644302769	1,6	DOWN
362	C610769.1	No match	-0,51305626	-0,544792946	-0,741394389	-0,779314114	-0,643093668	1,6	DOWN
363	C611067.1	No match	-0,714481162	-0,505978253	-0,638790213	-0,64697773	-0,642883972	1,6	DOWN
364	C707411.1	gb AAW26906.1 SJCHGC00905 protein [Schistosoma japonicum]; ref NP_001080498.1 excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) [Xenopus laevis] gb AAH43824.1 Ercc1-prov protein [Xenopus laevis]; gb AAW27225.1 SJCHGC04667 protein [Schistosoma japonicum]; ref NP_001107393.1 hypothetical protein LOC100135224 [Xenopus tropicalis] gb AAI57332.1 Unknown (protein for MGC:147821) [Xenopus tropicalis];	-0,641898072	-0,723440612	-0,610612014	-0,643021421	-0,642459747	1,6	DOWN

365	C611587.1	dbj BAB28672.1 unnamed protein product [Mus musculus]; ref NP_219486.1 hypothetical protein MGC9084 [Homo sapiens] sp O95568.1 CA156_HUMAN UPF0558 protein C1orf156 (Arsenic transactivated protein 2) (AsTP2) emb CAA23019.1 hypothetical protein [Homo sapiens] gb AAH08679.1 C1orf156 protein [Homo sapiens] emb CAG29326.1 MGC9084 [Homo sapiens] gb AAU95377.1 arsenic-transactivated protein 2 [Homo sapiens] emb CAI19361.1 chromosome 1 open reading frame 156 [Homo sapiens] gb EAW90861.1 chromosome 1 open reading frame 156, isoform CRA_a [Homo sapiens] gb EAW90862.1 chromosome 1 open reading frame 156, isoform CRA_a [Homo sapiens] dbj BAG36632.1 unnamed protein product [Homo sapiens]; ref XP_524959.1 PREDICTED: hypothetical protein MGC9084 isoform 3 [Pan troglodytes] ref XP_001139157.1 PREDICTED: hypothetical protein MGC9084 isoform 1 [Pan troglodytes] ref XP_001139315.1 PREDICTED: hypothetical protein MGC9084 isoform 2 [Pan troglodytes]; ref NP_001020839.1 hypothetical protein LOC304928 [Rattus norvegicus] sp Q4KM84.1 CA156_RAT UPF0558 protein C1orf156 homolog gb AAH98702.1 Similar to 2810422020Rik prot	-0,365895892	-0,47407021	-0,809629915	-0,898971932	-0,641850063	1,6	DOWN
366	C611810.1	No match	-0,494375929	-0,561834354	-0,721821452	-0,835776927	-0,641827903	1,6	DOWN
367	C610317.1	No match	-0,558599411	-0,60147784	-0,678622273	-0,733453271	-0,640050057	1,6	DOWN
368	C607250.1	No match	-0,496118432	-0,502237056	-0,777675808	-0,812976191	-0,639956432	1,6	DOWN
369	C603654.1	No match	-0,569878427	-0,484190584	-0,764699986	-0,707476372	-0,6386774	1,6	DOWN
370	C605489.1	gb ACE06931.1 unknown [Schistosoma japonicum]; gb AAP06215.1 hypothetical protein [Schistosoma japonicum];	-0,699429661	-0,670240853	-0,604693759	-0,470043375	-0,637467306	1,6	DOWN
371	C603825.1	gb AAW24827.1 SJCHGC09339 protein [Schistosoma japonicum];	-0,600926878	-0,550854045	-0,672889306	-0,766586385	-0,636908092	1,6	DOWN
372	C606983.1	gb AAD24794.1 AF120929_1 phosphoenolpyruvate carboxykinase [Schistosoma mansoni]; gb AAW25103.1 SJCHGC06900 protein [Schistosoma japonicum]; emb CAJ28913.1 phosphoenolpyruvate carboxykinase [Crassostrea gigas]; ref NP_001021590.1 R11A5.4d [Caenorhabditis elegans]; emb CAF31483.1 C. elegans protein R11A5.4d, confirmed by transcript evidence [Caenorhabditis elegans];	-0,351091528	-0,440657555	-0,831364788	-0,893474242	-0,636011172	1,6	DOWN
373	C606441.1	gb AAW25715.2 SJCHGC04764 protein [Schistosoma japonicum]; gb EDW57502.1 GJ18122 [Drosophila virilis]; gb EDW13455.1 GI18216 [Drosophila mojavensis]; gb EDW03178.1 GH11094 [Drosophila grimshawi];	-0,895186169	-0,882310797	-0,388923877	-0,294027742	-0,635617337	1,6	DOWN
374	C605169.1	No match	-0,26359896	-0,425037562	-0,902431538	-0,845815725	-0,635426644	1,6	DOWN
375	C611231.1	No match	-0,669655067	-0,795493051	-0,44705371	-0,600867179	-0,635261123	1,6	DOWN
376	C609409.1	No match	-0,41337467	-0,480824414	-0,957901976	-0,787326881	-0,634075648	1,6	DOWN
377	C611476.1	gb ABG78546.1 forkhead transcription factor [Schistosoma mansoni];	-0,632585707	-0,627285405	-0,665330406	-0,63523492	-0,633910314	1,6	DOWN

378	C612653.1	gb AAW24976.1 SJCHGC08993 protein [Schistosoma japonicum]; ref XP_972067.1 PREDICTED: similar to Protein C20orf11 (Two hybrid associated protein 1 with RanBPM) (Twa1) [Tribolium castaneum]; ref XP_001600429.1 PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis]; ref XP_392965.2 PREDICTED: similar to BWK-1 isoform 1 [Apis mellifera] ref XP_623151.1 PREDICTED: similar to BWK-1 isoform 2 [Apis mellifera];	-0,551944485	-0,381848367	-0,950221559	-0,713386319	-0,632665402	1,6	DOWN
379	C601526.1	gb AAW25382.1 SJCHGC03376 protein [Schistosoma japonicum]; ref NP_001084550.1 hypothetical protein LOC414499 [Xenopus laevis] gb AAH68951.1 MGC83218 protein [Xenopus laevis]; ref NP_001007290.1 ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) [Danio rerio] gb AAH85542.1 Ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) [Danio rerio]; gb AAH67177.1 Rpia protein [Danio rerio];	-0,586304257	-0,550036021	-0,677975668	-0,732893745	-0,632139963	1,5	DOWN
380	C606453.1	gb ABA40782.1 SJCHGC02235 protein [Schistosoma japonicum]; gb AAX31017.1 SJCHGC09722 protein [Schistosoma japonicum];	-0,655068825	-0,597432542	-0,609560961	-0,654263601	-0,631912281	1,5	DOWN
381	C609670.1	No match	-0,830752613	-1,119959115	-0,432793736	-0,194690998	-0,631773175	1,5	DOWN
382	C606327.1	gb ABN14897.1 mitochondrial ribosomal protein L15 [Taenia asiatica]; gb AAX25668.2 SJCHGC06954 protein [Schistosoma japonicum]; gb EDV52517.1 GG13310 [Drosophila erecta]; gb EDX11241.1 GD12186 [Drosophila simulans];	-0,729354313	-0,768026379	-0,500860577	-0,532717218	-0,631035766	1,5	DOWN
383	C607294.1	No match	-0,700750699	-0,853038241	-0,560816071	-0,544355967	-0,630783385	1,5	DOWN
384	C611746.1	gb AAX25413.2 SJCHGC05296 protein [Schistosoma japonicum]; gb AAW27491.1 SJCHGC07173 protein [Schistosoma japonicum];	0,075829924	-0,27690037	-1,041861604	-0,984353649	-0,63062701	1,5	DOWN
385	C602194.1	No match	-0,486610323	-0,52438707	-0,79546358	-0,73513202	-0,629759545	1,5	DOWN
386	C604764.1	gb AAW27023.1 SJCHGC06275 protein [Schistosoma japonicum]; gb AAX30014.1 Ubc9 [Schistosoma mansoni] gb AAX30015.1 Ubc9 [Schistosoma mansoni]; ref NP_001040407.1 ubiquitin-conjugating enzyme E2 [Bombyx mori] gb ABF51329.1 ubiquitin-conjugating enzyme E2 isoform 1 [Bombyx mori]; ref XP_001640489.1 predicted protein [Nematostella vectensis] gb EDO48426.1 predicted protein [Nematostella vectensis];	-0,353660369	-0,408217564	-0,849990515	-0,857817803	-0,62910404	1,5	DOWN
387	C602079.1	gb AAX24641.2 SJCHGC04887 protein [Schistosoma japonicum];	-0,433515551	-0,56958375	-0,718074665	-0,687802087	-0,628692919	1,5	DOWN
388	C603705.1	gb AAW26476.1 SJCHGC01111 protein [Schistosoma japonicum]; gb AAX24756.2 SJCHGC07014 protein [Schistosoma japonicum]; ref NP_694818.2 eukaryotic translation initiation factor 2C, 2 [Mus musculus] dbj BAC15767.1 Piwi/Argonaute family protein meiF2C2 [Mus musculus]; sp Q8CJG0 2C2_MOUSE Eukaryotic translation initiation factor 2C 2 (eIF2C 2) (eIF-2C 2) (Argonaute-2) (Slicer protein) (Piwi/argonaute family protein meiF2C2);	-0,429868748	-0,525439575	-0,729949127	-0,810828813	-0,627694351	1,5	DOWN
389	C606335.1	tpe CAJ00252.1 TPA: gag-pol polyprotein [Schistosoma mansoni];	-0,584702823	-0,501043739	-0,668468778	-0,697702867	-0,626585801	1,5	DOWN
390	C609801.1	gb AAW25936.1 SJCHGC05387 protein [Schistosoma japonicum];	-0,627373244	-0,624148854	-0,654393351	-0,603214794	-0,625761049	1,5	DOWN
391	C606909.1	No match	-0,293359501	-0,427218902	-0,822712418	-0,927728819	-0,62496566	1,5	DOWN

