

**Table S1. List of camera eye-specific genes commonly expressed in cephalopods and vertebrates**

| sid          | Annotations                           | best_hit by BLAST<br>searches against<br>vertebrate eye ESTs | e_value  | bit_score | GO annotation                                           | GO_id                                                       | domain         | dN/dS<br>mean |
|--------------|---------------------------------------|--------------------------------------------------------------|----------|-----------|---------------------------------------------------------|-------------------------------------------------------------|----------------|---------------|
| 00016_Oc_016 |                                       | gi 19004791 gb <br>BM691533.1 <br>BM691533                   | 8.00E-05 | 41.8      | mediator of rna<br>polymerase iisubunit<br>28           |                                                             |                |               |
| 00048_Oc_048 |                                       | gi 62889664 gb <br>DN904901.1 <br>DN904901                   | 0        | 174       | inositol-1(or 4)-<br>monophosphatase 1                  | F:GO:0005488                                                |                |               |
| 00058_Oc_061 |                                       | gi 62854000 gb <br>DN884045.1 <br>DN884045                   | 0.004    | 44.1      |                                                         |                                                             |                |               |
| 00123_Oc_022 |                                       | gi 75848117 gb <br>DT878377.1 DT878377                       | 0        | 222       | comm domain<br>containing 2                             | P:GO:0008150,C:GO:<br>0005575                               |                | 0.11667       |
| 00164_Oc_074 |                                       | BY795245                                                     | 6.00E-40 | 129       | nadh dehydrogenase1<br>beta19kda                        | C:GO:0044464                                                |                | 1.0398        |
| 00258_Oc_073 |                                       | gi 75832801 gb <br>DT863061.1 DT863061                       | 3.00E-09 | 41.4      | mitochondrial<br>ribosomal protein l32-<br>like protein |                                                             |                | 0.82538       |
| 00342_Oc_059 | <b>Embryo specific<br/>expression</b> | gi 62850164 gb <br>DN880209.1 <br>DN880209                   | 0        | 202       | p300 cbp-associated                                     |                                                             | Acetyltransf_1 |               |
| 00348_Oc_062 |                                       | gi 13288556 gb <br>BG395108.1 <br>BG395108                   | 0        | 250       | vacuolar atp synthase<br>subunit e                      |                                                             |                | 0.11737       |
| 00431_Oc_040 |                                       | gi 37636484 gb <br>CF740146.1 CF740146                       | 1.00E-06 | 56        |                                                         |                                                             | DSS1_SEM1      |               |
| 00547_Oc_066 |                                       | gi 41338221 gb <br>CK617335.1 <br>CK617335                   | 0        | 210       | fumarate hydratase 1                                    | F:GO:0043565,F:GO:<br>0003700,C:GO:<br>0005634,P:GO:0006355 | Lyase_1        |               |
| 00659_Oc_082 |                                       | gi 22810228 gb <br>BU503995.1 <br>BU503995                   | 0.001    | 28.1      |                                                         |                                                             |                |               |
| 00672_Oc_096 | <b>GO annotation</b>                  | gi 85198094 gb <br>DW604467.1 <br>DW604467                   | 0        | 262       | six homeobox 2                                          | F:GO:0043565,F:GO:<br>0003700,C:GO:<br>0005634,P:GO:0006355 | Homeobox       |               |

|                |                                            |          |                                                                         |                               |                         |         |
|----------------|--------------------------------------------|----------|-------------------------------------------------------------------------|-------------------------------|-------------------------|---------|
| 00697_Oc_021   | gi 54449080 gb <br>CV560442.1 <br>CV560442 | 9.00E-33 | 140 26s proteasome non-<br>atpase regulatory<br>subunit 13              | C:GO:0044424,C:GO:<br>0043234 |                         | 0.8005  |
| 00722_Oc_057   | gi 49671858 gb <br>CO425564.1 <br>CO425564 | 2.00E-29 | 87.7 tho complex 5                                                      | F:GO:0005515,P:GO:<br>0045650 | FimP                    |         |
| 00738_Oc_073   | gi 24730764 gb <br>CA395363.1 <br>CA395363 | 0        | 133 26s protease<br>regulatory subunit 6a                               |                               | Pfam-B_6879,<br>DUF3713 | 0.80709 |
| 00760_Oc_092   | gi 58035732 gb <br>CX733258.1 <br>CX733258 | 7.00E-35 | 147 transmembrane<br>protein 66                                         | C:GO:0016021                  | DUF1183                 | 1.10953 |
| 00806_Oc_5_043 | gi 77503943 gb <br>DV215357.1 DV215357     | 6.00E-10 | 64.9 cg050 protein                                                      |                               | DUF2373                 |         |
| 00820_Oc_5_058 | gi 37628497 gb <br>CF732167.1 CF732167     | 4.00E-09 | 51.5 nsf1 cofactor p47                                                  |                               |                         |         |
| 00824_Oc_5_060 | gi 22681745 gb <br>BU167761.1 <br>BU167761 | 0.002    | 41.4 ligand-independent<br>activating molecule for<br>estrogen receptor | F:GO:0004872                  |                         |         |
| 00913_Oc_5_049 | gi 32174379 gb <br>CD672648.1 <br>CD672648 | 7.00E-23 | 106 mitochondrial<br>ribosomal protein s7                               |                               | Ribosomal_S7            |         |
| 01019_Oc_5_054 | gi 46813061 gb <br>CN500437.1 <br>CN500437 | 1.00E-25 | 115 diazepam binding<br>inhibitor                                       | F:GO:0008289                  | ACBP                    | 1.18378 |
| 01047_Oc_5_084 | gi 19116539 gb <br>BM799716.1 <br>BM799716 | 0.001    | 46.1                                                                    |                               |                         |         |
| 01239_Oc_5_084 | gi 46465385 gb <br>CN459659.1 <br>CN459659 | 0.001    | 41.4                                                                    |                               |                         |         |
| 01265_Oc_5_017 | gi 62847240 gb <br>DN877285.1 <br>DN877285 | 3.00E-08 | 57.4 novel proteinfamily<br>with sequence<br>similaritymember a         |                               | DUF676                  |         |
| 01271_Oc_5_020 | gi 62046375 gb <br>DN691721.1 <br>DN691721 | 5.61E-45 | 180 nadp<br>transhydrogenase                                            |                               | PNTB                    | 2.8457  |

Positive  
selection

|                |                                       |                                             |          |                            |                                                                     |                                                                              |                 |
|----------------|---------------------------------------|---------------------------------------------|----------|----------------------------|---------------------------------------------------------------------|------------------------------------------------------------------------------|-----------------|
| 01284_Oc_5_042 | BY795228                              | 5.00E-06                                    | 44.6     | mt-ezrin radixin<br>moesin |                                                                     | ERM                                                                          |                 |
| 01304_Oc_5_060 | <b>Positive<br/>selection</b>         | gi 40322928 gb <br>CK356996.1 <br>CK356996  | 1.00E-27 | 122                        | methylosome protein<br>50                                           |                                                                              | 2.65794         |
| 01319_Oc_5_068 |                                       | gi 14062519 gb <br>BG751866.1 <br>BG751866  | 2.00E-06 | 52.4                       | novel<br>proteinvertebrate<br>diacylglycerolbeta<br>90kda           |                                                                              |                 |
| 01349_Oc_5_003 |                                       | gi 62884021 gb <br>DN899258.1 <br>DN899258  | 0.0003   | 44.1                       | low-density lipoprotein<br>receptor-related<br>protein              | P:GO:0007160,F:GO:<br>0005509,C:GO:<br>0045178,P:GO:0040010                  | Ldl_recept_b    |
| 01372_Oc_5_030 |                                       | gi 32180675 gb <br>CD678944.1 <br>CD678944  | 2.00E-23 | 75.8                       | accessory gland<br>protein                                          |                                                                              |                 |
| 01421_Oc_5_071 |                                       | gi 54448708 gb <br>CV560260.1 <br>CV560260  | 0.002    | 42.8                       |                                                                     |                                                                              |                 |
| 01489_Oc_5_049 |                                       | gi 5033517 gb <br>AI716264.1 AI716264       | 3.00E-06 | 49.2                       | dipeptidylpeptidase 7                                               |                                                                              |                 |
| 01490_Oc_5_057 |                                       | gi 12040989 gb <br>BF725078.1 BF725078      | 2.00E-12 | 72.4                       | non-muscle myosin ii<br>heavy chain                                 | F:GO:0005524,F:GO:<br>0003779,F:GO:<br>0000166,F:GO:<br>0003774,C:GO:0016459 |                 |
| 01494_Oc_5_059 |                                       | gi 41338320 gb <br>CK617434.1 <br>CK617434  | 2.00E-24 | 111                        | kelch domain-<br>containing protein 8a                              |                                                                              | Kelch_1 0.90463 |
| 01510_Oc_5_075 |                                       | gi 19029697 gb <br>BM716439.1 <br>BM716439  | 1.00E-10 | 48.3                       | x-prolyl<br>aminopeptidase<br>(aminopeptidase p)<br>isoform cra_a   | F:GO:0008233                                                                 |                 |
| 01551_Oc_5_008 | <b>Embryo specific<br/>expression</b> | gi 119789144 gb <br>EH281703.1 <br>EH281703 | 6.00E-08 | 57.9                       | transmembrane<br>emp24 domain-<br>containing protein 5<br>precursor | C:GO:0016021                                                                 | EMP24_GP25<br>L |
| 01657_Oc_5_021 |                                       | gi 37633733 gb <br>CF737397.1 CF737397      | 3.00E-26 | 118                        | mgc68950 protein                                                    | P:GO:0040023                                                                 | CAP_GLY 0.69648 |

|                |                            |                                    |          |      |                                                                        |                                                                                            |              |         |
|----------------|----------------------------|------------------------------------|----------|------|------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|--------------|---------|
| 01718_Oc_5_091 | Embryo specific expression | gi 83525044 gb DB294194.1 DB294194 | 0        | 193  | riken cdna 1700022n24                                                  | F:GO:0008270,F:GO:0005515,C:GO:0016021                                                     | Pfam-B_14559 | 0.20541 |
| 01737_Oc_5_005 |                            | gi 22696303 gb BU182319.1 BU182319 | 0        | 228  | chaperonin subunit 3                                                   | P:GO:0006457,C:GO:0005737,F:GO:0051082,F:GO:0005524                                        | Cpn60_TCP1   | 0.9165  |
| 01791_Oc_5_056 | GO annotation              | gi 32463972 gb CD805146.1 CD805146 | 8.00E-24 | 58.3 | high mobility group b3b protein                                        | P:GO:0006355,C:GO:0000785,F:GO:0003677,C:GO:0005634                                        | HMG_box      |         |
| 01826_Oc_5_009 |                            | gi 18965694 gb BM661719.1 BM661719 | 2.00E-09 | 62.5 | upregulated during skeletal muscle growth 5                            | C:GO:0005739,C:GO:0016021,C:GO:0016020,C:GO:0005743                                        | Pfam-B_8509  |         |
| 01855_Oc_5_024 | Positive selection         | gi 62888698 gb DN903935.1 DN903935 | 0        | 200  | cytochrome c proximal                                                  | F:GO:0045155,F:GO:0005506,C:GO:0005759,F:GO:0020037,P:GO:0006118,P:GO:0006810,C:GO:0005746 | Cytochrom_C  | 10.1348 |
| 01868_Oc_5_046 |                            | BY796180                           | 2.00E-07 | 50.6 | ---NA---                                                               |                                                                                            |              |         |
| 01873_Oc_5_049 |                            | gi 19018745 gb BM705487.1 BM705487 | 9.00E-35 | 90.9 | signal recognition particle 14kda (homologous alu rna binding protein) | P:GO:0009987,F:GO:0005488,C:GO:0048500                                                     | SRP14        | 1.77853 |
| 01897_Oc_5_069 |                            | gi 19397619 gb BM938467.1 BM938467 | 7.00E-29 | 127  | riboflavin kinase                                                      | F:GO:0008531,P:GO:0009231,F:GO:0005524,F:GO:0000287,F:GO:0008270                           | Flavokinase  |         |
| 01915_Oc_5_086 |                            | gi 62881909 gb DN897146.1 DN897146 | 9.00E-12 | 47.8 | ---NA---                                                               |                                                                                            |              |         |
| 02082_Oc_5_073 |                            | gi 46825597 gb CN512973.1 CN512973 | 3.00E-26 | 115  | proteasome 26s non-atpase subunit 9                                    | C:GO:0043234,C:GO:0005829,P:GO:0008150,F:GO:0005515                                        | PDZ          | 0.2745  |
| 02158_Oc_5_047 | GO annotation              | gi 24725639 gb CA392686.1 CA392686 | 1.00E-05 | 47.3 | zinc finger with krab and scan domains 4                               |                                                                                            | zf-C2H2      |         |

|                |                                    |          |      |                                                                                                        |                           |            |         |
|----------------|------------------------------------|----------|------|--------------------------------------------------------------------------------------------------------|---------------------------|------------|---------|
| 02222_Oc_5_015 | gi 62880837 gb DN896074.1 DN896074 | 3.00E-24 | 66.6 | af498232_1peroxiredoxin v protein                                                                      | F:GO:0016491              | Redoxin    | 1.10022 |
| 02252_Oc_5_046 | gi 10202777 gb BE781579.1 BE781579 | 2.00E-05 | 46   | ---NA---                                                                                               |                           |            |         |
| 02461_Oc_5_055 | gi 41342286 gb CK621400.1 CK621400 | 4.00E-15 | 60.2 | transmembrane protein 33                                                                               |                           | UPF0121    | 3.5469  |
| 02464_Oc_5_064 | gi 85195332 gb DW603494.1 DW603494 | 2.00E-32 | 139  | sulfide:quinone oxidoreductase                                                                         |                           |            | 1.03437 |
| 02511_Oc_5_008 | gi 14976737 gb BI300457.1 BI300457 | 0.008    | 44.1 |                                                                                                        |                           |            |         |
| 02601_Oc_5_005 | gi 18266931 gb BM413635.1 BM413635 | 0.006    | 25.8 |                                                                                                        |                           |            |         |
| 02672_Oc_5_080 | gi 85198934 gb DW604770.1 DW604770 | 0.0002   | 48.1 |                                                                                                        |                           |            |         |
| 02680_Oc_5_092 | gi 19001706 gb BM688448.1 BM688448 | 3.00E-12 | 71.6 | marco_mesauame: full=macrophage receptor marcoame: full=macrophage receptor with collagenous structure | C:GO:0016020,F:GO:0004872 | SRCR       |         |
| 02683_Oc_5_086 | gi 24727425 gb CA393620.1 CA393620 | 6.00E-25 | 104  | sec6 protein                                                                                           |                           | Sec6       | 0.95688 |
| 02731_Oc_5_038 | gi 41338923 gb CK618037.1 CK618037 | 0        | 198  | briggsae cbr-ncx-3 protein                                                                             |                           | Arf        | 2.9608  |
| 02792_Oc_5_012 | gi 20365123 gb BQ189572.1 BQ189572 | 6.00E-21 | 101  |                                                                                                        |                           | Na_Ca_ex   | 0.7284  |
| 02894_Oc_5_015 | gi 40321164 gb CK355232.1 CK355232 | 8.00E-34 | 95.5 | chaperonin containingsubunit 8                                                                         | P:GO:0044267,F:GO:0005488 | Cpn60_TCP1 | 0.60428 |

|                |                            |                                    |          |      |                                                           |                                                                                                                      |                                    |
|----------------|----------------------------|------------------------------------|----------|------|-----------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|------------------------------------|
| 02945_Oc_5_065 | Embryo specific expression | gi 19116584 gb BM799761.1 BM799761 | 0        | 233  | rab5 protein                                              | Ras                                                                                                                  | 1.82924                            |
| 02990_Oc_5_015 |                            | gi 75850467 gb DT880727.1 DT880727 | 9.00E-19 | 64.3 | ---NA---                                                  | F:GO:0003779                                                                                                         | 0.0757                             |
| 03014_Oc_5_043 |                            | BY795503                           | 0.006    | 38.2 |                                                           |                                                                                                                      |                                    |
| 03026_Oc_5_057 |                            | gi 57592584 gb CX565555.1 CX565555 | 0        | 284  | syndecan binding isoform cra_a                            | C:GO:0005895,F:GO:0016491,F:GO:0005137,C:GO:0042470,F:GO:0047485,P:GO:0008152,F:GO:0046982,P:GO:0007265,F:GO:0042043 | PDZ 0.2029                         |
| 03032_Oc_5_060 |                            | gi 15711610 gb BI734597.1 BI734597 | 4.00E-12 | 71.2 | bromodomain and phd finger-containing protein 1 isoform 1 | C:GO:0005622,P:GO:0006829,F:GO:0008270,F:GO:0005515                                                                  |                                    |
| 03145_Oc_5_069 |                            | BY799086                           | 0.001    | 40.1 |                                                           |                                                                                                                      |                                    |
| 03192_Oc_5_028 |                            | gi 13063784 gb BG298784.1 BG298784 | 1.40E-45 | 182  | carnitine o-octanoyltransferase                           | C:GO:0005777,F:GO:0008458,P:GO:0006810,P:GO:0006631                                                                  | 1.94932                            |
| 03241_Oc_5_069 | Positive selection         | gi 85208728 gb DW608617.1 DW608617 | 0        | 343  | dihydrolipoamide dehydrogenase                            | P:GO:0045454,F:GO:0050660,F:GO:0004148                                                                               | Pyr_redox_dim 2.30203, Pyr_redox_2 |
| 03247_Oc_5_072 |                            | gi 41341343 gb CK620457.1 CK620457 | 0.007    | 41.4 | paf1 rna polymerase ii complex component                  | F:GO:0005515                                                                                                         |                                    |
| 03249_Oc_5_081 |                            | gi 37634296 gb CF737959.1 CF737959 | 3.00E-38 | 159  | dishevelled associated activator of morphogenesis 1 like  | P:GO:0016043,F:GO:0005515                                                                                            |                                    |
| 03250_Oc_5_089 |                            | gi 83528083 gb DB294582.1 DB294582 | 0.008    | 44.1 |                                                           |                                                                                                                      |                                    |
| 03253_Oc_5_083 |                            | gi 62046044 gb DN691552.1 DN691552 | 4.00E-40 | 165  | sorting nexin 4                                           |                                                                                                                      |                                    |

|                |                                            |          |      |                                                |                                                                                               |                    |         |
|----------------|--------------------------------------------|----------|------|------------------------------------------------|-----------------------------------------------------------------------------------------------|--------------------|---------|
| 03428_Oc_5_074 | gi 85206200 gb <br>DW607704.1 <br>DW607704 | 0        | 248  | phosphate<br>carriermitochondrial<br>precursor |                                                                                               | Mito_carr          | 0.27196 |
| 03440_Oc_5_080 | gi 18987504 gb <br>BM677608.1 <br>BM677608 | 0.002    | 46.1 |                                                |                                                                                               |                    |         |
| 03467_Oc_5_006 | GS004812                                   | 0.008    | 32.2 |                                                |                                                                                               |                    |         |
| 03515_Oc_5_054 | gi 41342643 gb <br>CK621757.1 <br>CK621757 | 0        | 134  | heat shock protein<br>90kda betamember 1       |                                                                                               | HSP90              | 0.11    |
| 03518_Oc_5_063 | gi 46823305 gb <br>CN510681.1 <br>CN510681 | 1.00E-26 | 120  | nop10<br>ribonucleoprotein<br>homolog          | C:GO:0005634                                                                                  | Nop10p             | 0.8304  |
| 03533_Oc_5_071 | gi 11529949 gb <br>BF460792.1 BF460792     | 1.00E-28 | 127  | rna-binding protein<br>nova-                   |                                                                                               | KH_1               | 0.65403 |
| 03597_Oc_5_039 | gi 76234086 gb <br>CJ133758.1 CJ133758     | 2.00E-35 | 96.4 | ribosomal protein l34                          | C:GO:0005840,F:GO:<br>0003735,P:GO:0006412                                                    | Ribosomal_L3<br>4e | 1.64326 |
| 03698_Oc_5_057 | gi 62843102 gb <br>DN873161.1 <br>DN873161 | 0        | 190  | transaldolase 1                                | C:GO:0005737,F:GO:<br>0005515,F:GO:<br>0004801,P:GO:0006098                                   | Transaldolase      | 0.16238 |
| 03711_Oc_5_056 | gi 40320392 gb <br>CK354460.1 <br>CK354460 | 0.007    | 44.1 |                                                |                                                                                               |                    |         |
| 03771_Oc_5_022 | gi 57592316 gb <br>CX565287.1 <br>CX565287 | 4.00E-07 | 51.8 | heat shock protein<br>90kda betamember 1       |                                                                                               | HSP90              |         |
| 03840_Oc_5_096 | gi 32273706 gb <br>CD722858.1 <br>CD722858 | 2.00E-12 | 49.6 | fatty acid amide<br>hydrolase                  | F:GO:0016884,C:GO:<br>0016021,F:GO:<br>0016787,C:GO:<br>0005615,C:GO:<br>0016020,C:GO:0005783 | Amidase            |         |
| 04021_Oc_5_083 | gi 18986794 gb <br>BM676898.1 <br>BM676898 | 0.004    | 36.3 |                                                |                                                                                               | Ribosomal_S4<br>Pg |         |
| 04055_Oc_5_020 | gi 19018438 gb <br>BM705180.1 <br>BM705180 | 4.00E-09 | 62   | mgc82791 protein                               | C:GO:0005737,P:GO:<br>0030100,F:GO:0005515                                                    | BAR                |         |

|                |                                                               |          |      |                                         |                                                     |                                                                                               |         |
|----------------|---------------------------------------------------------------|----------|------|-----------------------------------------|-----------------------------------------------------|-----------------------------------------------------------------------------------------------|---------|
| 04073_Oc_5_037 | gi 22346578 gb BQ931547.1 BQ931547                            | 2.00E-11 | 66.5 | protein disulfide isomerase             |                                                     |                                                                                               |         |
| 04200_Oc_5_076 | BY800402                                                      | 0.005    | 32.7 |                                         |                                                     |                                                                                               |         |
| 04207_Oc_5_072 | BY795432                                                      | 0.003    | 27.6 |                                         |                                                     |                                                                                               |         |
| 04320_Oc_5_096 | gi 58060652 gb CX733816.1 CX733816                            | 0        | 187  | elongation factor tu                    |                                                     |                                                                                               |         |
| 04396_Oc_5_078 | Embryo specific expression gi 62871980 gb DN887217.1 DN887217 | 0        | 213  | adenylate kinase                        | F:GO:0005524,F:GO:0004017,P:GO:0006139              | ADK                                                                                           | 0.76786 |
| 04423_Oc_5_004 | gi 75846801 gb DT877061.1 DT877061                            | 0.005    | 44.1 |                                         |                                                     |                                                                                               |         |
| 04466_Oc_5_057 | Embryo specific expression gi 62037377 gb DN687251.1 DN687251 | 0        | 216  | thymidine kinaseisoform cra_b           | C:GO:0005743,F:GO:0004797,P:GO:0006139,F:GO:0000166 | Pfam-B_4425, dNK                                                                              | 1.93953 |
| 04550_OC_5_043 | gi 22707146 gb BU193170.1 BU193170                            | 0.004    | 38.6 |                                         |                                                     |                                                                                               |         |
| 04609_OC_5_001 | GS008140                                                      | 0.002    | 32.2 |                                         |                                                     | Pfam-B_587, Pfam-B_14082, Pfam-B_8988, Pfam-B_18484, Pfam-B_18104, Pfam-B_11111, Pfam-B_14589 |         |
| 04613_OC_5_003 | gi 75846808 gb DT877068.1 DT877068                            | 9.00E-18 | 71.6 | wd repeat domain 74                     |                                                     |                                                                                               |         |
| 04619_OC_5_006 | gi 22667936 gb BU154404.1 BU154404                            | 0.004    | 44.1 |                                         |                                                     |                                                                                               |         |
| 04636_OC_5_030 | gi 62853575 gb DN883620.1 DN883620                            | 8.00E-32 | 137  | mitochondrial 28s ribosomal protein s28 |                                                     |                                                                                               | 1.25635 |

|                    |                                            |          |                                                   |                                                                                                                                                                   |                                                    |
|--------------------|--------------------------------------------|----------|---------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------|
| 04654_OC_5_04<br>7 | gi 16046496 gb <br>BI872821.1 BI872821     | 0.0002   | 35.9 ---NA---                                     |                                                                                                                                                                   | Pfam-B_11882 0.16963                               |
| 04658_OC_5_05<br>7 | gi 62832853 gb <br>DN863204.1 <br>DN863204 | 0.0005   | 48.1                                              |                                                                                                                                                                   | Pfam-B_2397                                        |
| 04670_OC_5_06<br>3 | gi 19039801 gb <br>BM720506.1 <br>BM720506 | 3.00E-07 | 56.1 ---NA---                                     |                                                                                                                                                                   | CortBP2,<br>Pfam-<br>B_14732,<br>Peptidase_M1<br>7 |
| 04681_OC_5_06<br>9 | gi 40322049 gb <br>CK356117.1 <br>CK356117 | 0        | 200 tho complex subunit 7<br>homolog              |                                                                                                                                                                   | 0.8632                                             |
| 04754_Oc_5_057     | gi 15710462 gb <br>BI733449.1 BI733449     | 0        | 209 kinh_lolpeame:<br>full=kinesin heavy<br>chain | P:GO:0007018,C:GO:<br>0005875,F:GO:<br>0005524,F:GO:<br>0003777,C:GO:0005874                                                                                      | Pfam-B_11578                                       |
| 04808_Oc_5_012     | GS014047                                   | 0.01     | 32.2                                              |                                                                                                                                                                   |                                                    |
| 04810_Oc_5_013     | gi 15009600 gb <br>BI326003.1 BI326003     | 0        | 153 mkiaa0109 protein                             | P:GO:0006461,F:GO:<br>0008289,F:GO:<br>0005515,F:GO:<br>0008565,P:GO:<br>0016192,P:GO:<br>0006886,C:GO:<br>0030141,C:GO:<br>0030131,C:GO:<br>0005739,C:GO:0030132 | Clat_adaptor_s 0.27841                             |
| 04856_Oc_5_060     | BY798495                                   | 0.009    | 38.2                                              |                                                                                                                                                                   |                                                    |
| 04920_Oc_5_028     | gi 75833046 gb <br>DT863306.1 DT863306     | 0.003    | 44.1                                              |                                                                                                                                                                   |                                                    |
| 04999_Oc_5_004     | gi 8984832 gb <br>BB284383.1 <br>BB284383  | 1.00E-11 | 54.2 rieske (fe-s) domain<br>containing           |                                                                                                                                                                   | Rieske                                             |
| 05143_Oc_5_052     | gi 18523576 gb <br>BM474534.1 <br>BM474534 | 3.00E-12 | 72.5                                              |                                                                                                                                                                   | Plexin_cytopl                                      |

|                |                                                                                  |          |      |                                                                                                                                                                                                               |                                                                                               |                              |
|----------------|----------------------------------------------------------------------------------|----------|------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|------------------------------|
| 05231_Oc_5_040 | gi 15586593 gb <br>BI671209.1 BI671209                                           | 0.0007   | 44.6 | aminopeptidase<br>puromycin sensitive                                                                                                                                                                         | P:GO:0006508,F:GO:<br>0004179,F:GO:<br>0008237,F:GO:<br>0016787,F:GO:<br>0008233,F:GO:0008270 |                              |
| 05276_Oc_5_094 | gi 19004616 gb <br>BM691358.1 <br>BM691358                                       | 9.00E-26 | 117  | nadh dehydrogenase<br>1 alpha subcomplex 2<br>variant 1                                                                                                                                                       | Pfam-<br>B_10394,<br>L51_S25_CI-<br>B8                                                        | 1.24034                      |
| 05440_Oc_5_064 | gi 49675657 gb <br>CO429363.1 <br>CO429363                                       | 0        | 238  | vacuolar atp synthase<br>subunit d 1                                                                                                                                                                          | C:GO:0016469,F:GO:<br>0046961                                                                 | vATP-<br>synt_AC39<br>0.5621 |
| 05443_Oc_5_066 | gi 54443551 gb <br>CV557712.1 <br>CV557712                                       | 6.00E-35 | 147  | baculoviral iap repeat-<br>containing 6                                                                                                                                                                       |                                                                                               |                              |
| 05555_Oc_5_082 | <b>Embryo specific<br/>expression</b> gi 85194722 gb <br>DW603282.1 <br>DW603282 | 8.00E-33 | 140  | gtp-binding protein 8                                                                                                                                                                                         | F:GO:0005525,C:GO:<br>0005622                                                                 | 1.0748                       |
| 05713_Oc_5_049 | gi 57592048 gb <br>CX565019.1 <br>CX565019                                       | 2.00E-16 | 85.8 | fk506 binding<br>proteinpartial                                                                                                                                                                               | F:GO:0005515                                                                                  | FKBP_C                       |
| 05819_Oc_5_054 | gi 46462071 gb <br>CN456345.1 <br>CN456345                                       | 1.00E-28 | 127  | ring finger protein<br>113a                                                                                                                                                                                   |                                                                                               | 0.0448                       |
| 05962_Oc_5_013 | gi 75851959 gb <br>DT882219.1 DT882219                                           | 1.00E-24 | 112  | barrier-to-<br>autointegration factor                                                                                                                                                                         | C:GO:0005634                                                                                  | BAF                          |
| 06098_Oc_5_057 | gi 46816556 gb <br>CN503932.1 <br>CN503932                                       | 2.00E-10 | 67.9 |                                                                                                                                                                                                               |                                                                                               | eIF3_subunit                 |
| 06176_Oc_5_032 | gi 24816591 gb <br>CA452171.1 <br>CA452171                                       | 1.00E-14 | 80.3 | zinc finger protein 271<br>(zinc finger protein 7)<br>(zinc finger protein<br>znfpheX133) (epstein-<br>barr virus-induced zinc<br>finger protein) (znf-eb)<br>(ct-zfp48) (zinc finger<br>protein dp) (znf-dp) |                                                                                               |                              |

|                |                            |                                    |          |      |                                                       |                                                                                                         |         |
|----------------|----------------------------|------------------------------------|----------|------|-------------------------------------------------------|---------------------------------------------------------------------------------------------------------|---------|
| 06182_Oc_5_043 | Embryo specific expression | gi 18529315 gb BM480273.1 BM480273 | 8.00E-09 | 57.4 | lim domain-containing                                 |                                                                                                         |         |
| 06249_Oc_5_005 |                            | gi 46824386 gb CN511762.1 CN511762 | 3.00E-39 | 160  | tata box binding protein-associated                   | TFIID-18kDa                                                                                             | 0.31415 |
| 06263_Oc_5_020 |                            | gi 62839671 gb DN869730.1 DN869730 | 0.004    | 40   |                                                       | Pfam-B_980                                                                                              |         |
| 06339_Oc_5_002 |                            | gi 15684799 gb BI709104.1 BI709104 | 5.00E-16 | 84.9 | cm037_xenlaame: full=upf0582 protein c13orf37 homolog | DUF3743                                                                                                 |         |
| 06431_Oc_5_088 |                            | gi 62842908 gb DN872967.1 DN872967 | 1.00E-07 | 57.4 | galectin-4 (galactoside-soluble 4)                    | F:GO:0005529                                                                                            |         |
| 06480_Oc_5_048 |                            | gi 19011060 gb BM697802.1 BM697802 | 3.00E-18 | 92.7 | myosin iiiia                                          | C:GO:0030175,F:GO:0060002,F:GO:0005516,F:GO:0043531,F:GO:0030898,C:GO:0031941,P:GO:0007605,P:GO:0046777 |         |
| 06506_Oc_5_077 |                            | gi 85205891 gb DW607568.1 DW607568 | 0        | 222  | calcium-transporting atpase 2c1                       |                                                                                                         |         |
| 06537_Oc_5_005 |                            | gi 41348034 gb CK627148.1 CK627148 | 9.00E-22 | 104  | nucleobindin 2b                                       | F:GO:0005509                                                                                            | 0.1616  |
| 06540_Oc_5_014 |                            | gi 37598621 gb CF724453.1 CF724453 | 1.00E-29 | 130  | cell division cycle 40 homolog                        | P:GO:0051301                                                                                            | 0.2629  |
| 06561_Oc_5_033 |                            | GS008194                           | 0.004    | 32.2 |                                                       | CAF1A, Pfam-B_8504, Pfam-B_15738, Nop14, Pfam-B_11288, Pfam-B_14006, Pfam-B_7566                        |         |

