

Table S2

Ratios and anataation of all *Bb* induced genes

Probe	Name	3 h	6 h	12 h	24 h	E-value	Annotation
sw09154	BGIBMGA000068	0.4821	0.46355	0.76555	14.9329	Bmb025244	4.00E-60
sw06120	BGIBMGA009132	1	1.4081	1	10.268	0	gi 10242162 gb AAG15316.1 beta tubulin [Notothenia coriiceps]
sw13662	BGIBMGA010288	1	1.3618	2.75155	9.87	2.00E-43	gi 4530427 gb AAD22027.1 antennal-enriched UDP-glycosyltransferase [Drosophila melanogaster]
sw10407	BGIBMGA010569	1.30985	1.38105	1.21125	9.4806	1.00E-09	gi 72006769 ref XP_782274.1 PREDICTED: similar to mitochondrial ribosomal protein L46 (predicted) [Strongylocentrotus purpuratus]
sw17791	BGIBMGA006893	1.81845	1.4161	0.64985	9.20615	No hits found	
sw19970	BGIBMGA013834	2.0471	1.67165	2.15655	8.8402	1.00E-53	gi 74229818 ref YP_309022.1 ecdysone glucose transferase (egt) [Trichoplusia ni SNPV] ecdysone glucose transferase (egt) [Trichoplusia ni SNPV]
sw15442	BGIBMGA002979	0.8267	1.1066	1.02635	8.68885	1.00E-32	gi 72071125 ref XP_794946.1 PREDICTED: similar to carbonyl reductase 3, partial [Strongylocentrotus purpuratus]
sw15815	BGIBMGA011495	2.1127	1.5315	0.66685	8.1517	2.00E-14	gi 20138941 sp P82818 MOR1_BOMMO Moricin-1 precursor moricin [Bombyx mori]
sw11479	BGIBMGA010207	0.97105	1.05325	1.383	8.1504	2.00E-28	gi 18417421 ref NP_568302.1 S-adenosylmethionine-dependent methyltransferase [Arabidopsis thaliana] unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis thaliana]
sw08325	BGIBMGA006462	0.8277	1.12195	1	7.92665	1.00E-86	gi 72014480 ref XP_783380.1 PREDICTED: similar to Translation initiation factor eIF-2B alpha subunit (eIF-2B GDP-GTP exchange factor) [Strongylocentrotus purpuratus]
sw01773	BGIBMGA005658	0.9721	0.5052	0.37945	7.8362	5.00E-93	gi 52421205 dbj BAD51473.1 gloverin-like protein 1 [Bombyx mori]
sw21466	BGIBMGA000837	1.5345	1.15445	1.46355	7.79595	Bmb020074	6.00E-69
sw04084	BGIBMGA006805	0.9338	1.0415	0.8619	7.77445	4.00E-58	gi 56788798 gb AAH88474.1 WD40 protein Ciao1 (predicted) [Rattus norvegicus] WD40 protein Ciao1 (predicted) [Rattus norvegicus]
sw16997	BGIBMGA007299	0.85585	1.21805	0.9166	7.5102	2.00E-61	gi 4680679 gb AAD27729.1 CGI-20 protein [Homo sapiens]
sw10334	BGIBMGA001496	1.0025	1.15365	1.30385	7.4953	2.00E-34	gi 58396113 ref XP_321671.2 ENSANGP00000011708 [Anopheles gambiae str. PEST] ENSANGP00000011708 [Anopheles gambiae str. PEST]
sw04532	BGIBMGA014244	1.5091	1.6585	1.9517	7.15805	5.00E-17	gi 45550460 ref NP_611375.2 CG15094-PA, isoform A [Drosophila melanogaster] CG15094-PA, isoform A [Drosophila melanogaster]
sw13311	BGIBMGA012038	0.82825	0.961	0.9307	7.12655	e-104	gi 32450641 gb AAH54300.1 Osgep-prov protein [Xenopus laevis] Probable O-sialoglycoprotein endopeptidase
sw09873	BGIBMGA002492	0.86235	1.07675	0.827	7.0131	5.00E-12	gi 54638565 gb EAL27967.1 GA18941-PA [Drosophila pseudoobscura]
sw17221	BGIBMGA007845	0.7962	1.01745	0.82795	6.5563	3.00E-23	gi 54645591 gb EAL34329.1 GA12045-PA [Drosophila pseudoobscura]
sw10647	BGIBMGA000281	2.9171	1.47705	1.1584	6.53775	2.00E-54	gi 3608259 dbj BAA33195.1 cuticle protein [Bombyx mori]
sw03580	BGIBMGA010930	1.31075	1.2657	1.7451	6.4873	5.00E-65	gi 87248489 gb ABD36297.1 rRNA processing protein Ebp2 [Bombyx mori]
sw10315	BGIBMGA006200	0.90015	1.2047	0.80575	6.2053	5.00E-63	gi 3170241 gb AAC18057.1 TU37B2 [Anopheles gambiae]
sw10771	BGIBMGA003177	1.41385	1.16195	1.2861	6.0671	4.00E-72	gi 66519665 ref XP_393830.2 PREDICTED: similar to angio-associated migratory cell protein [Apis mellifera]
sw08579	BGIBMGA003842	0.75425	0.6444	0.7357	6.05845	9.00E-44	gi 77814698 ref ZP_00813954.1 Catalytic LigB subunit of aromatic ring-opening dioxygenase [Shewanella putrefaciens CN-32] Catalytic LigB subunit of aromatic ring-opening dioxygenase [Shewanella putrefaciens CN-32]

sw22144	BGIBMGA004091	0.99695	1.1136	0.7859	6.0561	2.00E-16	gi 21430068 gb AAM50712.1 GM16138p [Drosophila melanogaster] CG40127-PA.3 [Drosophila melanogaster] CG40127-PA.3 [Drosophila melanogaster]
sw06224	BGIBMGA001805	1.2051	1.03965	1.00685	6.0322	4.00E-75	gi 73997238 ref XP_534855.2 PREDICTED: similar to mitochondrial ribosomal protein S35 [Canis familiaris]
sw12539	BGIBMGA004834	1.01355	1.2302	1.3682	6.0197	4.00E-28	gi 50740272 ref XP_419413.1 PREDICTED: similar to CGI-115 protein [Gallus gallus]
sw16054	BGIBMGA001137	0.7686	0.87105	1.2503	5.96815	Bmb037837	2.00E-81
sw11597	BGIBMGA001131	1.0424	1.17535	1.2059	5.94735	2.00E-48	gi 71724847 gb AAZ38885.1 3' exoribonuclease [Xenopus laevis]
sw21303	BGIBMGA002783	1.25765	1.42015	1.5501	5.9309	No hits found	
sw01095	BGIBMGA011561	1.5206	0.6888	1.00545	5.88535	No hits found	
sw16412	BGIBMGA009964	1.12705	1.17355	1.3214	5.8593	5.00E-44	gi 54020928 ref NP_001005708.1 holocytochrome c synthase (cytochrome c heme-lyase)
sw17034	BGIBMGA009262	0.8918	1.0836	1.1378	5.77555	5.00E-59	gi 73979520 ref XP_849027.1 PREDICTED: similar to Deoxycytidylate deaminase (dCMP deaminase) isoform 1 [Canis familiaris]
sw14427	BGIBMGA000925	0.68505	1.00685	0.7108	5.75855	3.00E-35	gi 48139949 ref XP_397061.1 PREDICTED: similar to ENSANGP00000014483 [Apis mellifera]
sw18369	BGIBMGA011727	2.173	1.0237	1.2144	5.7494	4.00E-05	gi 6560657 gb AAF16706.1 putative cuticle protein [Manduca sexta]
sw03360	BGIBMGA004913	1.23895	1.39015	1.29165	5.7308	5.00E-96	gi 68401632 ref XP_685461.1 PREDICTED: similar to RNA polymerase 1-1 isoform 1 [Danio rerio] RNA polymerase 1-1 [Danio rerio] RNA polymerase 1-1 [Danio rerio]
sw00547	BGIBMGA002335	0.66465	0.99205	0.78555	5.72835	2.00E-39	gi 66504524 ref XP_623875.1 PREDICTED: similar to GA11196-PA [Apis mellifera]
sw20519	BGIBMGA010638	0.84235	0.96365	0.97715	5.676	1.00E-37	gi 21292306 gb EAA04451.1 ENSANGP00000021617 [Anopheles gambiae str. PEST] ENSANGP00000021617 [Anopheles gambiae str. PEST]
sw14877	BGIBMGA000350	0.8162	1.113	0.92975	5.67565	2.00E-13	gi 89473776 gb ABD72700.1 unknown [Acyrtosiphon pisum]
sw20283	BGIBMGA012125	0.94635	1.2979	1.28935	5.62805	8.00E-06	gi 73958242 ref XP_848469.1 PREDICTED: similar to CG15877-PA [Canis familiaris]
sw08750	BGIBMGA010225	1.1596	1.1734	1.0893	5.58125	e-161	gi 87248557 gb ABD36331.1 peroxisomal biogenesis factor 3 [Bombyx mori]
sw21920	BGIBMGA006855	0.94105	1.13475	0.8208	5.4299	5.00E-70	gi 37182119 gb AAQ88862.1 DFIT212 [Homo sapiens]
sw17103	BGIBMGA001561	0.7134	0.68985	0.7184	5.21745	No hits found	
sw12094	BGIBMGA006918	1.02865	1.32225	1.35345	5.2109	No hits found	
sw16458	BGIBMGA006735	0.84335	1.04675	0.87775	5.1433	Bmb041868	2.00E-47
sw03972	BGIBMGA008513	1.31615	1	0.9673	5.1106	No hits found	
sw06396	BGIBMGA006806	0.97785	1.0539	1.00415	5.104	1.00E-67	gi 40215783 gb AAL39701.2 LD28566p [Drosophila melanogaster]
sw03300	BGIBMGA013243	0.72195	0.91495	0.85715	5.07955	1.00E-22	gi 76643547 ref XP_875018.1 PREDICTED: similar to Mitochondrial import inner membrane translocase subunit Tim22 isoform 2 [Bos taurus]
sw05146	BGIBMGA002439	1.2721	1.37505	1.5179	5.04485	e-107	gi 66556699 ref XP_624203.1 PREDICTED: similar to GA11422-PA, partial [Apis mellifera]
sw01772	BGIBMGA000464	1.1085	1.0477	1.04175	5.0383	1.00E-69	gi 55237266 gb EAA12840.2 ENSANGP00000019242 [Anopheles gambiae str. PEST] ENSANGP00000019242 [Anopheles gambiae str. PEST]
sw15455	BGIBMGA011999	0.7669	0.847	0.5541	4.9469	8.00E-15	gi 53734221 gb AAH83655.1 Mitochondrial ATP synthase regulatory component factor B [Rattus norvegicus] mitochondrial ATP synthase regulatory component factor B
sw22332	BGIBMGA004847	0.65875	0.9139	0.99995	4.9277	e-120	gi 47086987 ref NP_998500.1 SEC13-like 1 [Danio rerio] SEC13-like 1 [Danio rerio]

sw22347	BGIBMGA012999	1.8581	2.6587	4.22965	4.9108	e-122	gi 48094603 ref XP_394220.1 PREDICTED: similar to CG9518-PA [Apis mellifera]
sw06780	BGIBMGA001507	1.3057	2.0168	2.0887	4.89775	Bmb034436	2.00E-54
sw21623	BGIBMGA006899	0.9358	1.0279	0.9017	4.8919	Bmb044274	9.00E-12
sw18085	BGIBMGA012780	0.9419	1.09045	1.29165	4.88875	e-114	gi 73980931 ref XP_532985.2 PREDICTED: similar to succinate-CoA ligase, GDP-forming, alpha subunit [Canis familiaris]
sw21727	BGIBMGA007987	1.1756	1.15925	1.0606	4.88565	8.00E-87	gi 13359092 dbj BAB33295.1 Bacteriophage T7 lysozyme-like protein 2 (BTL-LP2) [Bombyx mori]
sw13022	BGIBMGA002880	0.814	1.10085	0.70235	4.87635	No hits found	
sw14285	BGIBMGA013625	1.15125	1.01765	1.01745	4.84265	9.00E-22	gi 73967373 ref XP_854028.1 PREDICTED: similar to candidate tumor suppressor in ovarian cancer 2 [Canis familiaris]
sw21881	BGIBMGA014064	1.16355	1.7853	1.11005	4.82495	4.00E-40	gi 50418445 gb AAH77670.1 MGC89796 protein [Xenopus tropicalis] MGC89796 protein [Xenopus tropicalis] Novel protein similar to hypothetcal protein LOC56902 [Xenopus tropicalis]
sw05948	BGIBMGA005489	2.23905	1.84965	1.3703	4.8233	7.00E-39	gi 56790262 ref NP_571369.1 superoxide dismutase 1, soluble [Danio rerio] Cu/Zn-superoxide dismutase [Danio rerio] Superoxide dismutase 1, soluble [Danio rerio] PREDICTED: similar to Cu/Zn-superoxide dismutase
sw07313	BGIBMGA010376	0.7587	0.91525	0.85165	4.8185	8.00E-35	gi 2815410 dbj BAA24526.1 similar to Drosophila I(3)S12 [Bombyx mori]
sw09785	BGIBMGA010318	1.312	1.33425	1.29985	4.77525	Bmb035915	1.00E-91
sw07058	BGIBMGA011328	0.97915	1.0938	0.8651	4.74945	Bmb041739	3.00E-10
sw12525	BGIBMGA010309	0.8526	1.08895	1.13425	4.749	1.00E-36	gi 49904020 gb AAH76688.1 MGC79718 protein [Xenopus tropicalis] MGC79718 protein [Xenopus tropicalis]
sw09702	BGIBMGA003155	1.0923	1.0193	0.9663	4.73675	1.00E-24	gi 54035102 gb AAH84076.1 LOC494992 protein [Xenopus laevis]
sw01217	BGIBMGA009305	1	2.2798	1	4.7284	No hits found	
sw10048	BGIBMGA009486	0.77315	2.4063	1.58695	4.7274	Bmb041345	e-119
sw15650	BGIBMGA000330	2.37955	0.8064	1.8387	4.71715	No hits found	
sw14758	BGIBMGA007642	0.9575	1.17845	1.0088	4.71	1.00E-19	gi 15718247 emb CAA83138.2 Hypothetical protein T16H12.5a [Caenorhabditis elegans] BTB and MATH domain containing family member (bath-43) [Caenorhabditis elegans] Hypothetical protein T16H12.5 in chromosome III
sw10047	BGIBMGA008110	6.8849	1	1	4.67525	Bmb041294	No hits found
sw05369	BGIBMGA008620	1.08005	1.0117	1.0926	4.6519	2.00E-51	gi 87248529 gb ABD36317.1 mitochondria-associated granulocyte macrophage CSF signaling molecule [Bombyx mori]
sw02921	BGIBMGA000800	0.74475	0.9466	0.8724	4.64455	7.00E-43	gi 76641811 ref XP_616687.2 PREDICTED: similar to Clathrin coat assembly protein AP17 (Clathrin coat associated protein AP17) (Plasma membrane adaptor AP-2 17 kDa protein)
sw12746	BGIBMGA011007	0.67415	0.93555	0.66105	4.62415	3.00E-55	gi 84781676 ref NP_001034092.1 5-methyltetrahydrofolate-homocysteine methyltransferase reductase [Rattus norvegicus] Mtrr protein [Rattus norvegicus]
sw17264	BGIBMGA003520	0.9035	1.08285	0.899	4.6146	6.00E-08	gi 52346150 ref NP_001005117.1 novel protein similar to mitochondrial ribosomal protein L53 mrpl53 [Xenopus tropicalis] Novel protein similar to mitochondrial ribosomal protein L53 mrpl53
sw16046	BGIBMGA011324	0.83605	1.01135	0.9949	4.6096	Bmb037794	8.00E-07
sw22880	BGIBMGA010437	1.1852	1.17225	1.06705	4.60875	8.00E-62	gi 72006802 ref XP_783718.1 PREDICTED: similar to beta-tubulin cofactor C [Strongylocentrotus purpuratus]
sw17911	BGIBMGA011592	1.0353	1.0663	1.18465	4.5845	2.00E-55	gi 56270497 gb AAH87528.1 LOC496097 protein [Xenopus laevis]
sw09105	BGIBMGA009395	1.15365	1.3337	1.70365	4.55455	1.00E-49	gi 51480426 gb AAH80252.1 WD repeat domain 18 [Danio rerio] WD repeat domain 18 [Danio rerio]
sw07146	BGIBMGA007739	0.8679	0.94455	1.1636	4.54955	5.00E-07	gi 72091540 ref XP_791287.1 PREDICTED: similar to butyrate-induced transcript 1 like (19.4 kD) (3G364) [Strongylocentrotus purpuratus]

sw13530	BGIBMGA006177	0.718	0.81695	0.66475	4.4744	2.00E-22	gi 6684113 gb AAF23489.1 312 protein [Drosophila melanogaster]
sw15089	BGIBMGA003987	0.78365	0.94545	0.9424	4.46545	7.00E-64	gi 47523746 ref NP_999508.1 quinoid dihydropteridine reductase [Sus scrofa] quinoid dihydropteridine reductase [Sus scrofa] Dihydropteridine reductase (HDHPR) (Quinoid dihydropteridine reductase)
sw10444	BGIBMGA010151	0.8559	1.06235	0.876	4.465	1.00E-33	gi 57089809 ref XP_537340.1 PREDICTED: similar to tumor necrosis factor superfamily, member 5-induced protein 1 [Canis familiaris]
sw08478	BGIBMGA005882	0.5603	0.83685	0.86265	4.45825	2.00E-28	gi 54645763 gb EAL34501.1 GA12251-PA [Drosophila pseudoobscura]
sw04014	BGIBMGA005693	1	2.0388	1.71045	4.45345	No hits found	
sw10815	BGIBMGA003838	0.97085	1.018	0.67025	4.44385	2.00E-19	gi 73969379 ref XP_531710.2 PREDICTED: similar to serine hydrolase-like 2 [Canis familiaris]
sw16472	BGIBMGA010577	1.323	1.2836	1.13815	4.4428	Bmb042047	1.00E-13
sw17152	BGIBMGA009118	0.72305	1.0022	0.9122	4.42585	5.00E-56	gi 57032918 gb AAH88818.1 LOC496302 protein [Xenopus laevis]
sw07768	BGIBMGA007559	0.7547	0.83265	0.75115	4.396	6.00E-32	gi 66556167 ref XP_624817.1 PREDICTED: similar to Ribosomal protein S29 [Apis mellifera]
sw18132	BGIBMGA006966	0.896	1.10025	0.8674	4.36665	9.00E-32	gi 48104167 ref XP_392921.1 PREDICTED: similar to nuclear transport factor 2 [Apis mellifera]
sw16002	BGIBMGA002835	1.33445	1.1532	1.05165	4.3348	3.00E-66	gi 72010073 ref XP_786273.1 PREDICTED: similar to claudin 12 [Strongylocentrotus purpuratus]
sw19410	BGIBMGA001027	0.89605	1.2749	1.09135	4.3253	6.00E-41	gi 57905728 ref XP_551123.1 ENSANGP00000027831 [Anopheles gambiae str. PEST] ENSANGP00000027831 [Anopheles gambiae str. PEST]
sw10082	BGIBMGA009068	0.823	1.02165	0.83465	4.31995	No hits found	
sw11463	BGIBMGA007233	1.02	1.0915	1.20605	4.3172	No hits found	
sw13390	BGIBMGA007367	1.11365	1.22515	0.861	4.30325	2.00E-41	gi 12804745 gb AAH01808.1 Nucleoside diphosphate kinase type 6 [Homo sapiens] Nucleoside diphosphate kinase type 6 [Homo sapiens] nucleoside diphosphate kinase type 6
sw18512	BGIBMGA005162	0.83115	0.9651	1.1618	4.2965	2.00E-23	gi 62083501 gb AAH62475.1 mitochondrial ribosomal protein L11 [Lysiphlebus testaceipes]
sw07841	BGIBMGA010651	1.38435	1.49075	1.3233	4.2944	2.00E-27	gi 52789335 gb AAH83014.1 LOC494842 protein [Xenopus laevis]
sw22048	BGIBMGA013200	0.7698	1.0694	1.07635	4.27535	3.00E-68	gi 66552883 ref XP_625026.1 PREDICTED: similar to ENSANGP00000012063 [Apis mellifera]
sw20415	BGIBMGA012624	1.52565	1.11905	1.34265	4.272	2.00E-91	gi 62286614 sp Q60HC5 DHC24_MACFA 24-dehydrocholesterol reductase precursor (3-beta-hydroxysterol delta-24-reductase)
sw17940	BGIBMGA006931	1.2198	1.31025	1.2858	4.269	No hits found	
sw13056	BGIBMGA011645	1.1104	1.28025	1.39555	4.2538	2.00E-17	gi 22297524 gb AAK32113.2 Mpv17-like protein [Mus musculus] Mpv17 transgene, kidney disease mutant-like [Mus musculus] Mpv17l protein [Mus musculus]
sw13666	BGIBMGA012460	0.91845	1.1253	0.998	4.2367	No hits found	
sw17771	BGIBMGA003095	2.5833	1.3329	1.97195	4.23325	2.00E-18	gi 290935 gb AAC37204.1 cuticle protein 66 Larval/pupal rigid cuticle protein 66 precursor (HCCP66)
sw04275	BGIBMGA010208	0.85085	0.865	1.23865	4.21965	No hits found	
sw09102	BGIBMGA009901	1.24245	1.1374	1.58715	4.21515	5.00E-29	gi 87248537 gb ABD36321.1 mitochondrial matrix protein p33 [Bombyx mori]
sw08920	BGIBMGA009051	0.73615	0.93465	0.74585	4.21495	1.00E-22	gi 72061380 ref XP_789080.1 PREDICTED: similar to disulfide isomerase [Strongylocentrotus purpuratus]
sw06189	BGIBMGA011234	1.00925	1.0255	1.1417	4.20425	No hits found	
sw08778	BGIBMGA010977	1.28135	1.26905	0.94345	4.1625	7.00E-12	gi 409430 gb AAA29312.1 ecdysteroid regulated protein

sw13706	BGIBMGA010819	0.90285	1.0661	0.50775	4.15685	2.00E-44	gi 72022689 ref XP_795397.1 PREDICTED: similar to Mitochondrial 28S ribosomal protein S25 (S25mt) (MRP-S25) [Strongylocentrotus purpuratus]
sw11888	BGIBMGA009983	1.58655	1.48875	1.52385	4.1394	e-100	gi 30580383 sp Q9VZE6 BXDC2_DROME Brix domain-containing protein 2 homolog (Ribosome biogenesis protein Brix homolog)
sw01903	BGIBMGA006154	0.6878	0.9907	0.79025	4.12635	2.00E-35	gi 87248405 gb ABD36255.1 suppressor of Lec15 glycosylation mutation-like protein [Bombyx mori]
sw00830	BGIBMGA002078	0.88505	1.1494	0.8921	4.12245	1.00E-18	gi 55632157 ref XP_520201.1 PREDICTED: similar to haloacid dehalogenase-like hydrolase domain containing 3; chromosome 9 open reading frame 158 [Pan troglodytes]
sw18036	BGIBMGA003762	0.7267	0.9089	0.9568	4.11825	1.00E-42	gi 14603259 gb AAH10089.1 ASMTL protein [Homo sapiens]
sw09281	BGIBMGA007741	0.86445	1.0596	0.88165	4.1066	6.00E-23	gi 55238957 gb EAA11211.2 ENSANGP00000017823 [Anopheles gambiae str. PEST] ENSANGP00000017823 [Anopheles gambiae str. PEST]
sw18363	BGIBMGA011884	0.88905	1.073	0.9493	4.0937	5.00E-37	gi 27819763 gb AAL68373.2 SD01117p [Drosophila melanogaster]
sw05953	BGIBMGA007258	1.1382	1.11185	1.11955	4.09205	5.00E-71	gi 48139441 ref XP_397008.1 PREDICTED: similar to Diacetyl/L-xylulose reductase [Apis mellifera]
sw05099	BGIBMGA012981	0.5653	0.92815	0.74575	4.07675	3.00E-65	gi 89273430 emb CAJ82650.1 transmembrane emp24 domain trafficking protein 2 [Xenopus tropicalis]
sw11923	BGIBMGA009834	0.80675	1.50395	1.33015	4.0751	No hits found	
sw14629	BGIBMGA004075	4.6135	2.34935	1.9541	4.0746	No hits found	
sw03192	BGIBMGA008176	0.76595	0.74295	0.61635	4.07235	3.00E-17	gi 400673 sp P31420 OMBP_MANSE Ommochrome-binding protein precursor (OBP) (YCP) ommochrome-binding protein
sw09013	BGIBMGA013029	0.8649	0.88355	0.9334	4.071	2.00E-05	gi 4733885 gb AAD28638.1 unknown [Drosophila melanogaster]
sw00926	BGIBMGA005991	1.2557	1.1018	1.15155	4.0685	2.00E-36	gi 73973167 ref XP_532185.2 PREDICTED: similar to DNA primase large subunit, 58kDa isoform 1 [Canis familiaris]
sw17483	BGIBMGA010061	2.1242	1.42655	1.43805	4.0534	2.00E-64	gi 6690636 gb AAF24228.1 trypsin-like PIT2c precursor [Plodia interpunctella]
sw06001	BGIBMGA002215	0.91935	0.9811	1.30515	4.05285	7.00E-42	gi 72006105 ref XP_783220.1 PREDICTED: similar to Mitochondrial import inner membrane translocase subunit Tim17 B (JM3) [Strongylocentrotus purpuratus]
sw01600	BGIBMGA003524	0.9754	0.81525	0.7923	4.0406	No hits found	
sw17903	BGIBMGA009888	1.1189	0.96665	1.178	4.0295	5.00E-60	gi 61583224 gb AAx47004.1 transformer-2 protein F [Bombyx mori]
sw04267	BGIBMGA008689	1.4616	1.25695	1.34655	4.0281	Bmb030313	9.00E-10
sw12191	BGIBMGA006919	0.99875	1.01995	1.09275	4.0259	Bmb010764	4.00E-65
sw13139	BGIBMGA003537	0.58995	0.9654	0.586	4.02295	1.00E-25	gi 72015284 ref XP_782825.1 PREDICTED: similar to putative protein, with a coiled coil-4 domain, of ancient origin (2H170) [Strongylocentrotus purpuratus]
sw17449	BGIBMGA003475	0.82175	1.35645	1.08945	4.0224	e-102	gi 12328436 dbj BAB21109.1 elongation factor 1 delta [Bombyx mori]
sw11688	BGIBMGA008813	1.23705	1.08965	1.33775	4.0178	4.00E-26	gi 49532884 dbj BAD26677.1 Juvenile hormone diol kinase [Plutella xylostella]
sw20069	BGIBMGA000924	0.91415	1.0906	1.0202	4.013	2.00E-87	gi 87248355 gb ABD36230.1 ribosomal protein L22 [Bombyx mori]
sw12176	BGIBMGA008312	0.80895	0.75175	0.999	4.00105	e-119	gi 87248567 gb ABD36336.1 mitochondrial prohibitin complex protein 2 [Bombyx mori]
sw01486	BGIBMGA013268	0.74455	1.0512	0.8324	3.99825	5.00E-07	gi 66499360 ref XP_396507.2 PREDICTED: similar to CG11550-PA [Apis mellifera]
sw11663	BGIBMGA001222	0.9246	1.0078	0.81735	3.98315	2.00E-15	gi 49522624 gb AAH75581.1 MGC89563 protein [Xenopus tropicalis] MGC89563 protein [Xenopus tropicalis]
sw16038	BGIBMGA010118	0.98005	1.1465	1.2156	3.98165	4.00E-17	gi 55246170 gb EAL41993.1 ENSANGP00000027810 [Anopheles gambiae str. PEST] ENSANGP00000027810 [Anopheles gambiae str. PEST]

sw08598	BGIBMGA007010	0.80945	1.2399	0.71395	3.9806	1.00E-15	gi 49257982 gb AAH74167.1 MGC81952 protein [Xenopus laevis] Charged multivesicular body protein 6-1 (Chromatin modifying protein 6-1)
sw03808	BGIBMGA005319	0.5746	0.95895	0.92705	3.95505	2.00E-44	gi 27501446 ref NP_003668.2 density-regulated protein [Homo sapiens] DENR protein [Homo sapiens] Density-regulated protein (DRP) (DRP1 protein) (Smooth muscle cell associated protein 3) (SMAP-3) SMAP-3 [Homo sapiens]
sw07050	BGIBMGA006662	1.2035	1.0268	1.35605	3.942	4.00E-07	gi 510500 emb CAA50796.1 GCR 1 protein [Drosophila melanogaster]
sw08933	BGIBMGA013364	0.8714	1.1236	1.14995	3.9358	4.00E-60	gi 6671690 ref NP_031646.1 carbonyl reductase 1 [Mus musculus] Carbonyl reductase [NADPH] 1 (NADPH-dependent carbonyl reductase 1) carbonyl reductase
sw17045	BGIBMGA000375	1.0199	1.2083	1.0551	3.9354	2.00E-35	gi 80478497 gb AAI09352.1 Dihydrouridine synthase 4-like [Mus musculus]
sw08947	BGIBMGA004112	0.7442	0.91845	0.69535	3.93305	Bmb022039	e-146
sw15293	BGIBMGA007878	1.0656	1.2752	0.9476	3.9297	Bmb031647	5.00E-13
sw06899	BGIBMGA009307	0.79465	1.0541	0.8801	3.9246	4.00E-78	gi 62860202 ref NP_001016646.1 thioredoxin-like 4A [Xenopus tropicalis] thioredoxin-like 4A [Xenopus tropicalis]
sw16033	BGIBMGA014453	1.93	1.14875	0.78355	3.923	6.00E-84	gi 62529862 gb AAX85203.1 aldo/keto reductase [Aedes aegypti]
sw15849	BGIBMGA008868	1.21075	1.1895	1.0667	3.91485	Bmb035884	1.00E-19
sw09825	BGIBMGA008699	1.036	1.1849	1.0907	3.9112	1.00E-76	gi 56270488 gb AAH87491.1 LOC496075 protein [Xenopus laevis]
sw20745	BGIBMGA000364	0.9692	1.0694	0.986	3.9094	7.00E-43	gi 72086794 ref XP_793560.1 PREDICTED: similar to lactation elevated 1, partial [Strongylocentrotus purpuratus]
sw22684	BGIBMGA000276	2.0627	1.6147	1	3.90655	7.00E-50	gi 3608259 dbj BAA33195.1 cuticle protein [Bombyx mori]
sw17005	BGIBMGA006242	0.69705	0.9564	0.9037	3.8852	1.00E-35	gi 24647481 ref NP_650561.1 CG14903-PA [Drosophila melanogaster] CG14903-PA [Drosophila melanogaster]
sw16983	BGIBMGA006984	0.78	0.9604	0.8421	3.8827	2.00E-83	gi 87248133 gb ABD36119.1 G10 protein [Bombyx mori]
sw14681	BGIBMGA006292	0.9122	1.22015	1.0464	3.88025	7.00E-67	gi 89521458 gb ABD76573.1 transcription-associated zinc ribbon protein [Bombyx mori]
sw00338	BGIBMGA005391	0.88295	1.0498	0.9083	3.8798	7.00E-22	gi 73586862 gb AAI03209.1 Pyridoxine 5'-phosphate oxidase [Bos taurus] pyridoxine 5'-phosphate oxidase [Bos taurus] Pyridoxine-5'-phosphate oxidase (Pyridoxamine-phosphate oxidase)
sw09145	BGIBMGA013011	0.8424	1.26215	0.96275	3.86375	No hits found	
sw21775	BGIBMGA005079	1.03775	1.21875	0.99545	3.8513	No hits found	
sw07663	BGIBMGA006799	1.1023	1.2427	1.6249	3.83725	7.00E-30	gi 54641496 gb EAL30246.1 GA10532-PA [Drosophila pseudoobscura]
sw13347	BGIBMGA004278	1.07305	1.0967	1.0178	3.837	9.00E-18	gi 18203570 sp Q9WTQ8 TIM23_MOUSE Mitochondrial import inner membrane translocase subunit Tim23 translocase of inner mitochondrial membrane 23 homolog
sw14472	BGIBMGA002755	0.7449	0.94925	0.8946	3.83025	5.00E-73	gi 62857721 ref NP_001016870.1 SUMO-1 activating enzyme subunit 1 [Xenopus tropicalis] SMT3 suppressor of mif two 3 homolog 1 (yeast) [Xenopus tropicalis]
sw05605	BGIBMGA001623	0.9114	1.05535	0.9138	3.82895	1.00E-13	gi 23508790 ref NP_701458.1 Zinc finger transcription factor (krox1) [Plasmodium falciparum 3D7] Krox-like protein [Plasmodium falciparum 3D7] Zinc finger transcription factor (krox1) [Plasmodium falciparum 3D7]
sw03347	BGIBMGA005636	1.05755	1.03405	1.2643	3.8256	8.00E-88	gi 14603167 gb AAH10048.1 RNA, U3 small nucleolar interacting protein 2 [Homo sapiens] RNA, U3 small nucleolar interacting protein 2 [Homo sapiens] RNA, U3 small nucleolar interacting protein 2
sw09479	BGIBMGA011469	0.68955	0.79465	0.7999	3.8204	2.00E-24	gi 76628923 ref XP_588837.2 PREDICTED: similar to chromosome 2 open reading frame 7 [Bos taurus]
sw05879	BGIBMGA005208	1.4507	0.8478	0.8166	3.8173	6.00E-26	gi 76630146 ref XP_582319.2 PREDICTED: similar to retinol dehydrogenase 14 (all-trans and 9-cis) [Bos taurus]
sw15610	BGIBMGA006376	0.6895	0.76355	0.87075	3.8069	9.00E-16	gi 1362727 pir B56211 progesterone receptor-related protein p23 - chicken
sw01677	BGIBMGA011771	0.6309	0.759	0.9597	3.80325	8.00E-28	gi 47225269 emb CAG09769.1 unnamed protein product [Tetraodon nigroviridis]

sw18010	BGIBMGA012134	1.18375	1.35815	1.2874	3.80225	6.00E-14	gi 27374388 gb AAO01125.1 CG13030-PA [Drosophila willistoni]
sw13521	BGIBMGA011070	0.8927	1.1285	0.9746	3.8009	3.00E-41	gi 45360855 ref NP_989103.1 Nif31bp1-prov protein [Xenopus tropicalis] Nif31bp1-prov protein [Xenopus tropicalis]
sw18194	BGIBMGA009614	1.3675	1.2788	0.9787	3.79655	2.00E-35	gi 87248347 gb ABD36226.1 lysosomal thiol reductase IP30 precursor isoform 1 [Bombyx mori]
sw06046	BGIBMGA010845	0.8194	1.1804	0.94285	3.79605	1.00E-20	gi 48140447 ref XP_397115.1 PREDICTED: similar to ENSANGP00000014264 [Apis mellifera]
sw12429	BGIBMGA006771	0.6558	0.781	0.8036	3.7781	2.00E-46	gi 50759473 ref XP_417658.1 PREDICTED: similar to peptidyl prolyl isomerase H; cyclophilin H; rotamase H [Gallus gallus]
sw11486	BGIBMGA000412	0.7044	0.97255	1.03	3.7749	7.00E-43	gi 12653357 gb AAH00448.1 THUMP domain containing 1 [Homo sapiens] THUMP domain containing 1 [Homo sapiens] THUMP domain-containing protein 1
sw14453	BGIBMGA011281	0.8466	1.1639	0.7589	3.7645	Bmb025362	6.00E-18
sw13670	BGIBMGA011532	0.9167	1.142	1.2154	3.75325	2.00E-52	gi 82999323 ref XP_920157.1 PREDICTED: similar to Protein FRA10AC1 homolog [Mus musculus]
sw07451	BGIBMGA011737	0.8821	0.9949	1.00635	3.73595	2.00E-23	gi 47938836 gb AAH71528.1 General transcription factor IIA, 1, 19/37kDa [Danio rerio]
sw15319	BGIBMGA013759	0.918	1.03985	0.856	3.73525	No hits found	
sw13384	BGIBMGA012571	0.52445	0.9904	0.65455	3.73465	3.00E-31	gi 1016766 gb AAA79181.1 signal recognition particle 19 kDa protein
sw18770	BGIBMGA012376	0.95855	1.00605	1.0005	3.71535	9.00E-07	gi 39591361 emb CAE73415.1 Hypothetical protein CBG20858 [Caenorhabditis briggsae]
sw15870	BGIBMGA006100	0.65725	0.9475	0.7754	3.7095	Bmb036020	3.00E-35
sw09660	BGIBMGA004919	1.03815	1.1799	0.9264	3.7032	7.00E-78	gi 72006159 ref XP_785239.1 PREDICTED: similar to bisphosphate nucleotidase 1 [Strongylocentrotus purpuratus]
sw12216	BGIBMGA012075	0.78255	1.05675	1.0026	3.70265	3.00E-36	gi 7542478 gb AAF63472.1 H protein [Oryctolagus cuniculus] Glycine cleavage system H protein, mitochondrial precursor
sw01819	BGIBMGA012772	0.80015	0.8565	1.19915	3.69495	0	gi 73986746 ref XP_533895.2 PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 isoform 1 [Canis familiaris]
sw14711	BGIBMGA007955	1.32535	1.44	1.63805	3.6877	No hits found	
sw09767	BGIBMGA012459	0.7214	0.9415	0.5915	3.6876	2.00E-42	gi 58569313 gb AAW79027.1 GekBS181P [Gekko japonicus]
sw04603	BGIBMGA003390	0.7291	0.9446	0.9034	3.675	2.00E-40	gi 85720047 gb ABC75592.1 N-acetyltransferase 9 [Ictalurus punctatus]
sw06731	BGIBMGA004099	0.86205	1.03945	0.7686	3.6723	Bmb033309	1.00E-34
sw03726	BGIBMGA007259	0.8022	1.08195	1.0462	3.6712	2.00E-44	gi 48139441 ref XP_397008.1 PREDICTED: similar to Diacetyl/L-xylulose reductase [Apis mellifera]
sw15217	BGIBMGA012934	0.99465	1.24035	1.1165	3.6656	9.00E-74	gi 41388936 gb AAH65899.1 Actin related protein 2/3 complex subunit 4 [Danio rerio] actin related protein 2/3 complex, subunit 4, like [Danio rerio] Actin related protein 2/3 complex, subunit 4, like
sw16492	BGIBMGA010768	1.6068	2.23365	1.84785	3.66425	Bmb042252	2.00E-07
sw01325	BGIBMGA011759	2.7865	1.66795	1.26465	3.6627	4.00E-35	gi 28261395 gb AAO32819.1 putative cuticle protein [Manduca sexta] putative cuticle protein [Manduca sexta]
sw04436	BGIBMGA001197	1.10135	1.1996	1.07385	3.6625	1.00E-23	gi 72013764 ref XP_784928.1 PREDICTED: similar to Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP exchange factor) [Strongylocentrotus purpuratus]
sw11296	BGIBMGA009849	1.51205	1.1164	1.4853	3.6599	e-107	gi 7688192 emb CAB89811.1 RNA 3'-terminal phosphate cyclase-like protein [Homo sapiens]
sw18237	BGIBMGA005557	0.72085	1.2755	1.35295	3.64915	1.00E-60	gi 87248267 gb ABD36186.1 ATP binding protein [Bombyx mori]
sw01709	BGIBMGA010387	0.74205	1.03645	0.91	3.64905	9.00E-84	gi 5815357 gb AAD52652.1 J domain containing protein [Bombyx mori] J domain containing protein

sw04647	BGIBMGA004933	0.751	0.97595	0.7222	3.64715	5.00E-06	gi 12653931 gb AAH00759.1 NTF2-like export factor 1 [Homo sapiens] NTF2-like export factor 1 [Homo sapiens] NTF2-like export factor 1 [Homo sapiens] NTF2-like export factor 1 [Homo sapiens] NXT1
sw20346	BGIBMGA007678	1.5597	0.8628	1.3605	3.63995	8.00E-44	gi 66514096 ref XP_392261.2 PREDICTED: similar to ENSANGP00000015840 [Apis mellifera]
sw03016	BGIBMGA002151	0.8939	1.0902	1.0261	3.6391	7.00E-30	gi 70984713 ref XP_747863.1 peptidyl prolyl cis-trans isomerase [Aspergillus fumigatus Af293] peptidyl prolyl cis-trans isomerase (CypC), putative [Aspergillus fumigatus Af293]
sw00595	BGIBMGA003062	1.8259	1.33625	1.12435	3.6383	1.00E-21	gi 2961127 gb AAC05666.1 putative pupal-specific cuticular protein CP2b [Anopheles gambiae]
sw06251	BGIBMGA011764	1.68945	1.58705	1.23255	3.63475	No hits found	
sw03246	BGIBMGA011869	1.0103	1.3309	0.9941	3.63335	5.00E-06	gi 21356467 ref NP_649411.1 CG14450-PA [Drosophila melanogaster] RE67859p [Drosophila melanogaster] CG14450-PA [Drosophila melanogaster]
sw05747	BGIBMGA006794	0.9452	1.23065	1.10885	3.6298	3.00E-42	gi 7340062 gb AAF61067.1 testis enhanced gene transcript-like protein [Paralichthys olivaceus] Probable Bax inhibitor-1 (BI-1)
sw14297	BGIBMGA003840	0.70715	0.66265	1.01615	3.62745	2.00E-28	gi 17945870 gb AAL48981.1 RE39488p [Drosophila melanogaster]
sw17300	BGIBMGA007123	1.0195	0.99915	0.9744	3.6251	No hits found	
sw17048	BGIBMGA003698	0.6904	1.1089	0.8297	3.62485	3.00E-21	gi 28574095 ref NP_652562.2 CG18661-PA [Drosophila melanogaster] CG18661-PA [Drosophila melanogaster]
sw13398	BGIBMGA002540	0.92545	1.0469	1.0954	3.6243	1.00E-52	gi 6006703 gb AAF00577.1 protoporphyrinogen oxidase [Drosophila melanogaster]
sw05265	BGIBMGA001278	0.99985	1.1231	0.95765	3.6181	6.00E-50	gi 34899120 ref NP_910906.1 putative adenosine deaminase [Oryza sativa (japonica cultivar-group)] putative adenosine deaminase [Oryza sativa (japonica cultivar-group)]
sw08480	BGIBMGA000681	4.27915	1.57315	2.479	3.6104	1.00E-14	gi 6706437 emb CAB66004.1 Gly-rich protein [Drosophila melanogaster]
sw03796	BGIBMGA004009	0.7396	0.8941	0.8191	3.59665	1.00E-38	gi 4505369 ref NP_002486.1 NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) [Homo sapiens] NADH:ubiquinone oxidoreductase 18 kDa IP subunit
sw12210	BGIBMGA000948	1.0209	1.18395	0.74875	3.59435	7.00E-61	gi 87248261 gb ABD36183.1 anaphase promoting complex subunit 10 [Bombyx mori]
sw04194	BGIBMGA007193	0.9186	1.14815	1.0677	3.5941	3.00E-72	gi 40352976 gb AAH64593.1 DCP2 protein [Homo sapiens]
sw20297	BGIBMGA004524	1	1.4537	1.83195	3.5869	2.00E-35	gi 62637998 gb AAX92638.1 glucose transporter 8 [Solenopsis invicta]
sw13821	BGIBMGA011019	0.7455	1.00075	1.0145	3.58675	e-120	gi 87248121 gb ABD36113.1 endothelial-monocyte activating polypeptide II [Bombyx mori]
sw15711	BGIBMGA004218	0.7422	0.99545	0.796	3.5789	1.00E-63	gi 73992280 ref XP_867233.1 PREDICTED: similar to Dolichol-phosphate mannosyltransferase (Dolichol-phosphate mannose synthase) (Dolichyl-phosphate beta-D-mannosyltransferase)
sw11028	BGIBMGA010841	0.91325	0.99595	0.83235	3.57765	4.00E-13	gi 25012207 gb AAN71219.1 GM25447p [Drosophila melanogaster]
sw21957	BGIBMGA000086	1.02405	1.2405	1.1237	3.57555	3.00E-57	gi 66500131 ref XP_392131.2 PREDICTED: similar to MGC68697 protein [Apis mellifera]
sw14956	BGIBMGA005943	0.8959	0.95345	0.8299	3.5745	3.00E-98	gi 55235413 gb EAA14740.2 ENSANGP00000015949 [Anopheles gambiae str. PEST] ENSANGP00000015949 [Anopheles gambiae str. PEST]
sw17819	BGIBMGA010975	0.8697	1.19725	1.1201	3.566	5.00E-49	gi 74095893 ref NP_001027774.1 FRG1 protein [Takifugu rubripes] FRG1 [Takifugu rubripes] FRG1 [Takifugu rubripes] FRG1 protein
sw11182	BGIBMGA004978	0.9477	0.97135	0.89185	3.5588	1.00E-23	gi 55239530 gb EAA10573.2 ENSANGP00000021605 [Anopheles gambiae str. PEST] ENSANGP00000021605 [Anopheles gambiae str. PEST]
sw21012	BGIBMGA006507	0.6543	0.93395	0.78225	3.5569	2.00E-92	gi 3283068 gb AAC72298.1 reverse transcriptase [Caenorhabditis elegans]
sw20307	BGIBMGA006760	0.80795	1.12135	0.8075	3.5563	6.00E-12	gi 47217972 emb CAG02255.1 unnamed protein product [Tetraodon nigroviridis]
sw17807	BGIBMGA010560	1	0.4504	0.53785	3.5443	0	gi 73994438 ref XP_849294.1 PREDICTED: similar to phosphatidylinositol transfer protein, membrane-associated 2 isoform 2 [Canis familiaris]
sw10037	BGIBMGA007549	1.00735	1.08195	0.5945	3.537	5.00E-09	gi 76642627 ref XP_593949.2 PREDICTED: similar to tigger transposable element derived 1 [Bos taurus]

sw10747	BGIBMGA009830	1.1275	1.45765	1.40725	3.5298	e-112	gi 50416646 gb AAH77665.1 Integrin beta 4 binding protein [Xenopus tropicalis] integrin beta 4 binding protein [Xenopus tropicalis] integrin beta 4 binding protein [Xenopus tropicalis] integrin beta 4 binding protein [Xenopus tropicalis]
sw18585	BGIBMGA010745	1.37205	1.0557	1.40475	3.52605	e-102	gi 49899179 gb AAH75765.1 IMP4, U3 small nucleolar ribonucleoprotein, homolog [Danio rerio] IMP4, U3 small nucleolar ribonucleoprotein, homolog [Danio rerio]
sw22978	BGIBMGA005460	0.9712	1.10585	1.1601	3.5258	1.00E-95	gi 68397044 ref XP_708002.1 PREDICTED: similar to Ftsj homolog isoform 2 [Danio rerio] PREDICTED: similar to Ftsj homolog isoform 2 [Danio rerio]
sw07699	BGIBMGA009454	0.82615	1.407	1	3.5196	1.00E-64	gi 76630905 ref XP_873154.1 PREDICTED: similar to chromosome 9 open reading frame 78 isoform 2 isoform 2 [Bos taurus]
sw00299	BGIBMGA007734	1.02835	1.1505	1.25265	3.51875	8.00E-90	gi 66509665 ref XP_397030.2 PREDICTED: similar to bystin [Apis mellifera]
sw20314	BGIBMGA012866	1.54545	0.83625	0.338	3.50685	1.00E-72	gi 13359090 dbj BAB33294.1 Bacteriophage T7 lysozyme-like protein 1 (BTL-LP1) [Bombyx mori]
sw14167	BGIBMGA003386	0.6473	1.14135	1.03695	3.4988	3.00E-14	gi 9930610 gb AAG02114.1 steroid receptor RNA activator isoform 1 [Homo sapiens]
sw05478	BGIBMGA009559	0.65585	0.895	0.77325	3.4921	9.00E-32	gi 62648312 ref XP_342783.2 PREDICTED: similar to CGI-141 protein [Rattus norvegicus]
sw04453	BGIBMGA009033	1.10195	1.2061	1.01635	3.4918	1.00E-58	gi 7862150 gb AAF70499.1 3-dehydroecdysone 3alpha-reductase [Spodoptera littoralis]
sw22960	BGIBMGA010563	2.26375	1.46315	2.29005	3.48925	6.00E-42	gi 37591031 dbj BAC98835.1 juvenile hormone acid methyltransferase [Bombyx mori]
sw22947	BGIBMGA009009	1.0098	1.1762	1.30555	3.4869	3.00E-31	gi 34870767 ref XP_220504.2 PREDICTED: similar to novel zinc finger protein [Rattus norvegicus]
sw12949	BGIBMGA009279	1	1	1	3.45635	2.00E-06	gi 26006205 dbj BAC41445.1 mKIAA0701 protein [Mus musculus]
sw08936	BGIBMGA006859	0.91025	0.9405	0.79585	3.45035	3.00E-10	gi 68364782 ref XP_690709.1 PREDICTED: similar to mitochondrial NADH-ubiquinone oxidoreductase ESSS subunit precursor [Danio rerio]
sw09007	BGIBMGA014563	1.2087	1.2125	1.28455	3.44805	8.00E-51	gi 55641019 ref XP_510046.1 PREDICTED: similar to chromosome 14 open reading frame 169; NO66 [Pan troglodytes]
sw13748	BGIBMGA001943	0.8259	1.11345	0.932	3.44715	3.00E-38	gi 50539666 ref NP_001002298.1 arsA arsenite transporter, ATP-binding, homolog 1 [Danio rerio] ArsA arsenite transporter, ATP-binding, homolog 1 [Danio rerio]
sw11723	BGIBMGA008621	1.2601	1.21135	1.3012	3.44515	6.00E-81	gi 72006882 ref XP_780014.1 PREDICTED: similar to 3-hydroxyacyl-CoA dehydrogenase type II (Type II HADH) (Scully protein) isoform 1 [Strongylocentrotus purpuratus]
sw03582	BGIBMGA010723	0.752	0.8222	0.99735	3.44095	1.00E-36	gi 50417589 gb AAH77664.1 MGC89748 protein [Xenopus tropicalis] MGC89748 protein [Xenopus tropicalis] small nuclear ribonucleoprotein D2 polypeptide 16.5kDa [Xenopus tropicalis]
sw08576	BGIBMGA012606	1.87615	0.71925	0.99895	3.434	No hits found	
sw03207	BGIBMGA007490	1.02715	1.0692	1.072	3.425	e-178	gi 90309026 gb ABA43638.2 glyceraldehyde-3-phosphate dehydrogenase [Bombyx mori]
sw08771	BGIBMGA011824	0.69305	0.90815	0.7418	3.42335	2.00E-36	gi 51261910 gb AAH79933.1 MGC79564 protein [Xenopus tropicalis] MGC79564 protein [Xenopus tropicalis] ARD1 homolog A, N-acetyltransferase
sw09115	BGIBMGA013923	0.7921	0.89075	0.8561	3.42315	8.00E-42	gi 73960888 ref XP_547528.2 PREDICTED: similar to mitochondrial ribosomal protein L24 isoform 1 [Canis familiaris]
sw13447	BGIBMGA010734	1	1	1	3.42255	No hits found	
sw04091	BGIBMGA002546	0.9758	1	0.76305	3.4214	5.00E-24	gi 72092440 ref XP_790987.1 PREDICTED: similar to peptide deformylase-like protein [Strongylocentrotus purpuratus]
sw09558	BGIBMGA011493	0.8274	1.24935	0.89325	3.41835	6.00E-36	gi 266752 sp P29702 PFTA_BOVIN Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit (CAAX farnesyltransferase alpha subunit)
sw09837	BGIBMGA009504	0.69285	1.04265	0.8559	3.41405	Bmb036914	9.00E-25
sw21496	BGIBMGA008878	0.75275	1.1699	0.84725	3.4119	Bmb025395	1.00E-24
sw11603	BGIBMGA011856	0.96625	1.02235	0.83465	3.41155	8.00E-38	gi 77403939 gb ABA81848.1 AT16804p [Drosophila melanogaster] CG10809-PA [Drosophila melanogaster] CG10809-PA [Drosophila melanogaster]
sw22043	BGIBMGA013864	1.09445	0.59215	0.5785	3.4076	5.00E-98	gi 52421209 dbj BAD51475.1 gloverin-like protein 3 [Bombyx mori]

sw03657	BGIBMGA012563	0.91325	1.34765	1	3.405	6.00E-18	gi 66560076 ref XP_624348.1 PREDICTED: similar to CG12114-PA [Apis mellifera]
sw17253	BGIBMGA012850	0.82675	1.1189	0.92825	3.39575	7.00E-08	gi 68373919 ref XP_691048.1 PREDICTED: similar to zinc finger protein 569 [Danio rerio]
sw15517	BGIBMGA010229	0.98975	1.1503	1.0609	3.3931	2.00E-10	gi 54311324 gb AAH84843.1 LOC495376 protein [Xenopus laevis]
sw08542	BGIBMGA009802	0.85365	1.2953	1.32085	3.38035	4.00E-09	gi 21292650 gb EAA04795.1 ENSANGP00000019625 [Anopheles gambiae str. PEST] ENSANGP00000019625 [Anopheles gambiae str. PEST]
sw16856	BGIBMGA004846	0.87925	0.97295	1.12755	3.3802	Bmb048286	6.00E-30
sw01422	BGIBMGA002563	1.5304	0.9244	0.9523	3.3738	No hits found	
sw13103	BGIBMGA012537	0.9488	1.29205	1.0426	3.36615	e-113	gi 87248541 gb ABD36323.1 mitochondrial ribosomal protein L32 [Bombyx mori]
sw06690	BGIBMGA004838	1.12365	1.14865	1.15845	3.3652	2.00E-13	gi 50756073 ref XP_415003.1 PREDICTED: similar to mitochondrial ribosomal protein S5; mitochondrial 28S ribosomal protein S5 [Gallus gallus]
sw04653	BGIBMGA007630	1	1.2298	1	3.3647	5.00E-31	gi 76608529 ref XP_883507.1 PREDICTED: similar to ZK1058.5 isoform 2 [Bos taurus]
sw07293	BGIBMGA010193	0.6423	0.9298	0.8057	3.3647	9.00E-59	gi 87248225 gb ABD36165.1 short-chain dehydrogenase/reductase [Bombyx mori]
sw01825	BGIBMGA007173	0.96575	1.21945	0.9587	3.3543	1.00E-69	gi 66553058 ref XP_623865.1 PREDICTED: similar to Syntaxin 18 (predicted) [Apis mellifera]
sw21459	BGIBMGA000039	0.7354	0.1754	0.29065	3.3526	No hits found	
sw11297	BGIBMGA009893	0.9997	1.19465	1.227	3.34885	5.00E-64	gi 72008188 ref XP_781285.1 PREDICTED: similar to Exosome complex exonuclease RRP40 (Ribosomal RNA processing protein 40) (Exosome component 3) (p10) [Strongylocentrotus purpuratus]
sw12164	BGIBMGA007676	1.49775	1.3862	1.09835	3.3473	0	gi 62647472 ref XP_216173.3 PREDICTED: similar to ubiquitin specific protease 39 [Rattus norvegicus]
sw17728	BGIBMGA008663	1.1776	1.1008	0.85105	3.34595	No hits found	
sw04446	BGIBMGA005384	0.70515	0.87545	0.7639	3.34545	2.00E-15	gi 12803607 gb AAH02638.1 P53-inducible cell-survival factor [Homo sapiens] P53-inducible cell-survival factor [Homo sapiens] p53-inducible cell-survival factor
sw18213	BGIBMGA006083	0.7592	0.8457	1.0532	3.34255	4.00E-25	gi 76608452 ref XP_874747.1 PREDICTED: similar to Carbonyl reductase [NADPH] 1 (NADPH-dependent carbonyl reductase 1)
sw18236	BGIBMGA006653	0.8619	1.009	1.07835	3.34035	No hits found	
sw04526	BGIBMGA007025	1.2407	0.98165	1.0806	3.33975	Bmb037524	6.00E-53
sw14459	BGIBMGA007146	1.3606	1.47215	1.1077	3.33585	e-124	gi 49329405 gb AAT60051.1 kynureninase [Bacillus thuringiensis serovar konkukian str. 97-27] kynureninase [Bacillus thuringiensis serovar konkukian str. 97-27]
sw22928	BGIBMGA002423	0.95615	1.1013	0.91865	3.33535	2.00E-34	gi 48098602 ref XP_394113.1 PREDICTED: similar to CG1458-PA [Apis mellifera]
sw13044	BGIBMGA011078	0.68935	1.19075	0.61055	3.33015	6.00E-05	gi 6560645 gb AAF16700.1 juvenile hormone binding protein precursor-like protein [Manduca sexta]
sw14233	BGIBMGA007266	1.00725	1.28295	0.9557	3.3296	Bmb023690	9.00E-52
sw19198	BGIBMGA006638	1.0057	1.17755	1.1188	3.3173	7.00E-22	gi 87248471 gb ABD36288.1 calcitonin gene-related peptide-receptor component protein [Bombyx mori]
sw13830	BGIBMGA004023	0.7419	0.8781	0.9364	3.31335	3.00E-44	gi 25013122 gb AAN71660.1 SD14834p [Drosophila melanogaster]
sw13406	BGIBMGA000112	0.9892	1.10855	1.05295	3.3108	3.00E-40	gi 90103466 gb ABD85577.1 unknown [Ictalurus punctatus]
sw22297	BGIBMGA011616	2.30325	1.5702	3.03355	3.3076	5.00E-23	gi 72016315 ref XP_783630.1 PREDICTED: similar to Fibrillin-2 precursor, partial [Strongylocentrotus purpuratus]
sw00457	BGIBMGA006631	0.96355	1.14375	1.01485	3.30645	9.00E-19	gi 56270469 gb AAH87416.1 LOC496023 protein [Xenopus laevis]