392	C610879.1	gb AAX25661.2 SJCHGC04404 protein [Schistosoma japonicum];	-1,534908831	-0,96565788	-0,281636732	-0,267473006	-0,623647306	1,5	DOWN
393	C610625.1	gb AAW25508.1 SJCHGC05689 protein [Schistosoma japonicum]; gb AAH84616.1 LOC495283 protein [Xenopus laevis]; emb CAF94336.1 unnamed protein product [Tetraodon nigroviridis]; ref NP_001006926.1 aminolevulinate, delta-, synthase 2 [Xenopus tropicalis] gb AAH76921.1 Aminolevulinate, delta-, synthase 2 [Xenopus tropicalis];	-0,608739319	-0,596021794	-0,667648924	-0,636878409	-0,622808864	1,5	DOWN
394	C606450.1	gb AAC62254.1 lysophospholipase homolog [Schistosoma mansoni]; gb ACE06918.1 unknown [Schistosoma japonicum]; gb AAD52700.1 AF091539_1 lysophospholipase [Schistosoma japonicum]; ref NP_001085785.1 MGC80756 protein [Xenopus laevis] gb AAH73342.1 MGC80756 protein [Xenopus laevis];	-0,589648598	-0,560578205	-0,698077507	-0,655923056	-0,622785827	1,5	DOWN
395	C607608.1	ref XP_001625612.1 predicted protein [Nematostella vectensis] gb EDO33512.1 predicted protein [Nematostella vectensis]; ref XP_623551.1 PREDICTED: similar to Recombination repair protein 1 (DNA-(apurinic or apyrimidinic site) lyase) [Apis mellifera]; ref ZP_02431429.1 hypothetical protein CLOSCI_01649 [Clostridium scindens ATCC 35704] gb EDS07306.1 hypothetical protein CLOSCI_01649 [Clostridium scindens ATCC 35704]; ref ZP_02272247.1 Exodeoxyribonuclease III [Fusobacterium nucleatum subsp. polymorphum ATCC 10953] gb EDK87855.1 exodeoxyribonuclease III [Fusobacterium nucleatum subsp. polymorphum ATCC 10953];	-0,550222463	-0,403879208	-0,779403384	-0,694505239	-0,622363851	1,5	DOWN
396	C602071.1	ref NP_998628.1 eukaryotic translation initiation factor 3, subunit C [Danio rerio] gb AAH57465.1 Eukaryotic translation initiation factor 3, subunit C [Danio rerio]; ref XP_623580.2 PREDICTED: similar to eIF3-S8 CG4954-PA [Apis mellifera]; ref XP_001807880.1 PREDICTED: similar to translation initiation factor 3, subunit S8, putative [Tribolium castaneum]; emb CAG07597.1 unnamed protein product [Tetraodon nigroviridis];	-0,71026866	-0,687807106	-0,553143181	-0,413168504	-0,620475144	1,5	DOWN
397	C601311.1	No match	-0,464074408	-0,483171632	-0,751961724	-0,778535408	-0,617566678	1,5	DOWN
398	C610638.1	No match	-0,677673307	-0,598892265	-0,630580394	-0,520729682	-0,61473633	1,5	DOWN
399	C611201.1	No match	-0,947065563	-1,03817599	-0,277276058	-0,281318559	-0,614192061	1,5	DOWN
400	C612132.1	No match	-0,30489902	-1,072573752	-0,52015886	-0,707872026	-0,614015443	1,5	DOWN
401	C703445.1	gb AAO17782.1 wnt5-like protein [Girardia tigrina]; ref NP_001006767.1 wingless-type MMTV integration site family, member 5B [Xenopus tropicalis] gb AAH75560.1 Wingless-type MMTV integration site family, member 5B [Xenopus tropicalis] emb CAJ83472.1 wingless-type MMTV integration site family, member 5B [Xenopus tropicalis]; ref NP_001080150.1 C. elegans WNT family member precursor (40.4 kD) (wnt-2) [Xenopus laevis] gb AAH56128.1 Wnt-2-prov protein [Xenopus laevis]; sp P33945 WNT5C_XENLA Protein Wnt-5c precursor (XWnt-5c) emb CAA51916.1 Xwnt-5c [Xenopus laevis];	-0,556005618	-0,363844036	-0,851619916	-0,671087658	-0,613546638	1,5	DOWN