|                |                                            |          |      |                                                                                                                                                     |                                                                              |                          |
|----------------|--------------------------------------------|----------|------|-----------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------|--------------------------|
| 06590_Oc_5_063 | gi 10199396 gb <br>BE778198.1 BE778198     | 0.005    | 29.9 |                                                                                                                                                     |                                                                              |                          |
| 06592_Oc_5_064 | gi 10204941 gb <br>BE783743.1 BE783743     | 0        | 138  | karyopherin alpha 2<br>(rag cohortimportin<br>alpha 1)                                                                                              | P:GO:0006886,C:GO:<br>0005634                                                | IBB, Arm                 |
| 06646_Oc_5_027 | BY798958                                   | 3.00E-41 | 163  | eukaryotic initiation<br>factor 5c                                                                                                                  |                                                                              | W2 0.55447               |
| 06647_Oc_5_020 | gi 16491534 gb <br>BB657708.1 <br>BB657708 | 1.00E-28 | 126  | small nuclear rna<br>activatingpolypeptide<br>1                                                                                                     | F:GO:0003674,P:GO:<br>0006350,P:GO:<br>0008150,C:GO:<br>0005634,F:GO:0003677 | SNAPc_SNAP 0.47385<br>43 |
| 06682_Oc_5_061 | gi 54479963 gb <br>CV574907.1 <br>CV574907 | 1.00E-40 | 165  | dead (asp-glu-ala-asp)<br>box polypeptide 18                                                                                                        | F:GO:0005524,F:GO:<br>0008026                                                |                          |
| 06730_Oc_5_013 | gi 85205936 gb <br>DW607590.1 <br>DW607590 | 7.00E-32 | 117  | manba_boviname:<br>full=beta-<br>mannosidaseame:<br>full=lysosomal beta a<br>mannosidaseame:<br>full=mannanase<br>short=mannase flags:<br>precursor | P:GO:0008152                                                                 | Pfam-B_67                |
| 06784_Oc_5_064 | GS004826                                   | 0.009    | 32.2 |                                                                                                                                                     |                                                                              | ATP-synt_E               |
| 06847_Oc_5_024 | gi 32465408 gb <br>CD806582.1 <br>CD806582 | 3.00E-27 | 122  | ferroxidaseprecursor -<br>rat                                                                                                                       |                                                                              | Cu-oxidase_3 1.2635      |
| 06955_Oc_5_038 | gi 83528618 gb <br>DB294616.1 <br>DB294616 | 1.00E-22 | 106  | bcl-2 inhibitor of<br>transcription                                                                                                                 | F:GO:0004045,C:GO:<br>0005739                                                | PTH2, Pfam-<br>B_7718    |
| 06969_Oc_5_053 | gi 62872333 gb <br>DN887570.1 <br>DN887570 | 2.00E-35 | 87.7 | mgc81115 protein                                                                                                                                    |                                                                              |                          |
| 07033_Oc_5_021 | gi 23655182 gb <br>BU730863.1 <br>BU730863 | 1.00E-22 | 71.2 | isoform cra_a                                                                                                                                       |                                                                              | 1.34866                  |
| 07075_Oc_5_066 | gi 62828429 gb <br>DN858780.1 <br>DN858780 | 0        | 276  | heat shock protein 70                                                                                                                               | F:GO:0005524,P:GO:<br>0006950                                                | Pfam-B_2482,<br>HSP70    |

|                |                                     |          |      |                                                    |                                                     |           |         |
|----------------|-------------------------------------|----------|------|----------------------------------------------------|-----------------------------------------------------|-----------|---------|
| 07131_Oc_5_022 | GS013851                            | 4.00E-05 | 40.1 |                                                    |                                                     |           |         |
| 07343_Oc_5_040 | BY797798                            | 0.007    | 38.2 |                                                    |                                                     | PLAC8     |         |
| 07345_Oc_5_049 | gi 62842025 gb DN872084.1 DN872084  | 2.00E-10 | 36.8 | gelsolin-like protein                              | F:GO:0003779                                        | Gelsolin  | 0.59383 |
| 07379_Oc_5_082 | gi 119789412 gb EH281971.1 EH281971 | 0.0001   | 32.2 | glutathione s-transferase                          |                                                     | GST_N     |         |
| 07421_Oc_5_023 | gi 62839565 gb DN869624.1 DN869624  | 8.00E-23 | 97.3 | mitochondrial fission 1 protein                    | F:GO:0005488                                        | TPR_1     | 0.86984 |
| 07462_Oc_5_075 | gi 32180796 gb CD679065.1 CD679065  | 2.00E-29 | 129  | pre-mrna-splicing factor syf2 (ccndbp1-interactor) |                                                     |           | 0.2483  |
| 07467_Oc_5_070 | gi 22802866 gb BU500987.1 BU500987  | 0        | 291  | mgc80278 protein                                   |                                                     |           | 5.49096 |
| 07471_Oc_5_072 | gi 23679207 gb BU740075.1 BU740075  | 0.008    | 44.1 |                                                    |                                                     |           |         |
| 07483_Oc_5_086 | gi 37638276 gb CF741937.1 CF741937  | 1.00E-07 | 57.4 | ubiquitin specific peptidase 30                    |                                                     |           |         |
| 07502_Oc_5_015 | gi 32273237 gb CD722389.1 CD722389  | 2.00E-22 | 105  | aldehyde dehydrogenase 3member d1                  | P:GO:0006081,F:GO:0016491,F:GO:0004030,C:GO:0005575 | Aldedh    | 0.7517  |
| 07566_Oc_5_079 | gi 62040485 gb DN688816.1 DN688816  | 0        | 118  | acyl-synthetase bubblegum family member 2          | F:GO:0016874,P:GO:0006629                           |           | 0.33408 |
| 07568_Oc_5_080 | gi 54471416 gb CV570665.1 CV570665  | 0.008    | 44.1 |                                                    |                                                     |           |         |
| 07602_Oc_5_025 | gi 9127816 gb BE257342.1 BE257342   | 5.00E-36 | 115  | phosducin-like 3                                   | C:GO:0005737,F:GO:0005515                           | Phosducin | 0.6116  |
| 07691_Oc_5_006 | gi 62841082 gb DN871141.1 DN871141  | 0        | 221  | atp synthase gamma                                 |                                                     | ATP-synt  | 0.64806 |

|                |                                                       |          |                                                          |                                                                  |                |
|----------------|-------------------------------------------------------|----------|----------------------------------------------------------|------------------------------------------------------------------|----------------|
| 07693_Oc_5_007 | gi 85200581 gb DW605304.1 DW605304                    | 2.00E-08 | 60.2 thiolester containing protein ii isoform c          |                                                                  |                |
| 07712_Oc_5_032 | GO annotation gi 13270222 gb BG373685.1 BG373685      | 2.00E-29 | 129 hla-b associated transcript 1                        | F:GO:0003676,F:GO:0005524,F:GO:0008026                           | 1.01186        |
| 07748_Oc_5_074 | gi 85205535 gb DW607393.1 DW607393                    | 3.00E-19 | 94.5 afg3(atpase family gene 3)-like 1                   |                                                                  | 0.67195        |
| 07796_Oc_5_026 | gi 58035650 gb CX733176.1 CX733176                    | 8.00E-11 | 67.5 coactivator-associated arginine methyltransferase 1 | P:GO:0006355,P:GO:0030518,F:GO:0003713,F:GO:0008276,P:GO:0016571 |                |
| 07841_Oc_5_065 | Positive selection gi 19353921 gb BM903952.1 BM903952 | 0        | 163 tumor suppressor candidate 3                         |                                                                  | 2.00297        |
| 07846_Oc_5_075 | gi 45305571 gb CK875940.1 CK875940                    | 6.00E-05 | 47.8 mitochondrial transcription factor isoform d        | F:GO:0003712,C:GO:0005759,P:GO:0006390                           | Coiled-coil_56 |
| 07897_Oc_5_021 | gi 75842858 gb DT873118.1 DT873118                    | 4.00E-10 | 65.2 amphiphysin bar domain from drosophila              |                                                                  | BAR            |
| 07917_Oc_5_039 | GS014086                                              | 8.00E-05 | 38.2                                                     |                                                                  |                |
| 07921_Oc_5_049 | gi 62872616 gb DN887853.1 DN887853                    | 0.01     | 35                                                       |                                                                  |                |
| 07944_Oc_5_076 | gi 21763104 gb BQ638645.1 BQ638645                    | 0        | 232 heat shock protein 90                                |                                                                  | HSP90          |
| 07952_Oc_5_080 | gi 85201773 gb DW605722.1 DW605722                    | 3.00E-35 | 105 brix domain containing 1                             |                                                                  | ERO1 1.09096   |
| 07976_Oc_5_012 | gi 10199520 gb BE778322.1 BE778322                    | 1.00E-19 | 96.4 endoplasmic oxidoreductin-1                         |                                                                  | 0.3883         |
| 08025_Oc_5_053 | gi 62049453 gb DN693253.1 DN693253                    | 2.00E-16 | 86.3 cg14782-pa isoform 2                                |                                                                  |                |

|                |                                                                      |          |      |                                                           |                                                                                                                      |                  |         |
|----------------|----------------------------------------------------------------------|----------|------|-----------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|------------------|---------|
| 08072_Oc_5_012 | gi 22709767 gb BU195783.1 BU195783                                   | 0        | 316  | clathrin coat assembly protein                            |                                                                                                                      | Clat_adaptor_s   | 0.03167 |
| 08078_Oc_5_015 | gi 85572315 gb DW712123.1 DW712123                                   | 0        | 242  | af266220_1proteasome subunit beta type 1                  | C:GO:0005839,F:GO:0005515,F:GO:0004298,P:GO:0006511,C:GO:0005634                                                     | Proteasome       | 0.5332  |
| 08081_Oc_5_017 | gi 62882572 gb DN897809.1 DN897809                                   | 2.00E-34 | 145  | na+ k+ atpase alpha subunit                               | F:GO:0015077,F:GO:0019870,F:GO:0005267,F:GO:0030955,C:GO:0005579,P:GO:0006813,P:GO:0008152,F:GO:0015662,F:GO:0000166 | Cation_ATPas e_C | 0.32584 |
| 08120_Oc_5_060 | gi 62041039 gb DN689091.1 DN689091                                   | 2.00E-18 | 92.7 | elegans proteinpartially confirmed by transcript evidence | P:GO:0007242,F:GO:0005515                                                                                            | C1_1             |         |
| 08204_Oc_5_046 | BY798237                                                             | 0.009    | 26.3 |                                                           |                                                                                                                      |                  |         |
| 08268_Oc_5_014 | gi 58061282 gb CX734446.1 CX734446                                   | 1.00E-11 | 70.3 | ---NA---                                                  |                                                                                                                      |                  | 0.80885 |
| 08322_Oc_5_073 | gi 10202867 gb BE781741.1 BE781741                                   | 3.00E-24 | 112  | af393635_1visual arrestin                                 | P:GO:0007600,P:GO:0007165                                                                                            | Arrestin_N       | 0.34364 |
| 08352_Oc_5_096 | gi 62827577 gb DN857928.1 DN857928                                   | 3.00E-06 | 52   |                                                           |                                                                                                                      |                  |         |
| 08363_Oc_5_006 | GS020748                                                             | 0.007    | 32.2 |                                                           |                                                                                                                      |                  |         |
| 08462_Oc_5_015 | gi 85203731 gb DW606507.1 DW606507                                   | 0.0001   | 47.3 | gelsolin-like protein                                     | F:GO:0003779                                                                                                         | Gelsolin         | 1.40875 |
| 08618_Oc_5_077 | gi 5034328 gb AI717072.1 AI717072                                    | 0        | 187  | proteaseome (prosome macropain) 28 subunit 3              |                                                                                                                      |                  | 0.22146 |
| 08656_Oc_5_016 | <b>Embryo specific expression</b> gi 46565708 gb CN484204.1 CN484204 | 0        | 219  | icarus cg9031-pa                                          |                                                                                                                      | Pfam-B_6730      | 0.14439 |

|                |                                                                                  |          |      |                                                                |                                                                                               |                       |         |
|----------------|----------------------------------------------------------------------------------|----------|------|----------------------------------------------------------------|-----------------------------------------------------------------------------------------------|-----------------------|---------|
| 08705_Oc_5_065 | gi 32177391 gb <br>CD675660.1 <br>CD675660                                       | 2.00E-08 | 59.7 | novel protein with a<br>dna<br>polymerasesubunit 4<br>domain   | P:GO:0006260,C:GO:<br>0005634                                                                 | DNA_pol_delta<br>_4   |         |
| 08730_Oc_5_093 | gi 29527710 gb <br>CB584259.1 <br>CB584259                                       | 0        | 114  | heat shock protein 5                                           | C:GO:0005788,F:GO:<br>0005515,C:GO:<br>0042470,F:GO:<br>0005524,P:GO:<br>0006983,F:GO:0043022 | Pfam-B_2482,<br>HSP70 |         |
| 08731_Oc_5_086 | gi 19353895 gb <br>BM903943.1 <br>BM903943                                       | 0        | 215  | glutamyl-prolyl-trna<br>synthetase                             | C:GO:0005737,F:GO:<br>0004827,P:GO:<br>0006433,F:GO:<br>0004818,P:GO:<br>0006424,F:GO:0005524 | HGTP_anticon<br>on    |         |
| 08745_Oc_5_005 | gi 32173164 gb <br>CD671424.1 <br>CD671424                                       | 3.00E-11 | 68.9 | williams-beuren<br>syndrome<br>chromosome region<br>16 homolog |                                                                                               | RCC1                  |         |
| 08767_Oc_5_024 | gi 13054197 gb <br>BG294000.1 <br>BG294000                                       | 0.01     | 40.5 | cell adhesion molecule                                         | F:GO:0005488                                                                                  | fn3                   |         |
| 08785_Oc_5_049 | gi 14063071 gb <br>BG752418.1 <br>BG752418                                       | 0.0001   | 50.1 |                                                                |                                                                                               |                       |         |
| 08786_Oc_5_057 | gi 22274904 gb <br>BQ882896.1 <br>BQ882896                                       | 0        | 118  | malic enzyme                                                   |                                                                                               | Malic_M               | 0.65495 |
| 08812_Oc_5_078 | <b>Embryo specific<br/>expression</b> gi 13298391 gb <br>BG373919.1 <br>BG373919 | 0.006    | 44.1 |                                                                |                                                                                               |                       |         |
| 08845_Oc_5_007 | gi 85196168 gb <br>DW603790.1 <br>DW603790                                       | 1.00E-16 | 86.3 | nmda receptor<br>glutamate-binding<br>chain isoform 2          |                                                                                               | UPF0005               |         |
| 08871_Oc_5_036 | <b>Embryo specific<br/>expression</b> BY800203                                   | 0.009    | 38.2 | sperm associated<br>antigenpartial                             | F:GO:0005525,P:GO:<br>0007338,F:GO:<br>0005488,F:GO:<br>0016787,F:GO:0000166                  |                       | 0.92387 |

|                |                                                                  |          |      |                                                  |                                                                                                                                   |                            |         |
|----------------|------------------------------------------------------------------|----------|------|--------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|----------------------------|---------|
| 08912_Oc_5_080 | gi 19016174 gb BM702916.1 BM702916                               | 8.00E-14 | 76.7 | calcyclin binding protein                        | C:GO:0005737,P:GO:0006512,C:GO:0005634                                                                                            | SGS                        |         |
| 08917_Oc_5_083 | BY800072                                                         | 0.0004   | 40.1 |                                                  |                                                                                                                                   |                            |         |
| 08953_Oc_5_021 | gi 46817532 gb CN504908.1 CN504908                               | 2.00E-40 | 146  | coiled-coil domain-containing protein 58         | P:GO:0008150,C:GO:0005575                                                                                                         | Cid2                       | 0.70103 |
| 08954_Oc_5_029 | gi 19028683 gb BM715425.1 BM715425                               | 0.0004   | 45.1 |                                                  |                                                                                                                                   |                            |         |
| 08991_Oc_5_056 | gi 75846603 gb DT876863.1 DT876863                               | 1.00E-39 | 163  | glutathione s-transferase theta 1                |                                                                                                                                   |                            | 0.61475 |
| 09022_Oc_5_095 | gi 41345608 gb CK624722.1 CK624722                               | 9.00E-08 | 57   | transmembrane protein 161b                       |                                                                                                                                   | Pfam-B_13263, Tmemb_161A B |         |
| 09100_Oc_5_078 | gi 9123773 gb BE253612.1 BE253612                                | 0        | 123  | sec13-like 1                                     |                                                                                                                                   | WD40                       |         |
| 09121_Oc_5_001 | gi 62840342 gb DN870401.1 DN870401                               | 1.40E-45 | 183  | exosome complex exonuclease                      |                                                                                                                                   |                            | 0.427   |
| 09132_Oc_5_014 | gi 57591990 gb CX564961.1 CX564961                               | 1.00E-15 | 83.5 | alveolar soft part sarcoma chromosomecandidate 1 |                                                                                                                                   |                            |         |
| 09156_Oc_5_042 | BY797489                                                         | 0.01     | 36.2 |                                                  |                                                                                                                                   |                            |         |
| 09165_Oc_5_039 | gi 32172937 gb CD671206.1 CD671206                               | 0        | 226  | inositol-3-phosphate synthase a                  | P:GO:0006021,F:GO:0005488,P:GO:0008654,F:GO:0004512                                                                               | NAD_binding_5              | 0.16312 |
| 09168_Oc_5_048 | Embryo specific expression<br>gi 50134996 gb CO469880.1 CO469880 | 0        | 305  | na+ k+ atpase alpha subunit                      | F:GO:0015077,F:GO:0005391,F:GO:0030955,F:GO:0005524,F:GO:0000287,F:GO:0031402,P:GO:0006813,C:GO:0016021,P:GO:0008152,P:GO:0006814 | Cation_ATPas e_C           | 0.42477 |

|                               |                                                                                  |          |      |                                                     |                                                             |                    |
|-------------------------------|----------------------------------------------------------------------------------|----------|------|-----------------------------------------------------|-------------------------------------------------------------|--------------------|
| 09189_Oc_5_067                | gi 19390803 gb <br>BM931630.1 <br>BM931630                                       | 0.008    | 44.1 |                                                     |                                                             |                    |
| 09225_Oc_5_005                | gi 50138203 gb <br>CO471352.1 <br>CO471352                                       | 0        | 200  | translation initiation<br>factor 1a                 |                                                             | 0.65996            |
| 09243_Oc_5_022                | gi 62852808 gb <br>DN882853.1 <br>DN882853                                       | 0.002    | 46.1 |                                                     | Pfam-B_6449                                                 |                    |
| 09302_Oc_5_091                | gi 46823183 gb <br>CN510559.1 <br>CN510559                                       | 1.00E-27 | 121  | ribosomal protein l                                 | C:GO:0005840,F:GO:<br>0003735,P:GO:0006412                  | Ribosomal_L2<br>_C |
| 09357_Oc_5_039                | <b>Embryo specific<br/>expression</b> gi 126524124 gb <br>EL647843.1 EL647843    | 0        | 194  | serine threonine<br>tyrosine-interacting<br>protein | P:GO:0006470,F:GO:<br>0008138                               |                    |
| 09365_Oc_5_051                | gi 54440614 gb <br>CV556259.1 <br>CV556259                                       | 0.002    | 46.1 |                                                     |                                                             |                    |
| 09370_Oc_5_061                | gi 75844397 gb <br>DT874657.1 DT874657                                           | 0        | 249  | peroxisomal trans-2-<br>enoyl-reductase             | F:GO:0005488,F:GO:<br>0016491,P:GO:<br>0008152,F:GO:0003824 | 0.25225            |
| 09412_Oc_5_010                | <b>Embryo specific<br/>expression</b> gi 85197393 gb <br>DW604221.1 <br>DW604221 | 1.00E-07 | 57.4 | kv channel-interacting<br>protein                   |                                                             |                    |
| 09429_Oc_5_019                | gi 11672321 gb <br>BF562591.1 BF562591                                           | 0.008    | 44.1 |                                                     |                                                             |                    |
| 09491_Oc_5_082                | gi 85203729 gb <br>DW606506.1 <br>DW606506                                       | 8.00E-11 | 68   | nucleoporin 50                                      | C:GO:0016020,P:GO:<br>0046907                               |                    |
| 09492_Oc_5_090                | gi 119778776 gb <br>EH278374.1 <br>EH278374                                      | 0.01     | 41   |                                                     |                                                             |                    |
| 5primeCluster00<br>02.Contig1 | BY795134                                                                         | 4.00E-09 | 38.2 | cg6180-pa isoform 2                                 |                                                             | PBP                |
| 5primeCluster00<br>02.Contig3 | gi 13406406 gb <br>BG474129.1 <br>BG474129                                       | 2.00E-19 | 96.7 | cg6180-pa isoform 2                                 |                                                             | PBP 0.72476        |

|                               |                                                                             |          |                                                       |                                            |                                                                                                           |         |
|-------------------------------|-----------------------------------------------------------------------------|----------|-------------------------------------------------------|--------------------------------------------|-----------------------------------------------------------------------------------------------------------|---------|
| 5primeCluster00<br>08.Contig2 | gi 22353925 gb <br>BQ938447.1 <br>BQ938447                                  | 0        | 105 cytochrome c oxidase<br>subunit ii                | F:GO:0046872,C:GO:<br>0005743,C:GO:0044425 | COX2_TM,<br>COX2                                                                                          | 0.61197 |
| 5primeCluster00<br>09.Contig1 | gi 62046021 gb <br>DN691540.1 <br>DN691540                                  | 0        | 208 crom_octdoame:<br>full=omega-crystallin           | F:GO:0005212,F:GO:<br>0016491,P:GO:0008152 | Aldedh                                                                                                    | 1.32732 |
| 5primeCluster00<br>21.Contig1 | BY794962                                                                    | 6.00E-06 | 46.4 atp synthetase subunit<br>6                      | C:GO:0016020                               | ATP-synt_A                                                                                                |         |
| 5primeCluster00<br>31.Contig1 | gi 14261392 gb <br>BG884300.1 <br>BG884300                                  | 5.00E-25 | 107 ribosomal protein lp1                             | C:GO:0005840,F:GO:<br>0003735,P:GO:0006414 | Ribosomal_60<br>s                                                                                         | 1.31863 |
| 5primeCluster00<br>36.Contig1 | BY794962                                                                    | 0.0002   | 41.4 atp synthetase subunit<br>6                      | C:GO:0044464                               | ATP-synt_A                                                                                                |         |
| 5primeCluster00<br>45.Contig3 | <b>Positive<br/>selection</b><br>gi 62873711 gb <br>DN888948.1 <br>DN888948 | 0        | 166 ---NA---                                          |                                            | TMF_DNA_bd,<br>ATG16,<br>Tropomyosin,<br>ERM, Pfam-<br>B_16520,<br>Tropomyosin,<br>Myosin_tail_1,<br>IncA | 4.01906 |
| 5primeCluster00<br>46.Contig1 | gi 54470231 gb <br>CV570080.1 <br>CV570080                                  | 4.00E-13 | 46 saposin isoform 1                                  |                                            | Pfam-B_328,<br>SapB_1,<br>SapB_2                                                                          |         |
| 5primeCluster00<br>48.Contig1 | gi 75839196 gb <br>DT869456.1 DT869456                                      | 1.00E-13 | 47.8 histone h1                                       | C:GO:0005694                               | Linker_histone                                                                                            | 0.15023 |
| 5primeCluster00<br>50.Contig2 | gi 41341803 gb <br>CK620917.1 <br>CK620917                                  | 0.0008   | 35.4 calmodulin 4 (calcium-<br>binding protein dd112) | F:GO:0005509,C:GO:<br>0005626,C:GO:0005625 | efhand                                                                                                    |         |
| 5primeCluster00<br>52.Contig1 | GS020536                                                                    | 0.003    | 34.2                                                  |                                            |                                                                                                           |         |

|                               |                       |                                     |          |      |                                                                                                  |                                                     |                                                                                                                                |         |
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| 5primeCluster00<br>52.Contig3 |                       | GS020536                            | 0.008    | 34.2 | gastrotropin(fatty acid-binding protein 6) (ileal lipid-binding protein) (porcine ileal peptide) |                                                     | Pfam-B_587,<br>Pfam-B_14296 ,<br>Pfam-B_18747,<br>Pfam-B_6927,<br>Pfam-B_3553,<br>Pfam-B_7642,<br>Pfam-B_8096,<br>Pfam-B_14082 |         |
| 5primeCluster00<br>59.Contig1 |                       | BY795013                            | 0        | 230  | ribosomal protein s15a                                                                           | C:GO:0005840,F:GO:0003735,P:GO:0006412              | Ribosomal_S8                                                                                                                   | 0.47553 |
| 5primeCluster00<br>59.Contig2 |                       | BY795013                            | 0        | 254  | ribosomal protein rps15a                                                                         | C:GO:0005840,F:GO:0003735,P:GO:0006412              | Ribosomal_S8                                                                                                                   | 0.26852 |
| 5primeCluster00<br>61.Contig1 |                       | gi 75839434 gb DT869694.1 DT869694  | 7.00E-41 | 166  | ribosomal protein s26                                                                            | C:GO:0030529                                        | Ribosomal_S2<br>6e                                                                                                             | 0.60336 |
| 5primeCluster00<br>61.Contig2 |                       | gi 119779873 gb EH278644.1 EH278644 | 1.00E-39 | 163  | rs26_octvuame: full=40s ribosomal protein s26                                                    | C:GO:0030529                                        | Ribosomal_S2<br>6e                                                                                                             | 0.06295 |
| 5primeCluster00<br>62.Contig1 |                       | gi 24544553 gb CA326455.1 CA326455  | 0        | 410  | ribosomal protein s5                                                                             | P:GO:0042254,F:GO:0003735,N:GO:0022627,P:GO:0006412 | Ribosomal_S7                                                                                                                   | 0.04041 |
| 5primeCluster00<br>64.Contig1 |                       | gi 119777845 gb EH278206.1 EH278206 | 0        | 210  | ribosomal protein l10                                                                            | C:GO:0005840,F:GO:0003735,P:GO:0006412              | Ribosomal_L1<br>6                                                                                                              | 0.0922  |
| 5primeCluster00<br>67.Contig1 |                       | BY795427                            | 6.00E-14 | 67.5 | aecombinant actophorin                                                                           | C:GO:0005737,F:GO:0003779,C:GO:0005622              | Pfam-B_8155,<br>Cofilin_ADF                                                                                                    | 1.42294 |
| 5primeCluster00<br>71.Contig1 |                       | gi 62828989 gb DN859340.1 DN859340  | 2.00E-37 | 124  | ribosomal protein s30                                                                            | P:GO:0044267,C:GO:0005622                           | ubiquitin,<br>Ribosomal_S3<br>0                                                                                                | 0.45407 |
| 5primeCluster00<br>71.Contig2 |                       | BY795000                            | 3.00E-38 | 117  | ribosomal protein s30                                                                            | P:GO:0044267,C:GO:0005622                           | ubiquitin,<br>Ribosomal_S3<br>0                                                                                                | 0.18231 |
| 5primeCluster00<br>73.Contig1 | Positive<br>selection | gi 37637396 gb CF741058.1 CF741058  | 2.00E-41 | 168  | 60s ribosomal protein l23                                                                        | C:GO:0005840,F:GO:0003735,P:GO:0006412              | Ribosomal_L1<br>4                                                                                                              | 7.68894 |
| 5primeCluster00<br>74.Contig1 |                       | gi 50140708 gb CO472492.1 CO472492  | 2.00E-11 | 69.8 | mitochondrial atp synthase f chain                                                               |                                                     | WRW                                                                                                                            | 1.11975 |

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| 5primeCluster00<br>75.Contig1 | gi 119779534 gb <br>EH278551.1 <br>EH278551 | 6.00E-24 | 113 transport protein<br>sec61 subunit gamma                    | P:GO:0006886,C:GO:<br>0016020                                                | SecE                             |         |
| 5primeCluster00<br>75.Contig2 | gi 85183876 gb <br>DW600023.1 <br>DW600023  | 4.00E-27 | 121 transport protein<br>sec61 gamma subunit                    | P:GO:0065002,C:GO:<br>0005789,F:GO:<br>0015450,P:GO:<br>0006605,C:GO:0016021 | SecE                             | 0.21347 |
| 5primeCluster00<br>76.Contig1 | gi 62854210 gb <br>DN884255.1 <br>DN884255  | 2.00E-23 | 108 40s ribosomal protein<br>s29                                | C:GO:0005840,F:GO:<br>0003735,F:GO:<br>0008270,P:GO:000641                   | Ribosomal_S1<br>4                |         |
| 5primeCluster00<br>76.Contig2 | gi 50140539 gb <br>CO472426.1 <br>CO472426  | 2.00E-25 | 115 ribosomal protein s29                                       | C:GO:0005840,F:GO:<br>0003735,F:GO:<br>0008270,P:GO:000641                   | Ribosomal_S1<br>4                | 1.94215 |
| 5primeCluster00<br>77.Contig1 | gi 10589311 gb <br>BE950645.1 BE950645      | 9.00E-29 | 117 ornithine<br>decarboxylase<br>antizymeisoform cra_a         |                                                                              | ODC_AZ                           | 0.36185 |
| 5primeCluster00<br>77.Contig2 | gi 10589311 gb <br>BE950645.1 BE950645      | 7.00E-28 | 113 ornithine<br>decarboxylase<br>antizyme                      | F:GO:0008073                                                                 | ODC_AZ                           | 1.534   |
| 5primeCluster00<br>87.Contig1 | gi 62031452 gb <br>DN684263.1 <br>DN684263  | 0        | 141 cathepsin I                                                 |                                                                              | Inhibitor_I29,<br>Peptidase_C1   |         |
| 5primeCluster00<br>88.Contig1 | gi 40318508 gb <br>CK352621.1 <br>CK352621  | 2.00E-39 | 162 translocon-associated<br>protein subunit delta<br>precursor | C:GO:0016021,C:GO:<br>0005783                                                | TRAP-delta,<br>SEF14_adhesi<br>n | 0.19836 |
| 5primeCluster00<br>88.Contig2 | gi 40318508 gb <br>CK352621.1 <br>CK352621  | 0        | 207 translocon-associated<br>protein subunit delta<br>precursor | F:GO:0004872,C:GO:<br>0016021,P:GO:0008150                                   | TRAP-delta,<br>SEF14_adhesi<br>n | 0.34097 |
| 5primeCluster00<br>91.Contig1 | gi 62888533 gb <br>DN903770.1 <br>DN903770  | 0        | 251 fatty aldehyde<br>dehydrogenase                             |                                                                              | Aldedh                           | 2.41432 |
| 5primeCluster00<br>94.Contig1 | gi 24559278 gb <br>CA341182.1 <br>CA341182  | 0        | 210 ribosomal protein<br>rpl26                                  | F:GO:0003735,C:GO:<br>0015934,P:GO:0006412                                   | KOW                              | 0.06808 |
| 5primeCluster00<br>94.Contig2 | gi 124701339 gb <br>EH999942.1 <br>EH999942 | 0        | 221 ribosomal protein<br>rpl26                                  | F:GO:0003735,C:GO:<br>0015934,P:GO:0006412                                   | KOW                              | 0.5299  |

|                               |                                            |          |                                                    |                                                                              |                                         |         |
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| 5primeCluster00<br>97.Contig1 | gi 45305112 gb <br>CK875481.1 <br>CK875481 | 0        | 187 60s ribosomal protein<br>l35                   | P:GO:0009987,C:GO:<br>0030529                                                | Ribosomal_L2<br>9                       | 1.3573  |
| 5primeCluster00<br>97.Contig2 | gi 91746892 gb <br>EB383547.1 EB383547     | 0        | 184 ribosomal protein l35                          |                                                                              | Ribosomal_L2<br>9                       | 0.70752 |
| 5primeCluster00<br>98.Contig1 | gi 24559069 gb <br>CA340973.1 <br>CA340973 | 0        | 222 60s ribosomal protein<br>l30                   | C:GO:0005840,F:GO:<br>0003735,P:GO:0006412                                   | Ribosomal_L7<br>Ae                      |         |
| 5primeCluster01<br>03.Contig1 | gi 46823889 gb <br>CN511265.1 <br>CN511265 | 0        | 349 arp2 3 complex 20 kd<br>subunit                | C:GO:0005856,P:GO:<br>0030041                                                | ARPC4                                   | 0.62763 |
| 5primeCluster01<br>04.Contig1 | gi 23654355 gb <br>BU730451.1 <br>BU730451 | 0        | 294 n-acetyltransferase 13                         | P:GO:0001756,C:GO:<br>0005737,P:GO:<br>0008152,F:GO:0008080                  | Acetyltransf_1                          |         |
| 5primeCluster01<br>07.Contig1 | gi 78181987 gb <br>DV552360.1 DV552360     | 9.81E-45 | 179 60s ribosomal protein<br>l14                   |                                                                              | Pfam-<br>B_12433,<br>Ribosomal_L1<br>4e | 0.2301  |
| 5primeCluster01<br>07.Contig2 | gi 78181987 gb <br>DV552360.1 DV552360     | 2.80E-45 | 182 ribosomal<br>proteinpartial                    |                                                                              | Pfam-<br>B_12433,<br>Ribosomal_L1<br>4e | 1.08392 |
| 5primeCluster01<br>12.Contig1 | gi 62889671 gb <br>DN904908.1 <br>DN904908 | 0        | 308 ribosomal protein s16                          | P:GO:0000022,F:GO:<br>0003735,C:GO:<br>0005811,N:GO:<br>0022627,P:GO:0006412 | Ribosomal_S9                            | 0.15204 |
| 5primeCluster01<br>13.Contig1 | gi 46818458 gb <br>CN505834.1 <br>CN505834 | 8.00E-24 | 79 translationally-<br>controlled tumor<br>protein | P:GO:0006412,F:GO:<br>0005509,C:GO:<br>0005737,C:GO:0005874                  | TCTP                                    | 0.9258  |
| 5primeCluster01<br>14.Contig1 | gi 85190796 gb <br>DW602403.1 <br>DW602403 | 0        | 203 ribosomal protein s24e                         | C:GO:0005840,F:GO:<br>0003735,P:GO:<br>0006412,F:GO:0000166                  | Ribosomal_S2<br>4e                      | 1.31471 |
| 5primeCluster01<br>14.Contig2 | BY795029                                   | 2.94E-44 | 168 40s ribosomal protein<br>s24                   | C:GO:0005840,F:GO:<br>0003735,P:GO:<br>0006412,F:GO:0000166                  | Ribosomal_S2<br>4e                      | 1.54532 |
| 5primeCluster01<br>20.Contig1 | BY798636                                   | 4.00E-26 | 112 gaba-a receptor<br>associated protein          | F:GO:0004872                                                                 | MAP1_LC3                                | 0.95724 |