sw16286	BGIBMGA006754	0.84045	1.08315	0.87625	3.3052	Bmb040031	e-161
sw04869	BGIBMGA011061	0.9434	0.9536	0.81315	3.30495	7.00E-12	gi 76676986 ref XP_591925.2 PREDICTED: similar to CG12379-PA [Bos taurus]
sw02779	BGIBMGA008137	1	0.8413	1	3.28305	1.00E-48	gi 21064791 gb AAM29625.1 RH67819p [Drosophila melanogaster]
sw17094	BGIBMGA011031	0.86565	1.21335	0.7647	3.2795	4.00E-20	gi 21357917 ref NP_650514.1 CG4287-PA [Drosophila melanogaster] GH08991p [Drosophila melanogaster] CG4287-PA [Drosophila melanogaster]
sw10439	BGIBMGA003563	0.87915	0.9284	0.88725	3.27885	3.00E-06	gi 72146037 ref XP_797557.1 PREDICTED: similar to Myc-induced mitochondria protein [Strongylocentrotus purpuratus]
sw15421	BGIBMGA000293	1.198	1.17985	1.081	3.27705	6.00E-31	gi 14211570 dbj BAB56112.1 conserved ERA-like GTPase [Homo sapiens]
sw18742	BGIBMGA009671	0.8869	0.90415	1.00255	3.27705	8.00E-47	gi 72005686 ref XP_780645.1 PREDICTED: similar to isochorismatase domain containing 1 [Strongylocentrotus purpuratus]
sw05567	BGIBMGA012403	1.48865	1.2945	1.48925	3.27485	9.00E-10	gi 54636883 gb EAL26286.1 GA10354-PA [Drosophila pseudoobscura]
sw09446	BGIBMGA002417	0.8522	1.17685	0.85535	3.27375	Bmb030081	4.00E-17
sw07006	BGIBMGA011450	1.0402	1.3244	1.11625	3.2687	Bmb040045	2.00E-84
sw05257	BGIBMGA009618	0.8471	0.78115	0.9092	3.26655	No hits found	
sw11364	BGIBMGA006632	0.91005	1.0876	1.17785	3.2657	3.00E-29	gi 72005635 ref XP_785582.1 PREDICTED: similar to WD repeat domain 58 [Strongylocentrotus purpuratus]
sw09679	BGIBMGA011697	0.8127	1.0748	0.8774	3.2649	3.00E-20	gi 41054111 ref NP_956148.1 ring finger protein 146 [Danio rerio] Ring finger protein 146 [Danio rerio]
sw14835	BGIBMGA002933	0.402	0.92545	0.68325	3.26435	No hits found	
sw06597	BGIBMGA003527	0.4496	1.17275	0.6386	3.2471	8.00E-51	gi 25012624 gb AAN71409.1 RE44531p [Drosophila melanogaster]
sw05314	BGIBMGA001283	1.06515	1.3651	1.4077	3.24645	3.00E-21	gi 27695162 gb AAH43795.1 Mak16l-prov protein [Xenopus laevis] MAK16-like protein RBM13 B (RNA binding motif protein 13-like B)
sw10989	BGIBMGA013497	1.20925	0.89395	1.2117	3.24645	5.00E-65	gi 27462217 gb AAO15385.1 DAP3 [Drosophila melanogaster]
sw22147	BGIBMGA003616	1.65545	1.78335	1.1662	3.24465	2.00E-18	gi 72111613 ref XP_791607.1 PREDICTED: similar to phospholipid scramblase 1 [Strongylocentrotus purpuratus]
sw08911	BGIBMGA013542	2.05445	1.6801	0.61215	3.2444	Bmb021438	No hits found
sw09671	BGIBMGA006920	0.74975	0.92775	0.69595	3.2443	1.00E-23	gi 72047001 ref XP_787000.1 PREDICTED: similar to programmed cell death 6 (1F340), partial [Strongylocentrotus purpuratus]
sw15014	BGIBMGA007408	0.8938	0.829	0.7816	3.244	9.00E-38	gi 74002101 ref XP_535685.2 PREDICTED: similar to Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precursor (HCDH) (Medium and short chain L-3-hydroxyacyl-coenzyme A dehydrogenase) isoform 1 [Canis familiaris]
sw05030	BGIBMGA004008	0.80415	0.9498	0.8453	3.2354	2.00E-07	gi 72024737 ref XP_799052.1 PREDICTED: similar to coiled-coil-helix-coiled-coil-helix domain containing 1 [Strongylocentrotus purpuratus]
sw06168	BGIBMGA006477	0.6352	0.7954	0.994	3.2348	3.00E-29	gi 72005469 ref XP_785869.1 PREDICTED: similar to prefoldin 5 [Strongylocentrotus purpuratus]
sw14679	BGIBMGA006574	1.0909	1.04885	1.35755	3.2331	3.00E-73	gi 68358710 ref XP_688730.1 PREDICTED: similar to heat shock 70kDa protein 14 isoform 1 [Danio rerio]
sw20681	BGIBMGA012873	0.8395	1.0868	0.8646	3.23285	2.00E-10	gi 20071201 gb AAH26744.1 Vacuolar protein sorting 37B [Mus musculus] vacuolar protein sorting 37B [Mus musculus]
sw09038	BGIBMGA010866	0.7214	0.87715	0.79915	3.22645	5.00E-91	gi 32029913 ref ZP_00132857.1 COG0451: Nucleoside-diphosphate-sugar epimerases [Haemophilus somnus 2336] COG0451: Nucleoside-diphosphate-sugar epimerases [Haemophilus somnus 129PT]
sw14128	BGIBMGA000882	0.57585	0.9283	0.7977	3.22165	1.00E-32	gi 87248177 gb ABD36141.1 ribosomal protein L27 [Bombyx mori]
sw14985	BGIBMGA000506	0.68965	0.9115	0.85555	3.2169	4.00E-32	gi 74006183 ref XP_545715.2 PREDICTED: similar to lysophospholipase-like 1 [Canis familiaris]

sw03143	BGIBMGA001444	1	0.8157	1.31645	3.21425	3.00E-91	gi 23096118 dbj BAC16225.1 cuticle protein [Bombyx mori]
sw05818	BGIBMGA009816	1.0969	1.2013	1.45765	3.21265	e-163	gi 50758198 ref XP_415805.1 PREDICTED: similar to splicing factor Prp8 [Gallus gallus]
sw17569	BGIBMGA007973	1	0.94995	1	3.20855	No hits found	
sw04361	BGIBMGA007744	0.8762	0.8888	0.6847	3.2076	7.00E-09	gi 46249482 gb AAH68670.1 MGC81062 protein [Xenopus laevis] Sld5 [Xenopus laevis]
sw11939	BGIBMGA006198	1.0896	1.0756	1.0358	3.20755	3.00E-32	gi 41529182 dbj BAD08441.1 mitochondrial ribosomal protein S18-2 [Sus scrofa] mitochondrial ribosomal protein S18-2 [Sus scrofa]
sw10616	BGIBMGA000801	1.31455	1.258	0.976	3.20745	No hits found	
sw20320	BGIBMGA005955	0.7528	1.07655	0.9219	3.20585	3.00E-23	gi 27465077 gb AAO12862.1 Camar1 transposase [Chymomyza amoena]
sw10358	BGIBMGA011578	0.95425	1.2916	1.19235	3.20015	4.00E-07	gi 62859459 ref NP_001016090.1 hypothetical protein LOC548844 [Xenopus tropicalis]
sw03481	BGIBMGA007780	1	1.89925	1	3.1979	1.00E-47	gi 77686775 ref ZP_00802100.1 Indigoidine synthase A like protein [Alkaliphilus metalliredigenes QYMF] Indigoidine synthase A like protein [Alkaliphilus metalliredigenes QYMF]
sw05264	BGIBMGA014607	0.75155	0.9502	0.71735	3.1974	8.00E-47	gi 87248417 gb ABD36261.1 translocase of inner mitochondrial membrane 8 homolog b [Bombyx mori]
sw15298	BGIBMGA013785	1.10375	1.13005	0.9218	3.1906	No hits found	
sw13309	BGIBMGA007688	0.98595	1.07175	0.8774	3.18185	7.00E-47	gi 48097408 ref XP_391891.1 PREDICTED: similar to zinc finger, ZZ domain containing 3 [Apis mellifera]
sw03458	BGIBMGA010016	0.97745	0.9744	1.0889	3.1805	4.00E-54	gi 87248389 gb ABD36247.1 rotamase Pin1 [Bombyx mori]
sw06454	BGIBMGA012774	0.95925	1.3744	1.2024	3.17425	8.00E-32	gi 24642095 ref NP_572999.1 CG15027-PA [Drosophila melanogaster] CG15027-PA [Drosophila melanogaster]
sw04870	BGIBMGA008492	1.0187	1.80415	1.7541	3.17275	8.00E-16	gi 54645636 gb EAL34374.1 GA10125-PA [Drosophila pseudoobscura]
sw18921	BGIBMGA009495	0.7584	0.9024	0.877	3.1722	0	gi 54290087 dbj BAD61055.1 RFC40 [Bombyx mori]
sw13377	BGIBMGA004056	0.8585	0.8798	0.93145	3.16985	2.00E-21	gi 62642817 ref XP_226716.3 PREDICTED: similar to Pentatricopeptide repeat domain 2 [Rattus norvegicus]
sw05505	BGIBMGA003422	0.74285	0.83585	0.57815	3.16935	5.00E-11	gi 55243996 gb EAA06017.3 ENSANGP00000017964 [Anopheles gambiae str. PEST] ENSANGP00000017964 [Anopheles gambiae str. PEST]
sw06665	BGIBMGA003070	0.8652	0.99665	0.8712	3.1649	4.00E-28	gi 14250353 gb AAH08607.1 Translocase of inner mitochondrial membrane 13 [Homo sapiens] translocase of inner mitochondrial membrane 13 [Homo sapiens] TIMM13b [Homo sapiens] small zinc finger-like protein
sw01123	BGIBMGA011459	1.05665	1.13105	0.9106	3.1648	Bmb016767	4.00E-25
sw14615	BGIBMGA005519	0.87205	0.95965	1.08345	3.16445	1.00E-04	gi 42733535 dbj BAD11364.1 TOM22 [Rattus norvegicus] TOM22 protein [Rattus norvegicus] TOM22 protein [Rattus norvegicus]
sw08356	BGIBMGA002886	1.06135	1.1467	0.78055	3.15895	3.00E-51	gi 55669751 pdb 1SNY A Chain A, Carbonyl Reductase Sniffer Of D. Melanogaster
sw13511	BGIBMGA005615	0.66375	0.8502	0.7176	3.15825	8.00E-50	gi 72121083 gb AAZ63269.1 Zinc-containing alcohol dehydrogenase superfamily [Ralstonia eutropha JMP134] Zinc-containing alcohol dehydrogenase superfamily [Ralstonia eutropha JMP134]
sw07771	BGIBMGA012478	0.7941	0.8599	1.05255	3.1573	9.00E-30	gi 2331217 gb AAB66878.1 trypsin [Anopheles stephensi]
sw03543	BGIBMGA007702	0.90555	1.09455	1.1075	3.14595	6.00E-79	gi 2285788 dbj BAA21658.1 Multiprotein bridging factor 1 [Bombyx mori]
sw08382	BGIBMGA002720	0.7397	1.1591	0.69985	3.14255	No hits found	
sw15595	BGIBMGA001490	0.8492	1.18575	1.81515	3.14135	e-133	gi 68160236 gb AAY86706.1 45 kDa immunophilin FKBP45 [Bombyx mori]
sw16230	BGIBMGA002445	0.83335	1.2076	1.26985	3.1344	3.00E-36	gi 89268189 emb CAJ83671.1 adenosine deaminase, tRNA-specific 1 [Xenopus tropicalis]

sw08133	BGIBMGA012474	0.7398	0.9055	0.9205	3.1324	1.00E-37	gi 66539173 ref XP_624932.1 PREDICTED: similar to Huntingtin interacting protein K, partial [Apis mellifera]
sw14639	BGIBMGA011782	1.0933	1.07795	1.0757	3.13045	1.00E-41	gi 73958726 ref XP_861741.1 PREDICTED: similar to exonuclease NEF-sp isoform 5 [Canis familiaris]
sw09583	BGIBMGA009113	0.6736	1.1058	0.98635	3.12725	2.00E-16	gi 76658212 ref XP_887786.1 PREDICTED: similar to Nucleoside diphosphate-linked moiety X motif 8, mitochondrial precursor (Nudix motif 8) isoform 2 [Bos taurus]
sw21578	BGIBMGA013054	0.811	1.17275	1.2009	3.1246	Bmb040067	e-123
sw16042	BGIBMGA004870	1.10735	1.25075	1.2345	3.12435	No hits found	
sw03532	BGIBMGA009360	0.9198	1.1711	0.90865	3.1235	1.00E-33	gi 66504312 ref XP_395230.2 PREDICTED: similar to DNA polymerase gamma [Apis mellifera]
sw04517	BGIBMGA008815	1.0526	1.17035	0.9006	3.1204	7.00E-63	gi 49532884 dbj BAD26677.1 Juvenile hormone diol kinase [Plutella xylostella]
sw07091	BGIBMGA004280	1.2673	0.96145	1.0756	3.11805	Bmb042783	2.00E-81
sw07852	BGIBMGA005306	0.39475	1.0466	0.65895	3.11385	2.00E-07	gi 72014822 ref XP_783246.1 PREDICTED: similar to sarcolemma associated protein [Strongylocentrotus purpuratus]
sw14170	BGIBMGA001806	0.9467	1.20165	1.1921	3.1078	e-106	gi 66499810 ref XP_624522.1 PREDICTED: similar to cleavage and polyadenylation specific factor 5 [Apis mellifera]
sw12428	BGIBMGA006568	0.8183	0.8749	0.92195	3.10595	1.00E-48	gi 55245504 gb EAA04466.2 ENSANGP00000018430 [Anopheles gambiae str. PEST] ENSANGP00000018430 [Anopheles gambiae str. PEST]
sw08641	BGIBMGA008494	0.94315	1.1391	0.9906	3.0993	Bmb017333	1.00E-20
sw08766	BGIBMGA011338	0.94795	0.9728	1.0491	3.09535	8.00E-98	gi 38176158 ref NP_003849.2 cyclin K [Homo sapiens] Cyclin K [Homo sapiens] cyclin K [Homo sapiens] cyclin K [Homo sapiens] cyclin K [Homo sapiens] cyclin K [synthetic construct] cyclin K [synthetic construct]
sw09618	BGIBMGA008478	0.79275	1.25265	1.09185	3.09505	Bmb032873	3.00E-29
sw15985	BGIBMGA012059	1.26765	1.276	1.35535	3.08205	8.00E-40	gi 27462213 gb AAO15383.1 multiple hat domains [Mus musculus]
sw06451	BGIBMGA002985	0.7175	1.0562	0.84065	3.0789	3.00E-73	gi 3983135 gb AAC83820.1 platelet-activating factor acetylhydrolase alpha subunit homolog [Drosophila melanogaster]
sw08302	BGIBMGA005659	0.8183	1.03505	0.86765	3.07785	1.00E-17	gi 25013071 gb AAN71628.1 RH67738p [Drosophila melanogaster]
sw08827	BGIBMGA012029	0.7413	0.92205	0.63255	3.07705	2.00E-42	gi 87248631 gb ABD36368.1 mitochondrial thioredoxin 2 [Bombyx mori]
sw19580	BGIBMGA010370	1.6497	0.88645	0.71975	3.07385	3.00E-47	gi 4160012 gb AAD05225.1 dissatisfaction [Drosophila melanogaster]
sw01104	BGIBMGA000320	1.0181	0.8504	1.1564	3.07275	2.00E-23	gi 68371190 ref XP_696017.1 PREDICTED: similar to programmed cell death 2 [Danio rerio]
sw06213	BGIBMGA010349	1.87405	1.715	1.4625	3.0638	4.00E-21	gi 15146427 gb AAK84661.1 retinoid-inducible serine carboxypeptidase precursor [Rattus norvegicus] serine carboxypeptidase 1 [Rattus norvegicus] Retinoid-inducible serine carboxypeptidase precursor (Serine carboxypeptidase 1)
sw15398	BGIBMGA009239	0.711	0.89365	0.8618	3.05875	Bmb032363	No hits found
sw09920	BGIBMGA001163	1	1	1	3.0581	e-127	gi 48094345 ref XP_394147.1 PREDICTED: similar to cyclic AMP-dependent catalytic subunit (41.4 kD) (kin-1) [Apis mellifera]
sw14215	BGIBMGA000926	0.6608	0.81265	0.79755	3.0561	9.00E-46	gi 12002054 gb AAG43169.1 transaldolase [Rattus norvegicus] Transaldolase
sw14910	BGIBMGA009706	1.07145	0.9293	0.91015	3.05515	3.00E-33	gi 55632729 ref XP_520400.1 PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa; NADH:ubiquinone oxidoreductase 19 kDa subunit; NADH:ubiquinone oxidoreductase PGIV subunit
sw11857	BGIBMGA007452	1.2332	1.23325	0.9803	3.0485	2.00E-09	gi 49618945 gb AAT68057.1 pinball wizard [Danio rerio] tryptophan rich basic protein [Danio rerio]
sw04522	BGIBMGA002766	1.18965	1.3139	1.38135	3.04575	2.00E-40	gi 62858747 ref NP_001016308.1 apoptosis antagonizing transcription factor [Xenopus tropicalis]
sw15787	BGIBMGA001340	0.84125	0.963	0.8362	3.03355	6.00E-90	gi 66515816 ref XP_392546.2 PREDICTED: similar to Pantothenate kinase 4 (Pantothenic acid kinase 4) (hPank4), partial [Apis mellifera]

sw10500	BGIBMGA012093	0.8445	0.8319	0.97855	3.0333	e-167	gi 6448449 dbj BAA86901.1 mitochondrial carrier homolog [Bombyx mori]
sw17844	BGIBMGA005739	0.4853	0.83325	0.6231	3.03025	3.00E-31	gi 68362888 ref XP_697922.1 PREDICTED: similar to DNA-directed RNA polymerase II 7.6 kDa polypeptide (RPB10) (RPB7.6) (RPABC5) [Danio rerio]
sw13376	BGIBMGA001464	0.94405	0.9608	1.17395	3.02825	1.00E-76	gi 55640387 ref XP_509840.1 PREDICTED: similar to oxidase (cytochrome c) assembly 1-like [Pan troglodytes]
sw14544	BGIBMGA005023	0.82485	1.1401	0.91945	3.0271	1.00E-23	gi 71153817 sp Q9NX58 LYAR_HUMAN Cell growth-regulating nucleolar protein
sw08769	BGIBMGA013896	0.8972	0.9976	1.2133	3.0229	2.00E-75	gi 56270437 gb AAH87307.1 LOC495942 protein [Xenopus laevis]
sw00137	BGIBMGA010231	3.29465	0.5963	1.481	3.02175	2.00E-24	gi 87248419 gb ABD36262.1 larval cuticle protein [Bombyx mori]
sw16228	BGIBMGA006401	0.5594	0.67325	0.84125	3.01805	Bmb039284	8.00E-19
sw16854	BGIBMGA007767	1.41845	0.73505	0.87545	3.0115	Bmb048271	1.00E-74
sw18883	BGIBMGA005897	0.79005	1.3136	1.1784	3.01135	2.00E-92	gi 28317069 gb AAO39553.1 RE01362p [Drosophila melanogaster]
sw06760	BGIBMGA012554	0.9475	0.88025	0.78175	3.01105	Bmb034003	8.00E-11
sw21407	BGIBMGA006219	0.7739	1.0804	0.75605	3.0108	4.00E-06	gi 62644944 ref XP_575113.1 PREDICTED: similar to Hypothetical UPF0184 protein C9orf16 homolog [Rattus norvegicus]
sw14203	BGIBMGA011656	0.9584	1.2901	1.2879	3.0102	2.00E-38	gi 54636912 gb EAL26315.1 GA11566-PA [Drosophila pseudoobscura]
sw11583	BGIBMGA001068	1.0169	1.02585	1.18075	3.00565	8.00E-95	gi 87248327 gb ABD36216.1 fumarylacetoacetate hydrolase isoform A [Bombyx mori]
sw21178	BGIBMGA001792	0.7409	1.0765	0.9675	3.00075	1.00E-24	gi 73949006 ref XP_544251.2 PREDICTED: similar to Artemis protein (DNA cross-link repair 1C protein) (SNM1-like protein) (A-SCID protein) (hSNM1C) isoform 1 [Canis familiaris]
sw17304	BGIBMGA001343	1.2077	1.09835	0.9301	3.0005	6.00E-45	gi 58476597 gb AAH89985.1 Fused toes (predicted) [Rattus norvegicus] fused toes (predicted) [Rattus norvegicus]
sw13351	BGIBMGA000332	1.44705	0.6839	1.02845	2.9922	5.00E-20	gi 3913392 sp O02388 CU22_BOMMO Larval cuticle protein LCP-22 precursor LCP22 [Bombyx mori]
sw22950	BGIBMGA000940	1.1445	1.19465	0.926	2.9866	1.00E-28	gi 66499360 ref XP_396507.2 PREDICTED: similar to CG11550-PA [Apis mellifera]
sw04913	BGIBMGA003663	1	1.085	1	2.98565	2.00E-40	gi 50750445 ref XP_421997.1 PREDICTED: similar to methionine aminopeptidase 1D; similar to methionine aminopeptidase-like 1 [Gallus gallus]
sw16343	BGIBMGA007263	1.08265	1.374	1.25415	2.9851	4.00E-05	gi 24582874 ref NP_609236.2 CG13096-PA [Drosophila melanogaster] CG13096-PA [Drosophila melanogaster]
sw12549	BGIBMGA008574	1.07775	1.54095	0.92855	2.9847	5.00E-06	gi 21617857 ref NP_660193.1 CG15107-PA [Drosophila melanogaster] LD14312p [Drosophila melanogaster] CG15107-PA [Drosophila melanogaster]
sw09644	BGIBMGA004054	0.9977	1.27535	1.0227	2.98465	Bmb033291	2.00E-91
sw10427	BGIBMGA010129	1.11935	1.10495	1.26995	2.9818	e-161	gi 66552237 ref XP_623630.1 PREDICTED: similar to ribonuclease L inhibitor homolog [Apis mellifera]
sw03985	BGIBMGA009934	1.1318	0.95975	0.7892	2.98015	No hits found	
sw16645	BGIBMGA010621	1	0.94375	1.375	2.9801	e-178	gi 73988085 ref XP_862223.1 PREDICTED: similar to Ribonucleoside-diphosphate reductase large subunit (Ribonucleoside-diphosphate reductase M1 subunit) (Ribonucleotide reductase large chain) isoform 5 [Canis familiaris]
sw10573	BGIBMGA010920	1.28975	1.42965	1.00545	2.97835	4.00E-08	gi 55245618 gb EAL41836.1 ENSANGP00000027947 [Anopheles gambiae str. PEST] ENSANGP00000027947 [Anopheles gambiae str. PEST]
sw07976	BGIBMGA011696	0.8792	0.92125	1.00585	2.97785	8.00E-16	gi 48102233 ref XP_392756.1 PREDICTED: similar to GA14405-PA [Apis mellifera]
sw17810	BGIBMGA012127	0.88685	1.1207	1.52025	2.97695	1.00E-65	gi 89886082 ref NP_989268.2 glutamate-rich WD repeat containing 1 [Xenopus tropicalis] glutamate-rich WD repeat containing 1 [Xenopus tropicalis]
sw12206	BGIBMGA000338	1.2652	0.6625	1.1206	2.97355	1.00E-34	gi 47605413 sp Q7M4F3 CUD2_SCHGR Endocuticle structural glycoprotein SgAbd-2

sw14293	BGIBMGA010919	1.42745	1.7126	1.1242	2.97145	2.00E-20	gi 54637590 gb EAL26992.1 GA19958-PA [Drosophila pseudoobscura]
sw16101	BGIBMGA011899	0.78455	1.1833	0.88885	2.96975	2.00E-11	gi 82498917 ref ZP_00884371.1 diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases [Caldicellulosiruptor saccharolyticus DSM 8903] diadenosine tetraphosphate
sw15166	BGIBMGA012118	1.04305	1.1025	1.11055	2.9672	Bmb030649	e-104
sw17076	BGIBMGA011846	0.76605	1.0312	0.7128	2.9672	8.00E-40	gi 50753715 ref XP_414101.1 PREDICTED: similar to hypothetical protein FLJ38101 [Gallus gallus] PREDICTED: similar to hypothetical protein FLJ38101 [Gallus gallus]
sw21910	BGIBMGA000616	0.8103	1.03495	0.9071	2.9664	8.00E-25	gi 54641436 gb EAL30186.1 GA21196-PA [Drosophila pseudoobscura]
sw14801	BGIBMGA014257	1.4169	1.44805	0.9596	2.9625	No hits found	
sw12651	BGIBMGA006160	0.5586	1.03655	1.44745	2.96225	e-170	gi 76496246 gb ABA43639.1 L-threonine dehydrogenase [Bombyx mori]
sw22908	BGIBMGA009021	0.86305	1.07115	0.9062	2.95935	2.00E-49	gi 66564402 ref XP_396161.2 PREDICTED: similar to Sip-prov protein [Apis mellifera]
sw17113	BGIBMGA000061	0.65185	0.84705	0.70765	2.94795	5.00E-30	gi 62859501 ref NP_001017111.1 mitochondrial ribosomal protein L35 [Xenopus tropicalis]
sw02239	BGIBMGA000664	0.7748	1.6878	1.283	2.94785	6.00E-42	gi 87248467 gb ABD36286.1 unknown [Bombyx mori]
sw18482	BGIBMGA009726	0.95295	0.923	1.2149	2.9461	e-132	gi 87248625 gb ABD36365.1 translin [Bombyx mori]
sw20510	BGIBMGA008676	0.74485	0.6635	0.71575	2.9431	No hits found	
sw20836	BGIBMGA005710	0.4171	0.77975	1.0747	2.94	e-109	gi 474339 gb AAA17752.1 reverse transcriptase [Bombyx mori]
sw10418	BGIBMGA010137	0.7156	1.08425	0.89055	2.93975	3.00E-16	gi 24667277 ref NP_649195.1 CG13813-PA [Drosophila melanogaster] IP11764p [Drosophila melanogaster] CG13813-PA [Drosophila melanogaster]
sw16297	BGIBMGA000936	0.75095	0.98915	1.0466	2.9376	2.00E-80	gi 55250104 gb AAH85542.1 Ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) [Danio rerio] ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) [Danio rerio]
sw10381	BGIBMGA010620	0.78545	1.10255	0.89415	2.9361	6.00E-57	gi 89268101 emb CAJ83820.1 syntaxin 5A [Xenopus tropicalis]
sw14247	BGIBMGA008971	1.5026	1.59105	1	2.93585	3.00E-22	gi 24643546 ref NP_608400.1 CG15453-PA [Drosophila melanogaster] CG15453-PA [Drosophila melanogaster]
sw17423	BGIBMGA014117	0.9256	0.9292	0.9705	2.93545	8.00E-71	gi 62857375 ref NP_001017177.1 dullard homolog [Xenopus tropicalis] dullard homolog (Xenopus laevis) [Xenopus tropicalis]
sw17297	BGIBMGA006604	0.87295	0.9047	0.86655	2.935	3.00E-23	gi 72113620 ref XP_795139.1 PREDICTED: similar to cytochrome b5 domain-containing protein like (3F409) [Strongylocentrotus purpuratus]
sw20342	BGIBMGA004100	0.724	0.98425	0.8814	2.93145	8.00E-22	gi 76779920 gb AAI06315.1 Fj13912-prov protein [Xenopus laevis] Fj13912-prov protein [Xenopus laevis] Psf3 [Xenopus laevis]
sw05469	BGIBMGA010478	1.1384	1.1261	1.30635	2.9282	1.00E-11	gi 54644737 gb EAL33477.1 GA20198-PA [Drosophila pseudoobscura]
sw10611	BGIBMGA012747	1.34995	1.49155	1.35915	2.9258	1.00E-09	gi 2791944 emb CAA76124.1 Drosophila multidendritic neurons sodium channel 1 [Drosophila melanogaster]
sw05749	BGIBMGA006173	1.0239	1.36025	1.18215	2.92505	3.00E-95	gi 8050580 gb AAF71710.1 transcription elongation factor TFIIS [Drosophila virilis]
sw13299	BGIBMGA013605	1.01995	1.16855	1.66615	2.92025	2.00E-53	gi 62859519 ref NP_001016076.1 eukaryotic translation initiation factor 4E member 2 [Xenopus tropicalis] novel protein similar to eukaryotic translation initiation factor 4E member 2 (eif4e2) [Xenopus tropicalis]
sw10058	BGIBMGA013141	0.75475	1.13215	1.15105	2.9199	No hits found	
sw09177	BGIBMGA007961	0.8957	1.69955	1.47515	2.9148	9.00E-59	gi 76608291 ref XP_615387.2 PREDICTED: similar to Developmentally regulated RNA-binding protein 1 (RB-1) [Bos taurus]
sw15425	BGIBMGA012547	1.11695	1.2948	1.32355	2.9124	6.00E-47	gi 4753704 emb CAB42049.1 Nmd3 protein [Drosophila melanogaster]
sw09540	BGIBMGA001920	0.7609	1.01835	0.82335	2.90675	Bmb031410	4.00E-25

sw12323	BGIBMGA003141	0.93965	1.0655	0.92035	2.9058	9.00E-56	gi 56269514 gb AAH87353.1 Aad-A-prov protein [Xenopus laevis] alpha-aspartyl dipeptidase Alpha-aspartyl dipeptidase (Asp-specific dipeptidase) (Dipeptidase E)
sw09815	BGIBMGA007711	0.87205	1.1595	1.0248	2.9055	4.00E-13	gi 49899853 gb AAH76885.1 MGC88947 protein [Xenopus tropicalis] MGC88947 protein [Xenopus tropicalis]
sw12338	BGIBMGA002601	2.38615	1.7417	1.23435	2.90505	No hits found	
sw14359	BGIBMGA001581	1.0146	1.0942	1.286	2.9049	7.00E-63	gi 74354109 gb AAI02594.1 Mortality factor 4 like 2 [Bos taurus] mortality factor 4 like 2 [Bos taurus]
sw13966	BGIBMGA012520	1.0226	0.9896	1.16155	2.9037	5.00E-61	gi 17946007 gb AAL49047.1 RE50565p [Drosophila melanogaster]
sw10979	BGIBMGA005216	1.174	1.51195	1.3552	2.90235	No hits found	
sw09861	BGIBMGA012857	1.09565	1.08055	1.02055	2.9023	Bmb037283	4.00E-23
sw04248	BGIBMGA007766	3.6876	2.844	2.26695	2.901	e-108	gi 32997080 dbj BAC79386.1 glycerophosphoryl diester phosphodiesterase [Bombyx mori]
sw03199	BGIBMGA013120	0.7967	0.87775	0.81305	2.90045	2.00E-29	gi 5031597 ref NP_005710.1 actin related protein 2/3 complex subunit 3 [Homo sapiens] PREDICTED: similar to Actin-related protein 2/3 complex subunit 3 (ARP2/3 complex 21 kDa subunit) (p21-ARC) isoform 1
sw11551	BGIBMGA000102	0.8571	0.88045	0.83145	2.8992	Bmb006555	7.00E-10
sw11902	BGIBMGA009775	1.84945	1.10005	1.1312	2.89855	2.00E-15	gi 3913399 sp Q24998 CUP52_GALME Pupal cuticle protein PCP52 precursor (GMPCP52) pupal cuticle protein [Galleria mellonella]
sw06092	BGIBMGA008514	1.02765	1.024	1.07705	2.8975	1.00E-79	gi 609526 gb AAA58743.1 chymotrypsinogen chymotrypsin
sw12396	BGIBMGA003920	0.8528	0.84435	0.65565	2.89165	1.00E-15	gi 74001269 ref XP_850052.1 PREDICTED: similar to lipase, member I [Canis familiaris]
sw21445	BGIBMGA013862	1.8573	2.11865	0.8267	2.8915	7.00E-09	gi 76665796 ref XP_587609.2 PREDICTED: similar to UDP-glucuronosyltransferase 2B4 precursor (UDPGT) (Hyodeoxycholic acid) (HLUG25) (UDPGTh-1) isoform 1 [Bos taurus]
sw08056	BGIBMGA002243	1.11865	1.17655	0.94905	2.89105	2.00E-56	gi 66548725 ref XP_623164.1 PREDICTED: similar to ENSANGP00000017632 [Apis mellifera]
sw06600	BGIBMGA011753	0.67895	1.00685	0.79895	2.88895	Bmb030745	1.00E-41
sw02668	BGIBMGA008562	0.80795	1.01845	1	2.88485	Bmb046946	1.00E-14
sw20582	BGIBMGA004001	0.97395	1.17135	1.1154	2.88085	e-148	gi 1772495 emb CAA52032.1 hydroxymethylglutaryl-CoA synthase [Blattella germanica] Hydroxymethylglutaryl-CoA synthase 1 (HMG-CoA synthase 1) (3-hydroxy-3-methylglutaryl coenzyme A synthase 1)
sw05128	BGIBMGA001008	1.361	1.00995	1.0833	2.87775	1.00E-19	gi 18860533 ref NP_573377.1 CG8051-PA [Drosophila melanogaster] SD10554p [Drosophila melanogaster] CG8051-PA [Drosophila melanogaster]
sw07225	BGIBMGA012569	0.951	1.1153	1.0194	2.87355	4.00E-27	gi 62661030 ref XP_344287.2 PREDICTED: similar to J domain of DnaJ-like-protein 1 - rat [Rattus norvegicus] J domain of DnaJ-like-protein 1 - rat
sw09098	BGIBMGA012728	1.1387	1.09055	1.0801	2.87275	e-110	gi 38679389 gb AAR26516.1 antennal esterase [Mamestra brassicae]
sw15434	BGIBMGA003244	0.9499	1	1	2.87255	No hits found	
sw10412	BGIBMGA010150	1.1649	1.28135	1.27095	2.8725	2.00E-15	gi 24644274 ref NP_649550.1 CG14671-PA [Drosophila melanogaster] CG14671-PA [Drosophila melanogaster]
sw11916	BGIBMGA006700	1.31625	1.1321	1.0831	2.87155	4.00E-16	gi 72014989 ref XP_782823.1 PREDICTED: similar to solute carrier family 25, member 35 [Strongylocentrotus purpuratus]
sw13199	BGIBMGA013998	0.7642	0.95805	0.7933	2.8666	2.00E-44	gi 55700047 dbj BAD69622.1 heme oxygenase [Apis mellifera] heme oxygenase [Apis mellifera]
sw01022	BGIBMGA003330	1.19345	2.03655	1	2.8663	Bmb014895	3.00E-22
sw04880	BGIBMGA006828	0.8917	1.01535	0.82915	2.86195	4.00E-75	gi 7688673 gb AAF67477.1 putative 55 kDa protein [Homo sapiens]
sw19005	BGIBMGA003004	0.69715	0.85725	1.19785	2.8606	Bmb028789	2.00E-82

sw07489	BGIBMGA006500	0.9682	1.02025	0.9918	2.85915	5.00E-25	gi 56541182 gb AAH87570.1 Hypothetical protein LOC496625 [Xenopus tropicalis] hypothetical protein LOC496625 [Xenopus tropicalis] novel protein containing RING finger [Xenopus tropicalis]
sw16162	BGIBMGA007613	1	1.6978	1	2.85885	1.00E-37	gi 55240040 gb EAA10029.2 ENSANGP00000000640 [Anopheles gambiae str. PEST] ENSANGP00000000640 [Anopheles gambiae str. PEST]
sw11657	BGIBMGA003536	0.80345	1.01455	0.83785	2.85745	1.00E-23	gi 66514013 ref XP_394387.2 PREDICTED: similar to Protein FAM20B precursor [Apis mellifera]
sw18291	BGIBMGA013676	1.0292	1.2041	0.9982	2.85545	1.00E-08	gi 30387346 ref NP_848425.1 unknown [Choristoneura fumiferana MNPV] unknown [Choristoneura fumiferana MNPV]
sw22170	BGIBMGA003027	1.24735	1.32545	1.282	2.8524	1.00E-18	gi 50924436 ref XP_472578.1 OSJNBa0006B20.1 [Oryza sativa (japonica cultivar-group)] OSJNBa0006B20.1 [Oryza sativa (japonica cultivar-group)]
sw14429	BGIBMGA012834	1.01075	1.1058	1.01435	2.851	6.00E-45	gi 73994713 ref XP_863164.1 PREDICTED: similar to NAD-dependent deacetylase sirtuin-4 (SIR2-like protein 4) isoform 3 [Canis familiaris]
sw08912	BGIBMGA003590	1.2338	0.72505	0.9817	2.85	No hits found	
sw03742	BGIBMGA007424	0.93305	1.00635	1.45905	2.84965	3.00E-83	gi 55235786 gb EAA14577.2 ENSANGP00000020940 [Anopheles gambiae str. PEST] ENSANGP00000020940 [Anopheles gambiae str. PEST]
sw08173	BGIBMGA013304	0.1102	1.05785	0.61205	2.84585	No hits found	
sw01504	BGIBMGA001273	1.23195	1.26535	1.3782	2.8458	4.00E-51	gi 68396543 ref XP_682831.1 PREDICTED: similar to trimethyllysine hydroxylase, epsilon [Danio rerio]
sw11056	BGIBMGA007527	1.0675	1.1989	0.7888	2.84555	4.00E-10	gi 400673 sp P31420 OMBP_MANSE Ommochrome-binding protein precursor (OBP) (YCP) ommochrome-binding protein
sw20497	BGIBMGA013985	0.91345	0.91905	0.9171	2.8431	4.00E-38	gi 66522177 ref XP_393590.2 PREDICTED: similar to Odag-pending-prov protein [Apis mellifera]
sw14638	BGIBMGA011699	1.69525	1.28	1.08965	2.8412	No hits found	
sw03654	BGIBMGA003153	0.92385	1.06795	1.1794	2.83825	Bmb016214	2.00E-99
sw15877	BGIBMGA007493	1.2232	1.0576	0.98165	2.83415	Bmb036074	8.00E-48
sw16419	BGIBMGA008493	0.79095	1.03635	0.87555	2.83305	3.00E-14	gi 33329087 gb AAQ09944.1 phosphonoformate immuno-associated protein 2 [Homo sapiens] LSMD1 protein [Homo sapiens] LSMD1 protein [Homo sapiens] LSMD1 protein [Homo sapiens]
sw08118	BGIBMGA013449	0.77845	0.90915	1.1347	2.82895	2.00E-25	gi 829221 emb CAA29061.1 histone H2 A.F/Z [Strongylocentrotus purpuratus] Histone H2A variant
sw20751	BGIBMGA007261	1.22165	1.184	1.0856	2.8273	3.00E-24	gi 89257466 gb ABD64957.1 hydrolase, NUDIX family protein [Brassica oleracea]
sw03106	BGIBMGA008525	0.79295	0.9173	0.8743	2.8264	5.00E-41	gi 24642023 ref NP_572974.1 CG14407-PA [Drosophila melanogaster] RH03087p [Drosophila melanogaster] CG14407-PA [Drosophila melanogaster]
sw02182	BGIBMGA014475	0.9184	1.04185	0.9647	2.82585	4.00E-23	gi 50755675 ref XP_414848.1 PREDICTED: similar to Growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration) [Gallus gallus]
sw04574	BGIBMGA007972	1.13345	1.1866	1.1417	2.8245	6.00E-34	gi 72088711 ref XP_795347.1 PREDICTED: similar to chronic myelogenous leukemia tumor antigen 66 [Strongylocentrotus purpuratus]
sw12245	BGIBMGA007849	0.91025	1.11085	0.79125	2.82445	2.00E-69	gi 66534975 ref XP_624114.1 PREDICTED: similar to Peptidylprolyl isomerase-like protein 3, isoform PPIL3b [Apis mellifera]
sw21866	BGIBMGA006264	1.04065	1.0008	0.8121	2.82135	5.00E-37	gi 66506576 ref XP_394468.2 PREDICTED: similar to Biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen) [Apis mellifera]
sw12242	BGIBMGA006081	1.0411	0.98785	1.2552	2.8191	3.00E-98	gi 38679389 gb AAR26516.1 antennal esterase [Mamestra brassicae]
sw21174	BGIBMGA010227	0.8875	1.146	1.2645	2.81625	2.00E-60	gi 57506562 dbj BAD86652.1 reverse transcriptase [Bombyx mori]
sw06572	BGIBMGA003596	0.8626	1.07595	0.98995	2.81455	9.00E-26	gi 76651259 ref XP_589337.2 PREDICTED: similar to Autosomal Highly Conserved Protein [Bos taurus]
sw00738	BGIBMGA000339	1.1584	0.9385	0.5097	2.8127	3.00E-07	gi 47605408 sp Q7M4E8 CUD6_SCHGR Endocuticle structural protein SgAbd-6
sw15742	BGIBMGA007962	0.82635	0.99125	0.80525	2.8109	5.00E-35	gi 49250357 gb AAH74666.1 MGC69249 protein [Xenopus tropicalis] MGC69249 protein [Xenopus tropicalis]

sw08557	BGIBMGA014189	0.99785	1.17085	1.32215	2.80645	4.00E-55	gi 55239363 gb EAL40125.1 ENSANGP00000029489 [Anopheles gambiae str. PEST] ENSANGP00000029489 [Anopheles gambiae str. PEST]
sw07804	BGIBMGA004644	0.95735	1.14935	1.00835	2.8039	4.00E-40	gi 73952516 ref XP_536345.2 PREDICTED: similar to translin-associated factor X isoform 1 [Canis familiaris]
sw17943	BGIBMGA003065	1.5741	0.5357	0.66185	2.80295	3.00E-18	gi 290935 gb AAC37204.1 cuticle protein 66 Larval/pupal rigid cuticle protein 66 precursor (HCCP66)
sw14566	BGIBMGA008982	0.8542	1.00465	0.9087	2.8022	e-124	gi 66503797 ref XP_624046.1 PREDICTED: similar to solute carrier family 41 member 1 [Apis mellifera]
sw22014	BGIBMGA009885	1.1845	1.1234	1.54995	2.8019	e-127	gi 72014529 ref XP_786173.1 PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 [Strongylocentrotus purpuratus]
sw08359	BGIBMGA009817	0.6547	0.94475	0.67015	2.8016	1.00E-68	gi 55700852 dbj BAD69791.1 Replication protein A small subunit [Bombyx mori]
sw09330	BGIBMGA013774	1.44635	1.12355	1.5468	2.7999	4.00E-27	gi 24581316 ref NP_722867.1 CG17224-PA, isoform A [Drosophila melanogaster] CG17224-PB, isoform B [Drosophila melanogaster] CG17224-PB, isoform B
sw15691	BGIBMGA011457	1.93685	1.22695	0.85835	2.7992	2.00E-23	gi 6560645 gb AAF16700.1 juvenile hormone binding protein precursor-like protein [Manduca sexta]
sw14228	BGIBMGA011009	1.0296	1	1.14835	2.79155	Bmb023634	6.00E-92
sw10803	BGIBMGA012262	2.1921	1.13055	0.76535	2.78335	3.00E-10	gi 27462828 gb AAO15603.1 sensory neuron membrane protein [Mamestra brassicae]
sw15045	BGIBMGA013171	1.1032	0.65385	0.7609	2.77715	5.00E-23	gi 17224425 gb AAL36972.1 phosphorylase kinase gamma [Homo sapiens] Phosphorylase kinase, gamma 1 (muscle) [Homo sapiens] Phosphorylase kinase, gamma 1 (muscle)
sw06207	BGIBMGA002407	0.49905	1.2055	0.8424	2.77105	3.00E-15	gi 74356259 gb AAI04710.1 LOC500420 protein [Rattus norvegicus]
sw19267	BGIBMGA003995	0.67005	0.9288	0.52095	2.77065	2.00E-10	gi 68427052 ref XP_687434.1 PREDICTED: similar to stimulated by retinoic acid 13 [Danio rerio]
sw18568	BGIBMGA002973	0.8514	1.01655	0.92365	2.7661	e-151	gi 87248341 gb ABD36223.1 interphase cytoplasmic foci protein 45 [Bombyx mori]
sw12688	BGIBMGA012456	1.3023	1.5136	1.43105	2.7603	6.00E-46	gi 17861638 gb AAL39296.1 GH16993p [Drosophila melanogaster]
sw15388	BGIBMGA010998	1.12125	1.28755	0.78255	2.7585	3.00E-32	gi 15082309 gb AAH12060.1 Guanine nucleotide binding protein beta-subunit-like polypeptide [Homo sapiens] guanine nucleotide binding protein beta-subunit-like polypeptide [Homo sapiens] G-protein beta subunit-like protein
sw21851	BGIBMGA013220	0.6794	1.38565	1.42155	2.75175	Bmb024303	1.00E-60
sw12704	BGIBMGA009902	0.87325	0.989	0.8855	2.74625	6.00E-68	gi 87248643 gb ABD36374.1 Wibg protein [Bombyx mori]
sw03426	BGIBMGA005533	0.995	1.0176	0.89255	2.74435	2.00E-06	gi 54644959 gb EAL33699.1 GA13693-PA [Drosophila pseudoobscura]
sw08785	BGIBMGA005011	0.9942	1.07075	0.9266	2.7434	7.00E-06	gi 45552839 ref NP_995945.1 CG33229-PA [Drosophila melanogaster] LD20362p [Drosophila melanogaster] CG33229-PA [Drosophila melanogaster]
sw15882	BGIBMGA011762	1.37045	1.0816	1.01765	2.7394	No hits found	
sw18206	BGIBMGA006055	0.87525	1.01585	0.7624	2.7377	0	gi 87248311 gb ABD36208.1 dermal papilla derived protein 13 [Bombyx mori]
sw20945	BGIBMGA010303	1.14895	1.0944	1.13545	2.73285	6.00E-52	gi 2738865 gb AAB94558.1 hemocyte protease-2 [Manduca sexta]
sw08864	BGIBMGA005939	0.89715	1.11115	0.8128	2.73255	1.00E-71	gi 48094717 ref XP_392172.1 PREDICTED: similar to ENSANGP00000016945 [Apis mellifera]
sw21707	BGIBMGA004038	0.8866	1.09775	1.1704	2.73205	4.00E-81	gi 87248487 gb ABD36296.1 microtubule-associated protein RP/EB family member 3 [Bombyx mori]
sw09424	BGIBMGA002501	1.00535	0.95805	0.74515	2.72905	2.00E-20	gi 74356259 gb AAI04710.1 LOC500420 protein [Rattus norvegicus]
sw13074	BGIBMGA003719	1.59705	1.19605	1.90195	2.72675	No hits found	
sw16773	BGIBMGA013074	1	1.0652	1	2.72515	3.00E-16	gi 74353801 gb AAI01851.1 Asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3-, glucosyltransferase) [Rattus norvegicus] asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3-, glucosyltransferase) [Rattus norvegicus]

sw21570	BGIBMGA004527	0.42065	2.07875	1.3684	2.72475	7.00E-27	gi 62637998 gb AAX92638.1 glucose transporter 8 [Solenopsis invicta]
sw01530	BGIBMGA014149	1	0.76955	1.0619	2.7225	3.00E-42	gi 2970687 gb AAC06038.1 beta-glucosidase precursor [Spodoptera frugiperda]
sw12423	BGIBMGA006751	0.8287	1.0399	1.31105	2.722	e-124	gi 87248587 gb ABD36346.1 GTP-binding nuclear protein Ran [Bombyx mori]
sw11453	BGIBMGA012371	1	1	1	2.72095	2.00E-13	gi 11121441 emb CAC14873.1 zinc/iron regulated transporter-related protein 1, DZIP1 protein [Drosophila melanogaster]
sw04090	BGIBMGA012496	0.8735	0.6389	0.9352	2.71875	9.00E-41	gi 1136134 gb AAC46955.1 DmORC2
sw09876	BGIBMGA008291	1.2653	1.22725	1.12595	2.7179	Bmb037681	6.00E-35
sw20480	BGIBMGA002208	1.11415	1.0367	1.1288	2.71755	7.00E-37	gi 54638579 gb EAL27981.1 GA20391-PA [Drosophila pseudoobscura]
sw09327	BGIBMGA008661	0.8652	0.96885	0.9886	2.717	Bmb027876	3.00E-36
sw00966	BGIBMGA010906	0.8838	0.8988	1.14165	2.71445	Bmb014069	4.00E-46
sw16619	BGIBMGA011775	0.7545	0.98095	0.8485	2.713	Bmb044249	No hits found
sw01257	BGIBMGA003303	1.2534	1.21285	0.905	2.7129	No hits found	
sw20650	BGIBMGA003462	1.06595	1.13555	1.0171	2.7119	5.00E-43	gi 72137689 ref XP_797513.1 PREDICTED: similar to RNA binding motif protein 17 [Strongylocentrotus purpuratus]
sw09566	BGIBMGA010322	1.34975	2.16305	1.6701	2.7115	3.00E-57	gi 28317202 gb AAO39608.1 GH22674p [Drosophila melanogaster]
sw03812	BGIBMGA007280	1.0947	1.46615	1.2448	2.7039	4.00E-23	gi 3004821 gb AAC39088.1 putative inorganic phosphate cotransporter [Drosophila ananassae] Putative inorganic phosphate cotransporter
sw05344	BGIBMGA000922	1.107	1.0337	1.00455	2.70365	1.00E-05	gi 50761690 ref XP_424803.1 PREDICTED: similar to mitochondrial ribosomal protein S27; mitochondrial 28S ribosomal protein S27 [Gallus gallus]
sw06559	BGIBMGA012123	1.08265	0.9453	1	2.70315	5.00E-56	gi 88946778 ref ZP_01149846.1 cysteine synthase [Desulfotomaculum reducens MI-1] cysteine synthase [Desulfotomaculum reducens MI-1]
sw20968	BGIBMGA009469	0.95715	1.109	1.23735	2.70195	e-113	gi 4493354 emb CAB39165.1 nucleolar protein, putative [Drosophila melanogaster]
sw08457	BGIBMGA005096	1.22905	1.14605	0.7664	2.7015	7.00E-14	gi 4090964 gb AAD09279.1 immune-related Hdd1 [Hyphantria cunea]
sw16441	BGIBMGA009987	0.7401	1.0698	0.7422	2.7014	1.00E-14	gi 72004372 ref XP_784178.1 PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa [Strongylocentrotus purpuratus]
sw07598	BGIBMGA004250	0.88225	1.05005	1.1466	2.70135	No hits found	
sw10316	BGIBMGA007796	0.7526	1.1086	0.68945	2.6984	2.00E-19	gi 27374248 gb AAO01007.1 CG15863-PA [Drosophila erecta]
sw05343	BGIBMGA001221	1.11345	1.02125	0.976	2.6966	7.00E-19	gi 27374230 gb AAO00992.1 CG9951-PA [Drosophila erecta]
sw12534	BGIBMGA000555	1.43135	0.9433	1.0677	2.6939	6.00E-25	gi 55241087 gb EAL40600.1 ENSANGP000000027190 [Anopheles gambiae str. PEST] ENSANGP000000027190 [Anopheles gambiae str. PEST]
sw22224	BGIBMGA014599	1.6495	1.45385	1.63975	2.69265	2.00E-50	gi 66520183 ref XP_392696.2 PREDICTED: similar to carboxylesterase [Apis mellifera]
sw09138	BGIBMGA006761	0.82945	0.99	0.91675	2.69045	1.00E-29	gi 60552380 gb AAH91052.1 MGC108292 protein [Xenopus tropicalis] MGC108292 protein [Xenopus tropicalis] novel protein [Xenopus tropicalis]
sw18970	BGIBMGA000498	1.21205	1.64615	1	2.68815	2.00E-20	gi 38176144 gb AAR13011.1 clock [Danaus plexippus]
sw03051	BGIBMGA009043	1.78365	1.2098	1.7273	2.68585	7.00E-64	gi 73971831 ref XP_854862.1 PREDICTED: similar to Glyoxylate reductase/hydroxypyruvate reductase [Canis familiaris]
sw09429	BGIBMGA002394	0.87505	1.0975	1.32725	2.68055	1.00E-32	gi 50369534 gb AAH76042.1 Metap1 protein [Danio rerio]

sw12031	BGIBMGA007005	1.02945	0.90165	0.89675	2.6802	3.00E-17	gi 27370858 gb AAH41215.1 MGC52693 protein [Xenopus laevis] apyrase [Xenopus laevis]
sw15847	BGIBMGA003466	0.7652	0.92435	0.7104	2.67485	Bmb035873	6.00E-11
sw03160	BGIBMGA013274	0.94245	0.88725	0.82915	2.67365	1.00E-32	gi 85857490 gb ABC86281.1 RE09672p [Drosophila melanogaster]
sw19365	BGIBMGA010098	0.3586	0.7338	0.84295	2.6727	2.00E-32	gi 17864686 ref NP_525007.1 UDP-glycosyltransferase 37c1 CG8652-PA [Drosophila melanogaster] EG:EG0003.4 [Drosophila melanogaster] CG8652-PA [Drosophila melanogaster]
sw20309	BGIBMGA005439	0.89935	0.86295	0.77505	2.66875	3.00E-68	gi 83638667 gb AAI09717.1 NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa [Bos taurus] NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa
sw06772	BGIBMGA011509	0.92775	1.2461	0.9406	2.6677	Bmb034208	2.00E-33
sw07509	BGIBMGA001188	0.9717	1.028	0.98545	2.6676	3.00E-67	gi 66529825 ref XP_624000.1 PREDICTED: similar to Exosome complex exonuclease RRP43 (Ribosomal RNA processing protein 43) (Exosome component 8) (p9) (Opa-interacting protein 2) [Apis mellifera]
sw06240	BGIBMGA011822	0.98065	1.07085	1.1869	2.66615	0	gi 72106184 ref XP_790294.1 PREDICTED: similar to guanine nucleotide binding protein-like 2 (nucleolar) [Strongylocentrotus purpuratus]
sw13043	BGIBMGA011820	1.41415	1.07185	1.06015	2.6623	Bmb015947	4.00E-48
sw18743	BGIBMGA003456	1.28995	1.40715	0.97965	2.66135	3.00E-34	gi 73999552 ref XP_535120.2 PREDICTED: similar to lactate dehydrogenase A -like [Canis familiaris]
sw03236	BGIBMGA005544	0.7791	0.9581	0.90535	2.6582	4.00E-18	gi 72109917 ref XP_793600.1 PREDICTED: similar to Rab geranylgeranyltransferase, beta subunit [Strongylocentrotus purpuratus]
sw14542	BGIBMGA006118	0.92755	1.0159	0.9842	2.65725	No hits found	
sw03443	BGIBMGA010459	1.02285	1.1099	1.401	2.657	3.00E-08	gi 50761351 ref XP_424699.1 PREDICTED: similar to arrestin domain containing 3 [Gallus gallus]
sw12075	BGIBMGA008398	1.3236	1.3255	0.8944	2.65155	8.00E-06	gi 9964462 ref NP_064930.1 putative core protein [Amsacta moorei entomopoxvirus] AMV148 [Amsacta moorei entomopoxvirus]
sw21098	BGIBMGA003658	0.90435	1.05615	1.1157	2.64815	1.00E-49	gi 50370224 gb AAH76913.1 MGC89088 protein [Xenopus tropicalis] MGC89088 protein [Xenopus tropicalis]
sw11644	BGIBMGA002809	0.87235	1.1026	0.88895	2.6478	1.00E-11	gi 25012983 gb AAN71576.1 RH42446p [Drosophila melanogaster]
sw17190	BGIBMGA011501	0.74675	1.07105	0.812	2.64555	3.00E-14	gi 66508472 ref XP_624484.1 PREDICTED: similar to CG2046-PA [Apis mellifera]
sw09003	BGIBMGA008459	1.38835	1.4287	1.03675	2.6422	e-112	gi 7758 emb CAA41263.1 crn [Drosophila melanogaster]
sw15238	BGIBMGA010627	1.13295	0.6917	0.77695	2.64055	Bmb031258	No hits found
sw18021	BGIBMGA002948	0.996	1.10075	1.10435	2.63925	Bmb023843	1.00E-18
sw13455	BGIBMGA013100	0.8726	0.9892	1.28455	2.6363	4.00E-42	gi 74007795 ref XP_534749.2 PREDICTED: similar to small nuclear ribonucleoprotein D3 [Canis familiaris]
sw17156	BGIBMGA000931	0.99775	1.12355	0.9198	2.6357	e-123	gi 25013002 gb AAN71585.1 RH46192p [Drosophila melanogaster]
sw13946	BGIBMGA001506	1.1311	2.08765	2.1563	2.63455	2.00E-60	gi 72172203 gb AAZ66799.1 lipase [Samia cynthia ricini] lipase-1 [Bombyx mori] lipase [Bombyx mori]
sw11846	BGIBMGA000250	1.3523	1.39345	1.40135	2.63295	2.00E-27	gi 24666794 ref NP_649121.1 CG9290-PA [Drosophila melanogaster] CG9290-PA [Drosophila melanogaster]
sw22385	BGIBMGA010824	0.90455	0.57225	0.7441	2.63295	No hits found	
sw07544	BGIBMGA013713	0.36805	0.8332	0.788	2.63	3.00E-21	gi 31324444 gb AAP47228.1 Sec61p gamma subunit [Gryllotalpa orientalis] Protein transport protein SEC61 gamma subunit
sw04230	BGIBMGA010017	1.0163	1.01555	1.22315	2.6263	3.00E-77	gi 87248299 gb ABD36202.1 COMMD4 protein [Bombyx mori]
sw04425	BGIBMGA012348	0.67655	1.09585	1.2681	2.6233	Bmb034386	1.00E-28

