

sequence ID	length	accession No.	homologous sequence which showed the lowest E-value	species of the left sequence	E-value	human eye	Human	Mouse	Fugu	Ciona	Fly	Mosquito	Worm
OctCluster0001.Contig1	527	sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	1.00E-59		+	+	+	+	+	+	+
OctCluster0001.Contig2	1267	sp P27012	S-CRYSTALLIN 4 (OL4)	giant octopus	4.00E-31			+		+			+
OctCluster0002.Contig1	487	gb AAD29640.1	O-crystallin	[Octopus dofleini]	4.00E-31	O	+	+	+	+	+	+	+
OctCluster0002.Contig2	545	gb AAD29640.1	O-crystallin	[Octopus dofleini]	3.00E-57	O	+	+	+	+	+	+	+
OctCluster0002.Contig3	539	gb AAD29640.1	O-crystallin	[Octopus dofleini]	1.00E-83	O	+	+	+	+	+	+	+
OctCluster0002.Contig4	860	gb AAD29640.1	O-crystallin	[Octopus dofleini]	1.00E-103	O	+	+	+	+	+	+	+
OctCluster0003.Contig1	387	ref NP_062839.1	cytochrome c oxidase subunit I	[Loligo bleekeri]	3.00E-50				+	+			
OctCluster0003.Contig2	555	ref NP_062839.1	cytochrome c oxidase subunit I	[Loligo bleekeri]	4.00E-45		+			+			
OctCluster0003.Contig3	450	gb AAC95074.1	cytochrome c oxidase subunit I	[Bathypolypus arcticus]	4.00E-41		+			+			
OctCluster0003.Contig4	1558	ref NP_062839.1	cytochrome c oxidase subunit I	[Loligo bleekeri]	1.00E-178		+		+	+			
OctCluster0004.Contig1	693	sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	1.00E-56		+	+	+	+	+	+	+
OctCluster0005.Contig1	900	ref NP_505818.1	actin	[Caenorhabditis elegans]	1.00E-152	O	+	+	+	+	+	+	+
OctCluster0005.Contig3	642	sp P17304	ACTIN, MUSCLE	[Aplysia californica]	2.00E-53	O	+	+	+	+	+	+	+
OctCluster0005.Contig4	1910	sp Q26065	ACTIN, ADDUCTOR MUSCLE		0	O	+	+	+	+	+	+	+
OctCluster0008.Contig1	674	ref NP_062840.1	cytochrome c oxidase subunit II	[Loligo bleekeri]	2.00E-59								
OctCluster0008.Contig2	706	ref NP_062840.1	cytochrome c oxidase subunit II	[Loligo bleekeri]	4.00E-67				+				
OctCluster0009.Contig1	1911	sp P30841	OMEGA-CRYSTALLIN	giant octopus	0	O	+	+	+	+	+	+	+
OctCluster0011.Contig1	809	ref NP_062833.1	cytochrome c oxidase subunit III	[Loligo bleekeri]	4.00E-73				+	+			
OctCluster0013.Contig1	1128	ref NP_148763.1	cytochrome b	[Arctoscopus japonicus]	1.00E-101				+	+			
OctCluster0015.Contig1	510	gb AAD34267.1	calmodulin mutant SYNCAM64A	[synthetic construct]	2.00E-17	O	+	+	+	+	+	+	+
OctCluster0015.Contig2	673	sp P04464	Calmodulin		2.00E-17	O	+	+	+	+	+	+	+
OctCluster0016.Contig2	525	dbj BAA95609.1	arginine kinase	[Octopus vulgaris]	4.00E-74	O	+	+	+	+	+	+	+
OctCluster0016.Contig3	1311	dbj BAA95609.1	arginine kinase	[Octopus vulgaris]	1.00E-167	O	+	+	+	+	+	+	+
OctCluster0017.Contig1	865	gb AAD29640.1	O-crystallin	[Octopus dofleini]	2.00E-61	O	+	+	+	+	+	+	+
OctCluster0019.Contig1	613	gb EAA00623.1	agCP9673	[Anopheles gambiae str. PEST]	1.00E-25	O	+	+	+	+	+	+	+
OctCluster0020.Contig1	552	dbj BAA21513.1	newt elongation factor 1-alpha	[Cynops pyrrhogaster]	3.00E-36	O	+	+	+	+	+	+	+
OctCluster0020.Contig2	1423	emb CAA70221.1	elongation factor 1A	[Geodia cydonium]	0	O	+	+	+	+	+	+	+
OctCluster0021.Contig1	680	ref NP_062845.1	ATP synthase F0 subunit 6	[Loligo bleekeri]	8.00E-27								
OctCluster0022.Contig1	553	gb AAL27684.1	heat shock protein HSP27-like protein	[Ciona intestinalis]	1.00E-05					+			
OctCluster0023.Contig1	375	ref NP_287374.1	putative DNA packaging protein of prophage CP-933X	[Escherichia coli O157:H7 EDL933]	4.00E-24								
OctCluster0024.Contig1	275	sp Q01821	GUANINE NUCLEOTIDE-BINDING PROTEIN GAMMA SUBUNIT	[Loligo forbesi]	6.00E-08								
OctCluster0024.Contig2	598	sp Q01821	GUANINE NUCLEOTIDE-BINDING PROTEIN GAMMA SUBUNIT	[Loligo forbesi]	1.00E-13								
OctCluster0024.Contig3	518	sp Q01821	GUANINE NUCLEOTIDE-BINDING PROTEIN GAMMA SUBUNIT	[Loligo forbesi]	8.00E-09								
OctCluster0025.Contig1	645	sp P22011	Peptidyl-prolyl cis-trans isomerase (PPIase)	[Candida albicans]	2.00E-50	O	+	+	+	+	+	+	+
OctCluster0030.Contig1	758	gb AAD29639.1	ferritin	[Octopus dofleini]	8.00E-73	O	+	+	+	+	+	+	+
OctCluster0031.Contig1	517	sp P02402	60S ACIDIC RIBOSOMAL PROTEIN P1 (EL12/ EL12'-P)	brine shrimp	1.00E-20	O	+	+	+	+	+	+	+
OctCluster0032.Contig1	854	emb CAC86921.1	methionine-rich repeat protein 1	[Loligo forbesi]	1.00E-20								
OctCluster0034.Contig1	517	ref NP_062836.1	NADH dehydrogenase subunit 6	[Loligo bleekeri]	2.00E-12								
OctCluster0035.Contig1	429	ref NP_652035.1	CG6105-PA	[Drosophila melanogaster]	2.00E-20		+	+	+		+		+
OctCluster0036.Contig1	680	ref NP_062845.1	ATP synthase F0 subunit 6	[Loligo bleekeri]	3.00E-19								
OctCluster0037.Contig1	761	sp P27012	S-CRYSTALLIN 4 (OL4)	giant octopus	5.00E-56		+	+	+	+	+	+	+
OctCluster0040.Contig1	800	emb CAB75721.1	cytochrome oxidase subunit III	[Octopus vulgaris]	1.00E-84				+	+			
OctCluster0041.Contig1	529	gb EAA05461.1	agCP10585	[Anopheles gambiae str. PEST]	1.00E-68	O	+	+	+	+	+	+	+
OctCluster0041.Contig2	574	sp Q06331	TUBULIN ALPHA CHAIN	giant octopus	6.00E-81	O	+	+	+	+	+	+	+
OctCluster0041.Contig3	524	sp Q06331	TUBULIN ALPHA CHAIN	giant octopus	9.00E-75	O	+	+	+	+	+	+	+
OctCluster0042.Contig1	472	gb EAA01685.1	agCP12635	[Anopheles gambiae str. PEST]	3.00E-79	O	+	+	+	+	+	+	+
OctCluster0042.Contig2	495	gb AAB07728.1	alpha-2 tubulin	[Hirudo medicinalis]	3.00E-86	O	+	+	+	+	+	+	+
OctCluster0042.Contig3	596	sp Q06331	TUBULIN ALPHA CHAIN	giant octopus	1.00E-110	O	+	+	+	+	+	+	+
OctCluster0043.Contig1	755	dbj BAA75668.1	collagen pro alpha-chain	[Haliotis discus]	2.00E-41	O	+	+	+	+		+	
OctCluster0044.Contig1	423	gb AAN35164.1	60S acidic ribosomal protein	[Euprymna scolopes]	9.00E-15	O		+	+	+	+		+
OctCluster0044.Contig2	451	gb AAN35164.1	60S acidic ribosomal protein	[Plasmodium lophurae]	3.00E-16	O		+	+	+	+	+	+
OctCluster0045.Contig1	395	gb AAC61869.1	tropomyosin	[Crassostrea virginica]	8.00E-08						+		+
OctCluster0045.Contig2	471	sp P42636	TROPOMYOSIN 1 (TMI) (BG39)		8.00E-43	O	+	+	+	+	+	+	+
OctCluster0045.Contig3	1067	gb AAG08987.1	tropomyosin	[Haliotis diversicolor]	1.00E-82	O	+	+	+	+	+	+	+
OctCluster0046.Contig1	1070	gb EAA13115.1	agCP2178	[Anopheles gambiae str. PEST]	5.00E-11	O	+	+	+	+	+	+	+
OctCluster0047.Contig1	866	sp P04929	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	[Plasmodium lophurae]	6.00E-25	O	+	+	+	+	+	+	+
OctCluster0047.Contig2	758	sp P04929	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	[Plasmodium lophurae]	3.00E-28	O	+	+	+	+	+	+	+
OctCluster0047.Contig3	423	sp P04929	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	[Plasmodium lophurae]	3.00E-06								

OctCluster0048.Contig1	817	emb CAC94904.1	histone H1	[Mytilus californianus]	1.00E-15	O	+	+		+	+	+	+
OctCluster0050.Contig2	656	sp Q9HFY6	Calmodulin (CaM)	[Blastocladiella emersonii]	7.00E-05								
OctCluster0051.Contig1	489	gb AAC60279.1	ubiquitin/ribosomal protein	[Gallus gallus]	4.00E-56	O	+	+	+	+	+	+	+
OctCluster0051.Contig2	545	gb AAC60279.1	ubiquitin/ribosomal protein	[Gallus gallus]	1.00E-59	O	+	+	+	+	+	+	+
OctCluster0053.Contig1	707	ref NP_062837.1	NADH dehydrogenase subunit 1	[Loligo bleekeri]	1.00E-59		+			+			
OctCluster0054.Contig1	401	gb AAK91296.1	ubiquitin	[Branchiostoma belcheri]	5.00E-42	O	+	+	+	+	+	+	+
OctCluster0054.Contig2	460	gb AAK91296.1	ubiquitin	[Branchiostoma belcheri]	2.00E-42	O	+	+	+	+	+	+	+
OctCluster0056.Contig1	622	gb AAG50052.1	fatty acid-binding protein	[Schistosoma japonicum]	3.00E-07		+	+					
OctCluster0058.Contig1	470	ref NP_524582.1	ribosomal protein L32	[Drosophila melanogaster]	6.00E-51	O	+	+	+	+	+		+
OctCluster0059.Contig1	387	ref NP_524709.1	ribosomal protein S15a, cytosolic	[Drosophila melanogaster]	1.00E-49	O	+	+	+	+	+		+
OctCluster0059.Contig2	454	ref NP_524709.1	ribosomal protein S15a, cytosolic	[Drosophila melanogaster]	4.00E-56	O	+	+	+	+	+		+
OctCluster0061.Contig1	372	sp P27085	40S ribosomal protein S26	[Octopus vulgaris]	1.00E-42		+	+	+	+	+	+	+
OctCluster0061.Contig2	417	sp P27085	40S ribosomal protein S26	[Octopus vulgaris]	3.00E-45		+	+	+	+	+	+	+
OctCluster0062.Contig1	684	ref NP_001000.2	ribosomal protein S5	[Homo sapiens]	5.00E-95	O	+	+	+	+	+		+
OctCluster0062.Contig2	563	ref NP_001000.2	ribosomal protein S5	[Homo sapiens]	8.00E-91	O	+	+	+	+	+		+
OctCluster0064.Contig1	296	gb EAA04923.1	agCP4253	[Anopheles gambiae str. PEST]	2.00E-44	O	+	+	+	+	+		+
OctCluster0064.Contig2	752	sp Q96647	60S ribosomal protein L10 (QM protein homolog)	[Bombyx mandarina]	1.00E-98	O	+	+	+	+	+		+
OctCluster0065.Contig1	877	sp P23232	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT	[Loligo forbesi]	0.00E+00	O	+	+	+	+	+	+	+
OctCluster0067.Contig1	813	sp P37167	Actophorin		2.00E-23	O	+	+	+	+	+	+	+
OctCluster0068.Contig1	531	gb AAN05586.1	ribosomal protein S19	[Argopecten irradians]	8.00E-60	O	+	+	+	+	+	+	+
OctCluster0070.Contig1	514	ref NP_073163.1	ribosomal protein S14	[Rattus norvegicus]	7.00E-57		+	+	+	+	+	+	+
OctCluster0070.Contig2	514	ref NP_073163.1	ribosomal protein S14	[Rattus norvegicus]	7.00E-57		+	+	+	+	+	+	+
OctCluster0071.Contig1	463	gb AAN05597.1	ribosomal protein S30	[Argopecten irradians]	2.00E-35	O	+	+	+	+	+	+	+
OctCluster0071.Contig2	492	gb AAN05597.1	ribosomal protein S30	[Argopecten irradians]	8.00E-37	O	+	+	+	+	+	+	+
OctCluster0073.Contig1	332	ref NP_523813.1	CG3661-PA	[Drosophila melanogaster]	4.00E-35	O	+	+	+	+	+	+	+
OctCluster0073.Contig2	482	ref NP_523813.1	CG3661-PA	[Drosophila melanogaster]	3.00E-69	O	+	+	+	+	+	+	+
OctCluster0074.Contig1	485	ref NP_611940.1	CG4692-PB	[Drosophila melanogaster]	3.00E-20	O	+	+	+		+	+	+
OctCluster0075.Contig1	323	ref NP_035473.1	Sec61, gamma subunit	[Mus musculus]	2.00E-16		+	+		+	+		+
OctCluster0075.Contig2	346	ref NP_035473.1	SEC61, gamma subunit	[Mus musculus]	1.00E-20		+	+		+	+		+
OctCluster0076.Contig1	332	ref NP_497263.1	40S ribosomal protein S29	[Caenorhabditis elegans]	6.00E-20	O	+	+	+	+	+	+	+
OctCluster0076.Contig2	326	gb AAL62474.1	ribosomal protein S29	[Spodoptera frugiperda]	1.00E-20	O	+	+	+	+	+	+	+
OctCluster0077.Contig1	607	pir	ornithine decarboxylase antizyme	[Homo sapiens]	4.00E-23	O	+	+	+	+	+	+	+
OctCluster0077.Contig2	637	pir	ornithine decarboxylase antizyme	[Homo sapiens]	4.00E-23	O	+	+	+	+	+	+	+
OctCluster0078.Contig1	589	ref NP_524004.2	CG3395-PA	[Drosophila melanogaster]	3.00E-79		+	+	+	+	+		+
OctCluster0078.Contig2	658	gb EAA09489.1	agCP14911	[Anopheles gambiae str. PEST]	5.00E-91	O	+	+	+	+	+	+	+
OctCluster0081.Contig1	934	ref NP_493415.1	Regulator of chromosome condensation (RCC1)	[Caenorhabditis elegans]	5.00E-22	O	+	+	+	+			+
OctCluster0083.Contig1	872	sp Q07167	16 KDA CALCIUM-BINDING PROTEIN (EGG ANTIGEN SME16)		2.00E-05			+					
OctCluster0084.Contig1	941	sp Q05975	RAS-RELATED PROTEIN RAB-2	[Lymnaea stagnalis]	0.00E+00	O	+	+	+	+	+	+	+
OctCluster0087.Contig1	1039	gb AAF19631.1	cysteine proteinase precursor	[Myxine glutinosa]	1.00E-72	O	+	+	+	+	+	+	+
OctCluster0088.Contig1	453	pir	TRAP-like protein precursor (clone X0286)	African clawed frog	9.00E-33	O	+	+	+	+	+	+	+
OctCluster0088.Contig2	573	pir	TRAP-like protein precursor (clone X0286)	African clawed frog	3.00E-43	O	+	+	+	+	+	+	+
OctCluster0089.Contig1	1162	ref NP_510663.1	alpha-2 type IV collagen	[Caenorhabditis elegans]	5.00E-39	O	+	+	+	+	+	+	+
OctCluster0090.Contig1	1093	gb AAK12348.1	elongation factor-2	[Mastigoproctus giganteus]	0.00E+00	O	+	+	+	+	+	+	+
OctCluster0091.Contig1	1047	ref XP_109269.1	aldehyde dehydrogenase family 3, subfamily A2	[Mus musculus]	5.00E-59	O	+	+	+	+	+	+	+
OctCluster0092.Contig1	682	ref NP_064313.1	Ubiquitin-like protein SMT3A	[Mus musculus]	1.00E-21	O	+	+	+	+	+		+
OctCluster0093.Contig1	577	gb AAM51563.1	thioredoxin	[Brugia malayi]	9.00E-31		+	+	+				+
OctCluster0094.Contig1	415	gb AAN05608.1	ribosomal protein L26	[Argopecten irradians]	7.00E-50	O	+	+	+	+	+	+	+
OctCluster0094.Contig2	516	gb AAN05608.1	ribosomal protein L26	[Argopecten irradians]	9.00E-53	O	+	+	+	+	+	+	+
OctCluster0097.Contig1	423	gb AAM34649.1	60S ribosomal protein L35	[Danio rerio]	1.00E-37	O	+	+	+	+	+	+	+
OctCluster0097.Contig2	583	gb AAM34649.1	60S ribosomal protein L35	[Danio rerio]	4.00E-36	O	+	+	+	+	+	+	+
OctCluster0098.Contig1	432	gb AAN05584.1	ribosomal protein L30	[Argopecten irradians]	5.00E-55	O	+	+	+	+	+	+	+
OctCluster0098.Contig2	401	gb AAN05584.1	ribosomal protein L30	[Argopecten irradians]	3.00E-53	O	+	+	+	+	+	+	+
OctCluster0100.Contig1	347	ref NP_062834.1	NADH dehydrogenase subunit 3	[Loligo bleekeri]	3.00E-10								
OctCluster0101.Contig1	1268	sp Q01241	70 kDa neurofilament protein (NF70)	longfin squid	0.00E+00	O	+	+	+	+	+	+	+
OctCluster0103.Contig1	890	emb CAA11175.1	actin related protein	[Lumbricus rubellus]	2.00E-80		+	+	+	+	+	+	+
OctCluster0104.Contig1	535	ref NP_082384.1	Mak3p homolog	[Mus musculus]	3.00E-66	O	+	+	+	+	+	+	+
OctCluster0105.Contig1	623	ref NP_651852.1	CG1746-PA	[Drosophila melanogaster]	1.00E-28	O	+	+	+	+	+	+	+
OctCluster0105.Contig2	573	ref NP_651852.1	CG1746-PA	[Drosophila melanogaster]	8.00E-25	O	+	+	+	+	+	+	+
OctCluster0106.Contig1	956	gb AAN05591.1	ribosomal protein L7	[Argopecten irradians]	1.00E-92	O	+	+	+	+	+	+	+