|                               |                                                                   |                                            |          |      |                                                                              |                                                                                               |                                                                     |         |
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| 5primeCluster01<br>28.Contig1 |                                                                   | BY795095                                   | 7.00E-42 | 133  | 60s ribosomal protein<br>l23a variant 1                                      | C:GO:0005840,F:GO:<br>0000166                                                                 | Ribosomal_L2<br>3eN,<br>Ribosomal_L2<br>3                           | 1.48442 |
| 5primeCluster01<br>29.Contig1 |                                                                   | gi 19026532 gb <br>BM713274.1 <br>BM713274 | 0        | 325  | dolichyl-phosphate<br>mannosyltransferase<br>polypeptidecatalytic<br>subunit | C:GO:0005789,F:GO:<br>0004582,P:GO:<br>0035269,P:GO:<br>0006506,F:GO:<br>0005515,F:GO:0004169 | Glycos_transf_<br>2                                                 | 0.46204 |
| 5primeCluster01<br>32.Contig2 |                                                                   | gi 85182524 gb <br>DW599548.1 <br>DW599548 | 0        | 365  | heat shock cognate 70                                                        | F:GO:0005524,P:GO:<br>0006950                                                                 | HSP70                                                               |         |
| 5primeCluster01<br>36.Contig2 |                                                                   | gi 62878283 gb <br>DN893520.1 <br>DN893520 | 0.003    | 42.3 | linker histone h1 and<br>h5 family protein                                   | C:GO:0000786,P:GO:<br>0006334,F:GO:0003677                                                    | Linker_histone,<br>Pfam-B_9326,<br>Pfam-<br>B_14006Pfam-<br>B_10197 |         |
| 5primeCluster01<br>36.Contig3 |                                                                   | gi 57592021 gb <br>CX564992.1 <br>CX564992 | 0.0002   | 46.9 | linker histone h1 and<br>h5 family protein                                   | C:GO:0043229                                                                                  | Pfam-<br>B_10197,<br>Linker_histone,<br>S10_plectin                 |         |
| 5primeCluster01<br>37.Contig2 | <b>Embryo specific<br/>expression</b>                             | gi 75844950 gb <br>DT875210.1 DT875210     | 0        | 135  | ribosomal protein s10                                                        | C:GO:0005840                                                                                  |                                                                     | 1.51048 |
| 5primeCluster01<br>38.Contig1 |                                                                   | gi 58035516 gb <br>CX733042.1 <br>CX733042 | 7.00E-18 | 62   | mitochondrial<br>nadh:ubiquinone<br>oxidoreductase                           |                                                                                               | GRIM-19                                                             | 0.78623 |
| 5primeCluster01<br>43.Contig1 |                                                                   | gi 126525667 gb <br>EL649386.1 EL649386    | 2.00E-42 | 172  | ribosomal protein l11                                                        | C:GO:0030529                                                                                  | Ribosomal_L5<br>_C                                                  |         |
| 5primeCluster01<br>45.Contig1 |                                                                   | gi 39889198 gb <br>CK300140.1 <br>CK300140 | 6.00E-41 | 168  | glutathione s-<br>transferase mu                                             |                                                                                               | GST_C                                                               | 2.87141 |
| 5primeCluster01<br>47.Contig1 | <b>Embryo specific<br/>expression,<br/>Positive<br/>selection</b> | gi 85171835 gb <br>DW596067.1 <br>DW596067 | 0        | 249  | peptidase<br>(mitochondrial<br>processing) beta<br>isoform 2                 |                                                                                               | Peptidase_M1<br>6_C                                                 | 0.75579 |

|                               |                       |                                            |          |                                                                          |                                                             |                                     |         |
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| 5primeCluster01<br>50.Contig1 |                       | gi 11534174 gb <br>BF464991.1 BF464991     | 1.00E-16 | 62.9 mgc88931 protein                                                    | C:GO:0000785,F:GO:<br>0003677,C:GO:<br>0005634,P:GO:0006355 | HMG_box                             |         |
| 5primeCluster01<br>51.Contig1 |                       | gi 22673837 gb <br>BU159927.1 <br>BU159927 | 2.00E-31 | 136 cg10233-isoform a                                                    |                                                             | MORN                                | 0.25777 |
| 5primeCluster01<br>53.Contig1 |                       | BY795011                                   | 0        | 148 ribosomal protein l21                                                | C:GO:0005622                                                | Ribosomal_L2<br>1e, Pfam-<br>B_3820 | 1.84    |
| 5primeCluster01<br>61.Contig1 |                       | gi 46819336 gb <br>CN506712.1 <br>CN506712 | 0        | 155 atp synthase<br>oligomycin sensitivity<br>conferral protein          |                                                             | OSCP                                | 1.31305 |
| 5primeCluster01<br>63.Contig1 |                       | gi 13104757 gb <br>BG307230.1 <br>BG307230 | 8.00E-28 | 76.2 60s ribosomal protein<br>l22 (development-<br>specific protein 217) | F:GO:0003735,P:GO:<br>0006412,C:GO:<br>0005840,C:GO:0005622 | Ribosomal_L2<br>2e                  | 0.83977 |
| 5primeCluster01<br>65.Contig1 |                       | gi 77502748 gb <br>DV214656.1 DV214656     | 0        | 196 ribosomal protein s17                                                | C:GO:0005840,F:GO:<br>0003735,P:GO:0006412                  | Ribosomal_S1<br>7e                  | 1.28725 |
| 5primeCluster01<br>69.Contig1 |                       | gi 126526025 gb <br>EL649744.1 EL649744    | 1.00E-18 | 92.7 ---NA---                                                            |                                                             | MMgT                                | 0.0725  |
| 5primeCluster01<br>69.Contig2 |                       | gi 126526025 gb <br>EL649744.1 EL649744    | 1.00E-17 | 90 ---NA---                                                              |                                                             | MMgT,<br>DUF962                     |         |
| 5primeCluster01<br>73.Contig1 | Positive<br>selection | BY795137                                   | 7.00E-28 | 118 ribosomal protein s25                                                | C:GO:0005840                                                | Ribosomal_S2<br>5                   | 3.18242 |
| 5primeCluster01<br>74.Contig1 |                       | gi 41343480 gb <br>CK622594.1 <br>CK622594 | 8.00E-16 | 83.5 cytochrome csubunit<br>vic                                          | C:GO:0005615,C:GO:<br>0005751,C:GO:<br>0016021,F:GO:0004129 | COX6C                               |         |
| 5primeCluster01<br>78.Contig1 |                       | gi 45305160 gb <br>CK875529.1 <br>CK875529 | 9.00E-39 | 159 40s ribosomal protein<br>s21                                         |                                                             | Ribosomal_S2<br>1e                  | 1.61541 |
| 5primeCluster01<br>78.Contig2 |                       | gi 58035040 gb <br>CX732566.1 <br>CX732566 | 1.00E-38 | 159 ribosomal protein s21                                                | F:GO:0003735,P:GO:<br>0006412,C:GO:0030529                  | Ribosomal_S2<br>1e                  | 1.95144 |
| 5primeCluster01<br>84.Contig1 |                       | GS008194                                   | 0.005    | 32.2                                                                     |                                                             |                                     |         |
| 5primeCluster01<br>88.Contig1 | Positive<br>selection | gi 75840163 gb <br>DT870423.1 DT870423     | 0        | 189 es1 protein                                                          |                                                             | DJ-1_Pfpl                           | 2.2695  |

|                               |                                         |                                            |          |      |                                                                                                                                                                                                                 |                                                                                                                |                          |         |
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| 5primeCluster01<br>91.Contig1 |                                         | gi 49672561 gb <br>CO426267.1 <br>CO426267 | 6.00E-13 | 74.8 | heat shock protein<br>gp96                                                                                                                                                                                      | P:GO:0006457,C:GO:<br>0005788,C:GO:<br>0042470,P:GO:<br>0006950,F:GO:<br>0005509,F:GO:<br>0005524,F:GO:0051082 | HSP90                    |         |
| 5primeCluster01<br>92.Contig1 |                                         | gi 40318338 gb <br>CK352451.1 <br>CK352451 | 3.00E-06 | 34.5 | zinc finger protein 346<br>variant 3                                                                                                                                                                            |                                                                                                                | zf-C2H2_jaz              |         |
| 5primeCluster01<br>93.Contig1 |                                         | gi 49672103 gb <br>CO425809.1 <br>CO425809 | 3.00E-38 | 159  | syntenin-1 (syndecan-<br>binding protein 1)<br>(melanoma<br>differentiation-<br>associated protein 9)<br>(mda-9) (scaffold<br>protein pbp1) (pro-tgf-<br>alpha cytoplasmic<br>domain-interacting<br>protein 18) | F:GO:0005137,P:GO:<br>0008152,C:GO:<br>0005895,F:GO:<br>0016491,P:GO:0007265                                   | PDZ                      | 0.78017 |
| 5primeCluster01<br>97.Contig1 |                                         | gi 32465408 gb <br>CD806582.1 <br>CD806582 | 1.00E-31 | 81.4 | ---NA---                                                                                                                                                                                                        |                                                                                                                | Cu-oxidase_3             |         |
| 5primeCluster02<br>02.Contig1 | GO annotation,<br>Positive<br>selection | gi 13056621 gb <br>BG295212.1 <br>BG295212 | 5.00E-41 | 168  | fgfr1 oncogene partner<br>2                                                                                                                                                                                     | C:GO:0005737                                                                                                   | DUF837                   | 2.241   |
| 5primeCluster02<br>04.Contig1 |                                         | gi 37628162 gb <br>CF731832.1 CF731832     | 0        | 154  | suc1a2 protein                                                                                                                                                                                                  | C:GO:0005739                                                                                                   | ATP-grasp_2              | 0.35182 |
| 5primeCluster02<br>05.Contig1 | Positive<br>selection                   | gi 62853918 gb <br>DN883963.1 <br>DN883963 | 0        | 318  | thioredoxin peroxidase<br>2                                                                                                                                                                                     | F:GO:0004601                                                                                                   | AhpC-TSA, 1-<br>cysPrx_C | 7.62969 |
| 5primeCluster02<br>08.Contig1 |                                         | gi 62037240 gb <br>DN687181.1 <br>DN687181 | 2.00E-32 | 59.8 | ---NA---                                                                                                                                                                                                        |                                                                                                                | Transferrin              | 1.0693  |
| 5primeCluster02<br>09.Contig1 |                                         | GS020551                                   | 0.002    | 32.2 |                                                                                                                                                                                                                 |                                                                                                                |                          |         |
| 5primeCluster02<br>14.Contig2 | GO annotation                           | gi 12042337 gb <br>BF726426.1 BF726426     | 0        | 202  | annexin a7                                                                                                                                                                                                      | F:GO:0005488,C:GO:<br>0044424                                                                                  | Annexin                  | 0.34138 |

|                               |                                            |          |                                                                                  |                                                                                               |                        |         |
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| 5primeCluster02<br>15.Contig1 | gi 8487330 gb <br>BE096399.1 BE096399      | 5.00E-37 | 155 g alpha q subunit                                                            | P:GO:0007186,F:GO:<br>0004871,P:GO:<br>0006471,F:GO:0005525                                   | G-alpha                | 0.42835 |
| 5primeCluster02<br>19.Contig1 | gi 18523312 gb <br>BM474270.1 <br>BM474270 | 0.0002   | 46.5 fusion (involved in tin<br>malignant<br>liposarcoma) isoform a<br>isoform 2 |                                                                                               |                        |         |
| 5primeCluster02<br>23.Contig1 | gi 45305796 gb <br>CK876165.1 <br>CK876165 | 3.00E-29 | 103 transport protein<br>sec61 subunit beta                                      |                                                                                               | Sec61_beta             |         |
| 5primeCluster02<br>24.Contig1 | gi 11536060 gb <br>BF466877.1 BF466877     | 6.00E-06 | 51.5 nuclear fragile x<br>mental retardation<br>protein interacting<br>protein 1 | F:GO:0003676,F:GO:<br>0008270,C:GO:0005622                                                    | Pfam-B_6194,<br>NUFIP1 |         |
| 5primeCluster02<br>27.Contig1 | gi 76146130 gb <br>CJ065007.1 CJ065007     | 1.00E-37 | 156 ceruloplasmin<br>precursorisoform 3                                          |                                                                                               | Cu-oxidase_2           | 0.5422  |
| 5primeCluster02<br>35.Contig1 | gi 37636035 gb <br>CF739697.1 CF739697     | 0        | 195 60s ribosomal protein<br>l27a                                                |                                                                                               | Ribosomal_L1<br>8e     | 0.38194 |
| 5primeCluster02<br>47.Contig1 | gi 62842068 gb <br>DN872127.1 <br>DN872127 | 7.00E-29 | 76.2 nadh dehydrogenase                                                          |                                                                                               |                        |         |
| 5primeCluster02<br>51.Contig1 | gi 32175032 gb <br>CD673301.1 <br>CD673301 | 4.00E-10 | 46 isoform a                                                                     |                                                                                               | HSP20                  | 0.5291  |
| 5primeCluster02<br>59.Contig1 | gi 62883263 gb <br>DN898500.1 <br>DN898500 | 2.00E-40 | 112 60s ribosomal protein<br>rpl35a                                              |                                                                                               | Ribosomal_L3<br>5Ae    | 0.71661 |
| 5primeCluster02<br>59.Contig2 | gi 62883263 gb <br>DN898500.1 <br>DN898500 | 1.40E-45 | 111 ribosomal protein<br>rpl35a                                                  |                                                                                               | Ribosomal_L3<br>5Ae    | 1.30327 |
| 5primeCluster02<br>60.Contig1 | gi 19004898 gb <br>BM691640.1 <br>BM691640 | 2.00E-15 | 59.3 zgc:92867 protein                                                           | F:GO:0046872,C:GO:<br>0005737,F:GO:<br>0000287,F:GO:<br>0016787,C:GO:<br>0005634,F:GO:0004649 | ADP_ribosyl_<br>GH     |         |
| 5primeCluster02<br>65.Contig1 | gi 18991779 gb <br>BM681883.1 <br>BM681883 | 5.00E-10 | 64.8 cmc1 protein                                                                |                                                                                               | Cmc1                   |         |

|                               |                                            |          |                                                                                                                                      |                                                             |                       |         |
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| 5primeCluster02<br>66.Contig1 | gi 50138916 gb <br>CO471675.1 <br>CO471675 | 2.00E-13 | 76.2 heterogeneous<br>nuclear<br>ribonucleoprotein m                                                                                 | F:GO:0000166,P:GO:<br>0008150,C:GO:0005575                  | RRM_1                 |         |
| 5primeCluster02<br>73.Contig1 | Positive<br>selection<br>BY796454          | 1.00E-20 | 67 ribosomal protein<br>rpl36a                                                                                                       |                                                             | Ribosomal_L4<br>4     | 2.43467 |
| 5primeCluster02<br>75.Contig1 | gi 62885542 gb <br>DN900779.1 <br>DN900779 | 8.00E-07 | 53.3 sjchgc01974 protein                                                                                                             |                                                             |                       |         |
| 5primeCluster02<br>81.Contig1 | BY799369                                   | 0.006    | 38.2                                                                                                                                 |                                                             |                       |         |
| 5primeCluster02<br>81.Contig2 | BY800453                                   | 5.00E-06 | 48.1                                                                                                                                 |                                                             |                       |         |
| 5primeCluster02<br>89.Contig1 | gi 19019796 gb <br>BM706538.1 <br>BM706538 | 3.00E-36 | 124 arpc1a protein                                                                                                                   |                                                             |                       |         |
| 5primeCluster02<br>91.Contig1 | gi 62880016 gb <br>DN895253.1 <br>DN895253 | 6.00E-25 | 76.1 beta chain spectrin                                                                                                             |                                                             | Pfam-B_1882,<br>PH    | 0.17895 |
| 5primeCluster02<br>95.Contig1 | BY794950                                   | 0        | 132 60s ribosomal protein<br>l13a                                                                                                    | F:GO:0003735,C:GO:<br>0015934,P:GO:0006412                  | Ribosomal_L1<br>3     | 0.29973 |
| 5primeCluster02<br>95.Contig2 | gi 13404527 gb <br>BG472153.1 <br>BG472153 | 0        | 302 60s ribosomal protein<br>l13a                                                                                                    | F:GO:0003735,C:GO:<br>0015934,P:GO:0006412                  | Ribosomal_L1<br>3     | 0.70766 |
| 5primeCluster03<br>02.Contig1 | gi 85183430 gb <br>DW599865.1 <br>DW599865 | 0        | 197 diacylglycerol kinase<br>beta (diglyceride<br>kinase beta) (dgk-<br>beta) (dag kinase<br>beta) (90 kda<br>diacylglycerol kinase) |                                                             | DAGK_cat,<br>DAGK_acc | 0.97363 |
| 5primeCluster03<br>08.Contig1 | gi 46461359 gb <br>CN455633.1 <br>CN455633 | 5.00E-34 | 144 mitochondrial<br>ribosomal protein l18                                                                                           | F:GO:0003735,P:GO:<br>0006412,C:GO:<br>0005840,C:GO:0005622 | Ribosomal_L1<br>8p    | 0.80462 |
| 5primeCluster03<br>08.Contig2 | gi 46461359 gb <br>CN455633.1 <br>CN455633 | 1.00E-27 | 123 mitochondrial<br>ribosomal protein l18                                                                                           | C:GO:0005615,C:GO:<br>0044424                               | Ribosomal_L1<br>8p    | 0.67993 |

|                               |                               |                                             |          |                                                          |                                                                                                                                 |                          |         |
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| 5primeCluster03<br>11.Contig1 | Positive<br>selection         | gi 14061563 gb <br>BG750910.1 <br>BG750910  | 0        | 249 pp2a inhibitor                                       | P:GO:0006334,C:GO:<br>0005634                                                                                                   | NAP,<br>Phage_Mu_Ga<br>m | 2.02108 |
| 5primeCluster03<br>14.Contig1 |                               | gi 9121881 gb <br>BE251750.1 BE251750       | 0        | 200 beta like 1                                          | C:GO:0005575                                                                                                                    | DUF1716                  | 0.5801  |
| 5primeCluster03<br>15.Contig1 |                               | gi 13299867 gb <br>BG375395.1 <br>BG375395  | 2.00E-19 | 68.4 f-box proteinisoform<br>cra_a                       | F:GO:0004386,F:GO:<br>0005524,P:GO:<br>0006281,F:GO:<br>0000166,P:GO:<br>0006512,C:GO:<br>0005634,F:GO:<br>0003677,F:GO:0004003 | UvrD-helicase            |         |
| 5primeCluster03<br>21.Contig1 | Embryo specific<br>expression | gi 77506145 gb <br>DV216390.1 DV216390      | 1.00E-24 | 83.5 twins cg6235-isoform<br>e isoform 1                 |                                                                                                                                 |                          | 1.228   |
| 5primeCluster03<br>22.Contig1 |                               | gi 10202505 gb <br>BE781307.1 BE781307      | 2.00E-16 | 86.3 ---NA---                                            |                                                                                                                                 | Pfam-B_1551              |         |
| 5primeCluster03<br>24.Contig1 |                               | gi 124699704 gb <br>EH998307.1 <br>EH998307 | 0        | 238 translation initiation<br>factorhelicase             |                                                                                                                                 | DEAD                     |         |
| 5primeCluster03<br>28.Contig1 | Positive<br>selection         | BY798303                                    | 0        | 139 cornichon homolog                                    | C:GO:0043231,C:GO:<br>0044444,P:GO:<br>0007165,C:GO:<br>0044425,P:GO:0006955                                                    | Cornichon                | 3.02565 |
| 5primeCluster03<br>34.Contig1 |                               | gi 85165653 gb <br>DW593375.1 <br>DW593375  | 0        | 188 fk506 binding protein 4                              | P:GO:0006457                                                                                                                    |                          | 0.12873 |
| 5primeCluster03<br>35.Contig1 |                               | gi 46820693 gb <br>CN508069.1 <br>CN508069  | 0        | 200 ribosome biogenesis<br>regulatory protein<br>homolog | F:GO:0003674,P:GO:<br>0042254                                                                                                   | RRS1                     | 1.38976 |
| 5primeCluster03<br>39.Contig1 |                               | gi 54471816 gb <br>CV570857.1 <br>CV570857  | 1.00E-16 | 68.9 phosphoinositide-3-<br>beta polypeptide             | P:GO:0009987,P:GO:<br>0065008,P:GO:<br>0032501,F:GO:0035004                                                                     | PI3Ka,<br>PI3K_C2        |         |
| 5primeCluster03<br>41.Contig1 |                               | gi 62888766 gb <br>DN904003.1 <br>DN904003  | 5.00E-26 | 98.7 methionine<br>adenosyltransferasebe<br>ta           |                                                                                                                                 | RmlD_sub_bin<br>d        | 0.4952  |
| 5primeCluster03<br>44.Contig1 |                               | gi 37635813 gb <br>CF739476.1 CF739476      | 2.00E-13 | 76.2 cytochrome c oxidase<br>polypeptide vb              | C:GO:0005740,F:GO:<br>0004129,P:GO:0006118                                                                                      | COX5B                    | 0.95183 |

|                               |                       |                                            |          |      |                                                  |                                                             |                                |         |
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| 5primeCluster03<br>44.Contig2 | Positive<br>selection | gi 58179118 gb <br>CX768765.1 <br>CX768765 | 4.00E-13 | 75.3 | cytochrome c oxidase<br>polypeptide vb           | C:GO:0005740,F:GO:<br>0004129,P:GO:0006118                  | COX5B                          | 2.75122 |
| 5primeCluster03<br>47.Contig2 | Positive<br>selection | gi 62847435 gb <br>DN877480.1 <br>DN877480 | 1.40E-45 | 182  | glyceraldehyde-3-<br>phosphate<br>dehydrogenase  | C:GO:0005737,F:GO:<br>0051287,P:GO:<br>0006096,F:GO:0004365 | Gp_dh_C                        | 2.9412  |
| 5primeCluster03<br>50.Contig1 |                       | gi 49677623 gb <br>CO431329.1 <br>CO431329 | 0.001    | 44.1 | collagen alpha 1chain                            |                                                             | Endostatin                     |         |
| 5primeCluster03<br>55.Contig1 | Positive<br>selection | gi 14060102 gb <br>BG749449.1 <br>BG749449 | 2.00E-37 | 155  | kinesin light chain                              | F:GO:0003777,C:GO:<br>0005874,F:GO:<br>0005488,C:GO:0005871 | Pfam-<br>B_18958,<br>Rab5-bind | 3.34686 |
| 5primeCluster03<br>57.Contig1 |                       | gi 77506418 gb <br>DV216527.1 DV216527     | 0        | 188  | eukaryotic translation<br>initiation factor 5a-1 | P:GO:0006413,F:GO:<br>0003743                               | eIF-5a, KOW                    | 1.68893 |
| 5primeCluster03<br>59.Contig1 |                       | BY797846                                   | 0.004    | 29.5 |                                                  |                                                             |                                |         |
| 5primeCluster03<br>60.Contig1 |                       | gi 62827783 gb <br>DN858134.1 <br>DN858134 | 0        | 188  | ---NA---                                         |                                                             | ELO                            |         |
| 5primeCluster03<br>64.Contig1 |                       | gi 76146130 gb <br>CJ065007.1 CJ065007     | 5.00E-39 | 151  | hephaestin isoform 1                             | P:GO:0030218,P:GO:<br>0000041                               | Cu-oxidase_2                   | 1.31773 |
| 5primeCluster03<br>69.Contig1 |                       | gi 68325747 gb <br>DR423731.1 <br>DR423731 | 0        | 279  | ribosomal protein s11                            |                                                             | Ribosomal_S1<br>7              |         |
| 5primeCluster03<br>71.Contig1 |                       | gi 46562702 gb <br>CN481198.1 <br>CN481198 | 0.0004   | 45.5 | ---NA---                                         |                                                             | Thyroglobulin_<br>1            | 0.86027 |
| 5primeCluster03<br>73.Contig1 |                       | gi 57595569 gb <br>CX568540.1 <br>CX568540 | 2.00E-16 | 76.2 | regulator of g-protein<br>signaling 4            | F:GO:0004871                                                | RGS                            |         |
| 5primeCluster03<br>77.Contig1 |                       | gi 46854478 gb <br>CN526704.1 <br>CN526704 | 9.00E-20 | 87.2 | ---NA---                                         |                                                             | EGF_CA                         | 0.52845 |
| 5primeCluster03<br>80.Contig1 |                       | gi 62883968 gb <br>DN899205.1 <br>DN899205 | 0.006    | 41.8 | ring finger-containing                           |                                                             | zf-C3HC4,<br>Pfam-B_14559      |         |

|                               |                                            |          |      |                                                                |                                                                                                                                                                                                     |                 |         |
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| 5primeCluster03<br>81.Contig1 | gi 41338264 gb <br>CK617378.1 <br>CK617378 | 0        | 193  | shwachman-bodian-<br>diamond syndrome<br>homolog               | F:GO:0003674,P:GO:<br>0008150,C:GO:0005575                                                                                                                                                          | SBDS,<br>SBDS_C |         |
| 5primeCluster03<br>84.Contig1 | gi 62041029 gb <br>DN689085.1 <br>DN689085 | 1.00E-12 | 73.5 | eukaryotic translation<br>initiation factorsubunit<br>2partial |                                                                                                                                                                                                     | Peroxin-13_N    |         |
| 5primeCluster03<br>88.Contig1 | gi 40321108 gb <br>CK355176.1 <br>CK355176 | 0        | 128  | mgc81086 protein                                               | P:GO:0046439,F:GO:<br>0046872,F:GO:<br>0017172,P:GO:<br>0006879,P:GO:0006826                                                                                                                        | CDO_I           | 1.26823 |
| 5primeCluster03<br>90.Contig1 | gi 54441716 gb <br>CV556808.1 <br>CV556808 | 0        | 201  | kinh_lolpeame:<br>full=kinesin heavy<br>chain                  | C:GO:0005737,P:GO:<br>0007018,C:GO:<br>0043227,P:GO:<br>0007028,C:GO:<br>0043005,F:GO:<br>0005515,P:GO:<br>0006839,C:GO:<br>0035253,F:GO:<br>0005524,C:GO:<br>0005871,F:GO:<br>0003777,C:GO:0005874 | Pfam-B_7610     | 0.88919 |
| 5primeCluster03<br>93.Contig1 | gi 46819113 gb <br>CN506489.1 <br>CN506489 | 0        | 326  | mgc80364 protein                                               | C:GO:0005839,F:GO:<br>0004298,P:GO:<br>0006511,C:GO:0005634                                                                                                                                         | Proteasome      | 0.55173 |
| 5primeCluster03<br>95.Contig1 | gi 62841825 gb <br>DN871884.1 <br>DN871884 | 0        | 127  | heterogeneous<br>nuclear<br>ribonucleoprotein I                | F:GO:0003676,F:GO:<br>0000166,C:GO:0030529                                                                                                                                                          | RRM_1           | 2.48957 |
| 5primeCluster03<br>98.Contig1 | gi 62842819 gb <br>DN872878.1 <br>DN872878 | 4.00E-36 | 151  | mgc89819 protein                                               | F:GO:0003674,C:GO:<br>0005575                                                                                                                                                                       | UMP1            | 0.32508 |
| 5primeCluster04<br>03.Contig1 | gi 85172771 gb <br>DW596524.1 <br>DW596524 | 1.00E-07 | 57.4 | loc563523 protein                                              |                                                                                                                                                                                                     | Fibrinogen_C    |         |
| 5primeCluster04<br>05.Contig1 | gi 62030807 gb <br>DN683939.1 <br>DN683939 | 3.00E-16 | 63.4 | hydroxysteroid<br>dehydrogenase                                |                                                                                                                                                                                                     | 3Beta_HSD       |         |

|                               |                                       |                                            |          |      |                                                                                           |                                                                              |                                                              |         |
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| 5primeCluster04<br>08.Contig1 |                                       | gi 76050321 gb <br>CJ053284.1 CJ053284     | 3.00E-08 | 59.3 | arystal structure of<br>dimethylarginine<br>dimethylaminohydrola<br>se i in complexigh ph | F:GO:0016403,P:GO:<br>0006809,F:GO:<br>0008270,P:GO:0017014                  | Amidinotransf                                                |         |
| 5primeCluster04<br>12.Contig1 |                                       | gi 85205026 gb <br>DW607143.1 <br>DW607143 | 3.00E-11 | 68.9 | adp-ribosylation factor<br>4                                                              |                                                                              | Arf                                                          |         |
| 5primeCluster04<br>15.Contig1 | <b>Embryo specific<br/>expression</b> | gi 62875839 gb <br>DN891076.1 <br>DN891076 | 0        | 253  | nadph-specific<br>isocitrate<br>dehydrogenase                                             |                                                                              | Iso_dh                                                       | 0.1571  |
| 5primeCluster04<br>18.Contig1 | <b>Embryo specific<br/>expression</b> | gi 54471554 gb <br>CV570733.1 <br>CV570733 | 5.61E-45 | 181  | sarco endoplasmic<br>reticulum calcium<br>transporting atpase                             | P:GO:0006816,F:GO:<br>0005524,C:GO:<br>0016021,P:GO:<br>0008152,F:GO:0005388 | Cation_ATPas<br>e_C                                          | 0.12589 |
| 5primeCluster04<br>21.Contig1 |                                       | gi 24722358 gb <br>CA390919.1 <br>CA390919 | 0        | 200  | hephaestin-like 1                                                                         |                                                                              |                                                              | 0.35915 |
| 5primeCluster04<br>33.Contig1 |                                       | gi 75845182 gb <br>DT875442.1 DT875442     | 1.00E-29 | 130  | transcription<br>elongation factor b<br>polypeptide 1                                     |                                                                              |                                                              | 0.07255 |
| 5primeCluster04<br>38.Contig1 |                                       | gi 41346236 gb <br>CK625350.1 <br>CK625350 | 2.00E-31 | 136  | enhancer of yellow 2<br>homolog                                                           |                                                                              | EnY2                                                         | 0.11278 |
| 5primeCluster04<br>42.Contig1 |                                       | gi 22700947 gb <br>BU186963.1 <br>BU186963 | 6.00E-14 | 59.3 | sema-1a cg18405-pa                                                                        |                                                                              | Sema                                                         |         |
| 5primeCluster04<br>44.Contig1 |                                       | gi 62840545 gb <br>DN870604.1 <br>DN870604 | 0.002    | 46.1 |                                                                                           |                                                                              |                                                              |         |
| 5primeCluster04<br>45.Contig1 |                                       | gi 12040839 gb <br>BF724928.1 BF724928     | 2.00E-16 | 86.3 | pre-b cell enhancing<br>factor precursor                                                  |                                                                              | NAPRTase                                                     | 0.6405  |
| 5primeCluster04<br>56.Contig1 |                                       | gi 37638284 gb <br>CF741945.1 CF741945     | 0        | 162  | ---NA---                                                                                  |                                                                              | Pfam-<br>B_11765,<br>Pfam-B_14559                            | 1.9314  |
| 5primeCluster04<br>61.Contig1 |                                       | gi 22679525 gb <br>BU165573.1 <br>BU165573 | 1.00E-33 | 143  | fk506-binding protein<br>4                                                                | F:GO:0005488                                                                 | Pfam-B_2967,<br>Pfam-B_6046,<br>Pfam-B_3120,<br>TPR_1, TPR_2 | 0.21562 |

|                               |                               |                                            |          |      |                                                                          |                                                                              |                         |         |
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| 5primeCluster04<br>67.Contig1 |                               | gi 13135773 gb <br>BG329335.1 <br>BG329335 | 3.00E-22 | 82.2 | cs042_humanname:<br>full=upf0608 protein<br>c19orf42 flags:<br>precursor |                                                                              |                         |         |
| 5primeCluster04<br>72.Contig1 |                               | gi 3396334 gb <br>AI070083.1 AI070083      | 0        | 210  | ribosomal protein l27                                                    | C:GO:0030529                                                                 | Ribosomal_L2<br>7e, KOW |         |
| 5primeCluster04<br>72.Contig2 | Embryo specific<br>expression | gi 62854559 gb <br>DN884604.1 <br>DN884604 | 0        | 231  | ribosomal protein l27                                                    | C:GO:0030529                                                                 | Ribosomal_L2<br>7e, KOW |         |
| 5primeCluster04<br>85.Contig1 |                               | gi 50140585 gb <br>CO472446.1 <br>CO472446 | 2.00E-19 | 90.9 | heat shock protein 90                                                    | P:GO:0006457,F:GO:<br>0051082,C:GO:<br>0005737,F:GO:<br>0005524,P:GO:0006950 | HSP90                   | 0.87799 |
| 5primeCluster04<br>95.Contig1 |                               | gi 20360391 gb <br>BQ184840.1 <br>BQ184840 | 0.007    | 44.1 |                                                                          |                                                                              |                         |         |
| 5primeCluster04<br>96.Contig1 |                               | gi 50138538 gb <br>CO471508.1 <br>CO471508 | 0        | 185  | brain protein 44-like<br>protein                                         |                                                                              | UPF0041                 | 0.3574  |
| 5primeCluster05<br>01.Contig1 |                               | gi 62854198 gb <br>DN884243.1 <br>DN884243 | 4.00E-18 | 91.8 | ubiquinol-cytochrome<br>c reductase complex                              |                                                                              | UCR_UQCRX<br>_QCR9      |         |
| 5primeCluster05<br>07.Contig1 | Embryo specific<br>expression | gi 22812700 gb <br>BU506467.1 <br>BU506467 | 2.00E-09 | 62.9 | family with sequence<br>similaritymember a                               | F:GO:0003674,P:GO:<br>0008150                                                |                         |         |
| 5primeCluster05<br>10.Contig1 |                               | gi 62879604 gb <br>DN894841.1 <br>DN894841 | 1.00E-15 | 83.5 | ns1 binding protein                                                      |                                                                              | Kelch_1,<br>Pfam-B_6141 |         |
| 5primeCluster05<br>14.Contig1 |                               | gi 62851579 gb <br>DN881624.1 <br>DN881624 | 1.00E-36 | 153  | ubiquinol-cytochrome<br>c reductase binding<br>protein                   | C:GO:0016020,C:GO:<br>0005739                                                | UCR_14kD                | 0.31422 |
| 5primeCluster05<br>15.Contig1 |                               | gi 24731375 gb <br>CA395682.1 <br>CA395682 | 9.00E-36 | 93.6 | ubiquitin-fold modifier<br>1                                             |                                                                              | Ufm1                    |         |
| 5primeCluster05<br>15.Contig2 |                               | gi 24731375 gb <br>CA395682.1 <br>CA395682 | 3.00E-40 | 165  | ubiquitin-fold modifier<br>1                                             |                                                                              | Ufm1                    |         |