402	C601194.1	dbj BAF83282.1 unnamed protein product [Homo sapiens]; ref XP_001116610.1 PREDICTED: similar to alpha isoform of regulatory subunit A, protein phosphatase 2 isoform 10 [Macaca mulatta] ref XP_001174541.1 PREDICTED: alpha isoform of regulatory subunit A, protein phosphatase 2 isoform 9 [Pan troglodytes]; emb CAG29336.1 PPP2R1A [Homo sapiens]; ref NP_055040.2 alpha isoform of regulatory subunit A, protein phosphatase 2 [Homo sapiens] ref XP_001116592.1 PREDICTED: similar to alpha isoform of regulatory subunit A, protein phosphatase 2 isoform 8 [Macaca mulatta] ref XP_001116604.1 PREDICTED: similar to alpha isoform of regulatory subunit A, protein phosphatase 2 isoform 9 [Macaca mulatta] ref XP_001116617.1 PREDICTED: similar to alpha isoform of regulatory subunit A, protein phosphatase 2 isoform 11 [Macaca mulatta] ref XP_001174546.1 PREDICTED: alpha isoform of regulatory subunit A, protein phosphatase 2 isoform 10 [Pan troglodytes] sp P30153 2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (PP2A, subunit A, PR65-alpha isoform) (PP2A, subunit A, R1-alpha	-0,723542192	-0,630323774	-0,51318119	-0,59223519	-0,611279482	1,5	DOWN
403	C601555.1	gb AAU34080.1 glutathione peroxidase-2 [Schistosoma mansoni]; gb ABK58680.1 PHGPx isoform 2 [Clonorchis sinensis]; gb ABE68811.1 phospholipid hydroperoxide glutathione peroxidase isoform 1 [Paragonimus westermani]; gb ABE68812.1 phospholipid hydroperoxide glutathione peroxidase isoform 2 [Paragonimus westermani];	-0,453957832	-0,545585477	-0,675683465	-0,68571532	-0,610634471	1,5	DOWN
404	C602425.1	No match	-0,457135175	-0,011191309	-0,777271652	-0,763460702	-0,610297939	1,5	DOWN
405	C603422.1	gb AAW26144.1 SJCHGC02223 protein [Schistosoma japonicum]; ref NP_955885.1 eukaryotic translation initiation factor 5 [Danio rerio] gb AAH49502.1 Eukaryotic translation initiation factor 5 [Danio rerio] gb AAH66614.1 Eukaryotic translation initiation factor 5 [Danio rerio] gb AAS92648.1 eukaryotic translation initiation factor 5 [Danio rerio] emb CAI21349.1 novel protein (zgc:77026) [Danio rerio]; ref XP_001507766.1 PREDICTED: similar to Eukaryotic translation initiation factor 5 [Ornithorhynchus anatinus]; ref XP_001366943.1 PREDICTED: hypothetical protein [Monodelphis domestica];	-0,446225568	-0,361967535	-0,799693893	-0,77186155	-0,609043559	1,5	DOWN
406	C603036.1	ref NP_001090412.1 hypothetical protein LOC779324 [Xenopus laevis] gb AAI23367.1 MGC154882 protein [Xenopus laevis]; ref XP_786594.2 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus] ref XP_001176705.1 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]; ref XP_001364011.1 PREDICTED: similar to C14orf126 protein [Monodelphis domestica]; ref XP_001512645.1 PREDICTED: similar to C14orf126 protein [Ornithorhynchus anatinus];	-0,484654255	-0,443022517	-0,729842536	-0,754922363	-0,607248396	1,5	DOWN
407	C602131.1	gb AAW24903.1 SJCHGC05946 protein [Schistosoma japonicum]; gb AAK29203.1 AF225905_1 ribosomal protein S15a [Taenia solium] gb AAP35026.1 ribosomal S15a protein [Taenia solium] gb AAP35027.1 ribosomal S15a protein [Taenia saginata]; gb ACD65146.1 putative 40S ribosomal protein RPS15A [Phoronis muelleri]; gb ABR27827.1 40S ribosomal protein S15/S22 [Triatoma infestans];	-0,395914531	-0,450841523	-0,803275038	-0,762606286	-0,606723905	1,5	DOWN

408	C705316.1	dbj BAG54197.1 unnamed protein product [Homo sapiens]; sp Q6NXD8.2 RA61L_DANRE RAB6IP1-like protein; ref XP_001477177.1 PREDICTED: similar to Rab6 interacting protein 1 [Mus musculus]; gb EDL16964.1 Rab6 interacting protein 1, isoform CRA_b [Mus musculus] gb EDL16965.1 Rab6 interacting protein 1, isoform CRA_b [Mus musculus];	-0,539797102	-0,576570663	-0,692698852	-0,634687162	-0,605628913	1,5	DOWN
409	C603342.1	gb AAX25143.2 SJCHGC07760 protein [Schistosoma japonicum];	-0,737839317	-0,595878173	-0,61351056	-0,436939804	-0,604694367	1,5	DOWN
410	C610415.1	gb AAW25037.1 SJCHGC03665 protein [Schistosoma japonicum]; ref NP_001072776.1 cyclin-dependent kinase 5 [Xenopus tropicalis] gb AAI18781.1 Cyclin-dependent kinase 5 [Xenopus tropicalis] gb AAI35927.1 Cyclin-dependent kinase 5 [Xenopus tropicalis]; ref NP_001084086.1 neuronal cyclin-dependent kinase 5 [Xenopus laevis] sp P51166 CDK5_XENLA Cell division protein kinase 5 (Cyclin-dependent kinase 5) (Neuronal cyclin-dependent kinase 5) gb AAB37091.1 neuronal cyclin-dependent kinase 5 gb AAH72894.1 Cdk5 protein [Xenopus laevis]; gb AAP36712.1 Homo sapiens cyclin-dependent kinase 5 [synthetic construct] gb AAQ02523.1 cyclin-dependent kinase 5 [synthetic construct] gb AAV38941.1 cyclin-dependent kinase 5 [synthetic construct] gb AAX36868.1 cyclin-dependent kinase 5 [synthetic construct] gb AAX43084.1 cyclin-dependent kinase 5 [synthetic construct] gb AAX43934.1 cyclin-dependent kinase 5 [synthetic construct] gb AAX43935.1 cyclin-dependent kinase 5 [synthetic construct];	-0,63842027	-0,639712526	-0,569342227	-0,413694723	-0,603881249	1,5	DOWN
411	C600552.1	No match	-0,443640744	-0,493804465	-0,713417271	-0,855040906	-0,603610868	1,5	DOWN
412	C610467.1	gb AAW27291.1 SJCHGC06584 protein [Schistosoma japonicum]; ref NP_001086339.1 MGC81898 protein [Xenopus laevis] gb AAH75131.1 MGC81898 protein [Xenopus laevis]; gb AAN71554.1 RH27395p [Drosophila melanogaster]; ref NP_001089775.1 hypothetical protein LOC734839 [Xenopus laevis] gb AAI06543.1 MGC131302 protein [Xenopus laevis];	-0,605379397	-0,597833669	-0,641487896	-0,593046429	-0,601606533	1,5	DOWN
413	C600632.1	gb AAX26725.2 SJCHGC04721 protein [Schistosoma japonicum]; ref XP_001950539.1 PREDICTED: similar to AGAP004743-PA [Acyrtosiphon pisum]; ref XP_791284.1 PREDICTED: similar to transmembrane protein [Strongylocentrotus purpuratus] ref XP_001179656.1 PREDICTED: similar to transmembrane protein [Strongylocentrotus purpuratus]; ref XP_971914.1 PREDICTED: similar to predicted protein [Tribolium castaneum];	-0,453723325	-0,826558102	-0,666803951	-0,535401289	-0,60110262	1,5	DOWN
414	C600861.1	gb ABG21818.1 B-cell receptor-associated protein-like protein [Schistosoma mansoni]; gb AAW27231.1 SJCHGC06848 protein [Schistosoma japonicum]; ref XP_001656331.1 bcr-associated protein, bap [Aedes aegypti] gb EAT45594.1 bcr-associated protein, bap [Aedes aegypti]; ref XP_001656330.1 bcr-associated protein, bap [Aedes aegypti] gb EAT45593.1 bcr-associated protein, bap [Aedes aegypti];	-0,596265219	-0,427561122	-0,617861767	-0,605422804	-0,600844012	1,5	DOWN