sw01563	BGIBMGA009760	0.5754	0.7759	0.8862	2.6227	4.00E-84	gi 87248373 gb ABD36239.1 nonclathrin coat protein zeta 1-COP [Bombyx mori]
sw14729	BGIBMGA005936	1.1297	1.1862	1.0978	2.62255	No hits found	
sw22885	BGIBMGA006723	0.9003	1.37795	1.19165	2.621	5.00E-24	gi 56269559 gb AAH87483.1 LOC496069 protein [Xenopus laevis]
sw12065	BGIBMGA007864	0.7271	0.6181	0.9974	2.6208	1.00E-55	gi 72021217 ref XP_795004.1 PREDICTED: similar to GLIS family zinc finger 2 [Strongylocentrotus purpuratus]
sw09947	BGIBMGA001265	0.79585	0.9675	1.21435	2.6198	No hits found	
sw17077	BGIBMGA004734	1.09235	1.0698	0.9154	2.61615	1.00E-16	gi 5809683 gb AAD40352.2 RP140-upstream [Drosophila melanogaster]
sw20245	BGIBMGA001372	1.4071	1.28445	1.52265	2.61495	1.00E-51	gi 38679389 gb AAR26516.1 antennal esterase [Mamestra brassicae]
sw12542	BGIBMGA012452	1.4982	0.85765	0.9194	2.61475	5.00E-59	gi 54639776 gb EAL29178.1 GA14959-PA [Drosophila pseudoobscura]
sw14514	BGIBMGA007239	1.43545	1.1856	1.5324	2.6101	Bmb025879	e-159
sw09645	BGIBMGA004059	0.7145	0.76295	0.89315	2.6074	Bmb033292	2.00E-40
sw08543	BGIBMGA005547	0.7449	0.877	1.1365	2.6012	Bmb016029	6.00E-05
sw00511	BGIBMGA000921	0.8692	0.966	0.78805	2.6004	1.00E-26	gi 85857748 gb ABC86409.1 IP09454p [Drosophila melanogaster]
sw09864	BGIBMGA002754	1.3072	1.0372	1.05735	2.5984	No hits found	
sw05029	BGIBMGA001918	0.79345	0.96085	0.85155	2.5979	4.00E-95	gi 72004713 ref XP_785235.1 PREDICTED: similar to phosphatidylinositol glycan, class K (predicted) [Strongylocentrotus purpuratus]
sw11034	BGIBMGA010172	0.8264	0.96515	0.79255	2.59665	1.00E-40	gi 458674 gb AAC46479.1 TFIID 22 kDa subunit
sw20207	BGIBMGA000305	0.73605	0.9895	0.8516	2.5966	8.00E-66	gi 57506562 dbj BAD86652.1 reverse transcriptase [Bombyx mori]
sw13235	BGIBMGA005559	0.7564	1.0194	1.0977	2.5963	1.00E-58	gi 66533332 ref XP_625023.1 PREDICTED: similar to ARMET-like protein precursor [Apis mellifera]
sw03695	BGIBMGA010450	0.9086	1.03075	0.9245	2.59545	No hits found	
sw13320	BGIBMGA010325	1.06055	1.03885	1.05545	2.59295	Bmb017661	2.00E-24
sw22830	BGIBMGA005485	1.12465	1.25555	0.86575	2.5913	Bmb048151	4.00E-18
sw03365	BGIBMGA004830	1.57225	1.4632	1.4773	2.5897	2.00E-90	gi 74831719 emb CAJ30028.1 carboxypeptidase B precursor [Helicoverpa zea]
sw15675	BGIBMGA010533	1.1621	0.69145	0.819	2.5862	No hits found	
sw14565	BGIBMGA008983	0.85765	0.8998	1.0321	2.5808	6.00E-19	gi 266685 sp P08461 ODP2_RAT Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (E2) (Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex)
sw15717	BGIBMGA002330	1.0664	1.158	0.7962	2.5797	4.00E-79	gi 87248205 gb ABD36155.1 proline synthetase co-transcribed bacterial-like protein [Bombyx mori]
sw07840	BGIBMGA001209	1.00695	1.09295	0.95845	2.5746	2.00E-46	gi 62857779 ref NP_001017238.1 COP9 constitutive photomorphogenic homolog subunit 3 [Xenopus tropicalis] COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis) [Xenopus tropicalis]
sw22940	BGIBMGA011742	0.5229	0.9643	0.87655	2.5742	No hits found	
sw10552	BGIBMGA006840	0.6821	0.9187	1.1223	2.5722	3.00E-57	gi 87248491 gb ABD36298.1 eukaryotic translation initiation factor 1A [Bombyx mori]
sw15011	BGIBMGA007723	0.7364	0.72785	0.8108	2.5673	2.00E-64	gi 10443892 gb AAG17630.1 esterase D [Sus scrofa] esterase D [Sus scrofa] Esterase D esterase D [Sus scrofa]

sw05520	BGIBMGA003988	1.06065	1.24775	1.1147	2.56685	No hits found	
sw15490	BGIBMGA002064	0.99615	1.20675	1.0183	2.565	1.00E-09	gi 55620992 ref XP_526288.1 PREDICTED: similar to adenylate cyclase 5; adenylyl cyclase type V [Pan troglodytes]
sw12099	BGIBMGA002943	0.9217	0.92815	1.1606	2.56225	1.00E-20	gi 56118552 ref NP_001007992.1 hpgd-prov protein [Xenopus tropicalis] Hpgd-prov protein [Xenopus tropicalis]
sw03003	BGIBMGA010141	0.78245	0.97275	1	2.56215	8.00E-17	gi 87248419 gb ABD36262.1 larval cuticle protein [Bombyx mori]
sw19438	BGIBMGA011975	1.15365	1.4438	1.3214	2.56205	2.00E-06	gi 54641702 gb EAL30452.1 GA21682-PA [Drosophila pseudoobscura]
sw10834	BGIBMGA007944	1.3197	1.1197	1.16735	2.5605	3.00E-81	gi 66555732 ref XP_623838.1 PREDICTED: similar to Zgc:92633 [Apis mellifera]
sw17661	BGIBMGA008016	1.49455	0.8778	0.8958	2.5569	4.00E-27	gi 48096076 ref XP_392394.1 PREDICTED: similar to WAP four-disulfide core domain 2 [Apis mellifera] PREDICTED: similar to WAP four-disulfide core domain 2 [Apis mellifera]
sw13779	BGIBMGA003236	0.81055	1.1993	1.00395	2.55615	2.00E-14	gi 50730609 ref XP_416969.1 PREDICTED: similar to cDNA sequence BC006662 [Gallus gallus]
sw08964	BGIBMGA001766	1.5144	1.0683	1.17375	2.5555	1.00E-75	gi 72159781 ref XP_798408.1 PREDICTED: similar to phosphatidylserine decarboxylase [Strongylocentrotus purpuratus]
sw14879	BGIBMGA011458	2.3441	1.43735	1.63085	2.5535	2.00E-40	gi 505621 gb AAA21588.1 high affinity nuclear juvenile hormone binding protein
sw09721	BGIBMGA006739	0.9123	1.1519	1.20065	2.55235	No hits found	
sw05062	BGIBMGA005455	1.12675	0.96825	0.934	2.55115	4.00E-13	gi 51709682 ref XP_485502.1 PREDICTED: similar to coiled-coil-helix-coiled-coil-helix domain containing 2 [Mus musculus] PREDICTED: similar to coiled-coil-helix-coiled-coil-helix domain containing 2 [Mus musculus]
sw03386	BGIBMGA004871	1.2034	1.50605	1.25075	2.54745	Bmb010006	No hits found
sw03480	BGIBMGA005494	1.0119	1.2789	0.96785	2.54675	1.00E-07	gi 75704935 gb ABA24611.1 ABC-type phosphate/phosphonate transport system periplasmic component-like
sw16427	BGIBMGA012936	0.98945	1.3559	1.3518	2.54615	2.00E-10	gi 66556093 ref XP_397089.2 PREDICTED: similar to CG3224-PA [Apis mellifera]
sw20893	BGIBMGA003440	0.8657	0.843	0.88935	2.545	2.00E-61	gi 56118905 ref NP_001008042.1 MGC79577 protein [Xenopus tropicalis] MGC79577 protein [Xenopus tropicalis]
sw14278	BGIBMGA007219	1.21935	1.17865	1.3716	2.5375	4.00E-08	gi 62656459 ref XP_220582.3 PREDICTED: similar to ubiquitin specific protease 43 [Rattus norvegicus]
sw12863	BGIBMGA010210	0.7222	0.96735	1.013	2.53605	5.00E-32	gi 56269224 gb AAH87482.1 LOC496068 protein [Xenopus laevis]
sw10448	BGIBMGA008074	1.01585	0.90745	0.8168	2.5312	1.00E-08	gi 4505797 ref NP_002634.1 phosphatidylinositol glycan, class F isoform 1 [Homo sapiens] Phosphatidylinositol glycan, class F, isoform 1 [Homo sapiens] PIGF
sw15029	BGIBMGA012719	0.7848	0.987	1.2037	2.5312	Bmb029558	2.00E-08
sw09668	BGIBMGA003014	1.03705	0.82735	0.67155	2.5296	7.00E-16	gi 15222687 ref NP_173958.1 B5 #6 [Arabidopsis thaliana] putative cytochrome b5 protein [Arabidopsis thaliana] cytochrome b5 [Arabidopsis thaliana] cytochrome b5
sw20302	BGIBMGA000287	0.933	1.1841	1.14595	2.5286	2.00E-48	gi 50926880 gb AAH78974.1 Osgepl1 protein [Rattus norvegicus]
sw21955	BGIBMGA013567	1.39025	1.25035	1.2365	2.5275	0	gi 18253047 gb AAL62468.1 ribosomal protein L3 [Spodoptera frugiperda]
sw20598	BGIBMGA004800	2.03385	2.15015	1.67795	2.52615	2.00E-90	gi 57506558 dbj BAD86650.1 reverse transcriptase [Bombyx mori]
sw13853	BGIBMGA011074	1.66445	1.1724	1.5427	2.525	9.00E-14	gi 66550509 ref XP_624977.1 PREDICTED: similar to interferon gamma-inducible protein 30 [Apis mellifera]
sw14742	BGIBMGA013269	2.84135	1.51605	1.00965	2.5249	1.00E-35	gi 66499360 ref XP_396507.2 PREDICTED: similar to CG11550-PA [Apis mellifera]
sw14040	BGIBMGA001536	0.8994	1.15275	0.94105	2.5227	8.00E-88	gi 76639590 ref XP_580699.2 PREDICTED: similar to Beta-ureidopropionase (Beta-alanine synthase) (N-carbamoyl-beta-alanine amidohydrolase) (BUP-1) [Bos taurus]
sw03701	BGIBMGA010032	0.772	1	1.00175	2.5219	7.00E-11	gi 21594291 gb AAH32101.1 Jagunal homolog 1 [Homo sapiens]

sw19175	BGIBMGA008280	0.6639	0.82295	0.77955	2.5218	4.00E-38	gi 60735591 gb AAZ35812.1 midgut chymotrypsin [Spodoptera exigua]
sw09581	BGIBMGA003430	0.94195	0.857	0.7378	2.5203	No hits found	
sw13071	BGIBMGA011456	2.44405	0.8438	1.4277	2.5197	3.00E-10	gi 70905642 gb AAZ14281.1 proteophosphoglycan 5 [Leishmania major strain Friedlin] Leishmania major strain Friedlin proteophosphoglycan 5 [Leishmania major strain Friedlin]
sw15879	BGIBMGA012025	1.4312	1.44445	1.45095	2.5154	9.00E-37	gi 62859003 ref NP_001017054.1 PAK1 interacting protein 1 [Xenopus tropicalis]
sw04389	BGIBMGA008671	0.9382	1.17755	0.89555	2.5121	7.00E-75	gi 2570798 gb AAB82275.1 cyclin H [Drosophila melanogaster]
sw09140	BGIBMGA000440	1.1209	1.1479	0.91705	2.51055	2.00E-34	gi 72124941 ref XP_793194.1 PREDICTED: similar to mitochondrial ribosomal protein L47 [Strongylocentrotus purpuratus]
sw20657	BGIBMGA009800	1.07005	0.86935	0.871	2.50665	Bmb035870	8.00E-34
sw07808	BGIBMGA004333	1.02385	1.1245	1.0191	2.5054	2.00E-19	gi 35193192 gb AAH58574.1 Dystrobrein binding protein 1 [Mus musculus] dystrobrein binding protein 1 [Mus musculus] Dystrobrein binding protein 1
sw15040	BGIBMGA013693	0.87775	0.9875	0.96005	2.50375	3.00E-15	gi 20306641 gb AAH28523.1 lct1 protein [Mus musculus] Immature colon carcinoma transcript 1 protein precursor
sw16055	BGIBMGA001578	0.9529	1.20335	1.0424	2.5022	Bmb037848	6.00E-24
sw08635	BGIBMGA003028	0.7106	0.8574	0.8753	2.5002	e-101	gi 87248385 gb ABD36245.1 proteasome beta-subunit [Bombyx mori]
sw09737	BGIBMGA006975	0.8017	0.9009	1.08255	2.4999	Bmb034988	6.00E-42
sw10850	BGIBMGA013703	1.0191	1.18615	1.0361	2.4993	7.00E-40	gi 50759728 ref XP_417753.1 PREDICTED: similar to CGI-94 protein; comparative gene identification transcript 94 [Gallus gallus]
sw04240	BGIBMGA000381	0.882	1.0049	1.00255	2.49885	2.00E-10	gi 87248553 gb ABD36329.1 nuclear migration protein nudC [Bombyx mori]
sw11361	BGIBMGA012068	1.22505	0.82295	1.05535	2.4977	3.00E-11	gi 62751745 ref NP_001015768.1 MGC108303 protein [Xenopus tropicalis] MGC108303 protein [Xenopus tropicalis]
sw22855	BGIBMGA014416	1.11415	0.92345	1.06525	2.4961	4.00E-07	gi 76262498 gb ABA41399.1 pherophorin-C1 protein precursor [Chlamydomonas reinhardtii]
sw06858	BGIBMGA011718	0.9611	1.13165	0.73145	2.49585	No hits found	
sw08546	BGIBMGA011455	1.3573	0.59905	0.97615	2.49175	No hits found	
sw10814	BGIBMGA004073	1.10285	0.72125	0.6911	2.4914	No hits found	
sw06776	BGIBMGA003962	1.1897	1.2387	1.13175	2.4896	1.00E-07	gi 58395480 ref XP_321280.2 ENSANGP00000008441 [Anopheles gambiae str. PEST] ENSANGP00000008441 [Anopheles gambiae str. PEST]
sw09363	BGIBMGA009985	1.06065	1.0518	0.82385	2.4895	2.00E-24	gi 49522321 gb AAH75305.1 Brain and reproductive organ-expressed (TNFRSF1A modulator) [Xenopus tropicalis] brain and reproductive organ-expressed (TNFRSF1A modulator) [Xenopus tropicalis]
sw12802	BGIBMGA013641	1.10945	1.31605	1.11665	2.4894	4.00E-20	gi 17901861 gb AAL47714.1 synaptic vesicle protein 2B [Rattus norvegicus] synaptic vesicle glycoprotein 2b [Rattus norvegicus] synaptic vesicle protein 2B
sw22797	BGIBMGA000239	1.306	1	1.31655	2.4883	Bmb043445	No hits found
sw04649	BGIBMGA013375	1.6956	0.97145	1.3158	2.48755	Bmb041349	No hits found
sw13451	BGIBMGA003404	0.484	1.24305	1.0731	2.48725	Bmb018503	1.00E-15
sw07381	BGIBMGA004055	0.94385	1.1345	0.9608	2.4871	3.00E-47	gi 20330554 gb AAM19101.1 PRP4 kinase [Homo sapiens] serine/threonine-protein kinase [Homo sapiens] Serine/threonine-protein kinase PRP4 homolog (PRP4 pre-mRNA-processing factor 4 homolog) (PRP4 kinase)
sw01751	BGIBMGA012490	1.2474	1.314	1.31585	2.48705	No hits found	
sw08671	BGIBMGA008732	1.00915	1.2958	1.0188	2.4869	No hits found	

sw13204	BGIBMGA007669	1.06795	1.23485	1.2978	2.48555	9.00E-39	gi 66554920 ref XP_395755.2 PREDICTED: similar to estrogen receptor binding protein [Apis mellifera]
sw07664	BGIBMGA011093	0.965	1.2346	1.18425	2.4837	2.00E-55	gi 1934852 emb CAA73031.1 putative organic cation transporter [Drosophila melanogaster]
sw13824	BGIBMGA003855	1.2189	0.7727	1.0059	2.48285	No hits found	
sw15808	BGIBMGA013786	1.1918	1.0391	1.0639	2.48235	Bmb035627	5.00E-13
sw09073	BGIBMGA004657	0.67855	0.7135	0.7093	2.4815	4.00E-65	gi 50748430 ref XP_421242.1 PREDICTED: similar to Proteasome subunit alpha type 6 (Proteasome iota chain) (Macropain iota chain) (Multicatalytic endopeptidase complex iota chain) [Gallus gallus]
sw07946	BGIBMGA000875	1.1881	1.3617	1.47805	2.4811	3.00E-63	gi 38679389 gb AAR26516.1 antennal esterase [Mamestra brassicae]
sw15426	BGIBMGA010010	0.9272	0.47635	0.86345	2.4807	8.00E-47	gi 87248401 gb ABD36253.1 sericotropin [Bombyx mori]
sw13773	BGIBMGA004306	0.83125	0.9389	0.76405	2.4801	No hits found	
sw13194	BGIBMGA003325	1.1829	1.50055	1.18355	2.47865	No hits found	
sw11751	BGIBMGA006530	0.67635	0.8655	0.78905	2.4784	Bmb007822	No hits found
sw06973	BGIBMGA014622	1.4251	1.1281	1.4232	2.47775	7.00E-14	gi 73975357 ref XP_539297.2 PREDICTED: similar to UDP-glucuronosyltransferase 2A1 precursor, microsomal [Canis familiaris]
sw10526	BGIBMGA000627	0.882	1.0975	0.88945	2.47395	e-100	gi 22474521 dbj BAC10625.1 ubiquitin conjugating enzyme-like protein [Bombyx mori] ubiquitin conjugating enzyme-like protein [Bombyx mori]
sw03131	BGIBMGA009732	0.86435	0.7711	1.0642	2.47295	e-145	gi 66519017 ref XP_393258.2 PREDICTED: similar to gARPX [Apis mellifera]
sw10652	BGIBMGA012761	1.03195	0.93345	1.0812	2.4694	e-100	gi 24641702 ref NP_572865.1 CG2453-PA [Drosophila melanogaster] CG2453-PA [Drosophila melanogaster] Ubiquinone biosynthesis methyltransferase COQ5, mitochondrial precursor
sw05464	BGIBMGA013414	1	1	1	2.4683	No hits found	
sw13472	BGIBMGA013491	1.09075	1.06145	0.92675	2.46795	3.00E-40	gi 66525531 ref XP_624212.1 PREDICTED: similar to Nucleoporin Nup43 (p42) [Apis mellifera]
sw16263	BGIBMGA006887	0.9271	0.9869	0.93835	2.46545	Bmb039770	1.00E-05
sw16529	BGIBMGA000361	1.1866	1.18895	0.9078	2.4627	Bmb042787	No hits found
sw08533	BGIBMGA010576	1	1.06105	1	2.46215	e-103	gi 158001 gb AAA28730.1 numb peptide (put.); putative
sw08430	BGIBMGA010740	0.75325	1.033	1.9917	2.46195	Bmb014557	e-117
sw17132	BGIBMGA005126	0.7895	0.9502	1.1252	2.4587	1.00E-65	gi 6636388 gb AAF20167.1 tryptophanyl-tRNA synthetase [Drosophila melanogaster]
sw01098	BGIBMGA001465	1.2643	1.47385	1.6359	2.4584	No hits found	
sw03653	BGIBMGA003165	0.95445	0.98795	0.94965	2.45745	e-134	gi 87248663 gb ABD36384.1 transmembrane BAX inhibitor motif-containing protein 5 [Bombyx mori]
sw01302	BGIBMGA012247	0.8353	0.8109	0.8377	2.4554	4.00E-53	gi 3367669 emb CAA19735.1 EG:73D1.1 [Drosophila melanogaster]
sw09643	BGIBMGA006822	1.09555	1.4226	0.84605	2.453	7.00E-19	gi 33186814 tpe CAD67592.1 TPA: putative C6.1A-like protease [Mus musculus] C6.1A-like [Mus musculus]
sw09557	BGIBMGA006260	1	1.1749	1.3798	2.45075	7.00E-27	gi 28317322 gb AAO39657.1 AT01548p [Drosophila melanogaster]
sw08391	BGIBMGA001550	0.82105	0.89435	0.9106	2.4451	8.00E-18	gi 1705720 sp P51953 CDK7_CARAU Cell division protein kinase 7 (40 kDa protein kinase) (P40 MO15) (CDC2/CDK2,4-activating kinase) MO15(cdk7) kinase [Carassius auratus] cdc2-related protein p40 MO15
sw07488	BGIBMGA006498	0.8926	1.1184	1	2.44455	2.00E-05	gi 50748926 ref XP_421460.1 PREDICTED: similar to chromosome 14 open reading frame 138 [Gallus gallus]

sw12728	BGIBMGA009042	0.728	1.16635	0.89655	2.4426	1.00E-09	gi 5852418 gb AAD54066.1 putative 2-hydroxyacid dehydrogenase [Homo sapiens]
sw05413	BGIBMGA007413	0.8786	1.02235	0.8544	2.4385	e-104	gi 50737124 ref XP_419160.1 PREDICTED: similar to sudD suppressor of bimD6 homolog isoform 1; homolog of the Aspergillus nidulans sudD gene product
sw06853	BGIBMGA006056	1.0273	0.94045	1.28615	2.433	4.00E-29	gi 50746777 ref XP_420650.1 PREDICTED: similar to nucleolar protein family A, member 1; H/ACA small nucleolar RNPs [Gallus gallus]
sw10865	BGIBMGA001022	1.2468	1.08635	1.17635	2.42775	7.00E-12	gi 758796 gb AAC46959.1 Sh23 [Schistosoma haematobium] 23 kDa integral membrane protein (Sh23)
sw14229	BGIBMGA013895	0.9117	0.9107	1.1458	2.42715	Bmb023648	No hits found
sw09682	BGIBMGA003552	1.28875	1.09955	1.1482	2.4257	No hits found	
sw15939	BGIBMGA001217	0.9121	1.05805	0.96765	2.41805	1.00E-83	gi 25013002 gb AAN71585.1 RH46192p [Drosophila melanogaster]
sw10402	BGIBMGA005926	0.7454	0.9876	0.8976	2.41755	1.00E-61	gi 62652296 ref XP_576244.1 PREDICTED: phosphatidylserine synthase 1 (predicted) [Rattus norvegicus]
sw05328	BGIBMGA004646	0.9441	1.0282	1.27845	2.41655	1.00E-42	gi 72015359 ref XP_780636.1 PREDICTED: similar to budding uninhibited by benzimidazoles 3 homolog isoform 1 [Strongylocentrotus purpuratus]
sw16069	BGIBMGA008416	0.89735	0.8564	0.9172	2.412	2.00E-24	gi 1314248 gb AAA99718.1 NADH:cytochrome c reductase
sw01248	BGIBMGA009750	1.43475	1.3775	1.53135	2.4111	5.00E-19	gi 158512 gb AAA28918.1 type II transmembrane protein
sw10878	BGIBMGA010285	1.51855	1.08915	1.03225	2.41055	1.00E-83	gi 32029913 ref ZP_00132857.1 COG0451: Nucleoside-diphosphate-sugar epimerases [Haemophilus somnus 2336] COG0451: Nucleoside-diphosphate-sugar epimerases [Haemophilus somnus 129PT]
sw14403	BGIBMGA007889	0.8986	1.1072	1.04815	2.41055	e-123	gi 50759828 ref XP_417800.1 PREDICTED: similar to Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor interacting protein 1) (TRIP-1) [Gallus gallus]
sw04364	BGIBMGA008096	0.7581	0.69685	0.95475	2.4095	e-105	gi 87248227 gb ABD36166.1 short-chain dehydrogenase/reductase 2 [Bombyx mori]
sw13402	BGIBMGA001115	0.904	1.2773	1.06385	2.40795	Bmb018159	2.00E-44
sw06424	BGIBMGA011079	0.374	1.59225	0.24925	2.40665	3.00E-07	gi 6560645 gb AAF16700.1 juvenile hormone binding protein precursor-like protein [Manduca sexta]
sw06402	BGIBMGA007256	1.65215	1.42945	0.9402	2.406	1.00E-74	gi 66516898 ref XP_391826.2 PREDICTED: similar to yellow [Apis mellifera]
sw08850	BGIBMGA009355	0.9743	1.13865	0.84715	2.40515	5.00E-43	gi 55236609 gb EAA13645.2 ENSANGP00000015954 [Anopheles gambiae str. PEST] ENSANGP00000015954 [Anopheles gambiae str. PEST]
sw01649	BGIBMGA009063	0.59135	0.5273	0.73125	2.4049	1.00E-37	gi 66517091 ref XP_397364.2 PREDICTED: similar to ENSANGP00000027134 [Apis mellifera]
sw08409	BGIBMGA010653	0.83485	0.9485	0.90255	2.40405	5.00E-10	gi 38505259 ref NP_081247.2 mitochondrial ribosomal protein L48 isoform 1 [Mus musculus]
sw04971	BGIBMGA011776	0.6742	1.02205	0.93225	2.40225	3.00E-15	gi 62859829 ref NP_001017011.1 programmed cell death 5 [Xenopus tropicalis]
sw14663	BGIBMGA005158	0.7342	0.9889	0.7119	2.40195	Bmb026823	2.00E-44
sw07939	BGIBMGA003088	1.14795	1.42925	1.0263	2.4019	No hits found	
sw08909	BGIBMGA005205	1.0697	0.88905	1.192	2.40175	9.00E-24	gi 3929381 sp Q24491 RX21_DROME RNA binding protein Rsf1 (RNA binding protein Rox21) RNA binding protein
sw08373	BGIBMGA001476	1.08225	1.2534	0.72125	2.40115	Bmb013847	3.00E-86
sw22877	BGIBMGA010595	0.9663	1.06165	1.19205	2.40045	1.00E-88	gi 73996969 ref XP_851691.1 PREDICTED: similar to heat shock 70kD protein binding protein [Canis familiaris]
sw13266	BGIBMGA008342	1.0062	1.1024	1.1623	2.39865	e-141	gi 46249602 gb AAH68838.1 MGC81483 protein [Xenopus laevis] NEDD8-activating enzyme E1 regulatory subunit (Amyloid protein-binding protein 1) (APP-BP1)
sw15132	BGIBMGA003335	0.6283	0.74015	0.71225	2.39805	2.00E-73	gi 2055299 dbj BAA19760.1 proteasome subunit Y [Xenopus laevis]

sw13806	BGIBMGA014209	1.0371	1.156	1.1833	2.39775	3.00E-83	gi 55242911 gb EAA07041.2 ENSANGP00000016729 [Anopheles gambiae str. PEST] ENSANGP00000016729 [Anopheles gambiae str. PEST]
sw15265	BGIBMGA001964	0.95475	1.2052	1.05325	2.3975	2.00E-72	gi 28317060 gb AAO39549.1 RE03380p [Drosophila melanogaster]
sw11068	BGIBMGA010147	0.8696	1.16595	1.291	2.3972	5.00E-48	gi 37595364 gb AAQ94568.1 potassium channel modulatory factor 1 [Danio rerio] Similar to potassium channel modulatory factor 1 [Danio rerio] potassium channel modulatory factor 1 [Danio rerio]
sw08127	BGIBMGA013114	0.542	0.7798	0.8022	2.39615	2.00E-17	gi 34883246 ref XP_347254.1 PREDICTED: similar to Williams-Beuren syndrome critical region protein 21 [Rattus norvegicus] PREDICTED: similar to Williams-Beuren syndrome critical region protein 21 [Rattus norvegicus]
sw22975	BGIBMGA008095	0.7365	0.74645	0.77405	2.39555	e-141	gi 87248227 gb ABD36166.1 short-chain dehydrogenase/reductase 2 [Bombyx mori]
sw18289	BGIBMGA007842	1.1387	1.13865	1.34265	2.39445	2.00E-44	gi 68356394 ref XP_707135.1 PREDICTED: similar to SKB1 homolog isoform 3 [Danio rerio]
sw10858	BGIBMGA001938	0.71895	1.05685	0.7663	2.3942	Bmb002061	2.00E-11
sw00530	BGIBMGA001307	0.70065	0.6014	0.70435	2.3935	1.00E-85	gi 40949813 gb AAR97568.1 Cu/Zn SOD [Bombyx mori] Superoxide dismutase [Cu-Zn]
sw15224	BGIBMGA004496	0.80965	1	1	2.3929	3.00E-57	gi 72073999 ref XP_791465.1 PREDICTED: similar to Tetratricopeptide repeat protein 4 (TPR repeat protein 4), partial [Strongylocentrotus purpuratus]
sw18176	BGIBMGA001303	0.6632	0.77195	0.78345	2.3922	1.00E-45	gi 50746955 ref XP_420692.1 PREDICTED: similar to tumor suppressor candidate 3 isoform b [Gallus gallus]
sw05172	BGIBMGA012707	1.2016	0.8592	1.21955	2.39055	4.00E-24	gi 74006595 ref XP_859139.1 PREDICTED: similar to spermine synthase isoform 4 [Canis familiaris]
sw13037	BGIBMGA011731	1.92055	1.48025	1.29535	2.38995	No hits found	
sw13591	BGIBMGA005469	0.90375	1.1894	0.95545	2.38955	3.00E-42	gi 83754534 pdb 2C35 G Chain G, Subunits Rpb4 And Rpb7 Of Human Rna Polymerase Ii Chain E, Subunits Rpb4 And Rpb7 Of Human Rna Polymerase Ii Chain C, Subunits Rpb4 And Rpb7 Of Human Rna Polymerase Ii Chain A
sw18769	BGIBMGA012827	0.8926	1.0213	0.9166	2.3879	Bmb013219	2.00E-27
sw01127	BGIBMGA010276	1.25865	1.26425	1.34445	2.3877	Bmb016838	1.00E-51
sw10000	BGIBMGA007518	0.80125	0.91265	0.9714	2.3867	5.00E-82	gi 89269046 emb CAJ81570.1 TAR DNA binding protein [Xenopus tropicalis]
sw20846	BGIBMGA012268	0.8286	1.0328	0.8875	2.3856	8.00E-26	gi 66505114 ref XP_624237.1 PREDICTED: similar to GA14985-PA [Apis mellifera]
sw09749	BGIBMGA002917	1.0399	1.0831	0.89385	2.3855	8.00E-75	gi 51859336 gb AAH81422.1 Lin7c protein [Danio rerio] lin7c protein [Danio rerio] neuroepithelial polarity protein [Danio rerio]
sw15446	BGIBMGA014522	1.06435	1.40155	1.1249	2.3851	No hits found	
sw08935	BGIBMGA007083	0.9264	1.08305	0.89715	2.38465	2.00E-46	gi 66539089 ref XP_624856.1 PREDICTED: similar to Potassium channel tetramerisation domain containing 5, partial [Apis mellifera]
sw01324	BGIBMGA004489	1.1834	1.02695	0.92925	2.38455	2.00E-27	gi 68697259 emb CAJ14152.1 putative dodecenoylCoA deltaisomerase [Anopheles gambiae]
sw02948	BGIBMGA004162	0.87045	1.0012	0.827	2.3828	1.00E-44	gi 55641779 ref XP_510278.1 PREDICTED: similar to chromosome 15 open reading frame 24; chromosome 15 hypothetical ATG/GTP binding protein [Pan troglodytes]
sw11158	BGIBMGA011920	0.8187	1.19005	1.58025	2.38175	2.00E-75	gi 847869 gb AAA67954.1 zinc finger protein
sw18473	BGIBMGA006784	0.97535	0.4775	0.9897	2.3813	5.00E-06	gi 37704389 ref NP_780751.2 rotatin [Mus musculus]
sw00139	BGIBMGA010142	1.33735	0.85485	1.02335	2.3804	6.00E-31	gi 1706194 sp P80683 CUA3A_TENMO Larval cuticle protein A3A (TM-A3A) (TM-LCP A3A)
sw11173	BGIBMGA010908	0.90935	1.1003	1.00565	2.37975	8.00E-85	gi 57090201 ref XP_537470.1 PREDICTED: similar to tRNA-(N1G37) methyltransferase [Canis familiaris]
sw20935	BGIBMGA006615	1.14065	1.1393	0.9764	2.3792	1.00E-11	gi 55234466 gb EAA00473.3 ENSANGP00000014085 [Anopheles gambiae str. PEST] ENSANGP00000014085 [Anopheles gambiae str. PEST]
sw12388	BGIBMGA001556	0.74865	1.04245	0.73865	2.3791	2.00E-86	gi 87248203 gb ABD36154.1 phosphomevalonate kinase [Bombyx mori]

sw13433	BGIBMGA001257	0.77045	0.8959	0.97965	2.37765	e-122	gi 66529639 ref XP_624926.1 PREDICTED: similar to Hypothetical protein MGC73254 [Apis mellifera]
sw18570	BGIBMGA010396	0.9835	0.9022	0.9817	2.3763	7.00E-35	gi 68360882 ref XP_709703.1 PREDICTED: similar to splicing factor, arginine/serine-rich 7 isoform 7 [Danio rerio]
sw15779	BGIBMGA005949	0.7595	1.07345	1.02775	2.37555	8.00E-31	gi 87248079 gb ABD36092.1 coiled-coil domain containing 25 protein [Bombyx mori]
sw14966	BGIBMGA003669	0.8499	1.1517	1.0892	2.37475	1.00E-33	gi 87248493 gb ABD36299.1 eukaryotic translation initiation factor 3 subunit 6 [Bombyx mori]
sw06193	BGIBMGA006980	1.00535	1.1179	1.148	2.3734	No hits found	
sw11250	BGIBMGA003398	0.6223	0.80095	0.72625	2.37225	Bmb004624	3.00E-27
sw03707	BGIBMGA010584	2.0209	1.4018	1.62485	2.37195	e-141	gi 87248295 gb ABD36200.1 chymotrypsinogen [Bombyx mori]
sw04986	BGIBMGA004441	1.2459	0.964	1.1721	2.36615	3.00E-25	gi 54311237 gb AAH84811.1 LOC495348 protein [Xenopus laevis]
sw04521	BGIBMGA011508	0.74295	0.94105	1.0988	2.36555	e-118	gi 74001082 ref XP_856031.1 PREDICTED: similar to T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta) isoform 3 [Canis familiaris]
sw15884	BGIBMGA006588	1.46795	1.48185	1.4751	2.36505	1.00E-45	gi 73995433 ref XP_543480.2 PREDICTED: similar to pescadillo homolog 1, containing BRCT domain [Canis familiaris]
sw22214	BGIBMGA012171	0.93855	1.0765	1.1641	2.36475	1.00E-15	gi 6446579 gb AA21249.2 beta-heavy-spectrin [Drosophila melanogaster]
sw12660	BGIBMGA000813	1.24105	0.9184	1.39915	2.36435	4.00E-22	gi 54636559 gb EAL25962.1 GA15878-PA [Drosophila pseudoobscura]
sw03204	BGIBMGA000937	0.70975	0.89055	0.8685	2.3642	2.00E-55	gi 73977144 ref XP_861870.1 PREDICTED: similar to Uroporphyrinogen decarboxylase (URO-D) (UPD) isoform 4 [Canis familiaris]
sw01725	BGIBMGA006812	1.106	1.0812	1.1884	2.36345	1.00E-27	gi 25246706 gb AAN72834.1 allantoinase [Ctenocephalides felis]
sw15536	BGIBMGA013340	0.8645	1.1495	1.0016	2.3627	3.00E-25	gi 6164599 gb AAF04459.1 dihydrofolate reductase [Heliothis virescens] Dihydrofolate reductase
sw11692	BGIBMGA006875	0.9063	1.05945	1.0775	2.3613	3.00E-18	gi 66513264 ref XP_392851.2 PREDICTED: similar to GA17793-PA [Apis mellifera]
sw06498	BGIBMGA001907	1.42715	0.99955	1.14375	2.36085	1.00E-53	gi 57966866 ref XP_562320.1 ENSANGP00000027535 [Anopheles gambiae str. PEST] ENSANGP00000027535 [Anopheles gambiae str. PEST]
sw18757	BGIBMGA003438	1	1.0499	1.422	2.35945	2.00E-24	gi 37537238 gb AAH23738.2 Kelch domain containing 4 [Mus musculus] Kelch domain-containing protein 4
sw00146	BGIBMGA001664	1	1.08615	1.02705	2.35825	5.00E-59	gi 73976676 ref XP_539554.2 PREDICTED: similar to Solute carrier family 2, facilitated glucose transporter, member 1 (Glucose transporter type 1, erythrocyte/brain) [Canis familiaris]
sw06175	BGIBMGA002730	1.22005	1.227	1.23535	2.3577	1.00E-38	gi 60677859 gb AAX33436.1 RE32747p [Drosophila melanogaster]
sw08978	BGIBMGA007363	1.1663	1.2517	1.3585	2.35665	1.00E-57	gi 15213838 gb AAK92194.1 ribosomal protein S26 [Spodoptera frugiperda]
sw21874	BGIBMGA005655	1.1068	1.02915	1.00085	2.35555	6.00E-20	gi 23128321 ref ZP_00110172.1 COG4886: Leucine-rich repeat (LRR) protein [Nostoc punctiforme PCC 73102]
sw15929	BGIBMGA013069	1.10575	0.99185	1.06605	2.3519	2.00E-14	gi 24645182 ref NP_649837.1 CG8359-PA [Drosophila melanogaster] LD09733p [Drosophila melanogaster] CG8359-PA [Drosophila melanogaster]
sw14703	BGIBMGA011314	0.8734	1.27365	1.17655	2.34955	2.00E-43	gi 18859921 ref NP_573044.1 CG7872-PA [Drosophila melanogaster] LD24870p [Drosophila melanogaster] CG7872-PA [Drosophila melanogaster]
sw06821	BGIBMGA013924	1.2808	1.57665	1.78045	2.3495	5.00E-17	gi 24640056 ref NP_727067.1 CG32750-PA [Drosophila melanogaster] CG32750-PA [Drosophila melanogaster] Vanin-like protein 3 precursor
sw10357	BGIBMGA011682	1.12185	1.20385	0.98775	2.3493	2.00E-40	gi 74004004 ref XP_535873.2 PREDICTED: similar to peroxisomal D3,D2-enoyl-CoA isomerase isoform 1 [Canis familiaris]
sw17127	BGIBMGA002361	0.7056	0.66355	0.7648	2.34735	2.00E-76	gi 87248251 gb ABD36178.1 WD repeat domain 61 [Bombyx mori]
sw01470	BGIBMGA002232	1	1.14165	1.2442	2.34595	No hits found	

sw03560	BGIBMGA002721	0.83235	0.98635	1.00825	2.3436	Bmb014019	5.00E-26
sw18664	BGIBMGA001966	1.06205	0.9283	1.1479	2.3422	5.00E-98	gi 132545 sp P01122 RHO_APLCA RAS-like GTP-binding protein RHO rho protein
sw03200	BGIBMGA007267	0.75395	0.94095	0.74545	2.34035	6.00E-24	gi 50755667 ref XP_414844.1 PREDICTED: similar to NADH-ubiquinone oxidoreductase PDSW subunit (Complex I-PDSW) (CI-PDSW) [Gallus gallus]
sw04152	BGIBMGA007873	1.1519	1.0026	0.713	2.34	No hits found	
sw10585	BGIBMGA006143	1	1.01855	1	2.33505	No hits found	
sw10650	BGIBMGA013784	0.76385	1.30625	0.8591	2.33295	2.00E-48	gi 10863157 gb AAG23916.1 imprinted and ancient [Mus musculus]
sw15825	BGIBMGA009012	0.79415	0.81475	1.02315	2.32895	Bmb035709	5.00E-55
sw03736	BGIBMGA001509	1.2058	1.08815	1.1597	2.32825	e-106	gi 72011152 ref XP_780300.1 PREDICTED: similar to Guanine nucleotide releasing protein (GNRP) (P140 Ras-GRF) [Strongylocentrotus purpuratus]
sw18390	BGIBMGA003500	1.26	1.484	1.4213	2.3269	2.00E-79	gi 9527 emb CAA47358.1 luciferase [Luciola lateralis] Luciferin 4-monooxygenase (Luciferase)
sw05196	BGIBMGA009700	1.2477	1.08665	0.976	2.3236	6.00E-07	gi 73952314 ref XP_852456.1 PREDICTED: similar to Cytochrome c oxidase polypeptide VIIc, mitochondrial precursor [Canis familiaris]
sw05842	BGIBMGA005678	2.288	1.03225	1.12805	2.32195	No hits found	
sw01621	BGIBMGA013585	0.84575	0.9463	0.9632	2.32165	5.00E-47	gi 85857460 gb ABC86266.1 RE45749p [Drosophila melanogaster]
sw21951	BGIBMGA001202	1.739	2.17935	2.6849	2.3214	e-125	gi 87248175 gb ABD36140.1 muscle LIM protein [Bombyx mori]
sw00581	BGIBMGA011651	1.05865	0.99945	0.96025	2.3198	5.00E-36	gi 50603837 gb AAH78404.1 Cytokine induced apoptosis inhibitor 1 [Danio rerio] cytokine induced apoptosis inhibitor 1 [Danio rerio]
sw00797	BGIBMGA000202	0.871	0.73855	0.58105	2.31945	No hits found	
sw11070	BGIBMGA012808	1.0123	1.28205	1.20455	2.31905	e-147	gi 55236224 gb EAA14338.2 ENSANGP00000006039 [Anopheles gambiae str. PEST] ENSANGP00000006039 [Anopheles gambiae str. PEST]
sw09461	BGIBMGA004078	1.08165	0.912	1.11435	2.31865	4.00E-82	gi 72007484 ref XP_781161.1 PREDICTED: similar to mitochondrial ribosomal protein S9 [Strongylocentrotus purpuratus]
sw09066	BGIBMGA009169	1.00945	0.64275	1.05615	2.3173	No hits found	
sw08193	BGIBMGA008284	0.80255	0.90275	1.0213	2.3167	2.00E-30	gi 68421636 ref XP_683350.1 PREDICTED: similar to ELAV-like 2 isoform 1 isoform 1 [Danio rerio]
sw01521	BGIBMGA011634	1	1	1	2.315	3.00E-18	gi 83763951 emb CAJ12162.1 cg12111 protein [Drosophila simulans]
sw21778	BGIBMGA011804	1.1491	1.39195	1.42375	2.31255	No hits found	
sw13440	BGIBMGA002304	1.1867	1.0756	1.23555	2.31215	Bmb018393	7.00E-23
sw13175	BGIBMGA004515	0.9027	1.67455	1.44745	2.3107	e-104	gi 56378323 dbj BAD74198.1 heat shock protein hsp23.7 [Bombyx mori]
sw14953	BGIBMGA010827	1.04885	1.13835	1.26335	2.30955	8.00E-12	gi 57107227 ref XP_534981.1 PREDICTED: similar to exosome component 1 isoform 1 [Canis familiaris]
sw04110	BGIBMGA004573	0.66985	0.73375	0.8717	2.3079	3.00E-21	gi 62083383 gb AAX62416.1 small nuclear ribonucleoprotein G [Lysiphlebus testaceipes]
sw15235	BGIBMGA011810	1.08815	1.0286	1.293	2.30455	7.00E-27	gi 4972738 gb AAD34764.1 unknown [Drosophila melanogaster]
sw18276	BGIBMGA000236	0.75375	0.83945	0.65015	2.3043	3.00E-15	gi 26788031 emb CAD58772.1 novel protein similar to human isovaleryl Coenzyme A dehydrogenase (IVD) [Danio rerio] Isovaleryl Coenzyme A dehydrogenase [Danio rerio]
sw09911	BGIBMGA002406	0.95795	1.27435	1.10525	2.3022	Bmb038389	4.00E-92

sw05068	BGIBMGA007535	0.84575	1.0148	1.00445	2.2999	8.00E-05	gi 54641026 gb EAL29777.1 GA12543-PA [Drosophila pseudoobscura]
sw05584	BGIBMGA009067	1.1001	1.34675	1.27775	2.2997	9.00E-60	gi 58395618 ref XP_321387.2 ENSANGP00000011567 [Anopheles gambiae str. PEST] ENSANGP00000011567 [Anopheles gambiae str. PEST]
sw06006	BGIBMGA000713	0.1349	0.586	0.6147	2.29745	Bmb018933	No hits found
sw22871	BGIBMGA002309	1.08325	1.1373	1.47225	2.29595	4.00E-96	gi 87248551 gb ABD36328.1 nucleoplasmin isoform 2 [Bombyx mori]
sw10352	BGIBMGA005930	0.94875	1.14605	1.1182	2.29525	0	gi 87248441 gb ABD36273.1 WD40 protein [Bombyx mori]
sw12837	BGIBMGA002083	0.9991	0.8748	0.67545	2.29445	8.00E-62	gi 1526415 dbj BAA09449.1 actin [Chlamydomonas reinhardtii] Actin actin [Chlamydomonas reinhardtii]
sw00334	BGIBMGA008278	0.88665	0.8061	0.8839	2.2906	6.00E-08	gi 56199440 gb AAV84209.1 chymotrypsin [Culicoides sonorensis]
sw15960	BGIBMGA006158	0.9567	0.90485	1.1805	2.28965	e-113	gi 87248645 gb ABD36375.1 prohibitin protein WPH [Bombyx mori]
sw06569	BGIBMGA012979	0.99295	0.8611	0.843	2.2883	3.00E-14	gi 55242208 gb EAL40896.1 ENSANGP00000027230 [Anopheles gambiae str. PEST] ENSANGP00000012173 [Anopheles gambiae str. PEST] ENSANGP00000027230
sw07764	BGIBMGA010952	0.91515	1.0075	0.80375	2.28465	No hits found	
sw05181	BGIBMGA007733	1.3369	1.551	1.3551	2.28395	8.00E-15	gi 66517218 ref XP_396168.2 PREDICTED: similar to RE58116p [Apis mellifera]
sw20723	BGIBMGA010101	1.20065	1.6396	1.3243	2.2837	No hits found	
sw12097	BGIBMGA002944	1.12845	1.35575	0.48835	2.2824	6.00E-28	gi 66518230 ref XP_623818.1 PREDICTED: similar to putative alcohol dehydrogenase [Apis mellifera]
sw22256	BGIBMGA011840	1.2008	1.1654	1	2.28175	2.00E-06	gi 55649967 ref XP_524400.1 PREDICTED: similar to zinc finger protein 524 [Pan troglodytes]
sw05506	BGIBMGA001335	1.555	1.35185	1.31225	2.27985	Bmb009933	e-105
sw03914	BGIBMGA010735	0.93445	1.05135	1.56335	2.27895	Bmb022011	3.00E-33
sw10405	BGIBMGA013918	0.82425	0.9437	0.73695	2.278	2.00E-54	gi 1834425 emb CAA71871.1 Trf-proximal protein [Drosophila melanogaster]
sw15827	BGIBMGA006344	0.80915	0.85005	1.1544	2.27675	Bmb035726	6.00E-06
sw14986	BGIBMGA007019	1.00825	0.94285	0.95315	2.2761	2.00E-12	gi 50758414 ref XP_415911.1 PREDICTED: similar to Mitochondrial ribosomal protein S23 [Gallus gallus]
sw03337	BGIBMGA004596	0.89835	1.031	1.12695	2.27585	9.00E-24	gi 18693297 gb AAL78310.1 PDZ domain containing protein NHERF-2 [Oryctolagus cuniculus] Na(+)/H(+) exchange regulatory cofactor NHE-RF2 (PDZ domain containing protein NHERF-2)
sw04512	BGIBMGA001898	0.94095	0.9373	0.8535	2.2757	6.00E-75	gi 1060912 dbj BAA07406.1 RPB5 [Homo sapiens]
sw07203	BGIBMGA003702	0.9556	1.27335	1.30025	2.27505	Bmb046601	3.00E-14
sw07321	BGIBMGA013551	0.90295	1.02045	0.9083	2.27495	3.00E-37	gi 66552919 ref XP_625097.1 PREDICTED: similar to CG6884-PA [Apis mellifera]
sw13579	BGIBMGA013514	1.3195	1.19995	1.26575	2.2724	2.00E-06	gi 37681861 gb AAQ97808.1 hypothetical protein BC013949 [Danio rerio] Zgc:77492 protein [Danio rerio] hypothetical protein LOC393537 [Danio rerio] Hypothetical protein MGC65939 [Danio rerio]
sw09044	BGIBMGA005628	0.9761	1.3278	1.0366	2.27155	e-157	gi 87248245 gb ABD36175.1 uridine 5'-monophosphate synthase [Bombyx mori]
sw04365	BGIBMGA008111	1.111	1.23385	0.7611	2.2691	6.00E-46	gi 7657611 ref NP_055095.1 DnaJ (Hsp40) homolog, subfamily C, member 8 [Homo sapiens] SPF31 [Homo sapiens]
sw04717	BGIBMGA013458	1.0529	1.0996	0.9505	2.26815	Bmb043844	3.00E-11
sw20508	BGIBMGA002971	0.91105	1.099	1.0143	2.26785	9.00E-64	gi 87313157 gb ABD37875.1 catsup protein [Drosophila melanogaster]

sw08924	BGIBMGA000603	0.63495	1	0.92285	2.2661	2.00E-18	gi 73966446 ref XP_852670.1 PREDICTED: similar to sperm associated antigen 9 isoform 1 isoform 2 [Canis familiaris]
sw12797	BGIBMGA006727	1.0466	1.4222	1.19375	2.2653	e-173	gi 66509122 ref XP_394574.2 PREDICTED: similar to CG11594-PA, isoform A [Apis mellifera]
sw18095	BGIBMGA010291	1.4322	1.48075	1.6351	2.2649	Bmb037490	7.00E-46
sw10478	BGIBMGA001554	1.50905	2.07925	1.9729	2.26425	3.00E-17	gi 19698929 gb AAL91200.1 unknown protein [Arabidopsis thaliana] unknown protein [Arabidopsis thaliana]
sw10996	BGIBMGA011897	0.96065	1.0196	1.14885	2.26395	No hits found	
sw08134	BGIBMGA003351	1.13415	0.98995	1.3533	2.2636	1.00E-48	gi 54290089 dbj BAD61056.1 MCM7 [Bombyx mori]
sw07899	BGIBMGA006869	0.9021	1.1187	0.3674	2.2625	2.00E-41	gi 55243516 gb EAA06508.2 ENSANGP00000014874 [Anopheles gambiae str. PEST] ENSANGP00000014874 [Anopheles gambiae str. PEST]
sw21457	BGIBMGA007844	1.0404	1.2234	1.10845	2.2618	2.00E-08	gi 27374352 gb AAO01093.1 Surf6-PA [Drosophila willistoni]
sw08984	BGIBMGA010658	0.9033	1.0095	0.9799	2.26085	Bmb022624	9.00E-07
sw16289	BGIBMGA012810	0.8472	1.0839	1.1496	2.26025	5.00E-53	gi 14211845 ref NP_115938.1 IMP2 inner mitochondrial membrane protease-like [Homo sapiens] inner mitochondrial membrane peptidase 2
sw06218	BGIBMGA011887	0.90465	0.9005	0.9633	2.26015	Bmb023115	1.00E-94
sw11664	BGIBMGA001223	0.94985	1.1198	1.06915	2.25735	0	gi 6014919 sp O61305 DBP80_DROME DEAD-box helicase Dbp80 DEAD-box helicase [Drosophila melanogaster]
sw06330	BGIBMGA008593	1.07975	1.20945	1.235	2.2529	No hits found	
sw22089	BGIBMGA011721	1.54605	0.8652	1.1719	2.25195	2.00E-18	gi 56308438 ref NP_649115.2 CG18294-PA [Drosophila melanogaster] RE51966p [Drosophila melanogaster] CG18294-PA [Drosophila melanogaster]
sw15316	BGIBMGA004827	0.9464	1.0722	0.99635	2.25175	6.00E-06	gi 27356613 gb AAO06952.1 MSTP052 [Homo sapiens]
sw02241	BGIBMGA004738	1	1	0.72155	2.2514	2.00E-30	gi 60677713 gb AAX33363.1 RH65810p [Drosophila melanogaster]
sw05296	BGIBMGA008248	1.0007	0.83925	1.13795	2.251	3.00E-46	gi 6594153 emb CAB63528.1 EG:BACH59J11.1 [Drosophila melanogaster]
sw14362	BGIBMGA000722	0.829	0.89965	0.87285	2.24855	Bmb024668	5.00E-18
sw11111	BGIBMGA008714	1.05795	0.97815	1.08745	2.24695	5.00E-64	gi 72137308 ref XP_793386.1 PREDICTED: similar to mitochondrial ribosomal protein L45 [Strongylocentrotus purpuratus]
sw16738	BGIBMGA005505	0.8071	1.3127	0.94295	2.2469	Bmb046240	4.00E-11
sw14091	BGIBMGA002654	1.44375	1.17685	1.50235	2.24375	2.00E-78	gi 499204 gb AAC14192.1 D-E-A-D box protein [Drosophila melanogaster]
sw16445	BGIBMGA000383	0.72365	1.07595	0.9863	2.2425	5.00E-19	gi 73960510 ref XP_537169.2 PREDICTED: similar to odorant response abnormal 4 isoform 1 [Canis familiaris]
sw05319	BGIBMGA005692	1.0139	1.1851	1.53875	2.2423	3.00E-54	gi 66499215 ref XP_624770.1 PREDICTED: similar to ENSANGP00000015190 [Apis mellifera]
sw00284	BGIBMGA004975	1.4421	1.11715	1.03405	2.23945	8.00E-05	gi 67846976 gb AAY82180.1 CG6547 [Drosophila melanogaster]
sw01671	BGIBMGA007377	0.8036	0.5139	0.5572	2.239	5.00E-72	gi 61191881 gb AAX39408.1 serine protease [Bombyx mandarina]
sw18899	BGIBMGA014171	0.8411	0.3805	0.77045	2.23705	4.00E-29	gi 102972 pir A28068 microvitellogenin precursor - tobacco hornworm MICROVITELLOGENIN PRECURSOR microvitellogenin microvitellogenin
sw13873	BGIBMGA007726	1.08005	0.9678	0.9294	2.23555	e-150	gi 28277919 gb AAH45990.1 Bcs1l protein [Danio rerio]
sw03556	BGIBMGA009259	1.39155	1.23065	0.79195	2.23475	Bmb013903	5.00E-05

sw16561	BGIBMGA012567	0.888	1.03705	0.9021	2.2345	Bmb043350	4.00E-34
sw00924	BGIBMGA003924	0.83575	0.823	0.8703	2.2332	e-116	gi 87248369 gb ABD36237.1 NADH dehydrogenase (ubiquinone) Fe-S protein 8 [Bombyx mori]
sw07571	BGIBMGA004776	1	1	1	2.2287	e-139	gi 76616634 ref XP_872845.1 PREDICTED: similar to heterogeneous nuclear ribonucleoprotein methyltransferase-like 4 [Bos taurus]
sw04011	BGIBMGA011062	0.7367	1.0387	0.752	2.22815	2.00E-37	gi 7657313 ref NP_055277.1 Lsm1 protein [Homo sapiens] Lsm1 protein [Homo sapiens] Lsm1 protein [Homo sapiens] CaSm [Homo sapiens] U6 snRNA-associated Sm-like protein LSM1 (Small nuclear ribonuclear CaSm)
sw03046	BGIBMGA011994	0.7632	1.00395	0.6681	2.22375	3.00E-21	gi 25012393 gb AAN71305.1 RE11282p [Drosophila melanogaster]
sw16221	BGIBMGA001916	0.7264	0.9271	0.83345	2.2219	Bmb039234	4.00E-34
sw06147	BGIBMGA009052	1.2195	1.03885	1.04735	2.22025	1.00E-84	gi 72163576 ref XP_793131.1 PREDICTED: similar to Glyoxylate reductase/hydroxypyruvate reductase [Strongylocentrotus purpuratus]
sw10495	BGIBMGA002752	1.06775	1	0.9236	2.21945	1.00E-17	gi 56269188 gb AAH87435.1 LOC496040 protein [Xenopus laevis]
sw13572	BGIBMGA012671	0.9722	1.11595	0.885	2.21885	4.00E-08	gi 27682127 ref XP_215228.1 PREDICTED: similar to Ubiquitin-like protein 4 (Ubiquitin-like protein GDX) [Rattus norvegicus]
sw04473	BGIBMGA013018	1.1785	1.22645	1.2148	2.218	Bmb035495	1.00E-12
sw15920	BGIBMGA001889	0.9262	0.8325	0.9043	2.2176	No hits found	
sw04166	BGIBMGA008400	1.1199	1.1543	1.3285	2.2169	No hits found	
sw21888	BGIBMGA013792	1.39595	1.0894	1.1388	2.21445	3.00E-69	gi 70909519 emb CAJ17183.1 ribosomal protein S11e [Eucinetus sp. APV-2005]
sw21243	BGIBMGA009696	0.9637	1.10795	0.92385	2.2131	Bmb032323	5.00E-24
sw12116	BGIBMGA012032	0.83225	1.0832	1.1484	2.2123	2.00E-25	gi 50416634 gb AAH77653.1 Heat shock 10kDa protein 1 (chaperonin 10) [Xenopus tropicalis] heat shock 10kDa protein 1 (chaperonin 10) [Xenopus tropicalis] heat shock 10kDa protein 1 (chaperonin 10) [Xenopus tropicalis]
sw03938	BGIBMGA001708	0.6963	0.5718	0.755	2.2116	1.00E-33	gi 66525368 ref XP_392073.2 PREDICTED: similar to Colorectal mutant cancer protein (MCC protein) [Apis mellifera]
sw01900	BGIBMGA004612	1.94495	1.5786	1.92665	2.21125	0	gi 46358051 dbj BAD15163.1 heat shock protein [Antheraea yamamai]
sw08152	BGIBMGA006935	1.22465	1.26095	1.25155	2.21125	1.00E-32	gi 24640068 ref NP_572300.1 CG14446-PA [Drosophila melanogaster] CG14446-PA [Drosophila melanogaster]
sw12581	BGIBMGA003415	0.905	0.89835	0.9727	2.2112	3.00E-45	gi 60594462 pdb 2BIU X Chain X, Crystal Structure Of Human Cyclophilin D At 1.7 A Resolution, Dmso Complex Chain X, Crystal Structure Of Human Cyclophilin D At 1.7 A Resolution
sw14722	BGIBMGA010720	0.98345	1.04865	1.2907	2.211	1.00E-34	gi 83022250 ref XP_918113.1 PREDICTED: similar to zinc finger protein 420 [Mus musculus]
sw20012	BGIBMGA012172	0.77885	0.82385	1.0531	2.211	2.00E-08	gi 73982258 ref XP_533172.2 PREDICTED: similar to thioredoxin-related transmembrane protein 2 isoform 1 [Canis familiaris]
sw04868	BGIBMGA005374	1.1328	1.09765	0.98005	2.2062	2.00E-43	gi 72007676 ref XP_785301.1 PREDICTED: similar to polynucleotide kinase 3-phosphatase [Strongylocentrotus purpuratus]
sw07971	BGIBMGA013182	0.94595	1.2033	0.7714	2.206	No hits found	
sw01642	BGIBMGA011514	0.76265	1.17205	0.8983	2.20455	4.00E-10	gi 50749218 ref XP_421538.1 PREDICTED: similar to nuclear receptor binding factor 2; nuclear receptor binding factor-2; comodulator of PPAR and RXR [Gallus gallus]
sw04041	BGIBMGA002430	1.19375	0.97915	1.25405	2.2018	Bmb025306	e-118
sw04644	BGIBMGA003119	1.23915	1.07805	1.16075	2.199	9.00E-55	gi 68362350 ref XP_696178.1 PREDICTED: similar to Elongation factor Ts, mitochondrial precursor (EF-Ts) (EF-TsMt) (2A3-2) [Danio rerio]
sw22252	BGIBMGA010793	0.87065	0.78745	1	2.1977	Bmb024272	1.00E-24
sw08472	BGIBMGA010234	0.7818	0.9708	0.8741	2.19625	2.00E-48	gi 87248209 gb ABD36157.1 DNA-directed RNA polymerase subunit 6-like protein [Bombyx mori]