OctCluster0107.Contig1	496 ref NP_075238.1	ribosomal protein L14	[Rattus norvegicus]	2.00E-37	O	+	+	+	+	+	+	+
OctCluster0107.Contig2	559 ref NP_075238.1	ribosomal protein L14	[Rattus norvegicus]	7.00E-38	O	+	+	+	+	+	+	+
OctCluster0108.Contig1	522 gb AAD26692.1	40S ribosomal protein S13	[Cricetulus griseus]	4.00E-77	O	+	+	+	+	+	+	+
OctCluster0110.Contig1	485 ref NP_497700.1	myosin regulatory light chain 2	[Caenorhabditis elegans]	2.00E-05		+	+	+	+	+	+	+
OctCluster0110.Contig2	717 ref XP_130617.1	similar to transient receptor protein 2	[Mus musculus]	3.00E-66	O	+	+	+	+	+	+	+
OctCluster0111.Contig1	527 gb AAL79538.1	40S ribosomal protein S12	[Branchiostoma belcheri]	1.00E-49		+	+	+	+	+	+	+
OctCluster0112.Contig1	491 ref NP_611685.1	CG4046-PA	[Drosophila melanogaster]	4.00E-68	O	+	+	+	+	+	+	+
OctCluster0113.Contig1	652 sp Q95VY2	Translationally-controlled tumor protein (TCTP)	[Branchiostoma belcheri]	7.00E-23	O	+	+	+	+	+	+	+
OctCluster0114.Contig1	477 gb AAL40881.1	ribosomal protein S24	[Aedes aegypti]	2.00E-42	O	+	+	+	+	+	+	+
OctCluster0114.Contig2	431 sp O42387	40S RIBOSOMAL PROTEIN S24	[Takifugu rubripes]	1.00E-34	O	+	+	+	+	+	+	+
OctCluster0115.Contig1	462 ref NP_035424.1	RNA polymerase II transcriptional coactivator	[Mus musculus]	1.00E-15	O	+	+	+	+	+	+	+
OctCluster0116.Contig1	422 gb EAA12143.1	agCP9085	[Anopheles gambiae str. PEST]	5.00E-24	O	+	+	+	+	+	+	+
OctCluster0120.Contig1	344 ref NP_727447.1	CG32672-PA	[Drosophila melanogaster]	1.00E-20	O	+	+	+	+	+	+	+
OctCluster0120.Contig2	596 ref NP_727447.1	CG32672-PA	[Drosophila melanogaster]	2.00E-59	O	+	+	+	+	+	+	+
OctCluster0121.Contig1	542 sp Q9WVA4	Transgelin 2	[Mus musculus]	4.00E-11	O	+	+	+	+	+	+	+
OctCluster0122.Contig1	548 gb AAC41251.1	14-3-3 protein epsilon	[Xenopus laevis]	1.00E-61	O	+	+	+	+	+	+	+
OctCluster0124.Contig1	673 sp P08052	Myosin regulatory light chain LC-2, mantle muscle (RLC)		7.00E-08								
OctCluster0125.Contig1	562 gb EAA00275.1	agCP9711	[Anopheles gambiae str. PEST]	2.00E-23						+	+	+
OctCluster0128.Contig1	555 gb AAH26656.1	ribosomal protein L23a	[Mus musculus]	1.00E-35		+	+	+	+	+	+	+
OctCluster0129.Contig1	534 ref NP_003850.1	dolichyl-phosphate mannosyltransferase polypeptide 1	[Homo sapiens]	2.00E-73	O	+	+	+	+	+	+	+
OctCluster0130.Contig1	572 pir	omega-crystallin	giant octopus	1.00E-93	O	+	+	+	+	+	+	+
OctCluster0131.Contig1	1402 ref NP_079009.1	hypothetical protein FLJ14345	[Homo sapiens]	0.00E+00	O	+	+	+				
OctCluster0132.Contig1	535 gb AAK31583.1	heat shock protein 70	[Ambystoma mexicanum]	4.00E-71	O	+	+	+	+	+	+	+
OctCluster0132.Contig2	505 dbj BAB72169.1	stress protein HSC70	[Xiphophorus maculatus]	8.00E-85	O	+	+	+	+	+	+	+
OctCluster0133.Contig1	519 sp P08052	Myosin regulatory light chain LC-2, mantle muscle (RLC)	Japanese flying squid	6.00E-70	O	+	+	+	+	+	+	+
OctCluster0135.Contig1	477 gb AAN05588.1	ribosomal protein L19	[Argopecten irradians]	1.00E-42		+	+	+	+	+	+	+
OctCluster0135.Contig2	628 gb AAN05588.1	ribosomal protein L19	[Argopecten irradians]	7.00E-66		+	+	+	+	+	+	+
OctCluster0136.Contig1	465 emb CAC94905.1	histone H1	[Mytilus chilensis]	4.00E-05		+						
OctCluster0136.Contig3	641 emb CAC94904.1	histone H1	[Mytilus californianus]	1.00E-06	O	+	+				+	+
OctCluster0137.Contig1	434 gb AAN52385.1	ribosomal protein S10	[Branchiostoma belcheri]	2.00E-46		+	+	+	+	+	+	+
OctCluster0137.Contig2	492 gb AAN52385.1	ribosomal protein S10	[Branchiostoma belcheri]	1.00E-52		+	+	+	+	+	+	+
OctCluster0138.Contig1	562 gb EAA13833.1	agCP8449	[Anopheles gambiae str. PEST]	4.00E-24		+	+	+	+	+	+	+
OctCluster0139.Contig1	799 gb EAA06264.1	agCP13194	[Anopheles gambiae str. PEST]	2.00E-14	O	+	+	+	+	+	+	+
OctCluster0140.Contig1	519 sp P21613	KINESIN HEAVY CHAIN	longfin squid	1.00E-05								
OctCluster0142.Contig1	526 gb AAN31640.1	high mobility group protein 1	[Biomphalaria glabrata]	2.00E-12	O	+	+					+
OctCluster0143.Contig1	467 gb AAN05587.1	ribosomal protein L11	[Argopecten irradians]	6.00E-38	O	+	+	+	+	+	+	+
OctCluster0143.Contig2	517 gb AAN05587.1	ribosomal protein L11	[Argopecten irradians]	1.00E-78	O	+	+	+	+	+	+	+
OctCluster0145.Contig1	717 ref NP_034490.1	glutathione S-transferase, mu 5	[Mus musculus]	1.00E-33	O	+	+	+	+			+
OctCluster0147.Contig1	519 ref NP_650401.1	CG3731-PB	[Drosophila melanogaster]	2.00E-55	O	+	+	+	+	+	+	+
OctCluster0148.Contig1	564 pir	protein disulfide-isomerase (EC 5.3.4.1) ER60 precursor	bovine	7.00E-57	O	+	+	+	+	+	+	+
OctCluster0149.Contig1	605 pir	superoxide dismutase (EC 1.15.1.1) (Cu-Zn)	chicken	2.00E-55	O	+	+	+	+	+	+	+
OctCluster0150.Contig1	480 gb AAN31640.1	high mobility group protein 1	[Biomphalaria glabrata]	3.00E-31	O	+	+	+	+	+	+	+
OctCluster0150.Contig2	505 gb AAN31640.1	high mobility group protein 1	[Biomphalaria glabrata]	1.00E-33	O	+	+	+	+	+	+	+
OctCluster0151.Contig1	792 ref XP_129339.1	similar to hypothetical protein	[Homo sapiens]	9.00E-27	O	+	+	+	+	+	+	+
OctCluster0152.Contig1	502 gb AAD31042.1	heat shock protein 70	[Crassostrea gigas]	5.00E-29	O	+	+	+	+	+	+	+
OctCluster0152.Contig2	471 pir	dnaK-type molecular chaperone hsc70	[Pleurodeles waltl]	2.00E-12	O	+	+	+	+	+	+	+
OctCluster0153.Contig1	750 gb AAN05604.1	ribosomal protein L21	[Argopecten irradians]	6.00E-48	O	+	+	+	+	+	+	+
OctCluster0156.Contig1	496 ref NP_001021.1	ribosomal protein S27	[Homo sapiens]	1.00E-30	O	+	+	+	+	+		+
OctCluster0156.Contig2	197 emb CAC44218.1	putative ribosomal protein S27 protein	[Oncorhynchus mykiss]	3.00E-18	O	+	+	+	+	+		+
OctCluster0156.Contig3	333 ref NP_001021.1	ribosomal protein S27	[Homo sapiens]	8.00E-36	O	+	+	+	+	+	+	+
OctCluster0157.Contig1	168 sp P20342	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)	African clawed frog	2.00E-22	O	+	+	+	+	+	+	+
OctCluster0157.Contig2	491 gb AAN05605.1	ribosomal protein S15	[Argopecten irradians]	1.00E-55	O	+	+	+	+	+	+	+
OctCluster0158.Contig1	503 gb AAN52390.1	ribosomal protein S18	[Branchiostoma belcheri]	3.00E-63	O	+	+	+	+	+	+	+
OctCluster0159.Contig1	488 gb AAL26580.1	ribosomal protein S4	[Spodoptera frugiperda]	7.00E-67	O	+	+	+	+	+	+	+
OctCluster0159.Contig2	613 gb AAL26580.1	ribosomal protein S4	[Spodoptera frugiperda]	4.00E-94	O	+	+	+	+	+	+	+
OctCluster0160.Contig1	875 ref NP_062841.1	NADH dehydrogenase subunit 5	[Loligo bleekeri]	1.00E-46							+	
OctCluster0161.Contig1	857 ref XP_081326.1	Oligomycin sensitivity-conferring protein	[Drosophila melanogaster]	2.00E-52	O	+	+	+	+	+	+	+
OctCluster0162.Contig1	479 emb CAC14789.1	40S ribosomal protein S23	[Lumbricus rubellus]	1.00E-72		+	+	+	+	+	+	+
OctCluster0163.Contig1	473 gb AAN52375.1	ribosomal protein L22	[Branchiostoma belcheri]	3.00E-26	O	+	+	+	+	+	+	+

OctCluster0165.Contig1	463	gb AAN05594.1	ribosomal protein S17	[Argopecten irradians]	4.00E-59	+	+	+	+	+	+	+
OctCluster0166.Contig1	459	ref NP_062838.1	NADH dehydrogenase subunit 2	[Loligo bleekeri]	1.00E-06							
OctCluster0167.Contig1	424	ref NP_061329.1	G-protein gamma-12 subunit	[Homo sapiens]	8.00E-10	O	+	+	+		+	
OctCluster0169.Contig1	364	gb EAA15151.1	agCP4567	[Anopheles gambiae str. PEST]	4.00E-15	O	+	+	+	+	+	+
OctCluster0169.Contig2	436	gb EAA15151.1	agCP4567	[Anopheles gambiae str. PEST]	4.00E-15	O	+	+	+		+	+
OctCluster0170.Contig1	642	sp Q90705	Elongation factor 2 (EF-2)		2.00E-73	O	+	+	+	+	+	+
OctCluster0171.Contig1	422	sp P27012	S-CRYSTALLIN 4 (OL4)	giant octopus	8.00E-18							
OctCluster0173.Contig1	412	gb AAN52391.1	ribosomal protein S25	[Branchiostoma belcheri]	1.00E-23	O	+	+	+	+	+	+
OctCluster0174.Contig1	353	ref NP_444301.1	cytochrome c oxidase, subunit VIc	[Mus musculus]	1.00E-12	O	+	+	+		+	+
OctCluster0174.Contig2	409	ref NP_444301.1	cytochrome c oxidase, subunit VIc	[Mus musculus]	2.00E-14	O	+	+	+		+	+
OctCluster0175.Contig1	474	emb CAC86921.1	methionine-rich repeat protein 1	[Loligo forbesi]	1.00E-16							
OctCluster0177.Contig1	482	ref NP_062842.1	NADH dehydrogenase subunit 4	[Loligo bleekeri]	3.00E-15							
OctCluster0178.Contig1	341	ref NP_079863.1	ribosomal protein S21	[Mus musculus]	1.00E-30		+	+	+	+	+	+
OctCluster0178.Contig2	337	ref NP_079863.1	ribosomal protein S21	[Mus musculus]	1.00E-31		+	+	+	+	+	+
OctCluster0179.Contig2	328	ref XP_106711.1	hypothetical protein XP_106711	[Homo sapiens]	1.00E-06	O	+	+			+	
OctCluster0180.Contig1	325	sp O61462	60S RIBOSOMAL PROTEIN L37A	[Cryptochiton stelleri]	3.00E-42	O	+	+	+	+	+	+
OctCluster0185.Contig1	945	gb AAD29639.1	ferritin	[Octopus dofleini]	7.00E-72	O	+	+	+	+	+	+
OctCluster0186.Contig1	590	ref NP_013633.1	cyclophilin-3 (cyclosporin-sensitive proline rotamase-3)	[Saccharomyces cerevisiae]	3.00E-49	O	+	+	+	+	+	+
OctCluster0187.Contig1	559	ref NP_648514.1	CG7283-PA	[Drosophila melanogaster]	3.00E-60	O	+	+	+	+	+	+
OctCluster0188.Contig1	531	ref NP_613067.1	DNA segment, Chr 10, Johns Hopkins University 81 expressed	[Mus musculus]	2.00E-41	O	+	+	+	+		
OctCluster0190.Contig1	794	gb EAA00330.1	agCP9609	[Anopheles gambiae str. PEST]	8.00E-42	O	+	+	+	+	+	+
OctCluster0191.Contig1	561	sp P08712	Endoplasmic (94 kDa glucose-regulated protein) (GRP94)	[Mesocricetus auratus]	3.00E-10	O	+	+	+	+	+	+
OctCluster0193.Contig1	557	ref NP_058087.1	syndecan binding protein	[Mus musculus]	4.00E-31	O	+	+	+	+	+	
OctCluster0194.Contig1	876	dbj BAA22852.1	troponin I	[Mizuhopecten yessoensis]	7.00E-31	O	+	+	+	+	+	+
OctCluster0195.Contig1	689	sp Q9D8Y0	Swiprosin 1	[Mus musculus]	1.00E-31	O	+	+	+	+	+	+
OctCluster0196.Contig1	537	ref NP_076465.1	TGF-beta resistance-associated protein	[Rattus norvegicus]	5.00E-25		+	+	+	+	+	+
OctCluster0197.Contig1	545	dbj BAA31673.2	KIAA0698 protein	[Homo sapiens]	9.00E-38	O	+	+	+	+		
OctCluster0199.Contig1	550	ref XP_128846.1	similar to 60S RIBOSOMAL PROTEIN L17 (L23)	[Mus musculus]	7.00E-68	O	+	+	+	+	+	+
OctCluster0201.Contig1	638	gb AAK95130.1	ribosomal protein L6	[Ictalurus punctatus]	2.00E-48	O	+	+	+	+	+	+
OctCluster0202.Contig1	489	dbj BAB26006.1	homolog to CDNA FLJ10672 FIS, CLONE NT2RP2006365-putative	[Mus musculus]	6.00E-40		+	+	+	+	+	+
OctCluster0203.Contig1	530	gb EAA08379.1	agCP2992	[Anopheles gambiae str. PEST]	2.00E-23		+	+	+	+	+	+
OctCluster0204.Contig1	541	sp O97580	Succinyl-CoA ligase	[ADP-forming]	2.00E-39	O	+	+	+	+	+	+
OctCluster0205.Contig1	540	dbj BAA32086.1	natural killer cell enhancing factor	[Cyprinus carpio]	2.00E-72	O	+	+	+	+	+	+
OctCluster0206.Contig1	502	dbj BAB67790.1	KIAA1897 protein	[Homo sapiens]	2.00E-32	O	+	+	+	+	+	+
OctCluster0208.Contig1	616	sp P79819	Serotransferrin precursor	[Oryzias latipes]	3.00E-42	O	+	+	+	+	+	+
OctCluster0212.Contig1	322	gb AAL54903.1	ribosomal protein L14	[Lapemis hardwickii]	2.00E-22	O	+	+	+	+	+	+
OctCluster0212.Contig2	531	emb CAA28689.1	ribosomal protein L14	[Xenopus laevis]	1.00E-46	O	+	+	+	+	+	+
OctCluster0212.Contig3	534	sp P35980	60S ribosomal protein L18	[Mus musculus]	1.00E-67	O	+	+	+	+	+	+
OctCluster0213.Contig1	533	ref NP_510434.1	zinc metalloprotease	[Caenorhabditis elegans]	1.00E-21					+		+
OctCluster0214.Contig1	530	ref NP_004025.1	annexin VII isoform 2	[Homo sapiens]	2.00E-39	O	+	+	+	+	+	+
OctCluster0214.Contig2	520	ref NP_033804.1	annexin A7	[Mus musculus]	1.00E-43	O	+	+	+	+	+	+
OctCluster0215.Contig1	596	sp P38412	Guanine nucleotide-binding protein G(q), alpha subunit	northern European squid	3.00E-39	O	+	+	+	+	+	+
OctCluster0217.Contig1	526	gb AAH32893.1	Unknown (protein for MGC:43081)	[Homo sapiens]	2.00E-29	O	+	+	+	+	+	+
OctCluster0218.Contig1	526	sp Q06331	TUBULIN ALPHA CHAIN	giant octopus	1.00E-76	O	+	+	+	+	+	+
OctCluster0218.Contig2	521	sp Q06331	TUBULIN ALPHA CHAIN	giant octopus	1.00E-87	O	+	+	+	+	+	+
OctCluster0219.Contig1	561	gb AAC35284.1	FUS/TLS protein	[Homo sapiens]	3.00E-05		+	+				
OctCluster0220.Contig1	525	ref NP_633480.1	Universal stress protein	[Methanosarcina mazei Goe1]	1.00E-09					+		
OctCluster0221.Contig1	496	ref NP_033479.1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF)	[Mus musculus]	2.00E-46	O	+	+	+	+	+	+
OctCluster0222.Contig1	881	ref NP_725896.1	CG9277-PA	[Drosophila melanogaster]	1.00E-99	O	+	+	+	+	+	+
OctCluster0223.Contig1	522	gb AAL54898.1	transport protein Sec61 beta subunit	[Lapemis hardwickii]	1.00E-24	O	+	+	+	+	+	+
OctCluster0223.Contig2	413	gb AAL54898.1	transport protein Sec61 beta subunit	[Lapemis hardwickii]	3.00E-23	O	+	+	+	+	+	+
OctCluster0224.Contig1	520	ref NP_038773.1	nuclear fragile X mental retardation protein interacting protein	[Mus musculus]	1.00E-12	O	+	+	+	+		
OctCluster0225.Contig1	517	ref NP_689416.1	inositol polyphosphate multikinase	[Homo sapiens]	1.00E-22		+	+	+	+	+	+
OctCluster0227.Contig1	517	dbj BAA31673.2	KIAA0698 protein	[Homo sapiens]	7.00E-31	O	+	+	+	+	+	
OctCluster0229.Contig1	356	gb EAA05425.1	agCP10575	[Anopheles gambiae str. PEST]	1.00E-30	O	+	+	+	+	+	+
OctCluster0229.Contig2	612	ref NP_523710.1	calmodulin A	[Drosophila melanogaster]	9.00E-78	O	+	+	+	+	+	+
OctCluster0230.Contig1	530	ref NP_000977.1	ribosomal protein L24	[Homo sapiens]	6.00E-52	O	+	+	+	+	+	+
OctCluster0233.Contig1	511	gb EAA12330.1	agCP11439	[Anopheles gambiae str. PEST]	1.00E-37	O	+	+	+	+	+	+
OctCluster0234.Contig1	743	ref NP_681058.1	nucleoside diphosphate kinase	[Thermosynechococcus elongatus BP-]	4.00E-48	O	+	+	+	+	+	+