415	C607157.1	ref XP_001923230.1 PREDICTED: alpha thalassemia/mental retardation syndrome X-linked, like [Danio rerio]; gb AAH57486.1 Atrxl protein [Danio rerio]; gb AAH47849.1 Atrxl protein [Danio rerio]; ref XP_001128623.2 PREDICTED: similar to putative DNA dependent ATPase and helicase [Homo sapiens];	-0,571726607	-0,614356122	-0,586139497	-0,686655948	-0,60024781	1,5	DOWN
416	C609195.1	No match	-0,445934252	-0,478288512	-0,788971516	-0,721799949	-0,600044231	1,5	DOWN
417	C602569.1	gb AAW26420.1 SJCHGC06602 protein [Schistosoma japonicum]; ref NP_001013487.1 signal peptidase complex subunit 2 homolog [Danio rerio] sp Q5BJ9 SPCS2_BRARE Probable signal peptidase complex subunit 2 (Microsomal signal peptidase 25 kDa subunit) (SPase 25 kDa subunit) gb AAH91463.1 Signal peptidase complex subunit 2 homolog (S. cerevisiae) [Danio rerio]; gb AAO27767.1 signal peptidase 25 kDa subunit [Gasterosteus aculeatus]; emb CAG02153.1 unnamed protein product [Tetraodon nigroviridis];	-0,208752419	-0,229425026	-0,986949005	-0,970317314	-0,59987117	1,5	DOWN
418	C610344.1	gb AAW27211.1 SJCHGC09295 protein [Schistosoma japonicum]; gb AAX25500.2 SJCHGC05365 protein [Schistosoma japonicum];	-0,553865619	-0,554316003	-0,752827672	-0,645273882	-0,599794943	1,5	DOWN
419	C604353.1	ref XP_001942806.1 PREDICTED: similar to CG10671 CG10671-PA [Acyrtosiphon pisum]; gb EDW93488.1 GE20570 [Drosophila yakuba]; gb EDW50561.1 GM13929 [Drosophila sechellia]; gb AAL13842.1 LD30661p [Drosophila melanogaster];	-0,392987957	-0,052494995	-0,93815732	-0,806277741	-0,599632849	1,5	DOWN
420	C612571.1	gb AAW25086.1 SJCHGC09282 protein [Schistosoma japonicum]; ref XP_001632964.1 predicted protein [Nematostella vectensis] gb EDO40901.1 predicted protein [Nematostella vectensis]; ref NP_998955.1 histidine triad protein member 5 [Sus scrofa] sp Q8MIZ3 DCPS_PIG Scavenger mRNA-decapping enzyme DcpS (DCS-1) (Hint-related 7meGMP-directed hydrolase) (Histidine triad protein member 5) (HINT-5) gb AAK91766.1 histidine triad protein member 5 [Sus scrofa]; sp Q8MJJ7 DCPS_BOVIN Scavenger mRNA-decapping enzyme DcpS (DCS-1) (Hint-related 7meGMP-directed hydrolase) (Histidine triad protein member 5) (HINT-5) gb AAM90585.1 HINT-5 [Bos taurus];	-0,392692867	-0,592429664	-0,605681233	-0,830351671	-0,599055449	1,5	DOWN
421	C610016.1	gb AAW24791.1 SJCHGC06107 protein [Schistosoma japonicum]; gb EDV98017.1 GH14373 [Drosophila grimshawi]; ref XP_624693.1 PREDICTED: similar to Aut1 CG6877-PA [Apis mellifera]; gb EDW19783.1 GI11317 [Drosophila mojavensis];	-0,487360129	-0,553694337	-0,707628338	-0,643837477	-0,598765907	1,5	DOWN
422	C606333.1	gb AAW27044.1 SJCHGC05003 protein [Schistosoma japonicum]; gb AAP06320.1 hypothetical protein [Schistosoma japonicum]; gb EDW76652.1 GK14546 [Drosophila willistoni]; ref NP_609619.1 CG16812 CG16812-PA [Drosophila melanogaster] gb AAF53264.1 CG16812-PA [Drosophila melanogaster] gb AAL13891.1 LD36945p [Drosophila melanogaster];	-0,419474551	-0,539298687	-0,65745261	-0,840725244	-0,598375649	1,5	DOWN
423	C605292.1	No match	-0,481950529	-0,395408405	-0,712955357	-0,779706149	-0,597452943	1,5	DOWN
424	C611615.1	No match	-0,452713782	-0,507253196	-0,729372472	-0,687121829	-0,597187513	1,5	DOWN

425	C600144.1	gb AAX27647.2 SJCHGC05167 protein [Schistosoma japonicum]; gb AAP06067.1 similar to NM_021205 CDC42-like GTPase; novel Ras family protein; Wrch-1; Ryu GTPase in Homo sapiens [Schistosoma japonicum]; gb AAX20136.1 ras-like protein Rhoua [Danio rerio]; ref NP_001007444.1 ras homolog gene family, member Ua [Danio rerio] gb AAH85398.1 Ras homolog gene family, member Ua [Danio rerio] emb CAK04404.1 ras homolog gene family, member Ua [Danio rerio] gb AAI65147.1 Rhoua protein [synthetic construct];	-0,519503109	-0,453792331	-0,67240096	-0,748779696	-0,595952035	1,5	DOWN
426	C604407.1	gb AAW26910.1 SJCHGC06873 protein [Schistosoma japonicum]; ref NP_001108317.1 hypothetical protein LOC558272 [Danio rerio] emb CAM16012.1 novel protein similar to vertebrate hexosaminidase A (alpha polypeptide) (HEXA) [Danio rerio]; gb AAB30707.2 beta-hexosaminidase beta subunit [Felis catus]; ref NP_001009333.1 hexosaminidase B [Felis catus] gb AAB67612.1 beta-N-acetylhexosaminidase beta subunit [Felis catus];	-0,486076452	-0,539022213	-0,652028404	-0,731317962	-0,595525309	1,5	DOWN
427	C611867.1	gb AAW26628.1 SJCHGC05347 protein [Schistosoma japonicum];	-0,682912309	-0,740449846	-0,507602545	-0,35248306	-0,595257427	1,5	DOWN
428	C610657.1	No match	-0,807871891	-0,7050261	-0,480252517	-0,468191458	-0,592639309	1,5	DOWN
429	C604912.1	gb ABK60662.1 conserved hypothetical protein [Clostridium novyi NT] gb ABK60736.1 conserved hypothetical protein [Clostridium novyi NT] gb ABK60862.1 conserved hypothetical protein [Clostridium novyi NT] gb ABK61024.1 conserved hypothetical protein [Clostridium novyi NT] gb ABK61536.1 conserved hypothetical protein [Clostridium novyi NT] gb ABK62404.1 conserved hypothetical protein [Clostridium novyi NT] gb ABK62644.1 conserved hypothetical protein [Clostridium novyi NT] gb ABK62651.1 conserved hypothetical protein [Clostridium novyi NT]; ref ZP_02863215.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] ref ZP_02863226.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] ref ZP_02863230.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] gb ABK62310.1 conserved hypothetical protein [Clostridium novyi NT] gb ABK62642.1 conserved hypothetical protein [Clostridium novyi NT] gb EDS76142.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] gb EDS76170.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] gb EDS76282.1 conse	-0,458535984	-0,231097205	-0,726422756	-0,790090652	-0,59247937	1,5	DOWN
430	C610488.1	No match	-0,503845811	-0,403741162	-0,724443281	-0,67525638	-0,589551096	1,5	DOWN
431	C608151.1	No match	-0,521168191	-0,812821882	-0,533040938	-0,645532565	-0,589286752	1,5	DOWN
432	C603564.1	No match	-0,397623895	-0,514751961	-0,662104166	-0,675515167	-0,588428064	1,5	DOWN
433	C601781.1	No match	-0,507521812	-0,477425344	-0,6945878	-0,668612803	-0,588067308	1,5	DOWN
434	C608034.1	gb AAB86568.1 unknown [Schistosoma mansoni]; gb AAB86567.1 unknown [Schistosoma mansoni]; gb AAW26969.1 SJCHGC04169 protein [Schistosoma japonicum];	-0,457090348	0,016264198	-1,155755247	-0,718781832	-0,58793609	1,5	DOWN
435	C610146.1	tpg DAA04497.1 TPA_exp: pol polyprotein [Schistosoma mansoni];	-0,602477053	-0,575168229	-0,600231111	-0,3697049	-0,58769967	1,5	DOWN
436	C611006.1	No match	-0,743273213	-0,844804471	-0,42967295	-0,383605637	-0,586473082	1,5	DOWN