|                               |                                                                                  |          |      |                                                                                                                                   |                                                                                               |      |         |
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| 5primeCluster05<br>16.Contig2 | BY798344                                                                         | 3.00E-37 | 149  | small nuclear<br>ribonucleoprotein<br>polypeptide g                                                                               | C:GO:0005732,F:GO:<br>0031202,C:GO:<br>0005681,F:GO:<br>0005515,C:GO:<br>0030532,P:GO:0000245 | LSM  | 0.08485 |
| 5primeCluster05<br>21.Contig1 | gi 9593874 gb <br>BB538374.1 <br>BB538374                                        | 0.0004   | 48.1 |                                                                                                                                   |                                                                                               |      |         |
| 5primeCluster05<br>22.Contig1 | <b>Embryo specific<br/>expression</b> gi 49673830 gb <br>CO427536.1 <br>CO427536 | 4.00E-38 | 134  | phosphoglycerate<br>mutase family protein                                                                                         |                                                                                               | PGAM | 1.62139 |
| 5primeCluster05<br>23.Contig1 | gi 20359663 gb <br>BQ184112.1 <br>BQ184112                                       | 0.006    | 44.1 |                                                                                                                                   |                                                                                               |      |         |
| 5primeCluster05<br>31.Contig1 | gi 91743724 gb <br>EB380379.1 EB380379                                           | 5.00E-23 | 107  | abhydrolase domain<br>containingisoform<br>cra_c                                                                                  |                                                                                               |      |         |
| 5primeCluster05<br>50.Contig1 | gi 49672810 gb <br>CO426516.1 <br>CO426516                                       | 2.00E-28 | 65.9 | fimbrin plastin                                                                                                                   |                                                                                               |      | 1.39176 |
| 5primeCluster05<br>53.Contig1 | gi 85176586 gb <br>DW597899.1 <br>DW597899                                       | 1.00E-20 | 87.7 | map2k6 protein                                                                                                                    | F:GO:0016301                                                                                  |      |         |
| 5primeCluster05<br>58.Contig1 | gi 62039933 gb <br>DN688542.1 <br>DN688542                                       | 2.00E-40 | 165  | eno_lolpeame:<br>full=enolaseame:<br>full=2-<br>phosphoglycerate<br>dehydrataseame:<br>full=2-phospho-d-<br>glycerate hydro-lyase | C:GO:0000015,F:GO:<br>0004634,F:GO:<br>0000287,P:GO:0006096                                   |      | 1.1131  |
| 5primeCluster05<br>61.Contig1 | gi 13103565 gb <br>BG306038.1 <br>BG306038                                       | 3.00E-14 | 78.5 | proteasome subunit<br>alpha type-3                                                                                                |                                                                                               |      |         |
| 5primeCluster05<br>92.Contig1 | gi 19021562 gb <br>BM708304.1 <br>BM708304                                       | 0.006    | 25.8 |                                                                                                                                   |                                                                                               |      |         |

|                               |                                             |          |                                                                   |                                                                                                                                |         |
|-------------------------------|---------------------------------------------|----------|-------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|---------|
| 5primeCluster05<br>96.Contig1 | gi 62049228 gb <br>DN693138.1 <br>DN693138  | 0.0001   | 46.4 calcium binding atopy-<br>related autoantigen 1<br>isoform 1 |                                                                                                                                |         |
| 5primeCluster05<br>98.Contig1 | gi 13268617 gb <br>BG372080.1 <br>BG372080  | 4.00E-23 | 98.7 heat shock protein 70                                        | F:GO:0005524,P:GO:<br>0006950,F:GO:0000166                                                                                     | 1.36164 |
| 5primeCluster06<br>02.Contig1 | gi 14060917 gb <br>BG750264.1 <br>BG750264  | 3.00E-16 | 84.5 cysteine-rich with egf-<br>like domains 1                    | F:GO:0005509,C:GO:<br>0005783,C:GO:0005576                                                                                     |         |
| 5primeCluster06<br>09.Contig1 | gi 119789801 gb <br>EH282359.1 <br>EH282359 | 1.00E-10 | 65.7 cytochrome csubunit                                          | F:GO:0004129,P:GO:<br>0006118                                                                                                  |         |
| 5primeCluster06<br>10.Contig1 | GS013952                                    | 0.008    | 26.7                                                              |                                                                                                                                |         |
| 5primeCluster06<br>21.Contig1 | BY795030                                    | 7.00E-19 | 87.2 ribosomal protein<br>rpl39                                   | C:GO:0005840,F:GO:<br>0003735,P:GO:0006412                                                                                     | 0.09322 |
| 5primeCluster06<br>21.Contig2 | BY795030                                    | 2.00E-21 | 95.9 ribosomal protein<br>rpl39                                   |                                                                                                                                | 1.63097 |
| 5primeCluster06<br>27.Contig1 | BY800472                                    | 0.003    | 38.2                                                              |                                                                                                                                |         |
| 5primeCluster06<br>30.Contig1 | GS004626                                    | 0.003    | 32.2                                                              |                                                                                                                                |         |
| Ika-1224-<br>No22_B03_002     | GS020645                                    | 0.005    | 34.2                                                              |                                                                                                                                |         |
| Ika-1224-<br>No22_B05_002     | gi 20363398 gb <br>BQ187847.1 <br>BQ187847  | 1.00E-05 | 47.6 fyn binding protein<br>(fyb-120 130)                         | P:GO:0006468,P:GO:<br>0007243,P:GO:<br>0045576,F:GO:<br>0005102,P:GO:<br>0006607,C:GO:<br>0005634,P:GO:<br>0006955,C:GO:001562 | SH3_2   |
| Ika-1224-<br>No22_C12_003     | gi 15709914 gb <br>BI732901.1 BI732901      | 0.008    | 44.1                                                              |                                                                                                                                |         |
| Ika-1224-<br>No22_D12_004     | BY797664                                    | 0.006    | 38.2                                                              |                                                                                                                                |         |
| Ika-1224-<br>No22_F04_002     | BY797751                                    | 0.002    | 38.2                                                              |                                                                                                                                |         |

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|---------------------------|------------------------------------------------------------------------------|----------|------|------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------|
| ika-1224-<br>No22_H01_004 | GS004743                                                                     | 0.008    | 27.6 |                                    |                                                                                                                                                                                                     |                              |
| ika-1224-<br>No9_A09_001  | <b>Embryo specific<br/>expression</b> gi 37600690 gb <br>CF726522.1 CF726522 | 0        | 186  | dynein light<br>intermediate chain | F:GO:0003777,F:GO:<br>0042623,P:GO:<br>0007052,F:GO:<br>0032555,P:GO:<br>0046605,C:GO:<br>0005868,P:GO:<br>0007018,F:GO:<br>0005515,P:GO:0048813                                                    | DLIC, Pfam-<br>B_8060 1.0469 |
| ika-1224-<br>No9_B03_002  | gi 14061917 gb <br>BG751264.1 <br>BG751264                                   | 0.008    | 35   |                                    |                                                                                                                                                                                                     |                              |
| ika-1224-<br>No9_D03_004  | gi 24559278 gb <br>CA341182.1 <br>CA341182                                   | 0        | 219  | ribosomal protein l26              | P:GO:0000022,P:GO:<br>0006412,P:GO:<br>0040010,F:GO:<br>0003723,P:GO:<br>0009792,C:GO:<br>0005739,F:GO:<br>0003735,P:GO:<br>0000003,P:GO:<br>0042254,P:GO:<br>0002119,F:GO:<br>0005515,N:GO:0022625 | KOW                          |
| ika-1224-<br>No9_D09_004  | gi 18980734 gb <br>BM670843.1 <br>BM670843                                   | 0.004    | 44.1 |                                    |                                                                                                                                                                                                     |                              |
| ika-1224-<br>No9_D12_004  | BY799310                                                                     | 0.01     | 38.2 |                                    |                                                                                                                                                                                                     |                              |
| ika-1224-<br>No9_E02_001  | BY797751                                                                     | 0.005    | 35.4 |                                    |                                                                                                                                                                                                     |                              |
| ika-1224-<br>No9_G11_003  | gi 37599375 gb <br>CF725207.1 CF725207                                       | 1.00E-05 | 50.6 | ccr4-not<br>transcriptionsubunit 3 |                                                                                                                                                                                                     | Not3                         |
| ika1119-<br>No8_A02_001   | gi 9617433 gb <br>BB546005.1 <br>BB546005                                    | 0.002    | 46.1 |                                    |                                                                                                                                                                                                     |                              |

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| ika1119-<br>No8_A06_001 | gi 13298901 gb <br>BG374429.1 <br>BG374429 | 0.004  | 44.1 |
| ika1119-<br>No8_B08_002 | BY798528                                   | 0.0006 | 42.1 |
| ika1119-<br>No8_D11_004 | BY796060                                   | 0.008  | 36.2 |

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|-------------------------|--------------------------------------------|----------|------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| ika1119-<br>No8_E03_001 | gi 54439388 gb <br>CV555651.1 <br>CV555651 | 1.00E-38 | 160 myosin heavy chain | P:GO:0048547,P:GO:<br>0030048,C:GO:<br>0043005,P:GO:<br>0055013,P:GO:<br>0030010,P:GO:<br>0035295,P:GO:<br>0007507,P:GO:<br>0051321,C:GO:<br>0030017,P:GO:<br>0030239,P:GO:<br>0016044,P:GO:<br>0022402,P:GO:<br>0016477,P:GO:<br>0044237,P:GO:<br>0050793,P:GO:<br>0000226,P:GO:<br>0019538,P:GO:<br>0000904,F:GO:<br>0032559,C:GO:<br>0044459,P:GO:<br>0031175,P:GO:<br>0021591,P:GO:<br>0051656,F:GO:<br>0042623,P:GO:<br>0006936,P:GO:<br>0000910,P:GO:<br>0048729,P:GO:<br>0000003,P:GO:<br>0050794,P:GO:<br>0002376,C:GO:<br>0005859,P:GO:<br>0065008,P:GO:<br>0007155,P:GO:<br>0030855,F:GO:<br>0003774,C:GO:<br>0044448,P:GO:<br>0002164,P:GO:<br>0002165,P:GO:<br>0007391,P:GO:<br>0006950,P:GO: | Myosin_tail_1 1.18944 |
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| ika1119-No8_F05_002  |                            | BY795248                           | 0.008    | 33.6               |                                                                                                                                   |       |         |
| ika1119-No8_F07_002  |                            | GS019919                           | 0.001    | 36.2               |                                                                                                                                   |       |         |
| ika1119_A04_001      |                            | GS004815                           | 0.007    | 32.2               |                                                                                                                                   |       |         |
| ika1124-No28_C02_003 |                            | BY800302                           | 0.001    | 40.1               |                                                                                                                                   |       |         |
| ika1124-No2_B09_002  | Positive selection         | gi 85169667 gb DW595248.1 DW595248 | 0        | 361 protein        | P:GO:0002119,F:GO:0005488,C:GO:0046540,C:GO:0005681,P:GO:0000003,P:GO:0009792,C:GO:0016021,P:GO:0040007,C:GO:0005829,P:GO:0000398 | PRP38 | 4.30403 |
| ika1124-No30_G07_003 |                            | BY795637                           | 0.001    | 40.1               |                                                                                                                                   |       |         |
| ika1125-No7_A04_001  |                            | BY798345                           | 0.009    | 38.2               |                                                                                                                                   |       |         |
| ika1224-No10_A05_001 |                            | gi 9125360 gb BE254927.1 BE254927  | 0.009    | 42.1               |                                                                                                                                   |       |         |
| ika1224-No10_A09_001 |                            | GS014141                           | 0.001    | 36.2               |                                                                                                                                   |       |         |
| ika1224-No10_B09_002 |                            | BY800108                           | 0.007    | 34.8               |                                                                                                                                   |       |         |
| ika1224-No10_E05_001 | Embryo specific expression | gi 16450468 gb BB600534.2 BB600534 | 5.00E-39 | 81.7 cxxc finger 6 | F:GO:0046872,F:GO:0003674,P:GO:0008150,F:GO:0008270,F:GO:0003677,C:GO:0005634                                                     |       | 1.25013 |
| ika1224-No11_A04_001 |                            | gi 62826716 gb DN857067.1 DN857067 | 0.003    | 42.3 ---NA---      |                                                                                                                                   |       |         |

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| ika1224-<br>No11_C10_003 | gi 18995135 gb <br>BM685239.1 <br>BM685239 | 0.008    | 44.1 |                                                 |                                                                                                                                                                                    |                     |
| ika1224-<br>No11_D12_004 | GS013792                                   | 0.005    | 34.2 |                                                 |                                                                                                                                                                                    |                     |
| ika1224-<br>No11_F04_002 | BY795080                                   | 0.01     | 38.2 |                                                 |                                                                                                                                                                                    |                     |
| ika1224-<br>No12_D09_004 | gi 40318733 gb <br>CK352846.1 <br>CK352846 | 3.00E-25 | 87.6 | transcription initiation<br>factor tfiid        | C:GO:0000124,C:GO:<br>0046695,P:GO:<br>0006367,C:GO:<br>0005730,P:GO:<br>0045944,F:GO:<br>0016251,F:GO:<br>0046983,F:GO:<br>0003700,F:GO:<br>0004402,P:GO:<br>0016573,C:GO:0005669 | TFIID_90kDa 0.76572 |
| ika1224-<br>No12_E07_001 | BY798380                                   | 0.01     | 36.2 |                                                 |                                                                                                                                                                                    |                     |
| ika1224-<br>No12_E08_001 | BY796056                                   | 0.002    | 38.2 |                                                 |                                                                                                                                                                                    |                     |
| ika1224-<br>No13_D05_004 | gi 16062248 gb <br>BB709079.1 <br>BB709079 | 0.008    | 44.1 |                                                 |                                                                                                                                                                                    |                     |
| ika1224-<br>No13_D07_004 | BY800118                                   | 0.0006   | 42.1 |                                                 |                                                                                                                                                                                    |                     |
| ika1224-<br>No13_E04_001 | BY797696                                   | 0.01     | 38.2 |                                                 |                                                                                                                                                                                    |                     |
| ika1224-<br>No13_F06_002 | BY795820                                   | 0.009    | 38.2 |                                                 |                                                                                                                                                                                    |                     |
| ika1224-<br>No13_H04_004 | gi 19044026 gb <br>BM723028.1 <br>BM723028 | 1.00E-06 | 49.6 | set domain and<br>mariner transposase<br>fusion |                                                                                                                                                                                    |                     |
| ika1224-<br>No14_C05_003 | gi 39890957 gb <br>CK301009.1 <br>CK301009 | 0.0004   | 43.7 | ---NA---                                        |                                                                                                                                                                                    |                     |

|                      |                                                                      |          |                                     |                           |             |
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| Ika1224-No14_E08_001 | GS014043                                                             | 0.004    | 34.2                                |                           |             |
| Ika1224-No14_F06_002 | gi 42746304 gb CK780626.1 CK780626                                   | 2.00E-12 | 73.5 ubiquitin specific peptidase 3 | P:GO:0009987,F:GO:0008234 | UCH, zf-UBP |
| Ika1224-No14_G09_003 | <b>Embryo specific expression</b> gi 46465385 gb CN459659.1 CN459659 | 0.009    | 44.1 hypothetical loc100131203      |                           |             |
| Ika1224-No14_G10_003 | gi 15714351 gb BI737338.1 BI737338                                   | 0.0001   | 47.3                                |                           |             |
| Ika1224-No15_A02_001 | GS020766                                                             | 0.004    | 34.2                                |                           |             |
| Ika1224-No15_B12_002 | gi 3399133 gb AI072939.1 AI072939                                    | 0.009    | 44.1                                |                           |             |
| Ika1224-No15_C08_003 | gi 24731064 gb CA395520.1 CA395520                                   | 0.003    | 44.1                                |                           |             |
| Ika1224-No15_E05_001 | BY797989                                                             | 0.009    | 36.2                                |                           | PB1         |

|                          |                               |                                            |          |                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                         |         |
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| Ika1224-<br>No15_G05_003 |                               | gi 62826682 gb <br>DN857033.1 <br>DN857033 | 2.00E-10 | 66.1 sequestosome 1   | F:GO:0019901,P:GO:<br>0016197,P:GO:<br>0006511,C:GO:<br>0005770,C:GO:<br>0005634,P:GO:<br>0030154,P:GO:<br>0043122,P:GO:<br>0006915,F:GO:<br>0046872,F:GO:<br>0042169,F:GO:<br>0030971,P:GO:<br>0051291,P:GO:<br>0008150,P:GO:<br>0045944,P:GO:<br>0007242,P:GO:<br>0006955,F:GO:<br>0005080,C:GO:<br>0005768,F:GO:<br>0043130,C:GO:<br>0005737,P:GO:<br>0006950,P:GO:<br>0008104,C:GO:<br>0005829,F:GO:<br>0008270,F:GO:<br>0005515,C:GO:0005575 |                         |         |
| Ika1224-<br>No16_D01_004 |                               | GS020666                                   | 0.005    | 34.2                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                         |         |
| Ika1224-<br>No16_D10_004 |                               | BY800091                                   | 0.003    | 40.1                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                         |         |
| Ika1224-<br>No16_F06_002 |                               | gi 46816516 gb <br>CN503892.1 <br>CN503892 | 0.004    | 44.1                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                         |         |
| Ika1224-<br>No16_G02_003 | Embryo specific<br>expression | gi 22667692 gb <br>BU154160.1 <br>BU154160 | 0        | 208 protein           | F:GO:0005097,C:GO:<br>0005625,F:GO:<br>0017137,P:GO:0043087                                                                                                                                                                                                                                                                                                                                                                                       | Pfam-B_598              | 0.9222  |
| Ika1224-<br>No16_G07_003 |                               | gi 19024339 gb <br>BM711081.1 <br>BM711081 | 1.00E-09 | 53.3 flj00022 protein | F:GO:0003674,C:GO:<br>0005737,C:GO:0005575                                                                                                                                                                                                                                                                                                                                                                                                        | Pfam-B_9625,<br>DUF2464 | 0.47633 |

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| Ika1224-<br>No17_F03_002 | BY794969                                                                         | 0.005  | 36.3 |
| Ika1224-<br>No17_H04_004 | GS004729                                                                         | 0.001  | 36.2 |
| Ika1224-<br>No18_B11_002 | gi 75833579 gb <br>DT863839.1 DT863839                                           | 0.002  | 46.1 |
| Ika1224-<br>No18_F06_002 | <b>Embryo specific<br/>expression</b> gi 23672012 gb <br>BU737013.1 <br>BU737013 | 0.0001 | 44.1 |

|                          |                                        |          |                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |     |         |
|--------------------------|----------------------------------------|----------|-----------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|---------|
| ika1224-<br>No19_E06_001 | gi 75851466 gb <br>DT881726.1 DT881726 | 5.00E-43 | 174 member ras oncogene<br>family | P:GO:0030100,P:GO:<br>0022416,C:GO:<br>0030140,C:GO:<br>0009536,C:GO:<br>0005802,P:GO:<br>0008103,P:GO:<br>0016360,C:GO:<br>0033116,P:GO:<br>0006913,P:GO:<br>0007269,F:GO:<br>0008565,P:GO:<br>0007349,C:GO:<br>0005624,P:GO:<br>0042052,P:GO:<br>0006355,C:GO:<br>0005579,P:GO:<br>0040011,C:GO:<br>0042470,F:GO:<br>0005525,C:GO:<br>0005764,P:GO:<br>0007317,P:GO:<br>0006887,C:GO:<br>0042175,C:GO:<br>0005829,C:GO:<br>0005770,P:GO:<br>0006928,C:GO:<br>0005741,P:GO:<br>0046887,P:GO:<br>0007264,C:GO:<br>0005813,F:GO:<br>0003677,C:GO:<br>0005795,P:GO:<br>0050807,C:GO:<br>0005769,P:GO:<br>0006888,P:GO:<br>0019730,C:GO:<br>0048471,C:GO:<br>0005811,P:GO:<br>0006895,F:GO:<br>0003924,P:GO: | Ras | 1.17698 |
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|                          |                                            |          |      |                              |                                                             |                           |
|--------------------------|--------------------------------------------|----------|------|------------------------------|-------------------------------------------------------------|---------------------------|
| ika1224-<br>No19_E09_001 | gi 62876140 gb <br>DN891377.1 <br>DN891377 | 8.00E-05 | 44.1 |                              |                                                             | zf-C2H2                   |
| ika1224-<br>No19_F11_002 | GS020725                                   | 0.005    | 34.2 |                              |                                                             |                           |
| ika1224-<br>No19_G03_003 | gi 9129088 gb <br>BE258596.1 BE258596      | 0.008    | 42.1 |                              |                                                             |                           |
| ika1224-<br>No19_G04_003 | gi 62878866 gb <br>DN894103.1 <br>DN894103 | 0.008    | 44.1 |                              |                                                             |                           |
| ika1224-<br>No19_G05_003 | gi 18989049 gb <br>BM679153.1 <br>BM679153 | 6.00E-34 | 144  | 50s ribosomal protein<br>l22 | C:GO:0005762,F:GO:<br>0003735,P:GO:<br>0009792,P:GO:0006412 | Ribosomal_L2 0.20137<br>2 |

|                          |                                            |          |                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |     |
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| Ika1224-<br>No20_A07_001 | gi 22369065 gb <br>BQ953587.1 <br>BQ953587 | 3.00E-33 | 141 adp-ribosylation factor | P:GO:0016358,F:GO:<br>0005154,C:GO:<br>0005802,F:GO:<br>0005057,P:GO:<br>0009792,P:GO:<br>0008360,P:GO:<br>0006891,P:GO:<br>0007155,P:GO:<br>0006893,P:GO:<br>0030866,P:GO:<br>0040010,P:GO:<br>0007269,F:GO:<br>0008565,C:GO:<br>0005624,F:GO:<br>0003956,P:GO:<br>0040011,C:GO:<br>0005935,P:GO:<br>0007030,F:GO:<br>0005525,P:GO:<br>0044408,P:GO:<br>0031529,P:GO:<br>0007173,F:GO:<br>0016004,P:GO:<br>0018996,P:GO:<br>0006886,C:GO:<br>0005829,P:GO:<br>0006471,P:GO:<br>0007520,P:GO:<br>0006928,C:GO:<br>0001726,C:GO:<br>0005934,P:GO:<br>0016197,P:GO:<br>0006915,P:GO:<br>0002119,P:GO:<br>0006888,P:GO:<br>0048261,P:GO:<br>0000723,C:GO:<br>0005768,P:GO:<br>0035020,P:GO:<br>0007276,P:GO: | Arf |
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| Ika1224-<br>No20_B05_002 | gi 62846056 gb <br>DN876115.1 <br>DN876115 | 0.0006   | 48.1                              |                                                                                                                                                                                                                      |         |         |
| Ika1224-<br>No20_C02_003 | gi 19046236 gb <br>BM724905.1 <br>BM724905 | 5.00E-40 | 147 cdc37                         | C:GO:0005829,P:GO:<br>0000910,F:GO:<br>0051879,F:GO:<br>0051087,P:GO:<br>0000003,P:GO:<br>0007169,P:GO:<br>0006605,F:GO:<br>0030296,F:GO:<br>0000166,F:GO:<br>0051082,P:GO:<br>0007275,P:GO:<br>0009653,P:GO:0000079 | CDC37_M | 0.20548 |
| Ika1224-<br>No20_C07_003 | GS004636                                   | 0.008    | 32.2                              |                                                                                                                                                                                                                      |         |         |
| Ika1224-<br>No20_H11_004 | gi 40679977 gb <br>CK431159.1 <br>CK431159 | 6.00E-08 | 41.9 hypoxia associated<br>factor | P:GO:0006397,C:GO:<br>0005634,P:GO:<br>0008380,C:GO:<br>0005737,F:GO:<br>0003674,P:GO:<br>0008629,C:GO:<br>0005575,C:GO:<br>0005681,C:GO:<br>0005829,P:GO:<br>0007050,P:GO:0045585                                   | SART-1  |         |
| Ika1224-<br>No21_B06_002 | GS004683                                   | 0.005    | 34.2                              |                                                                                                                                                                                                                      |         |         |
| Ika1224-<br>No21_B07_002 | gi 16401319 gb <br>BB281433.2 <br>BB281433 | 0.009    | 44.1                              |                                                                                                                                                                                                                      |         |         |
| Ika1224-<br>No21_B09_002 | BY799853                                   | 6.00E-06 | 42.8 myosin iiiA                  | F:GO:0004672,F:GO:<br>0000166                                                                                                                                                                                        |         |         |
| Ika1224-<br>No21_D10_004 | GS013988                                   | 0.01     | 32.2                              |                                                                                                                                                                                                                      |         |         |

|                          |                                       |                                            |          |                         |                                                                                                                                                                                    |                     |
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| Ika1224-<br>No21_E12_001 |                                       | gi 18979080 gb <br>BM669183.1 <br>BM669183 | 0.008    | 44.1                    |                                                                                                                                                                                    |                     |
| Ika1224-<br>No21_F06_002 |                                       | gi 62881247 gb <br>DN896484.1 <br>DN896484 | 1.00E-30 | 133 multicopper oxidase | F:GO:0005507,P:GO:<br>0006825,P:GO:<br>0007584,F:GO:<br>0004322,C:GO:<br>0005615,P:GO:<br>0030218,P:GO:<br>0030005,F:GO:<br>0005515,P:GO:<br>0007568,C:GO:<br>0046658,P:GO:0007596 | Cu-oxidase_2 1.1544 |
| Ika1224-<br>No21_H04_004 | <b>Embryo specific<br/>expression</b> | gi 57590282 gb <br>CX563253.1 <br>CX563253 | 0.009    | 44.1                    |                                                                                                                                                                                    |                     |
| Ika1224-<br>No23_B07_002 |                                       | GS004703                                   | 0.002    | 34.2                    |                                                                                                                                                                                    |                     |
| Ika1224-<br>No23_C08_003 |                                       | gi 62830113 gb <br>DN860464.1 <br>DN860464 | 0.004    | 40                      |                                                                                                                                                                                    |                     |
| Ika1224-<br>No23_D01_004 | <b>Embryo specific<br/>expression</b> | GS004674                                   | 0.003    | 29.9                    |                                                                                                                                                                                    |                     |
| Ika1224-<br>No23_G04_003 | <b>Embryo specific<br/>expression</b> | gi 77506621 gb <br>DV216629.1 DV216629     | 0        | 187 spermidine synthase | C:GO:0005737,P:GO:<br>0006597,P:GO:<br>0008295,P:GO:<br>0009926,F:GO:<br>0004766,P:GO:<br>0015940,P:GO:<br>0010087,F:GO:<br>0016768,C:GO:<br>0005634,N:GO:0010487                  | Spermine_synt<br>h  |
| Ika1224-<br>No24_A03_001 |                                       | BY799341                                   | 0.007    | 36.2                    |                                                                                                                                                                                    |                     |

|                          |                               |                                            |          |                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                        |
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| Ika1224-<br>No24_A06_001 | Embryo specific<br>expression | gi 16780503 gb <br>BM051236.1 <br>BM051236 | 3.00E-16 | 75.3 o-methyltransferase | P:GO:0044238,F:GO:<br>0008171,P:GO:<br>0009058,F:GO:<br>0008757,C:GO:<br>0044464,P:GO:0044237                                                                                                                                                                                                                                                                                                                                                                                                                                          | Methyltransf_3         |
| Ika1224-<br>No24_B08_002 |                               | GS020505                                   | 0.004    | 34.2                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                        |
| Ika1224-<br>No24_C12_003 |                               | gi 32175750 gb <br>CD674019.1 <br>CD674019 | 2.00E-19 | 71.6 abc transporter     | P:GO:0033344,C:GO:<br>0000139,C:GO:<br>0043190,F:GO:<br>0015485,F:GO:<br>0005548,F:GO:<br>0008565,P:GO:<br>0009720,P:GO:<br>0010033,P:GO:<br>0045542,C:GO:<br>0005615,F:GO:<br>0043531,P:GO:<br>0043691,P:GO:<br>0015031,C:GO:<br>0005789,F:GO:<br>0005543,P:GO:<br>0006911,P:GO:<br>0055091,F:GO:<br>0046982,N:GO:<br>0034041,C:GO:<br>0005768,P:GO:<br>0045449,P:GO:<br>0032367,P:GO:<br>0033700,P:GO:<br>0042987,F:GO:<br>0042803,F:GO:<br>0019534,C:GO:<br>0005887,F:GO:<br>0005524,F:GO:<br>0017127,C:GO:<br>0009898,P:GO:0042632 | DUF258,<br>Pfam-B_5069 |
| Ika1224-<br>No24_D04_004 |                               | BY796668                                   | 0.004    | 38.2                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                        |

|                          |                                            |          |      |                                                            |                                                                                                                                                                                                                                                        |       |
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| Ika1224-<br>No24_D06_004 | gi 18528421 gb <br>BM479379.1 <br>BM479379 | 0.0005   | 48.1 |                                                            |                                                                                                                                                                                                                                                        |       |
| Ika1224-<br>No24_D08_004 | gi 62832186 gb <br>DN862537.1 <br>DN862537 | 0        | 237  | actin-related protein 2<br>3 complex subunit 4             | C:GO:0005885,P:GO:<br>0040010,F:GO:<br>0030674,P:GO:<br>0000147,P:GO:<br>0009792,P:GO:<br>0007015,P:GO:<br>0008360,F:GO:<br>0051015,P:GO:<br>0030041,P:GO:<br>0006911,C:GO:<br>0042995,P:GO:<br>0030031,F:GO:<br>0005200,P:GO:<br>0045010,C:GO:0005737 | ARPC4 |
| Ika1224-<br>No24_E05_001 | GS004645                                   | 0.004    | 34.2 |                                                            |                                                                                                                                                                                                                                                        |       |
| Ika1224-<br>No24_F05_002 | GS013936                                   | 0.005    | 34.2 |                                                            |                                                                                                                                                                                                                                                        |       |
| Ika1224-<br>No24_F07_002 | GS013783                                   | 0.001    | 36.2 |                                                            |                                                                                                                                                                                                                                                        |       |
| Ika1224-<br>No24_F11_002 | BY798838                                   | 0.009    | 38.2 |                                                            |                                                                                                                                                                                                                                                        |       |
| Ika1224-<br>No24_G01_003 | gi 21174067 gb <br>BQ434991.1 <br>BQ434991 | 8.00E-11 | 67.5 | heterogeneous<br>nuclear<br>ribonucleoprotein u-<br>like 1 | P:GO:0006915,F:GO:<br>0003677,F:GO:<br>0003723,C:GO:<br>0005634,P:GO:<br>0006355,F:GO:0000166                                                                                                                                                          | ASP   |
| Ika1224-<br>No24_H08_004 | GS014020                                   | 0.001    | 34.2 |                                                            |                                                                                                                                                                                                                                                        |       |

|                          |                                            |          |      |                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                        |         |
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| Ika1224-<br>No25_D03_004 | gi 22701704 gb <br>BU187720.1 <br>BU187720 | 0        | 184  | kinesin heavy chain | C:GO:0043005,F:GO:<br>0008574,P:GO:<br>0040010,P:GO:<br>0007269,C:GO:<br>0035253,C:GO:<br>0005624,P:GO:<br>0040011,P:GO:<br>0007317,C:GO:<br>0005874,P:GO:<br>0048311,P:GO:<br>0007303,P:GO:<br>0047496,F:GO:<br>0008017,P:GO:<br>0019227,P:GO:<br>0002009,P:GO:<br>0008045,P:GO:<br>0008088,P:GO:<br>0047497,P:GO:<br>0007310,P:GO:<br>0010171,C:GO:<br>0048471,C:GO:<br>0005871,F:GO:<br>0005524,P:GO:<br>0006839,P:GO:<br>0001754,C:GO:0005739 | ADIP,<br>Microtub_asso<br>c, H00K, Pfam-<br>B_7610, Cenp-<br>F_leu_zip | 1.30177 |
| Ika1224-<br>No25_D05_004 | BY797834                                   | 0.01     | 38.2 |                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                        |         |
| Ika1224-<br>No25_G02_003 | gi 85207344 gb <br>DW608201.1 <br>DW608201 | 8.00E-06 | 54   |                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                        |         |
| Ika1224-<br>No25_G04_003 | gi 13105897 gb <br>BG308370.1 <br>BG308370 | 8.00E-05 | 50.1 |                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                        |         |
| Ika1224-<br>No25_G08_003 | GS020701                                   | 0.004    | 34.2 |                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                        |         |