OctCluster0235.Contig1	510 gb AAM27202.1	ribosomal protein L27a	[Epinephelus coioides]	2.00E-42	O	+	+	+	+	+	+	+
OctCluster0235.Contig2	289 emb CAC34300.1	ribosomal protein 27a-4	[Entamoeba histolytica]	1.00E-19	O	+	+	+	+	+	+	+
OctCluster0237.Contig1	500 dbj BAC02914.1	retinal degeneration B beta	[Mus musculus]	2.00E-35	O	+	+	+	+	+	+	+
OctCluster0238.Contig1	458 sp Q26481	60S RIBOSOMAL PROTEIN L5	[Styela clava]	3.00E-43		+	+	+	+	+	+	+
OctCluster0238.Contig2	497 gb AAM33437.1	ribosomal protein L5	[Branchiostoma belcheri tsingtaunese]	2.00E-59		+	+	+	+	+	+	+
OctCluster0239.Contig1	501 gb AAM28852.1	ribosomal protein S20	[Branchiostoma belcheri tsingtaunese]	9.00E-55	O	+	+	+	+	+	+	+
OctCluster0239.Contig2	451 gb AAM28852.1	ribosomal protein S20	[Branchiostoma belcheri tsingtaunese]	3.00E-55	O	+	+	+	+	+	+	+
OctCluster0240.Contig1	756 gb EAA11049.1	agCP5847	[Anopheles gambiae str. PEST]	3.00E-12		+	+	+	+	+	+	+
OctCluster0242.Contig1	619 gb AAC23561.1	ADP/ATP carrier	[Trypanosoma brucei brucei]	5.00E-68	O	+	+	+	+	+	+	+
OctCluster0243.Contig1	491 ref NP_062841.1	NADH dehydrogenase subunit 5	[Loligo bleekeri]	8.00E-37								
OctCluster0244.Contig1	495 ref NP_062835.1	cytochrome b	[Loligo bleekeri]	8.00E-47				+	+			
OctCluster0244.Contig2	497 ref NP_062835.1	cytochrome b	[Loligo bleekeri]	2.00E-51				+	+			
OctCluster0245.Contig1	496 ref NP_062839.1	cytochrome c oxidase subunit I	[Loligo bleekeri]	9.00E-60				+	+			
OctCluster0246.Contig1	453 ref NP_080888.1	homolog to NADH-ubiquitone oxidoreductase aggg subunit precursor	[Mus musculus]	1.00E-14		+	+	+			+	+
OctCluster0247.Contig1	501 gb EAA14441.1	agCP8218	[Anopheles gambiae str. PEST]	5.00E-29		+	+	+	+	+	+	+
OctCluster0248.Contig1	434 dbj BAB41209.1	90-kDa heat shock protein	[Bombyx mori]	6.00E-47	O	+	+	+	+	+	+	+
OctCluster0249.Contig1	490 ref NP_062836.1	NADH dehydrogenase subunit 6	[Loligo bleekeri]	1.00E-31								
OctCluster0250.Contig1	892 ref NP_722589.1	CG31973-PA	[Drosophila melanogaster]	4.00E-33						+	+	+
OctCluster0251.Contig1	486 ref NP_608326.1	CG14207-PA	[Drosophila melanogaster]	2.00E-20	O	+	+	+	+	+	+	+
OctCluster0255.Contig1	636 gb AAN05602.1	ribosomal protein S7	[Argopecten irradians]	3.00E-76	O	+	+	+	+	+	+	+
OctCluster0256.Contig1	416 pir	microtubule-associated protein tau type 2	[Mus musculus]	4.00E-12	O	+	+	+	+	+	+	+
OctCluster0257.Contig1	558 sp Q9PTW9	Proteasome subunit alpha type 7 (Proteasome subunit alpha 4)	[Carassius auratus]	3.00E-77	O	+	+	+	+	+	+	+
OctCluster0259.Contig1	402 ref NP_067087.1	ribosomal protein L35a	[Rattus norvegicus]	1.00E-34			+	+	+	+	+	+
OctCluster0259.Contig2	445 ref NP_067087.1	ribosomal protein L35a	[Rattus norvegicus]	8.00E-40			+	+	+	+	+	+
OctCluster0260.Contig1	454 ref XP_131693.1	similar to hypothetical protein FLJ20446	[Homo sapiens]	3.00E-17		+	+	+	+	+	+	+
OctCluster0264.Contig1	694 gb EAA14597.1	agCP8839	[Anopheles gambiae str. PEST]	1.00E-30	O	+	+	+	+	+	+	+
OctCluster0265.Contig1	443 ref NP_609803.1	CG17996-PA	[Drosophila melanogaster]	7.00E-22	O		+	+	+	+	+	+
OctCluster0266.Contig1	397 emb CAA50897.1	almost identical to nRNP M protein, acc.L03532	[Homo sapiens]	9.00E-10	O	+	+	+	+	+	+	+
OctCluster0268.Contig1	398 sp P02268	Histone H2A	common cuttlefish	3.00E-51	O	+	+	+	+	+	+	+
OctCluster0273.Contig1	218 sp P90702	60S ribosomal protein L44	[Brugia malayi]	1.00E-21	O	+	+	+	+	+	+	+
OctCluster0273.Contig2	362 gb AAM94276.1	ribosomal protein L44	[Chlamys farreri]	5.00E-50	O	+	+	+	+	+	+	+
OctCluster0274.Contig1	423 sp P49395	40S RIBOSOMAL PROTEIN S3A (LYSINE-RICH PROTEIN KRP-A)	[Aplysia californica]	3.00E-45	O	+	+	+	+	+	+	+
OctCluster0279.Contig1	329 ref NP_062834.1	NADH dehydrogenase subunit 3	[Loligo bleekeri]	1.00E-14								
OctCluster0288.Contig1	609 pir	calcium-dependent protein kinase (EC 2.7.1.-), calmodulin-independent	maize	3.00E-15		+	+	+	+	+	+	+
OctCluster0289.Contig1	508 ref NP_006400.2	actin related protein 2/3 complex subunit 1A	[Homo sapiens]	1.00E-37	O	+	+	+	+	+	+	+
OctCluster0289.Contig2	597 ref NP_112408.1	suppressor of profilin/p41 of actin-related complex 2/3	[Rattus norvegicus]	6.00E-15	O	+	+	+	+	+	+	+
OctCluster0290.Contig1	470 dbj BAA22381.1	beta-tubulin	[Halocynthia roretzi]	1.00E-73	O	+	+	+	+	+	+	+
OctCluster0290.Contig2	597 dbj BAA22381.1	beta-tubulin	[Halocynthia roretzi]	0.00E+00	O	+	+	+	+	+	+	+
OctCluster0291.Contig1	593 gb EAA05634.1	agCP10465	[Anopheles gambiae str. PEST]	7.00E-27	O	+	+	+	+	+	+	+
OctCluster0291.Contig2	522 gb EAA05634.1	agCP10465	[Anopheles gambiae str. PEST]	6.00E-18	O	+	+	+	+	+	+	+
OctCluster0292.Contig1	593 gb EAA12214.1	agCP11195	[Anopheles gambiae str. PEST]	1.00E-35	O	+	+	+	+	+	+	+
OctCluster0293.Contig1	638 sp P17139	Collagen alpha 1(IV) chain precursor	[Caenorhabditis elegans]	7.00E-20	O	+	+	+	+	+	+	+
OctCluster0295.Contig1	404 gb AAH04900.1	ribosomal protein L13a	[Homo sapiens]	4.00E-40	O	+	+	+	+	+	+	+
OctCluster0295.Contig2	589 ref NP_036555.1	ribosomal protein L13a	[Homo sapiens]	9.00E-67	O	+	+	+	+	+	+	+
OctCluster0298.Contig1	567 ref NP_003338.1	ubiquitin-conjugating enzyme E2L 3	[Homo sapiens]	1.00E-63	O	+	+	+	+	+	+	+
OctCluster0299.Contig1	579 gb AAK61550.1	heart-type fatty acid-binding protein	[Fundulus heteroclitus]	9.00E-08		+	+					
OctCluster0300.Contig1	574 ref NP_694508.1	mucosa associated lymphoid tissue lymphoma translocation gene 1	[Danio rerio]	1.00E-10			+	+	+	+	+	+
OctCluster0302.Contig1	639 ref NP_062177.1	Diacylglycerol kinase 90kDa	[Rattus norvegicus]	4.00E-84	O	+	+	+	+	+	+	+
OctCluster0305.Contig1	473 gb AAH39185.1	Similar to transcription elongation regulator 1 (CA150)	[Mus musculus]	2.00E-35	O	+	+	+	+	+	+	+
OctCluster0306.Contig1	505 gb EAA14324.1	ebiP6196	[Anopheles gambiae str. PEST]	2.00E-50	O	+	+	+	+	+	+	+
OctCluster0307.Contig1	538 sp Q9DG68	60S acidic ribosomal protein P0 (L10E)	[Rana sylvatica]	2.00E-65	O	+	+	+	+	+	+	+
OctCluster0308.Contig1	562 ref NP_080586.1	homolog to MITOCHONDRIAL 39S RIBOSOMAL PROTEIN L18 (MRP-L)	[Mus musculus]	9.00E-28	O	+	+	+	+	+	+	+
OctCluster0308.Contig2	456 ref NP_080586.1	homolog to MITOCHONDRIAL 39S RIBOSOMAL PROTEIN L18 (MRP-L)	[Mus musculus]	1.00E-22	O	+	+	+	+	+	+	+
OctCluster0310.Contig1	537 ref NP_650774.1	CG6008-PA	[Drosophila melanogaster]	7.00E-14	O					+	+	
OctCluster0311.Contig1	570 gb AAB62936.1	PP2A inhibitor	[Tetraodon fluviatilis]	2.00E-75	O	+	+	+	+	+	+	+
OctCluster0312.Contig1	536 ref NP_055075.1	HLA class II region expressed gene KE2	[Homo sapiens]	3.00E-29		+	+	+	+	+	+	+
OctCluster0313.Contig1	554 sp P46088	Glutathione S-transferase (GST class-sigma)	Sloane's squid	5.00E-26	O	+	+		+	+	+	+
OctCluster0314.Contig1	553 ref NP_110517.2	catenin, beta like 1	[Homo sapiens]	2.00E-48	O	+	+	+		+	+	+
OctCluster0315.Contig1	555 gb AAH04036.1	Unknown (protein for IMAGE:3495765)	[Mus musculus]	2.00E-25	O	+	+		+			

OctCluster0316.Contig1	527 gb EAA00894.1	agCP12416	[Anopheles gambiae str. PEST]	9.00E-08				+	+		+	
OctCluster0317.Contig1	551 gb AAB60497.1	elongation factor 2		3.00E-50	O		+	+	+	+	+	+
OctCluster0320.Contig1	525 ref XP_110082.1	similar to chromosome 1 open reading frame 27	[Mus musculus]	8.00E-23			+	+		+	+	
OctCluster0321.Contig1	547 pir	phosphoprotein phosphatase (EC 3.1.3.16) 2A regulatory B chain	[Drosophila melanogaster]	2.00E-20	O		+	+	+	+	+	+
OctCluster0322.Contig1	548 ref XP_033003.1	similar to evidence:NAS~hypothetical protein~putative	[Homo sapiens]	8.00E-13				+	+			
OctCluster0323.Contig1	513 ref NP_612451.1	hypothetical protein BC013949	[Homo sapiens]	6.00E-22	O		+	+	+	+	+	+
OctCluster0324.Contig1	546 ref XP_147230.1	eukaryotic translation initiation factor 4A2	[Mus musculus]	3.00E-52	O		+	+	+	+	+	+
OctCluster0325.Contig1	540 gb AAC34595.1	ADP/ATP carrier protein	[Candida parapsilosis]	4.00E-43	O		+	+	+	+	+	+
OctCluster0325.Contig2	545 gb AAC23561.1	ADP/ATP carrier	[Trypanosoma brucei brucei]	4.00E-48	O		+	+	+	+	+	+
OctCluster0326.Contig1	544 dbj BAB21109.1	elongation factor 1 delta	[Bombyx mori]	7.00E-24	O		+	+	+	+	+	+
OctCluster0327.Contig1	544 pir	transcription factor IID 30k chain	[Homo sapiens]	2.00E-35	O		+	+	+	+	+	+
OctCluster0328.Contig1	530 ref NP_005767.1	cornichon-like	[Homo sapiens]	8.00E-41	O		+	+	+	+	+	+
OctCluster0331.Contig1	562 ref NP_572921.1	CG11103-PA	[Drosophila melanogaster]	2.00E-41	O		+	+	+	+	+	+
OctCluster0333.Contig1	537 emb CAC94905.1	histone H1	[Mytilus chilensis]	5.00E-12	O		+	+		+	+	+
OctCluster0334.Contig1	494 ref NP_508026.1	FKBP-type peptidyl-prolyl cis-trans isomerases	[Caenorhabditis elegans]	1.00E-37	O		+	+	+	+	+	+
OctCluster0335.Contig1	487 ref NP_055984.1	homolog of yeast ribosome biogenesis regulatory protein RRS1	[Homo sapiens]	4.00E-45			+	+	+	+	+	+
OctCluster0336.Contig1	538 ref NP_542366.1	eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD)	[Mus musculus]	8.00E-60	O		+	+	+	+	+	+
OctCluster0338.Contig1	645 gb AAA97543.1	S-crystallin		6.00E-75					+		+	
OctCluster0339.Contig1	510 ref NP_445933.1	phosphatidylinositol 3-kinase, catalytic subunit, beta isoform	[Rattus norvegicus]	9.00E-23			+	+	+	+	+	+
OctCluster0341.Contig1	530 ref NP_598778.1	expressed sequence A1182287	[Mus musculus]	4.00E-23	O		+	+	+	+	+	+
OctCluster0342.Contig1	556 ref NP_059129.2	myosin IIIA	[Homo sapiens]	1.00E-60	O		+	+	+			
OctCluster0344.Contig1	529 gb EAA10211.1	agCP15298	[Anopheles gambiae str. PEST]	1.00E-27	O		+	+	+	+	+	+
OctCluster0344.Contig2	520 gb EAA10211.1	agCP15298	[Anopheles gambiae str. PEST]	1.00E-29	O		+	+	+		+	+
OctCluster0345.Contig1	529 ref NP_036182.1	ribosomal protein S3	[Mus musculus]	4.00E-80	O		+	+	+		+	+
OctCluster0347.Contig1	528 pir	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	Yeast	6.00E-54	O		+	+	+	+	+	+
OctCluster0347.Contig2	480 pir	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	American lobster	6.00E-42	O		+	+	+	+	+	+
OctCluster0352.Contig1	686 gb EAA09713.1	agCP4381	[Anopheles gambiae str. PEST]	2.00E-08	O		+	+	+	+	+	+
OctCluster0353.Contig1	626 gb AAD02197.1	putative ferritin-1 heavy chain	[Schistosoma japonicum]	5.00E-37	O		+	+	+	+	+	+
OctCluster0355.Contig1	525 sp P46825	Kinesin light chain (KLC)		6.00E-66	O		+	+	+	+	+	+
OctCluster0357.Contig1	524 sp Q07460	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)	[validated]	4.00E-45	O		+	+	+	+	+	+
OctCluster0360.Contig1	493 gb EAA11304.1	agCP6167	[Anopheles gambiae str. PEST]	1.00E-45			+	+	+	+	+	+
OctCluster0361.Contig1	552 pir	omega-crystallin	giant octopus	2.00E-88			+	+	+	+	+	+
OctCluster0362.Contig1	501 ref NP_652042.1	CG9762-PA	[Drosophila melanogaster]	5.00E-18	O		+	+	+	+	+	
OctCluster0363.Contig1	499 ref NP_725886.1	CG9325-PB	[Drosophila melanogaster]	4.00E-22						+	+	+
OctCluster0364.Contig1	555 ref NP_034547.1	hephaestin	[Mus musculus]	2.00E-40	O		+	+	+	+	+	
OctCluster0365.Contig1	522 sp Q25481	Ecdysteroid regulated 16 kDa protein precursor	[Manduca sexta]	3.00E-16			+	+	+	+	+	
OctCluster0367.Contig1	521 gb AAF29081.1	HSPC117	[Homo sapiens]	2.00E-57	O		+	+	+	+	+	+
OctCluster0368.Contig1	498 ref NP_564870.1	copper homeostasis factor, putative	[Arabidopsis thaliana]	2.00E-08			+	+	+	+	+	+
OctCluster0369.Contig1	521 ref NP_001006.1	ribosomal protein S11	[Homo sapiens]	1.00E-61	O		+	+	+	+	+	+
OctCluster0370.Contig1	480 ref NP_068753.1	hypothetical protein FLJ11773	[Homo sapiens]	2.00E-43	O		+	+	+	+	+	+
OctCluster0371.Contig1	520 gb EAA11049.1	agCP5847	[Anopheles gambiae str. PEST]	1.00E-13			+	+	+		+	+
OctCluster0372.Contig1	501 gb EAA08406.1	agCP2931	[Anopheles gambiae str. PEST]	3.00E-11						+	+	
OctCluster0373.Contig1	493 gb AAF70201.1	RGS4 protein	[Xenopus laevis]	2.00E-16	O		+	+	+	+	+	+
OctCluster0375.Contig1	575 sp P27014	S-CRYSTALLIN 2	[Octopus vulgaris]	1.00E-47			+	+	+	+	+	+
OctCluster0376.Contig1	519 ref NP_008850.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3	[Homo sapiens]	3.00E-33	O		+	+	+	+	+	+
OctCluster0377.Contig1	519 ref NP_032019.1	fibrillin 1	[Mus musculus]	3.00E-23	O		+	+	+	+	+	+
OctCluster0378.Contig1	488 ref NP_598516.1	tubulin, gamma complex associated protein 2	[Mus musculus]	1.00E-52	O		+	+	+	+	+	+
OctCluster0379.Contig1	848 dbj BAA95677.1	prosaposin	[Bos taurus]	2.00E-17	O		+	+	+	+	+	+
OctCluster0380.Contig1	608 gb AAB95013.3	Hypothetical protein W04H10.3	[Caenorhabditis elegans]	2.00E-08	O		+	+	+	+		+
OctCluster0381.Contig1	518 ref XP_132423.1	similar to Protein 22A3	[Mus musculus]	4.00E-56	O		+	+		+	+	+
OctCluster0384.Contig1	509 dbj BAA88906.1	PEX13	[Cricetulus griseus]	3.00E-09	O		+	+	+	+	+	+
OctCluster0386.Contig1	529 gb EAA09299.1	agCP13948	[Anopheles gambiae str. PEST]	2.00E-54	O		+	+	+		+	+
OctCluster0387.Contig1	517 gb EAA10598.1	agCP4445	[Anopheles gambiae str. PEST]	2.00E-19			+	+	+		+	
OctCluster0388.Contig1	663 ref NP_001792.1	cysteine dioxygenase, type 1	[Homo sapiens]	3.00E-47	O		+	+	+	+	+	+
OctCluster0389.Contig1	517 ref XP_134591.1	similar to ATP-dependent RNA helicase DDX19 (DEAD-box protein 19)	[Mus musculus]	8.00E-46	O		+	+	+	+	+	+
OctCluster0390.Contig1	521 sp P21613	KINESIN HEAVY CHAIN	longfin squid	5.00E-58	O		+	+	+	+	+	+
OctCluster0391.Contig1	516 gb EAA06334.1	agCP13167	[Anopheles gambiae str. PEST]	3.00E-15	O		+	+	+	+	+	
OctCluster0393.Contig1	806 ref NP_002785.1	proteasome beta 2 subunit	[Homo sapiens]	4.00E-73	O		+	+	+	+	+	+
OctCluster0394.Contig1	515 gb AAC13268.1	reductase-related protein	[Aplysia californica]	4.00E-28								+

OctCluster0395.Contig1	509	gb AAN71009.1	AT01055p	[Drosophila melanogaster]	6.00E-49	O	+	+	+	+	+	+	+
OctCluster0397.Contig1	513	gb AAL85626.1	probable transport protein Sec61 alpha subunit	[Aedes aegypti]	7.00E-66	O	+	+	+	+	+	+	+
OctCluster0398.Contig1	514	ref NP_079900.1	RIKEN cDNA 2510048O06	[Mus musculus]	2.00E-27		+	+	+	+	+	+	
OctCluster0401.Contig1	643	ref XP_128256.1	similar to tubulin alpha 1	[Mus musculus]	0.00E+00	O	+	+	+	+	+	+	+
OctCluster0403.Contig1	529	dbj BAC11164.1	unnamed protein product	[Homo sapiens]	3.00E-09	O	+	+	+	+	+	+	
OctCluster0405.Contig1	509	gb EAA10767.1	agCP5828	[Anopheles gambiae str. PEST]	3.00E-17	O	+	+	+	+	+	+	+
OctCluster0405.Contig2	511	gb EAA10767.1	agCP5828	[Anopheles gambiae str. PEST]	1.00E-11	O	+	+	+		+	+	
OctCluster0407.Contig1	509	ref NP_082203.1	RIKEN cDNA 1110020M19	[Mus musculus]	4.00E-26	O	+	+	+	+	+	+	+
OctCluster0408.Contig1	514	ref NP_071633.1	dimethylarginine dimethylaminohydrolase 1	[Rattus norvegicus]	6.00E-11		+	+	+	+		+	
OctCluster0409.Contig1	510	sp P27013	S-CRYSTALLIN 1	[Octopus vulgaris]	7.00E-15								
OctCluster0412.Contig1	507	dbj BAB21999.1	ADP-ribosylation factor 4	[Mus musculus]	4.00E-07	O	+	+	+	+	+	+	+
OctCluster0413.Contig1	478	ref NP_038749.1	ribosomal protein L7a	[Mus musculus]	1.00E-48	O	+	+	+	+	+	+	+
OctCluster0415.Contig1	680	gb EAA08466.1	agCP2956	[Anopheles gambiae str. PEST]	3.00E-95	O	+	+	+	+	+	+	+
OctCluster0416.Contig1	435	gb AAH31719.1	Similar to dCMP deaminase	[Mus musculus]	4.00E-47		+	+	+	+	+	+	+
OctCluster0417.Contig1	504	ref NP_649840.1	CG9836-PA	[Drosophila melanogaster]	1.00E-55	O	+	+	+	+	+	+	+
OctCluster0418.Contig1	490	dbj BAA37143.1	calcium-ATPase	[Mizuhopecten yessoensis]	6.00E-40	O	+	+	+	+	+	+	+
OctCluster0419.Contig1	742	pdb 1CKJ	Chain A, Casein Kinase I Delta Truncation Mutant Containing Residues 1		1.00E-88	O	+	+	+	+	+	+	+
OctCluster0421.Contig1	511	ref XP_146812.1	similar to hephaestin	[Mus musculus]	7.00E-44	O	+	+	+	+			
OctCluster0426.Contig1	497	gb EAA11811.1	agCP6171	[Anopheles gambiae str. PEST]	8.00E-11	O	+	+	+	+	+	+	+
OctCluster0427.Contig1	497	ref NP_002992.1	succinate dehydrogenase complex, subunit C precursor	[Homo sapiens]	6.00E-30	O	+	+	+	+	+	+	+
OctCluster0429.Contig1	471	ref NP_648054.1	CG8519-PA	[Drosophila melanogaster]	2.00E-15	O	+	+	+	+	+	+	+
OctCluster0432.Contig1	491	gb AAM73989.1	alpha-tubulin 2	[Strongylocentrotus droebachiensis]	3.00E-80	O	+	+	+	+	+	+	+
OctCluster0433.Contig1	573	pdb 1LM8	Chain C, Structure Of A Hif-1a-Pvhl-Elonginb-Elongin Complex		1.00E-23	O	+	+	+	+	+	+	+
OctCluster0434.Contig1	493	ref XP_126850.1	similar to cytochrome c oxidase subunit VIIa polypeptide 2-like	[Mus musculus]	4.00E-09	O	+	+	+			+	
OctCluster0435.Contig1	493	ref XP_087346.1	similar to RIKEN cDNA 2610002K22	[Homo sapiens]	6.00E-60	O	+	+	+	+	+	+	+
OctCluster0436.Contig1	492	ref NP_254272.2	CG8144-PA	[Drosophila melanogaster]	6.00E-18		+	+	+	+	+	+	+
OctCluster0438.Contig1	489	ref NP_064574.1	DC6 protein	[Homo sapiens]	8.00E-26	O	+	+	+	+	+	+	+
OctCluster0439.Contig1	471	gb EAA15121.1	ebiP5193	[Anopheles gambiae str. PEST]	1.00E-27					+	+	+	
OctCluster0442.Contig1	489	ref NP_609243.1	CG18405-PB	[Drosophila melanogaster]	1.00E-29	O	+	+	+	+	+	+	+
OctCluster0445.Contig1	485	emb CAB65409.1	pre-B-cell colony-enhancing factor	[Suberites domuncula]	1.00E-30	O	+	+	+				
OctCluster0448.Contig1	486	ref XP_034890.4	similar to fibrillin	[Homo sapiens]	8.00E-31	O	+	+	+	+	+	+	+
OctCluster0450.Contig1	483	ref NP_445979.1	cell division cycle 5-like	[Rattus norvegicus]	1.00E-20	O	+	+	+	+	+	+	+
OctCluster0453.Contig1	474	ref NP_006801.1	for protein disulfide isomerase-related	[Homo sapiens]	3.00E-15		+			+	+	+	+
OctCluster0456.Contig1	481	dbj BAB67810.2	KIAA1917 protein	[Homo sapiens]	5.00E-41	O	+	+	+	+	+	+	+
OctCluster0458.Contig1	481	dbj BAB89359.1	calmodulin	[Strongylocentrotus intermedius]	1.00E-17	O	+	+	+	+	+	+	+
OctCluster0461.Contig1	478	gb AAH02887.1	Similar to FK506-binding protein 4 (59kD)	[Homo sapiens]	5.00E-28	O	+	+	+	+	+	+	+
OctCluster0467.Contig1	522	ref XP_180018.1	hypothetical protein XP_180018	[Mus musculus]	2.00E-10	O			+	+			
OctCluster0470.Contig1	473	ref NP_496500.1	VF13D12L.3.p	[Caenorhabditis elegans]	8.00E-38				+	+	+	+	+
OctCluster0472.Contig1	473	gb AAN52379.1	ribosomal protein L27	[Branchiostoma belcheri]	2.00E-45	O	+	+	+	+	+	+	+
OctCluster0472.Contig2	468	gb AAN52379.1	ribosomal protein L27	[Branchiostoma belcheri]	4.00E-50	O	+	+	+	+	+		+
OctCluster0473.Contig1	386	ref NP_705780.1	hypothetical protein MGC28284	[Mus musculus]	3.00E-35	O	+	+	+	+	+	+	+
OctCluster0475.Contig1	461	ref NP_651595.1	CG12259-PA	[Drosophila melanogaster]	3.00E-26	O	+	+	+	+	+	+	+
OctCluster0483.Contig1	462	ref NP_033107.1	ribosomal protein L28	[Mus musculus]	5.00E-38	O	+	+	+	+	+	+	+
OctCluster0484.Contig1	506	dbj BAB22732.1	homolog to SEC13-RELATED PROTEIN	[Mus musculus]	2.00E-59	O	+	+	+	+	+	+	+
OctCluster0485.Contig1	573	gb AAC21566.1	heat shock protein hsp90beta	[Danio rerio]	3.00E-17	O	+	+	+	+	+	+	+
OctCluster0487.Contig1	684	ref NP_731941.1	CG7425-PA	[Drosophila melanogaster]	4.00E-58	O	+	+	+	+	+	+	+
OctCluster0489.Contig1	403	emb CAC36306.1	octopine dehydrogenase	[Sepia officinalis]	2.00E-64								
OctCluster0494.Contig1	399	gb AAL48947.1	RE34669p	[Drosophila melanogaster]	2.00E-08		+	+		+	+		
OctCluster0496.Contig1	464	gb EAA01075.1	agCP12752	[Anopheles gambiae str. PEST]	2.00E-39	O	+	+	+	+	+	+	+
OctCluster0498.Contig1	432	gb AAN52381.1	ribosomal protein L36	[Branchiostoma belcheri]	2.00E-29		+	+	+	+	+	+	+
OctCluster0500.Contig1	440	ref NP_065707.2	actopaxin	[Rattus norvegicus]	8.00E-32	O	+	+	+	+	+	+	+
OctCluster0501.Contig1	441	pdb 1BCC	Chain J, Cytochrome Bc1 Complex From Chicken	Chiken	8.00E-15	O	+		+	+	+	+	
OctCluster0503.Contig1	429	dbj BAB23225.1	related to CG11024 PROTEIN	[Mus musculus]	6.00E-34	O	+	+	+	+	+	+	+
OctCluster0504.Contig1	256	sp Q90YS3	40S ribosomal protein S2	[Ictalurus punctatus]	1.00E-07	O	+	+	+	+			
OctCluster0504.Contig2	439	sp Q90YS3	40S ribosomal protein S2	[Ictalurus punctatus]	1.00E-44	O	+	+	+	+	+	+	+
OctCluster0505.Contig1	439	sp P27012	S-CRYSTALLIN 4 (OL4)	giant octopus	2.00E-10								
OctCluster0507.Contig1	457	gb AAH09074.1	Similar to CGI-62 protein	[Homo sapiens]	7.00E-07	O	+	+		+	+	+	
OctCluster0508.Contig1	430	ref NP_035181.1	programmed cell death 6	[Mus musculus]	2.00E-23	O	+	+	+	+	+	+	+
OctCluster0509.Contig1	489	gb EAA06789.1	agCP7485	[Anopheles gambiae str. PEST]	1.00E-09						+	+	