437	C601609.1	gb AAW25659.1 SJCHGC01319 protein [Schistosoma japonicum]; gb AAO86771.1 casein kinase II beta subunit [Schistosoma japonicum]; gb AAP06151.1 similar to NM_131187 casein kinase 2 beta in Danio rerio [Schistosoma japonicum]; gb AAP06476.1 similar to NM_009975 Casein kinase II beta subunit in Homo sapiens [Schistosoma japonicum];	-0,513865068	-0,205575041	-1,043355309	-0,657722888	-0,585793978	1,5	DOWN
438	C605137.1	sp Q5BQX9.1 SJ766_SCHJA Uncharacterized protein SJCHGC09766 precursor gb AAX31057.1 SJCHGC09766 protein [Schistosoma japonicum]; sp Q5BQU6.1 SJ803_SCHJA Uncharacterized protein SJCHGC09803 precursor gb AAX31090.1 SJCHGC09803 protein [Schistosoma japonicum]; sp Q5BQU9.1 SJ800_SCHJA Uncharacterized protein SJCHGC09800 precursor gb AAX31087.1 SJCHGC09800 protein [Schistosoma japonicum];	-0,136049634	-0,235286221	-0,935911741	-1,016223612	-0,585598981	1,5	DOWN
439	C609659.1	gb AAW24768.1 SJCHGC00713 protein [Schistosoma japonicum];	-0,415926235	-0,390740434	-0,755111263	-0,795693536	-0,585518749	1,5	DOWN
440	C603157.1	gb AAX27791.2 SJCHGC02238 protein [Schistosoma japonicum]; ref NP_997856.1 syndecan binding protein [Danio rerio] gb AAH44454.1 Syndecan binding protein (syntenin) [Danio rerio] gb AAQ97846.1 syndecan binding protein [Danio rerio] gb AAH65851.1 Syndecan binding protein (syntenin) [Danio rerio] gb AAI64064.1 Sdcbp protein [synthetic construct]; ref NP_001079704.1 similar to syndecan binding protein (syntenin) [Xenopus laevis] gb AAH48018.1 MGC52622 protein [Xenopus laevis]; ref XP_001843453.1 syntenin-1 [Culex pipiens quinquefasciatus] gb EDS32612.1 syntenin-1 [Culex quinquefasciatus];	-0,43412785	-0,492545137	-0,6897555	-0,678194339	-0,585369738	1,5	DOWN
441	C610329.1	No match	-0,235246876	-0,262418863	-0,907713129	-0,940831568	-0,585065996	1,5	DOWN
442	C609515.1	No match	-0,536716329	-0,688588191	-0,596599712	-0,573272664	-0,584936188	1,5	DOWN
443	C603215.1	No match	-0,421296662	-0,445475866	-0,773149084	-0,72177162	-0,583623743	1,5	DOWN
444	C711508.1	ref XP_001869981.1 dihydrolipoamide dehydrogenase [Culex pipiens quinquefasciatus] gb EDS31040.1 dihydrolipoamide dehydrogenase [Culex quinquefasciatus]; ref NP_502753.2 LLC1.3 [Caenorhabditis elegans] emb CAB05249.2 C. elegans protein LLC1.3, confirmed by transcript evidence [Caenorhabditis elegans]; ref XP_320877.4 AGAP011629-PA [Anopheles gambiae str. PEST] gb EAA00422.4 AGAP011629-PA [Anopheles gambiae str. PEST]; ref XP_782447.2 PREDICTED: similar to Dihydrolipoyl dehydrogenase, mitochondrial precursor (Dihydrolipoamide dehydrogenase) [Strongylocentrotus purpuratus] ref XP_001194682.1 PREDICTED: similar to Dihydrolipoyl dehydrogenase, mitochondrial precursor (Dihydrolipoamide dehydrogenase) [Strongylocentrotus purpuratus];	-0,65035121	-0,828077704	-0,469232079	-0,515010602	-0,582680906	1,5	DOWN
445	C602785.1	No match	-0,261847988	-0,491553059	-0,733865616	-0,672768141	-0,5821606	1,5	DOWN
446	C612007.1	gb ACE06877.1 unknown [Schistosoma japonicum]; gb AAP06287.1 similar to GenBank Accession Number AE003423 CG3073 gene product in Drosophila melanogaster [Schistosoma japonicum];	-0,481324537	-0,465134382	-0,680861196	-0,899840936	-0,581092867	1,5	DOWN
447	C601690.1	No match	-0,704471502	-1,097268164	-0,413682996	-0,455428108	-0,579949805	1,5	DOWN

448	C609870.1	gb AAX27166.2 SJCHGC05459 protein [Schistosoma japonicum]; gb AAI23082.1 LOC779589 protein [Xenopus tropicalis]; ref XP_001376019.1 PREDICTED: hypothetical protein [Monodelphis domestica]; ref NP_001006148.1 bromodomain containing 8 [Gallus gallus] emb CAG32596.1 hypothetical protein [Gallus gallus];	-0,438708471	-0,450391997	-0,709017591	-0,711211245	-0,579704794	1,5	DOWN
449	C608304.1	gb EDV42819.1 GF16839 [Drosophila ananassae]; gb EDW25876.1 GL14258 [Drosophila persimilis]; gb EDW66433.1 GJ15556 [Drosophila virilis]; gb EDW06198.1 GI16044 [Drosophila mojavensis];	-0,535481578	-0,398993516	-0,790334289	-0,622273721	-0,57887765	1,5	DOWN
450	C607711.1	gb AAW26347.1 SJCHGC02297 protein [Schistosoma japonicum]; emb CAF90783.1 unnamed protein product [Tetraodon nigroviridis]; gb EDL30780.1 Yip1 domain family, member 1, isoform CRA_d [Mus musculus]; emb CAM23043.1 Yip1 domain family, member 1 [Mus musculus];	-0,925319792	-0,964556831	-0,180332261	-0,23141968	-0,578369736	1,5	DOWN
451	C603814.1	emb CAD21542.1 hypothetical protein [Taenia solium];	-0,40843961	-0,247203522	-0,74369658	-0,743071916	-0,575755763	1,5	DOWN
452	C611329.1	gb AAP05966.1 hypothetical protein [Schistosoma japonicum]; gb AAW27241.1 SJCHGC02711 protein [Schistosoma japonicum];	-0,677547302	-0,628212448	-0,519671804	-0,447098753	-0,573942126	1,5	DOWN
453	C605963.1	No match	-0,660033729	-0,559647905	-0,588227861	-0,414009757	-0,573937883	1,5	DOWN
454	C608763.1	ref XP_001488649.2 PREDICTED: similar to Splicing factor 3b, subunit 4 [Equus caballus]; ref XP_001926524.1 PREDICTED: similar to Splicing factor 3b, subunit 4 [Sus scrofa]; ref XP_001365466.1 PREDICTED: similar to Splicing factor 3b, subunit 4 [Monodelphis domestica]; ref XP_423721.2 PREDICTED: similar to Splicing factor 3b, subunit 4 [Gallus gallus];	-0,224782498	-0,285323824	-0,862235636	-1,090589893	-0,57377973	1,5	DOWN
455	C600467.1	gb AAX28044.2 SJCHGC08177 protein [Schistosoma japonicum]; gb AAX25108.2 SJCHGC02950 protein [Schistosoma japonicum];	-0,624784085	-0,575466451	-0,570056454	-0,518032065	-0,572761453	1,5	DOWN
456	C600512.1	gb AAW25846.1 SJCHGC06777 protein [Schistosoma japonicum]; gb AAW27680.1 SJCHGC02820 protein [Schistosoma japonicum];	-0,648024099	-0,629196787	-0,515192196	-0,486003702	-0,572194492	1,5	DOWN
457	C608846.1	No match	-0,37612044	-0,387014357	-0,75578106	-0,826621685	-0,571397709	1,5	DOWN
458	C604746.1	prf 2019440B Sm65 antigen; gb AAX26501.2 SJCHGC07856 protein [Schistosoma japonicum];	-0,756843404	-0,647937596	-0,400594744	-0,493458047	-0,570697822	1,5	DOWN
459	C602619.1	gb AAW24565.1 SJCHGC03729 protein [Schistosoma japonicum];	-0,358444384	-0,506075389	-0,631962644	-0,842245983	-0,569019017	1,5	DOWN
460	C610620.1	No match	-0,698217761	-0,670807079	-0,465592953	-0,346095888	-0,568200016	1,5	DOWN
461	C600271.1	gb AAX30374.1 SJCHGC03136 protein [Schistosoma japonicum]; gb AAX25849.2 SJCHGC03094 protein [Schistosoma japonicum]; gb AAW27225.1 SJCHGC04667 protein [Schistosoma japonicum];	-0,584208771	-0,436358994	-0,592678	-0,551277928	-0,56774335	1,5	DOWN