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| Ika1224-<br>No26_B09_002 | gi 19389351 gb <br>BM930178.1 <br>BM930178 | 0.0005   | 48.1 | exosome component<br>10 | C:GO:0000176,P:GO:<br>0006396,C:GO:<br>0005634,F:GO:<br>0016787,P:GO:<br>0006364,F:GO:<br>0003676,F:GO:<br>0003723,F:GO:<br>0004527,C:GO:<br>0005730,P:GO:<br>0006139,C:GO:<br>0005622,P:GO:<br>0000184,F:GO:<br>0004518,C:GO:<br>0000178,F:GO:0008408 |
| Ika1224-<br>No26_D12_004 | gi 23675980 gb <br>BU738643.1 <br>BU738643 | 0.002    | 46.1 |                         |                                                                                                                                                                                                                                                        |
| Ika1224-<br>No26_E05_001 | gi 19393251 gb <br>BM934099.1 <br>BM934099 | 6.00E-05 | 47.8 |                         |                                                                                                                                                                                                                                                        |
| Ika1224-<br>No26_G11_003 | gi 62873057 gb <br>DN888294.1 <br>DN888294 | 0.008    | 44.1 |                         |                                                                                                                                                                                                                                                        |
| Ika1224-<br>No26_G12_003 | gi 62856864 gb <br>DN886909.1 <br>DN886909 | 0.009    | 44.1 |                         |                                                                                                                                                                                                                                                        |
| Ika1224-<br>No27_A02_001 | BY800039                                   | 0.003    | 40.1 |                         |                                                                                                                                                                                                                                                        |

|                          |                                            |          |                                  |                                                                                                                                                                                                                                                                                                                                                                                                |                   |
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| Ika1224-<br>No27_B03_002 | gi 22811032 gb <br>BU504799.1 <br>BU504799 | 9.00E-15 | 80.8 insulin-degrading<br>enzyme | F:GO:0031626,P:GO:<br>0007548,P:GO:<br>0051291,F:GO:<br>0008270,C:GO:<br>0005625,F:GO:<br>0004871,C:GO:<br>0031597,P:GO:<br>0043171,F:GO:<br>0043559,C:GO:<br>0005615,P:GO:<br>0051603,C:GO:<br>0009986,P:GO:<br>0045861,P:GO:<br>0042447,F:GO:<br>0005524,P:GO:<br>0050435,F:GO:<br>0016887,P:GO:<br>0007165,F:GO:<br>0004231,P:GO:<br>0051289,F:GO:<br>0042803,C:GO:<br>0005782,C:GO:0005634 | Peptidase_M1<br>6 |
| Ika1224-<br>No27_B08_002 | gi 19396614 gb <br>BM937462.1 <br>BM937462 | 1.00E-07 | 55.1                             |                                                                                                                                                                                                                                                                                                                                                                                                |                   |
| Ika1224-<br>No27_C07_003 | GS004891                                   | 0.003    | 34.2                             |                                                                                                                                                                                                                                                                                                                                                                                                |                   |
| Ika1224-<br>No27_D11_004 | gi 14977218 gb <br>BI300938.1 BI300938     | 4.00E-06 | 51.9 ---NA---                    |                                                                                                                                                                                                                                                                                                                                                                                                |                   |
| Ika1224-<br>No27_G04_003 | GS020571                                   | 0.001    | 36.2                             |                                                                                                                                                                                                                                                                                                                                                                                                |                   |

|                          |                                                |       |      |                                    |                                                                                                                                                                                                                                                                                                                            |                                       |
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| Ika1224-<br>No27_G06_003 | gi 62021563 gb <br>DN679604.1 <br>DN679604     | 0     | 234  | vacuolar atp synthase<br>subunit h | F:GO:0046961,P:GO:<br>0009792,F:GO:<br>0005515,F:GO:<br>0008553,P:GO:<br>0040007,F:GO:<br>0046933,P:GO:<br>0015991,P:GO:<br>0040011,P:GO:<br>0040002,P:GO:<br>0007035,P:GO:<br>0018996,P:GO:<br>0008340,F:GO:<br>0001671,P:GO:<br>0015986,P:GO:<br>0006897,P:GO:<br>0002119,C:GO:<br>0000221,C:GO:<br>0000300,F:GO:0005524 | V-<br>ATPase_H_N,<br>V-<br>ATPase_H_C |
| Ika1224-<br>No27_H05_004 | gi 46820176 gb <br>CN507552.1 <br>CN507552     | 0.007 | 44.1 |                                    |                                                                                                                                                                                                                                                                                                                            |                                       |
| Ika1224-<br>No27_H10_004 | GS008123                                       | 0.001 | 34.2 |                                    |                                                                                                                                                                                                                                                                                                                            |                                       |
| Ika1224-<br>No4_E08_001  | <b>Embryo specific<br/>expression</b> GS008153 | 0.004 | 31.3 |                                    |                                                                                                                                                                                                                                                                                                                            |                                       |
| Ika1224-<br>No4_G10_003  | gi 62837041 gb <br>DN867100.1 <br>DN867100     | 0.003 | 42.8 |                                    |                                                                                                                                                                                                                                                                                                                            |                                       |
| Ika1224_C06_00<br>3      | gi 32180633 gb <br>CD678902.1 <br>CD678902     | 0     | 306  |                                    |                                                                                                                                                                                                                                                                                                                            |                                       |

|                     |                       |                                            |          |      |                                       |                                                                                                                                                                                                                                                                         |              |        |
|---------------------|-----------------------|--------------------------------------------|----------|------|---------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------|--------|
| ikaD2-2_B11_00<br>2 | Positive<br>selection | GS020581                                   | 0.003    | 31.3 | thermosome                            | F:GO:0008565,P:GO:<br>0009792,C:GO:<br>0005856,P:GO:<br>0006457,P:GO:<br>0007010,P:GO:<br>0040007,C:GO:<br>0005832,P:GO:<br>0040035,P:GO:<br>0007283,F:GO:<br>0005524,P:GO:<br>0002119,P:GO:<br>0044408,P:GO:<br>0040011,F:GO:<br>0051082,P:GO:<br>0051131,P:GO:0008340 | Cpn60_TCP1   | 3.0724 |
| ikaD2-6_B10_00<br>2 |                       | GS020581                                   | 0.003    | 31.3 |                                       |                                                                                                                                                                                                                                                                         |              |        |
| ika_c11             |                       | BY799535                                   | 0.01     | 35.4 |                                       |                                                                                                                                                                                                                                                                         |              |        |
| ika_c24             |                       | gi 58031468 gb <br>CX729011.1 <br>CX729011 | 0.008    | 44.1 |                                       |                                                                                                                                                                                                                                                                         |              |        |
| ika_c29             |                       | BY799800                                   | 0.0007   | 42.1 |                                       |                                                                                                                                                                                                                                                                         |              |        |
| ika_c36             |                       | BY797277                                   | 2.00E-11 | 64.8 |                                       |                                                                                                                                                                                                                                                                         |              |        |
| ika_c37             |                       | gi 15706568 gb <br>BI729555.1 BI729555     | 3.00E-05 | 52   | cg11148-isoform a<br>isoform 1        |                                                                                                                                                                                                                                                                         | Pfam-B_18091 |        |
| ika_c61             |                       | GS013929                                   | 0.004    | 34.2 |                                       |                                                                                                                                                                                                                                                                         |              |        |
| ika_c67             |                       | gi 83161863 gb <br>DB384234.1 <br>DB384234 | 1.00E-05 | 49.2 | tnf receptor-<br>associated protein 1 |                                                                                                                                                                                                                                                                         |              |        |

|         |                               |                                            |   |             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                       |
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| ika_c70 | Embryo specific<br>expression | gi 62040790 gb <br>DN688965.1 <br>DN688965 | 0 | 131 protein | P:GO:0030100,C:GO:<br>0030122,P:GO:<br>0000003,C:GO:<br>0009536,C:GO:<br>0005802,P:GO:<br>0009792,P:GO:<br>0006726,P:GO:<br>0008286,P:GO:<br>0040007,P:GO:<br>0006898,P:GO:<br>0006461,P:GO:<br>0007269,C:GO:<br>0030123,F:GO:<br>0008565,P:GO:<br>0016183,P:GO:<br>0040011,P:GO:<br>0006886,F:GO:<br>0030276,P:GO:<br>0048268,P:GO:<br>0048072,P:GO:<br>0002119,P:GO:<br>0006896,C:GO:<br>0008021,P:GO:<br>0007040,C:GO:<br>0030121,P:GO:<br>0010171,C:GO:0005739 | Clat_adaptor_s 0.1915 |
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|----------------------|-------------------------------------------------------------------|--------------------------------------------|----------|----------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------|---------|
| ika_c8               | <b>Embryo specific<br/>expression,<br/>Positive<br/>selection</b> | gi 22695458 gb <br>BU181474.1 <br>BU181474 | 0        | 252 high density<br>lipoprotein binding<br>protein | F:GO:0005515,P:GO:<br>0007275,P:GO:<br>0051276,P:GO:<br>0048518,P:GO:<br>0006323,C:GO:<br>0044427,P:GO:<br>0044237,P:GO:<br>0040011,P:GO:<br>0051179,P:GO:<br>0048856,P:GO:<br>0006629,F:GO:<br>0003677,C:GO:<br>0012505,C:GO:<br>0044444,C:GO:0005634 | KH_1, Pfam-<br>B_12719 | 2.39913 |
| OctEye_0033F_0<br>34 |                                                                   | gi 13059618 gb <br>BG296702.1 <br>BG296702 | 0.007    | 44.1                                               |                                                                                                                                                                                                                                                        |                        |         |
| OctEye_0148F_0<br>59 |                                                                   | BY795189                                   | 9.00E-07 | 45.1 ribosomal protein l34                         |                                                                                                                                                                                                                                                        | Ribosomal_L3<br>4e     |         |
| OctEye_0206F_0<br>16 |                                                                   | gi 62842158 gb <br>DN872217.1 <br>DN872217 | 3.00E-07 | 54.2 briggsae cbr-aat-1<br>protein                 | C:GO:0005886                                                                                                                                                                                                                                           |                        |         |
| OctEye_0307F_0<br>19 |                                                                   | gi 62889367 gb <br>DN904604.1 <br>DN904604 | 0.005    | 44.1                                               |                                                                                                                                                                                                                                                        |                        |         |
| OctEye_0317F_0<br>24 |                                                                   | GS013987                                   | 0.001    | 36.2                                               |                                                                                                                                                                                                                                                        |                        |         |
| OctEye_0487F_0<br>05 |                                                                   | gi 62878532 gb <br>DN893769.1 <br>DN893769 | 0.0001   | 50.1                                               |                                                                                                                                                                                                                                                        |                        |         |
| OctEye_0591F_0<br>17 |                                                                   | gi 62023994 gb <br>DN677464.1 <br>DN677464 | 0.005    | 41.8                                               |                                                                                                                                                                                                                                                        |                        |         |
| OctEye_0659F_0<br>83 |                                                                   | gi 75838361 gb <br>DT868621.1 DT868621     | 0.004    | 38.6                                               |                                                                                                                                                                                                                                                        |                        |         |
| OctEye_0745F_0<br>70 |                                                                   | gi 75835824 gb <br>DT866084.1 DT866084     | 1.00E-07 | 57.1 isoform a                                     |                                                                                                                                                                                                                                                        |                        |         |

|                      |                                            |          |                                                          |                                                                                                                                                  |         |
|----------------------|--------------------------------------------|----------|----------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------|---------|
| OctEye_0789F_0<br>20 | gi 32173308 gb <br>CD671568.1 <br>CD671568 | 1.00E-07 | 53.3 coiled-coil domain-<br>containing protein 94        | DUF572                                                                                                                                           |         |
| OctEye_0826F_0<br>62 | BY798607                                   | 0.0006   | 38.6                                                     | DUF2154                                                                                                                                          |         |
| OctEye_0912F_0<br>57 | gi 77501382 gb <br>DV213912.1 DV213912     | 1.00E-25 | 116 ---NA---                                             | NDUF_B7                                                                                                                                          | 1.72221 |
| OctEye_1096F_0<br>45 | GS020542                                   | 0.008    | 30.2                                                     |                                                                                                                                                  |         |
| OctEye_1119F_0<br>65 | GS020677                                   | 0.009    | 32.2                                                     |                                                                                                                                                  |         |
| OctEye_1134F_0<br>80 | gi 58032450 gb <br>CX729993.1 <br>CX729993 | 0.007    | 44.1                                                     |                                                                                                                                                  |         |
| OctEye_1164F_0<br>15 | BY796496                                   | 0.009    | 38.2                                                     |                                                                                                                                                  |         |
| OctEye_1182F_0<br>32 | gi 62844591 gb <br>DN874650.1 <br>DN874650 | 0.002    | 46.1                                                     |                                                                                                                                                  |         |
| OctEye_1263F_0<br>17 | gi 62828798 gb <br>DN859149.1 <br>DN859149 | 4.00E-28 | 124 cytochrome c oxidase<br>subunit via<br>polypeptide 1 |                                                                                                                                                  |         |
| OctEye_1302F_0<br>60 | gi 62038659 gb <br>DN687898.1 <br>DN687898 | 0.002    | 41.4 zgc:55406 protein                                   | F:GO:0004568,F:GO:<br>0043169,F:GO:<br>0008061,P:GO:<br>0005975,C:GO:<br>0005576,F:GO:<br>0003824,F:GO:<br>0004553,P:GO:<br>0006032,P:GO:0006030 |         |
| OctEye_1343F_0<br>97 | gi 62038852 gb <br>DN687996.1 <br>DN687996 | 3.00E-06 | 46.9 collagen type vi alpha<br>4                         |                                                                                                                                                  |         |
| OctEye_1353F_0<br>06 | gi 62828989 gb <br>DN859340.1 <br>DN859340 | 5.00E-08 | 54.7 ---NA---                                            |                                                                                                                                                  |         |

|                  |                                    |          |                                              |                           |         |
|------------------|------------------------------------|----------|----------------------------------------------|---------------------------|---------|
| OctEye_1499F_055 | gi 85188936 gb DW601763.1 DW601763 | 0        | 191 mitochondrial trifunctional beta subunit | F:GO:0003988,P:GO:0008152 | 0.5225  |
| OctEye_1534F_096 | gi 58031885 gb CX729428.1 CX729428 | 1.00E-06 | 51.9 mgc89819 protein                        |                           |         |
| OctEye_1560F_029 | gi 32178782 gb CD677051.1 CD677051 | 7.00E-23 | 107 atph+mitochondrial f1o subunit           | F:GO:0015078              | 1.57288 |
| OctEye_1579F_039 | BY798633                           | 0.004    | 38.2                                         |                           |         |
| OctEye_1586F_058 | gi 18973569 gb BM666120.1 BM666120 | 0.01     | 37.3                                         |                           |         |
| OctEye_1592F_061 | BY796454                           | 0.002    | 34.1                                         |                           |         |
| OctEye_1748F_027 | gi 40319367 gb CK353480.1 CK353480 | 8.97E-44 | 177 homolog precursor                        |                           | 0.1216  |
| OctEye_1812F_091 | GS014021                           | 0.0006   | 30.9                                         |                           |         |
| OctEye_1825F_002 | gi 24559221 gb CA341125.1 CA341125 | 1.00E-09 | 65.9 arge subunit family member (rpl-)       |                           |         |
| OctEye_1832F_013 | gi 62031964 gb DN684517.1 DN684517 | 0.007    | 42.1                                         |                           |         |
| OctEye_2031F_017 | GS008102                           | 0.0002   | 38.2                                         |                           |         |
| OctEye_2085F_068 | BY794980                           | 5.00E-16 | 75.8 ribosomal protein s17                   |                           |         |
| OctEye_2126F_016 | gi 6516364 gb AW210424.1 AW210424  | 0.008    | 30.4                                         |                           |         |
| OctEye_2221F_008 | gi 24734171 gb CA397140.1 CA397140 | 0.0004   | 48.1                                         |                           |         |

|                      |                                                                             |          |      |                                           |                                                                                                                                 |         |
|----------------------|-----------------------------------------------------------------------------|----------|------|-------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|---------|
| OctEye_2262F_0<br>60 | gi 119785924 gb <br>EH279915.1 <br>EH279915                                 | 4.00E-14 | 78.5 | selenoprotein1                            | F:GO:0008430,C:GO:<br>0005739,C:GO:<br>0005886,F:GO:0003954                                                                     | 0.91171 |
| OctEye_2384F_0<br>89 | GS020757                                                                    | 0.008    | 30.2 |                                           |                                                                                                                                 |         |
| OctEye_2498F_0<br>10 | BY799605                                                                    | 0.004    | 36.2 |                                           |                                                                                                                                 |         |
| OctEye_2597F_0<br>04 | gi 58178287 gb <br>CX767934.1 <br>CX767934                                  | 0        | 254  | atp synthase                              | C:GO:0045261,F:GO:<br>0046933,C:GO:<br>0005743,P:GO:<br>0015986,F:GO:<br>0046872,F:GO:<br>0005524,F:GO:<br>0005515,F:GO:0046961 |         |
| OctEye_2648F_0<br>61 | GS019927                                                                    | 0.009    | 32.2 |                                           |                                                                                                                                 |         |
| OctEye_2674F_0<br>90 | <b>Positive<br/>selection</b><br>gi 58035934 gb <br>CX733460.1 <br>CX733460 | 4.00E-34 | 144  | coatomer<br>proteinsubunit alpha          | P:GO:0006461,F:GO:<br>0005515,F:GO:<br>0008565,P:GO:<br>0016192,P:GO:<br>0006886,C:GO:<br>0030126,F:GO:0005198                  | 6.37134 |
| OctEye_2694F_0<br>12 | GS020566                                                                    | 0.003    | 32.2 |                                           |                                                                                                                                 |         |
| OctEye_2707F_0<br>19 | GS020537                                                                    | 0.009    | 32.2 |                                           |                                                                                                                                 |         |
| OctEye_2728F_0<br>45 | gi 119790103 gb <br>EH282661.1 <br>EH282661                                 | 0.0001   | 43.7 | antioxidant enzyme                        | F:GO:0046872,P:GO:<br>0030001                                                                                                   |         |
| OctEye_2790F_0<br>12 | gi 46816584 gb <br>CN503960.1 <br>CN503960                                  | 2.00E-11 | 69.9 | actin 5c                                  |                                                                                                                                 |         |
| OctEye_2879F_0<br>97 | gi 37634583 gb <br>CF738246.1 CF738246                                      | 3.00E-34 | 145  | u2small nuclear rna<br>auxiliary factor 1 | F:GO:0003723,C:GO:<br>0005634,F:GO:<br>0000166,F:GO:0008270                                                                     | 0.31488 |
| OctEye_2993F_0<br>19 | gi 58060940 gb <br>CX734104.1 <br>CX734104                                  | 2.00E-19 | 96.6 | ---NA---                                  |                                                                                                                                 |         |

|                  |                                     |          |      |                                            |                                                                  |         |
|------------------|-------------------------------------|----------|------|--------------------------------------------|------------------------------------------------------------------|---------|
| OctEye_3104F_032 | gi 5209870 gb AI763935.1 AI763935   | 7.00E-42 | 170  | nadh dehydrogenase                         | C:GO:0016020,C:GO:0005739                                        | 0.95984 |
| OctEye_3179F_006 | gi 75834465 gb DT864725.1 DT864725  | 1.00E-21 | 57.4 | translationally controlled tumor protein   | F:GO:0005262,F:GO:0005509,P:GO:0006816,F:GO:0019855              |         |
| OctEye_3268F_012 | gi 119779499 gb EH278533.1 EH278533 | 0.0002   | 42.8 |                                            |                                                                  |         |
| OctEye_3507F_052 | gi 58033286 gb CX730812.1 CX730812  | 0.01     | 26.7 |                                            |                                                                  |         |
| OctEye_3723F_072 | gi 126522970 gb EL646689.1 EL646689 | 8.00E-33 | 139  | af486842_160s ribosomal protein l37        | F:GO:0046872,F:GO:0003723,C:GO:0030529                           | 0.92411 |
| OctEye_3881F_039 | gi 46825733 gb CN513109.1 CN513109  | 0        | 221  | delta-aminolevulinic acid dehydratase      | F:GO:0046872,F:GO:0004655,P:GO:0006779                           |         |
| OctEye_3919F_082 | gi 32464719 gb CD805893.1 CD805893  | 0        | 308  | centaurin gamma                            |                                                                  | 2.48762 |
| OctEye_3974F_045 | gi 50135821 gb CO470232.1 CO470232  | 6.00E-40 | 163  | glyceraldehyde-3-phosphate dehydrogenase-2 | F:GO:0051287,P:GO:0006096,F:GO:0004365                           | 1.2506  |
| OctEye_4022F_093 | BY796351                            | 0.009    | 26.7 |                                            |                                                                  |         |
| OctEye_4025F_087 | GS020566                            | 0.004    | 34.2 |                                            |                                                                  |         |
| OctEye_4048F_026 | BY795001                            | 5.00E-05 | 42.1 |                                            |                                                                  |         |
| OctEye_4133F_005 | gi 40319296 gb CK353409.1 CK353409  | 0.002    | 28.6 |                                            |                                                                  |         |
| OctEye_4228F_012 | gi 19017266 gb BM704008.1 BM704008  | 8.00E-23 | 105  | mgc84219 protein                           | C:GO:0005737,F:GO:0003779,C:GO:0030054,C:GO:0045202,F:GO:0004864 | 0.82442 |

Positive  
selection

Embryo specific  
expression

RPEL

|                  |                                                                       |          |      |                                                       |                                                                                                         |              |         |
|------------------|-----------------------------------------------------------------------|----------|------|-------------------------------------------------------|---------------------------------------------------------------------------------------------------------|--------------|---------|
| OctEye_4486F_077 | gi 62882487 gb DN897724.1 DN897724                                    | 9.00E-11 | 53.8 | cystatin b                                            | F:GO:0004866,C:GO:0005622                                                                               | Cystatin     |         |
| OctEye_4502F_093 | <b>Embryo specific expression</b> gi 126522032 gb EL645883.1 EL645883 | 6.00E-06 | 52   |                                                       |                                                                                                         |              |         |
| OctEye_4528F_026 | BY795027                                                              | 0.009    | 38.2 |                                                       |                                                                                                         |              |         |
| OctEye_4530F_027 | gi 5210219 gb AI764284.1 AI764284                                     | 0.002    | 46.1 |                                                       |                                                                                                         | Coatomer_E   |         |
| OctEye_4536F_030 | gi 41347505 gb CK626619.1 CK626619                                    | 3.00E-15 | 80.3 | epsilon subunit of coatomer protein complex isoform a | P:GO:0016192,F:GO:0005488,C:GO:0031410,P:GO:0016043,C:GO:0044425,C:GO:0031090,C:GO:0012505,C:GO:0044431 |              | 0.1668  |
| OctEye_4576F_074 | <b>GO annotation</b> gi 40549930 gb CK396398.1 CK396398               | 0        | 182  | lim and sh3 domain protein                            |                                                                                                         | Nebulin, LIM | 1.56255 |
| OctEye_4608F_102 | gi 85192029 gb DW602650.1 DW602650                                    | 0.005    | 42.1 |                                                       |                                                                                                         |              |         |
| OctEye_4725F_021 | gi 46822989 gb CN510365.1 CN510365                                    | 3.99E-43 | 175  | u424_dropsame: full=upf0424 protein ga19395           | F:GO:0003674,P:GO:0008150,C:GO:0005575                                                                  | PITH         | 0.46073 |
| OctEye_4771F_068 | gi 37631811 gb CF735475.1 CF735475                                    | 2.00E-24 | 109  | hyperplastic discs cg9484-pa isoform 1                |                                                                                                         | HECT         |         |
| OctEye_4817F_018 | GS014020                                                              | 0.004    | 32.2 |                                                       |                                                                                                         |              |         |
| OctEye_4872F_077 | gi 18501048 gb BM452008.1 BM452008                                    | 1.00E-14 | 79.8 |                                                       |                                                                                                         |              |         |
| OctEye_4900F_011 | gi 46566151 gb CN484647.1 CN484647                                    | 4.00E-12 | 73.8 |                                                       |                                                                                                         |              |         |

|                      |                                            |          |                                                                  |                               |                            |         |
|----------------------|--------------------------------------------|----------|------------------------------------------------------------------|-------------------------------|----------------------------|---------|
| OctEye_4909F_0<br>08 | gi 62873918 gb <br>DN889155.1 <br>DN889155 | 0        | 178 ---NA---                                                     | F:GO:0042578,P:GO:<br>0005975 |                            | 1.43801 |
| OctFet_0406F_0<br>28 | gi 85169445 gb <br>DW595187.1 <br>DW595187 | 3.00E-05 | 46.9 cat eye syndrome<br>candidate region 5<br>protein           | P:GO:0008152,F:GO:<br>0016787 |                            |         |
| OctFet_0464F_0<br>89 | gi 46815207 gb <br>CN502583.1 <br>CN502583 | 6.00E-12 | 71.2 mitochondrial atp<br>synthase f chain                       |                               | WRW                        | 1.26487 |
| OctFet_0712F_0<br>45 | gi 37635937 gb <br>CF739599.1 CF739599     | 3.00E-40 | 126 cytochrome c oxidase<br>subunit va                           | F:GO:0004129,P:GO:<br>0006118 |                            | 0.88096 |
| OctRet_0020F_0<br>27 | BY797441                                   | 1.00E-27 | 76.7 cg14235 cg14235-pa                                          | F:GO:0004129                  | Pfam-<br>B_10366,<br>COX6B | 1.41544 |
| OctRet_0045F_0<br>40 | GS020503                                   | 0.008    | 32.2                                                             |                               |                            |         |
| OctRet_0075F_0<br>71 | BY799424                                   | 0.0004   | 38.6                                                             |                               |                            |         |
| OctRet_0094F_0<br>96 | BY799942                                   | 3.00E-08 | 54                                                               |                               |                            |         |
| OctRet_0150F_0<br>60 | BY800189                                   | 9.00E-07 | 35                                                               |                               |                            |         |
| OctRet_0176F_0<br>89 | gi 18524913 gb <br>BM475871.1 <br>BM475871 | 0.008    | 41.4                                                             |                               |                            |         |
| OctRet_0203F_0<br>17 | gi 57590691 gb <br>CX563662.1 <br>CX563662 | 2.00E-13 | 73 adaptor-related protein<br>complexbeta 1 subunit<br>isoform 2 |                               | Adaptin_N                  |         |
| OctRet_0788F_0<br>27 | gi 18522948 gb <br>BM473906.1 <br>BM473906 | 2.00E-11 | 69.9                                                             |                               |                            |         |
| OctRet_0840F_0<br>77 | gi 22684611 gb <br>BU170627.1 <br>BU170627 | 0.0006   | 46.1                                                             |                               |                            |         |
| OctRet_0859F_0<br>87 | GS004651                                   | 0.0002   | 38.2                                                             |                               |                            |         |

|                      |                                                |          |      |                                                                                                                                                                                                |
|----------------------|------------------------------------------------|----------|------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| OctRet_0879F_0<br>17 | GS020645                                       | 0.008    | 26.7 |                                                                                                                                                                                                |
| OctRet_0892F_0<br>31 | gi 54449888 gb <br>CV560841.1 <br>CV560841     | 4.00E-14 | 79   | alpha 2 type i collagen C:GO:0005615,P:GO:<br>0007169,F:GO:0005198                                                                                                                             |
| OctRet_0896F_0<br>41 | gi 41341368 gb <br>CK620482.1 <br>CK620482     | 0.004    | 40.9 |                                                                                                                                                                                                |
| OctRet_0914F_0<br>58 | gi 19046508 gb <br>BM725177.1 <br>BM725177     | 2.00E-07 | 55.6 | ---NA--- VHP                                                                                                                                                                                   |
| OctRet_0921F_0<br>54 | gi 24721811 gb <br>CA390626.1 <br>CA390626     | 0.008    | 44.1 | two-component response regulator P:GO:0000160,P:GO:<br>0006355,F:GO:<br>0000156,P:GO:<br>0006350,F:GO:0003677                                                                                  |
| OctRet_1082F_0<br>32 | BY796825                                       | 0.009    | 35.4 | integral membrane protein C:GO:0016021                                                                                                                                                         |
| OctRet_1112F_0<br>63 | <b>Embryo specific<br/>expression</b> BY797271 | 0.01     | 38.2 |                                                                                                                                                                                                |
| OctRet_1170F_0<br>26 | GS020760                                       | 0.008    | 28.1 |                                                                                                                                                                                                |
| OctRet_1234F_0<br>90 | BY798709                                       | 5.00E-16 | 81.8 | ---NA---                                                                                                                                                                                       |
| OctRet_1240F_0<br>93 | gi 15711152 gb <br>BI734139.1 BI734139         | 4.00E-10 | 42.3 | nadh dehydrogenase subunit 2 C:GO:0005746,C:GO:<br>0016020,C:GO:<br>0005743,F:GO:<br>0008137,C:GO:<br>0005739,P:GO:<br>0006810,P:GO:<br>0006118,P:GO:<br>0006120,F:GO:<br>0016491,P:GO:0042773 |
| OctRet_1255F_0<br>05 | gi 22673683 gb <br>BU159773.1 <br>BU159773     | 9.00E-06 | 52   |                                                                                                                                                                                                |
| OctRet_1272F_0<br>29 | BY798753                                       | 0.009    | 38.2 |                                                                                                                                                                                                |

|                  |                                        |          |      |                                      |                                        |
|------------------|----------------------------------------|----------|------|--------------------------------------|----------------------------------------|
| OctRet_1283F_035 | GS004800                               | 0.0006   | 34.2 |                                      |                                        |
| OctRet_1295F_049 | gi 18986831 gb BM676935.1 BM676935     | 0.0003   | 46   |                                      |                                        |
| OctRet_1300F_059 | gi 3512121 gb AI112172.1 AI112172      | 1.00E-06 | 53.3 | glutathione s-transferase            | F:GO:0005212                           |
| OctRet_1353F_008 | Embryo specific expression<br>BY797166 | 0.003    | 38.2 |                                      |                                        |
| OctRet_1370F_032 | GS013955                               | 0.004    | 34.2 |                                      |                                        |
| OctRet_1398F_062 | gi 20363398 gb BQ187847.1 BQ187847     | 0.0003   | 45.4 | fyn-binding protein                  |                                        |
| OctRet_1427F_085 | gi 119789076 gb EH281635.1 EH281635    | 5.00E-43 | 174  | zinc finger protein 593              | F:GO:0005488 0.29657                   |
| OctRet_1452F_025 | BY794943                               | 0.008    | 31.8 | major facilitator superfamily mfs_1  | P:GO:0006810,C:GO:0016021,F:GO:0005215 |
| OctRet_1465F_024 | gi 62873846 gb DN889083.1 DN889083     | 0        | 314  | gtp-binding nuclear protein ran      | 0.70779                                |
| OctRet_1493F_054 | gi 18501600 gb BM452560.1 BM452560     | 2.00E-06 | 56   |                                      |                                        |
| OctRet_1499F_065 | gi 19025292 gb BM712034.1 BM712034     | 1.00E-41 | 169  | developmental embryonic b cg16792-pa | 1.1496                                 |
| OctRet_1960F_047 | gi 15682370 gb BI706675.1 BI706675     | 9.00E-26 | 73   | nadh dehydrogenase subunit 1         | C:GO:0016020,F:GO:0016491              |
| SquidNo3_D02_004 | gi 13297760 gb BG404312.1 BG404312     | 0.006    | 44.1 |                                      |                                        |
| DB910987         | gi 75836302 gb DT866562.1 DT866562     | 1.00E-05 | 50.6 | ---NA---                             | RRM_1                                  |
| DB911028         | GS013811                               | 0.001    | 36.2 |                                      |                                        |
| DB911039         | GS013856                               | 0.005    | 34.2 |                                      |                                        |

|          |                                            |          |      |                                                                               |                                                             |                     |         |
|----------|--------------------------------------------|----------|------|-------------------------------------------------------------------------------|-------------------------------------------------------------|---------------------|---------|
| DB911042 | BY797854                                   | 0.0007   | 42.1 |                                                                               |                                                             |                     |         |
| DB911058 | gi 85202102 gb <br>DW605836.1 <br>DW605836 | 1.00E-06 | 53.8 | farnesyl diphosphate<br>synthase                                              | P:GO:0008299                                                | polyprenyl_syn<br>t |         |
| DB911092 | BY799768                                   | 0.001    | 38.2 |                                                                               |                                                             |                     |         |
| DB911095 | GS020506                                   | 0.003    | 32.2 |                                                                               |                                                             |                     |         |
| DB911100 | gi 18988393 gb <br>BM678497.1 <br>BM678497 | 0.0005   | 37.3 |                                                                               |                                                             |                     |         |
| DB911114 | GS020551                                   | 0.0008   | 33.6 |                                                                               |                                                             | Pfam-B_4326         |         |
| DB911116 | BY795311                                   | 2.00E-05 | 44.1 | collagen triple helix<br>repeat protein                                       |                                                             | Pfam-B_7579         |         |
| DB911121 | gi 37631583 gb <br>CF735247.1 CF735247     | 0        | 233  | ubiquitin-protein<br>ligase                                                   |                                                             | HECT                |         |
| DB911129 | gi 19118735 gb <br>BM801912.1 <br>BM801912 | 5.00E-26 | 111  | eif4g1 protein                                                                | F:GO:0003743,P:GO:<br>0006446,P:GO:<br>0016070,F:GO:0005515 | MA3                 | 1.03727 |
| DB911135 | GS013972                                   | 0.005    | 34.2 |                                                                               |                                                             |                     |         |
| DB911138 | gi 10204034 gb <br>BE782836.1 BE782836     | 0.008    | 30.4 |                                                                               |                                                             |                     |         |
| DB911148 | GS020598                                   | 0.004    | 34.2 |                                                                               |                                                             |                     |         |
| DB911154 | gi 37599777 gb <br>CF725609.1 CF725609     | 2.00E-22 | 73   | beclin 1                                                                      | C:GO:0005737                                                | APG6                | 0.18435 |
| DB911160 | gi 16087554 gb <br>BI880283.1 BI880283     | 6.00E-23 | 108  | novel proteinbtaf1 rna<br>polymeraseb-tfiid<br>transcription<br>factor-170kda |                                                             | SNF2_N              |         |
| DB911164 | gi 10664305 gb <br>BE988186.1 BE988186     | 0.009    | 44.1 |                                                                               |                                                             |                     |         |
| DB911166 | gi 45306394 gb <br>CK876763.1 <br>CK876763 | 0.0006   | 46.1 |                                                                               |                                                             |                     |         |
| DB911193 | gi 2221038 gb <br>AA490163.1 AA490163      | 4.00E-06 | 39.6 | ---NA---                                                                      |                                                             |                     |         |
| DB911208 | GS004835                                   | 0.004    | 34.2 |                                                                               |                                                             |                     |         |