sw09637	BGIBMGA005145	1.102	1.04335	0.92655	2.1949	6.00E-24	gi 55297200 dbj BAD68874.1 glycine cleavage T protein-like [Oryza sativa (japonica cultivar-group)] glycine cleavage T protein-like [Oryza sativa (japonica cultivar-group)]
sw22882	BGIBMGA005064	1.22665	1.05575	0.9807	2.19385	e-124	gi 85740627 gb ABC79691.1 glutathione S-transferase 4 [Bombyx mori]
sw18808	BGIBMGA012505	0.78265	0.85265	0.8679	2.1932	9.00E-17	gi 71031052 ref XP_765168.1 protein disulfide isomerase [Theileria parva strain Muguga] protein disulfide isomerase [Theileria parva]
sw05420	BGIBMGA000360	0.9091	1.19575	0.81675	2.1905	5.00E-17	gi 57918265 ref XP_556948.1 ENSANGP00000026833 [Anopheles gambiae str. PEST] ENSANGP00000026833 [Anopheles gambiae str. PEST]
sw18382	BGIBMGA003336	0.7564	1.0092	0.95625	2.19025	5.00E-91	gi 76651937 ref XP_882268.1 PREDICTED: similar to RNA (guanine-7-) methyltransferase isoform 4 [Bos taurus]
sw16288	BGIBMGA011566	0.7301	1.01965	0.937	2.1878	5.00E-14	gi 50749705 ref XP_421721.1 PREDICTED: similar to DPCD protein [Gallus gallus]
sw17084	BGIBMGA010398	0.9278	1.0241	1	2.1868	8.00E-05	gi 66510656 ref XP_393387.2 PREDICTED: similar to ENSANGP00000008952 [Apis mellifera]
sw20128	BGIBMGA005411	0.8433	0.9568	1.0302	2.1863	Bmb033703	e-123
sw09541	BGIBMGA006802	1.2295	1.2016	1.11895	2.18415	9.00E-24	gi 57033124 gb AAH88913.1 LOC496323 protein [Xenopus laevis]
sw18672	BGIBMGA013624	1.09625	1.06015	1.25025	2.183	3.00E-72	gi 57096845 ref XP_532690.1 PREDICTED: similar to tigger transposable element derived 4 [Canis familiaris]
sw22325	BGIBMGA002288	1.0308	1.0051	0.4899	2.1828	6.00E-67	gi 9651929 gb AAF91316.1 immulectin-2 [Manduca sexta]
sw08246	BGIBMGA000520	1	1	1	2.18275	6.00E-72	gi 68989037 dbj BAE06188.1 glycine rich protein [Bombyx mori]
sw07403	BGIBMGA004741	1.143	1.2685	0.89985	2.18065	6.00E-65	gi 74009016 ref XP_538183.2 PREDICTED: similar to HIV TAT specific factor 1 [Canis familiaris]
sw01366	BGIBMGA005369	1.17705	1.0279	1.11475	2.18045	3.00E-19	gi 1244518 gb AAA93257.1 allatostatin neuropeptide precursor [Pseudaletia unipuncta]
sw06276	BGIBMGA003661	1.26135	0.7638	0.89995	2.1804	No hits found	
sw09973	BGIBMGA003909	0.81455	1.07925	0.8694	2.17955	5.00E-30	gi 38492611 pdb 1OE0 D Chain D, Crystal Structure Of Drosophila Deoxyribonucleoside Kinase In Complex With Dttp Chain C, Crystal Structure Of Drosophila Deoxyribonucleoside Kinase In Complex With Dttp Chain B
sw15259	BGIBMGA001921	0.8379	0.93205	1.05495	2.17905	2.00E-85	gi 558568 emb CAA50674.1 actin related protein [Drosophila melanogaster] actin-related protein
sw03335	BGIBMGA009111	1.0233	1.05355	0.97665	2.17545	2.00E-24	gi 20177053 gb AAM12288.1 RE13587p [Drosophila melanogaster]
sw07936	BGIBMGA006800	1.2314	1.33215	0.9734	2.1741	7.00E-38	gi 58476259 gb AAH89602.1 1700023B02Rik protein [Mus musculus]
sw15396	BGIBMGA009714	3.9267	1.615	1.2362	2.17255	Bmb032353	No hits found
sw11108	BGIBMGA002242	0.0501	0.6385	0.6398	2.17145	No hits found	
sw17801	BGIBMGA001829	1.0979	1.24205	1.1656	2.1714	3.00E-35	gi 82884290 ref XP_903599.1 PREDICTED: XPMC2 prevents mitotic catastrophe 2 homolog isoform 5 [Mus musculus]
sw13760	BGIBMGA001159	0.94765	0.99935	0.82945	2.17015	7.00E-94	gi 50418088 gb AAH77615.1 MGC84611 protein [Xenopus laevis] Vacuolar protein sorting protein 36
sw11720	BGIBMGA007100	0.9727	0.867	0.80195	2.16975	2.00E-89	gi 14041150 emb CAC38761.1 leukotriene B4 [Geodia cydonium]
sw12317	BGIBMGA009476	1.1448	1.21215	0.84735	2.16955	5.00E-44	gi 74831719 emb CAJ30028.1 carboxypeptidase B precursor [Helicoverpa zea]
sw18489	BGIBMGA010278	1.46225	1.54515	1.5254	2.16855	1.00E-16	gi 18129616 ref NP_082504.1 PIN2/TRF1-interacting protein [Mus musculus] Pin2-interacting protein X1 [Mus musculus] LPTS1 [Mus musculus] Pin2-interacting protein X1 (TRF1-interacting protein 1)
sw11674	BGIBMGA001711	0.8581	0.9512	0.88055	2.1683	4.00E-63	gi 55244531 gb EAA05402.2 ENSANGP00000019750 [Anopheles gambiae str. PEST] ENSANGP00000019750 [Anopheles gambiae str. PEST]
sw16454	BGIBMGA013305	1	1	1	2.1643	Bmb041849	6.00E-43

sw04142	BGIBMGA006085	1.37935	1.0062	1.707	2.1625	0	gi 6433838 emb CAB60723.1 DNop5 protein [Drosophila melanogaster]
sw03846	BGIBMGA012204	1.1828	1.0006	0.97045	2.1601	1.00E-64	gi 71725396 ref NP_001025161.1 D14Ert209e protein [Mus musculus]
sw06845	BGIBMGA009073	0.7973	1.0846	0.78215	2.15985	8.00E-10	gi 1836157 gb AAB46908.1 fungal protease inhibitor F; FPI-F [Bombyx mori] Fungal protease inhibitor F precursor (FPI-F) fungal protease-specific inhibitor-F [Bombyx mori]
sw17051	BGIBMGA012550	0.51685	0.79585	0.74475	2.15955	5.00E-96	gi 87248607 gb ABD36356.1 signal peptidase 18 kDa subunit [Bombyx mori]
sw03909	BGIBMGA008211	1.17635	0.95555	1.1138	2.1587	1.00E-13	gi 73980977 ref XP_855121.1 PREDICTED: similar to bolA-like 3 [Canis familiaris]
sw09544	BGIBMGA007716	1.2122	1.0999	0.9352	2.15855	e-180	gi 87248077 gb ABD36091.1 arginase [Bombyx mori]
sw19539	BGIBMGA006159	0.758	0.96695	1.0401	2.15725	9.00E-63	gi 68394187 ref XP_687166.1 PREDICTED: similar to inosine triphosphatase isoform a [Danio rerio]
sw01149	BGIBMGA006032	1.38115	0.97885	1.10795	2.15705	2.00E-18	gi 61889092 ref NP_077325.2 adenylate kinase 1 [Rattus norvegicus] Adenylate kinase 1 [Rattus norvegicus]
sw13759	BGIBMGA002179	0.608	1.11675	0.8875	2.15675	No hits found	
sw02931	BGIBMGA000282	0.7687	0.88885	0.6396	2.1551	2.00E-16	gi 117622 sp P11734 CU08_LOCM1 Cuticle protein 8 (LM-8) (LM-ACP 8)
sw07325	BGIBMGA011686	1.04165	1.18405	0.70475	2.1528	5.00E-76	gi 66517442 ref XP_623871.1 PREDICTED: similar to ENSANGP00000013944 [Apis mellifera]
sw12193	BGIBMGA013506	1.25545	1.28805	1.1581	2.1506	5.00E-55	gi 72098763 ref XP_799251.1 PREDICTED: similar to Protein C20orf43 [Strongylocentrotus purpuratus]
sw16074	BGIBMGA008956	0.9734	1.23915	0.90935	2.14855	Bmb038011	e-104
sw16663	BGIBMGA004848	1.28045	1.2879	1.224	2.14725	5.00E-44	gi 55247392 gb EAA01895.3 ENSANGP00000013804 [Anopheles gambiae str. PEST] ENSANGP00000015666 [Anopheles gambiae str. PEST] ENSANGP00000015666 [Anopheles gambiae str. PEST]
sw08168	BGIBMGA004994	1.02585	1.09985	1.1477	2.14525	e-143	gi 40645085 dbj BAD06461.1 homologue of DNA-directed RNA polymerase II subunit [Antheraea pernyi] homologue of DNA-directed RNA polymerase II subunit [Antheraea pernyi]
sw02528	BGIBMGA003564	0.72985	0.6492	0.8163	2.1418	Bmb043020	No hits found
sw08622	BGIBMGA000668	0.87785	0.9543	0.70695	2.14	1.00E-18	gi 49900160 gb AAH977030.1 MGC89869 protein [Xenopus tropicalis] MGC89869 protein [Xenopus tropicalis]
sw18227	BGIBMGA008049	0.9308	1.04315	1.4078	2.1396	2.00E-07	gi 66531974 ref XP_393396.2 PREDICTED: similar to putative monoacylglycerol acyltransferase 1 [Apis mellifera]
sw03037	BGIBMGA010345	1.88725	2.05275	1.71725	2.1388	No hits found	
sw18400	BGIBMGA004727	0.22395	0.6916	0.4914	2.1383	Bmb027076	4.00E-05
sw09770	BGIBMGA006329	0.7855	1.00645	0.8829	2.13815	6.00E-21	gi 66910579 gb AAH97374.1 ADP-ribosylation factor-like 6 interacting protein 4 [Rattus norvegicus] ADP-ribosylation factor-like 6 interacting protein 4 [Rattus norvegicus]
sw19962	BGIBMGA010938	1.44945	1.369	0.7186	2.13725	4.00E-68	gi 57966866 ref XP_562320.1 ENSANGP00000027535 [Anopheles gambiae str. PEST] ENSANGP00000027535 [Anopheles gambiae str. PEST]
sw07883	BGIBMGA012714	0.71465	0.8088	0.8629	2.13685	5.00E-13	gi 28077083 ref NP_291081.2 amnionless [Mus musculus] amnionless precursor protein [Mus musculus] amnionless precursor protein [Mus musculus] Amnionless [Mus musculus] Amnionless protein precursor
sw15413	BGIBMGA005336	1.4101	1.2596	1.1751	2.13555	3.00E-31	gi 58395895 ref XP_321568.2 ENSANGP00000011533 [Anopheles gambiae str. PEST] ENSANGP00000011533 [Anopheles gambiae str. PEST]
sw07985	BGIBMGA000419	1.628	1.7097	1.2878	2.13515	1.00E-46	gi 72156944 ref XP_794386.1 PREDICTED: similar to Lambda-crystallin homolog [Strongylocentrotus purpuratus]
sw14783	BGIBMGA002939	0.7981	1.1418	0.96835	2.135	5.00E-31	gi 56118552 ref NP_001007992.1 hpgd-prov protein [Xenopus tropicalis] Hpgd-prov protein [Xenopus tropicalis]
sw06082	BGIBMGA005878	0.9099	1.0804	1.1478	2.13235	5.00E-60	gi 228300 prf I1802389A transcription factor IIE:SUBUNIT=beta
sw18220	BGIBMGA009106	1.4047	1.16185	0.98535	2.1309	4.00E-70	gi 3514020 gb AAC34097.1 glutathione transferase; PiGSTII [Platynota idaeusalis]

sw22924	BGIBMGA001060	0.7506	0.8669	0.79815	2.13015	4.00E-37	gi 3065729 gb AAC14276.1 clathrin light chain [Drosophila melanogaster]
sw09598	BGIBMGA010739	0.99455	1.1308	1.70585	2.12935	Bmb032483	e-113
sw08971	BGIBMGA002768	0.9068	1.11755	0.8439	2.12875	2.00E-10	gi 89268302 emb CAJ83054.1 suppressor of Ty 7 (S. cerevisiae)-like;STAF65(gamma) [Xenopus tropicalis]
sw13208	BGIBMGA009776	1.90535	1.04695	1.0717	2.12715	2.00E-25	gi 6560689 gb AAF16722.1 putative cuticle protein [Manduca sexta]
sw09714	BGIBMGA003010	1	1	1	2.12625	1.00E-69	gi 50734127 ref XP_418979.1 PREDICTED: similar to Werner helicase interacting protein 1; Werner syndrome homolog (human) interacting protein [Gallus gallus]
sw20862	BGIBMGA009285	0.91965	1.0347	1.1505	2.126	Bmb009445	1.00E-38
sw14169	BGIBMGA014214	0.4841	0.7689	0.8131	2.12525	No hits found	
sw05142	BGIBMGA000365	1.1546	1.1735	1.2839	2.1251	4.00E-40	gi 72086744 ref XP_792890.1 PREDICTED: similar to RAB, member of RAS oncogene family-like 3 [Strongylocentrotus purpuratus]
sw03474	BGIBMGA005425	0.80235	0.92485	1.1197	2.1232	Bmb011946	1.00E-68
sw16063	BGIBMGA012718	0.8898	1.1182	1.2806	2.12285	2.00E-36	gi 76621180 ref XP_613288.2 PREDICTED: similar to solute carrier family 35, member E1 [Bos taurus]
sw19533	BGIBMGA005431	1	1	0.87455	2.1215	2.00E-40	gi 62471655 ref NP_001014495.1 pickpocket 13 CG33508-PA [Drosophila melanogaster] pickpocket 13 [Drosophila melanogaster] CG33508-PA [Drosophila melanogaster]
sw05309	BGIBMGA006778	0.8327	1.0596	0.71245	2.12115	No hits found	
sw15615	BGIBMGA012200	0.80445	1.01505	1.09215	2.1191	4.00E-06	gi 72141202 ref XP_791628.1 PREDICTED: similar to mitochondrial ribosomal protein L43 isoform b [Strongylocentrotus purpuratus]
sw07662	BGIBMGA007301	1.23265	1.1855	0.9169	2.1181	1.00E-24	gi 23308325 gb AAN18132.1 At5g47240/MQL5_10 [Arabidopsis thaliana] AT5g47240/MQL5_10 [Arabidopsis thaliana]
sw11627	BGIBMGA011108	1.43175	1.48205	1.2007	2.11715	3.00E-36	gi 78058375 gb ABB17552.1 NADH-dependent retinal reductase [Oryctolagus cuniculus]
sw13068	BGIBMGA008020	0.95905	0.9941	1.134	2.11635	2.00E-28	gi 68404433 ref XP_694901.1 PREDICTED: similar to cubilin, partial [Danio rerio]
sw06692	BGIBMGA007632	0.97965	1.07365	1	2.113	6.00E-26	gi 55664893 emb CAH70763.1 novel protein (FLJ13150) [Homo sapiens] C1orf82 protein [Homo sapiens]
sw11800	BGIBMGA008749	1.3631	1.06635	1.1529	2.11235	3.00E-94	gi 87248451 gb ABD36278.1 adenylate cyclase [Bombyx mori]
sw18756	BGIBMGA000254	1.00125	1	0.8761	2.11225	8.00E-37	gi 55245976 gb EAA04147.2 ENSANGP00000013342 [Anopheles gambiae str. PEST] ENSANGP00000013342 [Anopheles gambiae str. PEST]
sw11935	BGIBMGA008301	0.84525	0.9884	0.84605	2.1113	2.00E-19	gi 29124593 gb AAH49041.1 Mitochondrial ribosomal protein L14 [Danio rerio] mitochondrial ribosomal protein L14 [Danio rerio]
sw14651	BGIBMGA007269	0.3166	1.0556	0.89875	2.1101	3.00E-16	gi 72067168 ref XP_795216.1 PREDICTED: similar to putative protein of bilateral origin (49.2 kD) (3G698), partial [Strongylocentrotus purpuratus]
sw05401	BGIBMGA012017	0.7111	0.79425	0.8676	2.10895	No hits found	
sw16679	BGIBMGA009157	0.97995	1.05955	0.8194	2.10765	Bmb045273	7.00E-20
sw08752	BGIBMGA000157	1.2406	1.11285	0.95245	2.10705	4.00E-27	gi 76654393 ref XP_876322.1 PREDICTED: similar to Transcription factor MafK (Erythroid transcription factor NF-E2 p18 subunit) [Bos taurus]
sw17949	BGIBMGA003741	0.7984	0.73215	0.7132	2.10615	3.00E-12	gi 72086632 ref XP_791549.1 PREDICTED: similar to interferon gamma inducible protein 30 [Strongylocentrotus purpuratus]
sw08626	BGIBMGA008003	1.1495	1.2593	1.26135	2.10515	7.00E-11	gi 2827498 emb CAA15707.1 EG:30B8.3 [Drosophila melanogaster]
sw06638	BGIBMGA005004	0.95575	1.06035	1.4765	2.10475	1.00E-19	gi 11121443 emb CAC14874.1 zinc/iron regulated transporter-related protein 3, DZIP3 protein [Drosophila melanogaster]
sw21738	BGIBMGA009907	0.7359	0.8809	1.16655	2.10295	0	gi 49022793 dbj BAD23983.1 broad-complex Z1-isoform [Bombyx mori] broad-complex B-Z1 isoform [Bombyx mori] broad-complex A-Z1 isoform [Bombyx mori] broad-complex Z1-isoform [Bombyx mori] Broad-Complex isoform Z1

sw14041	BGIBMGA001437	0.87095	0.9736	1.0348	2.10255	4.00E-80	gi 12654229 gb AAH00934.1 Eukaryotic translation initiation factor 2 beta [Homo sapiens]
sw12550	BGIBMGA008222	1.07345	1.11515	0.7422	2.10105	2.00E-05	gi 33285891 gb AAQ01563.1 promoting protein [Bombyx mori]
sw22929	BGIBMGA001351	1.8716	1.08665	1.16855	2.09995	2.00E-24	gi 62646831 ref XP_579660.1 PREDICTED: aldo-keto reductase family 1, member D1 [Rattus norvegicus]
sw11669	BGIBMGA008893	1	1.19675	0.83055	2.09555	8.00E-31	gi 50760443 ref XP_418024.1 PREDICTED: similar to Transcription initiation factor TFIIID subunit 11 (Transcription initiation factor TFIIID 28 kDa subunit) (TAF(II)28) (TAFII-28) (TAFII28) (TFIID subunit p30-beta) [Gallus gallus]
sw18379	BGIBMGA010388	1.1116	1.13135	1.309	2.0945	e-165	gi 38014373 gb AAH60375.1 WD repeats and SOF domain containing 1 [Mus musculus] WD repeats and SOF domain containing 1 [Mus musculus]
sw15483	BGIBMGA005372	0.82225	0.9053	0.78275	2.09225	5.00E-28	gi 55642481 ref XP_510542.1 PREDICTED: similar to Mesoderm development candidate 2 (UNQ1911/PRO4369) [Pan troglodytes] MESDC2 protein [Homo sapiens] MESDC2 protein [Homo sapiens] Y081
sw15076	BGIBMGA004021	1.11555	1.20605	1.3461	2.09185	No hits found	
sw21935	BGIBMGA003566	1.1065	1.4469	1.3035	2.09185	2.00E-99	gi 464960 sp P35047 TRYC_MANSE Trypsin, alkaline C precursor
sw21310	BGIBMGA009925	1.16125	0.89465	1	2.09175	2.00E-79	gi 48094605 ref XP_394221.1 PREDICTED: similar to ENSANGP00000024305 [Apis mellifera]
sw11036	BGIBMGA010197	0.52045	0.90595	0.73125	2.08785	1.00E-21	gi 76638444 ref XP_580345.2 PREDICTED: similar to short coiled-coil protein [Bos taurus]
sw16392	BGIBMGA002349	0.84825	1.02495	0.77275	2.087	Bmb041108	2.00E-10
sw15596	BGIBMGA005274	1.08425	1.16075	0.77275	2.0861	Bmb033885	1.00E-53
sw06684	BGIBMGA002353	0.99935	0.9917	1.161	2.08535	e-104	gi 87248527 gb ABD36316.1 lysophospholipase [Bombyx mori]
sw06803	BGIBMGA012859	0.89855	1.01225	0.9068	2.0851	Bmb035041	2.00E-76
sw05929	BGIBMGA003562	0.94725	0.93135	0.8557	2.08405	3.00E-30	gi 89272445 emb CAJ83085.1 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 [Xenopus tropicalis]
sw11628	BGIBMGA011105	0.9849	1	1	2.0833	No hits found	
sw22686	BGIBMGA005953	1.2381	1.1816	1.1779	2.0831	1.00E-67	gi 55234500 gb EAA43295.2 ENSANGP00000022827 [Anopheles gambiae str. PEST] ENSANGP00000022827 [Anopheles gambiae str. PEST]
sw16116	BGIBMGA009046	1.26135	1.47885	1.2874	2.08155	8.00E-09	gi 1280151 gb AAA98017.1 Nudix family protein 3 [Caenorhabditis elegans] NuDIX family member (ndx-3) [Caenorhabditis elegans] Nudix hydrolase 3
sw00949	BGIBMGA009329	1	1	1.0616	2.0807	1.00E-67	gi 58569859 gb AAW79050.1 GekBS204P [Gekko japonicus]
sw15954	BGIBMGA002150	1.35635	1.36145	1.3165	2.0806	4.00E-05	gi 89271263 emb CAJ82958.1 serum response factor binding protein 1 [Xenopus tropicalis]
sw11427	BGIBMGA011500	0.96845	0.9231	1.4399	2.07995	Bmb005745	e-106
sw19244	BGIBMGA000269	1.6252	0.66225	0.91305	2.07955	6.00E-28	gi 117622 sp P11734 CU08_LOCM1 Cuticle protein 8 (LM-8) (LM-ACP 8)
sw01225	BGIBMGA002001	1.05705	1.09535	0.9823	2.0794	No hits found	
sw13724	BGIBMGA006525	1.01035	1	0.88775	2.07735	4.00E-14	gi 62857681 ref NP_001016776.1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 [Xenopus tropicalis] DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 [Xenopus tropicalis]
sw13775	BGIBMGA002945	1.28555	1.1993	1.07835	2.0768	7.00E-13	gi 66518233 ref XP_392596.2 PREDICTED: similar to putative alcohol dehydrogenase [Apis mellifera]
sw16220	BGIBMGA009115	0.93695	1.1023	0.73275	2.07645	Bmb039222	8.00E-05
sw07775	BGIBMGA010385	0.83045	1.0916	0.93815	2.0764	2.00E-38	gi 85857488 gb ABC86280.1 RE08574p [Drosophila melanogaster]
sw13145	BGIBMGA008021	1	1	1	2.07625	No hits found	

sw06309	BGIBMGA009041	0.955	1.1642	0.92185	2.0759	8.00E-18	gi 72171239 ref XP_783401.1 PREDICTED: similar to zinc finger, HIT domain containing 1 [Strongylocentrotus purpuratus]
sw08844	BGIBMGA006775	1.0683	0.9359	0.95405	2.0759	1.00E-79	gi 6016491 sp P55796 LEB3_BOMMO Lebocin-3 precursor (LEB 3) lebocin 3 [Bombyx mori]
sw18784	BGIBMGA003377	1.0114	0.996	1.0742	2.0736	4.00E-86	gi 72072160 ref XP_787339.1 PREDICTED: similar to replication factor C subunit RFC4 [Strongylocentrotus purpuratus]
sw13224	BGIBMGA013781	1.139	1.14905	0.7665	2.0734	3.00E-07	gi 3868784 dbj BAA34219.1 MBF2 [Samia cynthia]
sw21082	BGIBMGA005521	1.1005	1.1813	1.2816	2.07265	Bmb021757	2.00E-44
sw02328	BGIBMGA001396	0.7687	0.95055	0.74415	2.07175	4.00E-12	gi 72045503 ref XP_797188.1 PREDICTED: similar to butyrate-induced transcript 1 [Strongylocentrotus purpuratus]
sw00838	BGIBMGA010590	0.9947	1.8814	1.8615	2.0716	9.00E-90	gi 51094376 gb AAT95356.1 trypsin III precursor [Sesamia nonagrioides]
sw17121	BGIBMGA012220	0.8696	1.08255	0.99725	2.0715	2.00E-20	gi 66512914 ref XP_623446.1 PREDICTED: similar to Tetratricopeptide repeat protein 1 (TPR repeat protein 1) [Apis mellifera]
sw00917	BGIBMGA004302	0.79015	1.0056	1.2162	2.0709	e-120	gi 27462592 gb AAO15491.1 eIF2 alpha subunit [Spodoptera frugiperda]
sw18990	BGIBMGA005827	0.8581	1.011	1.0819	2.06895	7.00E-33	gi 66518233 ref XP_392596.2 PREDICTED: similar to putative alcohol dehydrogenase [Apis mellifera]
sw16014	BGIBMGA004044	1.6034	1	2.6336	2.0674	Bmb037504	5.00E-11
sw11213	BGIBMGA005002	0.8297	1.18	0.83805	2.06725	2.00E-94	gi 72048292 ref XP_784158.1 PREDICTED: similar to potassium channel tetramerisation domain containing 3 [Strongylocentrotus purpuratus]
sw15512	BGIBMGA004019	0.68675	0.98245	0.81985	2.06715	7.00E-42	gi 49523218 gb AAH75271.1 Thyroid autoantigen 70kDa (Ku antigen) [Xenopus tropicalis] thyroid autoantigen 70kDa (Ku antigen) [Xenopus tropicalis]
sw01796	BGIBMGA012009	1.2347	0.9317	0.9907	2.0652	Bmb028063	No hits found
sw12743	BGIBMGA008595	0.66385	0.6982	0.74595	2.0638	2.00E-85	gi 68390942 ref XP_683479.1 PREDICTED: similar to proteasome 26S non-ATPase subunit 8 [Danio rerio]
sw15831	BGIBMGA006266	1	1	1	2.0635	No hits found	
sw06503	BGIBMGA011204	1.03045	0.9386	1.02885	2.06245	2.00E-78	gi 13360618 dbj BAB34581.1 periplasmic glucose-1-phosphatase [Escherichia coli O157:H7] periplasmic glucose-1-phosphatase [Escherichia coli O157:H7] periplasmic glucose-1-phosphatase
sw06403	BGIBMGA013366	0.83885	0.9135	0.71995	2.0607	1.00E-60	gi 66550162 ref XP_396097.2 PREDICTED: similar to Zgc:103697 [Apis mellifera]
sw17345	BGIBMGA006913	1.0225	0.94225	0.89265	2.0601	7.00E-15	gi 9864185 gb AAG01337.1 Crossveinless 2 [Drosophila melanogaster]
sw15802	BGIBMGA010446	1.3912	1.21075	1.29625	2.0597	Bmb035584	1.00E-40
sw13997	BGIBMGA003583	1	1.6518	1	2.05765	Bmb022107	4.00E-07
sw13300	BGIBMGA008477	0.7111	1.03885	0.75545	2.0567	9.00E-45	gi 62083517 gb AAX62483.1 mitochondrial ribosomal protein L17 [Lysiphlebus testaceipes]
sw22672	BGIBMGA003402	0.61755	0.73525	0.7417	2.05635	Bmb028151	2.00E-48
sw11289	BGIBMGA000898	0.98995	1.01045	1.0686	2.05485	Bmb004833	4.00E-40
sw20321	BGIBMGA000232	0.7756	0.90565	0.8371	2.0538	1.00E-38	gi 6560653 gb AAF16704.1 calcyphosine-like protein [Manduca sexta]
sw16093	BGIBMGA008194	0.8624	0.94485	0.9479	2.0521	1.00E-31	gi 66500960 ref XP_395396.2 PREDICTED: similar to ENSANGP00000024290 [Apis mellifera]
sw22941	BGIBMGA005488	0.7896	0.85845	0.9228	2.0508	e-126	gi 87248211 gb ABD36158.1 replication factor C (activator 1) 5 [Bombyx mori]
sw19766	BGIBMGA007829	1.0696	1.36325	1.40585	2.0475	e-162	gi 6691117 gb AAF24495.1 SP71 [Drosophila melanogaster]

sw03637	BGIBMGA009232	1.4407	1.0586	1.0158	2.0473	9.00E-30	gi 71557964 gb AAZ37175.1 aldose 1-epimerase [Pseudomonas syringae pv. phaseolicola 1448A] aldose 1-epimerase [Pseudomonas syringae pv. phaseolicola 1448A]
sw07546	BGIBMGA005799	1.04505	0.89325	1.05215	2.0451	5.00E-44	gi 34871962 ref XP_341067.1 PREDICTED: similar to Williams-Beuren syndrome chromosome region 16 homolog [Rattus norvegicus]
sw10137	BGIBMGA005565	0.5099	1.22355	0.54005	2.04355	Bmb044116	5.00E-16
sw03095	BGIBMGA009277	1.1129	0.9976	0.90815	2.04345	Bmb003877	7.00E-22
sw12631	BGIBMGA006990	1.21425	1.30555	1.30935	2.04265	1.00E-40	gi 55242673 gb EAA07189.2 ENSANGP00000013724 [Anopheles gambiae str. PEST] ENSANGP00000013724 [Anopheles gambiae str. PEST]
sw03975	BGIBMGA006641	0.73255	1.1262	0.89385	2.04065	e-118	gi 87248395 gb ABD36250.1 ras-related GTP-binding protein 4b [Bombyx mori]
sw02046	BGIBMGA009240	1.24405	1.06895	0.7687	2.04055	4.00E-35	gi 62859495 ref NP_001017001.1 NMDA receptor regulated 1-like [Xenopus tropicalis]
sw05918	BGIBMGA003136	0.9144	1.03445	1.1242	2.04045	4.00E-12	gi 28839294 gb AAH47776.1 FLJ31795 protein [Homo sapiens]
sw06198	BGIBMGA011602	1.08725	1.0242	0.79495	2.0399	1.00E-08	gi 66516901 ref XP_393666.2 PREDICTED: similar to mKIAA0981 protein [Apis mellifera]
sw09451	BGIBMGA007508	2.2004	1.42785	1.2052	2.0384	5.00E-76	gi 73991331 ref XP_542897.2 PREDICTED: similar to Hydroxyacid oxidase 1 (HAOX1) (Glycolate oxidase) (GOX) isoform 1 [Canis familiaris]
sw03170	BGIBMGA012069	1.36325	1.44845	1.47215	2.0364	e-127	gi 72141411 ref XP_793660.1 PREDICTED: similar to RIO kinase 1 [Strongylocentrotus purpuratus]
sw05224	BGIBMGA004064	1.10595	1.0799	0.65365	2.0362	0	gi 87248335 gb ABD36220.1 glutamyl-tRNA amidotransferase subunit B [Bombyx mori]
sw21123	BGIBMGA000056	1	1.0062	1	2.03525	No hits found	
sw01951	BGIBMGA000951	1.25055	1.2173	1.26465	2.03415	No hits found	
sw14689	BGIBMGA014140	1.5652	1.2809	1.57725	2.03415	No hits found	
sw22883	BGIBMGA000955	1.20195	1.20675	1.10365	2.03405	5.00E-37	gi 27819803 gb AAO24950.1 RE53824p [Drosophila melanogaster]
sw12476	BGIBMGA002640	0.6549	0.7802	0.78455	2.033	5.00E-66	gi 54035222 gb AAH84116.1 LOC495025 protein [Xenopus laevis]
sw20366	BGIBMGA013929	0.8701	0.64285	0.824	2.0304	5.00E-25	gi 90025232 gb ABD85119.1 juvenile hormone epoxide hydrolase [Spodoptera exigua]
sw11949	BGIBMGA007545	0.84555	1.2806	1.6103	2.03015	5.00E-56	gi 38679389 gb AAR26516.1 antennal esterase [Mamestra brassicae]
sw09590	BGIBMGA007098	1.172	1.11775	0.8985	2.02955	Bmb032267	5.00E-89
sw11955	BGIBMGA002750	1.11465	0.8622	1.08295	2.02895	1.00E-70	gi 25012844 gb AAN71511.1 RH05604p [Drosophila melanogaster]
sw12248	BGIBMGA008807	1.21135	0.72715	1	2.02765	1.00E-64	gi 57914803 ref XP_555244.1 ENSANGP00000027403 [Anopheles gambiae str. PEST] ENSANGP00000027403 [Anopheles gambiae str. PEST]
sw04590	BGIBMGA005733	1.1634	1.2771	1.0759	2.0274	Bmb039328	3.00E-52
sw21942	BGIBMGA006982	0.3242	0.8611	0.8828	2.02655	No hits found	
sw10670	BGIBMGA013129	0.3553	1.1206	0.7204	2.0257	7.00E-14	gi 66511554 ref XP_393207.2 PREDICTED: similar to glucocerebrosidase precursor [Apis mellifera]
sw01501	BGIBMGA008552	0.53265	1	1	2.02405	7.00E-31	gi 77455216 gb ABA86417.1 CG9211 [Drosophila erecta]
sw01054	BGIBMGA013884	0.9779	1.0388	1.16345	2.0235	2.00E-27	gi 17863026 gb AAL39990.1 SD09147p [Drosophila melanogaster]
sw21138	BGIBMGA007107	1.0425	0.9319	1.2476	2.02195	0	gi 87248243 gb ABD36174.1 TPR-repeat protein [Bombyx mori]

sw16490	BGIBMGA014278	1.48445	1.1758	0.993	2.02115	Bmb042238	No hits found
sw13603	BGIBMGA003202	1.1971	1.2367	1.1439	2.02075	4.00E-29	gi 4007492 gb AAC95306.1 SNF4/AMP-activated protein kinase gamma subunit; SNF4A; noncatalytic subunit of the SNF/AMPK complex [Drosophila melanogaster]
sw11307	BGIBMGA013398	0.7905	1.0672	1.29785	2.02015	No hits found	
sw09395	BGIBMGA004965	0.20365	0.63825	0.65895	2.01865	2.00E-59	gi 22138087 gb AAM93421.1 ORF 4 [Spodoptera littoralis nucleopolyhedrovirus]
sw19688	BGIBMGA007361	1.41945	1.22995	0.99695	2.01845	1.00E-16	gi 47523722 ref NP_999496.1 L-3-hydroxyacyl-CoA dehydrogenase [Sus scrofa] L-3-hydroxyacyl-CoA dehydrogenase [Sus scrofa] Short chain 3-hydroxyacyl-CoA dehydrogenase
sw00316	BGIBMGA003815	1	1.08595	1.22755	2.01795	e-112	gi 220659 dbj BAA14397.1 dihydrolipoamide succinyltransferase [Rattus norvegicus]
sw16057	BGIBMGA010948	1.2905	1.0674	0.82485	2.0176	Bmb037901	1.00E-17
sw13618	BGIBMGA000777	0.8499	0.9974	1.09255	2.01735	7.00E-77	gi 66512713 ref XP_394697.2 PREDICTED: similar to carboxylesterase [Apis mellifera]
sw03397	BGIBMGA009613	1.1371	1.0537	1.1303	2.01645	8.00E-27	gi 26986579 ref NP_758476.1 prolyl-tRNA synthetase (mitochondrial)(putative) [Mus musculus] CDNA sequence BC027073 [Mus musculus] Probable prolyl-tRNA synthetase, mitochondrial precursor (Proline--tRNA ligase) (ProRS)
sw11377	BGIBMGA012905	0.8598	1.0147	1.10975	2.0158	4.00E-28	gi 48104416 ref XP_395776.1 PREDICTED: similar to small GTPase Ran binding protein 1; RanBP1 [Apis mellifera]
sw03140	BGIBMGA007977	0.94285	1.1189	1.34635	2.01455	6.00E-68	gi 76632367 ref XP_868926.1 PREDICTED: similar to chromosome 10 open reading frame 97 isoform 2 [Bos taurus]
sw18133	BGIBMGA009182	0.97195	1.10875	0.88315	2.01425	2.00E-11	gi 72077797 ref XP_783578.1 PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 [Strongylocentrotus purpuratus]
sw06948	BGIBMGA012590	0.1895	0.60005	0.8042	2.0137	No hits found	
sw13832	BGIBMGA012241	0.2067	0.5821	0.7234	2.0136	3.00E-08	gi 21357209 ref NP_648881.1 CG4893-PA [Drosophila melanogaster] RE55690p [Drosophila melanogaster] RE39465p [Drosophila melanogaster] CG4893-PA [Drosophila melanogaster] Hypothetical protein CG4893
sw06115	BGIBMGA005687	0.91045	1.2451	1.28705	2.0118	2.00E-75	gi 16877082 gb AAH16818.1 Phosphomannomutase 1 [Homo sapiens] Phosphomannomutase 1 [Homo sapiens] OTTHUMP00000028766 [Homo sapiens] PMM1 [Homo sapiens] phosphomannomutase
sw09793	BGIBMGA000803	0.91535	1.0547	1.07175	2.01055	Bmb036034	6.00E-61
sw13862	BGIBMGA009465	0.92615	1.16985	1.06955	2.01035	5.00E-16	gi 55243014 gb EAA06835.2 ENSANGP00000019057 [Anopheles gambiae str. PEST] ENSANGP00000019057 [Anopheles gambiae str. PEST]
sw20478	BGIBMGA001956	1.0064	1.03045	1.08095	2.01005	2.00E-54	gi 28569894 dbj BAC57926.1 reverse transcriptase [Bombyx mori]
sw13350	BGIBMGA000331	3.0576	0.79175	1.4101	2.0093	4.00E-24	gi 85857724 gb ABC86397.1 IP09958p [Drosophila melanogaster]
sw05428	BGIBMGA004926	1.025	1.14345	1.0486	2.00845	e-114	gi 66519538 ref XP_393739.2 PREDICTED: similar to CG6194-PA [Apis mellifera]
sw05239	BGIBMGA013876	1	1	1	2.007	No hits found	
sw19411	BGIBMGA009554	0.82175	0.73335	0.98795	2.0039	9.00E-95	gi 76576582 gb ABA53944.1 interleukin enhancer binding factor 2 [Ctenopharyngodon idella]
sw22661	BGIBMGA013207	0.406	0.9129	0.339	1.99965	2.00E-05	gi 74835158 dbj BAE44464.1 non-LTR retrotransposon CATS [Bombyx mori]
sw18380	BGIBMGA004567	2.4561	2.6275	2.37325	1.99215	8.00E-45	gi 62637998 gb AAX92638.1 glucose transporter 8 [Solenopsis invicta]
sw14949	BGIBMGA007192	2.15215	1.88055	1.6135	1.98365	3.00E-30	gi 89273996 emb CAJ81644.1 novel protein [Xenopus tropicalis] nin one binding protein [Xenopus tropicalis]
sw20178	BGIBMGA012263	2.46505	0.9876	0.54905	1.96755	1.00E-07	gi 66550559 ref XP_397430.2 PREDICTED: similar to sensory neuron membrane protein 1 [Apis mellifera]
sw05253	BGIBMGA002865	0.3305	1	0.65885	1.9608	No hits found	
sw16237	BGIBMGA006221	2.87735	1.8662	1.7472	1.9405	2.00E-85	gi 16758368 ref NP_446041.1 RAB14, member RAS oncogene family [Rattus norvegicus] Ras-related protein Rab-14 [Sus scrofa] small GTP binding protein RAB14 [Homo sapiens] Ras-related protein Rab-14

sw01401	BGIBMGA014092	0.4223	0.65125	0.6544	1.9386	No hits found	
sw20518	BGIBMGA011987	0.42725	0.7452	0.87945	1.92895	3.00E-31	gi 72027838 ref XP_794566.1 PREDICTED: similar to RNA pseudouridylate synthase domain containing 1 [Strongylocentrotus purpuratus]
sw09592	BGIBMGA006282	0.45845	0.6816	0.72985	1.8994	No hits found	
sw19025	BGIBMGA004509	0.32325	1.2454	0.9246	1.88205	1.00E-39	gi 55238404 gb EAA11457.2 ENSANGP00000007253 [Anopheles gambiae str. PEST] ENSANGP00000007253 [Anopheles gambiae str. PEST]
sw10798	BGIBMGA007677	1.92275	1.15735	2.6117	1.87125	Bmb001707	e-113
sw17805	BGIBMGA002747	0.56795	0.4119	0.5943	1.85365	e-112	gi 994849 gb AAB34519.1 attacin [Bombyx mori] Attacin precursor (Nuecin) nuecin [Bombyx mori]
sw06356	BGIBMGA013920	0.1621	0.632	0.5895	1.8354	5.00E-87	gi 66500267 ref XP_623297.1 PREDICTED: hypothetical protein XP_623294 [Apis mellifera]
sw22099	BGIBMGA005830	0.4342	1.049	0.8879	1.83205	3.00E-32	gi 66518233 ref XP_392596.2 PREDICTED: similar to putative alcohol dehydrogenase [Apis mellifera]
sw02728	BGIBMGA009558	0.40415	0.3566	1	1.8314	Bmb048846	8.00E-08
sw14234	BGIBMGA005803	0.1035	0.54945	0.5441	1.81435	No hits found	
sw16564	BGIBMGA011226	0.4485	0.97835	1.34815	1.79695	Bmb043407	4.00E-18
sw07605	BGIBMGA001007	2.0245	1.3865	1.4812	1.7926	2.00E-58	gi 55243048 gb EAA06899.2 ENSANGP00000001582 [Anopheles gambiae str. PEST] ENSANGP00000001582 [Anopheles gambiae str. PEST]
sw12914	BGIBMGA001839	0.09235	0.61305	0.6087	1.7825	No hits found	
sw00666	BGIBMGA007431	1.0868	1.16955	2.06445	1.77845	2.00E-70	gi 72014604 ref XP_787398.1 PREDICTED: similar to Aladin (Adracalin) [Strongylocentrotus purpuratus]
sw12271	BGIBMGA013646	0.57505	0.4812	0.62255	1.7662	2.00E-58	gi 33989989 gb AAH56253.1 Chromosome 6 open reading frame 71 [Homo sapiens]
sw03956	BGIBMGA004026	0.1861	0.593	0.66175	1.7579	1.00E-24	gi 49250900 gb AAH74631.1 MGC69557 protein [Xenopus tropicalis] MGC82513 protein [Xenopus laevis] MGC69557 protein [Xenopus tropicalis]
sw18893	BGIBMGA004121	1.5707	1.47525	2.24395	1.74305	No hits found	
sw20121	BGIBMGA002626	0.4386	0.82735	0.4647	1.74195	8.00E-59	gi 87248601 gb ABD36353.1 antennal binding protein [Bombyx mori]
sw16511	BGIBMGA010854	1.969	2.19685	1.14545	1.72535	Bmb042638	No hits found
sw11029	BGIBMGA010715	0.1905	1	0.678	1.7076	1.00E-24	gi 55644291 ref XP_511124.1 PREDICTED: similar to dynein, cytoplasmic, light polypeptide 2B; dynein light chain 2B; bithoraxoid-like protein; roadblock/LC7-like [Pan troglodytes]
sw22410	BGIBMGA006052	0.6745	0.5745	0.46885	1.7041	No hits found	
sw22573	BGIBMGA011001	2.13365	2.94145	2.3798	1.6842	0	gi 87248447 gb ABD36276.1 aminoacylase [Bombyx mori]
sw08108	BGIBMGA001333	2.2427	1.59245	1	1.6743	0	gi 76156035 gb ABA39861.1 uricase [Bombyx mori]
sw13079	BGIBMGA005673	2.05965	2.7684	2.0015	1.67305	6.00E-91	gi 24583491 ref NP_723607.1 CG31871-PA [Drosophila melanogaster] RE24765p [Drosophila melanogaster] CG31871-PA [Drosophila melanogaster]
sw21386	BGIBMGA010537	1.46275	2.0431	1.902	1.6639	e-155	gi 2970687 gb AAC06038.1 beta-glucosidase precursor [Spodoptera frugiperda]
sw13039	BGIBMGA005820	0.04305	0.52395	0.49515	1.6501	No hits found	
sw07934	BGIBMGA010161	1.25645	3.1151	1	1.6297	2.00E-14	gi 28317050 gb AAO39544.1 RE06501p [Drosophila melanogaster]
sw05120	BGIBMGA012291	2.11725	1.2521	1.67405	1.62755	No hits found	

sw15361	BGIBMGA004910	0.48405	0.96	0.72475	1.62115	6.00E-25	gi 27819749 gb AAL68388.2 SD08771p [Drosophila melanogaster]
sw17642	BGIBMGA001796	0.45075	0.64005	0.72715	1.61055	2.00E-05	gi 89293948 gb EAR91936.1 Viral A-type inclusion protein repeat containing protein [Tetrahymena thermophila SB210]
sw02976	BGIBMGA003178	0.51045	0.83475	1.232	1.61015	4.00E-59	gi 20070698 gb AAH26131.1 Solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 [Mus musculus] solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 [Mus musculus]
sw14496	BGIBMGA004947	0.2469	1	1	1.6076	9.00E-50	gi 40789008 dbj BAA76826.2 KIAA0982 protein [Homo sapiens]
sw01229	BGIBMGA005862	2.71685	2.74305	1.7736	1.6006	1.00E-37	gi 55650502 ref XP_514458.1 PREDICTED: similar to Protein C20orf54 [Pan troglodytes]
sw19517	BGIBMGA004538	0.391	1.31275	1.037	1.57195	2.00E-45	gi 55238404 gb EAA11457.2 ENSANGP00000007253 [Anopheles gambiae str. PEST] ENSANGP00000007253 [Anopheles gambiae str. PEST]
sw20638	BGIBMGA009632	0.37115	0.7689	0.59055	1.5684	8.00E-12	gi 5857 emb CAA41354.1 chorion protein [Bombyx mori] Chorion class CA protein ERA.5 precursor
sw02025	BGIBMGA010053	0.38565	0.5425	0.50505	1.56835	No hits found	
sw11960	BGIBMGA006713	0.36595	0.68325	0.49725	1.56145	9.00E-69	gi 5139701 dbj BAA81694.1 G protein a subunit 2 [Hydra magnipapillata]
sw02991	BGIBMGA013936	0.3368	0.67425	0.7889	1.55935	0	gi 13359380 dbj BAB33388.1 testis specific tektin [Bombyx mori]
sw01901	BGIBMGA002236	0.28045	0.8298	0.31755	1.5482	3.00E-92	gi 28416323 gb AAO42634.1 SD07139p [Drosophila melanogaster] Negative elongation factor A homolog
sw19507	BGIBMGA012332	0.0421	0.517	0.58365	1.5406	2.00E-06	gi 55235101 gb EAL38938.1 ENSANGP00000005174 [Anopheles gambiae str. PEST] ENSANGP00000005174 [Anopheles gambiae str. PEST]
sw06169	BGIBMGA013520	2.0081	1	1	1.53735	No hits found	
sw16532	BGIBMGA000158	0.13745	0.15465	0.2374	1.5367	4.00E-40	gi 72019779 ref XP_792493.1 PREDICTED: similar to choline dehydrogenase precursor [Strongylocentrotus purpuratus]
sw05294	BGIBMGA009058	0.1442	1	0.74055	1.536	8.00E-31	gi 66522084 ref XP_624399.1 PREDICTED: similar to Mitochondrial 2-oxoglutarate/malate carrier protein (OGCP) [Apis mellifera]
sw15101	BGIBMGA000289	0.1329	0.5571	0.5306	1.53455	Bmb030144	5.00E-05
sw14925	BGIBMGA011658	2.0413	1.85725	1.2505	1.53155	e-143	gi 87248507 gb ABD36306.1 glutathione S-transferase omega 2 [Bombyx mori]
sw08914	BGIBMGA001535	0.055	0.6105	0.67405	1.5292	No hits found	
sw05701	BGIBMGA009102	2.46035	1.435	1.73715	1.528	3.00E-64	gi 48108726 ref XP_393098.1 PREDICTED: similar to ENSANGP00000022305 [Apis mellifera]
sw05687	BGIBMGA002005	0.3162	0.64595	0.7022	1.5251	e-128	gi 28207648 gb AAO32325.1 ADP/ATP translocase [Manduca sexta]
sw05107	BGIBMGA004606	0.554	0.4493	0.64175	1.51345	8.00E-55	gi 56378319 dbj BAD74196.1 heat shock protein hsp20.1 [Bombyx mori]
sw16452	BGIBMGA001837	0.25365	0.72675	0.7387	1.5087	No hits found	
sw01237	BGIBMGA011236	0.12595	0.406	0.38245	1.49555	No hits found	
sw16082	BGIBMGA011795	0.31255	1.01625	0.45005	1.49255	No hits found	
sw08854	BGIBMGA010328	2.7317	1.72955	1.1654	1.49245	Bmb020629	2.00E-53
sw13009	BGIBMGA011468	1	1.7228	3.34165	1.47585	e-180	gi 1276940 gb AAC47018.1 juvenile hormone epoxide hydrolase Juvenile hormone epoxide hydrolase (Juvenile hormone-specific epoxide hydrolase) (JHEH) epoxide hydrolase
sw03184	BGIBMGA004650	0.08115	0.5321	0.45785	1.47155	3.00E-15	gi 44982930 gb AAS52160.1 ADR240Cp [Ashbya gossypii ATCC 10895] ADR240Cp [Eremothecium gossypii]
sw13683	BGIBMGA014380	0.03185	0.5906	0.57315	1.46215	No hits found	

sw20205	BGIBMGA005784	0.19215	0.63865	0.7535	1.45735	9.00E-33	gi 56378319 dbj BAD74196.1 heat shock protein hsp20.1 [Bombyx mori]
sw18395	BGIBMGA012952	1.75415	1.59635	2.36365	1.45295	1.00E-32	gi 72152404 ref XP_792972.1 PREDICTED: similar to glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID), partial [Strongylocentrotus purpuratus]
sw18642	BGIBMGA003409	2.094	1.27905	1.50525	1.45265	Bmb033794	1.00E-09
sw07308	BGIBMGA000677	0.4512	0.8003	0.7996	1.44925	3.00E-30	gi 62857673 ref NP_001016778.1 EF hand calcium binding domain 1 [Xenopus tropicalis]
sw15263	BGIBMGA013409	0.01085	0.4317	0.54235	1.438	No hits found	
sw20421	BGIBMGA008633	0.37615	0.56785	0.47385	1.43765	7.00E-83	gi 73987978 ref XP_860745.1 PREDICTED: similar to protein phosphatase methylesterase 1 isoform 4 [Canis familiaris] PREDICTED: similar to protein phosphatase methylesterase 1 isoform 1 [Canis familiaris]
sw08704	BGIBMGA007217	0.18045	0.5084	0.36645	1.43445	1.00E-95	gi 83306196 emb CAH59462.1 ATP-binding cassette transporter sub-family A [Pecten maximus]
sw21141	BGIBMGA003347	0.4338	0.8682	0.7294	1.4326	2.00E-05	gi 27374266 gb AAO01023.1 I(2)06496-PA [Drosophila erecta]
sw11832	BGIBMGA001003	2.4203	1.16765	1.91535	1.43025	8.00E-77	gi 58429859 gb AAW78325.1 cytochrome P450 family 4 [Chironomus tentans]
sw04660	BGIBMGA003100	0.2274	0.56695	0.37145	1.42805	Bmb041587	8.00E-06
sw14045	BGIBMGA013186	0.16705	1	0.50235	1.41665	No hits found	
sw06179	BGIBMGA000997	0.0611	0.55095	0.589	1.40755	4.00E-13	gi 14625425 dbj BAB61919.1 calmodulin NtCaM13 [Nicotiana tabacum]
sw12103	BGIBMGA004130	2.59595	1.17535	1.7725	1.40755	e-109	gi 55239333 gb EAA44260.2 ENSANGP00000025275 [Anopheles gambiae str. PEST] ENSANGP00000025275 [Anopheles gambiae str. PEST]
sw06897	BGIBMGA003745	0.08205	0.54615	0.6153	1.40645	No hits found	
sw08745	BGIBMGA003530	0.23005	0.54185	0.4096	1.40515	7.00E-09	gi 24651106 ref NP_733300.1 CG15506-PB, isoform B [Drosophila melanogaster] CG15506-PB, isoform B [Drosophila melanogaster]
sw00379	BGIBMGA000562	0.45865	1.03475	0.8985	1.4046	9.00E-44	gi 89243302 gb ABD64815.1 Dvir_CG10440 [Drosophila virilis]
sw08167	BGIBMGA002337	0.23175	0.67295	0.65755	1.3936	e-130	gi 86450230 gb ABC96322.1 enolase [Blattella germanica]
sw17553	BGIBMGA004115	2.43175	2.73085	4.9723	1.3839	No hits found	
sw20815	BGIBMGA000386	0.1438	0.5122	0.6586	1.3799	4.00E-27	gi 68585 pir AJFF2C glutamate-ammonia ligase (EC 6.3.1.2) 2, cytosolic - fruit fly (Drosophila melanogaster)
sw17004	BGIBMGA012421	0.1193	0.50345	0.54575	1.375	No hits found	
sw01141	BGIBMGA007900	0.4986	0.83625	0.667	1.3698	1.00E-24	gi 30178562 gb EAA45375.1 ENSANGP00000023091 [Anopheles gambiae str. PEST] ENSANGP00000023091 [Anopheles gambiae str. PEST]
sw03054	BGIBMGA000712	0.1957	0.6232	0.52695	1.3555	No hits found	
sw12305	BGIBMGA010642	0.3678	0.541	0.51485	1.3534	2.00E-40	gi 71122386 gb AAH99752.1 Uridine phosphorylase 1 [Rattus norvegicus] uridine phosphorylase 1 [Rattus norvegicus]
sw09312	BGIBMGA012380	0.24605	0.7174	0.75325	1.35075	e-106	gi 38181637 gb AAH61597.1 Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 [Xenopus tropicalis] solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
sw15356	BGIBMGA007043	0.4859	0.88495	0.6543	1.3428	3.00E-21	gi 72153363 ref XP_788906.1 PREDICTED: similar to Microsomal signal peptidase 12 kDa subunit (SPase 12 kDa subunit) (SPC12) [Strongylocentrotus purpuratus]
sw07075	BGIBMGA014151	0.12175	0.6052	0.52245	1.34165	Bmb042375	No hits found
sw20455	BGIBMGA003345	2.6338	1.11045	1.03945	1.33455	1.00E-77	gi 73992800 dbj BAE43413.1 hypothetical protein [Bombyx mori]
sw07617	BGIBMGA009108	2.12965	1.62525	1.296	1.33405	No hits found	