462	C606402.1	ref NP_705949.1 spinster homolog 1 [Danio rerio]; gb AAL69987.1 AF465772.1 not really started [Danio rerio]; sp Q7ZU13.1 SPNS1_DANRE Protein spinster homolog 1 (Spinster-like protein) (Protein not really started) gb AAH48024.1 Spinster homolog 1 (Drosophila) [Danio rerio] gb AAI65625.1 Spns1 protein [synthetic construct]; ref XP_972584.1 PREDICTED: similar to spinster CG8428-PC [Tribolium castaneum]; ref XP_001204134.1 PREDICTED: similar to RIKEN cDNA 2210013K02 gene, partial [Strongylocentrotus purpuratus] ref XP_787421.2 PREDICTED: similar to RIKEN cDNA 2210013K02 gene, partial [Strongylocentrotus purpuratus];	-0,772560883	-0,623084733	-0,49559909	-0,509846917	-0,566465825	1,5	DOWN
463	C609740.1	gb AAX30243.3 SJCHGC02237 protein [Schistosoma japonicum]; gb AAX28303.2 SJCHGC01433 protein [Schistosoma japonicum]; ref XP_971825.1 PREDICTED: similar to signal recognition particle receptor beta subunit [Tribolium castaneum]; ref XP_001641944.1 predicted protein [Nematostella vectensis] gb EDO49881.1 predicted protein [Nematostella vectensis];	-0,673945442	-0,541497434	-0,548120598	-0,584543969	-0,566332284	1,5	DOWN
464	C604860.1	gb AAW27060.1 SJCHGC04744 protein [Schistosoma japonicum];	-0,278580728	-0,370180473	-0,761679509	-0,763354563	-0,565929991	1,5	DOWN
465	C605752.1	No match	-0,487847117	-0,395952809	-0,64335145	-0,732923121	-0,565599284	1,5	DOWN
466	C609775.1	gb AAX27411.2 SJCHGC08952 protein [Schistosoma japonicum]; ref XP_395705.3 PREDICTED: similar to CG18497-PA, isoform A, partial [Apis mellifera]; ref XP_001606953.1 PREDICTED: similar to predicted protein [Nasonia vitripennis]; ref XP_001689173.1 AGAP009990-PA [Anopheles gambiae str. PEST] gb EDO63446.1 AGAP009990-PA [Anopheles gambiae str. PEST];	-0,757047431	-0,551697818	-0,43681148	-0,577878951	-0,564788385	1,5	DOWN
467	C609274.1	gb AAX26685.2 SJCHGC04347 protein [Schistosoma japonicum];	-0,416429591	-0,502755187	-0,625438157	-0,770881755	-0,564096672	1,5	DOWN
468	C602410.1	gb AAW26110.1 SJCHGC06773 protein [Schistosoma japonicum]; gb AAX25852.2 SJCHGC06264 protein [Schistosoma japonicum]; gb AAP06361.1 similar to GenBank Accession Number AK004968 putative ribophorin II in Mus musculus [Schistosoma japonicum]; ref NP_001079661.1 similar to ribophorin II [Xenopus laevis] gb AAH46727.1 MGC53764 protein [Xenopus laevis];	-0,174429685	-0,352305128	-0,808213396	-0,773134111	-0,56271962	1,5	DOWN
469	C716135.1	ref NP_001098258.1 caspase-8 [Oryzias latipes] gb AAS91704.1 caspase-8 [Oryzias latipes]; ref XP_001184391.1 PREDICTED: similar to caspase-3 [Strongylocentrotus purpuratus]; ref XP_792621.2 PREDICTED: similar to caspase-3, partial [Strongylocentrotus purpuratus] ref XP_001184344.1 PREDICTED: similar to caspase-3, partial [Strongylocentrotus purpuratus]; ref NP_001026949.1 caspase-8 [Sus scrofa] gb AAS91710.1 caspase-8 [Sus scrofa];	-0,564230198	-1,124543241	-0,557733057	-0,455824212	-0,560981628	1,5	DOWN

470	C604638.1	ref XP_789857.2 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus] ref XP_001176595.1 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]; ref NP_001093679.1 hypothetical protein LOC100101683 [Xenopus tropicalis] gb AAI35670.1 C19orf10 protein [Xenopus tropicalis]; emb CAG08012.1 unnamed protein product [Tetraodon nigroviridis]; ref XP_854682.1 PREDICTED: similar to chromosome 19 open reading frame 10 [Canis familiaris];	-0,492428549	-0,500130995	-0,620981498	-0,692742969	-0,560556247	1,5	DOWN
471	C605194.1	No match	-0,329761164	-0,36840612	-0,752355241	-0,755486133	-0,560380681	1,5	DOWN
472	C602592.1	gb AAW27615.1 SJCHGC02437 protein [Schistosoma japonicum];	-0,339392526	-0,362893851	-0,757859029	-0,761551717	-0,56037644	1,5	DOWN
473	C606545.1	ref ZP_02844269.1 hypothetical protein Tmz1tDRAFT_3429 [Thauera sp. MZ1T] gb EDS55905.1 hypothetical protein Tmz1tDRAFT_3429 [Thauera sp. MZ1T]; ref ZP_02008652.1 hypothetical protein Rpic12DDRAFT_1928 [Ralstonia pickettii 12D] gb EDN40584.1 hypothetical protein Rpic12DDRAFT_1928 [Ralstonia pickettii 12D]; ref ZP_02863229.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] gb EDS76152.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund]; ref ZP_02863215.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] ref ZP_02863226.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] ref ZP_02863230.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] gb ABK62310.1 conserved hypothetical protein [Clostridium novyi NT] gb ABK62642.1 conserved hypothetical protein [Clostridium novyi NT] gb EDS76142.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] gb EDS76170.1 conserved hypothetical protein [Clostridium botulinum C str. Eklund] gb EDS76282.1 conserved	-0,767242205	-0,483285576	-0,636508464	-0,466164158	-0,55989702	1,5	DOWN
474	C601120.1	gb AAW26691.1 SJCHGC07316 protein [Schistosoma japonicum]; ref NP_001002868.1 dpy-19-like 1, like [Danio rerio] gb AAT68046.1 KIAA0877-like [Danio rerio] gb AAI63534.1 Dpy-19-like 1, like (H. sapiens) [Danio rerio] gb AAI63516.1 Dpy-19-like 1, like (H. sapiens) [Danio rerio]; ref XP_001900769.1 Protein dpy-19 [Brugia malayi] gb EDP30524.1 Protein dpy-19, putative [Brugia malayi]; ref XP_785579.1 PREDICTED: similar to KIAA0877-like [Strongylocentrotus purpuratus] ref XP_001187578.1 PREDICTED: similar to KIAA0877-like [Strongylocentrotus purpuratus];	-0,501837456	-0,525096351	-0,594461905	-0,754229725	-0,559779128	1,5	DOWN
475	C600025.1	gb AAX30374.1 SJCHGC03136 protein [Schistosoma japonicum];	-0,532014102	-0,630108441	-0,586840209	-0,136408955	-0,559427156	1,5	DOWN
476	C601665.1	pdb 1VYF A Chain A, Schistosoma Mansoni Fatty Acid Binding Protein In Complex With Oleic Acid pdb 1VYG A Chain A, Schistosoma Mansoni Fatty Acid Binding Protein In Complex With Arachidonic Acid; sp P29498 FABP_SCHMA 14 kDa fatty acid-binding protein (Sm14) gb AAA63516.1 fatty acid binding protein gb AAL15461.1 fatty acid-binding protein Sm14 [Schistosoma mansoni]; gb AAM18480.1 AF492389_1 Sm14 fatty acid-binding protein isoform T20 [Schistosoma mansoni]; gb AAT39384.1 fatty acid binding protein 15 [Schistosoma bovis];	-0,246871758	-0,243071339	-0,950628782	-0,869929981	-0,55840087	1,5	DOWN