OctCluster0510.Contig1	450	gb EAA05952.1	agCP13832	[Anopheles gambiae str. PEST]	1.00E-19	O	+	+	+	+	+	+	+
OctCluster0512.Contig1	437	gb AAF79180.1	phospholipase C	[Loligo pealei]	1.00E-41	O	+					+	+
OctCluster0513.Contig1	431	ref XP_006997.6	similar to Ninjurin 2 (Nerve injury-induced protein 2)	[Homo sapiens]	1.00E-14		+	+	+			+	+
OctCluster0514.Contig1	431	sp P00129	Ubiquinol-cytochrome C reductase complex 14 kDa protein (Complex III subunit VI)		4.00E-31		+	+	+	+	+	+	+
OctCluster0515.Contig1	349	ref NP_057701.1	hypothetical protein BM-002	[Homo sapiens]	1.00E-28	O	+	+	+	+			+
OctCluster0515.Contig2	429	ref NP_057701.1	hypothetical protein BM-002	[Homo sapiens]	2.00E-33	O	+	+	+	+			+
OctCluster0516.Contig1	379	ref NP_003087.1	small nuclear ribonucleoprotein polypeptide G	[Homo sapiens]	1.00E-27	O	+	+	+	+	+	+	+
OctCluster0516.Contig2	428	ref NP_003087.1	small nuclear ribonucleoprotein polypeptide G	[Homo sapiens]	8.00E-29	O	+	+	+	+	+	+	+
OctCluster0522.Contig1	422	ref NP_212792.1	phosphoglycerate mutase (gpmA)	[Borrelia burgdorferi]	1.00E-46	O	+	+	+	+	+	+	+
OctCluster0525.Contig1	293	gb AAL62468.1	ribosomal protein L3	[Spodoptera frugiperda]	1.00E-22	O	+	+	+	+	+	+	+
OctCluster0525.Contig2	416	gb AAL62468.1	ribosomal protein L3	[Spodoptera frugiperda]	6.00E-56	O	+	+	+	+	+	+	+
OctCluster0527.Contig1	414	dbj BAA36517.1	paramyosin	[Mytilus galloprovincialis]	5.00E-11								
OctCluster0531.Contig1	402	pir	hypothetical protein DKFZp434P106.1	[Homo sapiens]	1.00E-18	O	+	+	+	+	+	+	+
OctCluster0538.Contig1	400	gb EAA12768.1	agCP11395	[Anopheles gambiae str. PEST]	7.00E-26	O	+	+	+	+	+	+	+
OctCluster0542.Contig1	393	ref XP_087346.1	similar to RIKEN cDNA 2610002K22	[Homo sapiens]	7.00E-22	O	+	+	+	+	+	+	+
OctCluster0547.Contig1	390	gb AAF22119.1	guanine nucleotide-binding protein	[Euprymna scolopes]	2.00E-53	O	+	+	+	+	+	+	+
OctCluster0549.Contig1	388	gb AAK61417.1	transposase	[Ceratitis rosa]	1.00E-11								
OctCluster0550.Contig1	384	ref NP_500061.1	Y104H12BR.1.p	[Caenorhabditis elegans]	3.00E-34	O	+	+	+			+	+
OctCluster0551.Contig1	387	sp O73817	Proteasome subunit beta type 3 (Proteasome theta chain)	[Oncorhynchus mykiss]	3.00E-42	O	+	+	+	+	+	+	+
OctCluster0553.Contig1	385	ref NP_571799.1	mitogen-activated protein kinase kinase 3	[Danio rerio]	7.00E-26	O	+	+	+	+	+	+	+
OctCluster0558.Contig1	376	sp O02654	Enolase (2-phosphoglycerate dehydratase)	[Loligo pealei]	1.00E-44	O	+	+	+	+	+	+	+
OctCluster0559.Contig1	379	gb AAL62465.1	60S acidic ribosomal protein P0	[Spodoptera frugiperda]	1.00E-22	O	+	+	+	+	+	+	+
OctCluster0561.Contig1	371	pir	multicatalytic endopeptidase complex (EC 3.4.99.46) chain XC8	clawed frog	2.00E-11		+	+	+	+			+
OctCluster0563.Contig1	399	gb AAL96264.2	helicase/primase complex protein	[Homo sapiens]	5.00E-10	O	+		+				
OctCluster0564.Contig1	362	ref NP_724427.1	CG8390-PB	[Drosophila melanogaster]	7.00E-05		+					+	+
OctCluster0565.Contig1	301	dbj BAA92649.1	KIAA1411 protein	[Homo sapiens]	6.00E-15	O	+		+	+	+	+	+
OctCluster0566.Contig1	364	sp P51971	Protein translation factor SUI1 homolog		7.00E-10	O	+	+	+	+	+	+	+
OctCluster0573.Contig1	357	gb AAC28863.1	ribosomal protein S8	[Apis mellifera]	1.00E-18	O	+	+	+	+	+	+	+
OctCluster0574.Contig1	356	gb AAL79525.1	ADP/ATP carrier	[Neocallimastix patriciarum]	4.00E-05								
OctCluster0575.Contig1	354	emb CAD40994.1	OSJNBa0072F16.18	[Oryza sativa (japonica cultivar-group)]	5.00E-05						+		
OctCluster0576.Contig1	352	ref NP_442422.1	unknown protein	[Synecocystis sp. PCC 6803]	3.00E-06								
OctCluster0582.Contig1	347	ref NP_732309.1	CG31196-PA	[Drosophila melanogaster]	5.00E-37	O	+	+	+	+	+	+	+
OctCluster0585.Contig1	340	gb AAA29403.1	S-crystallin		7.00E-13								
OctCluster0588.Contig1	343	gb EAA09529.1	agCP15016	[Anopheles gambiae str. PEST]	4.00E-09	O	+	+				+	+
OctCluster0589.Contig1	335	pir	omega-crystallin	giant octopus	4.00E-14								
OctCluster0590.Contig1	335	sp P08991	Histone H2A variant	[Strongylocentrotus purpuratus]	2.00E-47	O	+	+	+	+	+	+	+
OctCluster0598.Contig1	454	gb AAD31042.1	heat shock protein 70	[Crassostrea gigas]	4.00E-19	O	+	+	+	+	+	+	+
OctCluster0602.Contig1	266	gb AAA91469.1	HT protein		3.00E-14	O	+	+	+	+	+	+	+
OctCluster0606.Contig1	287	sp O97725	NADH-ubiquinone oxidoreductase subunit B17.2 (Complex I-B17.2)	[Bos taurus]	5.00E-20		+	+	+	+	+	+	+
OctCluster0609.Contig1	274	gb EAA04480.1	agCP3870	[Anopheles gambiae str. PEST]	6.00E-13		+	+	+			+	
OctCluster0619.Contig1	118	ref NP_062837.1	NADH dehydrogenase subunit 1	[Loligo bleekeri]	1.00E-07								
OctCluster0621.Contig1	229	gb AAK92174.1	ribosomal protein L39	[Spodoptera frugiperda]	4.00E-16	O	+	+	+	+	+	+	+
OctCluster0621.Contig2	239	gb AAN52382.1	ribosomal protein L39	[Branchiostoma belcheri]	1.00E-16	O	+	+	+	+	+	+	+
OctCluster0633.Contig1	93	gb AAD29639.1	ferritin	[Octopus dofleini]	1.00E-10	O	+	+	+				+
OctEye_0043F.orphan	492	ref NP_002614.2	prefoldin 4	[Homo sapiens]	1.00E-24		+		+	+	+	+	+
OctEye_0048F.orphan	480	emb CAA63003.1	melanotransferrin/EOS47	[Gallus gallus]	3.00E-16	O	+	+	+	+	+	+	+
OctEye_0172F.orphan	525	ref NP_005827.1	translational inhibitor protein p14.5	[Homo sapiens]	4.00E-38		+	+	+	+	+	+	+
OctEye_0206F.orphan	274	ref NP_501707.1	integral membrane protein E16 like	[Caenorhabditis elegans]	7.00E-11	O	+	+	+			+	+
OctEye_0249F.orphan	309	sp Q9Y3C8	Protein CGI-126 (Protein HSPC155)	[Homo sapiens]	4.00E-47	O	+	+	+	+	+	+	+
OctEye_0390F.orphan	527	gb AAL50218.1	zinc finger transcription factor	[Danio rerio]	7.00E-13	O	+	+	+	+	+	+	+
OctEye_0479F.orphan	511	dbj BAA11226.1	human 26S proteasome subunit p97	[Homo sapiens]	2.00E-61	O	+	+	+	+	+	+	+
OctEye_0590F.orphan	276	sp Q90YP3	40S ribosomal protein S28	[Ictalurus punctatus]	9.00E-20	O	+	+	+	+	+	+	+
OctEye_0675F.orphan	236	gb EAA06918.1	agCP7321	[Anopheles gambiae str. PEST]	3.00E-18	O	+	+	+	+	+	+	+
OctEye_0701F.orphan	338	gb AAF28975.1	HSPC297	[Homo sapiens]	5.00E-05	O					+		
OctEye_0729F.orphan	435	gb AAL34984.1	cathepsine L-like cysteine protease	[Rhodnius prolixus]	9.00E-33	O	+	+	+	+	+	+	+
OctEye_0740F.orphan	296	emb CAC27531.1	eukaryotic translation initiation factor 3 p42	[Platichthys flesus]	1.00E-16	O	+	+	+	+	+	+	+
OctEye_0745F.orphan	529	ref NP_726958.1	CG2861-PB	[Drosophila melanogaster]	2.00E-08		+	+	+	+	+		
OctEye_0789F.orphan	102	ref XP_140033.2	similar to RIKEN cDNA 2900016D05 gene	[Mus musculus]	6.00E-05	O					+	+	
OctEye_0811F.orphan	342	gb AAH36187.1	Similar to serine/arginine repetitive matrix 1	[Homo sapiens]	5.00E-33	O	+	+	+	+	+	+	+

OctEye 0875F.orphan	452 gb EAA12661.1	agCP11064	[Anopheles gambiae str. PEST]	1.00E-53		+	+	+	+	+	+
OctEye 0883F.orphan	468 gb AAH13878.1	Similar to thimet oligopeptidase 1	[Homo sapiens]	1.00E-35	O	+	+	+	+	+	+
OctEye 0907F.orphan	353 gb AAN40769.1	BCH domain-containing Cdc42GAP-like protein	[Homo sapiens]	9.00E-32	O	+	+	+	+	+	+
OctEye 0912F.orphan	480 gb EAA04597.1	agCP3297	[Anopheles gambiae str. PEST]	3.00E-31		+	+	+	+	+	+
OctEye 0979F.orphan	461 gb AAH29806.1	similar to RIKEN cDNA 0610010I12	[Homo sapiens]	1.00E-36		+	+	+	+	+	+
OctEye 1051F.orphan	340 sp P30736	60S RIBOSOMAL PROTEIN L15 (YL10)	[Chironomus tentans]	4.00E-25	O	+	+	+	+	+	+
OctEye 1206F.orphan	435 gb EAA01034.1	agCP12503	[Anopheles gambiae str. PEST]	2.00E-25	O	+	+	+	+	+	+
OctEye 1263F.orphan	446 ref NP_004364.2	cytochrome c oxidase subunit VIa polypeptide 1 precursor	[Homo sapiens]	4.00E-25	O	+	+	+	+	+	+
OctEye 1278F.orphan	542 ref NP_003414.1	zinc finger protein 43 (HTF6)	[Homo sapiens]	4.00E-42	O	+	+	+	+	+	+
OctEye 1285F.orphan	294 gb ZP_00073122.1	hypothetical protein	[Trichodesmium erythraeum IMS101]	9.00E-19	O	+	+	+	+	+	+
OctEye 1302F.orphan	274 gb AAN62848.1	variable region-containing chitin-binding protein 1	[Branchiostoma floridae]	5.00E-06		+		+	+		+
OctEye 1307F.orphan	533 ref NP_001906.1	cytochrome b-561	[Homo sapiens]	8.00E-18	O	+	+	+	+	+	+
OctEye 1343F.orphan	516 ref NP_031756.1	procollagen, type XII, alpha 1	[Mus musculus]	3.00E-09	O		+	+	+		+
OctEye 1353F.orphan	124 gb AAL49305.2	RH08962p	[Drosophila melanogaster]	9.00E-05	O	+	+		+	+	
OctEye 1499F.orphan	506 gb AAF04612.1	long-chain 3-ketoacyl-CoA thiolase	[Sus scrofa]	2.00E-63	O	+	+	+	+	+	+
OctEye 1556F.orphan	538 emb CAD43466.1	SI:PACKT90.1 (novel protein)	[Danio rerio]	4.00E-15	O	+	+	+	+	+	
OctEye 1560F.orphan	435 ref XP_081326.1	Oligomycin sensitivity-conferring protein	[Drosophila melanogaster]	1.00E-20	O		+	+	+	+	+
OctEye 1748F.orphan	463 gb EAA06793.1	agCP7480	[Anopheles gambiae str. PEST]	2.00E-32		+	+	+		+	+
OctEye 1798F.orphan	446 gb AAG48248.1	p70 ribosomal protein S6 kinase	[Artemia franciscana]	6.00E-66	O	+	+	+	+	+	+
OctEye 1824F.orphan	376 gb EAA06789.1	agCP7485	[Anopheles gambiae str. PEST]	8.00E-11						+	+
OctEye 2085F.orphan	110 gb AAN52389.1	ribosomal protein S17	[Branchiostoma belcheri]	4.00E-12		+	+	+	+	+	+
OctEye 2110F.orphan	346 gb EAA12227.1	agCP11263	[Anopheles gambiae str. PEST]	7.00E-26	O	+	+	+	+	+	+
OctEye 2116F.orphan	498 ref NP_611022.2	CG12954-PA	[Drosophila melanogaster]	7.00E-17	O		+		+	+	
OctEye 2262F.orphan	505 sp O15532	Selenoprotein W		3.00E-13	O	+	+		+		
OctEye 2302F.orphan	340 gb AAH19175.1	Similar to methylmalonyl-Coenzyme A mutase	[Mus musculus]	2.00E-48		+	+	+	+		+
OctEye 2363F.orphan	347 gb AAH30079.1	Unknown (protein for IMAGE:1379146)	[Mus musculus]	2.00E-07				+	+		
OctEye 2407F.orphan	99 ref NP_648920.1	CG9705-PA	[Drosophila melanogaster]	1.00E-06	O	+	+	+		+	+
OctEye 2597F.orphan	518 emb CAA39599.1	H(+)-transporting ATP synthase	[Rattus norvegicus]	1.00E-55	O	+	+	+	+	+	+
OctEye 2631F.orphan	403 ref NP_496824.1	Y48C3A.16.p	[Caenorhabditis elegans]	2.00E-44	O	+	+	+	+	+	+
OctEye 2667F.orphan	429 gb AAN71334.1	RE23632p	[Drosophila melanogaster]	2.00E-16	O			+	+	+	+
OctEye 2674F.orphan	442 gb AAH38447.1	Similar to coatomer protein complex, subunit alpha	[Homo sapiens]	4.00E-28		+	+	+	+	+	+
OctEye 2732F.orphan	497 ref NP_064628.1	mitochondrial import receptor Tom22	[Homo sapiens]	4.00E-11	O	+	+	+	+	+	+
OctEye 2761F.orphan	484 gb AAB30248.1	calponin alpha	[chickens, gizzard, Peptide, 292 aa]	6.00E-26	O	+	+	+	+	+	+
OctEye 2765F.orphan	288 ref NP_062839.1	cytochrome c oxidase subunit I	[Loligo bleekeri]	7.00E-32				+	+		
OctEye 2778F.orphan	485 gb EAA01174.1	agCP12107	[Anopheles gambiae str. PEST]	6.00E-60	O	+	+	+	+	+	+
OctEye 2790F.orphan	79 gb AAC06292.1	actin	[Ostertagia ostertagi]	2.00E-06	O	+	+	+	+	+	+
OctEye 2824F.orphan	484 gb EAA00285.1	agCP10016	[Anopheles gambiae str. PEST]	5.00E-27	O	+	+	+	+	+	+
OctEye 2852F.orphan	499 sp Q03443	CRYSTALLIN J1B	Jellyfish	9.00E-23							
OctEye 2877F.orphan	430 pdb 1FVH	Chain A, Crystall Structure Analysis Of Neuronal SecI	[Loligo pealei]	1.00E-69	O	+	+	+	+	+	+
OctEye 2879F.orphan	492 gb AAD13394.1	splicing factor U2AF35	[Takifugu rubripes]	5.00E-28	O	+	+	+	+	+	+
OctEye 2918F.orphan	440 dbj BAB32639.1	integrin alpha-4 subunit	[Bos taurus]	2.00E-24	O	+	+	+	+	+	+
OctEye 2993F.orphan	521 ref NP_647931.1	CG7509-PA	[Drosophila melanogaster]	7.00E-21	O	+	+	+	+	+	+
OctEye 3104F.orphan	455 sp P23935	NADH-ubiquinone oxidoreductase 13 kDa-B subunit (Complex I-13Kd-B)	[Bos taurus]	2.00E-34		+	+	+	+	+	+
OctEye 3179F.orphan	527 sp Q9DGGK4	Translationally-controlled tumor protein (TCTP)	[Danio rerio]	5.00E-25	O	+	+	+	+	+	+
OctEye 3262F.orphan	142 ref NP_651196.1	CG5854-PA	[Drosophila melanogaster]	2.00E-11					+	+	
OctEye 3391F.orphan	489 dbj BAB22103.1	homolog to CDNA FLJ13263 FIS, CLONE OVARC1000924	[Mus musculus]	7.00E-06		+	+				+
OctEye 3530F.orphan	353 gb AAA37061.1	CAD protein		6.00E-15	O	+	+	+	+	+	+
OctEye 3555F.orphan	421 gb EAA15143.1	agCP4709	[Anopheles gambiae str. PEST]	3.00E-06	O		+	+		+	
OctEye 3704F.orphan	369 pir	cytidine deaminase (EC 3.5.4.5)	[Homo sapiens]	4.00E-21		+	+	+	+	+	+
OctEye 3723F.orphan	347 gb AAL99981.1	60S ribosomal protein L37	[Aplysia californica]	1.00E-29		+	+	+	+	+	+
OctEye 3732F.orphan	381 gb AAB02297.1	reverse transcriptase		1.00E-09							
OctEye 3838F.orphan	187 sp P00508	Aspartate aminotransferase, mitochondrial precursor (Transaminase A)	chicken	5.00E-13	O	+	+	+	+	+	+
OctEye 3864F.orphan	476 ref NP_080581.1	RIKEN cDNA 0610040H15	[Mus musculus]	5.00E-25	O	+	+	+	+	+	+
OctEye 3881F.orphan	420 pir	delta-aminolevulinate dehydratase	[Homo sapiens]	2.00E-44		+	+	+	+	+	
OctEye 3893F.orphan	119 sp P91919	TRIOSEPHOSPHATE ISOMERASE (TIM)	[Culex pipiens]	2.00E-11		+	+	+	+	+	+
OctEye 3919F.orphan	500 ref NP_723849.1	CG31811-PB	[Drosophila melanogaster]	1.00E-74	O	+	+	+	+	+	+
OctEye 3974F.orphan	311 gb AAK49985.1	glyceraldehyde phosphate dehydrogenase	[Oncorhynchus mykiss]	6.00E-33	O	+	+	+	+	+	+
OctEye 4093F.orphan	255 gb AAB60655.1	lysosomal glycosylasparaginase	[Homo sapiens]	1.00E-14	O	+	+	+		+	+
OctEye 4166F.orphan	111 gb AAN52374.1	ribosomal protein L18a	[Branchiostoma belcheri]	5.00E-08	O	+	+	+			