sw06237	BGIBMGA004229	1.48985	1.6544	2.36655	1.3332	5.00E-48	gi 28317060 gb AAO39549.1 RE03380p [Drosophila melanogaster]
sw07690	BGIBMGA002991	0.1687	0.5494	0.7426	1.3217	No hits found	
sw15429	BGIBMGA001230	2.81275	1.3617	1	1.3186	Bmb032572	1.00E-84
sw13032	BGIBMGA005677	3.0774	0.9714	1.12555	1.31795	Bmb015897	No hits found
sw17947	BGIBMGA006176	2.3659	2.10905	1.58395	1.31595	4.00E-41	gi 76779438 gb AAI06213.1 LOC446918 protein [Xenopus laevis]
sw11317	BGIBMGA002073	2.0433	1	1	1.31415	3.00E-52	gi 27819801 gb AAO24949.1 RE59468p [Drosophila melanogaster]
sw22679	BGIBMGA012648	0.10245	0.7368	0.39975	1.31075	9.00E-59	gi 66555620 ref XP_624966.1 PREDICTED: similar to CG6113-PA [Apis mellifera]
sw04514	BGIBMGA001676	0.0491	0.4886	0.56765	1.3049	No hits found	
sw07989	BGIBMGA013726	0.26565	0.6998	0.74325	1.2958	6.00E-05	gi 66510443 ref XP_397485.2 PREDICTED: similar to CG6653-PA [Apis mellifera]
sw22922	BGIBMGA003885	0.3736	0.6353	0.7347	1.2914	1.00E-22	gi 27374204 gb AAN87276.1 CG13533 [Drosophila virilis]
sw14594	BGIBMGA010881	0.31	1.9238	0.83185	1.28695	5.00E-18	gi 28316894 gb AAO39469.1 RH04286p [Drosophila melanogaster]
sw11277	BGIBMGA004311	0.07265	0.6839	0.60645	1.28575	9.00E-06	gi 56270499 gb AAH87533.1 LOC496100 protein [Xenopus laevis]
sw07704	BGIBMGA007038	0.71165	0.49895	0.66005	1.2838	6.00E-56	gi 25012350 gb AAN71285.1 RE06328p [Drosophila melanogaster]
sw11301	BGIBMGA007153	2.1025	1.39835	1.7561	1.27425	3.00E-32	gi 76258691 ref ZP_00766345.1 Glycoside hydrolase, family 31 [Chloroflexus aurantiacus J-10-fl] Glycoside hydrolase, family 31 [Chloroflexus aurantiacus J-10-fl]
sw14637	BGIBMGA011698	0.4696	0.6479	0.5996	1.2709	7.00E-29	gi 66564529 ref XP_623716.1 PREDICTED: similar to Ribonuclease UK114 (14.5 kDa translational inhibitor protein) (p14.5) (UK114 antigen homolog) [Apis mellifera]
sw14400	BGIBMGA005753	5.3759	1.3806	1.69195	1.2636	No hits found	
sw11507	BGIBMGA000891	0.20415	0.60395	0.8261	1.26105	1.00E-05	gi 72016498 ref XP_783913.1 PREDICTED: similar to Gamma-aminobutyric-acid receptor alpha-5 subunit precursor (GABA(A) receptor) [Strongylocentrotus purpuratus]
sw14063	BGIBMGA010015	0.49955	0.8601	0.6799	1.25845	No hits found	
sw20654	BGIBMGA002525	0.45865	0.8692	0.49035	1.25505	e-112	gi 55239363 gb EAL40125.1 ENSANGP00000029489 [Anopheles gambiae str. PEST] ENSANGP00000029489 [Anopheles gambiae str. PEST]
sw02096	BGIBMGA001320	0.2954	0.14645	0.75875	1.25435	1.00E-35	gi 51094358 gb AAT95347.1 trypsin la precursor [Sesamia nonagrioides]
sw07346	BGIBMGA003969	1	1	4.19895	1.25115	3.00E-28	gi 25012479 gb AAN71344.1 RE26896p [Drosophila melanogaster]
sw07062	BGIBMGA012939	0.45575	0.43955	0.6009	1.2498	4.00E-77	gi 66546491 ref XP_624276.1 PREDICTED: similar to secretory component [Apis mellifera]
sw11397	BGIBMGA010747	2.25645	1.88045	1.55425	1.24855	3.00E-07	gi 14286129 sp P32866 GPRK2_DROME G protein-coupled receptor kinase 2
sw11347	BGIBMGA009838	1.6618	2.4447	1.69925	1.24725	3.00E-98	gi 55235355 gb EAA14774.2 ENSANGP00000019555 [Anopheles gambiae str. PEST] ENSANGP00000019555 [Anopheles gambiae str. PEST]
sw09094	BGIBMGA004546	2.01475	1.4162	1.34055	1.2466	No hits found	
sw06317	BGIBMGA007254	2.11605	1.1382	0.7737	1.2429	e-142	gi 86450717 gb ABC96694.1 yellow1 [Bombyx mori]
sw03939	BGIBMGA008460	0.29135	0.4863	0.5618	1.2359	No hits found	
sw20164	BGIBMGA009865	0.4445	0.6979	0.56615	1.23175	Bmb043467	3.00E-37

sw07726	BGIBMGA010976	0.2541	0.4517	0.34085	1.22745	2.00E-76	gi 66560187 ref XP_392698.2 PREDICTED: similar to carboxylesterase [Apis mellifera]
sw15683	BGIBMGA004120	0.2872	0.64095	0.90655	1.22245	5.00E-27	gi 68443719 ref XP_701274.1 PREDICTED: similar to inhibitor of Brutons tyrosine kinase, partial [Danio rerio]
sw14467	BGIBMGA006789	0.4814	1.1096	1.04935	1.22225	2.00E-75	gi 76639219 ref XP_593308.2 PREDICTED: similar to Protein KIAA0152 precursor [Bos taurus]
sw16168	BGIBMGA010213	2.07915	1.25435	1.11155	1.21205	1.00E-41	gi 441214 dbj BAA03374.1 intracellular coagulation inhibitor precursor [Tachypleus tridentatus]
sw07562	BGIBMGA004942	0.40825	0.70605	0.7259	1.20885	1.00E-43	gi 1490232 emb CAA67981.1 mitochondrial ATP synthase [Drosophila melanogaster]
sw02854	BGIBMGA007006	0.0522	0.5198	0.54485	1.2077	No hits found	
sw19774	BGIBMGA009646	0.33265	0.61405	0.73625	1.2015	No hits found	
sw12433	BGIBMGA008779	1.16325	2.61945	1.5224	1.2	2.00E-80	gi 50510635 dbj BAD32303.1 mKIAA0788 protein [Mus musculus]
sw13529	BGIBMGA002669	1.23735	1.68715	2.2502	1.1997	e-120	gi 72172203 gb AAZ66799.1 lipase [Samia cynthia ricini] lipase-1 [Bombyx mori] lipase [Bombyx mori]
sw22843	BGIBMGA014477	0.1448	0.473	0.3255	1.19745	6.00E-63	gi 32718005 gb AAP86970.1 testicular microtubules-related protein 3 [Mus musculus] novel protein [Mus musculus] tektin 3 [Mus musculus] Tektin-3
sw01592	BGIBMGA005069	0.1816	0.64625	0.3886	1.1962	No hits found	
sw10457	BGIBMGA000700	0.1062	0.5622	0.5547	1.1916	No hits found	
sw04120	BGIBMGA013611	1.37525	1.4308	2.1573	1.1906	7.00E-10	gi 18087833 ref NP_542393.1 peroxisomal biogenesis factor 11 gamma [Homo sapiens] Peroxisomal biogenesis factor 11 gamma [Homo sapiens] peroxin Pex11p gamma
sw03893	BGIBMGA010486	0.21955	0.6066	0.72475	1.1885	No hits found	
sw12994	BGIBMGA006747	0.35795	0.6103	1	1.18485	2.00E-21	gi 55235457 gb EAA14923.2 ENSANGP00000010625 [Anopheles gambiae str. PEST] ENSANGP00000010625 [Anopheles gambiae str. PEST]
sw10535	BGIBMGA003665	0.4013	0.75605	0.77645	1.18405	2.00E-08	gi 55237378 gb EAA12196.2 ENSANGP00000018278 [Anopheles gambiae str. PEST] ENSANGP00000018278 [Anopheles gambiae str. PEST]
sw11642	BGIBMGA006816	2.26595	2.0494	2.0041	1.17785	0	gi 3024509 sp Q91437 PYR1_SQUAC CAD protein [Includes: Glutamine-dependent carbamoyl-phosphate synthase ; Aspartate carbamoyltransferase ; Dihydroorotase] multifunctional protein CAD
sw20515	BGIBMGA013783	0.0311	0.60135	0.5252	1.17535	1.00E-64	gi 66513601 ref XP_623150.1 PREDICTED: similar to prophenoloxidase activating factor [Apis mellifera]
sw12992	BGIBMGA008810	1.9049	2.01105	1.622	1.17445	4.00E-13	gi 41618334 tpg DAA03106.1 TPA: TPA_inf: HDC11369 [Drosophila melanogaster] CG33290-PA [Drosophila melanogaster] CG33290-PA [Drosophila melanogaster]
sw15899	BGIBMGA014307	0.09255	0.54925	0.5819	1.16765	No hits found	
sw17054	BGIBMGA000702	0.1157	0.56435	0.57215	1.16765	No hits found	
sw11328	BGIBMGA000465	0.1712	0.4817	1	1.16185	No hits found	
sw05302	BGIBMGA000336	1.95845	1.678	2.1477	1.15905	1.00E-21	gi 47605412 sp Q7M4F2 CUD8_SCHGR Endocuticle structural glycoprotein SgAbd-8
sw22437	BGIBMGA001332	4.03835	2.46485	2.7747	1.15845	Bmb044299	2.00E-08
sw15726	BGIBMGA010895	0.16295	0.54885	0.5184	1.15665	No hits found	
sw19964	BGIBMGA004337	2.0586	1.40475	1.18085	1.1554	5.00E-06	gi 66507458 ref XP_623142.1 PREDICTED: similar to ENSANGP00000016918 [Apis mellifera]
sw05251	BGIBMGA002976	0.03075	0.5112	0.6792	1.1518	2.00E-38	gi 8927389 gb AAF82053.1 FOR I protein [Homo sapiens]
sw00199	BGIBMGA004540	0.313	0.70275	0.83285	1.1497	4.00E-98	gi 56378317 dbj BAD74195.1 heat shock protein hsp 19.9 [Bombyx mori]

sw15544	BGIBMGA001099	0.0146	0.45185	0.41165	1.14825	No hits found	
sw09231	BGIBMGA001596	0.44045	0.6647	0.52425	1.14435	2.00E-08	gi 72023261 ref XP_786653.1 PREDICTED: similar to Thioesterase superfamily member 2 (PNAS-27) (HT012) [Strongylocentrotus purpuratus]
sw00954	BGIBMGA009178	0.4428	0.5751	0.5327	1.1424	8.00E-31	gi 47117013 sp Q7M416 PA2_MEGPE Phospholipase A2 (Phosphatidylcholine 2-acylhydrolase)
sw00971	BGIBMGA000755	0.1593	0.6338	0.60125	1.142	No hits found	
sw06143	BGIBMGA011342	2.03015	1.29205	1.48345	1.13975	2.00E-26	gi 2804262 dbj BAA24442.1 cysteine proteinase [Sitophilus zeamais]
sw22125	BGIBMGA001620	0.43055	0.6882	0.58005	1.1396	2.00E-24	gi 70905642 gb AAZ14281.1 proteophosphoglycan 5 [Leishmania major strain Friedlin] Leishmania major strain Friedlin proteophosphoglycan 5 [Leishmania major strain Friedlin]
sw08481	BGIBMGA001626	0.4682	0.7593	0.656	1.1365	No hits found	
sw03831	BGIBMGA008976	0.063	0.523	0.57735	1.1321	4.00E-41	gi 48097950 ref XP_393932.1 PREDICTED: similar to molting fluid carboxypeptidase A [Apis mellifera]
sw13405	BGIBMGA005697	0.2918	0.9089	0.6814	1.1318	No hits found	
sw14786	BGIBMGA008167	2.74815	1.89655	1.7882	1.1283	6.00E-23	gi 58396460 ref XP_321914.2 ENSANGP00000013861 [Anopheles gambiae str. PEST] ENSANGP00000013861 [Anopheles gambiae str. PEST]
sw21382	BGIBMGA005822	0.2016	0.6548	0.68865	1.12525	No hits found	
sw03565	BGIBMGA013574	0.38715	0.6879	0.87	1.12505	No hits found	
sw22881	BGIBMGA002604	0.13695	0.6485	0.60905	1.12435	3.00E-45	gi 66508910 ref XP_623146.1 PREDICTED: similar to GA10372-PA [Apis mellifera]
sw12376	BGIBMGA000610	0.1414	0.6342	0.1196	1.12305	2.00E-44	gi 55241598 gb EAA08488.2 ENSANGP00000014719 [Anopheles gambiae str. PEST] ENSANGP00000014719 [Anopheles gambiae str. PEST]
sw02067	BGIBMGA007216	0.2359	0.8122	0.48385	1.11865	2.00E-47	gi 48096263 ref XP_394650.1 PREDICTED: similar to ENSANGP00000012511 [Apis mellifera]
sw02018	BGIBMGA001308	0.3424	1.5086	0.3915	1.11665	Bmb031686	4.00E-24
sw06049	BGIBMGA005403	0.14715	0.57695	0.63155	1.11635	5.00E-36	gi 387422 gb AAA39509.1 malate dehydrogenase
sw16470	BGIBMGA012040	0.17645	0.49145	0.5204	1.115	1.00E-07	gi 73997460 ref XP_853137.1 PREDICTED: similar to myosin regulatory light chain-like [Canis familiaris]
sw21899	BGIBMGA006623	2.30675	1.29985	0.79105	1.1135	e-112	gi 3510719 gb AAC33576.1 immunoelectin-A precursor [Manduca sexta]
sw08555	BGIBMGA000993	0.30845	0.6848	0.67395	1.1107	No hits found	
sw19720	BGIBMGA010834	0.13675	0.4788	0.7155	1.10995	No hits found	
sw12672	BGIBMGA003645	4.66495	1.6954	2.0591	1.1087	6.00E-62	gi 50730416 ref XP_416893.1 PREDICTED: similar to lipoyltransferase 1 [Gallus gallus]
sw18729	BGIBMGA000731	3.2003	1.2652	0.97225	1.10685	9.00E-37	gi 74229818 ref YP_309022.1 ecdysone glucose transferase (egt) [Trichoplusia ni SNPV] ecdysone glucose transferase (egt) [Trichoplusia ni SNPV]
sw14331	BGIBMGA007286	0.4465	0.64975	0.52605	1.10465	7.00E-61	gi 400673 sp P31420 OMBP_MANSE Ommochrome-binding protein precursor (OBP) (YCP) ommochrome-binding protein
sw09897	BGIBMGA005795	0.18395	0.6919	0.7158	1.1045	No hits found	
sw06150	BGIBMGA011959	0.3919	0.9204	1	1.0985	No hits found	
sw18703	BGIBMGA010812	2.6714	2.10235	2.6688	1.09535	Bmb025436	e-169
sw12286	BGIBMGA003199	0.1101	0.64555	0.7385	1.0947	7.00E-54	gi 76632826 ref XP_879048.1 PREDICTED: similar to polyamine oxidase isoform 1 isoform 11 [Bos taurus]

sw09814	BGIBMGA001021	0.04765	0.54655	0.4177	1.09235	No hits found	
sw16275	BGIBMGA009685	1.1433	1.42515	2.2439	1.08795	Bmb039916	No hits found
sw03059	BGIBMGA007637	0.46535	1.15335	1.0144	1.08745	0	gi 87248659 gb ABD36382.1 glycyI-tRNA synthetase [Bombyx mori]
sw08664	BGIBMGA005704	0.4614	0.9525	0.9518	1.08545	No hits found	
sw15953	BGIBMGA014418	0.42565	0.93915	0.7447	1.0791	7.00E-22	gi 54642185 gb EAL30934.1 GA14782-PA [Drosophila pseudoobscura]
sw22963	BGIBMGA001859	0.2281	0.7038	0.49695	1.07775	No hits found	
sw00035	BGIBMGA011472	0.43965	0.75515	0.66315	1.0756	No hits found	
sw13273	BGIBMGA007008	0.41435	0.7479	1	1.0635	No hits found	
sw04295	BGIBMGA003296	0.12305	0.2817	0.3204	1.0625	e-162	gi 402174 emb CAA52906.1 beta-tubulin [Bombyx mori] Tubulin beta chain (Beta tubulin)
sw13389	BGIBMGA007398	0.21945	0.7087	0.7499	1.0623	No hits found	
sw17922	BGIBMGA001013	0.15385	0.50965	0.6292	1.05975	Bmb002484	1.00E-46
sw20612	BGIBMGA006165	0.10035	0.54025	0.61415	1.05025	No hits found	
sw01378	BGIBMGA012166	0.4526	0.7311	0.7529	1.0418	1.00E-22	gi 66525741 ref XP_397234.2 PREDICTED: similar to WD repeat domain 34 [Apis mellifera]
sw08729	BGIBMGA000655	0.2195	0.60065	0.62075	1.0383	3.00E-05	gi 89301406 gb EAR99394.1 hypothetical protein THERM_00133600 [Tetrahymena thermophila SB210]
sw17607	BGIBMGA005168	0.3294	0.5308	0.43475	1.03555	0	gi 13446608 emb CAC35050.1 putative helicase Ski2 [Drosophila melanogaster]
sw19416	BGIBMGA007811	0.02825	0.45855	0.52315	1.02945	5.00E-18	gi 1226168 gb AAA92249.1 ORF B (bases 1850-5560) first start codon at 2306
sw03486	BGIBMGA010818	0.0833	0.6134	0.60375	1.0279	No hits found	
sw12583	BGIBMGA011053	0.14935	0.7266	0.5551	1.02505	No hits found	
sw18898	BGIBMGA004541	0.4982	1.2154	0.3939	1.0237	2.00E-94	gi 11120618 gb AAG30944.1 heat shock protein hsp20.8 [Bombyx mori] heat shock protein hsp20.8A [Bombyx mori]
sw09596	BGIBMGA010902	0.12315	0.45745	1	1.0222	No hits found	
sw14912	BGIBMGA004041	0.4351	0.91845	0.5957	1.01755	4.00E-29	gi 77415578 emb CAJ01458.1 hypothetical protein [Bombyx mori]
sw20682	BGIBMGA004525	0.2889	0.82155	0.80395	1.0155	Bmb043387	1.00E-18
sw11415	BGIBMGA006854	0.68855	0.3664	0.24375	1.01535	No hits found	
sw18441	BGIBMGA004618	0.29725	0.78015	0.8078	1.0022	0	gi 72065171 ref XP_791790.1 PREDICTED: similar to tubulin, beta, 2 [Strongylocentrotus purpuratus]
sw00748	BGIBMGA004906	2.6885	1	1	1	2.00E-61	gi 66508985 ref XP_624902.1 PREDICTED: similar to ENSANGP00000010432 [Apis mellifera]
sw01458	BGIBMGA011005	2.0268	1	1	1	4.00E-15	gi 54639187 gb EAL28589.1 GA18365-PA [Drosophila pseudoobscura]
sw03148	BGIBMGA006267	0.45615	1	0.5308	1	3.00E-54	gi 66499116 ref XP_395333.2 PREDICTED: similar to Odorant receptor 83b, partial [Apis mellifera]
sw03415	BGIBMGA007255	2.94585	1	1	1	1.00E-61	gi 66516898 ref XP_391826.2 PREDICTED: similar to yellow [Apis mellifera]

sw04223	BGIBMGA010082	0.134	0.54445	0.57525	1	No hits found	
sw05553	BGIBMGA000688	6.962	1	1	1	6.00E-51	gi 29788985 ref NP_705933.1 solute carrier family 24 member 4 isoform 2 precursor [Homo sapiens] K-dependent Na/Ca exchanger NCKX4 [Homo sapiens]
sw06614	BGIBMGA007238	3.1439	1	1	1	e-131	gi 3158392 gb AAC39036.1 MAP kinase kinase 4 [Drosophila melanogaster]
sw07086	BGIBMGA008333	2.6456	1	1	1	2.00E-35	gi 55237990 gb EAA43983.2 ENSANGP00000023009 [Anopheles gambiae str. PEST] ENSANGP00000023009 [Anopheles gambiae str. PEST]
sw08448	BGIBMGA010063	4.36115	2.0319	3.1085	1	6.00E-38	gi 6690636 gb AAF24228.1 trypsin-like PIT2c precursor [Plodia interpunctella]
sw08470	BGIBMGA005215	0.1696	1	0.71475	1	6.00E-52	gi 75516537 gb AAI01520.1 Testis-specific gene A2 [Homo sapiens] testis-specific gene A2 [Homo sapiens] Testis-specific gene A2 protein (Male meiotic metaphase chromosome-associated acidic protein)
sw08901	BGIBMGA009827	1	2.2925	1	1	9.00E-25	gi 66531593 ref XP_624704.1 PREDICTED: similar to GA21651-PA [Apis mellifera]
sw09295	BGIBMGA014054	1.32415	2.23735	0.73585	1	3.00E-17	gi 24644778 ref NP_649706.1 CG14606-PA [Drosophila melanogaster] IP11886p [Drosophila melanogaster] CG14606-PA [Drosophila melanogaster]
sw09459	BGIBMGA011041	1.68865	2.0717	1	1	Bmb030337	No hits found
sw09515	BGIBMGA008985	0.4023	0.7586	0.80445	1	2.00E-08	gi 74145314 gb AAZ99885.1 membrane occupation and recognition nexus protein 1 [Toxoplasma gondii]
sw10934	BGIBMGA013914	2.4836	1.82055	1	1	Bmb002530	4.00E-08
sw11020	BGIBMGA007654	0.08735	0.57135	0.6188	1	1.00E-09	gi 73995649 ref XP_534748.2 PREDICTED: similar to Rhabdoid tumor deletion region protein 1 isoform 1 [Canis familiaris]
sw11494	BGIBMGA003053	1.4334	1.32725	2.0434	1	1.00E-52	gi 40674148 gb AAH64831.1 HMT1 hnRNP methyltransferase-like 3 [Homo sapiens] HMT1 hnRNP methyltransferase-like 3 [Homo sapiens] HMT1 hnRNP methyltransferase-like 3
sw12194	BGIBMGA013504	1	0.4328	1	1	3.00E-11	gi 66524513 ref XP_624132.1 PREDICTED: similar to MGC80265 protein [Apis mellifera]
sw12614	BGIBMGA007379	1	4.80935	3.816	1	3.00E-05	gi 90111982 sp Q9H9A7 CI076_HUMAN Protein C9orf76
sw13012	BGIBMGA007058	0.08045	0.4751	1	1	e-162	gi 76617111 ref XP_874104.1 PREDICTED: similar to tubulin tyrosine ligase-like 1 (predicted) isoform 2 [Bos taurus]
sw13094	BGIBMGA008101	1	1	0.34805	1	5.00E-10	gi 58533151 gb AAW78933.1 trypsin [Anopheles sinensis]
sw13391	BGIBMGA004067	0.8717	1.17465	0.4881	1	1.00E-10	gi 77415706 emb CAJ01522.1 hypothetical protein [Anopheles gambiae] putative sensory appendage protein SAP-2 [Anopheles gambiae] ENSANGP00000011748
sw13872	BGIBMGA009422	0.098	0.56255	0.67095	1	3.00E-16	gi 15218966 ref NP_173553.1 ATEXT3 (EXTENSIN 3); structural constituent of cell wall
sw14075	BGIBMGA001231	2.7854	1.7448	1.32485	1	2.00E-25	gi 54644247 gb EAL32988.1 GA17385-PA [Drosophila pseudoobscura]
sw14227	BGIBMGA005237	0.38035	0.64615	1	1	4.00E-05	gi 66547599 ref XP_623499.1 PREDICTED: similar to Beat VII [Apis mellifera]
sw14502	BGIBMGA008031	0.10385	0.778	0.5543	1	7.00E-06	gi 53133880 emb CAG32269.1 hypothetical protein [Gallus gallus] hypothetical protein LOC416598 [Gallus gallus]
sw14865	BGIBMGA005191	0.3363	0.6735	1	1	2.00E-06	gi 10444078 gb AAG17699.1 mitochondrial malate dehydrogenase precursor [Nucella lapillus]
sw15568	BGIBMGA001156	0.43165	0.79945	0.72515	1	1.00E-49	gi 72025672 ref XP_792004.1 PREDICTED: similar to mitochondrial malate dehydrogenase precursor [Strongylocentrotus purpuratus]
sw15581	BGIBMGA004598	0.13535	0.6073	1	1	9.00E-24	gi 9294518 dbj BAB02780.1 dual-specificity protein phosphatase-like protein [Arabidopsis thaliana]
sw15966	BGIBMGA001757	0.0853	0.44275	0.5094	1	No hits found	
sw16060	BGIBMGA006472	0.09615	0.599	1	1	No hits found	
sw16556	BGIBMGA003746	0.318	0.6545	0.7532	1	No hits found	

sw16752	BGIBMGA012871	1	1.67115	2.5879	1	Bmb046498	5.00E-05
sw19095	BGIBMGA014144	2.3389	1	1	1	4.00E-28	gi 20334294 dbj BAB91145.1 beta-glucosidase [Neotermes koshunensis]
sw20799	BGIBMGA014242	6.7311	2.5926	2.29675	1	Bmb006459	3.00E-93
sw20883	BGIBMGA012265	2.34115	1.1885	0.92425	1	1.00E-12	gi 48474335 sp Q60417 SCRB1_CRIGR Scavenger receptor class B member 1 (SRB1) (SR-BI) (HaSR-BI) haSR-BI
sw22231	BGIBMGA004528	0.25075	1.2309	0.78955	1	2.00E-11	gi 79464734 ref NP_192384.2 carbohydrate transporter/ sugar porter [Arabidopsis thaliana]
sw22269	BGIBMGA001374	0.11	0.25565	0.21795	1	No hits found	
sw22271	BGIBMGA010680	0.44955	1.07535	0.468	1	2.00E-15	gi 9105718 gb AAF83628.1 endo-1,4-beta-glucanase [Xylella fastidiosa 9a5c] endo-1,4-beta-glucanase [Xylella fastidiosa 9a5c]
sw22288	BGIBMGA004708	2.7738	1	1	1	e-104	gi 87248427 gb ABD36266.1 triacylglycerol lipase [Bombyx mori]
sw22607	BGIBMGA010045	2.86025	1	1.78005	1	1.00E-16	gi 4239700 emb CAA10770.1 reverse transcriptase-like [Bos taurus]
sw22695	BGIBMGA003395	0.2266	0.65665	0.4827	1	1.00E-26	gi 55666027 emb CAH74051.1 OTTHUMP00000065631 [Homo sapiens] OTTHUMP00000065631 [Homo sapiens] OTTHUMP00000065631
sw22716	BGIBMGA010116	0.4707	0.80735	0.6005	1	No hits found	
sw00011	BGIBMGA009446	0.4385	0.694	0.7712	0.99595	No hits found	
sw11825	BGIBMGA003374	1.01005	2.24665	1.32105	0.98645	e-136	gi 27374348 gb AAO01089.1 CG4733-PA [Drosophila willistoni]
sw22171	BGIBMGA000423	0.2832	0.37345	0.32785	0.9827	No hits found	
sw09159	BGIBMGA008119	0.4277	0.61415	0.64435	0.98035	Bmb025309	7.00E-05
sw08186	BGIBMGA009324	0.3687	0.7438	0.7524	0.98015	No hits found	
sw04095	BGIBMGA005598	1.5945	1.4924	2.095	0.97075	Bmb026464	2.00E-26
sw13441	BGIBMGA000013	0.05605	0.8469	0.3692	0.9658	2.00E-10	gi 54638658 gb EAL28060.1 GA13834-PA [Drosophila pseudoobscura]
sw13920	BGIBMGA011965	0.494	0.83565	0.69615	0.9527	e-133	gi 66524404 ref XP_623193.1 PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 5, partial [Apis mellifera]
sw13737	BGIBMGA011695	0.6495	0.65345	0.4226	0.94835	e-117	gi 1923274 gb AAC47506.1 Tpr homolog [Drosophila melanogaster]
sw04258	BGIBMGA011058	0.2539	0.7685	0.1437	0.9466	No hits found	
sw18399	BGIBMGA008824	2.293	4.27355	3.3477	0.9437	0	gi 102886 pir S19607 alkaline phosphatase (EC 3.1.3.1) - silkworm
sw13077	BGIBMGA007091	0.0998	0.6261	0.6535	0.9414	No hits found	
sw05455	BGIBMGA009467	1.9794	2.1042	1.91805	0.94125	1.00E-83	gi 73974968 ref XP_858777.1 PREDICTED: similar to glucosamine-6-phosphate deaminase 2 isoform 3 [Canis familiaris]
sw13753	BGIBMGA012101	0.6943	0.67175	0.37235	0.94	3.00E-26	gi 24649778 ref NP_651285.1 CG13634-PA [Drosophila melanogaster] CG13634-PA [Drosophila melanogaster]
sw20476	BGIBMGA007307	0.1575	0.64985	0.6155	0.91955	2.00E-38	gi 1490236 emb CAA67980.1 oligomycin sensitivity conferring protein precursor [Drosophila melanogaster]
sw15838	BGIBMGA001609	2.216	1.5924	1.59785	0.91905	e-152	gi 25012519 gb AAN71363.1 RE31673p [Drosophila melanogaster]
sw22856	BGIBMGA013408	0.07955	0.5735	0.63685	0.91525	No hits found	

sw09712	BGIBMGA010403	0.41895	0.53645	0.56755	0.91375	Bmb034569	e-116
sw18137	BGIBMGA007251	0.0844	0.5428	0.55365	0.91025	No hits found	
sw08476	BGIBMGA009245	0.2864	0.5403	0.41425	0.90475	6.00E-58	gi 85861035 gb ABC86467.1 IPO4174p [Drosophila melanogaster]
sw03028	BGIBMGA000089	0.39085	0.72265	0.62165	0.9037	2.00E-11	gi 19572382 emb CAD27928.1 putative G-protein coupled receptor [Anopheles gambiae] ENSANGP00000018168 [Anopheles gambiae str. PEST] ENSANGP00000018168 [Anopheles gambiae str. PEST]
sw17363	BGIBMGA013260	0.3358	0.6193	0.3097	0.9037	2.00E-49	gi 55235212 gb EAA14862.2 ENSANGP00000013993 [Anopheles gambiae str. PEST] ENSANGP00000013993 [Anopheles gambiae str. PEST]
sw12770	BGIBMGA009753	0.3557	0.58725	0.73245	0.90195	No hits found	
sw07921	BGIBMGA009061	0.0811	0.59375	0.5822	0.9012	No hits found	
sw15465	BGIBMGA003452	0.03905	0.63075	0.74495	0.89685	1.00E-12	gi 55244897 gb EAA05228.3 ENSANGP00000012660 [Anopheles gambiae str. PEST] ENSANGP00000012660 [Anopheles gambiae str. PEST]
sw00599	BGIBMGA002774	0.1069	0.6094	0.4788	0.89665	1.00E-26	gi 56270199 gb AAH87372.1 LOC495986 protein [Xenopus laevis]
sw03447	BGIBMGA013571	0.3203	0.6755	0.79085	0.8961	No hits found	
sw01620	BGIBMGA007228	2.23205	1.8417	1.6814	0.89375	Bmb025093	e-127
sw22932	BGIBMGA010889	0.76525	0.4989	0.68455	0.8937	3.00E-16	gi 72077548 ref XP_796448.1 PREDICTED: similar to riddle like (86.6 kD) (5O189) [Strongylocentrotus purpuratus]
sw17796	BGIBMGA008829	0.0283	0.67575	0.2981	0.89065	6.00E-08	gi 17942678 pdb 1K9O I Chain I, Crystal Structure Of Michaelis Serpin-Trypsin Complex
sw18048	BGIBMGA011843	0.07905	0.80435	1	0.8898	No hits found	
sw10040	BGIBMGA010807	0.0757	0.6579	0.6793	0.88965	No hits found	
sw13243	BGIBMGA006116	0.0718	0.63175	0.63205	0.88725	1.00E-13	gi 50751424 ref XP_422391.1 PREDICTED: similar to adenylate kinase 5 isoform 1; adenylate kinase 6; ATP-AMP transphosphorylase [Gallus gallus]
sw18815	BGIBMGA001348	1.38275	0.473	0.57655	0.8861	1.00E-62	gi 50764028 ref XP_422928.1 PREDICTED: similar to aldose reductase [Gallus gallus]
sw05653	BGIBMGA002038	0.04405	0.5796	0.63285	0.88555	1.00E-28	gi 24581791 ref NP_608886.1 CG14043-PA [Drosophila melanogaster] CG14043-PA [Drosophila melanogaster]
sw13517	BGIBMGA008859	1	2.9164	1	0.88535	e-162	gi 2625150 gb AAB86646.1 moderately methionine rich hexamerin precursor; MMtH [Hyalophora cecropia]
sw11316	BGIBMGA007850	0.0612	0.4622	0.43535	0.87355	No hits found	
sw15875	BGIBMGA006235	0.4254	0.85295	0.61605	0.87245	Bmb036048	5.00E-18
sw00170	BGIBMGA004943	0.1182	0.58105	0.66255	0.87225	5.00E-68	gi 73995987 ref XP_850513.1 PREDICTED: similar to serine/threonine kinase 22B (spermiogenesis associated) (predicted) [Canis familiaris]
sw06190	BGIBMGA001122	0.2441	1	1	0.87175	e-107	gi 87248307 gb ABD36206.1 peptidyl-prolyl cis-trans isomerase E [Bombyx mori]
sw11883	BGIBMGA002125	1.45315	2.02865	1.41775	0.8668	3.00E-18	gi 27374312 gb AAO01060.1 ap-PA [Drosophila willistonii]
sw03301	BGIBMGA013242	2.9008	1.18495	1	0.86435	6.00E-05	gi 76791840 ref ZP_00774344.1 General substrate transporter [Pseudoalteromonas atlantica T6c] General substrate transporter [Pseudoalteromonas atlantica T6c]
sw19465	BGIBMGA013329	0.3989	0.57155	0.5711	0.86405	7.00E-08	gi 72115693 ref XP_782070.1 PREDICTED: similar to predicted CDS, reverse transcriptase family member (XB968) [Strongylocentrotus purpuratus]
sw09114	BGIBMGA010771	0.2106	1	0.73535	0.86395	No hits found	
sw00678	BGIBMGA006703	0.2436	0.6517	0.76625	0.85335	e-100	gi 68584 pir AJFF1M glutamate-ammonia ligase (EC 6.3.1.2) 1, mitochondrial - fruit fly (Drosophila melanogaster)

sw08067	BGIBMGA004990	0.27105	0.68825	0.76495	0.8504	4.00E-27	gi 72130450 ref XP_795609.1 PREDICTED: similar to TNF receptor-associated factor 3 interacting protein 1 (predicted), partial [Strongylocentrotus purpuratus]
sw13013	BGIBMGA005749	2.6142	2.5225	1	0.8455	2.00E-27	gi 10442636 gb AAG17398.1 gamma-syntrophin-like protein SYN2 [Drosophila melanogaster]
sw16249	BGIBMGA012879	0.1498	0.66365	0.68655	0.8449	Bmb039561	1.00E-43
sw09076	BGIBMGA003577	0.09965	0.6134	0.63625	0.842	No hits found	
sw02176	BGIBMGA001201	0.6989	0.4896	0.7828	0.84025	3.00E-72	gi 90567700 emb CAI30053.1 muscular protein 20 [Hydroporus erythrocephalus]
sw18850	BGIBMGA011059	0.1465	0.634	0.35765	0.8396	2.00E-46	gi 72067669 ref XP_798203.1 PREDICTED: similar to reverse transcriptase family member (1F383) [Strongylocentrotus purpuratus]
sw03198	BGIBMGA011432	0.75545	0.8793	0.2894	0.83715	3.00E-05	gi 57972112 ref XP_564944.1 ENSANGP00000027953 [Anopheles gambiae str. PEST] ENSANGP00000027953 [Anopheles gambiae str. PEST]
sw15814	BGIBMGA006125	0.42825	0.8472	0.7054	0.83455	Bmb035645	No hits found
sw03247	BGIBMGA013360	0.08545	0.60305	0.6612	0.8337	No hits found	
sw06863	BGIBMGA004028	0.19535	0.57295	0.58195	0.8315	3.00E-83	gi 72012777 ref XP_780667.1 PREDICTED: similar to testis-specific serine kinase 4 [Strongylocentrotus purpuratus]
sw03217	BGIBMGA005787	3.3007	3.0253	1.67145	0.8298	2.00E-87	gi 66503826 ref XP_392190.2 PREDICTED: similar to RH44796p [Apis mellifera]
sw09306	BGIBMGA010127	0.23905	0.5477	0.4526	0.82615	No hits found	
sw08418	BGIBMGA006385	0.4462	0.6361	0.64385	0.82525	3.00E-35	gi 86515380 ref NP_001034519.1 abdominal-B [Tribolium castaneum] abdominal-B [Tribolium castaneum]
sw04137	BGIBMGA012680	1.921	1.64625	2.82885	0.8215	2.00E-34	gi 66517541 ref XP_393694.2 PREDICTED: similar to CG32171-PD, isoform D [Apis mellifera]
sw03311	BGIBMGA008828	0.08985	0.66275	0.32335	0.8171	1.00E-07	gi 217291 dbj BAA00639.1 antitrypsin precursor [Bombyx mori] Antitrypsin precursor (AT)
sw03590	BGIBMGA013868	0.49725	0.7061	0.53775	0.81525	1.00E-52	gi 66506650 ref XP_625203.1 PREDICTED: similar to Dscam [Apis mellifera]
sw10691	BGIBMGA004051	0.11	0.5677	0.57975	0.8113	1.00E-09	gi 26454107 dbj BAC44437.1 DNA topoisomerase IV subunit A [Mycoplasma penetrans HF-2] DNA topoisomerase IV subunit A [Mycoplasma penetrans HF-2]
sw16450	BGIBMGA012894	0.6217	0.87235	0.45415	0.81065	No hits found	
sw03575	BGIBMGA010438	0.4397	0.57415	0.31915	0.8051	2.00E-10	gi 68076941 ref XP_680390.1 MAEBL [Plasmodium berghei strain ANKA] MAEBL, putative [Plasmodium berghei]
sw19086	BGIBMGA014542	0.0775	0.4695	0.7655	0.80205	1.00E-04	gi 77387268 gb ABA78453.1 F1-ATP synthase beta subunit [Rhodobacter sphaeroides 2.4.1] ATP synthase subunit B
sw03882	BGIBMGA004398	0.4284	0.8142	0.6299	0.80055	8.00E-33	gi 126417 sp P09336 LP3_BOMMO Low molecular 30 kDa lipoprotein PBMHPC-19 precursor 30K lipoprotein precursor [Bombyx mori]
sw00440	BGIBMGA005786	2.688	1.80735	1.4433	0.79945	5.00E-06	gi 76617327 ref XP_585387.2 PREDICTED: similar to Inositol oxygenase (Myo-inositol oxygenase) (Aldehyde reductase-like 6) (Renal-specific oxidoreductase) (Kidney-specific protein 32) [Bos taurus]
sw16133	BGIBMGA013229	0.35435	0.8094	0.6852	0.79595	2.00E-06	gi 74096211 ref NP_001027646.1 axonemal p66.0 [Ciona intestinalis] axonemal p66.0 [Ciona intestinalis]
sw02395	BGIBMGA010038	2.11825	1.4194	1.27615	0.79475	2.00E-28	gi 60393084 gb AAX19492.1 slalom PAPS transporter [Lucilia sericata]
sw19831	BGIBMGA007986	0.48395	0.6244	0.60705	0.7911	3.00E-07	gi 37589499 gb AAH59895.1 Pik4cb protein [Mus musculus]
sw15978	BGIBMGA010039	0.1037	0.4127	0.41545	0.78995	2.00E-05	gi 53148471 dbj BAD52263.1 antennal binding protein [Plutella xylostella] sericotropin-like protein [Plutella xylostella]
sw04440	BGIBMGA006954	0.3074	0.50385	0.37915	0.7835	8.00E-06	gi 54636037 gb EAL25440.1 GA10629-PA [Drosophila pseudoobscura]
sw12530	BGIBMGA008358	0.4194	0.5254	0.53745	0.7831	Bmb012777	7.00E-54

sw02266	BGIBMGA013770	0.35215	0.634	0.45255	0.78045	No hits found	
sw08839	BGIBMGA001797	0.47465	0.9065	0.71755	0.7802	2.00E-81	gi 56377671 dbj BAD74067.1 chromosome 2 open reading frame 4 short form [Homo sapiens]
sw03818	BGIBMGA003662	0.17025	0.6453	0.7711	0.7733	2.00E-34	gi 72096309 ref XP_797414.1 PREDICTED: similar to t-complex-associated testis expressed 1 [Strongylocentrotus purpuratus]
sw06412	BGIBMGA003032	0.4515	0.8195	0.7819	0.7704	e-104	gi 66519838 ref XP_391911.2 PREDICTED: similar to GA10180-PA [Apis mellifera] PREDICTED: similar to GA10180-PA [Apis mellifera]
sw20316	BGIBMGA013237	2.0269	0.9817	1.6017	0.76835	2.00E-68	gi 81248546 gb ABB69054.1 cytochrome P450 [Helicoverpa armigera]
sw14661	BGIBMGA010104	0.4134	0.61355	0.4949	0.76295	1.00E-32	gi 54648000 gb AAH84947.1 LOC495430 protein [Xenopus laevis]
sw06770	BGIBMGA012737	1	1	0.35995	0.7628	Bmb034180	No hits found
sw17451	BGIBMGA011145	0.36095	0.7673	0.5179	0.76195	Bmb028728	1.00E-57
sw07866	BGIBMGA013235	0.4833	1	0.8409	0.76015	Bmb006539	3.00E-89
sw05679	BGIBMGA002689	0.1978	0.76385	0.34035	0.7599	No hits found	
sw12826	BGIBMGA003277	0.3082	0.675	0.5694	0.757	No hits found	
sw01327	BGIBMGA002780	0.42065	0.66845	0.5433	0.75615	3.00E-79	gi 68367804 ref XP_695826.1 PREDICTED: similar to tripartite motif-containing 37 protein [Danio rerio]
sw00752	BGIBMGA006087	0.37415	1	1	0.75405	e-125	gi 2494216 sp Q16960 DYI3_ANTCR Dynein intermediate chain 3, ciliary dynein intermediate chain 3 [Anthodiaris crassispina]
sw15315	BGIBMGA004826	0.44055	0.6637	0.98125	0.75375	8.00E-29	gi 72015103 ref XP_781418.1 PREDICTED: similar to DNA polymerase epsilon, catalytic subunit A (DNA polymerase II subunit A) [Strongylocentrotus purpuratus]
sw15945	BGIBMGA004630	1.0991	1.4282	0.2501	0.7535	8.00E-57	gi 56378319 dbj BAD74196.1 heat shock protein hsp20.1 [Bombyx mori]
sw14737	BGIBMGA006103	0.378	0.7459	0.5702	0.74705	8.00E-05	gi 68390118 ref XP_694565.1 PREDICTED: similar to autoantigen RCD8 [Danio rerio]
sw00728	BGIBMGA012264	2.19	1.3607	1.3008	0.74565	5.00E-21	gi 27261765 gb AAN86085.1 lysozyme [Penaeus semisulcatus]
sw03453	BGIBMGA005122	0.19445	0.5382	0.6389	0.74545	Bmb011340	No hits found
sw05367	BGIBMGA005623	0.1184	0.47105	0.55015	0.74425	No hits found	
sw04945	BGIBMGA009530	0.0442	0.50805	0.5175	0.74375	1.00E-37	gi 13365633 dbj BAB39164.1 testis-specific ATPase inhibitor-like protein [Bombyx mori]
sw05534	BGIBMGA013115	1.8705	2.32265	2.10675	0.74345	4.00E-57	gi 13591614 dbj BAB40959.1 prophenoloxidase-2s [Bombyx mori]
sw12357	BGIBMGA000895	0.0244	0.63975	0.68205	0.74275	2.00E-13	gi 14423760 sp P93203 MFP1_LYCES MAR binding filament-like protein 1 MFP1 protein [Lycopersicon esculentum]
sw15671	BGIBMGA007787	0.3562	0.3586	0.3632	0.7351	0	gi 29420459 dbj BAC66474.1 anceropsin [Antheraea pernyi]
sw09635	BGIBMGA012427	2.68015	3.387	2.53755	0.7349	Bmb033167	6.00E-55
sw16538	BGIBMGA004726	1	1.47415	0.47005	0.73375	Bmb042912	2.00E-28
sw06658	BGIBMGA002175	1.0037	0.3754	0.3937	0.73095	Bmb031781	2.00E-18
sw22862	BGIBMGA014231	0.0954	0.5196	0.6223	0.72205	No hits found	
sw13232	BGIBMGA010449	2.0431	1.1627	1	0.71775	e-151	gi 66506401 ref XP_624756.1 PREDICTED: similar to CG11490-PA [Apis mellifera]

sw09626	BGIBMGA002379	0.4207	0.4669	0.58915	0.7168	2.00E-64	gi 72679333 gb AAI00144.1 Dctn4 protein [Rattus norvegicus] p62 dynactin subunit [Rattus norvegicus]
sw13340	BGIBMGA009206	0.0898	0.68505	0.73985	0.71465	Bmb017778	3.00E-41
sw13090	BGIBMGA003269	0.46345	0.723	0.5443	0.71415	1.00E-06	gi 62739281 gb AAH94228.1 Leucine-rich repeats and immunoglobulin-like domains 2 [Mus musculus] leucine-rich repeats and immunoglobulin-like domains 2
sw03241	BGIBMGA003865	5.5432	2.92495	1.80485	0.71	6.00E-36	gi 34366066 emb CAE18120.1 glycine cleavage system protein H [Crassostrea gigas]
sw15658	BGIBMGA006290	0.0924	0.5991	0.66855	0.70775	Bmb034448	6.00E-67
sw13680	BGIBMGA013857	0.102	0.63605	0.5946	0.70765	No hits found	
sw12461	BGIBMGA000734	0.17305	0.5658	0.5333	0.70285	No hits found	
sw11741	BGIBMGA005330	0.3064	1	0.74855	0.70165	4.00E-13	gi 85857620 gb ABC86345.1 IP13967p [Drosophila melanogaster]
sw10497	BGIBMGA005698	0.183	0.57625	0.6758	0.69485	No hits found	
sw15894	BGIBMGA011224	0.3714	0.7871	1	0.69035	5.00E-25	gi 55239363 gb EAL40125.1 ENSANGP00000029489 [Anopheles gambiae str. PEST] ENSANGP00000029489 [Anopheles gambiae str. PEST]
sw22218	BGIBMGA004384	0.27695	0.6209	0.77425	0.68775	No hits found	
sw17493	BGIBMGA009393	0.46435	0.91245	0.72025	0.6802	Bmb037261	e-121
sw09048	BGIBMGA009927	1.44505	1.45305	2.09225	0.67945	1.00E-50	gi 68393171 ref XP_688756.1 PREDICTED: similar to Calcitonin gene-related peptide type 1 receptor precursor (CGRP type 1 receptor) (Calcitonin receptor-like receptor) [Danio rerio]
sw00322	BGIBMGA004209	0.2499	0.5961	0.42265	0.67705	Bmb004470	2.00E-10
sw11700	BGIBMGA004190	0.9739	2.14125	2.39275	0.6745	1.00E-10	gi 66536215 ref XP_624664.1 PREDICTED: similar to GA15552-PA [Apis mellifera]
sw04327	BGIBMGA007804	0.4216	0.69275	0.57505	0.66945	Bmb031754	e-131
sw06775	BGIBMGA000314	0.34175	0.7494	0.74205	0.665	No hits found	
sw13482	BGIBMGA000563	2.65235	2.2217	1.0097	0.66365	Bmb018665	2.00E-95
sw12823	BGIBMGA010944	2.1599	1.2749	1.1063	0.66325	5.00E-07	gi 28569894 dbj BAC57926.1 reverse transcriptase [Bombyx mori]
sw17671	BGIBMGA002056	0.1666	0.64005	0.7073	0.66175	2.00E-12	gi 60551660 gb AAH91500.1 ODF2 protein [Homo sapiens]
sw17454	BGIBMGA007622	0.4325	0.6906	0.59405	0.6565	1.00E-11	gi 72005907 ref XP_781514.1 PREDICTED: similar to Nuclear pore complex protein Nup205 (Nucleoporin Nup205) (205 kDa nucleoporin) [Strongylocentrotus purpuratus]
sw15602	BGIBMGA014224	0.39895	0.7933	0.39165	0.6548	Bmb033954	2.00E-67
sw21169	BGIBMGA009782	0.1506	0.65105	0.73255	0.65335	1.00E-78	gi 474339 gb AAA17752.1 reverse transcriptase [Bombyx mori]
sw18977	BGIBMGA011215	0.47375	0.68235	0.58855	0.6527	7.00E-19	gi 5911296 gb AAD55740.1 BcDNA.LD27979 [Drosophila melanogaster]
sw10102	BGIBMGA007935	2.33715	2.156	1.82665	0.6523	Bmb043060	3.00E-14
sw03554	BGIBMGA006720	0.17395	0.65765	0.6171	0.646	2.00E-26	gi 76628450 ref XP_606462.2 PREDICTED: similar to leucine rich repeat containing 45, partial [Bos taurus]
sw03396	BGIBMGA005653	0.4749	0.721	0.5734	0.64435	No hits found	
sw11929	BGIBMGA013306	0.4617	0.64245	0.56725	0.6423	No hits found	

sw05348	BGIBMGA006649	0.1481	1	1	0.6407	2.00E-27	gi 76628450 ref XP_606462.2 PREDICTED: similar to leucine rich repeat containing 45, partial [Bos taurus]
sw18181	BGIBMGA012486	2.5286	2.0179	0.88725	0.64055	1.00E-59	gi 295756 emb CAA33113.1 TU-36B protein [Drosophila melanogaster]
sw06613	BGIBMGA006213	2.2885	1.18715	1.744	0.6333	e-104	gi 28317017 gb AAO39528.1 RE22242p [Drosophila melanogaster]
sw07419	BGIBMGA001368	0.2814	0.6726	0.70325	0.6304	No hits found	
sw13957	BGIBMGA012211	1	2.0871	1	0.6296	5.00E-24	gi 4158234 emb CAA75614.1 MA3 [Suberites domuncula]
sw14437	BGIBMGA012586	0.3161	0.6954	0.5105	0.62755	Bmb025239	2.00E-47
sw03890	BGIBMGA014445	0.3841	0.6239	0.50195	0.62615	4.00E-13	gi 66514931 ref XP_395624.2 PREDICTED: similar to broad complex isoform Z1 [Apis mellifera]
sw09008	BGIBMGA000224	0.4934	0.7554	1	0.621	4.00E-31	gi 72049850 ref XP_787337.1 PREDICTED: similar to solute carrier family 2, (facilitated glucose transporter), member 8 [Strongylocentrotus purpuratus]
sw19541	BGIBMGA004402	0.1582	0.6129	0.3905	0.61895	6.00E-82	gi 10907 emb CAA38531.1 30K protein [Bombyx mori] Low molecular mass 30 kDa lipoprotein 21G1 precursor
sw13880	BGIBMGA014287	0.12105	0.56645	0.4446	0.61675	2.00E-06	gi 41407340 ref NP_960176.1 PstA [Mycobacterium avium subsp. paratuberculosis K-10] PstA [Mycobacterium avium subsp. paratuberculosis K-10]
sw11356	BGIBMGA004681	0.0392	0.51035	0.5689	0.6145	2.00E-75	gi 62526540 gb AAX84656.1 alpha-tubulin [Tyrophagus putrescentiae]
sw02940	BGIBMGA001213	0.13705	0.2046	0.13175	0.6062	No hits found	
sw11380	BGIBMGA005514	0.082	0.7278	0.88345	0.60455	No hits found	
sw16519	BGIBMGA004436	2.02545	1.3108	1.3945	0.60425	7.00E-16	gi 28316894 gb AAO39469.1 RH04286p [Drosophila melanogaster]
sw03884	BGIBMGA013543	0.20895	0.50965	0.3297	0.6013	e-106	gi 48104652 ref XP_395824.1 PREDICTED: similar to transcription factor IIB [Apis mellifera]
sw02475	BGIBMGA009791	0.41625	0.99555	0.80215	0.5964	Bmb041791	2.00E-22
sw20990	BGIBMGA011460	0.0266	0.09555	0.0586	0.59525	5.00E-13	gi 6560645 gb AAF16700.1 juvenile hormone binding protein precursor-like protein [Manduca sexta]
sw19059	BGIBMGA014264	0.22095	0.6985	0.701	0.5904	1.00E-06	gi 89291452 gb EAR89440.1 HMG box family protein [Tetrahymena thermophila SB210]
sw22464	BGIBMGA008361	0.08235	0.40145	0.6248	0.58875	3.00E-06	gi 74009366 ref XP_849771.1 PREDICTED: similar to keratin associated protein 10-7 [Canis familiaris]
sw09993	BGIBMGA011628	0.29585	0.8751	0.5858	0.58695	Bmb039784	3.00E-12
sw12280	BGIBMGA008872	2.43545	2.3404	1.823	0.5816	4.00E-13	gi 72009524 ref XP_785536.1 PREDICTED: similar to Sialin (Solute carrier family 17 member 5) (Sodium/sialic acid cotransporter) (AST) (Membrane glycoprotein HP59) [Strongylocentrotus purpuratus]
sw17422	BGIBMGA004400	0.3487	0.8991	0.51785	0.57735	e-139	gi 266438 sp Q00802 L301_BOMMO Low molecular mass 30 kDa lipoprotein 19G1 precursor 30K protein [Bombyx mori]
sw19386	BGIBMGA012863	0.25035	0.71345	0.3407	0.57675	7.00E-63	gi 60099894 gb AAX13081.1 glucose dehydrogenase [Drosophila miranda]
sw04565	BGIBMGA009874	0.47145	0.6308	0.69915	0.5756	Bmb038486	3.00E-50
sw08318	BGIBMGA014102	0.13375	0.5121	0.6607	0.573	1.00E-05	gi 57914149 ref XP_554917.1 ENSANGP00000026385 [Anopheles gambiae str. PEST] ENSANGP00000026385 [Anopheles gambiae str. PEST]
sw06935	BGIBMGA009134	0.3764	0.68705	0.5667	0.5685	Bmb037859	7.00E-18
sw20743	BGIBMGA008668	2.05	1.4427	1.22315	0.56615	1.00E-83	gi 20372973 dbj BAB91156.1 serine protease [Bombyx mori]
sw13801	BGIBMGA013753	0.22785	0.73475	0.5534	0.56395	4.00E-08	gi 48097752 ref XP_393878.1 PREDICTED: similar to ENSANGP00000016890 [Apis mellifera]

sw19515	BGIBMGA003576	0.195	0.68785	0.80325	0.5639	8.00E-11	gi 83001004 ref XP_150403.5 PREDICTED: similar to fibrous sheath interacting protein 2 [Mus musculus] PREDICTED: similar to fibrous sheath interacting protein 2 [Mus musculus]
sw02159	BGIBMGA009641	2.31815	1.3921	1.40145	0.5581	Bmb034419	6.00E-06
sw17599	BGIBMGA009093	0.3566	0.7186	0.5184	0.55215	5.00E-09	gi 1836157 gb AAB46908.1 fungal protease inhibitor F; FPI-F [Bombyx mori] Fungal protease inhibitor F precursor (FPI-F) fungal protease-specific inhibitor-F [Bombyx mori]
sw15883	BGIBMGA006587	0.32385	0.66795	0.41435	0.5301	No hits found	
sw05186	BGIBMGA002691	0.4457	0.7238	0.62045	0.52915	4.00E-30	gi 66556657 ref XP_392741.2 PREDICTED: similar to ENSANGP00000009256 [Apis mellifera]
sw22776	BGIBMGA011702	0.3676	0.8467	0.71455	0.5271	e-108	gi 266438 sp Q00802 L301_BOMMO Low molecular mass 30 kDa lipoprotein 19G1 precursor 30K protein [Bombyx mori]
sw18255	BGIBMGA008059	1.1553	1.04595	1.2418	0.5262	0	gi 9802380 gb AAF99701.1 aminopeptidase-N [Epiphyas postvittana]
sw00114	BGIBMGA002331	0.4792	0.68125	0.50825	0.5256	No hits found	
sw12328	BGIBMGA010679	2.2333	1.5491	2.3216	0.52185	6.00E-99	gi 25009792 gb AAN71068.1 AT14391p [Drosophila melanogaster]
sw18516	BGIBMGA014051	2.25195	2.3268	1.5738	0.5191	Bmb038798	2.00E-26
sw08892	BGIBMGA013446	0.0227	0.563	0.61075	0.5174	2.00E-15	gi 89298896 gb EAR96884.1 EF hand family protein [Tetrahymena thermophila SB210]
sw02367	BGIBMGA012795	0.3029	0.6772	0.4892	0.51495	No hits found	
sw14775	BGIBMGA003551	0.25935	0.6381	0.47755	0.5141	4.00E-08	gi 24584084 ref NP_609635.1 CG15639-PA [Drosophila melanogaster] CG15639-PA [Drosophila melanogaster]
sw20411	BGIBMGA011039	1.10595	0.95445	1.13175	0.5123	0	gi 1335781 gb AAC47078.1 Cap
sw09361	BGIBMGA014458	0.04405	0.605	0.6375	0.51145	No hits found	
sw10237	BGIBMGA011530	1	1	1	0.51075	Bmb047540	2.00E-19
sw00689	BGIBMGA009276	2.7305	1.3968	0.99665	0.5107	2.00E-63	gi 85070116 gb ABC69733.1 vermilion [Mayetiola destructor]
sw08370	BGIBMGA011219	1	1	1	0.50845	7.00E-05	gi 89299669 gb EAR97657.1 hypothetical protein TTHERM_00617800 [Tetrahymena thermophila SB210]
sw13495	BGIBMGA002543	0.8842	1.44845	1	0.50705	1.00E-27	gi 45554605 ref NP_996387.1 Moesin CG10701-PJ, isoform J [Drosophila melanogaster] CG10701-PJ, isoform J [Drosophila melanogaster] Moesin/ezrin/radixin homolog 1
sw18226	BGIBMGA009415	0.1069	0.58365	0.73915	0.50605	3.00E-35	gi 74096331 ref NP_001027762.1 protofilament ribbon protein [Ciona intestinalis] protofilament ribbon protein [Ciona intestinalis]
sw06874	BGIBMGA011827	0.9761	1.1317	1.1057	0.50535	Bmb036467	e-117
sw19093	BGIBMGA007583	0.8701	0.91145	0.88865	0.5049	0	gi 12006108 gb AAG44738.1 IRA1 [Mus musculus]
sw02606	BGIBMGA004767	1	1	1	0.50475	Bmb044985	5.00E-07
sw13722	BGIBMGA007416	1.11015	1.26845	1.4392	0.50455	Bmb020359	4.00E-07
sw13248	BGIBMGA012800	1	1	1	0.50415	6.00E-59	gi 68369674 ref XP_706825.1 PREDICTED: similar to Solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 isoform 3 [Danio rerio]
sw02667	BGIBMGA003825	1	1.0819	1.6455	0.5032	4.00E-25	gi 66555679 ref XP_396164.2 PREDICTED: similar to kinesin family member 3A [Apis mellifera]
sw19228	BGIBMGA010386	1	1	1	0.5028	No hits found	
sw15828	BGIBMGA006540	1.11345	0.97395	0.81945	0.50205	No hits found	