477	C610449.1	ref XP_974489.2 PREDICTED: similar to Ankyrin repeat domain-containing protein 17 (Gene trap ankyrin repeat protein) (Serologically defined breast cancer antigen NY-BR-16) [Tribolium castaneum]; ref XP_393472.3 PREDICTED: similar to ankyrin repeat domain protein 17 isoform a [Apis mellifera];	-0,334925688	-0,506935508	-0,609820773	-0,981156552	-0,558378141	1,5	DOWN
478	C609610.1	No match	-0,564289129	-0,445764395	-0,667775416	-0,547865951	-0,55607754	1,5	DOWN
479	C600581.1	gb AAX26169.2 SJCHGC04821 protein [Schistosoma japonicum]; ref XP_001949000.1 PREDICTED: similar to Protein ADRM1 homolog (p42E) [Acyrthosiphon pisum]; ref XP_968223.1 PREDICTED: similar to AT08455p [Tribolium castaneum]; ref XP_001632164.1 predicted protein [Nematostella vectensis] gb EDO40101.1 predicted protein [Nematostella vectensis];	-0,56098336	-0,649637281	-0,549222147	-0,369855247	-0,555102754	1,5	DOWN
480	C609632.1	No match	-0,52018272	-0,601473353	-0,513348633	-0,589268214	-0,554725467	1,5	DOWN
481	C612205.1	gb AAW27894.1 SJCHGC05945 protein [Schistosoma japonicum];	-0,691848589	-0,299056061	-0,624473714	-0,479066743	-0,551770229	1,5	DOWN
482	C601522.1	gb ACE06902.1 unknown [Schistosoma japonicum]; gb AAP05958.1 similar to GenBank Accession Number AE003576 CG3652 gene product in Drosophila melanogaster [Schistosoma japonicum];	-0,573944618	-0,405977205	-0,993545803	-0,529315262	-0,55162994	1,5	DOWN
483	C601838.1	gb AAX24832.2 SJCHGC09189 protein [Schistosoma japonicum];	-0,612720802	-0,573684245	-0,5290195	-0,520322003	-0,551351873	1,5	DOWN
484	C600255.1	gb AAW26014.1 SJCHGC04863 protein [Schistosoma japonicum]; ref NP_001026661.1 TBC1 domain family, member 22A [Gallus gallus] emb CAG31060.1 hypothetical protein [Gallus gallus]; ref XP_001500326.1 PREDICTED: similar to MGC137912 protein [Equus caballus]; gb EAX03942.1 TBC1 domain family, member 22B, isoform CRA_d [Homo sapiens];	-0,389157728	-0,564850421	-0,659077953	-0,532975004	-0,548912713	1,5	DOWN
485	C600527.1	gb AAX28087.2 SJCHGC00998 protein [Schistosoma japonicum]; gb ABA40363.1 SJCHGC09384 protein [Schistosoma japonicum]; ref NP_001069240.1 WD repeat domain 53 [Bos taurus] sp Q32KQ2.1 WDR53_BOVIN WD repeat-containing protein 53 gb AAI09980.1 WD repeat domain 53 [Bos taurus]; ref XP_001364201.1 PREDICTED: similar to WD repeat domain 53 [Monodelphis domestica];	-0,843098247	-0,472959361	-0,592478587	-0,50452195	-0,548500269	1,5	DOWN
486	C610977.1	No match	-0,475320333	-0,621627147	-0,624316627	-0,354967604	-0,54847374	1,5	DOWN
487	C607402.1	sp Q01137 SODC_SCHMA Superoxide dismutase [Cu-Zn] gb AAA29936.1 superoxide dismutase; gb AAC14467.1 [Cu/Zn-superoxide dismutase [Schistosoma mansoni]; pdb 1TO4 A Chain A, Structure Of The Cytosolic Cu,Zn Sod From S. Mansoni pdb 1TO4 B Chain B, Structure Of The Cytosolic Cu,Zn Sod From S. Mansoni pdb 1TO4 C Chain C, Structure Of The Cytosolic Cu,Zn Sod From S. Mansoni pdb 1TO4 D Chain D, Structure Of The Cytosolic Cu,Zn Sod From S. Mansoni pdb 1TO5 A Chain A, Structure Of The Cytosolic Cu,Zn Sod From S. Mansoni pdb 1TO5 B Chain B, Structure Of The Cytosolic Cu,Zn Sod From S. Mansoni pdb 1TO5 C Chain C, Structure Of The Cytosolic Cu,Zn Sod From S. Mansoni pdb 1TO5 D Chain D, Structure Of The Cytosolic Cu,Zn Sod From S. Mansoni; gb AAA29935.1 superoxide dismutase;	-0,430240677	-0,321798817	-0,957808292	-0,66650072	-0,548370699	1,5	DOWN

488	C610255.1	gb AAW26926.1 SJCHGC05742 protein [Schistosoma japonicum]; emb CAG05279.1 unnamed protein product [Tetraodon nigroviridis];	-0,367123133	-0,464635552	-0,666017955	-0,631921248	-0,5482784	1,5	DOWN
489	C608373.1	gb AAC46898.1 similar to human carbonyl reductase (NADPH), PIR Accession Number A61271; Method: conceptual translation supplied by author; gb AAW25778.1 SJCHGC00683 protein [Schistosoma japonicum]; ref XP_001641607.1 predicted protein [Nematostella vectensis] gb EDO49544.1 predicted protein [Nematostella vectensis]; gb AAL16062.1 AF420278_1 carbonyl reductase [Anguilla japonica];	-0,652188438	-0,763883813	-0,443276959	-0,432464651	-0,547732699	1,5	DOWN
490	C612352.1	No match	-0,840541366	-0,873349511	-0,251186278	-0,21364632	-0,545863822	1,5	DOWN
491	C606731.1	No match	-0,893309444	-0,570925014	-0,51954135	-0,456934908	-0,545233182	1,5	DOWN
492	C609954.1	ref XP_973078.1 PREDICTED: similar to AGAP007538-PA [Tribolium castaneum]; ref NP_035917.2 autocrine motility factor receptor [Mus musculus] gb AAH34538.1 Autocrine motility factor receptor [Mus musculus] gb AAH40338.1 Autocrine motility factor receptor [Mus musculus] dbj BAE41974.1 unnamed protein product [Mus musculus]; ref NP_998328.1 autocrine motility factor receptor [Danio rerio] gb AAH57411.1 Autocrine motility factor receptor [Danio rerio]; gb AAD56721.1 AF124144_1 autocrine motility factor receptor [Mus musculus];	-0,537828717	-0,746412338	-0,549427284	-0,50839747	-0,543628001	1,5	DOWN
493	C605625.1	gb AAA19732.1 glucose transport protein; gb AAX26581.2 SJCHGC02813 protein [Schistosoma japonicum]; gb AAB05920.1 glucose transporter TGTP2 [Taenia solium]; ref NP_001036186.1 solute carrier family 2 (facilitated glucose transporter), member 2 [Danio rerio] gb AAZ43092.1 glucose transporter 2 [Danio rerio];	-0,717931426	-0,577564398	-0,502487601	-0,435606237	-0,540026	1,5	DOWN
494	C601197.1	gb AAX30542.1 SJCHGC04779 protein [Schistosoma japonicum]; gb ABK22541.1 unknown [Picea sitchensis]; ref XP_001187173.1 PREDICTED: similar to SNRPF protein [Strongylocentrotus purpuratus]; ref XP_796806.2 PREDICTED: similar to SNRPF protein, partial [Strongylocentrotus purpuratus];	-0,570896261	-0,505769599	-0,575927609	-0,394504931	-0,53833293	1,5	DOWN
495	C601689.1	gb AAX25664.2 SJCHGC03360 protein [Schistosoma japonicum]; ref XP_001952785.1 PREDICTED: similar to beta1,4 mannosyltransferase [Acyrtosiphon pisum]; gb EDV19433.1 hypothetical protein TRIADDRAFT_33634 [Trichoplax adhaerens]; ref XP_623777.2 PREDICTED: similar to beta-1,4-mannosyltransferase [Apis mellifera];	-0,794542789	-0,348316407	-0,555235711	-0,519550451	-0,537393081	1,5	DOWN
496	C610592.1	gb AAX25907.2 SJCHGC09404 protein [Schistosoma japonicum];	0,582847299	0,431967193	0,568732694	0,887551061	0,575789997	1,5	UP
497	C604083.1	No match	0,70485699	0,713294937	0,469678973	0,443485847	0,587267982	1,5	UP
498	C610809.1	gb AAX25746.2 SJCHGC05130 protein [Schistosoma japonicum]; gb EDW72378.1 GK20895 [Drosophila willistoni]; gb EDW91955.1 GE14079 [Drosophila yakuba]; gb EDW31890.1 GL11356 [Drosophila persimilis];	0,79856799	0,734062214	0,492819019	0,479336162	0,613440617	1,5	UP