|          |                                                                  |          |      |                                                        |                                                                                               |                   |         |
|----------|------------------------------------------------------------------|----------|------|--------------------------------------------------------|-----------------------------------------------------------------------------------------------|-------------------|---------|
| DB911215 | gi 9120961 gb <br>BE250824.1 BE250824                            | 1.00E-19 | 96.8 | mnp1 protein                                           |                                                                                               | RRM_1             | 1.54995 |
| DB911218 | GS020693                                                         | 0.001    | 32.7 |                                                        |                                                                                               |                   |         |
| DB911219 | gi 49680852 gb <br>CO434558.1 <br>CO434558                       | 7.00E-20 | 84   | protocadherin<br>gamma-b1 precursor<br>(pcdh-gamma-b1) |                                                                                               | Cadherin,Cadherin |         |
| DB911220 | gi 49677571 gb <br>CO431277.1 <br>CO431277                       | 4.00E-24 | 88.1 | protocadherin 2 alpha<br>b 6                           | F:GO:0005262,F:GO:<br>0005509,P:GO:<br>0006816,F:GO:<br>0004872,C:GO:<br>0016020,F:GO:0019855 | Cadherin,Cadherin |         |
| DB911222 | gi 13303397 gb <br>BG378925.1 <br>BG378925                       | 6.00E-22 | 104  | acidic coiled-coil<br>containing protein 3             |                                                                                               | CSD               | 1.82423 |
| DB911228 | GS020461                                                         | 0.002    | 24.9 |                                                        |                                                                                               |                   |         |
| DB911231 | GS020499                                                         | 0.001    | 36.2 |                                                        |                                                                                               |                   |         |
| DB911242 | <b>Embryo specific</b> gi 9592398 gb <br>BB536898.1 <br>BB536898 | 0.006    | 44.1 |                                                        |                                                                                               |                   |         |
| DB911252 | gi 37632734 gb <br>CF736398.1 CF736398                           | 0.0001   | 43.7 |                                                        |                                                                                               |                   |         |
| DB911287 | BY795259                                                         | 5.00E-05 | 43.2 | prothoracicostatic<br>peptide precursor                | F:GO:0005179,P:GO:<br>0007218,F:GO:<br>0003674,C:GO:<br>0005615,P:GO:<br>0002168,C:GO:0005576 |                   |         |
| DB911294 | GS013930                                                         | 0.007    | 30.4 |                                                        |                                                                                               |                   |         |
| DB911295 | gi 10589030 gb <br>BE950364.1 BE950364                           | 0.007    | 44.1 |                                                        |                                                                                               |                   |         |
| DB911297 | gi 37638356 gb <br>CF742017.1 CF742017                           | 1.00E-24 | 84.5 | lethalk05713 cg8256-<br>isoform c                      |                                                                                               |                   |         |
| DB911307 | BY800436                                                         | 0.003    | 40.1 |                                                        |                                                                                               |                   |         |
| DB911311 | gi 29801445 gb <br>CB734270.1 <br>CB734270                       | 0.009    | 40.1 |                                                        |                                                                                               |                   |         |

|          |                                    |          |      |                                                                    |                                                     |                        |         |
|----------|------------------------------------|----------|------|--------------------------------------------------------------------|-----------------------------------------------------|------------------------|---------|
| DB911319 | gi 46814677 gb CN502053.1 CN502053 | 9.00E-40 | 116  | regulator of g protein signaling                                   |                                                     | RGS                    | 0.64515 |
| DB911322 | BY795816                           | 0.0008   | 42.1 |                                                                    |                                                     |                        |         |
| DB911332 | gi 62883314 gb DN898551.1 DN898551 | 2.00E-25 | 75.3 | n-ethylmaleimide sensitive fusion protein attachment protein alpha | C:GO:0005783,C:GO:0005794,P:GO:0006886,F:GO:0005488 |                        |         |
| DB911351 | gi 54445890 gb CV558860.1 CV558860 | 2.00E-32 | 128  | loc100037132 protein                                               |                                                     | HEAT,Pfam-B_7274       |         |
| DB911354 | gi 62829115 gb DN859466.1 DN859466 | 4.00E-06 | 48.7 | sjhgc04589 protein                                                 |                                                     | Alpha_adaptin_C        |         |
| DB911365 | GS020607                           | 0.004    | 34.2 |                                                                    |                                                     |                        |         |
| DB911367 | GS020638                           | 0.001    | 36.2 |                                                                    |                                                     |                        |         |
| DB911370 | <b>Embryo specific</b> BY799356    | 0.007    | 38.2 |                                                                    |                                                     |                        |         |
| DB911375 | gi 41338165 gb CK617279.1 CK617279 | 2.00E-41 | 169  | isoform cra_a                                                      | C:GO:0016021                                        | DUF872                 | 0.1498  |
| DB911409 | GS004694                           | 0.005    | 34.2 | fvriamide neuropeptide precursor                                   |                                                     |                        |         |
| DB911412 | gi 20361740 gb BQ186189.1 BQ186189 | 0.002    | 46.1 |                                                                    |                                                     |                        |         |
| DB911425 | gi 54446990 gb CV559416.1 CV559416 | 0        | 325  | cell division cycleisoform cra_c                                   |                                                     | Pfam-B_614,TPR_2,TPR_1 |         |
| DB911430 | BY796875                           | 0.0008   | 38.6 | ---NA---                                                           |                                                     |                        |         |
| DB911432 | gi 58031823 gb CX729366.1 CX729366 | 1.00E-13 | 74.4 | synapsin s-syn-long                                                | P:GO:0007269,C:GO:0008021,F:GO:0005524,F:GO:0003824 | Synapsin               | 1.10337 |
| DB911433 | gi 75851599 gb DT881859.1 DT881859 | 3.00E-26 | 118  | ghitm-prov protein                                                 | C:GO:0016021                                        |                        | 0.14023 |
| DB911436 | BY795783                           | 0.01     | 38.2 |                                                                    |                                                     |                        |         |

|          |                                            |          |      |                                                           |                                                             |                                                                        |         |
|----------|--------------------------------------------|----------|------|-----------------------------------------------------------|-------------------------------------------------------------|------------------------------------------------------------------------|---------|
| DB911442 | gi 19050388 gb <br>BM729055.1 <br>BM729055 | 5.00E-10 | 58.3 | n-<br>acetylglucosamine-1-<br>phosphodiester alpha-<br>n- |                                                             |                                                                        |         |
| DB911447 | gi 37601933 gb <br>CF727765.1 CF727765     | 3.00E-32 | 93.2 | protein dpy-19<br>homolog 1 (dpy-19-<br>like protein 1)   |                                                             | Dpy19                                                                  |         |
| DB911490 | gi 22697937 gb <br>BU183953.1 <br>BU183953 | 3.00E-41 | 169  | 26s proteasome non-<br>atpase regulatory<br>subunit 13    | P:GO:0007127,C:GO:<br>0005838,F:GO:0004175                  |                                                                        | 0.20873 |
| DB911493 | BY795421                                   | 0.008    | 38.2 |                                                           |                                                             |                                                                        |         |
| DB911510 | gi 23668550 gb <br>BU735783.1 <br>BU735783 | 0.002    | 46.1 |                                                           |                                                             | Pfam-<br>B_13263,Pfam-<br>B_4326,<br>Pfam-<br>B_13263,Pfam-<br>B_4326  |         |
| DB911512 | GS020659                                   | 0.005    | 30.9 |                                                           |                                                             |                                                                        |         |
| DB911532 | gi 40549684 gb <br>CK396152.1 <br>CK396152 | 0.0006   | 48.1 |                                                           |                                                             |                                                                        |         |
| DB911549 | gi 46816411 gb <br>CN503787.1 <br>CN503787 | 0        | 244  | aspartate<br>aminotransferase                             | F:GO:0030170,F:GO:<br>0004069,P:GO:<br>0006520,P:GO:0009058 | Aminotran_1_2                                                          | 0.86328 |
| DB911573 | BY799426                                   | 0.0006   | 42.1 |                                                           |                                                             |                                                                        |         |
| DB911577 | gi 10653523 gb <br>BE982898.1 BE982898     | 6.00E-39 | 116  | ring finger protein 166                                   | F:GO:0046872,F:GO:<br>0008270,F:GO:<br>0005515,C:GO:0005622 | zf-C3HC4,<br>Pfam-<br>B_10993,<br>Di19,Pfam-<br>B_49, Pfam-<br>B_14559 | 0.2121  |
| DB911585 | gi 54449824 gb <br>CV560809.1 <br>CV560809 | 0        | 372  | actin related protein 2<br>3 complex subunit 2            |                                                             | P34-<br>Arc,PmbA_Tld<br>D                                              | 0.08341 |

|          |                                                           |          |      |                                                  |                                                     |                                         |         |
|----------|-----------------------------------------------------------|----------|------|--------------------------------------------------|-----------------------------------------------------|-----------------------------------------|---------|
| DB911601 | gi 62046427 gb DN691747.1 DN691747                        | 1.00E-08 | 61.1 | kelch domain containing 10                       | F:GO:0003674,P:GO:0008150                           | Kelch_2, Kelch_1, Pfam-B_15464, Kelch_1 |         |
| DB911607 | <b>Embryo specific</b> gi 37635569 gb CF739232.1 CF739232 | 2.00E-06 | 53.3 | ---NA---                                         |                                                     |                                         |         |
| DB911620 | gi 54444728 gb CV558300.1 CV558300                        | 3.00E-15 | 68.9 | fatty acid synthase                              | F:GO:0004312                                        | Thioesterase, AroM                      |         |
| DB911623 | gi 62847148 gb DN877193.1 DN877193                        | 0        | 220  | g protein a subunit o class                      | P:GO:0007186,F:GO:0004871,F:GO:0005525              | G-alpha, G-alpha                        |         |
| DB911626 | gi 23675414 gb BU738380.1 BU738380                        | 2.00E-27 | 123  | protoheme ix                                     |                                                     | UbiA                                    |         |
| DB911632 | gi 37638356 gb CF742017.1 CF742017                        | 2.00E-09 | 59.2 | elegans protein confirmed by transcript evidence |                                                     |                                         |         |
| DB911636 | gi 85193203 gb DW602890.1 DW602890                        | 4.00E-17 | 88.1 | proline dehydrogenase1                           | P:GO:0009064                                        |                                         |         |
| DB911657 | gi 9129209 gb BE258716.1 BE258716                         | 6.00E-33 | 130  | ribosomal protein s24                            | C:GO:0005840,P:GO:0006412,F:GO:0000166              | Ribosomal_S2 4e                         | 2.10946 |
| DB911685 | BY796756                                                  | 5.61E-45 | 163  | peanut cg8705-isoform a                          | C:GO:0031105,P:GO:0007049,F:GO:0005515,F:GO:0005525 | Septin,Pfam-B_6895                      | 0.2253  |
| DB911733 | gi 49675470 gb CO429176.1 CO429176                        | 3.00E-21 | 58.8 | ---NA---                                         |                                                     | DEAD                                    |         |
| DB911734 | gi 57592667 gb CX565638.1 CX565638                        | 5.00E-31 | 134  | alsin isoform 1                                  |                                                     | VPS9                                    |         |
| DB911735 | GS019915                                                  | 0.001    | 36.2 |                                                  |                                                     |                                         |         |
| DB911736 | gi 45305310 gb CK875679.1 CK875679                        | 3.00E-09 | 58.3 | ubiquinol-cytochrome c reductase core protein ii |                                                     | Peptidase_M1 6_C                        |         |

|          |                                    |          |      |                                                     |                                                                  |                  |         |
|----------|------------------------------------|----------|------|-----------------------------------------------------|------------------------------------------------------------------|------------------|---------|
| DB911746 | gi 54449981 gb CV560887.1 CV560887 | 9.00E-30 | 121  | parkinson disease 7 domain containing 1             | C:GO:0005576                                                     |                  | 1.00135 |
| DB911755 | gi 49670748 gb CO424537.1 CO424537 | 0        | 132  | ank2 cg7462-isoform b                               |                                                                  |                  | 2.2658  |
| DB911758 | gi 19024436 gb BM711178.1 BM711178 | 6.00E-12 | 54.2 | acid phosphatase-like 2 isoform 7                   |                                                                  | Acid_phosphat_A  |         |
| DB911789 | gi 23690556 gb BU743218.1 BU743218 | 0.0005   | 44.1 |                                                     |                                                                  |                  |         |
| DB911792 | gi 62881333 gb DN896570.1 DN896570 | 9.00E-32 | 134  | plasma alpha-l-fucosidase                           | P:GO:0005975,F:GO:0043169,F:GO:0004560                           | Alpha_L_fucos    | 1.50302 |
| DB911794 | gi 15712379 gb BI735366.1 BI735366 | 1.00E-11 | 55.1 | organic anion transporter                           |                                                                  | OATP             |         |
| DB911802 | gi 19121051 gb BM804228.1 BM804228 | 0.003    | 41.8 |                                                     |                                                                  |                  |         |
| DB911803 | GS020635                           | 0.001    | 32.7 |                                                     |                                                                  |                  |         |
| DB911817 | gi 18519436 gb BM470394.1 BM470394 | 0        | 125  | chromosome 12 open reading frame 11 isoform 3       |                                                                  | DUF2151, DUF2151 |         |
| DB911823 | gi 49671586 gb CO425292.1 CO425292 | 1.00E-42 | 172  | novel protein (zgc:100937)                          | C:GO:0005576,F:GO:0016787                                        | Pfam-B_10797     |         |
| DB911825 | gi 32273159 gb CD722311.1 CD722311 | 0        | 187  | isoform cra_a                                       | C:GO:0030176,C:GO:0005794,P:GO:0046856,F:GO:0016791,C:GO:0005579 | Syja_N, Syja_N   | 0.5172  |
| DB911830 | gi 22673755 gb BU159845.1 BU159845 | 0        | 222  | novel proteinvertebrate asparaginyl-trna synthetase |                                                                  | tRNA_anti        | 0.28049 |
| DB911835 | GS020564                           | 0.004    | 31.3 |                                                     |                                                                  |                  |         |
| DB911845 | GS008151                           | 0.004    | 30.9 |                                                     |                                                                  |                  |         |

|          |                                    |          |      |                         |                                                                                            |                                  |         |
|----------|------------------------------------|----------|------|-------------------------|--------------------------------------------------------------------------------------------|----------------------------------|---------|
| DB911846 | gi 62848950 gb DN878995.1 DN878995 | 0.0001   | 50.1 |                         |                                                                                            |                                  |         |
| DB911849 | gi 62848099 gb DN878144.1 DN878144 | 4.06E-44 | 177  | glutamine synthetase    | F:GO:0004356,P:GO:0006542                                                                  | Gln-synt_C                       | 1.68752 |
| DB911867 | gi 57595696 gb CX568667.1 CX568667 | 2.00E-38 | 107  | unc-13 cg2999-pc        |                                                                                            | Membr_traf_M<br>HD               |         |
| DB911869 | gi 6515841 gb AW209901.1 AW209901  | 5.00E-31 | 134  | phosphoglycerate kinase | P:GO:0006096,F:GO:0004618                                                                  | PGK                              | 0.88533 |
| DB911882 | GS014134                           | 0.005    | 34.2 | isoform d               |                                                                                            | PNP_UDP_1                        | 1.0885  |
| DB911896 | gi 18500742 gb BM451702.1 BM451702 | 1.00E-34 | 147  | t-complex 11            |                                                                                            | Baculo_p24,<br>Tcp11             | 0.89087 |
| DB911898 | gi 85169082 gb DW595077.1 DW595077 | 2.00E-32 | 70.8 | nervous system adducin  | F:GO:0046872                                                                               | Aldolase_II                      | 0.6202  |
| DB911907 | GS013851                           | 0.004    | 34.2 |                         |                                                                                            |                                  |         |
| DB911910 | BY797251                           | 0.002    | 31.3 |                         |                                                                                            |                                  |         |
| DB911944 | gi 62851116 gb DN881161.1 DN881161 | 0.004    | 42.1 |                         |                                                                                            |                                  |         |
| DB911946 | gi 21761521 gb BQ637062.1 BQ637062 | 1.00E-07 | 58   | splicing factor u2af35  |                                                                                            |                                  |         |
| DB911981 | gi 58035234 gb CX732760.1 CX732760 | 4.00E-07 | 55.1 | cacna1d protein         | C:GO:0043234,C:GO:0009925,C:GO:0016021,P:GO:0050910,F:GO:0005245,P:GO:0050885,P:GO:0030001 | Ion_trans                        | 4.0402  |
| DB911987 | GS020461                           | 0.005    | 30.9 |                         |                                                                                            |                                  |         |
| DB912007 | gi 85209205 gb DW608782.1 DW608782 | 3.00E-43 | 152  | dynamin 1-like          | C:GO:0005579,C:GO:0005737,F:GO:0003924,F:GO:0005525                                        | Dynamin_M,<br>NUC202,DUF1<br>308 |         |

|          |                                            |          |      |                                                                                                              |                                                                                                                                 |                                     |        |
|----------|--------------------------------------------|----------|------|--------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|-------------------------------------|--------|
| DB912010 | BY795488                                   | 0.003    | 36.2 |                                                                                                              |                                                                                                                                 |                                     |        |
| DB912015 | gi 85198668 gb <br>DW604674.1 <br>DW604674 | 0        | 279  | nadh<br>dehydrogenasefe-s<br>protein 1 isoform 1                                                             |                                                                                                                                 | Molybdopterin                       | 0.063  |
| DB912017 | gi 62040333 gb <br>DN688742.1 <br>DN688742 | 0        | 209  | eukaryotic initiation<br>factor 4a                                                                           | C:GO:0005737,F:GO:<br>0008026,P:GO:<br>0043581,F:GO:<br>0003723,F:GO:<br>0005524,F:GO:<br>0003743,P:GO:0006412                  | DEAD                                | 1.7499 |
| DB912030 | gi 62882476 gb <br>DN897713.1 <br>DN897713 | 0.003    | 42.8 | ring finger and fyve-<br>like domain containing<br>1                                                         |                                                                                                                                 | FYVE                                |        |
| DB912036 | gi 75850091 gb <br>DT880351.1 DT880351     | 0        | 164  | zinc finger protein 403<br>isoform 2                                                                         |                                                                                                                                 | Pfam-B_14984                        | 1.11   |
| DB912038 | gi 62850341 gb <br>DN880386.1 <br>DN880386 | 0.003    | 38.2 |                                                                                                              |                                                                                                                                 |                                     |        |
| DB912040 | gi 18500266 gb <br>BM451226.1 <br>BM451226 | 3.00E-34 | 119  | membrane-bound<br>transcription factorsite<br>2                                                              | P:GO:0006629,F:GO:<br>0008233,P:GO:0001501                                                                                      | Peptidase_M5<br>0                   |        |
| DB912055 | gi 15682687 gb <br>BI706992.1 BI706992     | 5.00E-20 | 98.2 | rpa43_danreame:<br>full=dna-directed rna<br>polymerase i subunit<br>rpa43ame: full=twist<br>neighbor protein | P:GO:0006355,P:GO:<br>0006353,F:GO:<br>0003899,P:GO:<br>0031564,C:GO:0005634                                                    | RNA_pol_Rpb<br>7_N, Pfam-<br>B_7275 | 0.8213 |
| DB912058 | gi 46465840 gb <br>CN460114.1 <br>CN460114 | 7.00E-07 | 51   | cationic amino acid<br>transporter                                                                           |                                                                                                                                 |                                     |        |
| DB912064 | gi 85200105 gb <br>DW605137.1 <br>DW605137 | 0.009    | 44.1 | carboxypeptidase a2                                                                                          | F:GO:0046872,F:GO:<br>0004182,P:GO:<br>0006508,F:GO:<br>0004180,F:GO:<br>0008237,F:GO:<br>0008233,F:GO:<br>0008270,C:GO:0005576 | Pfam-B_5672,<br>Propep_M14          |        |

|          |                    |                                    |          |      |                                                                |                                                                                            |              |         |
|----------|--------------------|------------------------------------|----------|------|----------------------------------------------------------------|--------------------------------------------------------------------------------------------|--------------|---------|
| DB912071 |                    | gi 77506737 gb DV216687.1 DV216687 | 5.00E-15 | 78.4 | voltage-dependent anion channel 2                              | P:GO:0006820,F:GO:0008308,C:GO:0016021,C:GO:0005741                                        | Porin_3      |         |
| DB912078 |                    | GS020765                           | 0.0005   | 34.1 |                                                                |                                                                                            |              |         |
| DB912083 |                    | BY795194                           | 3.00E-24 | 103  | septin 5                                                       | C:GO:0031105,P:GO:0007049,F:GO:0005515,F:GO:0005525                                        | Septin       |         |
| DB912108 |                    | gi 46867400 gb CN539244.1 CN539244 | 4.00E-37 | 107  | cg31064-isoform a                                              |                                                                                            |              |         |
| DB912109 | Positive selection | gi 62890243 gb DN905480.1 DN905480 | 0        | 253  | adp-ribosylation factor isoform cra_a                          | F:GO:0005525,C:GO:0005794,F:GO:0005515,F:GO:0008565,P:GO:0016192,P:GO:0006886,P:GO:0007264 | Arf          | 6.51203 |
| DB912128 |                    | gi 18983922 gb BM674024.1 BM674024 | 0.008    | 44.1 |                                                                |                                                                                            |              |         |
| DB912132 |                    | gi 18987621 gb BM677725.1 BM677725 | 0.0007   | 40.5 | ralbp1 associated eps domain containing 1                      | F:GO:0005509                                                                               |              | 1.43775 |
| DB912165 |                    | gi 11661619 gb BF551895.1 BF551895 | 6.00E-42 | 171  | spermatogenesis associated 5 isoform 1                         |                                                                                            | AAA          |         |
| DB912188 |                    | gi 46466837 gb CN461111.1 CN461111 | 0        | 184  | taf1 rna polymerase tata box binding protein-associated factor | F:GO:0003677,F:GO:0016301,C:GO:0005669,P:GO:0007049,F:GO:0005524,P:GO:0006352,P:GO:0006355 | Pfam-B_17638 | 1.2438  |
| DB912210 |                    | GS008140                           | 0.003    | 34.2 |                                                                |                                                                                            |              |         |
| DB912235 |                    | GS020592                           | 0.004    | 34.2 |                                                                |                                                                                            |              |         |
| DB912260 |                    | gi 32465039 gb CD806213.1 CD806213 | 6.00E-06 | 37.7 |                                                                |                                                                                            |              |         |

|          |                                            |          |      |                                                                                 |                                                             |                                             |         |
|----------|--------------------------------------------|----------|------|---------------------------------------------------------------------------------|-------------------------------------------------------------|---------------------------------------------|---------|
| DB912261 | gi 85195632 gb <br>DW603601.1 <br>DW603601 | 0.0005   | 41.8 |                                                                                 |                                                             |                                             |         |
| DB912271 | GS004800                                   | 0.005    | 34.2 |                                                                                 |                                                             |                                             |         |
| DB912272 | <b>Embryo specific</b> GS014137            | 0.003    | 31.3 |                                                                                 |                                                             |                                             |         |
| DB912276 | gi 54444960 gb <br>CV558410.1 <br>CV558410 | 0        | 304  | tfg beta signaling<br>pathway factor                                            |                                                             | MH2                                         | 0.92965 |
| DB912284 | gi 18511337 gb <br>BM462297.1 <br>BM462297 | 2.00E-39 | 162  | peptidase<br>(mitochondrial<br>processing) alpha                                | F:GO:0004222,P:GO:<br>0006508,F:GO:0008270                  | Peptidase_M1<br>6_C,<br>Peptidase_M1<br>6   | 1.05023 |
| DB912290 | gi 62829138 gb <br>DN859489.1 <br>DN859489 | 0        | 322  | hippocampus<br>abundant gene<br>transcript 1                                    | P:GO:0015904,C:GO:<br>0016021,P:GO:<br>0046677,F:GO:0015520 | MFS_1                                       |         |
| DB912291 | BY799598                                   | 0.003    | 36.2 |                                                                                 |                                                             |                                             |         |
| DB912292 | BY798825                                   | 0.002    | 40.1 |                                                                                 |                                                             |                                             |         |
| DB912296 | gi 13102735 gb <br>BG305208.1 <br>BG305208 | 0        | 194  | histone h4                                                                      |                                                             | Histone                                     |         |
| DB912302 | gi 14063722 gb <br>BG753069.1 <br>BG753069 | 0        | 156  | novel<br>proteinvertebrate imp<br>(inosine<br>monophosphate)<br>dehydrogenase 1 | F:GO:0003938,P:GO:<br>0006177                               | IMPDH,<br>IMPDH                             |         |
| DB912310 | gi 8486815 gb <br>BE095884.1 BE095884      | 0.002    | 42.8 |                                                                                 |                                                             | Pfam-B_4326,<br>Pfam-B_4326,<br>Pfam-B_4326 |         |
| DB912312 | gi 48584931 gb <br>CO044391.1 <br>CO044391 | 0.002    | 46.1 |                                                                                 |                                                             |                                             |         |
| DB912317 | gi 62026626 gb <br>DN681905.1 <br>DN681905 | 3.00E-41 | 166  | guanine nucleotide-<br>binding protein rho                                      | C:GO:0005622,C:GO:<br>0005886,F:GO:<br>0005525,P:GO:0007264 | Ras                                         | 0.45133 |
| DB912318 | gi 75837350 gb <br>DT867610.1 DT867610     | 0        | 334  | thioredoxin<br>peroxidase                                                       |                                                             | 1-<br>cysPrx_C,Ahp<br>C-TSA                 | 0.30859 |

|          |                                    |          |      |                                                                                           |                                                                  |                                              |         |
|----------|------------------------------------|----------|------|-------------------------------------------------------------------------------------------|------------------------------------------------------------------|----------------------------------------------|---------|
| DB912336 | gi 22675937 gb BU162027.1 BU162027 | 0        | 284  | dihydrolipoamide dehydrogenase                                                            | P:GO:0045454,C:GO:0005759,P:GO:0006118,F:GO:0050660,F:GO:0004148 | Pyr_redox_2,<br>Pyr_redox                    | 0.73524 |
| DB912343 | gi 62886290 gb DN901527.1 DN901527 | 0.001    | 34.1 |                                                                                           |                                                                  |                                              |         |
| DB912355 | BY799220                           | 0.01     | 38.2 |                                                                                           |                                                                  |                                              |         |
| DB912367 | gi 49675765 gb CO429471.1 CO429471 | 2.00E-26 | 119  | 17beta-hydroxysteroid dehydrogenase                                                       | F:GO:0042802                                                     | MaoC_dehydratas                              |         |
| DB912384 | GS020656                           | 0.007    | 30.4 |                                                                                           |                                                                  | Pfam-B_13263,<br>Pfam-B_4326,<br>Pfam-B_4326 |         |
| DB912394 | gi 62882970 gb DN898207.1 DN898207 | 0        | 327  | eukaryotic translation initiation factor 5b (eif-5b) (translation initiation factor if-2) |                                                                  | IF-2                                         | 2.34655 |
| DB912397 | gi 10201276 gb BE780078.1 BE780078 | 0.0007   | 40.9 |                                                                                           |                                                                  |                                              |         |
| DB912402 | gi 9889423 gb BE618485.1 BE618485  | 0        | 161  | ---NA---                                                                                  |                                                                  | Pfam-B_2320                                  |         |
| DB912418 | gi 37598576 gb CF724408.1 CF724408 | 1.00E-12 | 71.2 | atp-dependent bile acid permease                                                          |                                                                  | ABC_membrane                                 |         |
| DB912433 | BY796799                           | 1.00E-05 | 48.1 |                                                                                           |                                                                  |                                              |         |
| DB912448 | gi 18979105 gb BM669208.1 BM669208 | 8.00E-29 | 127  | macro domain containing 2                                                                 |                                                                  | Macro                                        | 0.93433 |
| DB912452 | BY798426                           | 0.008    | 38.2 |                                                                                           |                                                                  |                                              |         |
| DB912477 | gi 62842873 gb DN872932.1 DN872932 | 0        | 303  | traf2 and nck interactingtnik                                                             |                                                                  | CNH                                          |         |
| DB912483 | GS020551                           | 0.009    | 29.9 |                                                                                           |                                                                  |                                              |         |
| DB912526 | BY796100                           | 0.009    | 38.2 |                                                                                           |                                                                  |                                              |         |

|          |                                    |          |      |                                             |                                                                               |                                                                                                                                              |         |
|----------|------------------------------------|----------|------|---------------------------------------------|-------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|---------|
| DB912527 | gi 49679435 gb CO433141.1 CO433141 | 6.00E-33 | 141  | kiaa1636 protein                            |                                                                               | Ank, Ank, Ank, Ank, Ank                                                                                                                      | 0.90513 |
| DB912528 | gi 37633763 gb CF737427.1 CF737427 | 1.00E-07 | 57.4 | ---NA---                                    |                                                                               | Pfam-B_10577                                                                                                                                 |         |
| DB912532 | <b>Embryo specific</b> GS008127    | 2.00E-05 | 34.1 |                                             |                                                                               |                                                                                                                                              |         |
| DB912537 | gi 10203700 gb BE782502.1 BE782502 | 3.00E-23 | 109  | synovial apoptosis inhibitorsynoviolin      | F:GO:0016874,P:GO:0006829,C:GO:0005579,C:GO:0005786,P:GO:0009968,F:GO:0008270 | Pfam-B_1065, Pfam-B_133, Pfam-B_5058, Pfam-B_11973, Pfam-B_16964, Pfam-B_17208, Pfam-B_10669, Pfam-B_39, Pfam-B_14559, zf-C3HC4, Pfam-B_4755 |         |
| DB912542 | BY795001                           | 0.005    | 30.9 |                                             |                                                                               |                                                                                                                                              |         |
| DB912546 | BY795304                           | 0.002    | 37.7 |                                             |                                                                               |                                                                                                                                              |         |
| DB912549 | gi 19046685 gb BM725354.1 BM725354 | 0.002    | 46.1 |                                             |                                                                               |                                                                                                                                              |         |
| DB912575 | gi 57591445 gb CX564416.1 CX564416 | 5.00E-11 | 68.4 | sjchgc04791 protein                         |                                                                               |                                                                                                                                              |         |
| DB912582 | gi 62045919 gb DN691488.1 DN691488 | 2.80E-45 | 182  | subfamilymember 2                           |                                                                               | DnaJ_C                                                                                                                                       | 0.78315 |
| DB912590 | gi 19047029 gb BM725696.1 BM725696 | 3.00E-10 | 65.7 | atp-binding sub-family b (mdr tap) member 6 | F:GO:0042626,P:GO:0006810,F:GO:0005524,C:GO:0016021,C:GO:0005741              |                                                                                                                                              |         |
| DB912621 | BY799703                           | 0.002    | 37.7 |                                             |                                                                               |                                                                                                                                              |         |