sw13776	BGIBMGA005847	1	1	1	0.502	2.00E-13	gi 55637015 ref XP_508774.1 PREDICTED: similar to multi-transmembrane domain immunoglobulin-like protein [Pan troglodytes]
sw14006	BGIBMGA007332	0.71815	0.8286	1.0654	0.5015	3.00E-19	gi 51262008 gb AAH80137.1 26S protease regulatory subunit 7 [Xenopus tropicalis]
sw12787	BGIBMGA005014	1	0.8143	1.05785	0.5014	Bmb014393	8.00E-27
sw12759	BGIBMGA008725	0.96505	1.155	1.29915	0.5011	Bmb014178	0
sw12453	BGIBMGA007081	1	1	1	0.5009	2.00E-72	gi 6678403 ref NP_033436.1 topoisomerase (DNA) III alpha [Mus musculus] Topoisomerase (DNA) III alpha [Mus musculus] topoisomerase (DNA) III alpha [Mus musculus] DNA topoisomerase III alpha topoisomerase III [Mus musculus]
sw13708	BGIBMGA002823	1	1	1	0.5005	2.00E-09	gi 55238357 gb EAL39856.1 ENSANGP00000025455 [Anopheles gambiae str. PEST] ENSANGP00000025455 [Anopheles gambiae str. PEST]
sw15904	BGIBMGA011445	1.01865	1.0818	1.31745	0.5005	No hits found	
sw01994	BGIBMGA007728	0.69965	0.75045	0.9522	0.50025	Bmb031269	4.00E-50
sw16144	BGIBMGA008746	0.87265	1.0275	0.8905	0.4999	Bmb038552	4.00E-31
sw03617	BGIBMGA008719	1	1	1	0.4997	e-132	gi 50756593 ref XP_415231.1 PREDICTED: similar to cain [Gallus gallus]
sw17479	BGIBMGA009941	0.8262	0.941	1.2255	0.4995	3.00E-24	gi 73997326 ref XP_867414.1 PREDICTED: similar to Ubiquitin isopeptidase T isoform 4 [Canis familiaris]
sw21175	BGIBMGA000302	1	1	1	0.49925	9.00E-95	gi 49903743 gb AAH76951.1 MGC89333 protein [Xenopus tropicalis] MGC89333 protein [Xenopus tropicalis]
sw09464	BGIBMGA003016	1	1	1	0.49915	e-105	gi 55237368 gb EAA12425.2 ENSANGP00000018252 [Anopheles gambiae str. PEST] ENSANGP00000018252 [Anopheles gambiae str. PEST]
sw16277	BGIBMGA008061	1.8968	1.4994	1.8734	0.49915	2.00E-39	gi 2687733 emb CAA10950.1 aminopeptidase N [Plutella xylostella]
sw02073	BGIBMGA011733	0.8892	0.94335	0.8051	0.4991	2.00E-38	gi 55614029 ref XP_515921.1 PREDICTED: similar to G protein-coupled receptor 155 [Pan troglodytes]
sw14292	BGIBMGA007975	1	1	1	0.4988	6.00E-34	gi 82891212 ref XP_915569.1 PREDICTED: similar to early estrogen-induced gene 1 protein [Mus musculus]
sw21282	BGIBMGA001739	1	1	0.91885	0.4988	Bmb035015	9.00E-39
sw19341	BGIBMGA007497	1.0785	0.8713	1.1468	0.4987	2.00E-13	gi 18204091 gb AAH21382.1 Methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) [Mus musculus] methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) [Mus musculus]
sw13288	BGIBMGA010068	1	1	1	0.49865	4.00E-68	gi 37681881 gb AAQ97818.1 N-ethylmaleimide-sensitive factor attachment protein, alpha [Danio rerio] N-ethylmaleimide sensitive fusion protein attachment protein alpha
sw19089	BGIBMGA013662	1.1869	1.1276	1	0.4985	1.00E-69	gi 72133877 ref XP_788695.1 PREDICTED: similar to predicted CDS, reverse transcriptase family member (10881) [Strongylocentrotus purpuratus]
sw18280	BGIBMGA013223	1.38775	0.9026	1.1243	0.49835	1.00E-40	gi 68697272 emb CAJ14165.1 BEL12_AG transposon polyprotein [Anopheles gambiae]
sw12809	BGIBMGA008139	0.57605	0.80405	0.7336	0.49825	2.00E-76	gi 25009665 gb AAN71009.1 AT01055p [Drosophila melanogaster]
sw19867	BGIBMGA007441	1	1	1	0.49785	e-112	gi 21483348 gb AAM52649.1 GM13306p [Drosophila melanogaster]
sw13960	BGIBMGA008063	1	1	1	0.4978	Bmb021898	6.00E-13
sw03188	BGIBMGA002999	0.9438	1.0292	1.07095	0.49745	9.00E-13	gi 66734432 gb AAY53605.1 tetraspanin family protein [Branchiostoma belcheri tsingtaunese]
sw18185	BGIBMGA014217	1.0471	1.107	1.30895	0.49735	2.00E-61	gi 67938380 ref ZP_00530906.1 Acetyl-CoA hydrolase/transferase [Chlorobium phaeobacteroides BS1] Acetyl-CoA hydrolase/transferase [Chlorobium phaeobacteroides BS1]
sw08505	BGIBMGA003615	1	1	1	0.49695	4.00E-41	gi 28317242 gb AAO39628.1 GH01001p [Drosophila melanogaster]
sw11338	BGIBMGA009280	1.0438	1.009	1.1422	0.4966	1.00E-11	gi 55661397 ref XP_525616.1 PREDICTED: protein kinase C and casein kinase substrate in neurons 2 [Pan troglodytes]

sw20627	BGIBMGA002460	1.0743	1.01205	1.3058	0.49655	e-123	gi 13446610 emb CAC35051.1 putative exoribonuclease DIS3 [Drosophila melanogaster]
sw03847	BGIBMGA002370	1.1255	1.08535	1.0468	0.49645	9.00E-22	gi 72011764 ref XP_780861.1 PREDICTED: similar to ring finger protein 111 [Strongylocentrotus purpuratus]
sw06585	BGIBMGA000624	1	1	1	0.4963	0	gi 22474516 dbj BAC10620.1 Titin-like protein [Bombyx mori]
sw20393	BGIBMGA007769	1	1	1	0.49625	8.00E-62	gi 62484234 ref NP_609215.3 CG7627-PA [Drosophila melanogaster] CG7627-PA [Drosophila melanogaster]
sw11411	BGIBMGA004281	0.29325	0.63425	0.64015	0.4962	2.00E-06	gi 66546699 ref XP_393497.2 PREDICTED: similar to ENSANGP00000007226 [Apis mellifera]
sw16215	BGIBMGA000715	0.68865	0.7152	0.7437	0.4961	Bmb039191	6.00E-43
sw09610	BGIBMGA013588	1	1	1	0.49595	2.00E-08	gi 89307050 gb EAS05038.1 Protein kinase domain containing protein [Tetrahymena thermophila SB210]
sw10128	BGIBMGA001936	1	1	1	0.4956	Bmb043791	No hits found
sw04620	BGIBMGA007806	0.9626	0.7959	1.0125	0.4952	1.00E-07	gi 66506776 ref XP_395965.2 PREDICTED: similar to CG5859-PA [Apis mellifera]
sw08112	BGIBMGA010701	1.09325	1.02725	1.24175	0.49515	1.00E-49	gi 72132938 ref XP_794780.1 PREDICTED: similar to Sideroflexin-1 (Tricarboxylate carrier protein) [Strongylocentrotus purpuratus]
sw12526	BGIBMGA005140	1.08675	0.9006	1.04735	0.49515	3.00E-12	gi 1234789 gb AAC59866.1 fos-related antigen-2
sw20057	BGIBMGA002286	1	1	1	0.4951	3.00E-24	gi 66532890 ref XP_395425.2 PREDICTED: similar to GA13874-PA [Apis mellifera]
sw20466	BGIBMGA007283	0.0094	0.57985	0.7322	0.4951	2.00E-27	gi 50758492 ref XP_425404.1 PREDICTED: similar to NaDC-2 [Gallus gallus]
sw18131	BGIBMGA007772	1.74765	1.34885	0.91275	0.49505	2.00E-31	gi 72043224 ref XP_787838.1 PREDICTED: similar to TPR repeat containing protein (XH300), partial [Strongylocentrotus purpuratus]
sw08436	BGIBMGA013698	1.17255	1.0619	1.25225	0.495	1.00E-14	gi 71834271 gb AAZ41808.1 AT28579p [Drosophila melanogaster]
sw11778	BGIBMGA003505	1	1	1	0.49455	7.00E-29	gi 48095153 ref XP_392250.1 PREDICTED: similar to PDZ domain containing 3 [Apis mellifera]
sw11236	BGIBMGA010816	1	1	1	0.49445	Bmb004519	2.00E-18
sw03881	BGIBMGA000450	1	1	1	0.4938	4.00E-24	gi 18858733 ref NP_571286.1 GATA-binding protein 3 [Danio rerio] GATA-binding protein 3 [Danio rerio] transcription factor; GATA 3 homolog [Danio rerio] Transcription factor GATA-3 (GATA-binding factor 3)
sw02097	BGIBMGA011797	1	1	1	0.49325	e-132	gi 904101 gb AAA74931.1 helicase
sw10602	BGIBMGA007763	1	1	1	0.4931	No hits found	
sw08422	BGIBMGA012370	1	1	1	0.49305	2.00E-09	gi 72157704 ref XP_787309.1 PREDICTED: similar to protein tyrosine phosphatase, receptor type, T, partial [Strongylocentrotus purpuratus]
sw11815	BGIBMGA000745	0.7771	1.1142	1.3569	0.49295	1.00E-18	gi 28972592 dbj BAC65712.1 mKIAA1049 protein [Mus musculus]
sw11167	BGIBMGA008523	0.9054	0.82185	0.9167	0.49275	8.00E-34	gi 66562766 ref XP_625122.1 PREDICTED: similar to ATP-binding cassette, sub-family B, member 10 [Apis mellifera]
sw12034	BGIBMGA011646	0.81095	0.8295	0.85655	0.4927	6.00E-46	gi 54643291 gb EAL32035.1 GA14705-PA [Drosophila pseudoobscura]
sw20109	BGIBMGA005944	0.8033	0.81395	0.83995	0.4926	5.00E-70	gi 66529633 ref XP_395559.2 PREDICTED: similar to PNUTSDm protein [Apis mellifera]
sw20807	BGIBMGA006561	0.6429	0.6714	0.96685	0.4924	1.00E-26	gi 600837 gb AAC46947.1 mariner transposase mariner transposase
sw12259	BGIBMGA008926	0.76225	1	1	0.4921	1.00E-37	gi 28972347 dbj BAC65627.1 mKIAA0684 protein [Mus musculus]
sw16574	BGIBMGA004976	1	1	1	0.4916	Bmb043588	No hits found

sw17562	BGIBMGA004344	0.9686	1.0089	1.13115	0.4916	e-118	gi 3913717 sp O16118 GNAS_HOMAM Guanine nucleotide-binding protein G(s), alpha subunit (Adenylate cyclase-stimulating G alpha protein) G-protein alpha s subunit [Homarus americanus]
sw14906	BGIBMGA009912	1	1	1	0.4915	1.00E-62	gi 72050581 ref XP_795530.1 PREDICTED: similar to Protein-S-isoprenylcysteine O-methyltransferase (Isoprenylcysteine carboxylmethyltransferase)
sw16397	BGIBMGA012910	1.01825	0.94705	0.9983	0.4914	Bmb041158	2.00E-18
sw02208	BGIBMGA007189	1	1	1	0.49125	3.00E-08	gi 68432309 ref XP_687509.1 PREDICTED: similar to zinc finger protein ZFP235, partial [Danio rerio]
sw06259	BGIBMGA005386	1	1	1	0.49115	9.00E-61	gi 40254842 ref NP_036419.2 centaurin, beta 2 [Homo sapiens] Centaurin, beta 2 [Homo sapiens]
sw18260	BGIBMGA009993	1.01145	1.0162	1.1017	0.4911	3.00E-17	gi 25012713 gb AAN71450.1 RE59368p [Drosophila melanogaster]
sw20577	BGIBMGA004785	0.8212	0.88695	1.14845	0.4911	3.00E-35	gi 29122957 gb AAO65770.1 SEL1L [Rattus norvegicus] Sel1 (suppressor of lin-12) 1 homolog [Rattus norvegicus]
sw00009	BGIBMGA004744	1.01155	1.0598	1.30105	0.49105	No hits found	
sw19571	BGIBMGA003292	0.5308	0.82355	0.6202	0.4909	No hits found	
sw17637	BGIBMGA001929	1.6046	1.32155	1.5941	0.49075	2.00E-82	gi 1881831 gb AAB49519.1 17 beta-hydroxysteroid dehydrogenase type IV; HSD IV [Rattus sp.] Peroxisomal multifunctional enzyme type 2 (MFE-2) (D-bifunctional protein) (DBP)
sw14699	BGIBMGA009420	0.85965	0.91855	0.99795	0.4901	e-126	gi 66540209 ref XP_624722.1 PREDICTED: similar to Zgc:92093 [Apis mellifera]
sw08986	BGIBMGA011572	1	1	1	0.49005	5.00E-72	gi 66513007 ref XP_392473.2 PREDICTED: similar to jumonji domain containing 1B [Apis mellifera]
sw05363	BGIBMGA002524	1.30135	1.11705	1.85605	0.48985	No hits found	
sw18679	BGIBMGA005426	1.0438	1.128	1.17635	0.48975	4.00E-12	gi 1519345 gb AAB61684.1 Pdd1p [Tetrahymena thermophila] Pdd1p [Tetrahymena thermophila]
sw21533	BGIBMGA014091	1.2412	1.10745	1.2435	0.48975	Bmb031776	6.00E-39
sw10030	BGIBMGA014491	1	1	1	0.4897	Bmb040649	2.00E-22
sw17713	BGIBMGA008199	0.8495	0.7935	0.9031	0.4895	Bmb041949	No hits found
sw08310	BGIBMGA008133	1	1	1	0.4892	Bmb012854	5.00E-08
sw05659	BGIBMGA005625	1	1	1	0.4888	1.00E-46	gi 51094446 gb EAL23707.1 unc-84 homolog A (C. elegans) [Homo sapiens]
sw03660	BGIBMGA000408	0.8416	0.81845	0.98335	0.4886	0	gi 6978595 ref NP_036651.1 calcium/calmodulin-dependent protein kinase II, delta [Rattus norvegicus] Calcium/calmodulin-dependent protein kinase type II delta chain (CaM-kinase II delta chain) (CaM kinase II delta subunit)
sw15792	BGIBMGA007188	0.75305	0.8185	0.9222	0.48805	Bmb035519	6.00E-09
sw00343	BGIBMGA007515	1.18505	0.9829	1.01485	0.488	Bmb004810	5.00E-22
sw15583	BGIBMGA013228	0.8999	1.0036	1.17245	0.488	4.00E-22	gi 25012345 gb AAN71283.1 RE05346p [Drosophila melanogaster]
sw08772	BGIBMGA013516	1	1	1	0.48785	No hits found	
sw18052	BGIBMGA001754	0.7906	0.9647	0.9049	0.4876	3.00E-14	gi 4574742 gb AAD24195.1 fragmin A [Physarum polycephalum]
sw13622	BGIBMGA011708	0.90395	1.108	0.8801	0.48755	2.00E-16	gi 72085257 ref XP_796113.1 PREDICTED: similar to cytochrome P450, family 2, subfamily U, polypeptide 1 [Strongylocentrotus purpuratus]
sw02944	BGIBMGA013134	0.85405	1	1.03555	0.4875	0	gi 2257629 dbj BAA21483.1 Bm cdc2 [Bombyx mori]
sw08085	BGIBMGA002787	1	1	1	0.4875	No hits found	

sw12981	BGIBMGA011963	1.10685	1.0018	1.02085	0.48735	8.00E-18	gi 75766090 pdb 2A7L B Chain B, Structure Of The Human Hypothetical Ubiquitin-Conjugating Enzyme, Loc55284 Chain A, Structure Of The Human Hypothetical Ubiquitin-Conjugating Enzyme, Loc55284
sw21120	BGIBMGA005931	1.3421	1.0924	1.5224	0.4868	e-104	gi 1705537 sp P52826 CACP_COLLI Carnitine O-acetyltransferase precursor (Carnitine acetylase) (CAT) (Carnitine acetyltransferase) (CrAT) carnitine acetyltransferase
sw12975	BGIBMGA002013	1.39895	1.11425	1.2106	0.48645	2.00E-49	gi 28557675 gb AAO45243.1 GH01576p [Drosophila melanogaster]
sw01551	BGIBMGA009184	0.7233	0.82515	0.7954	0.4863	1.00E-50	gi 6448469 dbj BAA86911.1 homologue of Sarcophaga 26,29kDa proteinase [Periplaneta americana]
sw19182	BGIBMGA005899	1.15945	0.9304	1.1003	0.4863	0	gi 998377 gb AAC60521.1 chitooligosaccharidolytic beta-N-acetylglucosaminidase; beta-GlcNAcase [Bombyx mori] Chitooligosaccharidolytic beta-N-acetylglucosaminidase precursor (Beta-GlcNAcase) (Beta-hexosaminidase)
sw21436	BGIBMGA004679	1	1	1	0.4855	Bmb015733	e-121
sw04342	BGIBMGA009045	0.9818	0.99325	1.0633	0.4854	7.00E-46	gi 54643209 gb EAL31953.1 GA10697-PA [Drosophila pseudoobscura]
sw08981	BGIBMGA001031	0.32505	0.65995	0.5313	0.48535	No hits found	
sw01718	BGIBMGA003361	2.0572	1.40725	1.6631	0.48515	Bmb026803	e-163
sw14816	BGIBMGA009392	1.40235	1.09305	0.8807	0.48505	3.00E-19	gi 18921163 ref NP_572733.1 CG1561-PA, isoform A [Drosophila melanogaster] HL08023p [Drosophila melanogaster] CG1561-PA, isoform A [Drosophila melanogaster]
sw15044	BGIBMGA008214	1.2036	1.3133	1.50075	0.48465	1.00E-10	gi 2429444 gb AAB70982.1 Fumarase protein 1, isoform a [Caenorhabditis elegans] FUMarase family member (fum-1) [Caenorhabditis elegans] Probable fumarate hydratase, mitochondrial precursor (Fumarase)
sw14872	BGIBMGA005056	1	1	1	0.4846	1.00E-24	gi 68365252 ref XP_683807.1 PREDICTED: similar to Potential helicase MOV-10 (Moloney leukemia virus 10 protein) [Danio rerio]
sw01916	BGIBMGA006246	0.7103	0.8057	1.0679	0.48455	Bmb029821	5.00E-07
sw06500	BGIBMGA007579	0.9858	0.9712	0.8829	0.4842	Bmb028550	4.00E-06
sw17505	BGIBMGA001982	1	1	1	0.4841	Bmb039542	2.00E-08
sw06013	BGIBMGA008612	1	1	1	0.48375	7.00E-67	gi 76654637 ref XP_584546.2 PREDICTED: similar to phosphatidylinositol 4-kinase type II isoform 1 [Bos taurus]
sw19478	BGIBMGA013251	1.06245	1	0.8891	0.48345	No hits found	
sw12571	BGIBMGA010030	1.193	1.0443	0.93045	0.4834	3.00E-05	gi 54114942 tpg DAA01820.1 TPA: TPA_inf: HN1-like protein [Anopheles gambiae]
sw00586	BGIBMGA001883	0.797	1.0591	1.02395	0.4831	No hits found	
sw18406	BGIBMGA005190	1	1	1	0.4831	2.00E-15	gi 66506685 ref XP_392322.2 PREDICTED: similar to 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1 (Phosphoinositide phospholipase C) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-I) (PLC-154) [Apis mellifera]
sw22526	BGIBMGA008831	0.2487	0.32995	0.2859	0.4831	Bmb006706	3.00E-12
sw11177	BGIBMGA009836	1	1	1	0.48265	8.00E-11	gi 71980134 gb AAZ57345.1 RE33938p [Drosophila melanogaster]
sw12936	BGIBMGA012958	1.2202	1.05595	0.96765	0.48265	No hits found	
sw06996	BGIBMGA009453	1.0119	1.05165	1	0.4825	Bmb039791	1.00E-13
sw09256	BGIBMGA003034	0.6843	1	0.7545	0.48215	6.00E-26	gi 46329861 gb AAH68420.1 Wu:f56a04 protein [Danio rerio]
sw05389	BGIBMGA011675	1	0.88225	1	0.48135	1.00E-57	gi 66514417 ref XP_396199.2 PREDICTED: similar to Nuclear pore complex protein Nup160 homolog [Apis mellifera]
sw16324	BGIBMGA013348	0.86955	1.0123	1.2337	0.48115	3.00E-60	gi 25282451 ref NP_741992.1 damage-specific DNA binding protein 1 [Rattus norvegicus] damage-specific DNA binding protein 1 [Rattus norvegicus]
sw19824	BGIBMGA014503	1.41625	1.18185	1.4305	0.48115	e-135	gi 54261662 gb AAH84614.1 LOC495282 protein [Xenopus laevis]

sw01281	BGIBMGA008442	1.8548	1.2141	1.42995	0.48095	0	gi 550486 gb AAB64306.1 pyruvate carboxylase [Aedes aegypti]
sw21184	BGIBMGA010472	1	1	1	0.4809	e-165	gi 28416396 gb AAO42670.1 AT10293p [Drosophila melanogaster]
sw00060	BGIBMGA003143	1	1	1	0.48065	8.00E-88	gi 24640586 ref NP_572476.2 CG12125-PA [Drosophila melanogaster] RE13562p [Drosophila melanogaster] CG12125-PA [Drosophila melanogaster]
sw21481	BGIBMGA010159	1	1	1	0.48065	2.00E-41	gi 68697272 emb CAJ14165.1 BEL12_AG transposon polyprotein [Anopheles gambiae]
sw11740	BGIBMGA000661	0.77255	0.9003	0.94075	0.4805	3.00E-48	gi 68366688 ref XP_683991.1 PREDICTED: similar to Protein disulfide-isomerase A5 precursor (Protein disulfide isomerase-related protein) [Danio rerio]
sw08817	BGIBMGA000097	1	1	1.2215	0.48	2.00E-44	gi 66505197 ref XP_394928.2 PREDICTED: similar to calpain B [Apis mellifera]
sw13228	BGIBMGA009370	0.82175	1.05055	1.07955	0.47985	4.00E-38	gi 74002990 ref XP_545165.2 PREDICTED: similar to Carboxypeptidase N subunit 2 precursor (Carboxypeptidase N polypeptide 2) (Carboxypeptidase N 83 kDa chain) (Carboxypeptidase N regulatory subunit)
sw15267	BGIBMGA007626	0.37545	0.6649	0.5048	0.4798	6.00E-36	gi 422486 pir A40734 Pas (Passover) protein - fruit fly (Drosophila melanogaster) passover
sw00085	BGIBMGA009829	1.1777	0.97055	1	0.4797	2.00E-27	gi 86563230 ref NP_001033372.1 T15B12.1b [Caenorhabditis elegans]
sw18488	BGIBMGA011368	1.24315	1	1.44545	0.47965	Bmb036336	1.00E-88
sw19381	BGIBMGA002114	1	1	1	0.47945	0	gi 157804 gb AAA28664.1 laminin B2 chain
sw08473	BGIBMGA014226	1	1	1	0.4792	0	gi 55236350 gb EAA43619.2 ENSANGP00000025304 [Anopheles gambiae str. PEST] ENSANGP00000025304 [Anopheles gambiae str. PEST]
sw05210	BGIBMGA000175	0.91275	0.99645	1.05535	0.47915	7.00E-48	gi 72016095 ref XP_786114.1 PREDICTED: similar to testis expressed gene 2 [Strongylocentrotus purpuratus]
sw01110	BGIBMGA003129	0.8711	1.2437	1.73625	0.479	2.00E-27	gi 55244191 gb EAL41409.1 ENSANGP00000027433 [Anopheles gambiae str. PEST] ENSANGP00000027433 [Anopheles gambiae str. PEST]
sw10534	BGIBMGA003525	1.1379	1.0823	1.0144	0.47895	No hits found	
sw00266	BGIBMGA001435	1	1	1	0.47865	2.00E-97	gi 12053709 emb CAC20419.1 a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 12 [Homo sapiens] ADAMTS-12 precursor
sw20958	BGIBMGA003261	0.6892	1.13025	1.2142	0.47865	No hits found	
sw15943	BGIBMGA006848	1.09115	1.0954	1.1319	0.4786	3.00E-12	gi 87162631 gb ABD28426.1 RNA-directed DNA polymerase (Reverse transcriptase); HMG-I and HMG-Y, DNA-binding [Medicago truncatula]
sw06716	BGIBMGA012439	0.7479	0.3609	0.85685	0.4785	5.00E-65	gi 66522495 ref XP_393918.2 PREDICTED: similar to subtilisin-related protease SPC3 [Apis mellifera]
sw18519	BGIBMGA008389	1	1	1	0.47845	3.00E-57	gi 61815768 gb AAX56336.1 ikk-like protein [Pinctada fucata]
sw09407	BGIBMGA006153	1.27705	1.0442	1.13265	0.478	6.00E-28	gi 76686050 ref XP_598148.2 PREDICTED: similar to tubulin tyrosine ligase-like family, member 3 isoform 1 [Bos taurus]
sw03208	BGIBMGA007491	1.0491	0.9533	1.07075	0.47795	7.00E-26	gi 34098381 sp O54916 REPS1_MOUSE RalBP1-associated Eps domain-containing protein 1 (RalBP1-interacting protein 1) RalBP1 associated Eps domain containing protein [Mus musculus] RalBP1-associated EH domain protein Reps1 [M
sw17476	BGIBMGA004017	1.04045	1	1.36385	0.47755	Bmb034239	2.00E-76
sw05148	BGIBMGA002404	1	1.3195	1	0.4774	7.00E-06	gi 72126814 ref XP_790069.1 PREDICTED: similar to step II splicing factor SLU7 [Strongylocentrotus purpuratus]
sw12902	BGIBMGA013725	1.0536	0.8513	1.0187	0.4773	4.00E-14	gi 54644089 gb EAL32831.1 GA10154-PA [Drosophila pseudoobscura]
sw21300	BGIBMGA011190	1	1	1	0.4773	2.00E-59	gi 83595261 gb ABC25082.1 MAP kinase activated protein-kinase-2 [Glossina morsitans morsitans]
sw19519	BGIBMGA012042	0.7581	0.6963	0.6869	0.4772	Bmb009746	2.00E-23
sw18746	BGIBMGA009879	1	1	1	0.47715	1.00E-75	gi 55239964 gb EAA10272.2 ENSANGP00000012355 [Anopheles gambiae str. PEST] ENSANGP00000012355 [Anopheles gambiae str. PEST]

sw07485	BGIBMGA009929	1	1	1	0.47695	Bmb001229	e-132
sw07781	BGIBMGA008409	0.27185	0.64455	0.5084	0.47675	No hits found	
sw22270	BGIBMGA001572	1	1	1	0.47675	2.00E-52	gi 72036140 ref XP_797170.1 PREDICTED: similar to DEAH (Asp-Glu-Ala-His) box polypeptide 34 isoform 1, partial [Strongylocentrotus purpuratus]
sw08841	BGIBMGA006895	1	1	1	0.4767	6.00E-26	gi 72128018 ref XP_782784.1 PREDICTED: similar to cell division cycle 27 homolog [Strongylocentrotus purpuratus]
sw20782	BGIBMGA000312	0.99745	0.9009	1.3984	0.4767	4.00E-46	gi 42542379 ref NP_005830.2 serine/arginine repetitive matrix 1 [Homo sapiens] serine/arginine repetitive matrix 1 [Homo sapiens] serine/arginine repetitive matrix 1 [Homo sapiens] Serine/arginine repetitive matrix protein 1 (Ser/Arg-related
sw02310	BGIBMGA005381	0.74495	0.86105	1.00455	0.4764	4.00E-79	gi 72179523 ref XP_786725.1 PREDICTED: similar to HIV-1 Rev binding protein 2 homolog [Strongylocentrotus purpuratus]
sw06061	BGIBMGA005520	1	1	1	0.47595	Bmb020029	1.00E-84
sw01968	BGIBMGA012310	1	1	1	0.4756	Bmb030765	No hits found
sw09834	BGIBMGA013098	1.1761	1.30185	1.0472	0.47545	3.00E-15	gi 4090968 gb AAD09281.1 immune-related Hdd13 [Hyphantria cunea]
sw16590	BGIBMGA001038	1	1	1	0.47545	Bmb043759	2.00E-16
sw02009	BGIBMGA011071	1	1	1	0.4753	2.00E-49	gi 7242181 ref NP_035246.1 phospholipase D family, member 3 [Mus musculus] Pld3 protein [Mus musculus] schwannoma-associated protein [Mus musculus]
sw17762	BGIBMGA008582	1.3874	1.40495	0.7273	0.4753	2.00E-45	gi 2058458 gb AAB53257.1 p260 [Bombyx mori]
sw01173	BGIBMGA008336	1	1	1	0.47495	7.00E-24	gi 33604134 gb AAH56332.1 Glycogen synthase kinase 3 alpha [Danio rerio] Glycogen synthase kinase 3 alpha [Danio rerio] glycogen synthase kinase 3 alpha [Danio rerio] glycogen synthase kinase 3 alpha [Danio rerio]
sw22349	BGIBMGA001979	0.7122	0.7865	0.9687	0.47495	Bmb033615	5.00E-33
sw16072	BGIBMGA012362	1	1	1	0.47475	2.00E-11	gi 1572721 gb AAB09089.1 megakaryocyte stimulating factor; MSF [Homo sapiens]
sw00076	BGIBMGA009332	1.1022	1.16605	1.25125	0.4745	4.00E-05	gi 40675335 gb AAH64870.1 Nolc1-prov protein [Xenopus tropicalis]
sw09439	BGIBMGA000189	1	1	1	0.4744	3.00E-08	gi 66564860 ref XP_396938.2 PREDICTED: similar to Zgc:100945 [Apis mellifera]
sw12154	BGIBMGA004365	1	1	1	0.4744	e-136	gi 66546886 ref XP_392978.2 PREDICTED: similar to A disintegrin and metalloproteinase with thrombospondin motifs like [Apis mellifera]
sw09934	BGIBMGA005037	1	1	1	0.47415	9.00E-91	gi 62859265 ref NP_001016149.1 SCY1-like 1 [Xenopus tropicalis] SCY1-like 1 (S. cerevisiae) [Xenopus tropicalis]
sw04615	BGIBMGA004037	1.0333	0.91955	1.0599	0.474	No hits found	
sw11052	BGIBMGA006475	0.921	0.99005	1.02385	0.47385	1.00E-20	gi 58332274 ref NP_001011285.1 Novel protein similar to ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) [Xenopus tropicalis] Novel protein similar to ras-related C3 botulinum toxin substrate 1 (rho fam
sw19303	BGIBMGA013241	2.51715	1	5.5106	0.47385	1.00E-73	gi 81248546 gb ABB69054.1 cytochrome P450 [Helicoverpa armigera]
sw00240	BGIBMGA011161	0.89105	0.8879	1.12185	0.4737	2.00E-26	gi 55637015 ref XP_508774.1 PREDICTED: similar to multi-transmembrane domain immunoglobulin-like protein [Pan troglodytes]
sw04136	BGIBMGA001746	1.091	1.10715	1.19115	0.47365	9.00E-06	gi 25012376 gb AAN71297.1 RE10019p [Drosophila melanogaster]
sw10762	BGIBMGA001091	1.655	1.1852	1.2883	0.47365	e-170	gi 58394466 ref XP_320745.2 ENSANGP00000008856 [Anopheles gambiae str. PEST] ENSANGP00000008856 [Anopheles gambiae str. PEST]
sw16625	BGIBMGA003913	1.01355	1.02855	0.9757	0.4733	2.00E-06	gi 55242814 gb EAA07246.2 ENSANGP00000016000 [Anopheles gambiae str. PEST] ENSANGP00000016000 [Anopheles gambiae str. PEST]
sw05774	BGIBMGA004413	1	1.2193	1	0.47325	8.00E-91	gi 6690786 gb AAF24342.1 Short stop/Kakapo truncated isoform [Drosophila melanogaster]
sw17987	BGIBMGA006908	1	1	1	0.4731	4.00E-59	gi 6746588 gb AAF27637.1 ecdysone-inducible gene E1 [Drosophila melanogaster]

sw06909	BGIBMGA004860	0.8923	0.8492	0.91325	0.473	No hits found	
sw07696	BGIBMGA012705	0.86975	1.03355	1.1208	0.47295	No hits found	
sw15449	BGIBMGA006374	1	1	1	0.4729	1.00E-27	gi 50417096 gb AAH77105.1 Zgc:110543 protein [Danio rerio]
sw06556	BGIBMGA002539	1.15075	1.3131	1.49925	0.47285	e-134	gi 5852166 emb CAB55500.1 vacuolar ATPase subunit a [Manduca sexta]
sw07516	BGIBMGA007912	0.933	0.94945	0.9173	0.47265	5.00E-55	gi 62857739 ref NP_001017231.1 retinol dehydrogenase 14 (all-trans and 9-cis) [Xenopus tropicalis] retinol dehydrogenase 14 (all-trans and 9-cis) [Xenopus tropicalis]
sw01185	BGIBMGA006298	1.1829	0.7722	1.14265	0.4724	No hits found	
sw01562	BGIBMGA010477	1	0.86775	1	0.472	8.00E-48	gi 19920884 ref NP_609121.1 CG12789-PB, isoform B [Drosophila melanogaster] GH23019p [Drosophila melanogaster] CG12789-PB, isoform B [Drosophila melanogaster]
sw12903	BGIBMGA003733	0.5505	0.7905	0.94585	0.47195	2.00E-54	gi 14318618 gb AAH09107.1 Microtubule associated serine/threonine kinase-like [Homo sapiens] novel protein kinase domain containing protein [Homo sapiens] Microtubule-associated serine/threonine-protein kinase-like
sw18569	BGIBMGA006643	1	0.69605	1	0.47155	No hits found	
sw02688	BGIBMGA000002	1.0264	0.9973	1.09035	0.4714	No hits found	
sw20197	BGIBMGA002833	0.26265	0.6422	0.84225	0.47115	6.00E-32	gi 28569894 dbj BAC57926.1 reverse transcriptase [Bombyx mori]
sw18354	BGIBMGA001675	1	1	1	0.47105	Bmb022212	1.00E-05
sw22656	BGIBMGA012864	1	1	1	0.47065	8.00E-05	gi 42780628 ref NP_977875.1 peptidase, M23/M37 family [Bacillus cereus ATCC 10987] peptidase, M23/M37 family [Bacillus cereus ATCC 10987]
sw19421	BGIBMGA007182	1.11535	1.20385	1	0.47055	1.00E-05	gi 66514893 ref XP_623699.1 PREDICTED: similar to hypothetical protein [Apis mellifera]
sw00734	BGIBMGA005695	1	1	1	0.47045	0	gi 87248427 gb ABD36266.1 triacylglycerol lipase [Bombyx mori]
sw13075	BGIBMGA003718	0.6258	1.0061	1.28135	0.47035	2.00E-23	gi 57033136 gb AAH88952.1 LOC398231 protein [Xenopus laevis]
sw04135	BGIBMGA002475	1.1144	0.9889	1.0629	0.47025	2.00E-06	gi 50748275 ref XP_426430.1 PREDICTED: similar to papilin [Gallus gallus]
sw13650	BGIBMGA006843	1.21335	1.0163	0.96775	0.47	e-142	gi 82582269 sp Q6NN85 SSH_DROME Protein phosphatase Slingshot MAP kinase phosphatase [Drosophila melanogaster]
sw05769	BGIBMGA005348	1	1	1	0.46975	3.00E-61	gi 77403901 gb ABA81829.1 LP20363p [Drosophila melanogaster]
sw19875	BGIBMGA004580	1.44565	1.34015	1.89905	0.46935	8.00E-10	gi 66525417 ref XP_393163.2 PREDICTED: similar to LIM domain protein [Apis mellifera]
sw21147	BGIBMGA009702	1	1	1	0.46935	7.00E-65	gi 55625576 ref XP_518161.1 PREDICTED: mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase [Pan troglodytes]
sw13631	BGIBMGA005815	1.3336	1.1196	1.0373	0.4693	2.00E-22	gi 27374226 gb AAO00988.1 CG9715-PA [Drosophila erecta]
sw17508	BGIBMGA007020	0.95985	1.05165	0.9168	0.4693	Bmb040665	6.00E-16
sw11161	BGIBMGA007407	1.05785	1.0239	1.082	0.46925	9.00E-11	gi 28376664 ref NP_777550.1 AN1, ubiquitin-like, homolog [Homo sapiens] ubiquitin-like fusion protein [Homo sapiens]
sw14431	BGIBMGA013163	1.3623	1.0402	0.8759	0.4687	4.00E-05	gi 48427980 sp P82120 CUO7_BLACR Cuticle protein 7 (BcNCP15.0)
sw08189	BGIBMGA009770	1	1.1388	1	0.4684	Bmb011161	6.00E-16
sw08237	BGIBMGA011482	1.44795	0.834	1.1394	0.46795	1.00E-72	gi 62243588 ref NP_001009573.2 unc-13 homolog D [Mus musculus]
sw18527	BGIBMGA009139	1.19625	1.0796	0.8368	0.46795	Bmb039398	3.00E-49

sw07654	BGIBMGA002463	1	0.9869	0.9511	0.4679	9.00E-08	gi 70795028 gb AAZ08477.1 relish [Nasutitermes fumigatus]
sw06920	BGIBMGA009812	1	0.9618	0.94095	0.46775	2.00E-09	gi 76635779 ref XP_613206.2 PREDICTED: similar to SWAP-70 protein, partial [Bos taurus]
sw12042	BGIBMGA010596	1.302	1.3354	1.49745	0.46735	e-172	gi 66504706 ref XP_394350.2 PREDICTED: similar to Retinoblastoma-binding protein 2 (RBBP-2) [Apis mellifera]
sw18327	BGIBMGA010574	0.97565	0.95615	1.172	0.4669	Bmb019451	3.00E-11
sw06208	BGIBMGA004251	1	1	1	0.46685	5.00E-83	gi 18859145 ref NP_571876.1 ornithine decarboxylase 1 [Danio rerio] Odc1 protein [Danio rerio] Ornithine decarboxylase 1 [Danio rerio] Odc1 protein [Danio rerio] ornithine decarboxylase [Danio rerio] ornithine decarboxylase [Danio rerio]
sw03056	BGIBMGA012226	1	1	1	0.4667	0	gi 18389427 dbj BAB84191.1 flavoprotein subunit of succinate dehydrogenase [Ascaris suum]
sw05795	BGIBMGA006185	1.6475	1.45195	1.30615	0.46655	4.00E-34	gi 27374255 gb AAO01012.1 CG30194-PA [Drosophila erecta]
sw08009	BGIBMGA004127	0.56895	0.7822	0.64375	0.4665	1.00E-13	gi 48102198 ref XP_392753.1 PREDICTED: similar to CG8069-PB, isoform B [Apis mellifera]
sw18350	BGIBMGA008168	1.0012	0.84775	1.22735	0.4664	7.00E-16	gi 9635413 ref NP_059311.1 ORF163 [Xestia c-nigrum granulovirus] ORF163 [Xestia c-nigrum granulovirus]
sw09524	BGIBMGA004373	1	1	1	0.46625	2.00E-46	gi 66500590 ref XP_624299.1 PREDICTED: similar to methyltransferase like 3 [Apis mellifera]
sw15406	BGIBMGA004639	0.96035	0.9161	1.0308	0.46595	e-109	gi 83318899 emb CAJ29888.1 putative frizzled receptor precursor [Paracentrotus lividus]
sw01243	BGIBMGA007449	1	1.00705	1.00905	0.4658	Bmb018637	e-123
sw09161	BGIBMGA014110	1	0.96715	1	0.4657	Bmb025329	1.00E-11
sw22913	BGIBMGA000807	1.31605	1.07965	1.35875	0.4656	e-132	gi 76613083 ref XP_886710.1 PREDICTED: similar to adenosine monophosphate deaminase 2 (isoform L) isoform 2 isoform 6 [Bos taurus]
sw17551	BGIBMGA001752	1.05965	1.06145	1.03515	0.46545	No hits found	
sw18459	BGIBMGA006039	0.9727	1.1169	1.0061	0.46545	Bmb033073	1.00E-57
sw15031	BGIBMGA013462	1	1	1	0.46525	Bmb029562	e-108
sw05600	BGIBMGA011412	0.8806	0.96775	1.06805	0.46495	e-146	gi 55246316 gb EAA03807.2 ENSANGP00000013512 [Anopheles gambiae str. PEST] ENSANGP00000013512 [Anopheles gambiae str. PEST]
sw12148	BGIBMGA003350	0.90505	0.8747	1.11095	0.4648	Bmb010467	7.00E-09
sw13431	BGIBMGA009605	1.0252	1.086	1	0.46475	Bmb018356	2.00E-39
sw05999	BGIBMGA009000	0.9841	0.9879	1.0848	0.46465	Bmb018748	9.00E-71
sw22935	BGIBMGA002149	0.81375	0.86875	0.9751	0.46465	1.00E-28	gi 72083766 ref XP_786661.1 PREDICTED: similar to HLA-B associated transcript 5 [Strongylocentrotus purpuratus]
sw16481	BGIBMGA007922	1.2512	0.91545	1.1665	0.4644	No hits found	
sw22957	BGIBMGA007904	0.84965	1.0666	1.06945	0.4642	4.00E-81	gi 7672773 gb AAF66635.1 thioredoxin-like protein TXL [Drosophila melanogaster]
sw12334	BGIBMGA008114	1.2777	1.22225	1.1134	0.4637	Bmb011600	e-139
sw12680	BGIBMGA005473	0.9568	0.905	1.06165	0.46365	0	gi 68354800 ref XP_692515.1 PREDICTED: similar to ATP-binding cassette, sub-family B, member 6, mitochondrial precursor (Mitochondrial ABC transporter 3) (Mt-ABC transporter 3) (ABC transporter umat) [Danio rerio]
sw01726	BGIBMGA010918	1	1	1	0.46355	1.00E-52	gi 54637592 gb EAL26994.1 GA18806-PA [Drosophila pseudoobscura]
sw14750	BGIBMGA005842	1	1	1	0.46335	Bmb027448	2.00E-23

sw00690	BGIBMGA003072	1	1.004	0.8325	0.463	4.00E-58	gi 28317277 gb AAO39638.1 AT18914p [Drosophila melanogaster]
sw19070	BGIBMGA002857	1.27895	1.3453	1.1539	0.46295	2.00E-70	gi 55235344 gb EAA15146.2 ENSANGP00000017210 [Anopheles gambiae str. PEST] ENSANGP00000017210 [Anopheles gambiae str. PEST]
sw14517	BGIBMGA009875	0.96455	1.08945	1.06355	0.4623	2.00E-17	gi 45382201 ref NP_990133.1 dynamitin [Gallus gallus] dynamitin [Gallus gallus]
sw18111	BGIBMGA005360	1	1	1	0.4622	Bmb039864	1.00E-44
sw09113	BGIBMGA011813	1.06015	0.95365	1	0.4621	e-146	gi 66543768 ref XP_624319.1 PREDICTED: similar to CG5547-PD, isoform D [Apis mellifera]
sw11861	BGIBMGA009576	0.9507	1.1735	1.03155	0.4617	Bmb008522	No hits found
sw16241	BGIBMGA002779	1.054	1.235	1.35	0.46155	e-163	gi 27544248 dbj BAC54898.1 supressor of Ty element 16 [Drosophila melanogaster]
sw21613	BGIBMGA005468	0.36605	0.6952	0.56875	0.46125	Bmb043785	5.00E-11
sw06910	BGIBMGA014194	1.06625	1.0108	1.275	0.461	1.00E-84	gi 76640328 ref XP_871841.1 PREDICTED: similar to vacuolar protein sorting 35 isoform 2 [Bos taurus]
sw18097	BGIBMGA006001	1	1	1	0.46095	Bmb037557	4.00E-24
sw12382	BGIBMGA014602	0.47865	0.62295	1	0.4609	3.00E-07	gi 4322670 gb AAD16120.1 dentin phosphoryn [Homo sapiens]
sw03369	BGIBMGA008914	1.0034	0.9653	1.0706	0.46085	Bmb009582	0
sw00850	BGIBMGA007400	0.89675	0.8393	0.83085	0.46065	3.00E-11	gi 54637002 gb EAL26405.1 GA14087-PA [Drosophila pseudoobscura]
sw14035	BGIBMGA000772	0.22435	0.4665	0.7387	0.46045	e-175	gi 73921301 gb AAG42021.2 juvenile hormone esterase precursor [Manduca sexta]
sw09553	BGIBMGA007554	1	1	1	0.46015	Bmb031613	No hits found
sw15607	BGIBMGA005884	1	1	1	0.46015	1.00E-44	gi 437310 gb AAA62850.1 nodulin
sw07919	BGIBMGA002675	0.8808	0.9358	1.10605	0.46	5.00E-50	gi 25012709 gb AAN71448.1 RE59077p [Drosophila melanogaster]
sw14653	BGIBMGA005500	1	1	1	0.46	1.00E-19	gi 72009576 ref XP_781168.1 PREDICTED: similar to Beta-glucuronidase precursor (Beta-G1) [Strongylocentrotus purpuratus]
sw05069	BGIBMGA007533	1	1	1	0.4597	No hits found	
sw13964	BGIBMGA009814	0.5042	0.9989	0.84195	0.4597	2.00E-06	gi 66564941 ref XP_396130.2 PREDICTED: similar to Phosphoserine phosphatase (predicted) [Apis mellifera]
sw15492	BGIBMGA007760	1	1	1	0.4597	3.00E-07	gi 11037277 gb AAG27544.1 BRCT-domain protein MUS101 [Drosophila melanogaster]
sw05761	BGIBMGA008140	1	1	1	0.4595	No hits found	
sw12431	BGIBMGA001064	0.5358	0.707	0.8628	0.4595	2.00E-33	gi 73993635 ref XP_848946.1 PREDICTED: similar to GalNAc transferase 10 isoform a [Canis familiaris]
sw15990	BGIBMGA009705	1	1	1	0.45905	No hits found	
sw20454	BGIBMGA007507	1.47775	1	1	0.4586	4.00E-48	gi 66508571 ref XP_395447.2 PREDICTED: similar to FAM [Apis mellifera]
sw18217	BGIBMGA014109	0.9927	1.11705	1.229	0.45855	7.00E-63	gi 8919867 emb CAB96203.1 acGAP protein [Drosophila melanogaster]
sw12378	BGIBMGA001142	1	1	1	0.45815	Bmb011862	2.00E-25
sw12804	BGIBMGA011577	1	1	1	0.45795	No hits found	

sw10986	BGIBMGA012320	1.0015	1.7574	1.08755	0.45785	1.00E-37	gi 50752092 ref XP_422648.1 PREDICTED: similar to ubiquitin-conjugating enzyme E2G 2; ubiquitin-conjugating enzyme 7 homolog [Gallus gallus]
sw13461	BGIBMGA009778	0.9711	1.0939	1.0962	0.4576	2.00E-28	gi 27526238 emb CAC82378.1 Lasp protein [Drosophila melanogaster]
sw13819	BGIBMGA012296	0.4716	0.69235	0.7315	0.4574	No hits found	
sw11982	BGIBMGA009263	1.09445	1.007	1.023	0.45735	Bmb009304	8.00E-08
sw08742	BGIBMGA005508	1.18395	0.9792	0.93645	0.45715	3.00E-87	gi 85857668 gb ABC86369.1 IP11908p [Drosophila melanogaster]
sw22878	BGIBMGA007971	0.7124	0.9394	1.05065	0.45715	3.00E-40	gi 72110057 ref XP_795453.1 PREDICTED: similar to Vesicle trafficking protein SEC22b (SEC22 vesicle trafficking protein-like 1) [Strongylocentrotus purpuratus]
sw12475	BGIBMGA010521	1	1	1	0.457	1.00E-44	gi 27806053 ref NP_776841.1 c-GMP stimulated phosphodiesterase [Bos taurus] cGMP-dependent 3',5'-cyclic phosphodiesterase (Cyclic GMP-stimulated phosphodiesterase) (CGS-PDE) (cGSPDE) cyclic nucleotide phosphodiesterase
sw16402	BGIBMGA005083	0.99265	1.0578	0.9791	0.4568	1.00E-67	gi 217346 dbj BAA01464.1 prospero [Drosophila melanogaster]
sw02008	BGIBMGA001874	1	1	1	0.45605	3.00E-41	gi 76639910 ref XP_876225.1 PREDICTED: similar to Synaptic vesicle membrane protein VAT-1 homolog [Bos taurus]
sw15251	BGIBMGA012514	0.5398	0.58165	0.8912	0.4559	Bmb031361	5.00E-83
sw11872	BGIBMGA000544	1	1	1	0.4554	3.00E-35	gi 28317039 gb AAO39539.1 RE09158p [Drosophila melanogaster]
sw07047	BGIBMGA006909	1	1	1	0.45535	3.00E-11	gi 55245839 gb EAA45449.2 ENSANGP00000023755 [Anopheles gambiae str. PEST] ENSANGP00000023755 [Anopheles gambiae str. PEST]
sw18001	BGIBMGA002649	1.13305	0.9909	1.11705	0.4551	3.00E-58	gi 66521630 ref XP_393870.2 PREDICTED: similar to suppressor of forked protein; Su(f) protein [Apis mellifera]
sw04420	BGIBMGA009007	1	1	1	0.455	No hits found	
sw06038	BGIBMGA004394	0.2231	0.8486	0.42615	0.45485	e-137	gi 126415 sp P09334 LP1_BOMMO Low molecular 30 kDa lipoprotein PBMHP-6 precursor 30K protein precursor [Bombyx mori]
sw18149	BGIBMGA001211	0.83675	0.9238	1.05735	0.45435	2.00E-47	gi 3024649 sp Q60416 SRBP1_CRIGR Sterol regulatory element-binding protein 1 (SREBP-1) (Sterol regulatory element-binding transcription factor 1) sterol regulatory element binding protein-1
sw09259	BGIBMGA001645	1.00485	1.0848	1.12875	0.45425	No hits found	
sw10855	BGIBMGA007875	0.9541	0.9469	1.2003	0.45395	2.00E-05	gi 89001107 ref NP_055023.2 dentin sialophosphoprotein preproprotein [Homo sapiens]
sw18633	BGIBMGA001300	1.0431	1.022	1.08125	0.4539	2.00E-98	gi 72034333 ref XP_798150.1 PREDICTED: similar to Alpha-fetoprotein enhancer binding protein (AT motif-binding factor) (AT-binding transcription factor 1) [Strongylocentrotus purpuratus]
sw20312	BGIBMGA012488	1	1	1	0.4533	Bmb025867	0
sw22884	BGIBMGA002918	1.01065	1.07925	1.0936	0.45325	8.00E-65	gi 62661108 ref XP_341289.2 PREDICTED: similar to ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) [Rattus norvegicus]
sw11474	BGIBMGA012907	1	1	1	0.4532	5.00E-50	gi 55243855 gb EAA06063.2 ENSANGP00000015314 [Anopheles gambiae str. PEST] ENSANGP00000015314 [Anopheles gambiae str. PEST]
sw03540	BGIBMGA005036	1.1444	1.01915	1.0256	0.45285	8.00E-20	gi 73989867 ref XP_850213.1 PREDICTED: similar to haloacid dehalogenase-like hydrolase domain containing 4 [Canis familiaris]
sw14021	BGIBMGA006781	1	1.13125	1	0.4528	No hits found	
sw20662	BGIBMGA006347	1	1.3296	1.0136	0.45275	Bmb036732	5.00E-69
sw07818	BGIBMGA009333	1	1	1	0.45225	5.00E-05	gi 1657752 gb AAC50805.1 FE65-like protein
sw18603	BGIBMGA014265	0.98545	0.67695	0.7802	0.4522	3.00E-60	gi 66549046 ref XP_393144.2 PREDICTED: similar to GA10777-PA [Apis mellifera]
sw09273	BGIBMGA008015	1	1	1	0.4521	3.00E-06	gi 14018320 emb CAC38353.1 aminopeptidase [Aspergillus niger]

sw22530	BGIBMGA010250	1	1	1	0.45205	No hits found	
sw11040	BGIBMGA010913	1.7618	1.29225	1.41965	0.45185	Bmb003179	2.00E-10
sw12830	BGIBMGA006977	0.59365	1.05935	0.97935	0.45155	1.00E-38	gi 4557233 ref NP_000008.1 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain precursor [Homo sapiens] acyl-CoA dehydrogenase [Homo sapiens] short chain acyl CoA dehydrogenase [Homo sapiens] Acyl-CoA dehydrogenas
sw06913	BGIBMGA012977	1	1	1	0.4515	Bmb037282	5.00E-62
sw15487	BGIBMGA006464	0.99995	1.3431	1.05995	0.45095	Bmb033087	2.00E-15
sw18118	BGIBMGA010689	0.87785	1.2357	1.15185	0.45075	3.00E-29	gi 66558407 ref XP_624445.1 PREDICTED: similar to ring finger protein 153 [Apis mellifera]
sw04759	BGIBMGA010476	1	1	1	0.4505	Bmb045545	4.00E-09
sw09549	BGIBMGA011040	1.2133	1.0022	1.1347	0.4505	Bmb031586	5.00E-77
sw12833	BGIBMGA008808	1	1	1	0.4503	4.00E-44	gi 1388166 gb AAB17949.1 Bowel
sw08031	BGIBMGA003874	1.16975	1.07725	1.30215	0.45015	2.00E-18	gi 27820023 gb AAO25043.1 GM10395p [Drosophila melanogaster]
sw00332	BGIBMGA002635	1.88475	1.33835	1.19615	0.45	1.00E-85	gi 55245443 gb EAA04375.2 ENSANGP00000009437 [Anopheles gambiae str. PEST] ENSANGP00000009437 [Anopheles gambiae str. PEST]
sw05201	BGIBMGA006127	1	1	1	0.45	Bmb004590	7.00E-30
sw16250	BGIBMGA001583	0.9982	0.9428	1.03515	0.45	1.00E-20	gi 45551904 ref NP_732009.2 Tropomyosin 1 CG4898-PI, isoform I [Drosophila melanogaster] Tropomyosin 1 CG4898-PC, isoform C [Drosophila melanogaster] GH09289p [Drosophila melanogaster] LD11194p
sw18283	BGIBMGA007137	0.8568	0.9406	1.0921	0.44995	6.00E-66	gi 66532439 ref XP_396968.2 PREDICTED: similar to vacuolar protein sorting protein 18, partial [Apis mellifera]
sw08886	BGIBMGA007295	1	1	1	0.4498	4.00E-10	gi 2104845 emb CAA93441.1 platelet glycoprotein V [Mus musculus] Platelet glycoprotein V precursor (GPV) (CD42D antigen)
sw18524	BGIBMGA004740	1	1	1	0.4496	2.00E-05	gi 37595925 gb AAQ94739.1 signal transducer and activator of transcription [Penaeus monodon]
sw10943	BGIBMGA005916	0.90895	1.021	1.10355	0.4492	5.00E-92	gi 3005601 gb AAC09329.1 katanin p80 subunit [Strongylocentrotus purpuratus] katanin p80 subunit [Strongylocentrotus purpuratus] Katanin p80 WD40-containing subunit B1 (Katanin p80 subunit B1) (p80 katanin)
sw11220	BGIBMGA001828	1.2557	1.1407	1.12055	0.449	No hits found	
sw09342	BGIBMGA007584	0.9094	0.8298	0.8951	0.44885	Bmb028131	1.00E-12
sw04210	BGIBMGA005356	1	1	1	0.44875	4.00E-06	gi 2618772 gb AAC98527.1 cytochrome P450 CYP12A2 [Musca domestica] Cytochrome P450 CYP12A2 (CYPXIIA2)
sw05778	BGIBMGA002642	0.87625	0.94205	0.849	0.44865	4.00E-06	gi 72011023 ref XP_780724.1 PREDICTED: hypothetical protein XP_775631 [Strongylocentrotus purpuratus]
sw03036	BGIBMGA014187	1.1031	1.0777	1.1397	0.4484	0	gi 87248313 gb ABD36209.1 DnaJ-like protein isoform A [Bombyx mori]
sw01764	BGIBMGA008071	1	0.9724	1.26165	0.4478	1.00E-10	gi 11870000 gb AAG40582.1 nuclear matrix transcription factor [Rattus norvegicus] Zinc finger protein 384 (Nuclear matrix transcription factor 4) (Cas-associated zinc finger protein)
sw06104	BGIBMGA002096	1	1	1	0.4477	3.00E-85	gi 66511984 ref XP_392429.2 PREDICTED: similar to protein tyrosine phosphatase [Apis mellifera]
sw14706	BGIBMGA006997	1.00775	0.8661	1.0275	0.44745	Bmb027140	2.00E-11
sw03233	BGIBMGA006063	0.7349	0.9089	0.9792	0.4474	No hits found	
sw17381	BGIBMGA007072	0.63035	0.811	0.57535	0.44685	3.00E-66	gi 86450725 gb ABC96698.1 yellow5 [Bombyx mori]
sw11286	BGIBMGA007516	0.25745	0.72145	0.7481	0.4466	0	gi 62526112 ref NP_001014993.1 elongation factor 1-alpha [Apis mellifera] elongation factor-1alpha F2 [Apis mellifera]