499	C606657.1	gb AAX27370.2 SJCHGC05548 protein [Schistosoma japonicum]; ref NP_001090456.1 hypothetical protein LOC779369 [Xenopus laevis] sp Q6GPC6 TB1RB_XENLA F-box-like/WD repeat-containing protein TBL1XR1-B (Transducin beta-like 1X-related homolog 1-B) (Nuclear receptor corepressor/HDAC3 complex subunit TBLR1-B) (TBL1-related protein 1-B) gb AAH73215.1 MGC80502 protein [Xenopus laevis]; ref XP_424555.2 PREDICTED: hypothetical protein [Gallus gallus]; ref NP_001120367.1 hypothetical protein LOC100145441 [Xenopus tropicalis] gb AAI61057.1 Unknown (protein for MGC:184829) [Xenopus tropicalis];	0,510740533	0,433362485	0,820691738	0,725695431	0,618217982	1,5	UP
500	C607838.1	gb AAX28366.2 SJCHGC04923 protein [Schistosoma japonicum]; ref NP_499890.2 T21D12.3 [Caenorhabditis elegans] gb AAC48091.2 Hypothetical protein T21D12.3 [Caenorhabditis elegans]; ref XP_001671977.1 Hypothetical protein CBG10545 [Caenorhabditis briggsae AF16] emb CAP29955.1 Hypothetical protein CBG10545 [Caenorhabditis briggsae]; ref XP_001897165.1 WW domain containing protein [Brugia malayi] gb EDP34005.1 WW domain containing protein [Brugia malayi];	0,92923856	0,379304522	0,683728639	0,576503088	0,630115864	1,5	UP
501	C611430.1	No match	0,725784894	0,712694652	0,511791322	0,548447257	0,630570955	1,5	UP
502	C602742.1	No match	0,713579092	0,651261449	0,519988334	0,615319759	0,633290604	1,6	UP
503	C609745.1	No match	0,978049607	0,583970157	0,703205829	0,358333903	0,643587993	1,6	UP
504	C601437.1	No match	0,821603348	0,706224159	0,58995484	0,470754327	0,6480895	1,6	UP
505	C707555.1	ref XP_001372990.1 PREDICTED: similar to multidrug resistance protein 2; MRP2 [Monodelphis domestica]; gb EDL41913.1 ATP-binding cassette, sub-family C (CFTR/MRP), member 2 [Mus musculus]; ref NP_038834.2 ATP-binding cassette, sub-family C, member 2 [Mus musculus] gb AAL36986.1 AF282773_1 sub-family C member 2 ATP-binding cassette protein [Mus musculus]; sp Q8VI47 MRP2_MOUSE Canalicular multispecific organic anion transporter 1 (ATP-binding cassette sub-family C member 2) gb AAL36985.1 AF282772_1 sub-family C member 2 ATP-binding cassette protein [Mus musculus];	0,920328291	0,691603702	0,606901739	0,467461095	0,649252721	1,6	UP
506	C612590.1	No match	0,7036255	0,667244993	0,632998305	0,605454397	0,650121649	1,6	UP
507	C610554.1	ref XP_001624897.1 predicted protein [Nematostella vectensis] gb EDO32797.1 predicted protein [Nematostella vectensis]; ref XP_001620718.1 hypothetical protein NEMVEDRAFT_v1g222786 [Nematostella vectensis] gb EDO28618.1 predicted protein [Nematostella vectensis]; gb EDV28510.1 hypothetical protein TRIADDRAFT_19202 [Trichoplax adhaerens]; gb AAI42592.1 Checkpoint protein [Xenopus laevis];	0,599851215	0,77456969	0,442319012	0,702816421	0,651333818	1,6	UP
508	C607914.1	gb AAW24719.1 SJCHGC06079 protein [Schistosoma japonicum];	0,779666181	0,733899351	0,586940969	0,509901896	0,66042016	1,6	UP
509	C604775.1	No match	0,895432933	0,861612153	0,463441062	0,45539218	0,662526608	1,6	UP

510	C608834.1	ref NP_001107473.1 hypothetical protein LOC100135324 [Xenopus tropicalis] emb CAK11162.1 novel protein (zgc:114074) [Danio rerio] gb AAI52590.1 Tmem115 protein [Danio rerio] gb AAI57623.1 Unknown (protein for MGC:181014) [Xenopus tropicalis]; ref NP_001028917.1 transmembrane protein 115 [Danio rerio] gb AAH97136.1 Transmembrane protein 115 [Danio rerio]; gb AAI09436.1 Tmem115 protein [Danio rerio]; ref XP_001518365.1 PREDICTED: hypothetical protein [Ornithorhynchus anatinus];	0,826650308	0,788796872	0,549654111	0,53488998	0,669225492	1,6	UP
511	C603612.1	No match	0,838393469	0,449050605	0,568413716	0,784252059	0,676332888	1,6	UP
512	C607124.1	gb AAX28476.2 SJCHGC03500 protein [Schistosoma japonicum]; ref XP_974514.1 PREDICTED: similar to putative cholesterol transporter BmStart1 [Tribolium castaneum]; ref NP_001006799.1 START domain containing 3 [Xenopus tropicalis] gb AAH76666.1 START domain containing 3 [Xenopus tropicalis]; ref NP_571737.1 START domain containing 3 [Danio rerio] sp Q9DFS4.2 STAR3_DANRE STAR-related lipid transfer protein 3 (START domain-containing protein 3) (SIARD3) (MLN64-like protein) gb AAH56766.1 START domain containing 3 [Danio rerio] emb CAK04971.2 START domain containing 3 [Danio rerio];	0,817945713	0,797367436	0,577276275	0,602302778	0,699835107	1,6	UP
513	C604589.1	ref XP_001663199.1 brefeldin A-inhibited guanine nucleotide-exchange protein [Aedes aegypti] gb EAT34779.1 brefeldin A-inhibited guanine nucleotide-exchange protein [Aedes aegypti]; ref XP_001846441.1 brefeldin A-inhibited guanine nucleotide-exchange protein 1 [Culex pipiens quinquefasciatus] gb EDS43578.1 brefeldin A-inhibited guanine nucleotide-exchange protein 1 [Culex quinquefasciatus]; ref XP_319652.3 AGAP008906-PA [Anopheles gambiae str. PEST] gb EAA14874.4 AGAP008906-PA [Anopheles gambiae str. PEST]; emb CAG00665.1 unnamed protein product [Tetraodon nigroviridis];	0,936987878	0,807889232	0,601560939	0,440349309	0,704725086	1,6	UP
514	C718538.1	gb EDL26904.1 mCG9866 [Mus musculus]; ref NP_035019.1 nebulin [Mus musculus]; emb CAM21137.1 nebulin [Mus musculus] emb CAM17920.1 nebulin [Mus musculus]; ref NP_001101201.1 nebulin [Rattus norvegicus] gb EDM00439.1 nebulin (predicted) [Rattus norvegicus];	0,467692317	0,705251841	0,83789667	0,72165147	0,713451656	1,6	UP
515	C600335.1	ref XP_540384.2 PREDICTED: similar to component of oligomeric golgi complex 5 isoform 1 [Canis familiaris]; ref XP_001509241.1 PREDICTED: similar to component of oligomeric golgi complex 5 [Ornithorhynchus anatinus]; ref XP_001076141.1 PREDICTED: similar to component of oligomeric golgi complex 5 isoform 1 [Rattus norvegicus]; ref XP_001163243.1 PREDICTED: component of oligomeric golgi complex 5 isoform 3 [Pan troglodytes];	0,985779499	0,369668891	0,93572651	0,502815567	0,719271039	1,6	UP
516	C606481.1	No match	0,894351677	0,962555422	0,669389237	0,711528535	0,802940106	1,7	UP
517	C610534.1	No match	0,801126245	0,792410649	1,068879471	1,258068235	0,935002858	1,9	UP
= 2 ^ median log2 (test/control)									
** Up- or down-regulation refers to a significant (q< 0.01) increase or decrease (respectively) in the expression level of that gene in <i>S. mansoni</i> worms recovered from mice vaccinated with rSm29 plus adjuvant (test), in relation to control mice injected only with adjuvant (control).									