|          |                                            |          |      |                                                                |                                                                                                                                                  |                                                                            |         |
|----------|--------------------------------------------|----------|------|----------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------|---------|
| DB912631 | gi 62887310 gb <br>DN902547.1 <br>DN902547 | 0.009    | 44.1 |                                                                |                                                                                                                                                  |                                                                            |         |
| DB912649 | gi 21762007 gb <br>BQ637548.1 <br>BQ637548 | 5.00E-07 | 54.9 | ran gtpase-activating<br>protein                               | F:GO:0005515                                                                                                                                     | RanGAP1_C,<br>Pfam-<br>B_12569,Nop1<br>4, Pfam-<br>B_2333, Pfam-<br>B_5586 |         |
| DB912660 | GS004800                                   | 0.004    | 34.2 |                                                                |                                                                                                                                                  |                                                                            |         |
| DB912664 | gi 21765658 gb <br>BQ641486.1 <br>BQ641486 | 2.00E-39 | 93.7 | annexin a7                                                     |                                                                                                                                                  | Annexin,<br>Annexin                                                        |         |
| DB912668 | GS004800                                   | 0.003    | 34.2 |                                                                |                                                                                                                                                  |                                                                            |         |
| DB912676 | gi 37637992 gb <br>CF741653.1 CF741653     | 0.0003   | 45.7 | thioester-containing<br>protein                                | F:GO:0004866,F:GO:<br>0005515,C:GO:0005576                                                                                                       | A2M_comp                                                                   |         |
| DB912681 | BY795985                                   | 0.009    | 35.9 |                                                                |                                                                                                                                                  |                                                                            |         |
| DB912686 | GS013829                                   | 0.004    | 34.2 |                                                                |                                                                                                                                                  |                                                                            |         |
| DB912687 | BY798965                                   | 3.00E-17 | 71.8 | fascin homolog 1-<br>actin-bundling protein                    | F:GO:0030674                                                                                                                                     | DUF3656,<br>Fascin,Fascin                                                  |         |
| DB912700 | gi 19028434 gb <br>BM715176.1 <br>BM715176 | 2.00E-13 | 76.2 | -like subfamily b<br>member 6                                  | F:GO:0031072                                                                                                                                     |                                                                            |         |
| DB912701 | gi 22345651 gb <br>BQ930620.1 <br>BQ930620 | 1.00E-16 | 57.9 | classmember 2                                                  |                                                                                                                                                  | Glyco_hydro_3<br>8C                                                        | 0.8353  |
| DB912707 | gi 24722033 gb <br>CA390743.1 <br>CA390743 | 0        | 325  | bone marrow stromal<br>cell-derived ubiquitin-<br>like protein | P:GO:0006512                                                                                                                                     | ubiquitin                                                                  |         |
| DB912714 | gi 85205120 gb <br>DW607189.1 <br>DW607189 | 0        | 377  | nadh<br>dehydrogenaseflavopr<br>otein51kda                     | P:GO:0006120,F:GO:<br>0051287,F:GO:<br>0008137,F:GO:<br>0005506,F:GO:<br>0010181,P:GO:<br>0006118,P:GO:<br>0006810,F:GO:<br>0051539,C:GO:0005746 | Complex1_51<br>K, SLBB                                                     | 0.09373 |

|          |                                    |          |      |                                            |                                                                                                         |                               |         |
|----------|------------------------------------|----------|------|--------------------------------------------|---------------------------------------------------------------------------------------------------------|-------------------------------|---------|
| DB912738 | gi 24543901 gb CA325803.1 CA325803 | 6.00E-16 | 85.4 | mitochondrial carrier homologisoform a     | C:GO:0005739                                                                                            |                               | 0.40836 |
| DB912745 | gi 75835694 gb DT865954.1 DT865954 | 7.00E-22 | 54.3 | survival motor neuron domain containing 1  | F:GO:0003676,F:GO:0003723,P:GO:0006397,P:GO:0000245,C:GO:0005634                                        | Pfam-B_7939, Pfam-B_2444, SMN | 0.49777 |
| DB912762 | gi 62044561 gb DN690812.1 DN690812 | 2.00E-26 | 113  | ubiquinone biosynthesis monooxygenase coq6 | P:GO:0006725,F:GO:0016491,C:GO:0005615,P:GO:0006744,P:GO:0008152,F:GO:0016709,C:GO:0005575,F:GO:0050660 |                               | 1.48683 |
| DB912768 | gi 62871874 gb DN887111.1 DN887111 | 7.00E-13 | 74.8 | chloride channelpartial                    |                                                                                                         | CBS                           |         |
| DB912772 | gi 32466934 gb CD808108.1 CD808108 | 1.40E-45 | 183  | kiaa0020 protein                           |                                                                                                         |                               |         |
| DB912773 | gi 62843107 gb DN873166.1 DN873166 | 7.00E-16 | 84.9 | nuclear lamin I1                           |                                                                                                         | FYVE, IBR                     |         |
| DB912776 | BY795642                           | 2.00E-06 | 44.6 |                                            |                                                                                                         | bZIP_2                        |         |
| DB912793 | gi 77502459 gb DV214503.1 DV214503 | 2.00E-06 | 52.8 | zinc finger                                |                                                                                                         | Pfam-B_1393                   | 0.7937  |
| DB912802 | gi 58178950 gb CX768597.1 CX768597 | 4.00E-18 | 91.8 | pyruvate dehydrogenasecomponentpartial     |                                                                                                         | 2-oxoacid_dh                  | 0.29127 |
| DB912820 | GS020723                           | 0.002    | 32.2 |                                            |                                                                                                         |                               |         |
| DB912827 | gi 37632506 gb CF736170.1 CF736170 | 0        | 307  | eukaryotic peptide chain release factor    |                                                                                                         | eRF1_3                        |         |
| DB912831 | gi 62024788 gb DN680985.1 DN680985 | 2.00E-18 | 52.8 | lethalk09913 cg3082-pc                     |                                                                                                         | DUF829                        |         |

|          |                                            |          |      |                                                                                                                      |                                                                                                         |               |         |
|----------|--------------------------------------------|----------|------|----------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|---------------|---------|
| DB912832 | gi 32175105 gb <br>CD673374.1 <br>CD673374 | 0        | 244  | fig4 homolog                                                                                                         |                                                                                                         |               | 0.96493 |
| DB912835 | gi 22337291 gb <br>BQ922260.1 <br>BQ922260 | 0        | 106  | mannose-6-phosphate isomerase                                                                                        |                                                                                                         | PMI_type1     | 0.73762 |
| DB912837 | gi 62839120 gb <br>DN869179.1 <br>DN869179 | 0        | 371  | adaptor-related protein complexmu 1a                                                                                 | P:GO:0006461,F:GO:0008289,C:GO:0005579,F:GO:0008565,P:GO:0016192,P:GO:0006886,C:GO:0030131,C:GO:0030132 | Adap_comp_sub | 0.3036  |
| DB912843 | gi 62033477 gb <br>DN685282.1 <br>DN685282 | 2.00E-27 | 122  | 26s proteasome non-atpase regulatory subunit 3                                                                       |                                                                                                         |               | 0.90891 |
| DB912845 | gi 19013482 gb <br>BM700224.1 <br>BM700224 | 6.00E-24 | 107  | c-terminal srcisoform g                                                                                              | F:GO:0035014,P:GO:0002119,P:GO:0006468,C:GO:0005942,F:GO:0005515,F:GO:0005524,F:GO:0004713,F:GO:0004674 | Pkinase_Tyr   |         |
| DB912849 | gi 4563757 gb <br>AI579381.1 AI579381      | 0.009    | 44.1 |                                                                                                                      |                                                                                                         |               |         |
| DB912863 | gi 22811051 gb <br>BU504818.1 <br>BU504818 | 9.00E-21 | 100  | tfp11_boviname: full=tuftelin-interacting protein 11ame: full=septin and tuftelin-interacting protein 1 short=stip-1 | F:GO:0003676,C:GO:0005622                                                                               | Pfam-B_6436   |         |
| DB912872 | GS014037                                   | 0.001    | 36.2 |                                                                                                                      |                                                                                                         |               |         |
| DB912880 | gi 12354902 gb <br>BF937582.1 BF937582     | 3.00E-30 | 88.9 | fasciculation and elongation protein zeta 1 (zygin i) isoform 3                                                      |                                                                                                         | FEZ           |         |

|          |                                                           |          |      |                                                                                                                                                                                                                                                                |                                                                  |                             |        |
|----------|-----------------------------------------------------------|----------|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|-----------------------------|--------|
| DB912893 | <b>Embryo specific</b> gi 62836036 gb DN866387.1 DN866387 | 5.00E-15 | 82   | kiaa1738 protein                                                                                                                                                                                                                                               | F:GO:0003674,P:GO:0008150                                        | DUF2404,<br>SOG2            |        |
| DB912907 | gi 19011979 gb BM698721.1 BM698721                        | 1.40E-45 | 112  | flj39378 protein isoform 2                                                                                                                                                                                                                                     |                                                                  | RILP                        |        |
| DB912914 | gi 119789254 gb EH281813.1 EH281813                       | 0.002    | 39.8 |                                                                                                                                                                                                                                                                |                                                                  |                             |        |
| DB912940 | GS020580                                                  | 0.0008   | 36.2 |                                                                                                                                                                                                                                                                |                                                                  |                             |        |
| DB912945 | gi 54480453 gb CV575153.1 CV575153                        | 4.00E-05 | 52   |                                                                                                                                                                                                                                                                |                                                                  |                             |        |
| DB912963 | gi 12040252 gb BF724343.1 BF724343                        | 7.00E-39 | 134  | kuzbanian cg7147-isoform a                                                                                                                                                                                                                                     |                                                                  | Pfam-B_14539                |        |
| DB912969 | gi 37600899 gb CF726731.1 CF726731                        | 0.003    | 43.2 | ---NA---                                                                                                                                                                                                                                                       |                                                                  |                             |        |
| DB912977 | gi 15716370 gb BI739357.1 BI739357                        | 0.009    | 44.1 |                                                                                                                                                                                                                                                                |                                                                  |                             |        |
| DB912982 | gi 85171716 gb DW596007.1 DW596007                        | 1.00E-25 | 81.4 | odo2_fugruame: full=dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenasemitochondrial: full=dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex short=e2ame: full=e2k flags: precursor | C:GO:0045252,F:GO:0004149,P:GO:0006099,F:GO:0031405,C:GO:0005739 | 2-oxoacid_dh, Biotin_lipoyl | 1.4637 |
| DB912985 | gi 62842042 gb DN872101.1 DN872101                        | 0.009    | 44.1 |                                                                                                                                                                                                                                                                |                                                                  |                             |        |

|          |                 |                                            |          |                                                           |                                                             |                                                  |         |
|----------|-----------------|--------------------------------------------|----------|-----------------------------------------------------------|-------------------------------------------------------------|--------------------------------------------------|---------|
| DB912988 |                 | gi 9388719 gb <br>BB471530.1 <br>BB471530  | 0.01     | 44.1                                                      |                                                             |                                                  |         |
| DB912994 |                 | gi 85193203 gb <br>DW602890.1 <br>DW602890 | 0        | 176 proline<br>dehydrogenase1                             | F:GO:0004657,P:GO:<br>0006537,P:GO:0006562                  |                                                  |         |
| DB913003 |                 | gi 46563334 gb <br>CN481830.1 <br>CN481830 | 0.002    | 46.1                                                      |                                                             |                                                  |         |
| DB913024 |                 | GS013784                                   | 0.003    | 31.3                                                      |                                                             |                                                  |         |
| DB913029 |                 | BY797909                                   | 0.003    | 40.1                                                      |                                                             |                                                  |         |
| DB913033 |                 | GS014023                                   | 0.001    | 36.2                                                      |                                                             |                                                  |         |
| DB913048 |                 | gi 62024575 gb <br>DN680892.1 <br>DN680892 | 0        | 141 yip1 domainmember 1<br>isoform 6                      |                                                             | Pfam-B_3433,<br>Yip1                             |         |
| DB913064 |                 | BY799008                                   | 0.004    | 36.2                                                      |                                                             |                                                  |         |
| DB913066 |                 | gi 62828989 gb <br>DN859340.1 <br>DN859340 | 3.00E-38 | 123 ribosomal protein s30                                 | P:GO:0044267,C:GO:<br>0005622                               | ubiquitin,Pfam<br>-<br>B_13282,Ribo<br>somal_S30 | 0.17947 |
| DB913089 | GO annotation   | gi 6515598 gb <br>AW209658.1 <br>AW209658  | 0        | 202 ets-related isoform 4                                 |                                                             | Ets, Pfam-<br>B_2481                             | 0.7548  |
| DB913126 |                 | gi 49672968 gb <br>CO426674.1 <br>CO426674 | 8.00E-26 | 116 adaptin ear-binding<br>clathrin-associated<br>protein |                                                             | DUF1681                                          | 0.3036  |
| DB913128 |                 | gi 41339610 gb <br>CK618724.1 <br>CK618724 | 0        | 385 heat shock protein 90                                 | P:GO:0006457,F:GO:<br>0051082,F:GO:<br>0005524,P:GO:0006950 | HSP90                                            | 0.23848 |
| DB913131 |                 | gi 41345269 gb <br>CK624383.1 <br>CK624383 | 1.00E-11 | 70.7 spermatogenesis<br>e-rich 2                          |                                                             | DUF1387                                          |         |
| DB913138 | Embryo specific | GS020726                                   | 0.005    | 30.9 ---NA---                                             |                                                             |                                                  |         |

|          |                                                                                          |          |      |                                                |                                                     |                                                     |         |
|----------|------------------------------------------------------------------------------------------|----------|------|------------------------------------------------|-----------------------------------------------------|-----------------------------------------------------|---------|
| DB913145 | gi 24723938 gb CA391768.1 CA391768                                                       | 8.00E-06 | 43.7 |                                                |                                                     | Pfam-B_4326, Pfam-B_13263, Pfam-B_4326, Pfam-B_4326 |         |
| DB913153 | GS004679                                                                                 | 0.005    | 34.2 |                                                |                                                     |                                                     |         |
| DB913156 | gi 62040139 gb DN688645.1 DN688645                                                       | 1.00E-21 | 88.1 | mgc68804 protein                               |                                                     | Pfam-B_14351                                        | 1.1158  |
| DB913161 | gi 10204338 gb BE783140.1 BE783140                                                       | 7.00E-15 | 80.9 | son dna-binding protein                        |                                                     | Pfam-B_2818                                         |         |
| DB913165 | gi 40321032 gb CK355100.1 CK355100                                                       | 0        | 247  | proteasome subunit n3                          |                                                     | Proteasome                                          | 1.8665  |
| DB913168 | gi 57592920 gb CX565891.1 CX565891                                                       | 0        | 250  | adp-ribosylation factor interacting protein 2b | F:GO:0003674,C:GO:0005575                           | Arfaptin                                            |         |
| DB913174 | gi 9122814 gb BE252671.1 BE252671                                                        | 2.00E-28 | 108  | hcls1 binding protein 3                        |                                                     | PX                                                  | 1.9744  |
| DB913226 | <b>Embryo specific expression, Positive selection</b> gi 62846546 gb DN876605.1 DN876605 | 0        | 286  | g alpha i subunit                              | P:GO:0007186,F:GO:0004871,F:GO:0005525              | G-alpha                                             | 3.07597 |
| DB913236 | gi 13063968 gb BG298876.1 BG298876                                                       | 0.0005   | 48.1 |                                                |                                                     |                                                     |         |
| DB913237 | gi 15709338 gb BI732325.1 BI732325                                                       | 0        | 188  | taurine transporter                            | C:GO:0005887,F:GO:0005328,P:GO:0006836              | SNF                                                 | 1.32602 |
| DB913238 | GS020774                                                                                 | 0.003    | 29   |                                                |                                                     |                                                     |         |
| DB913240 | GS008202                                                                                 | 0.008    | 30.2 |                                                |                                                     |                                                     |         |
| DB913241 | BY799689                                                                                 | 0.002    | 40.1 |                                                |                                                     |                                                     |         |
| DB913244 | <b>Positive selection</b> gi 62832237 gb DN862588.1 DN862588                             | 2.00E-36 | 150  | 25-kda subunit rna polymerase                  | P:GO:0006350,F:GO:0003899,C:GO:0005634,F:GO:0003677 | RNA_pol_Rpb 5_N                                     | 5.44031 |
| DB913265 | gi 18801967 gb BM558864.1 BM558864                                                       | 3.00E-11 | 69.3 | hspb (heat shock 27kda) associated protein 1   |                                                     |                                                     |         |

|          |                                                                   |          |      |                                                |                                                                                                                |                            |         |
|----------|-------------------------------------------------------------------|----------|------|------------------------------------------------|----------------------------------------------------------------------------------------------------------------|----------------------------|---------|
| DB913273 | BY795432                                                          | 0.001    | 35.4 |                                                |                                                                                                                |                            |         |
| DB913319 | gi 58033543 gb <br>CX731069.1 <br>CX731069                        | 3.00E-41 | 104  | light polypeptide                              | C:GO:0030132,F:GO:<br>0005509                                                                                  | DUF1092,<br>Clathrin_lg_ch | 1.20868 |
| DB913324 | gi 37600957 gb <br>CF726789.1 CF726789                            | 0.006    | 35.4 |                                                |                                                                                                                |                            |         |
| DB913332 | gi 46825971 gb <br>CN513347.1 <br>CN513347                        | 0        | 227  | isoform a                                      | C:GO:0035003,C:GO:<br>0045211,F:GO:0005515                                                                     | Pfam-<br>B_4599,PDZ        | 0.02862 |
| DB913333 | gi 62888698 gb <br>DN903935.1 <br>DN903935                        | 0        | 194  | cytochrome c                                   | F:GO:0009055,F:GO:<br>0005506,C:GO:<br>0005759,F:GO:<br>0020037,P:GO:<br>0006118,P:GO:<br>0006810,C:GO:0005746 | Cytochrom_C                | 0.55094 |
| DB913334 | gi 85570838 gb <br>DW711454.1 <br>DW711454                        | 2.00E-08 | 51.3 | cleavage and<br>polyadenylation<br>specificity |                                                                                                                |                            |         |
| DB913335 | gi 18514281 gb <br>BM465239.1 <br>BM465239                        | 0.003    | 46.1 |                                                |                                                                                                                |                            |         |
| DB913340 | <b>Embryo specific</b> gi 22667862 gb <br>BU154330.1 <br>BU154330 | 0        | 184  | inositol trisphosphate<br>receptor             | F:GO:0005262,P:GO:<br>0006811,C:GO:0016020                                                                     |                            | 0.86123 |
| DB913348 | BY800050                                                          | 0.003    | 35   | ---NA---                                       |                                                                                                                |                            |         |
| DB913369 | gi 29772761 gb <br>CB715613.1 <br>CB715613                        | 0.0007   | 48.1 |                                                |                                                                                                                |                            |         |
| DB913375 | BY798681                                                          | 0.003    | 40.1 |                                                |                                                                                                                |                            |         |
| DB913395 | GS014081                                                          | 0.006    | 34.2 |                                                |                                                                                                                |                            |         |
| DB913418 | gi 3396572 gb <br>AI070321.1 AI070321                             | 0.002    | 46.1 |                                                |                                                                                                                |                            |         |
| DB913420 | gi 85179361 gb <br>DW598441.1 <br>DW598441                        | 0.0003   | 42.3 | prohormone<br>convertase 2                     | F:GO:0004289,P:GO:<br>0006508,F:GO:<br>0004252,F:GO:<br>0016787,F:GO:0008233                                   |                            |         |

|          |                                            |          |      |                                        |                                                             |                                        |         |
|----------|--------------------------------------------|----------|------|----------------------------------------|-------------------------------------------------------------|----------------------------------------|---------|
| DB913426 | gi 62046021 gb <br>DN691540.1 <br>DN691540 | 0        | 402  | retinal dehydrogenase                  | F:GO:0016491,P:GO:<br>0008152                               | Aldedh                                 | 1.1106  |
| DB913439 | BY795176                                   | 0        | 238  | von hippel-lindau<br>binding protein 1 | P:GO:0006457,C:GO:<br>0016272,C:GO:<br>0005634,F:GO:0005515 | Prefoldin                              | 0.89993 |
| DB913440 | gi 40549504 gb <br>CK395972.1 <br>CK395972 | 5.00E-05 | 48.7 | ---NA---                               |                                                             | Ldl_recept_a                           |         |
| DB913441 | gi 32176228 gb <br>CD674497.1 <br>CD674497 | 0.0002   | 50.1 |                                        |                                                             |                                        |         |
| DB913442 | gi 62037138 gb <br>DN687131.1 <br>DN687131 | 0        | 256  | actin-related protein 2<br>3           |                                                             | WD40, WD40                             |         |
| DB913449 | gi 9385047 gb <br>BB467858.1 <br>BB467858  | 0.009    | 44.1 |                                        |                                                             |                                        |         |
| DB913450 | gi 62885542 gb <br>DN900779.1 <br>DN900779 | 0.007    | 41.8 | ---NA---                               |                                                             |                                        |         |
| DB913487 | GS004800                                   | 0.004    | 34.2 |                                        |                                                             |                                        |         |
| DB913490 | GS013979                                   | 0.004    | 25.4 |                                        |                                                             |                                        |         |
| DB913493 | gi 19390371 gb <br>BM931198.1 <br>BM931198 | 2.00E-30 | 133  | small<br>subunitprocessomeho<br>molog  | F:GO:0003674,P:GO:<br>0008150                               | Fcf1                                   |         |
| DB913494 | gi 18510675 gb <br>BM461635.1 <br>BM461635 | 0        | 131  | gamma-glutamyl<br>carboxylase          | C:GO:0016020                                                | VKG_Carbox,<br>Phytoreo_P8,<br>Cupin_2 |         |
| DB913503 | gi 62040707 gb <br>DN688924.1 <br>DN688924 | 4.00E-35 | 149  | cg7766-isoform b<br>isoform 1          |                                                             | Pfam-B_1757                            |         |

|          |                                    |          |                                                            |                                                                                                                      |                                   |         |
|----------|------------------------------------|----------|------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|-----------------------------------|---------|
| DB913522 | gi 62847335 gb DN877380.1 DN877380 | 0        | 314 glycogen phosphorylase                                 | F:GO:0004645,P:GO:0005975,F:GO:0030170,F:GO:0043565,C:GO:0005622,F:GO:0003700,P:GO:0006355                           | Phosphorylase                     | 0.63607 |
| DB913528 | gi 85168270 gb DW594674.1 DW594674 | 1.00E-06 | 37.3 cl066_xenlaame: full=upf0536 protein c12orf66 homolog |                                                                                                                      | DUF2003                           |         |
| DB913535 | <b>Embryo specific</b> gi BY798736 | 0.01     | 29 serine arginine repetitive matrix 1                     | P:GO:0006397,F:GO:0003677,C:GO:0016363,P:GO:0008380,F:GO:0031202,F:GO:0003723,C:GO:0005681,P:GO:0000398,F:GO:0005515 |                                   |         |
| DB913547 | gi 75835685 gb DT865945.1 DT865945 | 0        | 223 ring-box protein 2                                     |                                                                                                                      |                                   | 1.07992 |
| DB913549 | gi 58061026 gb CX734190.1 CX734190 | 1.40E-45 | 184 run and fyve domain containing 2                       | F:GO:0046872,F:GO:0008270,C:GO:0005634                                                                               | Pfam-B_13880,Pfam-B_13880         | 1.5647  |
| DB913569 | gi 46823126 gb CN510502.1 CN510502 | 1.00E-15 | 62.9 h+v1 subunit f                                        |                                                                                                                      | ATP-synt_F                        |         |
| DB913590 | gi 32180832 gb CD679101.1 CD679101 | 0.003    | 46.1                                                       |                                                                                                                      |                                   |         |
| DB913606 | GS020725                           | 0.004    | 34.2 ---NA---                                              |                                                                                                                      |                                   |         |
| DB913609 | GS008119                           | 0.005    | 34.2                                                       |                                                                                                                      |                                   |         |
| DB913627 | gi 22339549 gb BQ924518.1 BQ924518 | 3.00E-05 | 49.6 protocadherin 17                                      | F:GO:0005509,C:GO:0016021,C:GO:0016020,F:GO:0005515                                                                  | Cadherin_2                        |         |
| DB913637 | gi 13298119 gb BG404671.1 BG404671 | 0        | 236 adaptor-related protein complexalpha 1 subunit         |                                                                                                                      | Alpha_adaptin_C, Alpha_adaptin C2 | 0.60157 |

|          |                                                              |          |      |                                                              |                                                                               |                       |         |
|----------|--------------------------------------------------------------|----------|------|--------------------------------------------------------------|-------------------------------------------------------------------------------|-----------------------|---------|
| DB913650 | gi 62046989 gb DN692025.1 DN692025                           | 3.00E-19 | 96.4 | novel protein (zgc:92136)                                    | C:GO:0044464                                                                  |                       | 0.7395  |
| DB913674 | gi 24729312 gb CA394606.1 CA394606                           | 0.0007   | 48.1 |                                                              |                                                                               | RRM_1                 |         |
| DB913685 | gi 62883652 gb DN898889.1 DN898889                           | 3.00E-20 | 73.5 | rho guanine exchange factor 15                               |                                                                               | SH3_1                 |         |
| DB913694 | BY795432                                                     | 1.00E-05 | 45.5 | ---NA---                                                     |                                                                               |                       |         |
| DB913697 | gi 37600573 gb CF726405.1 CF726405                           | 0        | 349  | frizzled 1                                                   |                                                                               | Frizzled, Frizzled    | 0.88177 |
| DB913711 | <b>Positive selection</b> gi 22695367 gb BU181383.1 BU181383 | 0        | 257  | cop9 constitutive photomorphogenic homolog subunit 3         | C:GO:0005737,C:GO:0008180                                                     |                       | 3.57667 |
| DB913719 | gi 77503914 gb DV215332.1 DV215332                           | 0        | 463  | rna binding motif protein 22                                 | P:GO:0008380,C:GO:0005681,F:GO:0003723,P:GO:0006397,F:GO:0008270              | zf-CCCH, Pfam-B_18962 | 4.4089  |
| DB913720 | gi 62038980 gb DN688060.1 DN688060                           | 0        | 233  | prolyl endopeptidase                                         | P:GO:0006508,F:GO:0004287                                                     | Peptidase_S9_N        | 0.6695  |
| DB913726 | gi 18527507 gb BM478465.1 BM478465                           | 0        | 245  | gdp dissociation inhibitor                                   | P:GO:0007269,P:GO:0043087,C:GO:0008021,P:GO:0016192,F:GO:0005093,P:GO:0015031 | GDI                   |         |
| DB913730 | gi 21765959 gb BQ641787.1 BQ641787                           | 0        | 183  | member ras oncogene family                                   |                                                                               | Ras                   | 0.0971  |
| DB913738 | gi 15586332 gb BI670948.1 BI670948                           | 2.00E-25 | 116  | zgc:153540 protein                                           | P:GO:0006546,F:GO:0004047                                                     | GCV_T, GCV_T_C        |         |
| DB913744 | gi 46465494 gb CN459768.1 CN459768                           | 0        | 334  | swi snfmatrixactin dependent regulator of subfamily member 1 |                                                                               | Pfam-B_9568, SLIDE    | 1.4354  |
| DB913750 | GS020461                                                     | 0.006    | 34.2 | mucin 2 precursor                                            | F:GO:0005488,C:GO:0009279,F:GO:0004519                                        |                       |         |

|          |                                                              |          |      |                                                                                     |                                        |                                      |         |
|----------|--------------------------------------------------------------|----------|------|-------------------------------------------------------------------------------------|----------------------------------------|--------------------------------------|---------|
| DB913764 | gi 54470159 gb CV570043.1 CV570043                           | 2.00E-25 | 88.6 | jnk sapk-associated                                                                 |                                        | Pfam-B_719                           |         |
| DB913779 | gi 21765084 gb BQ640625.1 BQ640625                           | 2.00E-19 | 59.3 | map-kinase activating death domain protein denn aex-3                               |                                        |                                      |         |
| DB913787 | <b>Positive selection</b> gi 62843453 gb DN873512.1 DN873512 | 0        | 411  | nadh dehydrogenase iron-sulfur proteinmitochondrial                                 | F:GO:0009055,F:GO:0051287              | Complex1_49k Da                      | 2.6864  |
| DB913792 | gi 57595939 gb CX568910.1 CX568910                           | 9.00E-34 | 144  | kiaa1738 protein                                                                    |                                        | Pfam-B_4326, Pfam-B_4326, Pfam-B_363 | 0.85265 |
| DB913797 | gi 10661657 gb BE986879.1 BE986879                           | 3.00E-39 | 114  | homolog dnj-2 precursor                                                             |                                        | DnaJ,Pfam-B_9221                     |         |
| DB913798 | gi 37635654 gb CF739317.1 CF739317                           | 0        | 173  | tbc1 domainmember 13                                                                | F:GO:0005515                           | TBC                                  | 1.6534  |
| DB913811 | gi 19402955 gb BM943092.1 BM943092                           | 1.00E-06 | 50.1 | ---NA---                                                                            |                                        | Peptidase_M13                        |         |
| DB913827 | GS020635                                                     | 0.003    | 31.8 |                                                                                     |                                        |                                      |         |
| DB913833 | gi 62021352 gb DN679501.1 DN679501                           | 8.00E-09 | 61.6 | novel proteinhuman and mouse amyotrophic lateral sclerosis 2chromosomecandida te 13 |                                        |                                      |         |
| DB913843 | BY796572                                                     | 0.002    | 40.1 |                                                                                     |                                        |                                      |         |
| DB913845 | gi 22704007 gb BU190023.1 BU190023                           | 0        | 188  | u2-associated sr140 protein 1                                                       | P:GO:0006396,F:GO:0003676,F:GO:0000166 | CTK3, Surp                           |         |
| DB913848 | gi 19118874 gb BM802051.1 BM802051                           | 0.007    | 44.1 |                                                                                     |                                        |                                      |         |
| DB913861 | gi 62046494 gb DN691780.1 DN691780                           | 2.00E-15 | 83.1 | ---NA---                                                                            |                                        | DUF1279                              |         |
| DB913888 | BY797846                                                     | 0.009    | 27.6 |                                                                                     |                                        |                                      |         |

|          |                                            |          |      |                                                       |                                                                                               |                     |
|----------|--------------------------------------------|----------|------|-------------------------------------------------------|-----------------------------------------------------------------------------------------------|---------------------|
| DB913900 | GS013868                                   | 0.009    | 29.9 |                                                       |                                                                                               |                     |
| DB913902 | GS020551                                   | 0.0006   | 34.5 |                                                       |                                                                                               | Pfam-B_13263        |
| DB913907 | gi 54474151 gb <br>CV572013.1 <br>CV572013 | 1.00E-25 | 116  | cysteinyl-trna<br>synthetase mitochondr<br>ial        | F:GO:0016874,F:GO:<br>0046872,C:GO:<br>0005739,F:GO:0000166                                   | tRNA-synt_1e 1.1404 |
| DB913915 | gi 58178353 gb <br>CX768000.1 <br>CX768000 | 1.00E-18 | 79.4 | dihydrolipoamide<br>branched chain<br>transacylase e2 | F:GO:0008415,F:GO:<br>0043754,F:GO:<br>0031405,P:GO:<br>0008152,C:GO:<br>0005739,F:GO:0005515 | 2-oxoacid_dh        |
| DB913916 | gi 24727839 gb <br>CA393839.1 <br>CA393839 | 4.00E-06 | 48.7 | tpr domain containing<br>protein                      |                                                                                               |                     |
| DB913919 | gi 49672429 gb <br>CO426135.1 <br>CO426135 | 0        | 364  | muscle glycogen<br>phosphorylase                      |                                                                                               | Phosphorylase       |
| DB913929 | gi 8487195 gb <br>BE096264.1 BE096264      | 5.00E-12 | 72.1 | chromosome 9 open<br>reading frame 30<br>isoform 2    |                                                                                               | Pfam-B_489          |
| DB913930 | gi 62039806 gb <br>DN688475.1 <br>DN688475 | 0.002    | 46.1 |                                                       |                                                                                               |                     |
| DB913934 | gi 62872274 gb <br>DN887511.1 <br>DN887511 | 0.0007   | 44.6 | ---NA---                                              |                                                                                               | Pfam-B_4326         |
| DB913937 | gi 24731276 gb <br>CA395630.1 <br>CA395630 | 0.002    | 46.1 |                                                       |                                                                                               | Baculo_11_kD<br>a   |

|          |                                                              |          |      |                                                  |                                                                                                                                                                          |                             |         |
|----------|--------------------------------------------------------------|----------|------|--------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|---------|
| DB913946 | BY797261                                                     | 0.004    | 37.3 | immunoglobulin a1 protease                       | C:GO:0009986,F:GO:0004222,C:GO:0016021,C:GO:0016020,F:GO:0016787,F:GO:0008270,F:GO:0008237,C:GO:0005576,P:GO:0006508,F:GO:0008233,C:GO:0005618,P:GO:0009405,F:GO:0046872 |                             |         |
| DB913952 | gi 19353745 gb BM903889.1 BM903889                           | 0        | 360  | phosphoribosyl pyrophosphate synthetase 1b       | F:GO:0046872,P:GO:0009156,F:GO:0004749,P:GO:0009116                                                                                                                      | Pribosyltran                |         |
| DB913956 | <b>Positive selection</b> gi 19030465 gb BM717207.1 BM717207 | 0        | 221  | trafficking protein particle complex 4           | P:GO:0006888,C:GO:0005783,C:GO:0005801                                                                                                                                   | Sybindin                    |         |
| DB913957 | <b>Positive selection</b> gi 57592559 gb CX565530.1 CX565530 | 0        | 357  | cytohesin 1                                      | P:GO:0032012,C:GO:0005622                                                                                                                                                | Sec7,Pfam-B_2207            | 2.74005 |
| DB913964 | gi 49674799 gb CO428505.1 CO428505                           | 0        | 184  | ---NA---                                         |                                                                                                                                                                          | DAGK_acc                    | 2.81749 |
| DB913966 | gi 29528388 gb CB584937.1 CB584937                           | 0.009    | 44.1 |                                                  |                                                                                                                                                                          |                             |         |
| DB913969 | gi 54480439 gb CV575146.1 CV575146                           | 2.00E-07 | 56.1 | williams-beuren syndrome critical region protein |                                                                                                                                                                          |                             |         |
| DB913985 | GS008211                                                     | 0.003    | 30.9 |                                                  |                                                                                                                                                                          |                             |         |
| DB913991 | gi 22812006 gb BU505773.1 BU505773                           | 6.00E-14 | 70.2 | g-protein signalling modulator 2 (ags3-elegans)  | F:GO:0005096,F:GO:0005488,P:GO:0007165                                                                                                                                   | GoLoco,GoLoco,GoLoco,GoLoco | 1.20823 |
| DB913996 | gi 62839638 gb DN869697.1 DN869697                           | 0.0002   | 46.9 |                                                  |                                                                                                                                                                          |                             |         |