sw14855	BGIBMGA006617	1.12115	1.1133	1.28	0.44625	2.00E-39	gi 60678219 gb AAX33616.1 AT12602p [Drosophila melanogaster]
sw03338	BGIBMGA009555	1	1	1	0.44615	5.00E-14	gi 4972778 gb AAD34784.1 unknown [Drosophila melanogaster]
sw14778	BGIBMGA000060	0.8216	0.87795	0.8176	0.44615	e-154	gi 76780833 ref NP_001029121.1 sperm phosphodiesterase 5 [Strongylocentrotus purpuratus] sperm phosphodiesterase 5 [Strongylocentrotus purpuratus]
sw17812	BGIBMGA001313	0.56085	0.85055	0.78745	0.44615	Bmb020198	7.00E-18
sw03136	BGIBMGA002530	1.58365	1	1	0.4461	9.00E-25	gi 78366543 ref ZP_00836822.1 Peptidyl-dipeptidase A [Shewanella sp. PV-4] Peptidyl-dipeptidase A [Shewanella sp. PV-4]
sw18772	BGIBMGA009946	0.58445	0.70295	1.1005	0.44605	5.00E-55	gi 55241158 gb EAA08957.2 ENSANGP00000019635 [Anopheles gambiae str. PEST] ENSANGP00000019635 [Anopheles gambiae str. PEST]
sw09199	BGIBMGA000902	1.58635	1.4441	1.22915	0.4457	7.00E-06	gi 66511341 ref XP_392407.2 PREDICTED: similar to mastermind [Apis mellifera]
sw02423	BGIBMGA008124	0.98405	1.15715	1.04075	0.44565	Bmb040286	2.00E-14
sw03643	BGIBMGA004745	1.3469	1.36415	0.83155	0.44555	5.00E-17	gi 72006355 ref XP_787711.1 PREDICTED: similar to Preli [Strongylocentrotus purpuratus]
sw14332	BGIBMGA006865	1.32885	1.27605	1.36695	0.44555	7.00E-87	gi 87248303 gb ABD36204.1 cAMP responsive element binding protein [Bombyx mori]
sw12007	BGIBMGA001190	1	0.9833	1	0.4455	6.00E-13	gi 7542567 gb AAF63501.1 SP1173 [Drosophila melanogaster]
sw14222	BGIBMGA001607	0.9226	1.00365	1.0844	0.44535	3.00E-11	gi 38677997 emb CAC83074.1 alpha-1,6-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase [Drosophila melanogaster]
sw19227	BGIBMGA009127	0.8953	0.9705	1.07955	0.44535	No hits found	
sw01949	BGIBMGA010566	1.05135	1.27025	1.30115	0.44525	3.00E-96	gi 68440549 ref XP_708445.1 PREDICTED: similar to prolyl 4-hydroxylase, alpha I subunit isoform 1 precursor isoform 2 [Danio rerio]
sw04231	BGIBMGA001248	0.22045	0.64525	0.75745	0.4448	5.00E-15	gi 89309236 gb EAS07224.1 Viral A-type inclusion protein repeat containing protein [Tetrahymena thermophila SB210]
sw16364	BGIBMGA011102	1.21405	1.0064	1.2786	0.44465	1.00E-55	gi 158485 gb AAB04680.1 son of sevenless protein
sw17344	BGIBMGA007565	1.4527	1.35195	1.3651	0.44465	2.00E-47	gi 1226168 gb AAA92249.1 ORF B (bases 1850-5560) first start codon at 2306
sw01032	BGIBMGA010235	1.1368	0.7347	1.07515	0.4446	0	gi 72083296 gb AAZ66313.1 RE64894p [Drosophila melanogaster]
sw13109	BGIBMGA004430	1	1	1	0.4446	No hits found	
sw19642	BGIBMGA004728	0.37015	1.3325	0.51565	0.44445	Bmb038818	2.00E-29
sw00401	BGIBMGA004459	1	0.9357	1	0.4443	Bmb005751	No hits found
sw10452	BGIBMGA007223	0.02615	0.58955	0.3962	0.44395	No hits found	
sw13642	BGIBMGA008216	1.0031	1.2047	1.0115	0.4439	8.00E-13	gi 56541238 gb AAH87598.1 Fumarate hydratase 1 [Rattus norvegicus]
sw15152	BGIBMGA009172	1	1	1	0.4439	1.00E-31	gi 68369754 ref XP_691790.1 PREDICTED: similar to Low-density lipoprotein receptor-related protein 2 precursor (Megalin) (Glycoprotein 330) (gp330) [Danio rerio]
sw13038	BGIBMGA002339	1.0032	1.04185	0.89665	0.44385	No hits found	
sw19527	BGIBMGA007030	1	1	1	0.4438	e-173	gi 476949 pir A47371 transcription initiation factor IID 230K chain - fruit fly (Drosophila melanogaster)
sw08906	BGIBMGA012839	0.3503	0.50755	1.0053	0.44325	1.00E-19	gi 52354744 gb AAH82822.1 Formyltetrahydrofolate dehydrogenase [Xenopus tropicalis] formyltetrahydrofolate dehydrogenase [Xenopus tropicalis] aldehyde dehydrogenase 1 family, member L1 [Xenopus tropicalis]
sw15310	BGIBMGA010786	0.29005	0.5847	0.43845	0.44315	No hits found	

sw20792	BGIBMGA013122	1	1	1	0.4429	1.00E-27	gi 83005715 ref XP_143000.5 PREDICTED: similar to Zinc finger protein Kr18 (HKr18) [Mus musculus]
sw19900	BGIBMGA006846	1.7273	1	1.49245	0.44275	Bmb034060	3.00E-27
sw10721	BGIBMGA011537	1	1	1	0.4427	3.00E-21	gi 66525753 ref XP_392953.2 PREDICTED: similar to CG8379-PA, isoform A [Apis mellifera]
sw01339	BGIBMGA009645	0.4418	0.54935	0.83675	0.4424	3.00E-35	gi 85857466 gb ABC86269.1 RE41071p [Drosophila melanogaster]
sw04333	BGIBMGA007475	1.39445	1.11215	1.2693	0.44235	4.00E-15	gi 29134779 dbj BAC66140.1 projectin [Procambarus clarkii]
sw05831	BGIBMGA012160	1.08795	0.9636	1.102	0.44235	2.00E-06	gi 21483564 gb AAM52757.1 SD02552p [Drosophila melanogaster]
sw15165	BGIBMGA012119	0.8777	0.82915	1.1373	0.4421	8.00E-24	gi 83595275 gb ABC25089.1 integrin linked kinase [Glossina morsitans morsitans]
sw08199	BGIBMGA006857	1.19055	1.3342	1	0.44185	9.00E-08	gi 2117117 emb CAA69649.1 neurotransmitter transporter [Drosophila melanogaster]
sw02084	BGIBMGA012997	1.09155	0.99	1.034	0.44125	8.00E-69	gi 55243915 gb EAA06000.2 ENSANGP00000015052 [Anopheles gambiae str. PEST] ENSANGP00000015052 [Anopheles gambiae str. PEST]
sw14650	BGIBMGA004961	0.90735	1.06525	1.0583	0.44085	No hits found	
sw18754	BGIBMGA013513	1	1	1	0.4406	2.00E-42	gi 66803723 gb AAY56634.1 mitochondrial ribosomal protein S11 [Drosophila simulans]
sw05130	BGIBMGA007946	1.03195	1.07905	1.16515	0.44015	2.00E-60	gi 7858 emb CAA79313.1 Dpbx [Drosophila melanogaster]
sw08534	BGIBMGA005497	1	1	1	0.43985	4.00E-14	gi 85861125 gb ABC86511.1 GH15984p [Drosophila melanogaster]
sw00649	BGIBMGA009219	1	1	1	0.4398	4.00E-25	gi 27374257 gb AAO01014.1 I(2)k09913-PA [Drosophila erecta]
sw03795	BGIBMGA000776	0.70705	0.5776	0.9456	0.4393	Bmb019598	1.00E-66
sw11478	BGIBMGA008579	1.4728	1.3349	1	0.4389	Bmb006092	3.00E-90
sw13917	BGIBMGA000631	1	1	1	0.4385	No hits found	
sw12056	BGIBMGA012240	1.26145	0.955	1.0983	0.4383	3.00E-22	gi 82895058 ref XP_919288.1 PREDICTED: similar to Basement membrane-specific heparan sulfate proteoglycan core protein precursor (HSPG) (Perlecan) (PLC) [Mus musculus]
sw01890	BGIBMGA013973	1	1.2235	1.5386	0.4382	4.00E-07	gi 55628412 ref XP_519039.1 PREDICTED: similar to hypothetical protein FLJ22313 [Pan troglodytes]
sw07039	BGIBMGA008873	0.7184	0.9003	0.85165	0.43815	No hits found	
sw12574	BGIBMGA009994	1.0413	1.07585	1.2251	0.4381	4.00E-23	gi 54038195 gb AAH84280.1 LOC495107 protein [Xenopus laevis]
sw17442	BGIBMGA010072	1.58555	1.3271	1.5659	0.4381	2.00E-52	gi 45382633 ref NP_990799.1 cortactin [Gallus gallus] Src substrate protein p85 (p80) (Cortactin) p80/85
sw05330	BGIBMGA005717	0.38705	0.60445	0.4684	0.43805	1.00E-48	gi 66545426 ref XP_392228.2 PREDICTED: similar to dihydropyrimidine amidohydrolase [Apis mellifera]
sw15180	BGIBMGA008314	1	1	1	0.43805	Bmb030779	3.00E-90
sw06384	BGIBMGA004713	1.01445	0.88365	1.08145	0.438	e-125	gi 28316835 gb AAO39441.1 SD01504p [Drosophila melanogaster]
sw11176	BGIBMGA009911	1.06155	0.89825	1.108	0.43755	0	gi 11874759 dbj BAB19357.1 ubiquitin activating enzyme [Xenopus laevis]
sw01733	BGIBMGA014009	1	1	1	0.4374	Bmb027059	e-144
sw13453	BGIBMGA012689	1.04135	1.07455	0.95305	0.43735	8.00E-29	gi 62859817 ref NP_001016691.1 midnolin [Xenopus tropicalis] MGC97762 protein [Xenopus tropicalis] MGC97762 protein [Xenopus tropicalis] midnolin [Xenopus tropicalis]

sw03124	BGIBMGA001611	1.3215	0.84885	0.96485	0.4373	6.00E-08	gi 28850409 gb AAO53177.1 similar to Dictyostelium discoideum (Slime mold). Adenylyl cyclase
sw12110	BGIBMGA008062	1.3642	1.13055	1.24825	0.4371	e-178	gi 2687733 emb CAA10950.1 aminopeptidase N [Plutella xylostella]
sw08022	BGIBMGA003803	1.1984	1	1.08545	0.43695	No hits found	
sw03440	BGIBMGA007448	0.6501	0.9582	0.9548	0.4369	4.00E-20	gi 25288036 pir C88700 protein K02B2.1 [imported] - Caenorhabditis elegans
sw15888	BGIBMGA004729	1.0586	1.06315	1.26525	0.43645	Bmb036205	4.00E-51
sw01148	BGIBMGA003624	1.55595	1	1	0.43615	6.00E-52	gi 55245484 gb EAA04134.2 ENSANGP00000019058 [Anopheles gambiae str. PEST] ENSANGP00000019058 [Anopheles gambiae str. PEST]
sw18887	BGIBMGA004417	1.11795	1.20635	1.1671	0.43615	2.00E-18	gi 6690788 gb AAF24343.1 Short stop/Kakapo long isoform [Drosophila melanogaster]
sw13698	BGIBMGA003614	1.2254	1.20025	1.19055	0.4361	1.00E-06	gi 57526849 ref NP_001009623.1 tumor necrosis factor (ligand) superfamily, member 13 (predicted) [Rattus norvegicus] Tumor necrosis factor (ligand) superfamily, member 13 (predicted) [Rattus norvegicus]
sw15790	BGIBMGA011320	1.28225	1.1205	0.8797	0.4361	3.00E-24	gi 33620734 ref NP_065924.2 leucine rich repeat neuronal 1 [Homo sapiens] Leucine rich repeat neuronal 1 [Homo sapiens]
sw03621	BGIBMGA011755	0.86805	0.945	1.0076	0.43575	e-124	gi 15082379 gb AAH12103.1 3-phosphoinositide dependent protein kinase-1 [Homo sapiens] 3-phosphoinositide dependent protein kinase-1 isoform 1 [Homo sapiens] PDPK1
sw16262	BGIBMGA002789	1.0872	0.8952	1.398	0.4354	1.00E-45	gi 14669808 dbj BAB33159.2 paxillin [Drosophila melanogaster]
sw08877	BGIBMGA006810	1.15155	1.26175	1.3775	0.435	e-111	gi 38566288 gb AAH62579.1 CDC2L1 protein [Homo sapiens]
sw04296	BGIBMGA007885	1.09325	0.90625	0.97845	0.4347	1.00E-14	gi 62659557 ref XP_222780.3 PREDICTED: similar to Ras GTPase-activating protein nGAP (RAS protein activator like 1) [Rattus norvegicus]
sw12277	BGIBMGA011630	1	1	1	0.4347	e-144	gi 27806391 ref NP_776615.1 supervillin [Bos taurus] supervillin; P205 [Bos taurus]
sw03823	BGIBMGA008162	1	1	1	0.4345	1.00E-14	gi 87248235 gb ABD36170.1 tetraspanin E [Bombyx mori]
sw06632	BGIBMGA007210	1	1	1	0.43445	1.00E-37	gi 27374353 gb AAO01094.1 CG4538-PA [Drosophila willistonii]
sw12652	BGIBMGA006161	0.90145	0.90345	1	0.4344	6.00E-26	gi 68438451 ref XP_700621.1 PREDICTED: similar to Golgi apparatus protein 1 precursor (Golgi sialoglycoprotein MG-160) (E-selectin ligand 1) (ESL-1) (Selel) [Danio rerio]
sw16745	BGIBMGA008226	0.99255	1.099	1.2799	0.43405	Bmb046429	6.00E-25
sw07536	BGIBMGA009237	1.1474	1.0346	1.33305	0.43385	2.00E-07	gi 68365954 ref XP_690947.1 PREDICTED: similar to cyclin-dependent kinase inhibitor 1B (P27) [Danio rerio]
sw18854	BGIBMGA011348	1	1	1	0.43355	3.00E-06	gi 55629778 ref XP_527965.1 PREDICTED: similar to polycystic kidney disease 1 like 3; polycystic kidney disease 1-like 3 [Pan troglodytes]
sw15684	BGIBMGA006360	0.85505	1.1681	1.018	0.43345	1.00E-07	gi 27261275 gb AAN87620.1 circumsporozoite protein [Plasmodium falciparum]
sw10936	BGIBMGA007120	1.12685	1.1308	1.2615	0.43325	8.00E-66	gi 55957148 emb CAI17931.1 OTTHUMP00000042146 [Homo sapiens] OTTHUMP00000042146 [Homo sapiens] Aconitase 2, precursor [Homo sapiens] aconitase 2 precursor
sw05299	BGIBMGA007034	1.30965	1.20925	1.16205	0.43315	2.00E-08	gi 24649234 ref NP_651131.2 Inwardly rectifying potassium channel CG6747-PA [Drosophila melanogaster] inwardly rectifying K+ channel protein [Drosophila melanogaster] CG6747-PA [Drosophila melanogaster]
sw18000	BGIBMGA005188	1	1	1	0.43305	4.00E-34	gi 54636303 gb EAL25706.1 GA14185-PA [Drosophila pseudoobscura]
sw15395	BGIBMGA004932	0.7469	0.95955	1.127	0.4326	5.00E-07	gi 50978924 ref NP_001003179.1 ribosome receptor [Canis familiaris] Ribosome-binding protein 1 (180 kDa ribosome receptor) (RRp) ribosome receptor [Canis familiaris]
sw21301	BGIBMGA000529	1.3782	0.87595	0.9376	0.43245	e-150	gi 13359138 dbj BAB33300.1 neutral endopeptidase 24.11 [Bombyx mori]
sw00705	BGIBMGA000461	1.0795	1.04365	1.10715	0.4324	No hits found	
sw05298	BGIBMGA000103	1.1214	1.1881	1.14085	0.4324	2.00E-44	gi 46249989 gb AAH68436.1 Heterogeneous nuclear ribonucleoprotein U-like 1 [Danio rerio] heterogeneous nuclear ribonucleoprotein U-like 1 [Danio rerio]

sw13915	BGIBMGA001475	1.014	1.05495	1.2454	0.43185	No hits found	
sw02654	BGIBMGA011259	1	1	0.91875	0.4318	5.00E-14	gi 34328063 ref NP_058672.1 glutamate receptor, metabotropic 1 [Mus musculus] metabotropic glutamate receptor type 1 [Mus musculus] Metabotropic glutamate receptor 1 precursor (mGluR1)
sw12063	BGIBMGA003318	0.9395	0.8735	0.8275	0.4318	Bmb009923	9.00E-07
sw15458	BGIBMGA011631	1	1	1	0.4317	2.00E-67	gi 68430827 ref XP_685621.1 PREDICTED: similar to ubiquitin specific protease 10 isoform 1 [Danio rerio]
sw19077	BGIBMGA007792	1	1	1	0.43155	6.00E-13	gi 474339 gb AAA17752.1 reverse transcriptase [Bombyx mori]
sw10857	BGIBMGA001886	1	1	1	0.43125	7.00E-17	gi 76647578 ref XP_588089.2 PREDICTED: similar to gamma tubulin ring complex protein (76p gene) [Bos taurus]
sw06801	BGIBMGA007288	1	1.0659	1	0.43095	Bmb035016	2.00E-40
sw09789	BGIBMGA012228	1	1	1	0.4308	4.00E-79	gi 68364958 ref XP_683834.1 PREDICTED: similar to IQ motif containing with AAA domain isoform 1 [Danio rerio]
sw07504	BGIBMGA005299	1.44575	1.09975	0.7382	0.43065	5.00E-07	gi 15146352 dbj BAB33387.2 XP8 [Xenopus laevis]
sw20448	BGIBMGA010298	1.0104	0.9638	0.8912	0.4306	4.00E-54	gi 4521269 dbj BAA76304.1 endonuclease and reverse transcriptase-like protein [Bombyx mori]
sw03476	BGIBMGA005305	0.93165	0.9843	1.0086	0.4302	9.00E-06	gi 66518870 ref XP_391883.2 PREDICTED: similar to zinc finger protein 236 [Apis mellifera]
sw12506	BGIBMGA005624	1	1	1	0.42995	No hits found	
sw17635	BGIBMGA000025	0.947	1.1011	0.88715	0.4299	No hits found	
sw08966	BGIBMGA009401	1	1	1	0.42975	No hits found	
sw02214	BGIBMGA012743	1	1	1	0.42965	Bmb035678	7.00E-40
sw04688	BGIBMGA009254	1	1	1	0.42965	Bmb042445	2.00E-19
sw18597	BGIBMGA011424	0.81125	0.62405	0.53695	0.42965	0	gi 136206 sp P22297 TRF_MANSE Transferrin precursor transferrin
sw00514	BGIBMGA013343	1	1	1	0.42955	Bmb007345	6.00E-31
sw11487	BGIBMGA010637	0.8984	0.9238	0.86535	0.42945	4.00E-77	gi 5410429 gb AAD43053.1 Recq helicase 5 [Drosophila melanogaster]
sw17432	BGIBMGA001402	1.21845	1.12715	1.307	0.42915	Bmb024182	9.00E-23
sw13610	BGIBMGA013851	1	1	1	0.4291	6.00E-07	gi 30696202 ref NP_176103.2 ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana]
sw22041	BGIBMGA001781	1	0.9066	0.65205	0.4291	7.00E-13	gi 474339 gb AAA17752.1 reverse transcriptase [Bombyx mori]
sw01716	BGIBMGA010554	1	1	1	0.42895	No hits found	
sw22759	BGIBMGA004610	0.99045	0.70665	0.86175	0.42895	No hits found	
sw15773	BGIBMGA004500	1.1694	1.19795	1.2427	0.42885	Bmb035374	2.00E-71
sw18575	BGIBMGA006415	1.20835	0.99925	0.9803	0.42875	0	gi 54401523 gb AAV34566.1 chorion b-ZIP transcription factor [Bombyx mori]
sw19295	BGIBMGA003655	1.3887	1.57885	1.3436	0.42845	e-160	gi 66515547 ref XP_394781.2 PREDICTED: similar to rTS beta protein isoform 2 [Apis mellifera]
sw04457	BGIBMGA013226	1.1865	1.0277	1.155	0.42815	3.00E-15	gi 52076246 dbj BAD45014.1 egalitarian-like [Oryza sativa (japonica cultivar-group)]

sw05764	BGIBMGA001666	1	1	1	0.428	No hits found	
sw21639	BGIBMGA007415	0.94845	1.2438	1.33235	0.42795	5.00E-07	gi 3860051 gb AAC72967.1 transcytosis associated protein p115 [Mus musculus]
sw17331	BGIBMGA006179	1.5174	1.17685	1.49015	0.4277	3.00E-06	gi 54645551 gb EAL34289.1 GA10719-PA [Drosophila pseudoobscura]
sw04173	BGIBMGA008687	1	1	1	0.42715	3.00E-05	gi 66516317 ref XP_392552.2 PREDICTED: similar to CG14307-PB, isoform B [Apis mellifera]
sw05614	BGIBMGA013995	1	1	1	0.42695	0	gi 29343830 gb AAO81591.1 glycosyl hydrolase, family 31/fibronectin type III domain protein [Enterococcus faecalis V583] glycosyl hydrolase, family 31/fibronectin type III domain protein [Enterococcus faecalis V583]
sw13861	BGIBMGA011183	1.0025	1.02645	1.08985	0.42685	Bmb021215	No hits found
sw21531	BGIBMGA005523	1.08395	1.0056	1.02625	0.4268	No hits found	
sw14740	BGIBMGA012136	1.2669	1.11485	1.26335	0.42655	7.00E-58	gi 47086073 ref NP_998413.1 ADP-ribosylation factor-like 7 [Danio rerio] ADP-ribosylation factor-like 7 [Danio rerio]
sw04125	BGIBMGA007784	1	1	1	0.4265	Bmb027120	4.00E-35
sw06036	BGIBMGA005475	0.98605	0.6934	0.89445	0.4264	5.00E-21	gi 72108948 ref XP_800584.1 PREDICTED: hypothetical protein XP_795491 [Strongylocentrotus purpuratus]
sw20229	BGIBMGA000760	1	1	1	0.4262	0	gi 73953679 ref XP_536399.2 PREDICTED: similar to polymerase (RNA) III (DNA directed) polypeptide A, 155kDa [Canis familiaris]
sw19878	BGIBMGA005522	1	1	1	0.42595	0	gi 6491999 gb AAF14115.1 SPT6 protein [Drosophila melanogaster]
sw20117	BGIBMGA011625	0.6158	0.98855	0.7981	0.42585	6.00E-33	gi 28569894 dbj BAC57926.1 reverse transcriptase [Bombyx mori]
sw05034	BGIBMGA012309	0.7929	1.0589	0.9183	0.4252	2.00E-38	gi 66803829 gb AAV56642.1 unknown [Drosophila simulans]
sw18837	BGIBMGA005925	1.17905	1.02825	1.06705	0.4252	Bmb012364	1.00E-55
sw14827	BGIBMGA010711	1	1	1	0.42475	Bmb028066	1.00E-10
sw01328	BGIBMGA005268	1	1	1.2919	0.42465	No hits found	
sw16327	BGIBMGA002977	1	1	1	0.4244	Bmb040403	3.00E-09
sw13503	BGIBMGA014181	1.2032	1.14815	1.33615	0.4241	1.00E-47	gi 47522760 ref NP_999131.1 long-chain 3-ketoacyl-CoA thiolase [Sus scrofa] long-chain 3-ketoacyl-CoA thiolase [Sus scrofa]
sw13202	BGIBMGA010004	1	1	1	0.42395	No hits found	
sw00781	BGIBMGA005536	1	1.0928	0.9943	0.42315	Bmb011411	0
sw02532	BGIBMGA009783	1.02155	0.9996	0.97655	0.42315	Bmb043166	No hits found
sw21215	BGIBMGA013894	1	1	1	0.42315	Bmb030178	3.00E-05
sw11197	BGIBMGA009156	1.14525	1.00925	1.12825	0.4227	Bmb004266	e-119
sw06889	BGIBMGA004301	1	1	1	0.4226	2.00E-22	gi 53766623 gb AAU93471.1 ubiquitin ligase [Mus musculus] ring finger protein 123 [Mus musculus]
sw07468	BGIBMGA003020	1	1	1	0.4225	3.00E-90	gi 66519954 ref XP_392911.2 PREDICTED: similar to CG2950-PB, isoform B [Apis mellifera]
sw19088	BGIBMGA007869	0.84605	1.06885	1.2732	0.4225	Bmb015999	e-124
sw20009	BGIBMGA010482	0.2766	0.7087	0.47965	0.42215	No hits found	

sw14947	BGIBMGA007604	1	1	1	0.42135	1.00E-08	gi 60677997 gb AAX33505.1 LP14866p [Drosophila melanogaster]
sw19450	BGIBMGA007218	1.5766	1.828	1.60905	0.42085	Bmb037633	2.00E-67
sw06417	BGIBMGA001346	1	1	1	0.4207	4.00E-05	gi 25009850 gb AAN71095.1 AT22221p [Drosophila melanogaster]
sw08876	BGIBMGA010177	1.25275	1.13295	1.1088	0.4207	Bmb020896	6.00E-14
sw05656	BGIBMGA013001	1	1	1	0.4205	0	gi 66499229 ref XP_624835.1 PREDICTED: similar to CG9514-PA [Apis mellifera]
sw02098	BGIBMGA003532	1	1	1	0.42015	6.00E-16	gi 62663165 ref XP_214420.3 PREDICTED: similar to nuclear ATP/GTP-binding protein [Rattus norvegicus]
sw11791	BGIBMGA006898	1.0213	0.9283	0.8165	0.42005	No hits found	
sw02234	BGIBMGA008858	1	1	1	0.4199	Bmb036249	8.00E-82
sw19332	BGIBMGA000508	1	1	1	0.4198	Bmb030748	7.00E-14
sw20506	BGIBMGA006491	1.0369	1.28255	1.03985	0.4195	6.00E-67	gi 37359874 dbj BAC97915.1 mKIAA0261 protein [Mus musculus]
sw01081	BGIBMGA002821	1	1	1	0.41935	Bmb015839	7.00E-58
sw15708	BGIBMGA000864	1	1	1	0.41935	Bmb034920	2.00E-37
sw05903	BGIBMGA000387	1.1186	1.2067	1.48055	0.4192	2.00E-05	gi 27316716 gb AAO05891.1 streptococcal hemagglutinin protein [Staphylococcus epidermidis ATCC 12228] streptococcal hemagglutinin protein [Staphylococcus epidermidis ATCC 12228]
sw00084	BGIBMGA009828	1	1	1	0.41905	2.00E-11	gi 49522839 gb AAH73969.1 NEFH protein [Homo sapiens] neurofilament protein [Homo sapiens] Neurofilament triplet H protein (200 kDa neurofilament protein) (Neurofilament heavy polypeptide) (NF-H)
sw17919	BGIBMGA013623	0.85475	0.8692	1.0252	0.41885	3.00E-18	gi 73959079 ref XP_864654.1 PREDICTED: similar to transcription elongation factor B (SIII), polypeptide 2 isoform 3 [Canis familiaris]
sw18960	BGIBMGA011754	1.1258	1.06705	1.1043	0.41885	e-165	gi 66524404 ref XP_623193.1 PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 5, partial [Apis mellifera]
sw16993	BGIBMGA011319	1.385	1.52995	1.3036	0.41875	5.00E-30	gi 73976657 ref XP_539546.2 PREDICTED: similar to aminoadipate-semialdehyde synthase [Canis familiaris]
sw00820	BGIBMGA013327	0.8194	1.2256	1.5914	0.41865	2.00E-14	gi 72180773 ref XP_798850.1 PREDICTED: similar to Staphylococcal nuclease domain containing protein 1 (p100 co-activator) (100 kDa coactivator) (4SNc-Tudor domain protein) [Strongylocentrotus purpuratus]
sw12892	BGIBMGA013088	1	1	1	0.41855	2.00E-09	gi 73966952 ref XP_548257.2 PREDICTED: similar to growth arrest-specific 2 like 2 [Canis familiaris]
sw15682	BGIBMGA000703	1.15705	0.8534	1.16855	0.4183	5.00E-98	gi 89272476 emb CAJ83048.1 procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 [Xenopus tropicalis]
sw17349	BGIBMGA001707	0.91605	0.9006	1.1551	0.4178	0	gi 2613141 gb AAB84297.1 beta-1 tubulin [Manduca sexta] Tubulin beta-1 chain (Beta-1 tubulin)
sw13693	BGIBMGA000939	1	1	1	0.41765	5.00E-21	gi 25009692 gb AAN71022.1 AT04406p [Drosophila melanogaster]
sw09883	BGIBMGA003393	1	1	1	0.4175	Bmb037812	2.00E-12
sw20669	BGIBMGA011222	1	1	1	0.41725	2.00E-18	gi 24586460 ref NP_724636.1 CG11198-PB, isoform B [Drosophila melanogaster] GH12002p [Drosophila melanogaster] CG11198-PB, isoform B [Drosophila melanogaster]
sw21348	BGIBMGA011032	1	1.0171	1	0.41715	No hits found	
sw14007	BGIBMGA008169	0.87085	1.10905	1.0868	0.4164	7.00E-23	gi 72004452 ref XP_779950.1 PREDICTED: similar to RN protein [Strongylocentrotus purpuratus]
sw22896	BGIBMGA007727	0.97935	0.82025	0.8806	0.41615	7.00E-49	gi 9992882 gb AAG11414.1 nicastrin [Drosophila melanogaster]
sw00397	BGIBMGA002165	1	1	1	0.4161	2.00E-08	gi 66516917 ref XP_391828.2 PREDICTED: similar to CG8312-PA, isoform A [Apis mellifera]

sw21135	BGIBMGA005745	1.0065	1.07295	0.99225	0.41515	Bmb025037	6.00E-38
sw04421	BGIBMGA008701	1	1	1	0.4151	No hits found	
sw10912	BGIBMGA007558	1.293	0.8929	1.14315	0.4149	4.00E-75	gi 74011918 ref XP_848765.1 PREDICTED: similar to inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) [Canis familiaris]
sw18920	BGIBMGA013723	1	1	1	0.41455	9.00E-41	gi 83415184 ref NP_787057.2 ARG99 protein [Homo sapiens]
sw13033	BGIBMGA000536	1	1	1	0.4142	No hits found	
sw19113	BGIBMGA013161	0.932	1.04925	1.02065	0.4139	2.00E-63	gi 7862150 gb AAF70499.1 3-dehydroecdysone 3alpha-reductase [Spodoptera littoralis]
sw22265	BGIBMGA012100	0.95345	0.9475	1	0.41355	2.00E-19	gi 56418289 gb AAV91103.1 unknown protein [Grouper iridovirus]
sw20921	BGIBMGA003644	0.9631	1.1688	0.8609	0.41345	1.00E-33	gi 68394337 ref XP_696675.1 PREDICTED: similar to Sorting nexin 17 [Danio rerio]
sw00374	BGIBMGA007028	1	1	1	0.41335	No hits found	
sw20984	BGIBMGA003288	0.9706	0.98345	1.1387	0.4128	No hits found	
sw00249	BGIBMGA007948	0.8155	0.8818	0.87985	0.41265	0	gi 82799714 ref XP_929387.1 PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II spectrin) (Fodrin alpha chain) isoform
sw17817	BGIBMGA009635	0.0964	0.64495	0.6667	0.4122	No hits found	
sw20046	BGIBMGA003008	1	1	1	0.41215	0	gi 73949889 ref XP_535315.2 PREDICTED: similar to Phosphorylase b kinase beta regulatory chain (Phosphorylase kinase beta subunit) isoform 1 [Canis familiaris]
sw22790	BGIBMGA002170	0.91875	0.82795	0.72375	0.4117	5.00E-11	gi 57163725 ref NP_001009188.1 cauxin [Felis catus] carboxylesterase-like urinary excreted protein [Felis catus]
sw12437	BGIBMGA002767	1.1991	1.01905	1.23065	0.41135	4.00E-36	gi 89039345 gb ABD60146.1 adipokinetic hormone receptor [Anopheles gambiae]
sw14479	BGIBMGA009409	0.9923	0.8632	1.1682	0.41135	Bmb025627	9.00E-99
sw09646	BGIBMGA005102	1	1	1	0.4113	e-140	gi 562793 emb CAA57539.1 kinesin-like protein 1 [Xenopus laevis] Chromosome-associated kinesin KLP1 (Chromokinesin)
sw10757	BGIBMGA001512	1	1	1	0.41115	5.00E-80	gi 28557643 gb AAO45227.1 LD28216p [Drosophila melanogaster]
sw09844	BGIBMGA013565	1	1	1	0.4109	Bmb037037	1.00E-09
sw17529	BGIBMGA007519	1.94665	1.8354	2.41355	0.4104	Bmb046033	5.00E-56
sw02168	BGIBMGA003145	1	1	1	0.4103	No hits found	
sw16234	BGIBMGA013799	1	1	1	0.40985	Bmb039414	1.00E-06
sw11241	BGIBMGA009731	1.0442	1.04215	1.19	0.40955	No hits found	
sw03799	BGIBMGA011489	1	1	0.86495	0.40885	2.00E-13	gi 88174321 gb ABD39318.1 monocarboxylate transporter 2 [Bos taurus]
sw09134	BGIBMGA012483	1.2189	0.9463	1.1453	0.40885	2.00E-74	gi 50745792 ref XP_420245.1 PREDICTED: similar to synaptotagmin-like 4 (granuphilin-a); granuphilin-a [Gallus gallus]
sw13141	BGIBMGA011983	0.7603	1.105	1.2581	0.40885	4.00E-44	gi 39595413 emb CAE60451.1 Hypothetical protein CBG04059 [Caenorhabditis briggsae]
sw21110	BGIBMGA005199	0.95595	1.08785	1	0.40885	Bmb023509	e-175
sw01913	BGIBMGA003021	1.1366	0.8014	0.9879	0.4085	1.00E-30	gi 8855 emb CAA30332.1 unnamed protein product [Drosophila melanogaster]

sw05562	BGIBMGA000455	1.33245	1.2124	1.64355	0.40825	No hits found	
sw15120	BGIBMGA002346	1.17395	1.14405	1.26515	0.4081	Bmb030342	e-176
sw12404	BGIBMGA014126	1.1069	0.98915	1.11075	0.40805	4.00E-16	gi 73988285 ref XP_534038.2 PREDICTED: similar to tripartite motif-containing 3 isoform 1 [Canis familiaris]
sw13634	BGIBMGA008170	1	1	1	0.40765	2.00E-38	gi 45552683 ref NP_995866.1 CG15609-PB, isoform B [Drosophila melanogaster] CG15609-PC, isoform C [Drosophila melanogaster] CG15609-PA, isoform A [Drosophila melanogaster] CG15609-PC, isoform C
sw01118	BGIBMGA013531	1.4801	1.11595	1.53265	0.4074	2.00E-56	gi 72065732 ref XP_798089.1 PREDICTED: similar to Myosin light chain kinase, smooth muscle and non-muscle isozymes (MLCK) [Strongylocentrotus purpuratus]
sw07891	BGIBMGA011611	1	0.7623	1.2143	0.40695	1.00E-25	gi 30851445 gb AAH52460.1 Activating transcription factor 7 interacting protein [Mus musculus] activating transcription factor 7 interacting protein [Mus musculus] Atf7ip protein [Mus musculus]
sw04003	BGIBMGA003015	1	1	1	0.4069	9.00E-80	gi 66519690 ref XP_393825.2 PREDICTED: similar to ENSANGP00000018249 [Apis mellifera]
sw16308	BGIBMGA009674	1.7167	1.18	1.1083	0.4065	Bmb040261	4.00E-26
sw08046	BGIBMGA003752	1.02055	1.11205	1.12855	0.40635	4.00E-58	gi 71834261 gb AAZ41803.1 GH05001p [Drosophila melanogaster]
sw15582	BGIBMGA008548	1.36985	1.1216	1	0.40635	2.00E-36	gi 66524943 ref XP_394073.2 PREDICTED: similar to ENSANGP00000021271 [Apis mellifera]
sw15666	BGIBMGA006921	1.02995	0.93995	1.50955	0.40615	No hits found	
sw05916	BGIBMGA007041	1	1	1	0.4061	8.00E-11	gi 5834394 gb AAD53951.1 sulfate transporter [Drosophila melanogaster]
sw15430	BGIBMGA003464	1	1	1	0.40595	2.00E-89	gi 74002920 ref XP_545139.2 PREDICTED: similar to solute carrier family 12, member 8 [Canis familiaris]
sw17421	BGIBMGA006461	1.0303	1.01985	1.1226	0.4058	8.00E-52	gi 66564370 ref XP_395279.2 PREDICTED: similar to GA14079-PA [Apis mellifera]
sw07693	BGIBMGA003939	1	1	1	0.4057	9.00E-35	gi 32997078 dbj BAC79385.1 transcription factor BmEts [Bombyx mori]
sw14240	BGIBMGA003515	1.24425	1.13395	1.15845	0.4056	1.00E-38	gi 28317136 gb AAD27865.2 LD24380p [Drosophila melanogaster]
sw18541	BGIBMGA006999	1	1	1	0.4056	Bmb040506	e-137
sw22022	BGIBMGA013519	1	1	1	0.4056	No hits found	
sw04273	BGIBMGA003831	1	1	1	0.4055	4.00E-32	gi 25072201 ref NP_739563.1 oocyte-testis gene 1 [Mus musculus] Protein C10orf118 homolog (Oocyte-testis gene 1 protein) oocyte-testis gene 1 [Mus musculus]
sw08691	BGIBMGA001608	0.9081	1.05465	1.0573	0.40525	5.00E-36	gi 38677997 emb CAC83074.1 alpha-1,6-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase [Drosophila melanogaster]
sw03623	BGIBMGA001237	0.93125	0.825	0.8514	0.40505	2.00E-39	gi 2342862 gb AAB67672.1 branched chain aminotransferase precursor [Homo sapiens]
sw09354	BGIBMGA011542	1	1	1	0.4049	1.00E-60	gi 57236096 gb AAW48725.1 dicer-2 [Aedes aegypti]
sw09068	BGIBMGA008554	0.9827	1.05085	1.0619	0.40485	2.00E-12	gi 50756101 ref XP_415017.1 PREDICTED: similar to chromosome 20 open reading frame 72 [Gallus gallus]
sw00459	BGIBMGA009057	0.86885	0.8464	1.2403	0.40475	2.00E-85	gi 55644901 ref XP_523558.1 PREDICTED: solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 [Pan troglodytes] solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 [Homo sapiens] Sol
sw13599	BGIBMGA007388	1	1	1	0.40395	3.00E-15	gi 28381027 gb AAO41480.1 AT31792p [Drosophila melanogaster]
sw09253	BGIBMGA000504	0.1725	0.6545	0.7512	0.40385	9.00E-22	gi 72147038 ref XP_794932.1 PREDICTED: similar to putative protein, with at least 6 transmembrane domains (53.0 kD) (XK70) [Strongylocentrotus purpuratus]
sw00359	BGIBMGA003481	1.21045	0.9945	1.179	0.40375	0	gi 17298115 dbj BAB78526.1 wing disc-specific protein [Bombyx mori]
sw15106	BGIBMGA000146	0.9798	1.0924	1.1015	0.4037	9.00E-60	gi 54636311 gb EAL25714.1 GA10531-PA [Drosophila pseudoobscura]

sw12091	BGIBMGA005747	1	1	1	0.4036	9.00E-96	gi 66505993 ref XP_396307.2 PREDICTED: similar to GA16078-PA, partial [Apis mellifera]
sw12938	BGIBMGA008450	0.307	0.64765	0.4723	0.40315	No hits found	
sw10846	BGIBMGA011426	0.9065	0.9104	1.0221	0.40295	2.00E-12	gi 1877189 emb CAA71853.1 mitochondrial protein [Drosophila melanogaster]
sw06982	BGIBMGA008730	1	1	1	0.4027	Bmb039305	No hits found
sw18019	BGIBMGA000976	1.1071	1.1556	1.14425	0.4025	Bmb023439	8.00E-17
sw01636	BGIBMGA008706	1.05915	0.98755	0.9317	0.40185	8.00E-07	gi 1125764 gb AA83588.1 Uncoordinated protein 78, isoform a [Caenorhabditis elegans] UNCoordinated family member (unc-78) [Caenorhabditis elegans] UNC-78 [Caenorhabditis elegans] Actin-interacting protein 1 (AIP1)
sw01139	BGIBMGA011703	1.1139	0.9233	0.9396	0.40165	1.00E-68	gi 87248125 gb ABD36115.1 EN protein binding/engrailed nuclear homeoprotein-regulated protein [Bombyx mori]
sw12143	BGIBMGA003555	0.9772	0.9605	1.0779	0.4012	e-117	gi 49904239 gb AAH76960.1 MGC89389 protein [Xenopus tropicalis] MGC89389 protein [Xenopus tropicalis]
sw07452	BGIBMGA012764	2.10635	1.62895	2.05445	0.40115	6.00E-55	gi 46396762 sp Q27451 PRP1_BOMMO Phenoloxidase subunit 1 precursor (Tyrosinase 1) (PO 1) prophenoloxidase subunit 1 [Bombyx mori]
sw01082	BGIBMGA000691	0.7228	0.5409	0.8891	0.401	5.00E-33	gi 7106224 gb AAF36090.1 flagelliform silk protein [Nephila clavipes]
sw12257	BGIBMGA008927	1.03015	0.93795	0.85505	0.4008	e-112	gi 74005720 ref XP_536066.2 PREDICTED: similar to actin related protein 2/3 complex subunit 2 [Canis familiaris]
sw16701	BGIBMGA004029	1	1	1	0.40055	Bmb045710	2.00E-28
sw20918	BGIBMGA002709	1	0.9609	1.1617	0.4005	8.00E-37	gi 56269147 gb AAH87370.1 LOC495984 protein [Xenopus laevis]
sw01814	BGIBMGA006603	1	1	1	0.4001	Bmb028324	0
sw14404	BGIBMGA002393	0.988	1.0235	1.22195	0.3997	1.00E-92	gi 6523177 emb CAB62169.1 ARALAR 1 protein [Drosophila melanogaster]
sw15323	BGIBMGA004517	0.42785	0.8152	1	0.3995	2.00E-09	gi 72094483 ref XP_792984.1 PREDICTED: similar to ACRC protein [Strongylocentrotus purpuratus]
sw21273	BGIBMGA009503	1	1	1	0.39945	e-113	gi 25009861 gb AAN71100.1 AT23409p [Drosophila melanogaster]
sw10003	BGIBMGA012921	1	1	1	0.3991	Bmb040113	1.00E-46
sw08368	BGIBMGA002435	1.05155	1.04585	0.93535	0.39875	No hits found	
sw20163	BGIBMGA010338	1.313	1.42945	1.30385	0.3987	No hits found	
sw12788	BGIBMGA000145	1	1	1	0.3986	1.00E-18	gi 24655499 ref NP_725862.1 CG10737-PA, isoform A [Drosophila melanogaster] CG10737-PA, isoform A [Drosophila melanogaster]
sw06810	BGIBMGA008146	0.9264	0.44585	0.4733	0.398	Bmb035169	2.00E-36
sw12413	BGIBMGA007032	1	1	1	0.39795	2.00E-06	gi 19921638 ref NP_610120.1 General receptor for phosphoinositides 1 CG11628-PA [Drosophila melanogaster] RE34385p [Drosophila melanogaster] CG11628-PA [Drosophila melanogaster]
sw14428	BGIBMGA004018	1	1	1	0.39745	e-116	gi 11493775 gb AAG35645.1 cyclin-dependent protein kinase 5 [Danio rerio] cyclin-dependent protein kinase 5 [Danio rerio]
sw09128	BGIBMGA002432	1.4285	1.12075	1.47905	0.39725	4.00E-94	gi 6815281 gb AAF28475.1 V-ATPase 110 kDa integral membrane subunit [Aedes aegypti]
sw08102	BGIBMGA003647	1.11515	0.8406	1.1316	0.3966	8.00E-31	gi 1022831 gb AAA79851.1 tyrosine kinase
sw10606	BGIBMGA012964	0.9896	0.906	1.2198	0.39625	e-117	gi 66535977 ref XP_624437.1 PREDICTED: similar to Nardilysin precursor (N-arginine dibasic convertase) (NRD convertase) (NRD-C) [Apis mellifera]
sw09237	BGIBMGA000634	1	1	1	0.39615	No hits found	

sw15072	BGIBMGA002517	1	1	1	0.39615	No hits found	
sw09525	BGIBMGA007317	0.02855	0.56055	0.61545	0.3958	7.00E-88	gi 66520408 ref XP_392848.2 PREDICTED: similar to Ubiquitin carboxyl-terminal hydrolase 7 (Ubiquitin thiolesterase 7) (Ubiquitin-specific processing protease 7) (Deubiquitinating enzyme 7) (Herpesvirus associated ubiquitin-specific protease 7)
sw02952	BGIBMGA006809	1.0099	0.94895	1.0096	0.3952	Bmb001061	6.00E-53
sw21115	BGIBMGA005435	0.9213	1.1153	1.0446	0.3939	3.00E-31	gi 57506562 dbj BAD86652.1 reverse transcriptase [Bombyx mori]
sw08191	BGIBMGA008857	1.2245	0.93105	1.22435	0.39345	5.00E-17	gi 58585102 ref NP_001011581.1 cGMP-dependent protein kinase foraging [Apis mellifera] cGMP-dependent protein kinase foraging [Apis mellifera]
sw12272	BGIBMGA007791	0.0951	0.7013	1	0.3932	9.00E-05	gi 82704981 ref XP_726778.1 chloroquine resistance marker protein [Plasmodium yoelii yoelii str. 17XNL] chloroquine resistance marker protein, putative [Plasmodium yoelii yoelii]
sw10247	BGIBMGA013007	1	1.0274	1.3095	0.39305	Bmb047837	2.00E-28
sw05877	BGIBMGA011979	0.94745	0.96425	1.0062	0.39285	Bmb016516	7.00E-67
sw06023	BGIBMGA007077	0.8272	1.05635	1.01395	0.3922	No hits found	
sw18955	BGIBMGA010022	0.1789	0.31565	0.07885	0.3918	7.00E-88	gi 415798 emb CAA81643.1 blastopia polyprotein [Drosophila melanogaster]
sw17998	BGIBMGA003613	1.5973	1.3666	1.2492	0.39165	Bmb020186	No hits found
sw03948	BGIBMGA008363	1	1	1	0.3912	7.00E-17	gi 70571741 dbj BAE06812.1 zinc finger protein [Ciona intestinalis]
sw02398	BGIBMGA013707	1.11	0.9797	1.2912	0.3907	No hits found	
sw16826	BGIBMGA010300	1	1	1	0.3903	Bmb047820	No hits found
sw03733	BGIBMGA008849	1.08825	1.03415	1.1158	0.3902	1.00E-14	gi 68441657 ref XP_698520.1 PREDICTED: similar to G protein-coupled receptor 158 [Danio rerio]
sw19848	BGIBMGA002375	0.97145	1.02925	1.1207	0.38995	Bmb026314	5.00E-55
sw07506	BGIBMGA005300	2.24045	0.82805	0.65335	0.38955	7.00E-71	gi 121150 sp P07314 GGT1_RAT Gamma-glutamyltranspeptidase 1 precursor (Gamma-glutamyltransferase 1) (GGT 1) (CD224 antigen) [Contains: Gamma-glutamyltranspeptidase 1 heavy chain; Gamma-glutamyltranspeptidase 1 light chain]
sw08808	BGIBMGA005404	0.0488	0.4103	0.363	0.389	No hits found	
sw15751	BGIBMGA009148	1.3972	1.36215	1.2607	0.38895	5.00E-18	gi 55237956 gb EAA12905.3 ENSANGP00000002431 [Anopheles gambiae str. PEST] ENSANGP00000002431 [Anopheles gambiae str. PEST]
sw09672	BGIBMGA009282	0.98885	0.9689	1.0581	0.38835	Bmb033756	2.00E-22
sw05837	BGIBMGA000699	1.02245	0.8858	0.8784	0.38735	2.00E-35	gi 38638820 gb AAR25648.1 Abnormal cell migration protein 10, isoform c [Caenorhabditis elegans] abnormal cell MIGration family member (mig-10) [Caenorhabditis elegans] Abnormal cell migration protein 10
sw15402	BGIBMGA009090	1	1	1	0.38695	No hits found	
sw13978	BGIBMGA011687	1.06485	1.15235	1.1382	0.38595	2.00E-75	gi 68388015 ref XP_692539.1 PREDICTED: similar to leukocyte receptor cluster (LRC) member 8 [Danio rerio]
sw19096	BGIBMGA001352	0.9658	1.09675	1.1177	0.38595	1.00E-47	gi 16758758 ref NP_446338.1 lectin, mannose-binding, 1 [Rattus norvegicus] ERGIC-53 protein precursor (ER-Golgi intermediate compartment 53 kDa protein) (Lectin, mannose-binding 1) (p58) p58 cis-Golgi/intermediate compartment protein
sw09062	BGIBMGA000621	1	1	1	0.38545	2.00E-64	gi 3043692 dbj BAA25510.1 KIAA0584 protein [Homo sapiens]
sw09797	BGIBMGA000710	1	1	1	0.38525	2.00E-30	gi 48138819 ref XP_393426.1 PREDICTED: similar to vesicle-associated membrane protein, associated protein B and C [Apis mellifera]
sw16651	BGIBMGA003704	1.0482	1.12445	1.042	0.38465	Bmb044821	No hits found
sw19010	BGIBMGA004010	1	1	1	0.3838	2.00E-96	gi 2058458 gb AAB53257.1 p260 [Bombyx mori]

sw13989	BGIBMGA002847	1	1	1	0.3829	Bmb022061	4.00E-21
sw05946	BGIBMGA006585	1	1	1	0.38265	6.00E-14	gi 25009879 gb AAN71108.1 AT27059p [Drosophila melanogaster]
sw19815	BGIBMGA009693	0.49995	0.68335	0.6096	0.38235	5.00E-23	gi 73965363 ref XP_548034.2 PREDICTED: similar to Angiotensin-converting enzyme, testis-specific isoform precursor (ACE-T) (Dipeptidyl carboxypeptidase I) (Kinase II) [Canis familiaris]
sw00306	BGIBMGA014211	1.06055	0.95085	1.2978	0.38225	e-175	gi 87248239 gb ABD36172.1 transketolase [Bombyx mori]
sw20350	BGIBMGA007121	0.92185	1.0731	1.08805	0.38225	Bmb034174	e-105
sw08116	BGIBMGA011429	1.09905	1.14945	1.19755	0.3815	e-167	gi 50751398 ref XP_422379.1 PREDICTED: similar to cAMP-dependent protein kinase catalytic subunit beta isoform 1; PKA C-beta [Gallus gallus]
sw19561	BGIBMGA001173	1	0.86105	1	0.3812	No hits found	
sw08164	BGIBMGA012313	1.1867	1.279	1.20485	0.3811	e-130	gi 60459962 gb AAX20152.1 AMPK-gamma subunit [Aedes aegypti]
sw14529	BGIBMGA000901	1.035	0.9724	1.116	0.38105	No hits found	
sw18325	BGIBMGA004276	0.52465	0.7175	0.77435	0.38085	4.00E-52	gi 73962512 ref XP_859768.1 PREDICTED: similar to mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor isoform 8 [Canis familiaris]
sw22019	BGIBMGA009725	1	1	1	0.38065	Bmb003937	1.00E-24
sw22045	BGIBMGA013442	0.5464	0.9625	0.58535	0.38065	No hits found	
sw11376	BGIBMGA011250	0.9746	1.0696	1.08905	0.3803	1.00E-87	gi 6946695 emb CAB72316.1 Wee1-like CDK Tyrosine kinase [Daphnia pulex]
sw13878	BGIBMGA004453	0.9184	1.06425	1.06065	0.38025	e-110	gi 76626083 ref XP_870049.1 PREDICTED: similar to Eyes absent homolog 4 isoform 2 [Bos taurus]
sw17684	BGIBMGA000623	1.73295	0.91525	0.9173	0.3795	0	gi 18700459 dbj BAB85197.1 Titin-like protein [Bombyx mori]
sw01589	BGIBMGA011363	1.0359	0.931	0.94325	0.3787	Bmb024438	1.00E-06
sw10856	BGIBMGA007876	1.5477	1.15995	1.1587	0.37865	7.00E-62	gi 76650863 ref XP_598872.2 PREDICTED: similar to Choline transporter-like protein 4 isoform 1 [Bos taurus]
sw10110	BGIBMGA007179	0.9661	1.03925	1.03565	0.37845	4.00E-16	gi 48109567 ref XP_393109.1 PREDICTED: similar to ENSANGP00000018996 [Apis mellifera]
sw11629	BGIBMGA005718	1	1	1	0.3784	5.00E-19	gi 28194049 gb AAO33382.1 dihydropyrimidine amidohydrolase [Drosophila melanogaster]
sw01251	BGIBMGA001988	1.67805	1.49135	0.837	0.3778	2.00E-07	gi 60678129 gb AAX33571.1 HL05615p [Drosophila melanogaster]
sw00221	BGIBMGA001218	1.10285	1.16575	1.2889	0.37695	0	gi 73983932 ref XP_533297.2 PREDICTED: similar to Heat shock 70 kDa protein 4L (Osmotic stress protein 94) (Heat shock 70-related protein APG-1) isoform 1 [Canis familiaris]
sw09572	BGIBMGA003642	2.0094	0.51615	1.26415	0.3768	No hits found	
sw09593	BGIBMGA005106	1.1474	1.2813	1.2933	0.3766	Bmb032355	1.00E-21
sw00225	BGIBMGA004379	1.05635	1.07265	1.2847	0.37635	1.00E-58	gi 28972560 dbj BAC65696.1 mKIAA0979 protein [Mus musculus]
sw20591	BGIBMGA001349	1	1	1	0.3763	Bmb026435	9.00E-44
sw16021	BGIBMGA009599	1.41965	0.9777	0.9311	0.3759	Bmb037573	No hits found
sw17845	BGIBMGA001776	1	1	1	0.3754	1.00E-55	gi 72092399 ref XP_790598.1 PREDICTED: similar to helitron 3 helitron-like transposon replicase/helicase/endonuclease [Strongylocentrotus purpuratus]
sw20954	BGIBMGA006808	1	1	1	0.3753	2.00E-29	gi 72090091 ref XP_788672.1 PREDICTED: similar to MondoA [Strongylocentrotus purpuratus]

sw01299	BGIBMGA004403	0.0916	0.43405	0.2457	0.37515	e-150	gi 10907 emb CAA38531.1 30K protein [Bombyx mori] Low molecular mass 30 kDa lipoprotein 21G1 precursor
sw18885	BGIBMGA007764	0.99015	0.9735	1.01455	0.3748	8.00E-05	gi 45382883 ref NP_990840.1 fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) [Gallus gallus] Tyrosine kinase receptor CEK2 precursor cek2 protein
sw06565	BGIBMGA009417	1	1	1	0.3746	5.00E-06	gi 55770707 ref XP_550395.1 putative MAR binding filament-like protein 1 [Oryza sativa (japonica cultivar-group)] putative MAR binding filament-like protein 1 [Oryza sativa (japonica cultivar-group)]
sw00708	BGIBMGA007315	1	1	1	0.37435	e-154	gi 76652847 ref XP_592719.2 PREDICTED: similar to ubiquitin specific protease 7 (herpes virus-associated) [Bos taurus]
sw20332	BGIBMGA011069	1	1	1	0.37355	No hits found	
sw17956	BGIBMGA005889	1.03045	1.3253	1.3701	0.37345	No hits found	
sw19250	BGIBMGA008060	1.31375	1.03955	1.41085	0.3731	0	gi 27818925 gb AAO23562.1 aminopeptidase N4 [Helicoverpa armigera]
sw18954	BGIBMGA014270	1.10395	0.94285	0.82785	0.3728	2.00E-54	gi 54643658 gb EAL32401.1 GA15301-PA [Drosophila pseudoobscura]
sw03783	BGIBMGA013475	1.2286	1	1	0.37235	2.00E-05	gi 48137797 ref XP_396816.1 PREDICTED: similar to inhibitory protein SMAD6 [Apis mellifera]
sw03891	BGIBMGA001730	0.9337	1.1112	1.2749	0.37215	4.00E-57	gi 1362608 pir A53909 gelsolin, secreted form precursor - fruit fly (Drosophila melanogaster) The biology of this fly protein has not yet been explored. Its identification as a secretory gelsolin is based on sequence comparison to the vertebrate
sw01846	BGIBMGA005135	0.56165	0.61475	0.73475	0.372	Bmb028716	2.00E-32
sw09024	BGIBMGA005181	1.3062	1.11325	1.0238	0.37195	2.00E-22	gi 88698232 gb AAY87162.2 trehalose 6-phosphate synthase [Helicoverpa armigera]
sw14296	BGIBMGA008429	0.83215	0.9954	1	0.37065	2.00E-62	gi 83015999 ref XP_917609.1 PREDICTED: similar to Zinc finger protein Kr18 (HKr18) [Mus musculus]
sw17710	BGIBMGA009443	1	1	1	0.3703	Bmb041188	2.00E-38
sw14924	BGIBMGA001847	1	0.98715	1	0.3701	4.00E-08	gi 73987473 ref XP_542180.2 PREDICTED: similar to nicalin [Canis familiaris]
sw13752	BGIBMGA003185	1	1	1	0.37005	Bmb020551	1.00E-21
sw04261	BGIBMGA008018	1	1.30745	1.61635	0.3698	Bmb030094	2.00E-77
sw14339	BGIBMGA005549	1.03755	0.98885	1.01945	0.3695	Bmb024531	1.00E-17
sw20886	BGIBMGA013812	0.4982	0.691	0.68365	0.3694	e-121	gi 24416622 db BAC22502.1 putative pheromone-degrading enzyme [Antheraea polyphemus]
sw22364	BGIBMGA013477	1	1	1	0.3694	6.00E-60	gi 72133877 ref XP_788695.1 PREDICTED: similar to predicted CDS, reverse transcriptase family member (10881) [Strongylocentrotus purpuratus]
sw16197	BGIBMGA010698	0.80675	0.7929	0.9112	0.36905	No hits found	
sw07824	BGIBMGA007568	1	1	1	0.3688	5.00E-27	gi 15430244 gb AAK98515.1 N-acetylglucosamine-6-sulfatase [Coturnix coturnix] Extracellular sulfatase Sulf-1 precursor (QSulf1)
sw12066	BGIBMGA000798	1	1	1	0.3685	1.00E-29	gi 25012554 gb AAN71378.1 RE36563p [Drosophila melanogaster]
sw13097	BGIBMGA012783	1	1	1	0.3682	3.00E-19	gi 47124478 gb AAH70104.1 KIAA1841 protein [Homo sapiens] KIAA1841 protein [Homo sapiens]
sw05336	BGIBMGA006870	1.5128	1.1495	1.63635	0.36805	9.00E-05	gi 54643010 gb EAL31754.1 GA13991-PA [Drosophila pseudoobscura]
sw14492	BGIBMGA007569	1.44765	0.87255	1	0.3662	2.00E-90	gi 21429186 gb AAM50312.1 SD04414p [Drosophila melanogaster]
sw01150	BGIBMGA009681	1.14395	0.96455	0.89145	0.36615	6.00E-10	gi 28317019 gb AAO39529.1 RE22259p [Drosophila melanogaster]
sw05071	BGIBMGA003428	1.0397	0.96475	1.4743	0.36595	Bmb002410	0