OctEye 4211F.orphan	336	ref NP_006545.1	metaxin 2	[Homo sapiens]	2.00E-22	O	+	+	+	+	+	+	+
OctEye 4228F.orphan	237	dbj BAB21824.1	KIAA1733 protein	[Homo sapiens]	1.00E-18	O	+	+	+	+	+	+	+
OctEye 4325F.orphan	530	dbj BAA07894.1	KIAA0098 protein	[Homo sapiens]	1.00E-62	O	+	+	+	+	+	+	+
OctEye 4332F.orphan	352	ref NP_648923.1	CG9710-PA	[Drosophila melanogaster]	7.00E-27	O	+	+	+	+	+	+	+
OctEye 4352F.orphan	402	gb AAK71636.1	protein disulfide isomerase-related protein P5 precursor	[Danio rerio]	1.00E-20		+	+	+	+	+	+	+
OctEye 4422F.orphan	330	ref NP_080077.1	RIKEN cDNA 0610042A05	[Mus musculus]	6.00E-34	O	+	+	+	+	+	+	+
OctEye 4436F.orphan	387	emb CAB40275.1	dJ708F5.1 (PUTATIVE novel Collagen alpha 1 LIKE protein)	[Homo sapiens]	1.00E-11	O	+	+	+	+			+
OctEye 4486F.orphan	494	gb AAN28679.1	cystatin B	[Theromyzon tessulatum]	3.00E-09		+	+	+				
OctEye 4536F.orphan	214	sp Q60445	COATOMER EPSILON SUBUNIT (EPSILON-COAT PROTEIN)	[Cricetulus griseus]	2.00E-12	O	+	+	+	+		+	+
OctEye 4559F.orphan	332	ref NP_062837.1	NADH dehydrogenase subunit 1	[Loligo bleekeri]	1.00E-38						+		
OctEye 4561F.orphan	432	gb EAA14832.1	agCP4971	[Anopheles gambiae str. PEST]	8.00E-40	O	+	+	+	+	+	+	
OctEye 4566F.orphan	432	ref NP_722590.1	CG31973-PB	[Drosophila melanogaster]	1.00E-12						+	+	
OctEye 4576F.orphan	455	ref NP_730192.1	CG3849-PB	[Drosophila melanogaster]	5.00E-45	O	+	+	+	+	+	+	+
OctEye 4582F.orphan	125	gb AAF45418.2	yip6 gene product	[alt 1]	3.00E-10		+		+	+	+	+	+
OctEye 4623F.orphan	537	ref XP_128879.1	similar to ribosomal protein L24-like	[Homo sapiens]	6.00E-60	O	+	+	+	+	+	+	+
OctEye 4675F.orphan	313	emb CAA46450.1	stathmin	[Gallus gallus]	2.00E-06	O	+	+	+	+		+	
OctEye 4700F.orphan	526	sp Q35589	NGFI-A binding protein 1 (EGR-1 binding protein 1)	[Mesocricetus auratus]	2.00E-20	O	+	+		+	+	+	+
OctEye 4703F.orphan	264	ref XP_126459.2	similar to Unconventional myosin from rat 4 for myosin I heavy chain	[Rattus norvegicus]	5.00E-12	O	+	+	+	+	+	+	+
OctEye 4725F.orphan	522	ref NP_609580.1	CG6153-PA	[Drosophila melanogaster]	4.00E-37	O	+	+	+	+	+	+	+
OctEye 4771F.orphan	162	ref NP_446441.1	progestin induced protein	[Rattus norvegicus]	4.00E-19	O	+	+		+	+	+	+
OctEye 4909F.orphan	557	sp O00757	Fructose-1,6-bisphosphatase isozyme 2 (D-fructose-1,6-bisphosphate 1-phosph	[Homo sapiens]	8.00E-51		+	+	+	+	+	+	+
OctEye 4911F.orphan	190	ref NP_506071.1	T04H1.5.p	[Caenorhabditis elegans]	2.00E-05								+
OctEye 4990F.orphan	314	gb AAD55725.1	calreticulin precursor	[Strongylocentrotus purpuratus]	6.00E-13		+	+	+	+		+	+
OctRet 0020F.orphan	391	ref NP_728295.1	CG14235-PB	[Drosophila melanogaster]	4.00E-27	O	+	+	+	+	+		+
OctRet 0033F.orphan	261	gb EAA11938.1	agCP6162	[Anopheles gambiae str. PEST]	5.00E-15	O	+	+	+	+	+	+	+
OctRet 0108F.orphan	592	gb AAN05606.1	ribosomal protein L9	[Argopecten irradians]	5.00E-65	O	+	+	+	+	+	+	+
OctRet 0176F.orphan	591	gb ZP_00128302.1	hypothetical protein	[Pseudomonas syringae pv. syringae B	1.00E-34								
OctRet 0188F.orphan	620	gb ZP_00086025.1	hypothetical protein	[Pseudomonas fluorescens]	6.00E-63						+		+
OctRet 0203F.orphan	87	gb AAH12150.1	Unknown (protein for IMAGE:4558274)	[Homo sapiens]	8.00E-10	O	+	+	+	+	+	+	+
OctRet 0230F.orphan	473	gb AAK09385.1	HSPC011-like protein	[Ophiophagus hannah]	1.00E-10	O	+	+	+	+	+	+	+
OctRet 0275F.orphan	153	gb AAM88922.1	cytochrome b	[Barbus ablabes]	9.00E-16				+				
OctRet 0338F.orphan	447	ref NP_610629.1	CG7712-PA	[Drosophila melanogaster]	1.00E-39		+	+		+	+	+	+
OctRet 0379F.orphan	367	gb ZP_00092717.1	hypothetical protein	[Azotobacter vinelandii]	2.00E-25							+	
OctRet 0428F.orphan	575	pir	murinoglobulin precursor		9.00E-07		+						
OctRet 0438F.orphan	447	gb AAA35521.1	alpha-tubulin	[Homo sapiens]	8.00E-16	O	+	+	+	+	+	+	+
OctRet 0443F.orphan	538	gb EAA13192.1	agCP2764	[Anopheles gambiae str. PEST]	2.00E-27	O	+	+	+		+	+	+
OctRet 0450F.orphan	560	gb EAA01238.1	agCP12425	[Anopheles gambiae str. PEST]	3.00E-06	O	+	+	+	+	+	+	
OctRet 0455F.orphan	512	ref NP_081187.1	similar to signal peptidase 12kDa	[Mus musculus]	1.00E-21		+	+	+	+	+	+	+
OctRet 0464F.orphan	462	ref NP_611940.1	CG4692-PB	[Drosophila melanogaster]	2.00E-22	O	+	+	+	+	+	+	+
OctRet 0498F.orphan	460	ref NP_396326.1	AGR_pAT_567p	[Agrobacterium tumefaciens]	7.00E-17							+	
OctRet 0538F.orphan	272	gb AAH12382.1	Unknown (protein for MGC:21495)	[Homo sapiens]	2.00E-09	O	+	+	+		+	+	
OctRet 0546F.orphan	529	ref NP_644488.1	conserved hypothetical protein	[Xanthomonas axonopodis pv. citri str.	6.00E-15								
OctRet 0600F.orphan	599	gb ZP_00085804.1	hypothetical protein	[Pseudomonas fluorescens]	6.00E-52								
OctRet 0625F.orphan	389	gb AAF16910.1	ING1 protein	[Mus musculus]	1.00E-11	O	+	+	+	+	+	+	
OctRet 0679F.orphan	494	pdb 1BCC	Chain J_Cytochrome Bc1 Complex	chicken	3.00E-12	O	+		+		+	+	
OctRet 0712F.orphan	583	gb EAA05128.1	agCP6973	[Anopheles gambiae str. PEST]	3.00E-47		+	+	+	+	+	+	+
OctRet 0880F.orphan	536	gb ZP_00024708.1	hypothetical protein	[Ralstonia metallidurans]	3.00E-71	O	+	+	+	+	+	+	+
OctRet 0892F.orphan	553	sp Q46392	Collagen alpha 2(I) chain precursor	[Canis familiaris]	1.00E-10	O	+	+	+	+	+		+
OctRet 0896F.orphan	281	ref NP_542293.1	unknown	[Sinorhizobium meliloti phage PBC5]	1.00E-14								
OctRet 0905F.orphan	408	gb ZP_00032343.1	hypothetical protein	[Burkholderia fungorum]	4.00E-28								
OctRet 0914F.orphan	389	gb EAA14915.1	agCP4966	[Anopheles gambiae str. PEST]	2.00E-10	O	+	+	+	+	+	+	+
OctRet 0921F.orphan	532	ref NP_253071.1	probable two-component response regulator	[Pseudomonas aeruginosa PA01]	2.00E-34							+	
OctRet 1029F.orphan	508	ref NP_608692.1	CG3214-PA	[Drosophila melanogaster]	1.00E-34		+	+	+	+	+	+	+
OctRet 1072F.orphan	528	ref NP_715982.1	conserved hypothetical protein	[Shewanella oneidensis MR-1]	4.00E-75								
OctRet 1082F.orphan	506	gb ZP_00086750.1	hypothetical protein	[Pseudomonas fluorescens]	1.00E-72							+	
OctRet 1084F.orphan	339	ref NP_062842.1	NADH dehydrogenase subunit 4	[Loligo bleekeri]	2.00E-10								
OctRet 1090F.orphan	522	gb ZP_00082897.1	hypothetical protein	[Pseudomonas fluorescens]	1.00E-60								
OctRet 1100F.orphan	429	sp P25391	Laminin alpha-1 chain precursor (Laminin A chain)	[Homo sapiens]	9.00E-12	O	+	+	+	+	+	+	+
OctRet 1108F.orphan	203	gb ZP_00124923.1	hypothetical protein	[Pseudomonas syringae pv. syringae B	2.00E-27								

OctRet 1114F.orphan	621 dbj BAB55383.1	unnamed protein product	[Homo sapiens]	3.00E-11		+			+										
OctRet 1118F.orphan	179 gb ZP_00033875.1	hypothetical protein	[Burkholderia fungorum]	5.00E-06															
OctRet 1125F.orphan	551 gb AAK00229.1	myosin VI	[Homo sapiens]	2.00E-31			+		+		+		+		+		+		+
OctRet 1240F.orphan	545 ref NP_062838.1	NADH dehydrogenase subunit 2	[Loligo bleekeri]	2.00E-18															
OctRet 1300F.orphan	357 sp P27013	S-CRYSTALLIN 1	[Octopus vulgaris]	8.00E-22			+		+										
OctRet 1323F.orphan	588 gb ZP_00031363.1	hypothetical protein	[Burkholderia fungorum]	5.00E-76	O		+		+		+		+		+		+		+
OctRet 1339F.orphan	556 ref XP_113111.1	hypothetical protein XP_113111	[Mus musculus]	2.00E-05	O		+												
OctRet 1398F.orphan	400 gb AAF62400.1	EVH1 domain binding protein	[Homo sapiens]	5.00E-06			+				+		+						
OctRet 1424F.orphan	312 ref NP_116136.1	hypothetical protein MGC14697	[Homo sapiens]	5.00E-06	O		+		+		+								
OctRet 1427F.orphan	444 ref NP_572335.1	CG3224-PA	[Drosophila melanogaster]	1.00E-27	O		+		+		+				+		+		+
OctRet 1443F.orphan	520 gb ZP_00083811.1	hypothetical protein	[Pseudomonas fluorescens]	3.00E-49															
OctRet 1452F.orphan	601 gb ZP_00086237.1	hypothetical protein	[Pseudomonas fluorescens]	2.00E-52	O														
OctRet 1460F.orphan	562 ref NP_543149.1	ankyrin repeat and SOCS box-containing protein 11	[Homo sapiens]	1.00E-08	O		+		+		+		+		+		+		+
OctRet 1462F.orphan	598 sp P09241	RHODOPSIN	[Octopus dofleini]	1.00E-72	O		+		+		+		+		+		+		+
OctRet 1465F.orphan	600 ref NP_499369.1	GTP-binding protein	[Caenorhabditis elegans]	1.00E-72	O		+		+		+		+		+		+		+
OctRet 1470F.orphan	610 gb EAA04691.1	ebiP9261	[Anopheles gambiae str. PEST]	3.00E-09			+		+						+		+		
OctRet 1479F.orphan	614 gb ZP_00089363.1	hypothetical protein	[Azotobacter vinelandii]	9.00E-54													+		
OctRet 1499F.orphan	380 ref XP_012145.3	similar to small nuclear ribonucleoprotein polypeptide F	[Homo sapiens]	3.00E-34	O		+		+		+		+		+		+		+
OctRet 1504F.orphan	592 ref NP_521747.1	Hypothetical periplasmic substrate binding ABC transporter protein	[Ralstonia solanacearum]	5.00E-21															
OctRet 1516F.orphan	639 gb ZP_00085585.1	hypothetical protein	[Pseudomonas fluorescens]	1.00E-30															
OctRet 1519F.orphan	608 gb ZP_00087663.1	hypothetical protein	[Pseudomonas fluorescens]	6.00E-88															+
OctRet 1522F.orphan	629 gb ZP_00124051.1	hypothetical protein	[Pseudomonas syringae pv. syringae B]	3.00E-43															
OctRet 1960F.orphan	360 ref NP_062837.1	NADH dehydrogenase subunit 1	[Loligo bleekeri]	3.00E-29											+				
OctRet 1962F.orphan	471 gb AAG28339.1	macrophage migration inhibitory factor	[Amblyomma americanum]	1.00E-24	O		+		+		+		+						+
OctRet 1978F.orphan	473 gb ZP_00027103.1	hypothetical protein	[Ralstonia metallidurans]	8.00E-20															
OctWhole 0016.orphan	546 ref NP_079481.1	endothelial-derived gene 1	[Homo sapiens]	1.00E-10			+		+		+				+		+		
OctWhole 0048.orphan	544 pdb 2HHM	Chain A, Human Inositol Monophosphatase (E.C.3.1.3.25) Dimer Complex	[Homo sapiens]	4.00E-50			+		+		+		+		+		+		+
OctWhole 0071.orphan	509 ref NP_477373.1	CG4008-PA	[Drosophila melanogaster]	2.00E-06											+				
OctWhole 0123.orphan	584 ref XP_037699.2	similar to My004 protein	[Homo sapiens]	3.00E-44			+		+		+		+		+		+		
OctWhole 0164.orphan	573 sp Q02372	NADH-ubiquinone oxidoreductase ASH1 subunit, mitochondrial precursor (C	[Bos taurus]	5.00E-34	O		+		+		+		+		+		+		+
OctWhole 0178.orphan	569 gb AAH12382.1	Unknown (protein for MGC:21495)	[Homo sapiens]	2.00E-10	O		+		+		+		+		+		+		
OctWhole 0180.orphan	512 ref NP_080546.1	RIKEN cDNA 1110012J22	[Mus musculus]	5.00E-06			+		+										
OctWhole 0190.orphan	417 ref NP_002482.1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	[Homo sapiens]	1.00E-13	O		+		+		+		+		+		+		+
OctWhole 0196.orphan	347 sp P50217	Isocitrate dehydrogenase	[NADP]	4.00E-11	O		+		+		+		+		+		+		+
OctWhole 0224.orphan	576 gb EAA06842.1	agCP7375	[Anopheles gambiae str. PEST]	4.00E-38	O		+		+		+		+		+		+		+
OctWhole 0232.orphan	346 gb AAC28863.1	ribosomal protein S8	[Apis mellifera]	1.00E-15	O		+		+		+		+		+		+		+
OctWhole 0257.orphan	559 ref NP_477376.1	CG4585-PA	[Drosophila melanogaster]	7.00E-14											+		+		
OctWhole 0258.orphan	533 ref NP_524606.1	CG12220-PA	[Drosophila melanogaster]	8.00E-23	O		+		+		+		+		+		+		+
OctWhole 0313.orphan	292 gb AAH13417.1	Unknown (protein for MGC:4811)	[Homo sapiens]	3.00E-12	O		+		+		+		+		+		+		+
OctWhole 0333.orphan	527 ref NP_572915.1	CG9941-PA	[Drosophila melanogaster]	3.00E-36	O		+		+		+				+		+		+
OctWhole 0342.orphan	294 dbj BAB59138.1	PCAF	[Gallus gallus]	3.00E-43	O		+		+		+		+		+		+		+
OctWhole 0343.orphan	375 ref NP_524867.2	CG4539-PA	[Drosophila melanogaster]	2.00E-30	O		+		+		+		+		+		+		+
OctWhole 0348.orphan	563 ref NP_524237.1		[Drosophila melanogaster]	1.00E-58	O		+		+		+		+		+		+		+
OctWhole 0350.orphan	522 ref NP_620470.1	CG8947-PA	[Drosophila melanogaster]	4.00E-51	O		+		+		+		+		+		+		+
OctWhole 0375.orphan	501 gb AAC00007.1	cyclophilin-33B	[Homo sapiens]	9.00E-55	O		+		+		+		+		+		+		+
OctWhole 0400.orphan	297 sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	6.00E-21															+
OctWhole 0442.orphan	417 ref XP_167448.1	similar to mitochondrial intermediate peptidase	[Homo sapiens]	1.00E-36	O		+		+		+		+		+		+		+
OctWhole 0507.orphan	446 sp O02654	Enolase (2-phosphoglycerate dehydratase)	[Loligo pealei]	6.00E-63	O		+		+		+		+		+		+		+
OctWhole 0514.orphan	370 ref NP_508911.1	F35C8.7.p	[Caenorhabditis elegans]	7.00E-18	O		+		+		+		+		+		+		+
OctWhole 0547.orphan	409 ref NP_058701.1	fumarate hydratase	[Rattus norvegicus]	7.00E-54	O		+		+		+		+		+		+		+
OctWhole 0590.orphan	353 ref NP_732901.1	CG10371-PA	[Drosophila melanogaster]	8.00E-17	O		+												
OctWhole 0605.orphan	112 sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	1.00E-08			+		+		+		+		+		+		+
OctWhole 0609.orphan	531 pir	myosin-VI	[similarity]	1.00E-23			+		+		+		+		+		+		+
OctWhole 0672.orphan	509 emb CAC86663.1	Six2 protein	[Platynereis dumerilii]	6.00E-78	O		+		+		+		+		+		+		+
OctWhole 0693.orphan	339 sp O02654	Enolase (2-phosphoglycerate dehydratase)	[Loligo pealei]	5.00E-35	O		+		+		+		+		+		+		+
OctWhole 0697.orphan	456 ref NP_036005.1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	[Mus musculus]	6.00E-29	O		+		+		+		+		+		+		+
OctWhole 0712.orphan	459 gb EAA02656.1	ebiP347	[Anopheles gambiae str. PEST]	3.00E-09											+			+	
OctWhole 0722.orphan	516 ref XP_109901.1	similar to gene from NF2/meningioma region of 22q12	[Mus musculus]	3.00E-24			+		+		+		+				+		
OctWhole 0724.orphan	437 gb ZP_00109643.1	hypothetical protein	[Nostoc punctiforme]	6.00E-08															

OctWhole 0732.orphan	388 gb EAA11712.1	agCP5938	[Anopheles gambiae str. PEST]	2.00E-38	O	+	+	+	+	+	+	+	+
OctWhole 0738.orphan	430 sp O42587	26S PROTEASE REGULATORY SUBUNIT 6A (TAT-BINDING PROTEIN)	[Xenopus laevis]	1.00E-48	O	+	+	+	+	+	+	+	+
OctWhole 0760.orphan	412 gb AAH24888.1	RIKEN cDNA 1810045K07 gene	[Mus musculus]	8.00E-29		+	+	+	+				+
OctWhole 0781.orphan	376 pir	Ku autoantigen 86k chain	Chinese hamster	1.00E-16	O	+	+	+	+				
OctWhole 0806.orphan	523 ref NP_082745.1	RIKEN cDNA 3110082I17	[Mus musculus]	2.00E-08		+	+	+	+				
OctWhole 0820.orphan	486 gb EAA09447.1	agCP15118	[Anopheles gambiae str. PEST]	5.00E-07	O	+	+	+	+	+	+		
OctWhole 0846.orphan	455 ref NP_727895.1	CG8962-PA	[Drosophila melanogaster]	5.00E-10	O	+	+	+		+	+		
OctWhole 0879.orphan	510 gb AAH18154.1	RIKEN cDNA 1300011D16 gene	[Mus musculus]	1.00E-31	O	+	+		+	+	+	+	+
OctWhole 0913.orphan	357 ref NP_057055.1	mitochondrial ribosomal protein S7	[Homo sapiens]	1.00E-18	O	+		+	+	+	+	+	+
OctWhole 0936.orphan	410 ref NP_115882.1	adaptor-related protein complex 1, mu 1 subunit	[Homo sapiens]	2.00E-38	O	+	+	+	+	+	+	+	+
OctWhole 0954.orphan	299 ref NP_491709.1	C34G6.2.p	[Caenorhabditis elegans]	3.00E-07	O					+			+
OctWhole 0964.orphan	537 gb AAH02178.1	Unknown (protein for IMAGE:3487040)	[Mus musculus]	9.00E-64	O	+	+	+	+	+	+	+	+
OctWhole 0966.orphan	502 ref NP_619649.1	hepatocellular carcinoma-associated protein HCA4	[Homo sapiens]	1.00E-16	O	+	+	+	+				
OctWhole 0982.orphan	127 gb AAK95155.1	ribosomal protein L28	[Ictalurus punctatus]	8.00E-06				+					
OctWhole 1011.orphan	388 emb CAA11261.1	trp-like protein	[Loligo forbesi]	1.00E-53	O	+	+	+	+	+	+	+	+
OctWhole 1012.orphan	436 ref NP_077169.1	RIKEN cDNA 1110021N07	[Mus musculus]	5.00E-24	O	+	+	+	+	+	+	+	+
OctWhole 1014.orphan	452 ref NP_651609.1	CG12870-PA	[Drosophila melanogaster]	3.00E-47	O	+	+	+	+	+	+	+	+
OctWhole 1019.orphan	308 dbj BAA34531.1	endozepine	[Sus scrofa]	2.00E-21	O	+	+	+	+	+	+	+	+
OctWhole 1089.orphan	452 pir	omega-crystallin	giant octopus	3.00E-37									
OctWhole 1124.orphan	399 gb AAH10182.1	Unknown (protein for MGC:20328)	[Homo sapiens]	2.00E-31	O	+	+	+	+	+	+	+	+
OctWhole 1176.orphan	301 gb AAA81355.1	HPRT gene product		5.00E-17	O	+	+	+	+				+
OctWhole 1215.orphan	335 sp P27016	S-CRYSTALLIN SL18		7.00E-08									
OctWhole 1265.orphan	259 ref NP_728588.1	CG32333-PA	[Drosophila melanogaster]	4.00E-17	O	+		+	+	+	+	+	
OctWhole 1271.orphan	334 gb EAA08455.1	agCP2976	[Anopheles gambiae str. PEST]	2.00E-40		+	+	+	+			+	+
OctWhole 1304.orphan	359 emb CAC36040.1	bA552M11.2.1 (novel protein (isoform 1))	[Homo sapiens]	8.00E-22	O	+	+	+					
OctWhole 1319.orphan	320 ref NP_037258.1	diacylglycerol kinase, gamma	[Rattus norvegicus]	7.00E-05	O	+							
OctWhole 1349.orphan	231 ref NP_506228.1	nidogen like	[Caenorhabditis elegans]	9.00E-05	O								+
OctWhole 1372.orphan	418 ref NP_055629.1	26S proteasome non-ATPase regulatory subunit 6	[Homo sapiens]	3.00E-18	O	+	+	+	+	+	+	+	+
OctWhole 1384.orphan	101 sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	2.00E-09									
OctWhole 1386.orphan	266 pir	polyubiquitin 5	[Volvox carter]	6.00E-39	O	+	+	+	+	+	+	+	+
OctWhole 1415.orphan	508 ref NP_572567.1	CG32701-PA	[Drosophila melanogaster]	5.00E-11	O	+	+	+	+	+	+	+	
OctWhole 1420.orphan	399 ref NP_062751.1	inhibitor of kappaB kinase epsilon	[Mus musculus]	3.00E-11		+	+	+	+	+	+	+	
OctWhole 1490.orphan	340 gb AAK85118.1	non-muscle myosin II heavy chain	[Loligo pealei]	5.00E-24	O	+	+	+	+	+	+		+
OctWhole 1494.orphan	376 gb AAH36076.1	hypothetical protein FLJ10748	[Homo sapiens]	2.00E-20	O	+	+	+	+	+	+	+	+
OctWhole 1496.orphan	312 gb EAA07212.1	agCP10770	[Anopheles gambiae str. PEST]	1.00E-10	O	+	+	+		+	+		
OctWhole 1510.orphan	307 ref NP_573479.1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	[Mus musculus]	2.00E-12	O	+	+	+	+	+	+	+	+
OctWhole 1551.orphan	439 ref NP_082721.1	CGI-100-like protein	[Mus musculus]	2.00E-05	O	+	+	+	+			+	
OctWhole 1657.orphan	360 emb CAA67333.1	dynactin	[Homo sapiens]	1.00E-23	O	+	+	+	+	+	+	+	+
OctWhole 1680.orphan	373 ref NP_084429.1	embryonic growth-associated	[Mus musculus]	4.00E-37	O	+	+	+	+	+	+	+	+
OctWhole 1718.orphan	367 ref NP_663330.1	similar to CG8974 gene product	[Mus musculus]	5.00E-41	O	+	+	+	+	+	+	+	+
OctWhole 1737.orphan	446 sp P50143	T-complex protein 1, gamma subunit (TCP-1-gamma) (CCT-gamma)		2.00E-52	O	+	+	+	+	+	+	+	+
OctWhole 1776.orphan	420 pdb 1Q GK	Chain A, Structure Of Importin Beta Bound To The Ibb Domain Of Importin Alpha	pdb	7.00E-50	O	+	+	+	+	+	+	+	+
OctWhole 1789.orphan	502 ref NP_690057.1	Lethal giant larvae (Drosophila) homolog 1	[Rattus norvegicus]	5.00E-37	O	+	+	+	+	+	+	+	+
OctWhole 1791.orphan	481 gb AAN31640.1	high mobility group protein 1	[Biomphalaria glabrata]	8.00E-42	O	+	+	+	+	+	+	+	+
OctWhole 1792.orphan	426 emb CAC17645.1	dJ776P7.2 (WD repeat domain 3)	[Homo sapiens]	8.00E-27		+	+	+	+	+	+	+	+
OctWhole 1808.orphan	407 gb AAN05595.1	ribosomal protein S8	[Argopecten irradians]	2.00E-52	O	+	+	+	+	+	+	+	+
OctWhole 1826.orphan	340 ref NP_116136.1	hypothetical protein MGC14697	[Homo sapiens]	3.00E-07	O	+	+	+					
OctWhole 1830.orphan	342 ref NP_001876.1	crystallin, alpha B	[Homo sapiens]	3.00E-17	O	+	+	+	+	+	+	+	+
OctWhole 1832.orphan	485 dbj BAB91363.1	chaperone-ABC1-like	[Homo sapiens]	6.00E-15	O			+	+	+	+	+	+
OctWhole 1833.orphan	411 gb AAN71504.1	RH01338p	[Drosophila melanogaster]	1.00E-06	O	+	+	+	+	+	+		
OctWhole 1834.orphan	502 gb AAL56441.1	similar to transmembrane receptor	[Oikopleura dioica]	7.00E-23					+				
OctWhole 1838.orphan	386 ref NP_005642.1	tryptophan 2,3-dioxygenase	[Homo sapiens]	1.00E-26		+	+	+	+	+	+	+	+
OctWhole 1852.orphan	381 sp O16110	Vacuolar ATP synthase 16 kDa proteolipid subunit (V-ATPase C-subunit)	[Aedes aegypti]	1.00E-12	O		+	+	+	+	+		+
OctWhole 1855.orphan	459 ref NP_477176.1	CG17903-PA	[Drosophila melanogaster]	2.00E-44	O	+	+	+	+	+			+
OctWhole 1856.orphan	483 ref NP_569715.1	protocadherin 18	[Mus musculus]	2.00E-17	O	+	+	+	+	+	+		
OctWhole 1857.orphan	391 sp P27012	S-CRYSTALLIN 4 (OL4)		9.00E-10									
OctWhole 1865.orphan	372 ref NP_659138.1	hypothetical protein MGC18784	[Mus musculus]	2.00E-11	O	+	+					+	
OctWhole 1868.orphan	445 ref XP_140685.2	similar to putative G-protein coupled receptor	[Homo sapiens]	5.00E-09									
OctWhole 1873.orphan	381 pir	Alu RNA-binding protein	[Homo sapiens]	7.00E-31	O	+	+	+	+	+			+

OctWhole	1897.orphan	457 gb AAH33521.1	RIKEN cDNA 0610038L10 gene	[Mus musculus]	1.00E-23	+	+	+	+	+	+	+
OctWhole	1915.orphan	318 ref NP_649015.2	CG5567-PA	[Drosophila melanogaster]	5.00E-12				+	+	+	+
OctWhole	2008.orphan	382 ref NP_054781.1	ART-4 protein	[Homo sapiens]	4.00E-21	O	+	+	+	+	+	+
OctWhole	2025.orphan	346 gb EAA00426.1	agCP9910	[Anopheles gambiae str. PEST]	3.00E-30	O		+	+	+	+	+
OctWhole	2027.orphan	415 gb EAA05145.1	agCP7124	[Anopheles gambiae str. PEST]	9.00E-57	O	+	+	+	+	+	+
OctWhole	2042.orphan	516 gb AAH14661.1	hypothetical protein FLJ12448	[Homo sapiens]	1.00E-05	O	+					
OctWhole	2046.orphan	464 gb EAA15143.1	agCP4709	[Anopheles gambiae str. PEST]	4.00E-07	O		+				+
OctWhole	2082.orphan	402 sp Q9CR00	26S proteasome non-ATPase regulatory subunit 9 (26S proteasome regulatory	[Mus musculus]	2.00E-22	O	+	+	+	+	+	+
OctWhole	2089.orphan	413 ref XP_128879.1	similar to ribosomal protein L24-like	[Homo sapiens]	9.00E-44	O	+	+	+	+	+	+
OctWhole	2106.orphan	391 sp Q9Z1E9	Golgi apparatus protein 1 precursor (Golgi sialoglycoprotein MG-160)		2.00E-31		+	+	+	+	+	+
OctWhole	2127.orphan	441 ref NP_610108.1	Na/K-ATPase beta subunit isoform 3	[Drosophila melanogaster]	3.00E-22	O	+	+	+	+	+	+
OctWhole	2139.orphan	477 sp Q16981	APLYCALCIN		4.00E-69	O	+	+	+	+	+	+
OctWhole	2149.orphan	104 sp P27012	S-CRYSTALLIN 4 (OL4)	giant octopus	3.00E-09		+	+				
OctWhole	2210.orphan	372 ref NP_057930.1	IQ motif containing GTPase activating protein 1	[Mus musculus]	2.00E-11	O	+	+	+	+		
OctWhole	2214.orphan	483 sp P82264	GLutamate dehydrogenase (GDH)		4.00E-32	O	+	+	+	+	+	+
OctWhole	2222.orphan	382 gb AAM18076.1	peroxiredoxin V protein	[Branchiostoma belcheri tsingtaunese]	2.00E-26	O	+	+	+		+	+
OctWhole	2239.orphan	441 emb CAC09491.1	contains similarity to F12A21.16	[Oryza sativa (indica cultivar-group)]	2.00E-05							
OctWhole	2294.orphan	479 sp P35574	Glycogen debranching enzyme (Glycogen debrancher)		7.00E-24		+	+		+	+	+
OctWhole	2310.orphan	269 ref NP_006126.1	F-actin capping protein alpha-1 subunit	[Homo sapiens]	2.00E-25	O	+	+	+	+	+	+
OctWhole	2325.orphan	374 gb AAH12382.1	Unknown (protein for MGC:21495)	[Homo sapiens]	1.00E-05	O	+	+				
OctWhole	2333.orphan	466 emb CAC87888.1	toad pancreatic chitinase	[Bufo japonicus]	5.00E-37		+	+	+	+	+	+
OctWhole	2350.orphan	422 gb EAA07830.1	agCP1746	[Anopheles gambiae str. PEST]	1.00E-05				+		+	
OctWhole	2388.orphan	441 sp O42131	DNA topoisomerase II, beta isozyme	[Gallus gallus]	1.00E-26	O	+	+	+	+	+	+
OctWhole	2414.orphan	529 ref NP_055629.1	KIAA0107 gene product	[Homo sapiens]	1.00E-73	O	+	+	+	+	+	+
OctWhole	2439.orphan	346 gb AAL48327.1	cytochrome oxidase subunit 1	[Goniobasis proxima]	1.00E-23		+			+		
OctWhole	2461.orphan	450 dbj BAB28224.1	homolog to CDNA FLJ13000 FIS	[Mus musculus]	1.00E-14	O	+	+		+	+	+
OctWhole	2462.orphan	429 gb ZP_00084442.1	hypothetical protein	[Pseudomonas fluorescens]	3.00E-38				+	+		
OctWhole	2464.orphan	530 gb AAF22029.1	PRO1975	[Homo sapiens]	5.00E-28		+	+	+	+	+	+
OctWhole	2490.orphan	498 ref NP_005585.1	nascent-polypeptide-associated complex alpha polypeptide	[Homo sapiens]	1.00E-46	O	+	+	+	+	+	+
OctWhole	2492.orphan	470 ref NP_689945.1	hypothetical protein FLJ30845	[Homo sapiens]	1.00E-14		+	+	+	+	+	+
OctWhole	2506.orphan	328 ref NP_648985.1	CG7580-PA	[Drosophila melanogaster]	2.00E-21	O	+	+	+	+	+	+
OctWhole	2509.orphan	529 ref NP_647860.1	CG14996-PB	[Drosophila melanogaster]	5.00E-25	O	+	+	+	+	+	+
OctWhole	2530.orphan	428 gb EAA14324.1	ebiP6196	[Anopheles gambiae str. PEST]	7.00E-30	O	+	+	+	+	+	+
OctWhole	2557.orphan	396 ref NP_609900.1	CG10343-PA	[Drosophila melanogaster]	2.00E-06	O	+	+	+	+	+	+
OctWhole	2561.orphan	461 ref NP_610220.1	CG15908-PA	[Drosophila melanogaster]	3.00E-27	O				+	+	+
OctWhole	2606.orphan	500 ref XP_127612.1	similar to SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALY	[Mus musculus]	2.00E-42	O	+	+	+	+	+	+
OctWhole	2656.orphan	492 ref NP_002790.1	proteasome beta 7 subunit proprotein	[Homo sapiens]	2.00E-56		+	+	+	+	+	+
OctWhole	2680.orphan	324 sp Q9WUB9	Macrophage receptor MARCO (Macrophage receptor with collagenous struct	[Mesocricetus auratus]	2.00E-16	O	+	+	+	+	+	+
OctWhole	2683.orphan	493 sp Q62825	Exocyst complex component Sec6 (rSec6)		5.00E-22	O		+	+	+	+	+
OctWhole	2731.orphan	509 ref NP_080135.1	RIKEN cDNA 2310008D22	[Mus musculus]	3.00E-48	O	+	+	+	+	+	+
OctWhole	2733.orphan	539 ref NP_497684.1	Y53G8AM.1.p	[Caenorhabditis elegans]	4.00E-11				+		+	+
OctWhole	2745.orphan	481 gb AAG45156.1	10.4 kDa basic protein	[Amblyomma hebraeum]	1.00E-21	O	+	+	+	+	+	+
OctWhole	2792.orphan	513 ref NP_501984.1	sodium/calcium exchanger protein like	[Caenorhabditis elegans]	6.00E-28	O	+	+	+	+	+	+
OctWhole	2871.orphan	231 ref NP_114159.1	MSTP043 protein	[Homo sapiens]	9.00E-15	O	+	+	+	+	+	+
OctWhole	2876.orphan	510 sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	3.00E-29							+
OctWhole	2894.orphan	481 gb AAD33728.1	Cctq	[Bos taurus]	2.00E-31	O	+	+	+	+	+	+
OctWhole	2936.orphan	508 ref NP_503917.1	F35F10.12.p	[Caenorhabditis elegans]	1.00E-06					+	+	+
OctWhole	2945.orphan	454 ref NP_002859.1	RAB5B, member RAS oncogene family	[Homo sapiens]	9.00E-54	O	+	+	+	+	+	+
OctWhole	2990.orphan	529 emb CAD43405.1	gelsolin-like protein	[Lumbricus terrestris]	3.00E-47	O	+	+	+	+	+	+
OctWhole	2993.orphan	525 ref NP_060769.1	hypothetical protein FLJ11011	[Homo sapiens]	2.00E-35	O	+	+	+	+	+	+
OctWhole	3002.orphan	531 emb CAB38081.1	Su(fu) protein	[Mus musculus]	2.00E-43	O	+	+	+	+	+	+
OctWhole	3026.orphan	516 ref NP_114192.1	syntenin	[Rattus norvegicus]	2.00E-63	O	+	+	+	+	+	+
OctWhole	3032.orphan	354 emb CAD28495.1	hypothetical protein	[Homo sapiens]	2.00E-09	O	+		+			
OctWhole	3052.orphan	501 ref NP_071609.1	aldehyde dehydrogenase family 9, subfamily A1	[Rattus norvegicus]	1.00E-39	O	+	+	+	+	+	+
OctWhole	3068.orphan	515 gb AAK12359.1	elongation factor-2	[Nereis virens]	5.00E-55	O	+	+	+	+	+	+
OctWhole	3069.orphan	402 gb AAA90933.1	L-isoaspartyl/D-aspartyl protein carboxyl methyltransferase		3.00E-12	O	+	+	+	+	+	+
OctWhole	3103.orphan	342 sp Q92119	Exosome complex exonuclease RRP41 (Ribosomal RNA processing protein 4	[Mus musculus]	5.00E-28	O		+	+	+	+	+
OctWhole	3192.orphan	547 ref NP_076222.1	carnitine O-octanoyltransferase	[Mus musculus]	3.00E-40	O	+	+	+	+	+	+
OctWhole	3215.orphan	510 ref NP_572928.1	CG10997-PA	[Drosophila melanogaster]	4.00E-09					+	+	