sw17641	BGIBMGA011223	1	1	1	0.3658	2.00E-26	gi 45382859 ref NP_990836.1 acetyl-Coenzyme A carboxylase alpha [Gallus gallus] Acetyl-CoA carboxylase (ACC) [Includes: Biotin carboxylase] acetyl-CoA carboxylase
sw10635	BGIBMGA008025	0.94345	0.9105	1.2705	0.3654	9.00E-80	gi 32141382 sp Q9UBL3 ASH2L_HUMAN Set1/Ash2 histone methyltransferase complex subunit ASH2 (ASH2-like protein) similar to Drosophila ash2 gene [Homo sapiens] similar to Drosophila ash2 [Homo sapiens]
sw12375	BGIBMGA005279	1.0634	0.98885	1.5038	0.36505	0	gi 21464370 gb AAM51988.1 RE10344p [Drosophila melanogaster]
sw03379	BGIBMGA006518	0.7941	0.67895	0.77895	0.3648	e-143	gi 66513288 ref XP_392481.2 PREDICTED: similar to peroxinectin [Apis mellifera]
sw12753	BGIBMGA000950	1.23195	1.05465	1.1842	0.3648	0	gi 50745998 ref XP_420332.1 PREDICTED: similar to THO complex subunit 2 (Tho2) [Gallus gallus]
sw05439	BGIBMGA013437	1	1	1	0.36405	2.00E-43	gi 5052592 gb AAD38626.1 BcDNA.GH08773 [Drosophila melanogaster]
sw18089	BGIBMGA008568	0.7759	1.1345	1.05245	0.364	Bmb036359	5.00E-08
sw19870	BGIBMGA002295	1	1	1	0.3637	9.00E-32	gi 25012968 gb AAN71569.1 RH35990p [Drosophila melanogaster]
sw09202	BGIBMGA004107	1	1	1	0.3636	2.00E-36	gi 40538865 ref NP_954889.1 cAMP-specific cyclic nucleotide phosphodiesterase PDE8 [Rattus norvegicus] cAMP-specific cyclic nucleotide phosphodiesterase PDE8 [Rattus norvegicus]
sw12398	BGIBMGA013328	0.6684	1.3033	2.05725	0.36335	e-106	gi 50417388 gb AAH77133.1 Staphylococcal nuclease domain containing 1 [Danio rerio]
sw11655	BGIBMGA009062	0.97215	0.98715	0.9721	0.36235	9.00E-11	gi 25013142 gb AAN71684.1 SD18148p [Drosophila melanogaster]
sw06073	BGIBMGA011882	1	1	1	0.36215	No hits found	
sw18055	BGIBMGA006767	1.2769	1.1886	1.1233	0.3621	Bmb029038	e-123
sw06122	BGIBMGA013717	0.73255	0.86025	1.0664	0.36135	Bmb020986	e-103
sw22552	BGIBMGA003575	0.7604	0.85055	0.5712	0.36	No hits found	
sw14149	BGIBMGA005292	1.1142	0.95385	1.09055	0.35935	Bmb023143	2.00E-34
sw08784	BGIBMGA010377	1.17655	1.02225	0.9609	0.35835	0	gi 2282473 dbj BAA21640.1 xanthine dehydrogenase [Bombyx mori]
sw03803	BGIBMGA011362	1	1	1	0.358	1.00E-19	gi 24585877 ref NP_724424.1 scarface CG11066-PA, isoform A [Drosophila melanogaster] scarface CG11066-PB, isoform B [Drosophila melanogaster] GH05918p [Drosophila melanogaster] CG11066-PB, isoform B
sw19927	BGIBMGA012507	1.0925	1.3935	1.3543	0.3579	Bmb039369	4.00E-08
sw13968	BGIBMGA005226	0.2331	0.51245	0.20095	0.35755	9.00E-48	gi 73955036 ref XP_853231.1 PREDICTED: similar to ATP-binding cassette, sub-family G, member 4 [Canis familiaris]
sw09217	BGIBMGA000630	1	1	1	0.35705	5.00E-82	gi 76613294 ref XP_878881.1 PREDICTED: similar to WD-repeat protein 47 isoform 3 [Bos taurus]
sw11275	BGIBMGA014206	1.6095	1.36905	1.28195	0.3567	1.00E-42	gi 24662101 ref NP_652439.1 dpr6 CG14162-PA [Drosophila melanogaster] LD13525p [Drosophila melanogaster] CG14162-PA [Drosophila melanogaster]
sw14337	BGIBMGA012195	1	1	1	0.35585	4.00E-06	gi 68366904 ref XP_687110.1 PREDICTED: similar to adenosine deaminase [Danio rerio]
sw05552	BGIBMGA010602	1	1	1	0.3556	0	gi 66506280 ref XP_394455.2 PREDICTED: similar to Protein KIAA0274 [Apis mellifera]
sw18675	BGIBMGA001723	0.19595	0.648	0.4237	0.35555	6.00E-33	gi 82950923 ref XP_898519.1 PREDICTED: similar to zinc finger protein 709 [Mus musculus]
sw14618	BGIBMGA001540	1	1	1	0.3555	0	gi 76620868 ref XP_612154.2 PREDICTED: similar to regulator of nonsense transcripts 1 [Bos taurus]
sw05220	BGIBMGA008017	1.68155	1.35665	1.76995	0.3552	0	gi 3402300 dbj BAA32140.1 aminopeptidase N [Bombyx mori]
sw17594	BGIBMGA013548	0.76825	0.91825	1.05425	0.3549	Bmb011738	3.00E-84

sw21343	BGIBMGA014532	1	1	1	0.3548	2.00E-21	gi 62642463 ref XP_219988.3 PREDICTED: similar to novel protein [Rattus norvegicus]
sw01505	BGIBMGA010999	0.84785	1.33385	1	0.3542	3.00E-25	gi 72172673 ref XP_780956.1 PREDICTED: similar to transmembrane protein 39a [Strongylocentrotus purpuratus]
sw15513	BGIBMGA005105	1	1	1	0.3539	Bmb033312	No hits found
sw11530	BGIBMGA012781	1	1	1	0.35355	2.00E-26	gi 66555036 ref XP_393093.2 PREDICTED: similar to ENSANGP00000013872 [Apis mellifera]
sw22430	BGIBMGA009441	1	1	1	0.35225	Bmb042980	6.00E-22
sw11624	BGIBMGA003720	1.42455	1.4187	0.70535	0.352	2.00E-08	gi 68367284 ref XP_707274.1 PREDICTED: similar to sphingomyelin phosphodiesterase 1, acid lysosomal isoform 2 precursor isoform 3 [Danio rerio]
sw18171	BGIBMGA004550	0.8582	1.04685	1.28255	0.35195	Bmb003499	e-118
sw18944	BGIBMGA000809	1	1	1	0.35185	Bmb014713	2.00E-32
sw15731	BGIBMGA000204	0.9138	1.1025	1.1066	0.35155	Bmb035060	2.00E-22
sw13734	BGIBMGA011364	0.88665	1.00215	1.04925	0.3496	Bmb020467	8.00E-63
sw20725	BGIBMGA007679	1	0.77665	1	0.3492	7.00E-33	gi 66546388 ref XP_392296.2 PREDICTED: similar to GA11585-PA [Apis mellifera]
sw11965	BGIBMGA005177	1.2406	1.03925	1.2109	0.3488	2.00E-91	gi 87248575 gb ABD36340.1 PTB-associated splicing factor [Bombyx mori]
sw02650	BGIBMGA004178	1	1.01745	1.0318	0.34835	Bmb046489	No hits found
sw20256	BGIBMGA011405	1	1	1	0.34785	0	gi 55645159 ref XP_511395.1 PREDICTED: similar to neurofibromin; Neurofibromin (neurofibromatosis, type I) [Pan troglodytes]
sw09418	BGIBMGA002695	1.0928	1.06965	1.0503	0.34765	No hits found	
sw01405	BGIBMGA009563	1.0599	1.0825	0.9961	0.3473	3.00E-39	gi 76654987 ref XP_879917.1 PREDICTED: similar to cyclin M2 isoform 2 isoform 9 [Bos taurus]
sw12458	BGIBMGA006506	1	1	1.23695	0.3472	3.00E-62	gi 28380977 gb AAO41456.1 RE20724p [Drosophila melanogaster]
sw03870	BGIBMGA000638	1	1	1	0.3471	1.00E-38	gi 47155829 gb AAT11862.1 iroquois-like protein [Tribolium castaneum]
sw17926	BGIBMGA008304	1.07205	1.06445	1.12855	0.347	Bmb004111	e-125
sw09265	BGIBMGA006906	1	1	1	0.3468	Bmb026874	2.00E-15
sw02555	BGIBMGA000866	1.671	1.03705	1.29415	0.3467	Bmb043733	1.00E-07
sw07171	BGIBMGA011207	1.2207	0.81085	1.02685	0.3464	Bmb045644	1.00E-13
sw15971	BGIBMGA003037	1.4468	1.04835	1.2142	0.34585	7.00E-37	gi 89243264 gb ABD64784.1 Bent [Drosophila virilis]
sw03125	BGIBMGA010725	0.74075	1.00915	1.26135	0.3451	e-104	gi 72167287 ref XP_796805.1 PREDICTED: similar to Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Strongylocentrotus purpuratus]
sw22078	BGIBMGA008083	1	1	1	0.34495	8.00E-14	gi 72043882 ref XP_793468.1 PREDICTED: similar to zn-finger, CCHC type and RNA-directed DNA polymerase and Integrase, catalytic domain containing protein (3J949) [Strongylocentrotus purpuratus]
sw12973	BGIBMGA003926	0.6738	1.2856	0.84715	0.3448	8.00E-95	gi 5759228 gb AAD51036.1 cytochrome P450 [Manduca sexta]
sw06028	BGIBMGA005338	1	1	1	0.3443	Bmb019370	4.00E-33
sw20460	BGIBMGA001272	1.5142	1.5026	1.83055	0.34425	Bmb008625	6.00E-81

sw09820	BGIBMGA012753	1.0547	1.00155	1.46245	0.34335	0	gi 431944 emb CAA53948.1 Ppk 98; a protein kinase [Sus scrofa] Endoplasmin precursor (94 kDa glucose-regulated protein) (GRP94) (GP96 homolog) (98 kDa protein kinase) (PPK 98) (ppk98)
sw20435	BGIBMGA013978	1	1	1	0.3428	4.00E-19	gi 8926400 gb AAF81829.1 DISCS LOST; dlt [Drosophila melanogaster]
sw03965	BGIBMGA005182	1	1	1	0.3426	0	gi 88698232 gb AAY87162.2 trehalose 6-phosphate synthase [Helicoverpa armigera]
sw00653	BGIBMGA012048	0.70625	0.7912	0.70135	0.341	1.00E-10	gi 1209648 gb AAC47002.1 protein tyrosine phosphatase DLAR protein tyrosine phosphatase (DLAR) precursor
sw20095	BGIBMGA008834	1.1235	1.1027	0.852	0.341	No hits found	
sw22610	BGIBMGA000379	0.9618	0.868	0.92515	0.3406	2.00E-21	gi 68398837 ref XP_697912.1 PREDICTED: similar to Zinc finger protein 184 (Kruppel-like) [Danio rerio]
sw17697	BGIBMGA004431	1	1	1	0.34035	Bmb036890	2.00E-21
sw04820	BGIBMGA012054	1.2277	1.18575	0.88915	0.33985	Bmb048235	2.00E-15
sw20255	BGIBMGA001126	0.48865	0.96765	1.0703	0.33975	2.00E-86	gi 10946670 ref NP_067325.1 choroideremia-like [Mus musculus] rab escort protein-2 [Mus musculus]
sw02441	BGIBMGA009109	1	1	1	0.3397	No hits found	
sw07527	BGIBMGA001794	1.4797	1.23285	1	0.3393	2.00E-06	gi 66562084 ref XP_395379.2 PREDICTED: similar to ENSANGP00000010681 [Apis mellifera]
sw11733	BGIBMGA001790	0.75355	0.85565	0.9777	0.3393	Bmb007728	2.00E-23
sw13774	BGIBMGA002092	0.34125	0.77245	0.38855	0.339	3.00E-18	gi 47086753 ref NP_997808.1 solute carrier family 35, member C2 [Danio rerio] Ovarian cancer overexpressed 1 [Danio rerio]
sw10718	BGIBMGA011333	1	1	1	0.3386	4.00E-14	gi 51471144 gb AAU04329.1 transformed mouse 3T3 cell double minute 2 [Mus caroli]
sw12815	BGIBMGA001579	1	1	1	0.3385	e-167	gi 4505343 ref NP_002477.1 nuclear cap binding protein subunit 1, 80kDa [Homo sapiens] nuclear cap binding protein subunit 1, 80kDa [Homo sapiens] nuclear cap binding protein subunit 1, 80kDa [Homo sapiens] 80 kDa nuclear cap-bindin
sw01427	BGIBMGA008871	1.08125	0.93175	1.33025	0.3377	1.00E-58	gi 55242794 gb EAA07084.3 ENSANGP00000016038 [Anopheles gambiae str. PEST] ENSANGP00000016038 [Anopheles gambiae str. PEST]
sw11321	BGIBMGA010911	1	1	1	0.3371	No hits found	
sw17936	BGIBMGA000672	1.323	1.14345	1.3928	0.3359	0	gi 41058938 gb AAR98861.1 mitochondrial citrate synthase precursor [Xiphias gladius]
sw14253	BGIBMGA005736	1.45445	1.05765	1.0525	0.3354	4.00E-91	gi 55244645 gb EAA05197.3 ENSANGP00000017954 [Anopheles gambiae str. PEST] ENSANGP00000017954 [Anopheles gambiae str. PEST]
sw12244	BGIBMGA007848	1.13745	1.03395	1.0081	0.3353	0	gi 73967590 ref XP_857927.1 PREDICTED: similar to sarcosine dehydrogenase isoform 3 [Canis familiaris]
sw11643	BGIBMGA002894	1.14955	1.0263	1.09235	0.33455	0	gi 5764409 gb AAD51291.1 DGP-1 protein [Drosophila melanogaster]
sw20970	BGIBMGA006959	0.8505	0.84895	0.92085	0.33395	0	gi 399056 sp Q02453 ARM_MUSDO Armadillo segment polarity protein armadillo protein
sw08517	BGIBMGA011119	0.43055	0.7939	0.79055	0.33375	No hits found	
sw13580	BGIBMGA007512	0.25805	0.7325	0.55705	0.33345	e-168	gi 790585 gb AAA85850.1 UDP-glucose:glycoprotein glucosyltransferase precursor
sw13955	BGIBMGA004691	1.3593	1.2494	1.0337	0.33345	1.00E-57	gi 22138110 gb AAM93435.1 PARP-E protein [Drosophila melanogaster]
sw06062	BGIBMGA008185	1	1	1	0.3333	3.00E-43	gi 73961507 ref XP_854829.1 PREDICTED: similar to F-box only protein 28 [Canis familiaris]
sw21674	BGIBMGA011334	1.2692	1.09745	0.90575	0.3332	2.00E-34	gi 66566395 ref XP_623926.1 PREDICTED: similar to GA18544-PA [Apis mellifera]
sw11208	BGIBMGA012248	1	1	1	0.33265	No hits found	

sw17606	BGIBMGA000509	1	1	1	0.33255	3.00E-05	gi 66546685 ref XP_395583.2 PREDICTED: similar to polyhomeotic 3 [Apis mellifera]
sw07932	BGIBMGA000147	1	1	1	0.3322	2.00E-25	gi 2467112 emb CAA75228.1 Lola-like protein [Drosophila hydei]
sw11253	BGIBMGA003971	1	1	1	0.3316	1.00E-25	gi 76154169 gb AAX25663.2 SJCHGC08483 protein [Schistosoma japonicum]
sw17651	BGIBMGA010274	0.0536	0.648	0.6212	0.33155	Bmb023886	2.00E-09
sw04234	BGIBMGA014531	1	1	1	0.33125	No hits found	
sw19907	BGIBMGA007184	1.676	0.9771	0.79115	0.33095	No hits found	
sw13690	BGIBMGA012030	0.65465	1.2146	1.1692	0.3301	No hits found	
sw19049	BGIBMGA002618	1.2562	1.0298	1.2259	0.3293	2.00E-28	gi 7682380 gb AAF67245.1 gp150 [Drosophila virilis]
sw05088	BGIBMGA000120	1.0096	1.095	1.1647	0.32805	e-123	gi 55238955 gb EAA10832.2 ENSANGP00000017705 [Anopheles gambiae str. PEST] ENSANGP00000017705 [Anopheles gambiae str. PEST]
sw07090	BGIBMGA012702	1	1	1	0.32765	Bmb042755	4.00E-31
sw19748	BGIBMGA004714	1	1	1	0.32675	1.00E-14	gi 72014020 ref XP_783244.1 PREDICTED: similar to cytochrome P450, family 4, subfamily v, polypeptide 2 [Strongylocentrotus purpuratus]
sw22874	BGIBMGA005130	1.16045	1.27945	0.9834	0.3263	8.00E-06	gi 33354081 dbj BAC81124.1 L1 cell adhesion molecule [Pongo pygmaeus]
sw09307	BGIBMGA008931	0.34445	0.65835	0.4997	0.32625	No hits found	
sw16006	BGIBMGA013378	1.0815	1.18605	0.81585	0.32615	Bmb037438	7.00E-38
sw00905	BGIBMGA007738	1	1	1	0.32605	3.00E-89	gi 76631800 ref XP_593336.2 PREDICTED: similar to ATP-binding cassette, sub-family C, member 4 [Bos taurus]
sw12281	BGIBMGA007633	1.60215	1.64975	2.17665	0.3259	6.00E-06	gi 73967692 ref XP_537809.2 PREDICTED: similar to adenylate kinase 3 isoform 1 [Canis familiaris]
sw14927	BGIBMGA008268	0.55355	0.57775	0.68505	0.3246	Bmb028811	e-152
sw20305	BGIBMGA004592	1	1.01145	0.9083	0.32445	4.00E-31	gi 50752056 ref XP_422633.1 PREDICTED: similar to calsyntenin-2 [Gallus gallus]
sw11598	BGIBMGA001132	0.8814	0.827	0.89765	0.3237	1.00E-67	gi 551090 gb AAA50238.1 DNA-binding protein
sw11048	BGIBMGA004712	1	1	1	0.32245	1.00E-08	gi 27316716 gb AAO05891.1 streptococcal hemagglutinin protein [Staphylococcus epidermidis ATCC 12228] streptococcal hemagglutinin protein [Staphylococcus epidermidis ATCC 12228]
sw15141	BGIBMGA001012	1	1	1	0.32245	2.00E-58	gi 33880192 gb AAH50772.2 Testis-specific serine kinase 1 [Mus musculus]
sw02984	BGIBMGA005477	1.16195	0.90025	1.0779	0.3224	0	gi 440144 emb CAA52155.1 integrin [Drosophila melanogaster]
sw11166	BGIBMGA003938	1	1	1	0.32105	Bmb004077	0
sw06172	BGIBMGA006559	1	1.1237	1	0.32095	4.00E-30	gi 76654169 ref XP_618212.2 PREDICTED: similar to neural stem cell-derived dendrite regulator [Bos taurus]
sw20313	BGIBMGA001183	1	1	1	0.32075	Bmb026077	2.00E-71
sw18783	BGIBMGA000528	1.1408	1.06255	1.2067	0.3204	No hits found	
sw20096	BGIBMGA000826	0.9601	0.93215	0.87915	0.32035	7.00E-38	gi 59939802 gb AAQ62963.2 transferrin [Romalea microptera]
sw02978	BGIBMGA004568	1	1	1	0.3198	e-109	gi 28972886 dbj BAC65859.1 mKIAA3002 protein [Mus musculus]

sw07109	BGIBMGA013544	1	1	1	0.3193	Bmb043396	2.00E-05
sw04705	BGIBMGA004786	1	1	1	0.31905	Bmb043440	6.00E-52
sw20203	BGIBMGA014105	1.4459	1.1992	1.67095	0.31885	3.00E-59	gi 3004821 gb AAC39088.1 putative inorganic phosphate cotransporter [Drosophila ananassae] Putative inorganic phosphate cotransporter
sw08603	BGIBMGA002043	0.44145	1.2861	0.6568	0.3188	No hits found	
sw12171	BGIBMGA012794	0.2108	0.57345	0.4372	0.3188	1.00E-26	gi 5815245 gb AAD52614.1 SANT domain protein SMRTER [Drosophila melanogaster]
sw15024	BGIBMGA000689	1.0561	1.05	1.2622	0.3188	Bmb029529	e-178
sw06336	BGIBMGA009138	0.8087	1.14735	1	0.3187	5.00E-26	gi 62897749 dbj BAD96814.1 aminopeptidase-like 1 variant [Homo sapiens]
sw00477	BGIBMGA010943	0.95155	1.0448	0.8655	0.31715	2.00E-76	gi 87248265 gb ABD36185.1 ADP-ribosylation factor-like protein [Bombyx mori]
sw11389	BGIBMGA008251	1.3557	1.37055	1.77125	0.31695	No hits found	
sw20748	BGIBMGA011671	1	1	1	0.3168	4.00E-21	gi 68364550 ref XP_690945.1 PREDICTED: similar to senataxin; DEAxQ-box helicase; tRNA splicing endonuclease regulator 1, partial [Danio rerio]
sw20474	BGIBMGA000850	1.19925	0.9267	1.24305	0.31615	3.00E-10	gi 41235797 ref NP_958738.1 SH3/ankyrin domain gene 2 isoform a [Rattus norvegicus] Shank2E [Rattus norvegicus]
sw00648	BGIBMGA007835	1.0709	1.1118	1.1215	0.3145	2.00E-79	gi 73988919 ref XP_542530.2 PREDICTED: similar to neuron navigator 2 isoform 2 [Canis familiaris]
sw22969	BGIBMGA011427	1	1	1	0.3142	No hits found	
sw12469	BGIBMGA003472	1	1	1	0.31385	e-168	gi 2547046 dbj BAA22868.1 bHLH-PAS transcription factor [Drosophila melanogaster]
sw15709	BGIBMGA006226	1	1	1	0.31385	Bmb034922	e-169
sw15794	BGIBMGA001836	0.7317	0.82395	0.69925	0.31375	1.00E-70	gi 1705995 sp P49747 COMP_HUMAN Cartilage oligomeric matrix protein precursor (COMP) cartilage oligomeric matrix protein [Homo sapiens] matrix protein
sw18498	BGIBMGA003458	1.2558	1.17535	1.21275	0.31365	Bmb037077	3.00E-61
sw08951	BGIBMGA009402	1	1	1.4617	0.313	0	gi 55243234 gb EAA06289.2 ENSANGP00000017306 [Anopheles gambiae str. PEST] ENSANGP00000017306 [Anopheles gambiae str. PEST]
sw14920	BGIBMGA012759	1.14825	0.93115	0.9319	0.31275	No hits found	
sw00665	BGIBMGA002139	0.3204	0.67655	0.5236	0.31255	No hits found	
sw02031	BGIBMGA002544	0.8898	0.8823	1.1425	0.31205	e-121	gi 473595 gb AAA19857.1 moesin/ezrin/radixin homolog
sw15086	BGIBMGA004113	1	1	1	0.3108	No hits found	
sw20167	BGIBMGA013819	1.24005	1.02785	1.06105	0.30995	No hits found	
sw12513	BGIBMGA003789	1	1	1	0.308	e-153	gi 1373390 gb AAB05596.1 SH2/SH3 adaptor protein
sw06051	BGIBMGA001271	1.029	0.95115	1.04605	0.3076	No hits found	
sw05711	BGIBMGA006106	1	1	1	0.30685	2.00E-11	gi 68440173 ref XP_683330.1 PREDICTED: similar to BTB/POZ domain containing protein 3 [Danio rerio]
sw13179	BGIBMGA008337	1.0928	0.95285	1.0602	0.30675	1.00E-33	gi 55640947 ref XP_510026.1 PREDICTED: similar to Butyrate response factor 1 (TIS11B protein) (EGF-response factor 1) (ERF-1) [Pan troglodytes]
sw19370	BGIBMGA010289	1	1	1	0.30655	1.00E-57	gi 24645837 ref NP_652625.2 Ugt86Dc CG4739-PA [Drosophila melanogaster] CG4739-PA [Drosophila melanogaster]

sw06003	BGIBMGA010323	1	1	1	0.30595	7.00E-07	gi 54637562 gb EAL26964.1 GA14328-PA [Drosophila pseudoobscura]
sw12898	BGIBMGA014227	1.33735	1.163	1.43615	0.30365	0	gi 28574239 ref NP_523587.4 Myosin heavy chain CG17927-PH, isoform H [Drosophila melanogaster] CG17927-PH, isoform H [Drosophila melanogaster]
sw18813	BGIBMGA011052	1.1088	1.01315	1.23915	0.3033	No hits found	
sw10899	BGIBMGA010644	1.1544	0.93765	1.09765	0.3031	0	gi 4165140 gb AAD08704.1 PIWI [Drosophila melanogaster]
sw04254	BGIBMGA010111	1	0.95585	1	0.303	1.00E-12	gi 27819785 gb AAO24941.1 RE65015p [Drosophila melanogaster]
sw19986	BGIBMGA003574	0.7738	0.7956	0.58085	0.30245	6.00E-80	gi 61554518 gb AAX46572.1 atlastin [Bos taurus]
sw20339	BGIBMGA002719	0.7915	0.8951	0.7901	0.30245	Bmb032487	No hits found
sw07497	BGIBMGA002882	1	1	1	0.302	6.00E-12	gi 29145087 gb AAH49104.1 Oxoglutarate dehydrogenase (lipoamide) [Mus musculus] 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor (Alpha-ketoglutarate dehydrogenase)
sw19762	BGIBMGA005738	1.24585	1.1023	1.1462	0.30125	7.00E-38	gi 72004925 ref XP_781695.1 PREDICTED: similar to ankyrin 3, epithelial isoform a [Strongylocentrotus purpuratus]
sw12943	BGIBMGA001971	0.13045	0.68745	0.3153	0.3002	No hits found	
sw01980	BGIBMGA014369	1.6899	1.00735	1.31545	0.29835	8.00E-05	gi 54641695 gb EAL30445.1 GA21796-PA [Drosophila pseudoobscura]
sw10995	BGIBMGA011993	1	1	1	0.2975	1.00E-14	gi 50740576 ref XP_419499.1 PREDICTED: similar to GTP binding protein 2 [Gallus gallus]
sw16843	BGIBMGA007680	1	1	1	0.29735	Bmb048080	No hits found
sw19701	BGIBMGA000132	0.68715	0.71415	0.9058	0.2972	5.00E-07	gi 76657688 ref XP_591861.2 PREDICTED: similar to alpha glucosidase II alpha subunit isoform 2 [Bos taurus]
sw15347	BGIBMGA007924	1	1	1	0.2963	Bmb031972	e-144
sw16391	BGIBMGA010699	0.82455	0.92135	0.9053	0.29565	7.00E-06	gi 72098908 ref XP_799322.1 PREDICTED: similar to ileal sodium/bile acid cotransporter (Ileal Na(+)/bile acid cotransporter) (Na(+)-dependent ileal bile acid transporter) (Ileal sodium-dependent bile acid transporter) (ISBT) (Sodium/tauroch
sw10866	BGIBMGA003411	1.2389	0.83	0.8238	0.29525	1.00E-43	gi 66515966 ref XP_396216.2 PREDICTED: similar to corin [Apis mellifera]
sw10062	BGIBMGA006852	1.1463	1.05665	1.124	0.2951	Bmb041700	1.00E-10
sw08905	BGIBMGA008090	1.3788	0.8599	0.9402	0.29445	No hits found	
sw19810	BGIBMGA014221	1.1467	1.0394	1.01015	0.29445	0	gi 2575865 dbj BAA23126.1 BmP109 [Bombyx mori]
sw18355	BGIBMGA004061	1	1	1	0.2943	0	gi 10801051 dbj BAB16608.1 210kDa protein [Sarcophaga peregrina]
sw19426	BGIBMGA002157	1	1	1	0.2941	4.00E-30	gi 1621281 emb CAA70088.1 GATA-6 protein [Xenopus laevis] GATA-binding factor 6-B (Transcription factor xGATA-6B)
sw12537	BGIBMGA004896	1	1	1	0.2938	7.00E-19	gi 40788939 dbj BAA13442.2 KIAA0013 [Homo sapiens]
sw03215	BGIBMGA005503	0.7993	0.89585	1.12805	0.2933	8.00E-56	gi 3983137 gb AAC83821.1 Lis1 homolog [Drosophila melanogaster]
sw11257	BGIBMGA014069	0.95685	0.98045	1.0687	0.2933	No hits found	
sw11565	BGIBMGA000910	1.2666	0.9709	1.0301	0.2926	5.00E-97	gi 12657593 dbj BAB21565.1 laminin [Bombyx mori]
sw08530	BGIBMGA000639	0.28835	0.64375	0.4299	0.29165	1.00E-36	gi 72049105 ref XP_795008.1 PREDICTED: similar to Iroquois-class homeodomain protein IRX-4 (Iroquois homeobox protein 4) (Homeodomain protein IRXA3) [Strongylocentrotus purpuratus]
sw11595	BGIBMGA010929	1	1	1	0.29095	2.00E-05	gi 24645680 ref NP_524775.1 CG17100-PA [Drosophila melanogaster] CG17100-PA [Drosophila melanogaster]

sw02946	BGIBMGA000622	1.71835	0.92215	1.50265	0.2909	0	gi 22474512 dbj BAC10617.1 KETTIN [Bombyx mori] BMKETTIN [Bombyx mori]
sw17139	BGIBMGA001498	1.06285	1.56295	0.9359	0.2895	2.00E-20	gi 66499643 ref XP_393415.2 PREDICTED: similar to ENSANGP00000012563 [Apis mellifera]
sw12077	BGIBMGA003667	1	0.96715	1	0.28945	e-117	gi 73999471 ref XP_535098.2 PREDICTED: similar to organic anion transporter polypeptide-related protein 4 [Canis familiaris]
sw18008	BGIBMGA002296	0.78025	1.07965	0.94095	0.2894	2.00E-06	gi 25012968 gb AAN71569.1 RH35990p [Drosophila melanogaster]
sw12755	BGIBMGA009101	1.4294	2.06265	1.4761	0.28915	No hits found	
sw20070	BGIBMGA004577	0.9036	1.0255	1.06665	0.2883	2.00E-46	gi 66513968 ref XP_394726.2 PREDICTED: similar to ENSANGP00000015204 [Apis mellifera]
sw04109	BGIBMGA011124	1.31655	1.21995	1.19675	0.2878	3.00E-48	gi 7943 emb CAA48327.1 elg [Drosophila melanogaster] DNA-binding protein D-ELG
sw00950	BGIBMGA003771	1.5056	1.06195	1	0.28755	9.00E-25	gi 37181975 gb AAQ88791.1 LLPL [Homo sapiens] lysophospholipase 3 (lysosomal phospholipase A2) [Homo sapiens] Lysophospholipase 3 (lysosomal phospholipase A2) [Homo sapiens] 1-O-acylceramide synthase precursor (ACS)
sw17939	BGIBMGA000447	1	1	1	0.28705	0	gi 6580808 gb AAF18300.1 N-ethylmaleimide sensitive fusion protein [Manduca sexta]
sw11085	BGIBMGA010939	0.80765	0.97425	0.9136	0.2867	No hits found	
sw16435	BGIBMGA008856	1	1	1	0.28625	4.00E-31	gi 58585102 ref NP_001011581.1 cGMP-dependent protein kinase foraging [Apis mellifera] cGMP-dependent protein kinase foraging [Apis mellifera]
sw20223	BGIBMGA013099	1	0.2221	0.36355	0.2858	6.00E-23	gi 89243283 gb ABD64800.1 Dvir_CG14130 [Drosophila virilis]
sw09808	BGIBMGA011525	1.3254	1.16315	0.8453	0.28515	Bmb036406	2.00E-21
sw08392	BGIBMGA001551	0.9424	0.8965	1.0503	0.28495	e-109	gi 73946504 ref XP_858102.1 PREDICTED: similar to ubiquitin 1 isoform 1 isoform 3 [Canis familiaris]
sw11999	BGIBMGA012308	1.00385	0.83555	1.14115	0.28455	No hits found	
sw21986	BGIBMGA009325	1	1	1	0.28335	8.00E-51	gi 66505065 ref XP_392243.2 PREDICTED: similar to rho-type GTPase-activating protein rhoGAPX-1 [Apis mellifera]
sw01142	BGIBMGA007303	0.2957	1.038	0.61325	0.28315	3.00E-09	gi 57087751 ref XP_546987.1 PREDICTED: similar to Basic helix-loop-helix protein MIST1 (Muscle, intestine and stomach expression 1) [Canis familiaris]
sw13263	BGIBMGA009857	1.08285	1.2173	1	0.28305	5.00E-99	gi 466258 gb AAA19591.1 myosin-IB
sw20505	BGIBMGA000613	1.1651	0.97025	1.3285	0.2823	3.00E-85	gi 10959 emb CAA41557.1 paramyosin [Drosophila melanogaster]
sw17725	BGIBMGA006043	0.8737	0.8671	1	0.28225	e-137	gi 87248413 gb ABD36259.1 stathmin [Bombyx mori]
sw18782	BGIBMGA014600	1	1	1	0.2822	5.00E-47	gi 66521636 ref XP_396241.2 PREDICTED: similar to ENSANGP00000010275, partial [Apis mellifera]
sw01513	BGIBMGA009974	1.21595	0.9889	1.0316	0.28205	Bmb023073	6.00E-81
sw05425	BGIBMGA011984	2.1819	1	1	0.28115	e-115	gi 50753737 ref XP_414111.1 PREDICTED: similar to alanine aminotransferase 2; glutamic-pyruvate transaminase 2 [Gallus gallus]
sw04154	BGIBMGA001570	1.14915	1.3521	0.95105	0.2792	e-141	gi 87248571 gb ABD36338.1 phosphoribosyl pyrophosphate synthetase [Bombyx mori]
sw11956	BGIBMGA004343	0.4774	1.11505	0.72175	0.27885	1.00E-04	gi 48096382 ref XP_392446.1 PREDICTED: similar to death-associated protein [Apis mellifera]
sw14909	BGIBMGA009161	1.36355	1.0846	0.9934	0.27845	No hits found	
sw02464	BGIBMGA010275	1.3635	0.94755	1.23415	0.2765	Bmb041571	No hits found
sw11512	BGIBMGA009962	1	1	1	0.27645	0	gi 66514814 ref XP_394762.2 PREDICTED: similar to CG32498-PO, isoform O [Apis mellifera]

sw20303	BGIBMGA006227	0.8707	1.0601	1.06605	0.27585	e-124	gi 7677032 gb AAF66996.1 timeless [Antheraea pernyi]
sw07785	BGIBMGA003506	1	1	1	0.27545	6.00E-23	gi 48095153 ref XP_392250.1 PREDICTED: similar to PDZ domain containing 3 [Apis mellifera]
sw04404	BGIBMGA012440	0.6825	0.4683	0.6968	0.27515	8.00E-12	gi 66522495 ref XP_393918.2 PREDICTED: similar to subtilisin-related protease SPC3 [Apis mellifera]
sw06057	BGIBMGA010761	1	1	1	0.2751	6.00E-66	gi 28626480 gb AAO49159.1 LD15982p [Drosophila melanogaster]
sw18259	BGIBMGA004852	0.709	1.1294	1.3714	0.275	0	gi 25012545 gb AAN71374.1 RE35250p [Drosophila melanogaster]
sw18818	BGIBMGA012221	1.03895	1.20855	1.3262	0.27485	5.00E-16	gi 34924891 sp Q26643 TRF_SARPE Transferrin precursor transferrin precursor [Sarcophaga peregrina]
sw06018	BGIBMGA002647	1.2126	1.2699	1.11765	0.2744	4.00E-65	gi 87248315 gb ABD36210.1 erythrocyte carbonic anhydrase [Bombyx mori]
sw19955	BGIBMGA012763	1.4839	1.91125	2.0136	0.2737	e-143	gi 46396762 sp Q27451 PRP1_BOMMO Phenoloxidase subunit 1 precursor (Tyrosinase 1) (PO 1) prophenoloxidase subunit 1 [Bombyx mori]
sw10890	BGIBMGA005341	1.1641	1.3672	1.0451	0.2732	No hits found	
sw02334	BGIBMGA007111	0.72595	0.7508	0.7914	0.2714	2.00E-26	gi 1561730 gb AAC47288.1 Dreg-3 protein [Drosophila melanogaster]
sw19471	BGIBMGA013173	1	1	1	0.27105	1.00E-30	gi 68398138 ref XP_684604.1 PREDICTED: similar to ROX protein [Danio rerio]
sw19621	BGIBMGA014011	1	1	1	0.27085	9.00E-30	gi 26190489 gb AAN17506.1 laccase 1 [Manduca sexta]
sw10272	BGIBMGA005876	1	1	1	0.2705	Bmb049073	1.00E-10
sw11770	BGIBMGA000608	1	1	1	0.2701	4.00E-07	gi 44985962 gb AAS54573.1 AGR084Cp [Ashbya gossypii ATCC 10895] AGR084Cp [Eremothecium gossypii]
sw04957	BGIBMGA008292	1	1	1	0.2689	2.00E-33	gi 72008255 ref XP_784488.1 PREDICTED: similar to polyglutamine-containing protein [Strongylocentrotus purpuratus]
sw20523	BGIBMGA000150	1	1	1	0.2688	8.00E-15	gi 72173283 ref XP_791277.1 PREDICTED: similar to reverse transcriptase family member (1F383) [Strongylocentrotus purpuratus]
sw12010	BGIBMGA013537	0.75565	1.64065	1.55565	0.2682	e-128	gi 72083934 ref XP_789316.1 PREDICTED: similar to ubiquitin-activating enzyme E1-domain containing 1 isoform 1, partial [Strongylocentrotus purpuratus]
sw20315	BGIBMGA012740	0.8417	0.76145	0.74415	0.2668	3.00E-63	gi 66513293 ref XP_623940.1 PREDICTED: similar to peroxidase [Apis mellifera]
sw14309	BGIBMGA000391	0.68305	0.78005	0.77265	0.26665	e-146	gi 16877801 gb AAH17135.1 Glycine decarboxylase [Mus musculus] glycine decarboxylase [Mus musculus] Glycine dehydrogenase [decarboxylating], mitochondrial precursor (Glycine decarboxylase) (Glycine cleavage system P-protein)
sw19884	BGIBMGA000223	1.34255	1.3305	1.2446	0.265	1.00E-08	gi 72049850 ref XP_787337.1 PREDICTED: similar to solute carrier family 2, (facilitated glucose transporter), member 8 [Strongylocentrotus purpuratus]
sw15021	BGIBMGA013972	1	1	1.35835	0.2648	4.00E-21	gi 50732950 ref XP_418840.1 PREDICTED: similar to hypothetical protein FLJ22313 [Gallus gallus]
sw20285	BGIBMGA006694	0.96155	1.22285	1.04335	0.2642	3.00E-99	gi 1346296 sp P98092 HMCT_BOMMO Hemocytin precursor (Humoral lectin) humoral lectin prepropeptide [Bombyx mori] hemocytin
sw13346	BGIBMGA007502	0.78355	1.0569	1.41205	0.26415	4.00E-49	gi 50761621 ref XP_424784.1 PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Gallus gallus]
sw05082	BGIBMGA009435	0.7238	0.6165	0.5686	0.26225	5.00E-05	gi 1030731 emb CAA32198.1 polyprotein [Drosophila melanogaster]
sw20514	BGIBMGA003617	1	1	1	0.26215	No hits found	
sw00551	BGIBMGA008989	1.14815	0.90035	1	0.2613	0	gi 77403867 gb ABA81812.1 RE66325p [Drosophila melanogaster]
sw13345	BGIBMGA014441	1.0167	1.0672	1.1973	0.25815	6.00E-86	gi 66556915 ref XP_395006.2 PREDICTED: similar to Expressed sequence AU040829, partial [Apis mellifera]
sw12019	BGIBMGA003830	1	1	1	0.25785	6.00E-10	gi 58255189 gb AAV43426.1 surface protein [Lactobacillus acidophilus NCFM] surface protein [Lactobacillus acidophilus NCFM]

sw16198	BGIBMGA005101	1	1	1	0.25625	0	gi 559307 dbj BAA07523.1 silk gland factor-1 [Bombyx mori] Silk gland factor 1 (SGF-1)
sw05452	BGIBMGA004950	2.3673	1.85645	1.50785	0.2559	0	gi 41016826 sp Q27772 C1TC_SPOFR C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Includes: Methylenetetrahydrofolate dehydrogenase ; Methenyltetrahydrofolate cyclohydrolase ; Formyltetrahydrofolate synthetase
sw00121	BGIBMGA009878	1.20685	0.9554	1.134	0.2554	No hits found	
sw11736	BGIBMGA013626	1	1	1	0.2551	e-100	gi 25013151 gb AAN71688.1 SD20577p [Drosophila melanogaster]
sw19436	BGIBMGA014356	0.4461	0.66635	0.5184	0.2546	4.00E-23	gi 72133877 ref XP_788695.1 PREDICTED: similar to predicted CDS, reverse transcriptase family member (1O881) [Strongylocentrotus purpuratus]
sw05100	BGIBMGA005144	0.9463	0.9797	0.83045	0.2535	Bmb002772	No hits found
sw21022	BGIBMGA001981	1.432	1.1299	1.3161	0.25345	1.00E-45	gi 59807717 gb AAH89375.1 Zswim5 protein [Mus musculus]
sw11640	BGIBMGA013439	0.316	0.6005	0.4431	0.25285	1.00E-09	gi 5052592 gb AAD38626.1 BcDNA.GH08773 [Drosophila melanogaster]
sw15109	BGIBMGA011852	1.04385	0.8361	0.9057	0.25225	Bmb030195	5.00E-27
sw13006	BGIBMGA001466	1	1	0.85855	0.25145	No hits found	
sw09717	BGIBMGA010171	1	1	1	0.2513	Bmb034639	3.00E-44
sw14141	BGIBMGA004984	0.87545	1.11835	1.1674	0.251	1.00E-06	gi 55235760 gb EAA14411.2 ENSANGP00000020885 [Anopheles gambiae str. PEST] ENSANGP00000020885 [Anopheles gambiae str. PEST]
sw05218	BGIBMGA007027	0.94815	0.84935	0.97245	0.2502	0	gi 68370302 ref XP_691456.1 PREDICTED: similar to sperm protein SSP411 [Danio rerio]
sw08786	BGIBMGA011477	1.1328	0.99725	1.12485	0.25005	3.00E-98	gi 77168470 gb ABA63172.1 hexokinase [Culex pipiens quinquefasciatus]
sw15226	BGIBMGA002958	0.73225	0.48955	0.3357	0.2497	Bmb031168	e-116
sw17734	BGIBMGA004806	1.42785	1.09845	1.43305	0.2484	0	gi 82940307 emb CAJ34654.1 chlorophyllide A binding protein precursor [Bombyx mori]
sw11270	BGIBMGA009303	1	1	1	0.24745	8.00E-31	gi 135084 sp P24507 SY63_DISOM Synaptotagmin C (Synaptic vesicle protein O-p65-C) synaptic vesicle protein
sw16267	BGIBMGA010352	0.63845	0.70135	0.82035	0.2468	Bmb039809	1.00E-20
sw20719	BGIBMGA001913	0.64205	0.6944	0.6419	0.24665	4.00E-16	gi 66500529 ref XP_392121.2 PREDICTED: similar to thrombospondin repeat protein 1 [Apis mellifera]
sw07960	BGIBMGA012935	0.9125	0.9697	0.9268	0.2465	0	gi 73966639 ref XP_867220.1 PREDICTED: similar to Clathrin heavy chain 1 (CLH-17) isoform 6 [Canis familiaris]
sw11259	BGIBMGA007783	0.1047	0.62535	0.4015	0.24595	e-148	gi 55236881 gb EAA13239.3 ENSANGP00000017707 [Anopheles gambiae str. PEST] ENSANGP00000017707 [Anopheles gambiae str. PEST]
sw03494	BGIBMGA012388	1.1328	1.12135	1.1253	0.24515	5.00E-87	gi 66510594 ref XP_624428.1 PREDICTED: similar to Zfr protein [Apis mellifera]
sw02003	BGIBMGA003652	1.0545	0.90185	1.11195	0.2447	1.00E-74	gi 66530257 ref XP_396670.2 PREDICTED: similar to nuclear lamin C protein, partial [Apis mellifera]
sw17350	BGIBMGA010471	1.45985	1.0922	1.34195	0.24445	e-135	gi 24417709 gb AAN60442.1 nesprin-1 [Homo sapiens] nesprin 1 longest [Homo sapiens]
sw14078	BGIBMGA009933	1	1	1	0.24425	Bmb022640	2.00E-35
sw14384	BGIBMGA010744	1.16195	1.08415	1.18565	0.24315	1.00E-58	gi 12619290 dbj BAB21529.1 cathepsin B mRNA 3'-untranslated-region-binding protein CBBP [Sarcophaga peregrina]
sw10845	BGIBMGA000424	1.24705	1.2404	1.10325	0.24095	4.00E-65	gi 66526767 ref XP_393136.2 PREDICTED: similar to ENSANGP00000013077 [Apis mellifera]
sw05816	BGIBMGA004752	1	1	1	0.2407	3.00E-37	gi 58396182 ref XP_321723.2 ENSANGP00000015183 [Anopheles gambiae str. PEST] ENSANGP00000015183 [Anopheles gambiae str. PEST]

sw17616	BGIBMGA007089	0.77045	0.85595	0.971	0.24015	Bmb016749	2.00E-71
sw15360	BGIBMGA004992	0.8451	0.8981	1.29	0.2396	1.00E-05	gi 61103060 gb AAX38000.1 hemomucin [Drosophila melanogaster]
sw13635	BGIBMGA001504	1.12	1.12335	1.30395	0.2385	No hits found	
sw07222	BGIBMGA008144	1	1	1	0.23675	No hits found	
sw13143	BGIBMGA013342	1.18895	1.01905	1.02575	0.2365	0	gi 2498144 sp Q25490 APLP_MANSE Apolipophorins precursor [Contains: Apolipophorin-2 (Apolipophorin II) (apoLp-2); Apolipophorin-1 (Apolipophorin I) (apoLp-1)] apolipophorin precursor protein
sw08444	BGIBMGA000612	1.3354	0.9275	1.472	0.23565	e-115	gi 10959 emb CAA41557.1 paramyosin [Drosophila melanogaster]
sw13134	BGIBMGA002930	1.093	1.2911	1.59235	0.23565	No hits found	
sw05530	BGIBMGA008541	0.79265	0.8124	0.719	0.23525	8.00E-46	gi 62858603 ref NP_001016344.1 fasciculation and elongation protein zeta 2 (zygin II) [Xenopus tropicalis] fasciculation and elongation protein zeta 2 (zygin II) [Xenopus tropicalis]
sw06323	BGIBMGA008545	1	0.7348	1	0.2345	2.00E-17	gi 76635459 ref XP_613108.2 PREDICTED: similar to leucine rich repeat containing 35 isoform 1 [Bos taurus]
sw22217	BGIBMGA006419	0.81425	1.0472	1.0895	0.2314	Bmb021298	0
sw06194	BGIBMGA010176	1	1	1	0.2297	No hits found	
sw16793	BGIBMGA011309	1	1	1	0.22775	Bmb047304	No hits found
sw22209	BGIBMGA009523	0.0677	0.1103	0.0681	0.22725	2.00E-87	gi 66551411 ref XP_397170.2 PREDICTED: similar to Probable cytochrome P450 301a1, mitochondrial precursor (CYPCCCIA1) [Apis mellifera]
sw18890	BGIBMGA006878	0.9342	0.92215	0.9817	0.22635	0	gi 157955 gb AAA28714.1 mysospheroid protein
sw01135	BGIBMGA014337	1.53955	1.1553	1.2914	0.22395	e-119	gi 68357106 ref XP_709875.1 PREDICTED: similar to Farsla protein isoform 5 [Danio rerio]
sw13036	BGIBMGA003516	1.1891	1.08965	1.18515	0.22275	1.00E-19	gi 28317136 gb AAD27865.2 LD24380p [Drosophila melanogaster]
sw14074	BGIBMGA011844	0.842	0.88585	0.95495	0.2226	e-139	gi 13775331 gb AAK39152.1 Protein disulfide isomerase protein 2, isoform a [Caenorhabditis elegans] Protein Disulfide Isomerase family member (pdi-2) [Caenorhabditis elegans] Protein disulfide-isomerase 2 precursor (PDI 1)
sw19121	BGIBMGA004808	1	1	1	0.22215	Bmb026871	3.00E-49
sw15337	BGIBMGA014548	1	1	1	0.2221	5.00E-58	gi 35505243 gb AAH57652.1 Moxd1 protein [Mus musculus]
sw00881	BGIBMGA002620	1.34165	1.2698	1.02155	0.22115	2.00E-21	gi 8421 emb CAA34861.1 Ref(2)P protein [Drosophila melanogaster]
sw22831	BGIBMGA001599	1.6685	0.8587	1.07935	0.2205	2.00E-13	gi 55234273 gb EAA00192.2 ENSANGP00000008929 [Anopheles gambiae str. PEST] ENSANGP00000008929 [Anopheles gambiae str. PEST]
sw09738	BGIBMGA014601	1	1	0.62335	0.21655	No hits found	
sw06110	BGIBMGA003681	1	1	1	0.2148	3.00E-40	gi 48097111 ref XP_391844.1 PREDICTED: similar to yes-associated protein 2 [Apis mellifera]
sw16010	BGIBMGA012196	1	1	1	0.21375	5.00E-11	gi 50732285 ref XP_418563.1 PREDICTED: similar to adenosine deaminase, RNA-specific, B2; RNA dependent adenosine deaminase 3; adenosine deaminase 3, RNA dependent [Gallus gallus]
sw19706	BGIBMGA003454	1	1	1	0.21365	0	gi 73948859 ref XP_544234.2 PREDICTED: similar to myosin IIIA [Canis familiaris]
sw13742	BGIBMGA001793	0.05995	0.65895	0.2155	0.2111	1.00E-16	gi 67930197 ref ZP_00523372.1 Protein kinase [Solibacter usitatus Ellin6076] Protein kinase [Solibacter usitatus Ellin6076]
sw22032	BGIBMGA000598	0.38865	1.02975	0.39315	0.2107	No hits found	
sw17590	BGIBMGA003994	1	1	1	0.2101	4.00E-05	gi 66514408 ref XP_394746.2 PREDICTED: similar to CG13643-PA [Apis mellifera]

sw20054	BGIBMGA005531	1	1	1	0.20965	No hits found	
sw14533	BGIBMGA005418	1.12305	1.07145	1.09505	0.20945	9.00E-50	gi 66561019 ref XP_393495.2 PREDICTED: similar to DNA excision repair protein ERCC-6 (Cockayne syndrome protein CSB) [Apis mellifera]
sw18151	BGIBMGA012002	0.03485	0.26765	0.0202	0.20925	No hits found	
sw14501	BGIBMGA003854	1.254	0.72985	0.7266	0.2076	e-106	gi 55236115 gb EAA14378.2 ENSANGP00000014757 [Anopheles gambiae str. PEST] ENSANGP00000014757 [Anopheles gambiae str. PEST]
sw10274	BGIBMGA008051	1	1	1	0.2038	Bmb049080	2.00E-11
sw01062	BGIBMGA003866	1.7359	1.70025	0.72395	0.20305	Bmb015651	0
sw11666	BGIBMGA002961	1.28165	1.24775	1.32565	0.1984	e-122	gi 83033256 gb ABB97082.1 chitin synthase [Ostrinia furnacalis]
sw21834	BGIBMGA000388	1.2504	0.91105	1.15205	0.197	2.00E-26	gi 28380950 gb AAO41442.1 RE39251p [Drosophila melanogaster]
sw07898	BGIBMGA011165	0.09145	0.09495	0.1129	0.19255	Bmb006912	5.00E-07
sw00791	BGIBMGA011479	1.02885	1.0462	0.7668	0.19225	Bmb011517	e-144
sw22899	BGIBMGA004474	1.44295	1.0727	1.3878	0.191	0	gi 82940307 emb CAJ34654.1 chlorophyllide A binding protein precursor [Bombyx mori]
sw07281	BGIBMGA000788	0.51735	0.6741	0.4633	0.1898	2.00E-06	gi 18447174 gb AAL68178.1 AT31946p [Drosophila melanogaster]
sw09703	BGIBMGA010573	1	1	1	0.18775	6.00E-47	gi 55243450 gb EAA06323.3 ENSANGP00000021951 [Anopheles gambiae str. PEST] ENSANGP00000021951 [Anopheles gambiae str. PEST]
sw20915	BGIBMGA001976	1.03665	0.97425	0.8362	0.1866	1.00E-93	gi 66510575 ref XP_392939.2 PREDICTED: similar to protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - horseshoe crab (Tachypleus tridentatus) [Apis mellifera]
sw18903	BGIBMGA002462	2.334	1.98525	0.98925	0.18635	0	gi 45384004 ref NP_990509.1 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Gallus gallus] 5-aminoimidazole-4-carboxamide-ribonucleotide transformylase-IMP cyclohydrolase; ATIC
sw00215	BGIBMGA005270	0.8315	1.06925	0.93515	0.1859	7.00E-42	gi 56427966 gb AAV91250.1 translocation protein 1 [Drosophila santomea]
sw18978	BGIBMGA009809	1.26105	1.1657	1.20845	0.17975	4.00E-08	gi 9630950 ref NP_047547.1 AcMNPV orf150 [Bombyx mori nucleopolyhedrovirus] AcMNPV orf150 [Bombyx mori nuclear polyhedrosis virus]
sw19806	BGIBMGA000917	0.4702	0.9886	0.4897	0.17705	No hits found	
sw18858	BGIBMGA007208	2.77705	1.8736	1.22815	0.17355	4.00E-84	gi 76639351 ref XP_870725.1 PREDICTED: similar to neurofilament, heavy polypeptide 200kDa isoform 2 [Bos taurus]
sw07856	BGIBMGA013818	1.1412	0.97095	1.13135	0.17245	2.00E-07	gi 26454107 dbj BAC44437.1 DNA topoisomerase IV subunit A [Mycoplasma penetrans HF-2] DNA topoisomerase IV subunit A [Mycoplasma penetrans HF-2]
sw20215	BGIBMGA014116	0.44205	0.26285	0.44215	0.16365	7.00E-32	gi 51243505 gb AAT99456.1 beta-N-acetylglucosaminidase isoform B [Bombyx mori]
sw07683	BGIBMGA007649	1	1	1	0.163	5.00E-68	gi 24641454 ref NP_727583.1 CG2467-PB, isoform B [Drosophila melanogaster] CG2467-PA, isoform A [Drosophila melanogaster] GH09980p [Drosophila melanogaster] CG2467-PB, isoform B [Drosophila melanogaster] CG2467-PA, isoform
sw20536	BGIBMGA011896	0.4913	0.8532	0.67825	0.1505	No hits found	
sw03123	BGIBMGA003682	1	1	1.2979	0.14665	5.00E-59	gi 48097111 ref XP_391844.1 PREDICTED: similar to yes-associated protein 2 [Apis mellifera]
sw16247	BGIBMGA007250	1	1	1	0.14545	Bmb039547	2.00E-67
sw17712	BGIBMGA005539	1	1	1	0.14205	Bmb041853	e-105
sw14648	BGIBMGA010419	1.1818	1.09295	1.1658	0.1354	3.00E-81	gi 2575865 dbj BAA23126.1 BmP109 [Bombyx mori]
sw22025	BGIBMGA002386	1	1	1	0.1345	3.00E-99	gi 68989041 dbj BAE06190.1 glycine rich protein [Bombyx mori]

sw13842	BGIBMGA010392	0.02785	0.18335	0.0366	0.1161	Bmb021115	2.00E-53
sw16501	BGIBMGA010765	1	1	1	0.11385	3.00E-15	gi 66500196 ref XP_393508.2 PREDICTED: similar to ENSANGP000000003319 [Apis mellifera]
sw19437	BGIBMGA000159	1	1	1	0.1118	No hits found	