OctWhole 3221.orphan	338 dbj BAB31587.1	homolog to UBINUCLEIN	[Mus musculus]	1.00E-06	O	+						
OctWhole 3223.orphan	548 gb EAA00937.1	agCP12672	[Anopheles gambiae str. PEST]	5.00E-25	O	+	+	+	+	+	+	+
OctWhole 3233.orphan	500 sp O77622	T-complex protein 1, zeta subunit (TCP-1-zeta) (CCT-zeta)	[Oryctolagus cuniculus]	1.00E-32	O	+	+	+	+	+	+	+
OctWhole 3241.orphan	513 sp P09623	DIHYDROLIPOAMIDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR		3.00E-77	O	+	+	+	+	+	+	+
OctWhole 3247.orphan	527 dbj BAA13382.2	Similar to Plasmodium falciparum glutamic acid-rich protein precursor (A545	[Homo sapiens]	9.00E-08		+		+				
OctWhole 3249.orphan	541 dbj BAA31641.1	KIAA0666 protein	[Homo sapiens]	6.00E-50	O	+	+	+	+	+	+	+
OctWhole 3253.orphan	548 ref NP_542124.1	sorting nexin 4	[Mus musculus]	7.00E-36	O	+	+	+	+	+	+	+
OctWhole 3293.orphan	542 ref NP_077167.1	RIKEN cDNA 1200003C05	[Mus musculus]	1.00E-30	O	+	+	+	+	+	+	+
OctWhole 3305.orphan	511 ref NP_002159.1	isocitrate dehydrogenase 2 (NADP+), mitochondrial	[Homo sapiens]	8.00E-46	O	+	+	+	+	+	+	+
OctWhole 3329.orphan	396 sp P27010	S-CRYSTALLIN 2 (OL2)	giant octopus	2.00E-20						+		
OctWhole 3343.orphan	316 ref XP_147855.1	RIKEN cDNA C030013D06	[Mus musculus]	8.00E-07	O	+	+	+	+		+	
OctWhole 3348.orphan	488 ref XP_130984.1	similar to RIKEN cDNA 2610034E18 gene	[Mus musculus]	6.00E-23		+	+	+	+			
OctWhole 3350.orphan	464 gb AAA35105.1	putative prf		6.00E-06				+				
OctWhole 3394.orphan	462 sp Q9XSK2	CD63 antigen	[Bos taurus]	3.00E-12	O	+	+	+	+	+	+	+
OctWhole 3418.orphan	440 gb EAA14314.1	agCP8431	[Anopheles gambiae str. PEST]	4.00E-39	O	+	+	+	+	+	+	+
OctWhole 3428.orphan	511 gb AAN04052.1	mitochondrial inorganic phosphate carrier	[Rana sylvatica]	6.00E-54		+	+	+	+	+	+	+
OctWhole 3452.orphan	472 gb EAA06328.1	agCP13512	[Anopheles gambiae str. PEST]	2.00E-18				+	+	+	+	+
OctWhole 3515.orphan	505 dbj BAB69766.1	glucose-regulated protein GRP94 precursor	[Bos taurus]	1.00E-55	O	+	+	+	+	+	+	+
OctWhole 3518.orphan	506 ref NP_061118.1	nucleolar protein family A, member 3	[Homo sapiens]	2.00E-19	O	+	+	+		+	+	+
OctWhole 3533.orphan	493 ref NP_524727.2	CG8144-PA	[Drosophila melanogaster]	2.00E-30		+	+	+	+	+	+	
OctWhole 3550.orphan	502 gb AAH16841.1	Similar to RAB34, member RAS oncogene family	[Homo sapiens]	3.00E-26	O	+	+	+	+	+	+	+
OctWhole 3564.orphan	512 ref NP_077814.1	CDK5 activator-binding protein C53	[Rattus norvegicus]	4.00E-14		+	+	+	+		+	
OctWhole 3568.orphan	450 gb EAA05650.1	agCP10616	[Anopheles gambiae str. PEST]	3.00E-07						+		+
OctWhole 3569.orphan	511 pir	phosphatidylinositol-specific phospholipase C	[Loligo forbesi]	6.00E-88	O	+	+	+	+	+	+	+
OctWhole 3586.orphan	487 dbj BAB12216.1	vasa homolog	[Ciona savignyi]	3.00E-49	O	+	+	+	+	+	+	+
OctWhole 3597.orphan	395 gb AAL62471.1	ribosomal protein L34	[Spodoptera frugiperda]	6.00E-29	O	+	+	+	+	+	+	+
OctWhole 3650.orphan	506 ref NP_062410.1	Down syndrome critical region protein 2	[Mus musculus]	4.00E-05		+	+	+				
OctWhole 3673.orphan	528 ref NP_609170.1	CG7224-PA	[Drosophila melanogaster]	4.00E-17		+	+	+	+	+		+
OctWhole 3678.orphan	529 sp P08429	60S ribosomal protein L4A (L1A)	[Xenopus laevis]	6.00E-37	O	+	+	+	+	+	+	+
OctWhole 3698.orphan	521 ref NP_006746.1	transaldolase 1	[Homo sapiens]	4.00E-39			+	+	+	+	+	+
OctWhole 3771.orphan	107 dbj BAB69766.1	glucose-regulated protein GRP94 precursor	[Bos taurus]	6.00E-05	O	+	+	+	+	+		+
OctWhole 3790.orphan	443 sp Q9Z1D1	Eukaryotic translation initiation factor 3 subunit 4 (eIF-3 delta)	[Mus musculus]	1.00E-13	O	+	+	+	+	+	+	
OctWhole 3792.orphan	493 pir	zinc-finger protein, BR140	[Homo sapiens]	6.00E-74	O	+	+	+	+	+	+	+
OctWhole 3814.orphan	489 dbj BAB47390.1	mitochondrial ATP synthase gamma-subunit	[Cyprinus carpio]	9.00E-38	O	+	+	+	+	+	+	+
OctWhole 3840.orphan	365 gb AAH06863.1	fatty acid amide hydrolase	[Mus musculus]	1.00E-18	O	+		+	+	+	+	+
OctWhole 3844.orphan	515 ref NP_062768.1	DnaJ (Hsp40) homolog, subfamily A, member 2	[Mus musculus]	7.00E-55	O	+	+	+	+	+	+	+
OctWhole 3850.orphan	517 gb EAA00401.1	agCP9498	[Anopheles gambiae str. PEST]	9.00E-08							+	
OctWhole 3901.orphan	516 gb EAA00947.1	agCP12126	[Anopheles gambiae str. PEST]	2.00E-46	O	+	+	+	+	+	+	+
OctWhole 3915.orphan	492 ref NP_496566.1	Y17G7B.10b.p	[Caenorhabditis elegans]	4.00E-08						+		+
OctWhole 3985.orphan	376 gb EAA00232.1	agCP9536	[Anopheles gambiae str. PEST]	5.00E-30	O		+	+	+	+	+	+
OctWhole 3986.orphan	120 sp P97275	Alkylldihydroxyacetonephosphate synthase, peroxisomal precursor (Alkyl-DH	[Cavia sp.]	1.00E-05	O	+	+	+				
OctWhole 4055.orphan	468 emb CAC83970.1	putative aggregation factor	[Geodia cydonium]	2.00E-08	O	+	+	+	+	+	+	
OctWhole 4073.orphan	122 gb AAA40619.1	iodothyronine 5'-monodeiodinase		2.00E-08	O	+		+	+	+	+	+
OctWhole 4145.orphan	551 gb AAF22119.1	guanine nucleotide-binding protein	[Euprymna scolopes]	7.00E-83	O	+	+	+	+	+	+	+
OctWhole 4165.orphan	514 gb EAA10674.1	agCP5405	[Anopheles gambiae str. PEST]	2.00E-42	O	+	+	+	+	+	+	+
OctWhole 4232.orphan	552 gb EAA13946.1	agCP8629	[Anopheles gambiae str. PEST]	4.00E-45		+	+	+	+	+	+	+
OctWhole 4243.orphan	497 sp P46023	G-protein coupled receptor GRL101 precursor	[Lymnaea stagnalis]	7.00E-22	O	+	+	+	+	+	+	+
OctWhole 4246.orphan	545 gb AAB62720.1	alpha 1,2-mannosidase	[Spodoptera frugiperda]	1.00E-09		+	+	+			+	
OctWhole 4317.orphan	485 gb EAA00852.1	agCP12079	[Anopheles gambiae str. PEST]	7.00E-40	O	+	+	+	+	+	+	+
OctWhole 4320.orphan	527 gb EAA04167.1	agCP3428	[Anopheles gambiae str. PEST]	3.00E-43	O		+	+	+	+	+	+
OctWhole 4396.orphan	521 gb EAA04739.1	agCP3470	[Anopheles gambiae str. PEST]	1.00E-47	O	+	+	+	+	+	+	+
OctWhole 4466.orphan	516 gb AAL55705.1	putative deoxyribonucleoside kinase	[Xenopus laevis]	7.00E-47	O	+	+	+	+	+	+	
OctWhole 4474.orphan	356 gb EAA08621.1	agCP2424	[Anopheles gambiae str. PEST]	5.00E-38	O	+	+	+	+	+	+	+
OctWhole 4561.orphan	514 ref NP_476667.1	CG5119-PA	[Drosophila melanogaster]	2.00E-06	O			+		+		+
OctWhole 4595.orphan	521 dbj BAB91862.1	putative carboxymethylglutaminase	[Oryza sativa (japonica cultivar-group)]	6.00E-17								
OctWhole 4597.orphan	480 ref NP_598485.1	RIKEN cDNA 2610101N07	[Mus musculus]	2.00E-15	O	+	+	+		+	+	
OctWhole 4613.orphan	482 ref NP_060563.1	hypothetical protein FLJ10439	[Homo sapiens]	1.00E-16	O	+	+	+	+			+
OctWhole 4636.orphan	552 gb EAA10773.1	agCP5749	[Anopheles gambiae str. PEST]	2.00E-27	O	+	+	+	+	+	+	+
OctWhole 4654.orphan	456 gb EAA00119.1	agCP9725	[Anopheles gambiae str. PEST]	1.00E-18					+	+	+	+

OctWhole 4670.orphan	515 gb AAC25716.1	suppressin	[Homo sapiens]	2.00E-05	O							
OctWhole 4674.orphan	472 ref XP_087420.1	similar to CG7049 gene product	[Homo sapiens]	8.00E-54		+	+	+	+	+	+	
OctWhole 4681.orphan	535 ref NP_079351.1	hypothetical protein FLJ23445	[Homo sapiens]	4.00E-42		+	+	+	+	+	+	+
OctWhole 4702.orphan	513 sp P13602	TUBULIN BETA-2 CHAIN	[Xenopus laevis]	6.00E-46	O	+	+	+	+	+	+	+
OctWhole 4754.orphan	521 sp P21613	KINESIN HEAVY CHAIN	longfin squid	3.00E-83	O	+	+	+	+	+	+	+
OctWhole 4793.orphan	486 dbj BAA91900.1	unnamed protein product	[Homo sapiens]	4.00E-11	O	+	+	+			+	+
OctWhole 4801.orphan	463 gb EAA13808.1	agCP8488	[Anopheles gambiae str. PEST]	1.00E-47	O	+	+	+	+	+	+	+
OctWhole 4810.orphan	497 pdb 1GW5	Chain M, Ap2 Clathrin Adaptor Core		6.00E-58	O	+	+	+	+	+	+	+
OctWhole 4811.orphan	514 ref NP_724278.1	CG2615-PB	[Drosophila melanogaster]	5.00E-56	O	+	+	+	+	+	+	+
OctWhole 4876.orphan	494 ref NP_006818.1	transmembrane trafficking protein	[Homo sapiens]	5.00E-44	O	+	+	+	+	+	+	+
OctWhole 4915.orphan	472 gb AAF34578.1	ADP-ribosylation factor	[Entamoeba histolytica]	9.00E-10	O	+	+	+	+	+	+	+
OctWhole 4999.orphan	481 ref XP_127465.1	similar to hypothetical gene supported by XM_059671	[Homo sapiens]	3.00E-13		+						
OctWhole 5031.orphan	206 dbj BAB23925.1	putative-synbindin	[Mus musculus]	8.00E-21		+	+	+	+	+	+	+
OctWhole 5077.orphan	455 gb AAL66295.1	hepatocellular carcinoma-associated antigen HCA557b	[Homo sapiens]	4.00E-13		+	+	+	+			
OctWhole 5143.orphan	517 ref NP_726627.1	CG11081-PB	[Drosophila melanogaster]	6.00E-12	O	+	+	+	+	+	+	+
OctWhole 5211.orphan	495 gb AAF81184.1	actin	[Japetella diaphana]	5.00E-89	O	+	+	+	+	+	+	+
OctWhole 5231.orphan	481 ref NP_032968.1	puromycin-sensitive aminopeptidase	[Mus musculus]	1.00E-11		+	+	+	+	+	+	
OctWhole 5276.orphan	521 ref NP_002479.1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	[Homo sapiens]	2.00E-20	O	+	+	+	+	+	+	+
OctWhole 5310.orphan	468 sp P33477	Annexin A11 (Annexin XI)	[Oryctolagus cuniculus]	2.00E-31	O	+	+	+	+	+	+	+
OctWhole 5377.orphan	335 ref NP_062845.1	ATP synthase F0 subunit 6	[Loligo bleekeri]	2.00E-21					+			
OctWhole 5388.orphan	416 ref NP_060916.1	glycosyltransferase AD-017	[Homo sapiens]	3.00E-21	O	+	+	+				
OctWhole 5440.orphan	420 sp Q25531	Vacuolar ATP synthase subunit d (V-ATPase d subunit)	[Manduca sexta]	3.00E-54	O	+	+	+	+	+	+	+
OctWhole 5443.orphan	469 ref NP_057336.1	baculoviral IAP repeat-containing 6	[Homo sapiens]	1.00E-29	O	+	+	+		+	+	
OctWhole 5472.orphan	456 ref NP_001705.1	Bicaudal D homolog 1 (Drosophila)	[Homo sapiens]	3.00E-14	O	+	+	+	+	+	+	
OctWhole 5555.orphan	540 ref XP_148358.1	hypothetical protein XP_148358	[Mus musculus]	2.00E-31		+	+	+			+	
OctWhole 5632.orphan	319 ref NP_035314.1	proteasome (prosome, macropain) subunit, alpha type 3	[Mus musculus]	3.00E-26	O	+	+	+	+	+	+	+
OctWhole 5658.orphan	540 dbj BAA76333.1	DUF87	[Xenopus laevis]	1.00E-22	O	+	+	+	+	+	+	+
OctWhole 5713.orphan	347 gb AAH03447.1	FK506 binding protein 4 (59 kDa)	[Mus musculus]	3.00E-13	O	+	+	+	+	+	+	+
OctWhole 5756.orphan	486 ref NP_060357.1	hypothetical protein FLJ20580	[Homo sapiens]	1.00E-44		+	+	+	+	+	+	+
OctWhole 5801.orphan	515 dbj BAB26488.1	homolog to TRANSCRIPTIONAL CO-ACTIVATOR CRSP34~putative	[Mus musculus]	1.00E-14		+	+	+	+	+	+	+
OctWhole 5819.orphan	519 gb EAA03925.1	agCP3191	[Anopheles gambiae str. PEST]	6.00E-25	O	+	+	+	+	+	+	+
OctWhole 5871.orphan	414 ref XP_086222.1	hypothetical protein XP_086222	[Homo sapiens]	1.00E-26		+	+	+	+	+	+	
OctWhole 5882.orphan	467 gb AAA66351.1	TB2		3.00E-33	O	+	+	+	+	+	+	+
OctWhole 5893.orphan	423 ref NP_650596.1	CG5169-PA	[Drosophila melanogaster]	3.00E-56	O	+	+	+	+	+	+	+
OctWhole 5898.orphan	344 ref NP_542123.1	transmembrane 9 superfamily member 2	[Mus musculus]	8.00E-44	O	+	+	+	+	+	+	+
OctWhole 5962.orphan	300 ref NP_446083.1	Breakpoint cluster region protein, uterine leiomyoma, 1	[Rattus norvegicus]	3.00E-17		+	+	+	+	+	+	+
OctWhole 6013.orphan	482 ref NP_498094.1	Mitochondrial carrier protein	[Caenorhabditis elegans]	1.00E-32		+	+	+	+	+	+	+
OctWhole 6062.orphan	425 dbj BAB26566.1	homolog to BRAIN MY042 PROTEIN~putative	[Mus musculus]	2.00E-29		+	+	+	+	+	+	
OctWhole 6141.orphan	521 ref NP_650523.1	CG5903-PA	[Drosophila melanogaster]	1.00E-08		+	+	+		+	+	+
OctWhole 6146.orphan	530 sp P56101	Cysteine string protein (CCCS1)	Pacific electric ray	2.00E-40	O	+	+	+	+	+	+	+
OctWhole 6150.orphan	539 gb AAC47022.1	chitinase prf		5.00E-36		+	+	+	+	+	+	+
OctWhole 6171.orphan	536 gb AAB08478.1	XFEN1b	[Xenopus laevis]	5.00E-55		+	+	+	+	+	+	+
OctWhole 6176.orphan	528 gb AAC51180.1	kruppel-related zinc finger protein		5.00E-12	O	+	+	+	+	+	+	+
OctWhole 6182.orphan	117 gb EAA11776.1	agCP5746	[Anopheles gambiae str. PEST]	5.00E-09	O	+	+	+	+	+	+	+
OctWhole 6187.orphan	320 gb AAH12382.1	Unknown (protein for MGC:21495)	[Homo sapiens]	7.00E-05	O							
OctWhole 6189.orphan	402 ref XP_040948.8	similar to cytoplasmic dynein heavy chain	[Homo sapiens]	2.00E-23	O	+	+	+	+	+		
OctWhole 6222.orphan	510 ref NP_062626.1	arsA (bacterial) arsenite transporter, ATP-binding, homolog 1	[Mus musculus]	1.00E-57	O	+	+	+	+	+	+	+
OctWhole 6227.orphan	512 ref NP_003483.1	chromosome X open reading frame 12	[Homo sapiens]	6.00E-08	O	+						
OctWhole 6234.orphan	507 gb AAA37418.1	chaperonin		2.00E-50	O	+	+	+	+	+	+	+
OctWhole 6242.orphan	228 gb EAA09489.1	agCP14911	[Anopheles gambiae str. PEST]	1.00E-20		+		+	+	+	+	+
OctWhole 6249.orphan	284 gb EAA12355.1	agCP11081	[Anopheles gambiae str. PEST]	6.00E-34		+	+		+	+	+	+
OctWhole 6324.orphan	504 ref NP_651601.1	CG5520-PA	[Drosophila melanogaster]	4.00E-48	O	+	+	+	+	+	+	+
OctWhole 6339.orphan	463 ref XP_140260.1	similar to Homeobox domain	[Caenorhabditis elegans]	9.00E-10		+	+	+	+			
OctWhole 6342.orphan	539 ref NP_492814.1	B0205.4.p	[Caenorhabditis elegans]	1.00E-15		+	+					+
OctWhole 6344.orphan	509 gb AAD50299.1	rac GTPase	[Xenopus laevis]	5.00E-68	O	+	+	+	+	+	+	+
OctWhole 6356.orphan	448 sp Q9R1R2	Tripartite motif protein 3 (RING finger protein 22)	[Mus musculus]	5.00E-17	O	+	+	+	+	+	+	+
OctWhole 6412.orphan	493 ref XP_135859.1	RIKEN cDNA 1810018L05	[Mus musculus]	2.00E-27	O	+	+	+	+			+
OctWhole 6414.orphan	508 gb EAA06334.1	agCP13167	[Anopheles gambiae str. PEST]	5.00E-68	O	+	+	+	+	+	+	+
OctWhole 6417.orphan	494 gb AAA60151.1	snRNP polypeptide B		2.00E-49	O	+	+	+	+	+	+	+

OctWhole	6431.orphan	527 gb AAF63406.1	galectin	[Haemonchus contortus]	3.00E-07		+					+
OctWhole	6441.orphan	543 ref XP_134444.2	similar to Hypothetical protein KIAA0513	[Mus musculus]	3.00E-28		+	+	+	+	+	+
OctWhole	6452.orphan	508 ref NP_611606.1	CG9878-PA	[Drosophila melanogaster]	4.00E-25		+	+	+	+	+	+
OctWhole	6480.orphan	562 ref NP_059129.2	myosin IIIA	[Homo sapiens]	3.00E-35	O	+	+	+	+	+	+
OctWhole	6496.orphan	539 emb CAC39613.1	LanC-like protein 1	[Danio rerio]	8.00E-36	O	+	+	+	+	+	+
OctWhole	6506.orphan	491 sp P98194	Calcium-transporting ATPase type 2C, member 1 (ATPase 2C1)		5.00E-46	O	+	+	+	+	+	+
OctWhole	6514.orphan	501 gb AAG44126.1	reptin	[Xenopus laevis]	6.00E-48	O	+	+	+	+	+	+
OctWhole	6529.orphan	488 gb AAM18076.1	peroxiredoxin V protein	[Branchiostoma belcheri tsingtaunese]	1.00E-05							
OctWhole	6537.orphan	550 gb AAF63957.1	CALNUC	[Spodoptera frugiperda]	1.00E-26	O	+	+	+	+	+	+
OctWhole	6540.orphan	549 sp Q9DC48	Pre-mRNA splicing factor PRP17	[Mus musculus]	1.00E-29	O	+	+	+	+	+	+
OctWhole	6543.orphan	520 gb EAA04429.1	agCP3657	[Anopheles gambiae str. PEST]	1.00E-14	O	+	+	+		+	+
OctWhole	6544.orphan	547 pir	hypothetical protein DKFZp586N1020.1	[Homo sapiens]	3.00E-37	O	+	+	+	+	+	+
OctWhole	6551.orphan	546 dbj BAB60813.1	calponin-like protein	[Mytilus galloprovincialis]	7.00E-49	O	+	+	+	+		+
OctWhole	6592.orphan	510 gb AAG42103.2	karyopherin alpha 2	[Sus scrofa]	4.00E-40	O	+	+	+	+	+	+
OctWhole	6600.orphan	522 pir	GTP-binding protein 2	[Homo sapiens]	4.00E-35	O	+	+	+	+	+	+
OctWhole	6608.orphan	538 gb AAB28640.1	mortalin mot-1=hsp70 homolog cytosolic form	[Mus musculus]	3.00E-42	O	+	+	+	+	+	+
OctWhole	6615.orphan	536 gb AAH27549.1	Similar to DC13 protein	[Mus musculus]	3.00E-13	O	+	+	+			+
OctWhole	6646.orphan	517 ref XP_045290.1	similar to RIKEN cDNA 1200015E15	[Homo sapiens]	2.00E-32	O	+	+	+	+	+	+
OctWhole	6647.orphan	521 ref XP_126943.1	similar to small nuclear RNA activating complex, polypeptide 1, 43kDa	[Homo sapiens]	3.00E-23		+	+	+	+	+	
OctWhole	6649.orphan	532 ref NP_523414.1	CG12530-PA	[Drosophila melanogaster]	2.00E-92	O	+	+	+	+	+	+
OctWhole	6681.orphan	499 ref NP_000099.1	dihydrolipoamide dehydrogenase precursor	[Homo sapiens]	2.00E-43	O	+	+	+	+	+	+
OctWhole	6682.orphan	268 gb AAH28246.1	RIKEN cDNA 2310005B10 gene	[Mus musculus]	1.00E-33	O	+	+	+	+	+	+
OctWhole	6730.orphan	506 sp Q29444	Beta-mannosidase precursor (Mannanase) (Mannase)	bovine	5.00E-44	O	+	+	+	+	+	+
OctWhole	6748.orphan	432 gb AAB00542.1	UNC-89		7.00E-14	O	+	+	+	+	+	+
OctWhole	6790.orphan	230 sp P46223	60S RIBOSOMAL PROTEIN L7A	[Drosophila melanogaster]	3.00E-11	O	+	+	+	+	+	+
OctWhole	6794.orphan	422 dbj BAA88638.1	glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	[Paralichthys olivaceus]	4.00E-58	O	+	+	+	+	+	+
OctWhole	6795.orphan	337 ref NP_648167.1	CG8209-PA	[Drosophila melanogaster]	9.00E-16		+	+	+		+	+
OctWhole	6847.orphan	505 ref NP_034547.1	hephaestin	[Mus musculus]	2.00E-28	O	+	+	+	+		
OctWhole	6890.orphan	402 emb CAC87273.1	Dbp5 protein	[Chironomus tentans]	5.00E-07	O	+	+	+			+
OctWhole	6902.orphan	225 sp P24635	TUBULIN ALPHA CHAIN	[Stecotopus vulgaris]	3.00E-14	O	+	+	+	+	+	+
OctWhole	6935.orphan	516 gb AAF73803.1	surface protein PspC	[Streptococcus pneumoniae]	3.00E-13	O	+	+	+	+	+	+
OctWhole	6955.orphan	510 ref NP_057161.1	CGI-147 protein	[Homo sapiens]	1.00E-18		+		+	+	+	
OctWhole	6969.orphan	533 dbj BAC03381.1	FLJ00277 protein	[Homo sapiens]	9.00E-32		+	+	+	+	+	+
OctWhole	6970.orphan	498 emb CAC86921.1	methionine-rich repeat protein 1	[Loligo forbesi]	1.00E-33							
OctWhole	7009.orphan	323 gb EAA13101.1	agCP2185	[Anopheles gambiae str. PEST]	7.00E-13							+
OctWhole	7033.orphan	526 ref NP_035732.1	talin	[Mus musculus]	1.00E-22	O	+	+	+	+	+	+
OctWhole	7048.orphan	447 gb EAA07129.1	agCP10646	[Anopheles gambiae str. PEST]	1.00E-09		+	+	+		+	+
OctWhole	7075.orphan	421 gb AAD31042.1	heat shock protein 70	[Crassostrea gigas]	3.00E-67	O	+	+	+	+	+	+
OctWhole	7188.orphan	561 gb AAF19611.1	fatvg	[Xenopus laevis]	1.00E-06					+		
OctWhole	7198.orphan	471 sp P42026	NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial precursor (	[Bos taurus]	8.00E-44		+	+	+	+	+	+
OctWhole	7200.orphan	506 gb EAA11776.1	agCP5746	[Anopheles gambiae str. PEST]	8.00E-62	O	+	+	+	+	+	+
OctWhole	7307.orphan	547 pir	calcium-binding protein (clone pMP41)	[Mus musculus]	9.00E-46	O	+	+	+	+	+	+
OctWhole	7328.orphan	548 gb AAH26190.1	similar to zinc finger protein from gene of uncertain exon structure	[Homo sapiens]	1.00E-29	O	+	+	+	+	+	+
OctWhole	7345.orphan	512 emb CAD43405.1	gelsolin-like protein	[Lumbricus terrestris]	3.00E-24	O				+		
OctWhole	7379.orphan	158 pir	glutathione transferase (EC 2.5.1.18)		5.00E-05		+	+	+	+	+	+
OctWhole	7421.orphan	494 gb AAH03540.1	Similar to CGI-135 protein	[Homo sapiens]	4.00E-33		+	+	+	+	+	+
OctWhole	7461.orphan	326 gb EAA03781.1	agCP14739	[Anopheles gambiae str. PEST]	3.00E-15	O	+	+	+	+	+	+
OctWhole	7462.orphan	538 ref NP_596908.1	GCIP-interacting protein p29	[Rattus norvegicus]	7.00E-24	O	+	+	+	+	+	+
OctWhole	7464.orphan	591 ref XP_115525.1	similar to putative E1-E2 ATPase	[Homo sapiens]	3.00E-35	O	+	+	+	+	+	+
OctWhole	7467.orphan	583 dbj BAA86474.1	KIAA1160 protein	[Homo sapiens]	8.00E-65	O	+	+	+	+	+	+
OctWhole	7483.orphan	544 gb AAH22094.1	Similar to hypothetical protein MGC10702	[Homo sapiens]	1.00E-12	O	+	+	+	+	+	+
OctWhole	7487.orphan	329 emb CAD32263.1	Sl:dZ150F13.6 (CR1 Danio rerio 2 reverse transcriptase)	[Danio rerio]	1.00E-05				+			
OctWhole	7502.orphan	519 gb AAK49121.1	aldehyde dehydrogenase	[Danio rerio]	4.00E-31	O	+	+	+	+	+	+
OctWhole	7566.orphan	532 ref NP_444408.1	lipidosin	[Mus musculus]	2.00E-48	O	+	+	+	+	+	+
OctWhole	7588.orphan	526 ref NP_004783.1	peptidyl-prolyl isomerase G (cyclophilin G)	[Homo sapiens]	4.00E-55	O	+	+	+	+	+	+
OctWhole	7595.orphan	489 ref NP_000146.2	galactose-1-phosphate uridylyltransferase isoform 1	[Homo sapiens]	2.00E-41	O	+	+	+	+	+	+
OctWhole	7602.orphan	509 ref NP_076970.1	hypothetical protein MGC3062	[Homo sapiens]	3.00E-29	O	+	+	+	+	+	
OctWhole	7614.orphan	468 gb AAG16898.1	z-protein	[Homo sapiens]	2.00E-41	O	+	+	+	+	+	+
OctWhole	7691.orphan	476 gb EAA12854.1	agCP11416	[Anopheles gambiae str. PEST]	6.00E-49	O	+	+	+	+	+	+

OctWhole 7693.orphan	535 ref NP_523506.1	CG7052-PA	[Drosophila melanogaster]	1.00E-17	O	+	+	+	+	+	+	+	+
OctWhole 7695.orphan	440 sp Q08696	Axoneme-associated protein MST101(2)	[Drosophila hydei]	4.00E-15	O	+	+	+	+	+	+	+	+
OctWhole 7712.orphan	500 emb CAD21558.1	HEL protein	[Chironomus tentans]	2.00E-24	O	+	+	+	+	+	+	+	+
OctWhole 7748.orphan	328 gb AAH22577.1	Unknown (protein for IMAGE:4012553)	[Mus musculus]	6.00E-15	O	+	+	+	+	+	+	+	+
OctWhole 7796.orphan	445 ref NP_649963.1	CG5358-PA	[Drosophila melanogaster]	9.00E-09	O	+	+	+	+	+	+	+	+
OctWhole 7815.orphan	507 ref XP_131970.1	RIKEN cDNA 0610007C21	[Mus musculus]	6.00E-17	O	+	+	+					
OctWhole 7841.orphan	533 sp Q13454	N33 protein	[Homo sapiens]	3.00E-51	O	+	+	+	+	+	+	+	+
OctWhole 7842.orphan	499 pir	inducible mast cell-415 protein	[Bos taurus]	1.00E-52		+	+	+	+	+	+	+	+
OctWhole 7846.orphan	419 gb EAA03318.1	agCP5168	[Anopheles gambiae str. PEST]	3.00E-10	O		+	+				+	+
OctWhole 7850.orphan	460 gb EAA09647.1	ebiP953	[Anopheles gambiae str. PEST]	8.00E-37	O	+	+	+	+	+	+	+	+
OctWhole 7895.orphan	506 ref NP_004999.1	NHP2 non-histone chromosome protein 2-like 1	[Homo sapiens]	9.00E-44	O	+	+	+	+	+	+	+	+
OctWhole 7897.orphan	450 ref NP_523717.1	CG8604-PA	[Drosophila melanogaster]	1.00E-08	O	+	+	+	+	+	+	+	+
OctWhole 7929.orphan	270 gb AAF35436.1	structural muscle protein titin	[Gallus gallus]	2.00E-08	O	+	+	+	+	+	+	+	+
OctWhole 7944.orphan	512 sp O61998	Heat shock protein 90	[Brugia pahangi]	1.00E-64	O	+	+	+	+	+	+	+	+
OctWhole 7952.orphan	549 ref XP_166303.1	similar to RIKEN cDNA 2810470K21 gene	[Homo sapiens]	3.00E-25	O	+	+	+	+	+	+	+	+
OctWhole 7976.orphan	434 ref NP_056589.1	ERO1-like (S. cerevisiae)	[Mus musculus]	2.00E-16	O	+	+	+	+	+	+	+	+
OctWhole 8025.orphan	470 ref XP_131308.1	similar to phafin 2	[Homo sapiens]	3.00E-13		+	+	+	+	+	+	+	+
OctWhole 8035.orphan	494 ref NP_728903.1	CG32263-PA	[Drosophila melanogaster]	2.00E-18		+	+	+	+	+	+	+	+
OctWhole 8052.orphan	327 sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	4.00E-17	O								
OctWhole 8067.orphan	525 gb EAA07781.1	agCP1091	[Anopheles gambiae str. PEST]	1.00E-43	O	+	+	+	+	+	+	+	+
OctWhole 8072.orphan	512 ref NP_001275.1	adaptor-related protein complex 3, sigma 1 subunit	[Homo sapiens]	3.00E-71	O	+	+	+	+	+	+	+	+
OctWhole 8078.orphan	505 gb AAG13340.1	proteasome subunit beta type 1	[Gillichthys mirabilis]	1.00E-52	O	+	+	+	+	+	+	+	+
OctWhole 8081.orphan	486 ref NP_571765.1	ATPase, Na+/K+ transporting, alpha 1b polypeptide	[Danio rerio]	3.00E-27	O	+	+	+	+	+	+	+	+
OctWhole 8120.orphan	463 ref NP_496417.1	DAG binding domain	[Caenorhabditis elegans]	6.00E-17	O	+	+	+	+	+	+	+	+
OctWhole 8133.orphan	495 sp Q93104	ENHANCER OF RUDIMENTARY HOMOLOG	[Aedes aegypti]	3.00E-28	O	+	+	+	+	+	+	+	+
OctWhole 8134.orphan	503 pir	omega-crystallin	giant octopus	1.00E-35									
OctWhole 8143.orphan	511 ref NP_649808.1	CG8021-PA	[Drosophila melanogaster]	9.00E-12	O	+	+	+	+	+	+	+	+
OctWhole 8159.orphan	498 ref NP_647836.2	CG10849-PA	[Drosophila melanogaster]	2.00E-52	O	+	+	+	+	+	+	+	+
OctWhole 8190.orphan	517 pir	troponin T	[Chlamys nipponensis]	5.00E-06									
OctWhole 8233.orphan	547 dbj BAB28500.1	LNR42	[Mus musculus]	1.00E-42		+	+	+	+	+	+	+	+
OctWhole 8258.orphan	527 dbj BAA29028.1	alpha 1 type I collagen	[Rana catesbeiana]	1.00E-35	O	+	+	+	+	+	+	+	+
OctWhole 8263.orphan	135 pir	14-3-3 protein isoform zeta	rat	6.00E-07	O	+	+	+	+	+	+	+	+
OctWhole 8268.orphan	528 gb EAA10868.1	agCP6086	[Anopheles gambiae str. PEST]	2.00E-24	O	+	+	+	+	+	+	+	+
OctWhole 8296.orphan	522 ref NP_476772.1	CG1913-PA	[Drosophila melanogaster]	1.00E-61	O	+	+	+	+	+	+	+	+
OctWhole 8322.orphan	493 gb AAK84368.1	visual arrestin	[Loligo pealei]	8.00E-29	O	+	+	+		+	+	+	+
OctWhole 8429.orphan	524 emb CAC38780.1	allograft inflammatory factor 1	[Suberites domuncula]	1.00E-24	O	+	+	+	+				+
OctWhole 8462.orphan	523 emb CAD43405.1	gelsolin-like protein	[Lumbricus terrestris]	2.00E-14		+		+					
OctWhole 8510.orphan	487 pir	protein-tyrosine-phosphatase (EC 3.1.3.48) pi	[Homo sapiens]	8.00E-26	O	+	+	+	+	+	+	+	+
OctWhole 8514.orphan	442 ref NP_610629.1	CG7712-PA	[Drosophila melanogaster]	5.00E-41		+	+		+	+	+	+	+
OctWhole 8520.orphan	502 dbj BAB26125.1	evidence:NAS-hypothetical protein-putative	[Mus musculus]	6.00E-19	O	+	+	+	+				
OctWhole 8523.orphan	486 gb EAA05555.1	agCP10511	[Anopheles gambiae str. PEST]	6.00E-22	O	+	+	+	+	+	+	+	+
OctWhole 8545.orphan	506 ref NP_648895.1	CG4561-PA	[Drosophila melanogaster]	7.00E-52	O	+	+	+	+	+	+	+	+
OctWhole 8547.orphan	520 gb EAA03538.1	agCP14233	[Anopheles gambiae str. PEST]	2.00E-10	O	+	+	+	+	+	+	+	+
OctWhole 8552.orphan	492 ref XP_131295.1	similar to Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial pr	[Mus musculus]	9.00E-12		+	+	+	+				+
OctWhole 8618.orphan	535 pir	Ki nuclear autoantigen	bovine	2.00E-38	O	+	+	+	+	+	+	+	+
OctWhole 8656.orphan	499 ref NP_036557.1	ras suppressor protein 1	[Homo sapiens]	4.00E-47	O	+	+	+	+	+	+	+	+
OctWhole 8676.orphan	121 ref XP_176918.1	similar to ribosomal protein L15	[Rattus norvegicus]	5.00E-08	O	+	+	+	+	+	+	+	+
OctWhole 8705.orphan	494 ref NP_081472.1	small subunit DNA polymerase delta p12	[Mus musculus]	1.00E-06		+	+						
OctWhole 8730.orphan	493 sp P06761	78 KD GLUCOSE-REGULATED PROTEIN PRECURSOR (GRP 78)	rat	4.00E-46	O	+	+	+	+	+	+	+	+
OctWhole 8731.orphan	400 gb EAA07591.1	agCP1363	[Anopheles gambiae str. PEST]	1.00E-49	O	+	+	+	+	+	+	+	+
OctWhole 8745.orphan	511 sp Q96151	Williams-Beuren syndrome chromosome region 16 protein	[Homo sapiens]	3.00E-35	O	+	+	+	+	+	+	+	+
OctWhole 8761.orphan	528 ref NP_073182.1	rexo70	[Rattus norvegicus]	5.00E-18	O		+	+	+	+	+	+	+
OctWhole 8762.orphan	495 ref NP_648504.1	CG6004-PB	[Drosophila melanogaster]	2.00E-07						+			
OctWhole 8767.orphan	433 gb EAA06433.1	agCP13649	[Anopheles gambiae str. PEST]	2.00E-16	O	+	+	+	+	+	+	+	+
OctWhole 8786.orphan	515 gb EAA06403.1	agCP13242	[Anopheles gambiae str. PEST]	3.00E-53	O	+	+	+	+	+	+	+	+
OctWhole 8836.orphan	527 sp P81431	ALCOHOL DEHYDROGENASE CLASS III	[Octopus]	2.00E-71	O	+	+	+	+	+	+	+	+
OctWhole 8845.orphan	369 ref NP_505501.1	N-methyl-D-aspartate receptor associated protein	[Caenorhabditis elegans]	6.00E-14	O	+	+	+	+	+	+	+	+
OctWhole 8858.orphan	347 sp P27013	S-CRYSTALLIN 1	[Octopus vulgaris]	2.00E-07									
OctWhole 8863.orphan	478 ref NP_003787.2	RPB5-mediating protein isoform a	[Homo sapiens]	2.00E-23	O	+	+	+	+	+	+	+	+

OctWhole	8871.orphan	483	ref NP_036161.1	sperm associated antigen 1	[Mus musculus]	2.00E-13		+	+	+	+	+				
OctWhole	8888.orphan	457	sp O42275	Acetylcholinesterase precursor (AChE)	[Electrophorus electricus]	9.00E-37	O	+	+	+	+	+	+	+	+	+
OctWhole	8895.orphan	472	gb AAH23905.1	Similar to SKB1 homolog (S. pombe)	[Mus musculus]	2.00E-56	O	+	+	+	+	+	+	+	+	+
OctWhole	8912.orphan	316	ref NP_055227.1	calyculin binding protein	[Homo sapiens]	9.00E-11	O	+	+	+	+	+	+	+	+	+
OctWhole	8913.orphan	262	gb AAC09337.2	cytochrome oxidase subunit I	[Rhyacodrilus falciformis]	1.00E-13						+				
OctWhole	8927.orphan	346	gb AAA97543.1	S-crystallin		4.00E-10										
OctWhole	8938.orphan	471	emb CAA67134.1	PR264/SC35	[Mus musculus]	2.00E-35	O	+	+	+	+	+	+	+	+	+
OctWhole	8953.orphan	501	ref XP_059492.2	hypothetical protein XP_059492	[Homo sapiens]	6.00E-26		+	+	+	+	+	+	+	+	+
OctWhole	8991.orphan	533	ref NP_728347.1	CG1702-PA	[Drosophila melanogaster]	1.00E-37		+	+	+	+	+	+	+	+	+
OctWhole	9011.orphan	565	gb AAB81017.1	alpha-tubulin	[Spirotrunculus barkeri]	4.00E-08	O	+	+	+	+	+	+	+	+	+
OctWhole	9014.orphan	518	gb AAK50016.1	pyridoxine	[Aspergillus nidulans]	3.00E-25						+				
OctWhole	9022.orphan	385	dbj BAB64452.1	hypothetical protein	[Macaca fascicularis]	6.00E-06	O	+	+	+	+	+	+	+	+	+
OctWhole	9060.orphan	497	ref XP_115658.2	similar to Zinc finger protein 208	[Homo sapiens]	2.00E-21	O	+	+	+	+	+				
OctWhole	9075.orphan	431	sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	2.00E-24										+
OctWhole	9098.orphan	500	dbj BAC20599.1	NADH dehydrogenase (ubiquinone) flavoprotein 1	[Macaca fascicularis]	5.00E-63	O	+	+	+	+	+	+	+	+	+
OctWhole	9100.orphan	511	sp P55735	SEC13-related protein		1.00E-58	O	+	+	+	+	+	+	+	+	+
OctWhole	9101.orphan	462	ref NP_003747.1	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa	[Homo sapiens]	5.00E-31	O	+	+	+	+	+	+	+	+	+
OctWhole	9104.orphan	423	dbj BAB91244.1	LBP (LPS binding protein)/BPI (bactericidal/permeability-increasing protein)	[Onchocerca mykiss]	3.00E-06										
OctWhole	9121.orphan	483	ref XP_005323.3	similar to Exosome complex exonuclease RRP40 (Ribosomal RNA processing)	[Homo sapiens]	7.00E-38	O	+	+		+	+				+
OctWhole	9132.orphan	526	ref XP_126555.1	similar to alveolar soft part sarcoma chromosome region, candidate 1	[Homo sapiens]	3.00E-12	O	+	+	+	+	+	+	+		
OctWhole	9133.orphan	515	gb AAF17190.1	prenylated rab acceptor 1	[Homo sapiens]	1.00E-27	O	+	+	+	+	+	+	+		
OctWhole	9142.orphan	438	ref NP_598510.1	RIKEN cDNA 2900064A13	[Mus musculus]	4.00E-17		+	+	+	+	+	+	+	+	+
OctWhole	9154.orphan	474	sp P41824	Y-box factor homolog (APY1)		5.00E-51	O	+	+	+	+	+	+	+	+	+
OctWhole	9165.orphan	507	ref NP_076116.1	myo-inositol 1-phosphate synthase A1	[Mus musculus]	1.00E-48		+	+	+			+	+	+	+
OctWhole	9168.orphan	489	gb AAL09322.1	SNaK1	[Schistosoma mansoni]	8.00E-74	O	+	+	+	+	+	+	+	+	+
OctWhole	9170.orphan	540	ref NP_064625.1	non-kinase Cdc42 effector protein SPEC2	[Homo sapiens]	2.00E-08		+	+	+	+	+	+	+	+	+
OctWhole	9173.orphan	493	ref NP_569097.1	src family associated phosphoprotein 2	[Rattus norvegicus]	1.00E-05				+	+					
OctWhole	9217.orphan	576	sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	1.00E-21		+	+							
OctWhole	9225.orphan	551	gb EAA08471.1	agCP2987	[Anopheles gambiae str. PEST]	2.00E-44	O	+	+	+	+	+	+	+	+	+
OctWhole	9228.orphan	481	ref NP_062845.1	ATP synthase F0 subunit 6	[Loligo bleekeri]	2.00E-09										
OctWhole	9229.orphan	513	ref NP_034610.1	heat shock protein, 86 kDa 1	[Mus musculus]	5.00E-85	O	+	+	+	+	+	+	+	+	+
OctWhole	9235.orphan	508	dbj BAB72169.1	stress protein HSC70	[Xiphophorus maculatus]	1.00E-51	O	+	+	+	+	+	+	+	+	+
OctWhole	9238.orphan	529	emb CAC35209.1	GRAAL2 protein	[Drosophila melanogaster]	2.00E-06						+				
OctWhole	9302.orphan	225	gb AAN05596.1	ribosomal protein L	[Argopecten irradians]	2.00E-25	O	+	+	+	+	+	+	+	+	+
OctWhole	9316.orphan	520	ref NP_598819.1	expressed sequence AA409897	[Mus musculus]	2.00E-58		+	+	+	+	+	+	+	+	+
OctWhole	9324.orphan	367	sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	9.00E-40				+		+	+	+	+	+
OctWhole	9326.orphan	350	ref NP_543172.1	heterogeneous nuclear ribonucleoprotein H1	[Rattus norvegicus]	3.00E-11	O	+	+	+	+	+	+			
OctWhole	9357.orphan	538	ref NP_062611.1	phosphoserine/threonine/tyrosine interaction protein	[Mus musculus]	6.00E-39	O	+	+	+	+	+	+	+	+	+
OctWhole	9361.orphan	537	ref XP_060025.1	similar to evidence:NAS~hypothetical protein~putative	[Homo sapiens]	3.00E-17	O	+	+	+	+	+	+	+	+	+
OctWhole	9367.orphan	463	dbj BAB22965.1	histone cell cycle regulation defective interacting protein 5~putative	[Mus musculus]	7.00E-23	O	+	+	+	+	+		+	+	+
OctWhole	9370.orphan	571	gb AAK28336.1	peroxisomal 2-enoyl-CoA reductase	[Mus musculus]	1.00E-50	O	+	+	+	+	+	+	+	+	+
OctWhole	9372.orphan	531	ref NP_498330.1	Y42G9A.3.p	[Caenorhabditis elegans]	5.00E-12	O	+	+	+	+	+	+	+	+	+
OctWhole	9380.orphan	578	sp Q9Y5W7	Sorting nexin 14	[Homo sapiens]	3.00E-15	O	+	+	+	+	+	+	+	+	+
OctWhole	9392.orphan	571	ref NP_057654.1	CDA14	[Homo sapiens]	4.00E-39	O	+	+	+	+	+	+	+	+	+
OctWhole	9412.orphan	543	gb EAA08579.1	agCP2531	[Anopheles gambiae str. PEST]	6.00E-07	O	+	+	+	+	+	+	+	+	+
OctWhole	9428.orphan	563	sp P97260	Sterol regulatory element binding protein cleavage-activating protein	[Cricetulus griseus]	2.00E-23	O	+	+	+	+	+	+	+	+	+
OctWhole	9460.orphan	416	sp P27011	S-CRYSTALLIN 3 (OL3)	giant octopus	5.00E-05										
OctWhole	9491.orphan	570	ref XP_010041.3	similar to Nucleoporin 50 kDa (Nuclear pore-associated protein 60 kDa-like)	[Homo sapiens]	3.00E-06		+	+	+						
OctWhole	9549.orphan	504	sp P27012	S-CRYSTALLIN 4 (OL4)	giant octopus	5.00E-45	O	+	+	+	+	+	+	+	+	+
OctWhole	9556.orphan	575	gb EAA06918.1	agCP7321	[Anopheles gambiae str. PEST]	2.00E-58	O	+	+	+	+	+	+	+	+	+