|          |                                            |          |      |                                                           |                                                                                                                                 |            |
|----------|--------------------------------------------|----------|------|-----------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|------------|
| DB914000 | gi 62031677 gb <br>DN684377.1 <br>DN684377 | 3.00E-25 | 93.6 | folate carrier protein                                    | Mito_carr                                                                                                                       | 0.36387    |
| DB914002 | BY796360                                   | 0.003    | 40.1 |                                                           |                                                                                                                                 |            |
| DB914006 | gi 37602996 gb <br>CF728828.1 CF728828     | 0.009    | 39.1 |                                                           |                                                                                                                                 |            |
| DB914027 | gi 62880674 gb <br>DN895911.1 <br>DN895911 | 0.008    | 44.1 |                                                           |                                                                                                                                 |            |
| DB914035 | gi 5033755 gb <br>AI716502.1 AI716502      | 5.00E-17 | 88.6 | ---NA---                                                  | DAGK_cat                                                                                                                        |            |
| DB914059 | gi 11004100 gb <br>AU142579.1 <br>AU142579 | 1.00E-05 | 51   | cwc22_debhaame:<br>full=pre-mrna-splicing<br>factor cwc22 | C:GO:0005681,F:GO:<br>0005488,C:GO:<br>0005737,P:GO:<br>0008380,P:GO:<br>0016070,P:GO:<br>0006397,F:GO:<br>0005515,C:GO:0005634 |            |
| DB914061 | gi 24721169 gb <br>CA390255.1 <br>CA390255 | 0.003    | 42.8 |                                                           |                                                                                                                                 |            |
| DB914076 | gi 13104116 gb <br>BG306589.1 <br>BG306589 | 0        | 326  | camp-specific<br>phosphodiesterase 4b                     | PDEase_I                                                                                                                        |            |
| DB914098 | GS004884                                   | 0.001    | 36.2 |                                                           |                                                                                                                                 |            |
| DB914103 | BY796077                                   | 7.00E-35 | 142  | agap006755-pa<br>isoform 1                                | U1snRNP70_N<br>,RRM_1                                                                                                           | 1.51713    |
| DB914109 | gi 22681849 gb <br>BU167865.1 <br>BU167865 | 0        | 326  | interleukin enhancer<br>binding factor45kda               | DZF                                                                                                                             |            |
| DB914123 | gi 57590120 gb <br>CX563091.1 <br>CX563091 | 7.00E-38 | 130  | vacuolar protein<br>sorting protein 18                    | P:GO:0015721,P:GO:<br>0045176,P:GO:<br>0008333,P:GO:<br>0043485,P:GO:<br>0048069,C:GO:<br>0044464,P:GO:0007634                  | Pep3_Vps18 |

|          |                                                              |          |      |                                             |                                                                                            |                                |         |
|----------|--------------------------------------------------------------|----------|------|---------------------------------------------|--------------------------------------------------------------------------------------------|--------------------------------|---------|
| DB914124 | gi 37598991 gb CF724823.1 CF724823                           | 7.00E-10 | 65.2 | espin-like protein                          | F:GO:0005515,C:GO:0015629,P:GO:0007010,C:GO:0042995                                        | Ank,Ank                        |         |
| DB914127 | gi 37600304 gb CF726136.1 CF726136                           | 5.00E-31 | 79   | heterochromatin proteinbinding protein 3    | C:GO:0005694,C:GO:0000786,:GO:0006334,F:GO:0003677,C:GO:0005634                            | Linker_histone, Linker_histone |         |
| DB914129 | gi 126523681 gb EL647400.1 EL647400                          | 0        | 314  | elongation factor-1 gamma                   | P:GO:0006414,F:GO:0003746,C:GO:0005853                                                     | GST_C, GST_N                   | 1.29333 |
| DB914152 | gi 19045875 gb BM724544.1 BM724544                           | 0.007    | 44.1 |                                             |                                                                                            |                                |         |
| DB914155 | gi 54479595 gb CV574729.1 CV574729                           | 6.00E-13 | 74.8 | zinc transporter                            |                                                                                            | Zip                            |         |
| DB914171 | gi 10596854 gb BE954383.1 BE954383                           | 0.006    | 41.8 |                                             |                                                                                            |                                |         |
| DB914180 | BY795432                                                     | 0.0009   | 34.1 |                                             |                                                                                            |                                |         |
| DB914187 | gi 24559062 gb CA340966.1 CA340966                           | 0.0002   | 50.1 |                                             |                                                                                            |                                |         |
| DB914192 | gi 62037319 gb DN687221.1 DN687221                           | 4.00E-10 | 66.1 | dentin sialophosphoprotein                  |                                                                                            |                                |         |
| DB914196 | gi 41337670 gb CK616784.1 CK616784                           | 0        | 219  | coatomer proteinsubunit beta 2 (beta prime) | P:GO:0006461,F:GO:0005515,C:GO:0030117,F:GO:0008565,P:GO:0016192,P:GO:0006886,F:GO:0005198 | Coatomer_WD AD                 | 1.30895 |
| DB914210 | BY798374                                                     | 0.0002   | 35.9 |                                             |                                                                                            |                                |         |
| DB914212 | <b>Positive selection</b> gi 49677750 gb CO431456.1 CO431456 | 1.00E-06 | 54.7 | cg1105 cg1105-pa                            | F:GO:0003674,P:GO:0008150                                                                  | Arrestin_N,Arrestin_C          | 2.46215 |
| DB914229 | gi 19399931 gb BM940779.1 BM940779                           | 0.01     | 44.1 |                                             |                                                                                            |                                |         |

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|----------|--------------------------------------------------------------|----------|------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|-------------------------------|
| DB914236 | <b>Positive selection</b> gi 75844134 gb DT874394.1 DT874394 | 0        | 340  | trafficking protein particle complex 3                                                                                                                                    | TRAPP                                                                                      | 3.0934                        |
| DB914244 | gi 13298246 gb BG404798.1 BG404798                           | 4.00E-33 | 142  | abc1 family protein                                                                                                                                                       | ABC1                                                                                       | 0.64775                       |
| DB914248 | gi 19041815 gb BM721716.1 BM721716                           | 0.002    | 44.1 | rhotekin 2                                                                                                                                                                | P:GO:0007165,C:GO:0005622                                                                  | PH                            |
| DB914253 | gi 18988555 gb BM678659.1 BM678659                           | 0.0007   | 46.1 |                                                                                                                                                                           |                                                                                            |                               |
| DB914269 | gi 37638272 gb CF741933.1 CF741933                           | 0        | 437  | dna directed rna polymerase ii polypeptide b                                                                                                                              | P:GO:0002119,F:GO:0003899,P:GO:0006350,P:GO:0040010,P:GO:0000003,P:GO:0009792,P:GO:0008340 | RNA_pol_Rpb2_7,RNA_pol_Rpb2_6 |
| DB914272 | GS020498                                                     | 0.0003   | 38.2 |                                                                                                                                                                           |                                                                                            |                               |
| DB914274 | <b>Positive selection</b> gi 46814587 gb CN501963.1 CN501963 | 9.00E-43 | 174  | rho gdp dissociation                                                                                                                                                      | Rho_GDI                                                                                    | 2.2603                        |
| DB914275 | BY799992                                                     | 0.008    | 35.9 |                                                                                                                                                                           |                                                                                            |                               |
| DB914278 | gi 85180004 gb DW598666.1 DW598666                           | 0        | 208  | fyve finger-containing phosphoinositide kinase (1-phosphatidylinositol-4-phosphate 5-kinase) (phosphatidylinositol-3-phosphate 5-kinase type iii)(nsp-5-kinase) isoform 1 | PIP5K                                                                                      |                               |
| DB914296 | gi 46566690 gb CN485186.1 CN485186                           | 2.00E-34 | 112  | elongation factor tu (ef-tu)                                                                                                                                              | GTP_EFTU_D3                                                                                | 0.8134                        |
| DB914300 | GS020635                                                     | 0.002    | 31.8 |                                                                                                                                                                           |                                                                                            |                               |

|          |                                    |          |      |                                                   |                                                                  |                                        |         |
|----------|------------------------------------|----------|------|---------------------------------------------------|------------------------------------------------------------------|----------------------------------------|---------|
| DB914308 | gi 62045584 gb DN691323.1 DN691323 | 1.00E-12 | 74.4 | amyloid precursor protein                         | F:GO:0005488,C:GO:0016021,F:GO:0004867                           | APP_amyloid, Pfam-B_16930, Pfam-B_1037 | 0.4179  |
| DB914314 | BY798122                           | 7.00E-24 | 105  | mediator complex subunit 11 cg6884-pa             |                                                                  | Med11                                  | 0.48202 |
| DB914322 | BY797251                           | 0.008    | 29   |                                                   |                                                                  |                                        |         |
| DB914347 | gi 11003833 gb AU142312.1 AU142312 | 2.00E-25 | 100  | required for meiotic nuclear division 5 homolog a |                                                                  | Pfam-B_49, DUF869                      | 1.31703 |
| DB914362 | gi 10205227 gb BE784029.1 BE784029 | 0        | 292  | af484088_1syntaxin 1a                             | C:GO:0016021,F:GO:0005484,P:GO:0016192,P:GO:0006886,P:GO:0006836 | Syntaxin,SNA RE                        |         |
| DB914365 | gi 41342595 gb CK621709.1 CK621709 | 3.00E-22 | 105  | c-jun protein                                     | F:GO:0003677,P:GO:0046686,P:GO:0051597                           | Jun                                    | 1.57635 |
| DB914372 | gi 62828798 gb DN859149.1 DN859149 | 2.00E-30 | 133  | cytochrome c oxidase subunit via polypeptide 1    |                                                                  | COX6A                                  |         |
| DB914374 | BY795858                           | 1.00E-27 | 117  | ornithine decarboxylase antizyme                  | F:GO:0008073                                                     | ODC_AZ                                 | 0.85583 |
| DB914380 | gi 40321099 gb CK355167.1 CK355167 | 0.002    | 33.1 |                                                   |                                                                  |                                        |         |
| DB914393 | gi 19016174 gb BM702916.1 BM702916 | 3.00E-15 | 82.2 | calcyclin binding protein                         | C:GO:0005737,P:GO:0006512,C:GO:0005634                           | SGS                                    |         |
| DB914415 | gi 40319267 gb CK353380.1 CK353380 | 0.001    | 25.4 |                                                   |                                                                  |                                        |         |
| DB914418 | gi 54440189 gb CV556048.1 CV556048 | 2.00E-07 | 57   | src kinase associated phosphoprotein 1            | C:GO:0005737,C:GO:0016020,P:GO:0006955,C:GO:0005634              | SH3_2                                  |         |

|          |                                            |          |      |                                                   |                               |                                     |        |
|----------|--------------------------------------------|----------|------|---------------------------------------------------|-------------------------------|-------------------------------------|--------|
| DB914431 | gi 32465039 gb <br>CD806213.1 <br>CD806213 | 0.002    | 43.7 |                                                   |                               |                                     |        |
| DB914445 | gi 62880016 gb <br>DN895253.1 <br>DN895253 | 5.00E-26 | 75.2 | beta chain spectrin                               |                               | Pfam-B_1882,<br>PH                  | 1.4125 |
| DB914464 | gi 24727633 gb <br>CA393729.1 <br>CA393729 | 2.00E-17 | 90.4 | lymphoid-restricted<br>membraneisoform<br>cra_a   |                               | MRVI1                               |        |
| DB914494 | gi 49674086 gb <br>CO427792.1 <br>CO427792 | 2.00E-20 | 100  | mediator of rna<br>polymerase ii<br>transcription | P:GO:0009987                  | Med24_N                             | 0.5669 |
| DB914496 | gi 22810544 gb <br>BU504311.1 <br>BU504311 | 0.001    | 35.4 |                                                   |                               |                                     |        |
| DB914502 | gi 16086838 gb <br>BI879567.1 BI879567     | 0.005    | 31.3 | transposase                                       |                               | Pfam-B_19958                        | 1.2465 |
| DB914521 | gi 19044026 gb <br>BM723028.1 <br>BM723028 | 9.00E-05 | 47.8 | set domain and<br>mariner transposase<br>fusion   | P:GO:0009987,F:GO:<br>0003824 |                                     |        |
| DB914525 | gi 18523633 gb <br>BM474591.1 <br>BM474591 | 7.00E-10 | 64.3 | pentatricopeptide<br>repeat protein 1             |                               |                                     |        |
| DB914526 | gi 37643689 gb <br>CF747346.1 CF747346     | 0.0007   | 48.1 |                                                   |                               |                                     |        |
| DB914527 | gi 29773470 gb <br>CB716322.1 <br>CB716322 | 0.01     | 44.1 |                                                   |                               |                                     |        |
| DB914529 | gi 58032704 gb <br>CX730231.1 <br>CX730231 | 5.00E-21 | 102  | agrin_disomame:<br>full=agrin                     |                               | Pfam-B_6679,<br>EGF<br>,Laminin_G_2 |        |
| DB914543 | gi 10661640 gb <br>BE986871.1 BE986871     | 0.0007   | 48.1 |                                                   |                               |                                     |        |
| DB914548 | gi 9126593 gb <br>BE256137.1 BE256137      | 0.009    | 35.9 |                                                   |                               |                                     |        |

|          |                                                              |          |      |                                                     |                                                     |                                 |         |
|----------|--------------------------------------------------------------|----------|------|-----------------------------------------------------|-----------------------------------------------------|---------------------------------|---------|
| DB914550 | gi 16491993 gb BB658168.1 BB658168                           | 0.003    | 46.1 |                                                     |                                                     |                                 |         |
| DB914606 | gi 41342768 gb CK621882.1 CK621882                           | 0        | 263  | calcium calmodulin-dependent protein kinaseii delta | F:GO:0004683,P:GO:0006468,F:GO:0005524,F:GO:0005516 | CaMKII_AD                       | 1.79304 |
| DB914609 | gi 49680679 gb CO434385.1 CO434385                           | 0.009    | 44.1 | kiaa0523 protein                                    |                                                     | WSC                             |         |
| DB914611 | gi 37634173 gb CF737836.1 CF737836                           | 8.00E-28 | 59.7 | integrin alpha fg-gap repeat containing 1           | F:GO:0005515                                        | Pfam-B_10882,FG-GAP,Pfam-B_2701 | 1.5911  |
| DB914618 | gi 85175473 gb DW597555.1 DW597555                           | 0.006    | 35.9 |                                                     |                                                     |                                 |         |
| DB914626 | <b>Positive selection</b> gi 13269951 gb BG373449.1 BG373449 | 0        | 277  | ma-binding protein luc7-like 1                      |                                                     | LUC7                            | 2.96008 |
| DB914647 | GS013972                                                     | 0.006    | 34.2 |                                                     |                                                     |                                 |         |
| DB914665 | gi 19018339 gb BM705081.1 BM705081                           | 0.0004   | 45.9 | glutamic acid-rich protein cnbl1500                 |                                                     | IQ                              |         |
| DB914701 | GS004835                                                     | 0.006    | 34.2 |                                                     |                                                     |                                 |         |
| DB914704 | gi 19045114 gb BM723783.1 BM723783                           | 0        | 263  | voltage and ligand gated potassium channel          |                                                     | cNMP_binding                    |         |
| DB914711 | gi 16045694 gb BI872019.1 BI872019                           |          | 0    | aspartate aminotransferase                          | P:GO:0008152,F:GO:0008483                           | Aminotran_1_2                   | 1.94034 |
| DB914715 | gi 15708152 gb BI731139.1 BI731139                           | 0        | 371  | plasma membrane calcium atpase                      |                                                     | Hydrolase_3, Cation_ATPas e_C   |         |
| DB914741 | BY798376                                                     | 0.009    | 36.1 | ---NA---                                            |                                                     |                                 |         |
| DB914754 | gi 13298781 gb BG374309.1 BG374309                           | 0.008    | 40.9 |                                                     |                                                     |                                 |         |

|          |                                            |          |      |                                                                                                     |                                                                              |                                                 |         |
|----------|--------------------------------------------|----------|------|-----------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------|-------------------------------------------------|---------|
| DB914755 | gi 62022742 gb <br>DN680198.1 <br>DN680198 | 0        | 248  | receptor-type<br>tyrosine-protein<br>phosphatase n2                                                 |                                                                              | Y_phosphatas<br>e                               | 0.0223  |
| DB914756 | GS020551                                   | 0.006    | 34.2 |                                                                                                     |                                                                              |                                                 |         |
| DB914758 | gi 14975170 gb <br>BI298890.1 BI298890     | 0.01     | 44.1 |                                                                                                     |                                                                              |                                                 |         |
| DB914759 | BY797937                                   | 5.00E-05 | 46.1 |                                                                                                     |                                                                              |                                                 |         |
| DB914768 | gi 18988103 gb <br>BM678207.1 <br>BM678207 | 1.00E-13 | 77.6 | loc779536 protein                                                                                   |                                                                              |                                                 |         |
| DB914775 | gi 83525008 gb <br>DB294182.1 <br>DB294182 | 0.002    | 46.1 |                                                                                                     |                                                                              |                                                 |         |
| DB914777 | gi 75840093 gb <br>DT870353.1 DT870353     | 5.00E-34 | 145  | cytochrome c oxidase<br>subunit iv                                                                  | F:GO:0004129,P:GO:<br>0006118                                                | COX4                                            | 1.82462 |
| DB914790 | gi 22811777 gb <br>BU505544.1 <br>BU505544 | 5.04E-44 | 110  | heterogeneous<br>nuclear<br>ribonucleoprotein l                                                     | F:GO:0005488                                                                 |                                                 | 1.66068 |
| DB914792 | gi 49675509 gb <br>CO429215.1 <br>CO429215 | 0        | 347  | udp-n-acetyl-alpha-d-<br>galactosamine:<br>polypeptide n-<br>acetylgalactosaminyltr<br>ansferase 13 | F:GO:0004653,F:GO:<br>0046872,F:GO:<br>0043169,P:GO:<br>0006493,C:GO:0016020 | Ricin_B_lectin,<br>Ricin_B_lectin               | 0.24575 |
| DB914798 | gi 55687806 gb <br>CV782866.1 <br>CV782866 | 9.00E-08 | 58.3 | protocadherin gamma<br>subfamily3 isoform 1<br>precursor isoform 4                                  |                                                                              | Cadherin,Cadh<br>erin                           |         |
| DB914800 | gi 62838255 gb <br>DN868314.1 <br>DN868314 | 0.001    | 33.1 | ---NA---                                                                                            |                                                                              | Pfam-B_4326,<br>Pfam-<br>B_4326,Pfam-<br>B_4326 |         |
| DB914805 | gi 49670616 gb <br>CO424453.1 <br>CO424453 | 2.00E-16 | 83.1 | dead box polypeptide<br>42 protein                                                                  | F:GO:0003723,F:GO:<br>0005524,C:GO:<br>0005634,F:GO:0008026                  |                                                 |         |
| DB914807 | gi 50135734 gb <br>CO470191.1 <br>CO470191 | 6.00E-14 | 78   | tubulin-specific<br>chaperone d                                                                     |                                                                              |                                                 |         |
| DB914811 | GS020613                                   | 0.006    | 34.2 |                                                                                                     |                                                                              |                                                 |         |

|          |                 |                                    |          |      |                                                                                                                                                                                        |                                                                                            |                    |
|----------|-----------------|------------------------------------|----------|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|--------------------|
| DB914825 | Embryo specific | GS014020                           | 0.005    | 34.2 |                                                                                                                                                                                        |                                                                                            |                    |
| DB914830 |                 | GS020737                           | 9.00E-05 | 40.1 |                                                                                                                                                                                        |                                                                                            |                    |
| DB914835 |                 | BY798120                           | 0.004    | 40.1 |                                                                                                                                                                                        |                                                                                            |                    |
| DB914837 |                 | gi 37633333 gb CF736997.1 CF736997 | 0        | 290  | component of oligomeric golgi complex 6P:GO:0015031,C:GO:0000139,C:GO:0017119                                                                                                          | COG6                                                                                       |                    |
| DB914853 |                 | gi 75833992 gb DT864252.1 DT864252 | 5.00E-07 | 55.1 | ubiquinol-cytochrome c reductase subunit-like                                                                                                                                          | QCR10,UCR_6-4kD                                                                            |                    |
| DB914855 |                 | gi 19042411 gb BM722079.1 BM722079 | 2.00E-10 | 66.6 | zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein dp) (znf-dp) | F:GO:0003676,F:GO:0008270,C:GO:0005622                                                     | zf-C2H2            |
| DB914862 |                 | BY795675                           | 0        | 213  | epsilon subunit of coatamer protein complex isoform 1                                                                                                                                  | P:GO:0016192,F:GO:0005488,C:GO:0030137,P:GO:0016043,C:GO:0044425,C:GO:0031090,C:GO:0012505 | Coatamer_E 1.50606 |
| DB914867 |                 | gi 46821517 gb CN508893.1 CN508893 | 1.00E-14 | 81.3 | tumor protein d52-like 2b                                                                                                                                                              |                                                                                            | TPD52              |
| DB914886 |                 | gi 37602491 gb CF728323.1 CF728323 | 0        | 229  | liquid facets                                                                                                                                                                          | Pfam-B_15358,ENTH                                                                          | 2.05756            |
| DB914895 |                 | gi 22347977 gb BQ932594.1 BQ932594 | 1.40E-45 | 139  | cop9 signalosome complex subunit                                                                                                                                                       | PCI                                                                                        | 0.26647            |
| DB914897 |                 | BY798777                           | 0.003    | 40.1 |                                                                                                                                                                                        |                                                                                            |                    |

|          |                    |                                     |          |      |                                          |                                                                                                                      |                            |         |
|----------|--------------------|-------------------------------------|----------|------|------------------------------------------|----------------------------------------------------------------------------------------------------------------------|----------------------------|---------|
| DB914898 |                    | gi 119785924 gb EH279915.1 EH279915 | 2.00E-27 | 123  | selenoprotein w                          | F:GO:0008430,C:GO:0005737,F:GO:0016491,C:GO:0005886                                                                  | Rdx                        | 0.93773 |
| DB914905 |                    | gi 32173367 gb CD671636.1 CD671636  | 0        | 186  | sulfatase-modifying factor 1 precursor   |                                                                                                                      | FGE-sulfatase              | 0.60223 |
| DB914917 |                    | GS013972                            | 0.006    | 34.2 |                                          |                                                                                                                      |                            |         |
| DB914919 | GO annotation      | gi 58032883 gb CX730410.1 CX730410  | 2.00E-22 | 102  | rhodopsin kinase                         | P:GO:0006468,F:GO:0004871,F:GO:0005524,P:GO:0007165,F:GO:0004703                                                     |                            |         |
| DB914921 |                    | gi 49672103 gb CO425809.1 CO425809  | 0        | 331  | syndecan bindingisoform cra_a            | C:GO:0005895,F:GO:0016491,F:GO:0005137,C:GO:0042470,F:GO:0047485,P:GO:0008152,F:GO:0046982,P:GO:0007265,F:GO:0042043 | PDZ, PDZ                   | 1.00847 |
| DB914924 |                    | gi 58032634 gb CX730161.1 CX730161  | 2.00E-13 | 76.7 | atp-dependent bile acid permease         |                                                                                                                      | ABC_membrane               | 1.0399  |
| DB914927 |                    | gi 62827356 gb DN857707.1 DN857707  | 0        | 225  | mitochondrial ribosomal                  | C:GO:0005622                                                                                                         |                            | 1.58155 |
| DB914952 |                    | gi 46464646 gb CN458920.1 CN458920  | 5.00E-34 | 75.3 | probable rna-binding protein 19          |                                                                                                                      | RRM_1, Pfam-B_1057,RRM_1   | 1.00403 |
| DB914954 | Positive selection | gi 46819175 gb CN506551.1 CN506551  | 0        | 442  | ribosome biogenesis protein nsa2 homolog |                                                                                                                      | Pfam-B_11758,Ribosomal_S8e | 3.08143 |
| DB914957 |                    | BY797925                            | 0.005    | 36.8 |                                          |                                                                                                                      |                            |         |
| DB914959 |                    | gi 9124583 gb BE254157.1 BE254157   | 4.00E-05 | 52   |                                          |                                                                                                                      |                            |         |
| DB914968 |                    | gi 50136911 gb CO470735.1 CO470735  | 3.00E-26 | 76.7 | transmembrane protein 50a                |                                                                                                                      | UPF0220,UPF0220            | 0.90197 |

|          |                                                                   |          |      |                                                                                                                                           |                                                                                                                                 |                                                    |         |  |
|----------|-------------------------------------------------------------------|----------|------|-------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------|---------|--|
| DB914971 | gi 10204034 gb <br>BE782836.1 BE782836                            | 0.0004   | 36.8 |                                                                                                                                           |                                                                                                                                 |                                                    |         |  |
| DB914981 | GS004685                                                          | 0.009    | 32.2 |                                                                                                                                           |                                                                                                                                 |                                                    |         |  |
| DB915001 | gi 40678063 gb <br>CK430204.1 <br>CK430204                        | 6.00E-11 | 61.6 | peptidylglycine alpha-<br>amidating<br>monooxygenase                                                                                      | F:GO:0004504,P:GO:<br>0006518,P:GO:<br>0009987,F:GO:<br>0005507,F:GO:<br>0003824,C:GO:<br>0016020,F:GO:<br>0004497,F:GO:0004867 | NHL                                                | 0.6148  |  |
| DB915010 | gi 62041170 gb <br>DN689160.1 <br>DN689160                        | 0        | 201  | atp-dependent<br>transporter                                                                                                              |                                                                                                                                 | Pfam-<br>B_11162,Pfam<br>-<br>B_11182,ABC_<br>tran |         |  |
| DB915022 | <b>Embryo specific</b> gi BY797574                                | 0.007    | 38.2 |                                                                                                                                           |                                                                                                                                 |                                                    |         |  |
| DB915040 | gi 37630580 gb <br>CF734247.1 CF734247                            | 0        | 152  | domain containing 1                                                                                                                       |                                                                                                                                 |                                                    | 1.2712  |  |
| DB915046 | <b>Embryo specific</b> gi 50134930 gb <br>CO469857.1 <br>CO469857 | 5.00E-05 | 52   |                                                                                                                                           |                                                                                                                                 |                                                    |         |  |
| DB915065 | gi 85187158 gb <br>DW601144.1 <br>DW601144                        | 0.0001   | 40.9 | ---NA---                                                                                                                                  |                                                                                                                                 |                                                    |         |  |
| DB915089 | gi 62842970 gb <br>DN873029.1 <br>DN873029                        | 0.006    | 33.6 | orcokinin precursor                                                                                                                       | P:GO:0007218,F:GO:<br>0005184,C:GO:0005576                                                                                      |                                                    |         |  |
| DB915090 | gi 22689959 gb <br>BU175975.1 <br>BU175975                        | 0.001    | 40.6 |                                                                                                                                           |                                                                                                                                 |                                                    |         |  |
| DB915094 | GS020443                                                          | 0.006    | 34.2 | pdx1_subdoame:<br>full=probable<br>pyridoxine<br>biosynthesis<br>snzerrame: full=pdx1<br>homologame:<br>full=ethylene response<br>protein | P:GO:0008615,F:GO:<br>0003824                                                                                                   | SOR_SNZ                                            | 0.38215 |  |

|          |                                            |          |      |                             |                                                                                               |                                     |
|----------|--------------------------------------------|----------|------|-----------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------|
| DB915096 | GS020567                                   | 0.006    | 30.9 |                             |                                                                                               |                                     |
| DB915118 | gi 32176841 gb <br>CD675110.1 <br>CD675110 | 2.00E-10 | 66.9 | subfamilymember 1           | F:GO:0051082,P:GO:<br>0006457,P:GO:<br>0045449,F:GO:<br>0031072,F:GO:<br>0003677,C:GO:0005634 | Myb_DNA-<br>binding                 |
| DB915122 | GS004800                                   | 0.001    | 36.2 |                             |                                                                                               |                                     |
| DB915128 | gi 75842167 gb <br>DT872427.1 DT872427     | 0        | 204  | protein                     |                                                                                               | eIF-1a 0.30832                      |
| DB915140 | gi 32273244 gb <br>CD722396.1 <br>CD722396 | 9.00E-36 | 151  | ---NA---                    |                                                                                               | PHD,<br>Bromodomain,<br>PHD         |
| DB915141 | GS013851                                   | 0.006    | 34.2 |                             |                                                                                               |                                     |
| DB915148 | GS004600                                   | 0.006    | 34.2 |                             |                                                                                               |                                     |
| DB915151 | BY795161                                   | 0.006    | 36.2 |                             |                                                                                               |                                     |
| DB915153 | gi 62826040 gb <br>DN856391.1 <br>DN856391 | 0        | 318  | myst histone                |                                                                                               | MOZ_SAS,Pfa<br>m-B_7698,<br>MOZ_SAS |
| DB915164 | gi 32464819 gb <br>CD805993.1 <br>CD805993 | 0        | 386  | glycogen brain              | F:GO:0030170,F:GO:<br>0004645                                                                 | Phosphorylase 0.04362               |
| DB915168 | gi 68325747 gb <br>DR423731.1 <br>DR423731 | 0        | 274  | ribosomal protein s11       | C:GO:0005840,F:GO:<br>0003735,P:GO:0006412                                                    | Ribosomal_S1<br>7                   |
| DB915191 | GS008298                                   | 0.01     | 30.4 |                             |                                                                                               |                                     |
| DB915213 | GS020603                                   | 0.006    | 34.2 |                             |                                                                                               |                                     |
| DB915221 | BY796397                                   | 0.004    | 40.1 | ---NA---                    |                                                                                               | Aminotran_5                         |
| DB915228 | gi 18500152 gb <br>BM451112.1 <br>BM451112 | 2.00E-11 | 51.5 | pap2 superfamily<br>protein | F:GO:0016787,F:GO:<br>0003824,C:GO:0016020                                                    | PAP2                                |
| DB915231 | BY797899                                   | 0.009    | 36.2 |                             |                                                                                               |                                     |
| DB915236 | GS020630                                   | 0.006    | 34.2 |                             |                                                                                               |                                     |
| DB915244 | gi 22678666 gb <br>BU164714.1 <br>BU164714 | 0        | 240  | orm1-like 1                 | C:GO:0005783,C:GO:<br>0044425                                                                 | ORMDL                               |
| DB915246 | BY799230                                   | 0.003    | 40.1 |                             |                                                                                               |                                     |

|          |                                                              |          |      |                                                   |                                                                                                                                                             |                                      |         |
|----------|--------------------------------------------------------------|----------|------|---------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------|---------|
| DB915252 | gi 20362619 gb BQ187068.1 BQ187068                           | 5.00E-14 | 57.4 | core-fucosyltransferase a                         | F:GO:0016757,C:GO:0016020                                                                                                                                   | Glyco_transf_1<br>0                  | 0.69855 |
| DB915290 | gi 50138615 gb CO471538.1 CO471538                           | 0        | 292  | rap guanine nucleotide exchange factor4           |                                                                                                                                                             | RasGEF,Sec7                          |         |
| DB915313 | BY798198                                                     | 0.003    | 36.2 |                                                   |                                                                                                                                                             |                                      |         |
| DB915332 | gi 46818123 gb CN505499.1 CN505499                           | 5.00E-28 | 108  | atp synthase lipid-bindingmitochondrial precursor | P:GO:0015986,C:GO:0045263,C:GO:0016021,C:GO:0016020,C:GO:0016469,P:GO:0006811,P:GO:0006810,F:GO:0015078,F:GO:0046933,F:GO:0046961,F:GO:0008289,P:GO:0015992 | ATP-synt_C                           |         |
| DB915334 | <b>Positive selection</b> gi 18521031 gb BM471989.1 BM471989 | 0        | 474  | gtp binding protein 4                             | F:GO:0005525                                                                                                                                                | NOG1                                 | 12.4053 |
| DB915355 | gi 46814772 gb CN502148.1 CN502148                           | 2.00E-07 | 57   | protein                                           |                                                                                                                                                             | Pfam-B_9880,Pfam-B_18588,Pfam-B_7249 |         |
| DB915358 | gi 32466998 gb CD808172.1 CD808172                           | 5.00E-06 | 44   | remodeling and spacing factor 1                   |                                                                                                                                                             |                                      |         |
| DB915364 | GS004835                                                     | 0.006    | 34.2 |                                                   |                                                                                                                                                             |                                      |         |
| DB915366 | gi 85164424 gb DW592739.1 DW592739                           | 0        | 185  | non-erythrocytic 1 (alpha-fodrin)                 | C:GO:0005737,C:GO:0005856,P:GO:0051016,F:GO:0003779,F:GO:0005509,F:GO:0005516                                                                               | efhand_Ca_ins en,efhand              | 0.76977 |
| DB915381 | gi 37630736 gb CF734403.1 CF734403                           | 3.00E-15 | 61.6 | nicotinic acetylcholine receptor subunit type i   | F:GO:0004872,F:GO:0005230,P:GO:0006810,C:GO:0044425,C:GO:0045202                                                                                            | Neur_chan_me mb                      |         |

|          |                                                              |          |      |                                                                                                                                     |                                        |                       |         |
|----------|--------------------------------------------------------------|----------|------|-------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------|-----------------------|---------|
| DB915390 | gi 62878361 gb DN893598.1 DN893598                           | 2.00E-40 | 166  | gtp binding protein 4                                                                                                               | F:GO:0005525,P:GO:0007264              | Pfam-B_1475,NOGCT     |         |
| DB915398 | GS020721                                                     | 0.006    | 34.2 |                                                                                                                                     |                                        |                       |         |
| DB915414 | gi 85204141 gb DW606709.1 DW606709                           | 3.00E-27 | 110  | wd repeat domain 59                                                                                                                 |                                        | Pfam-B_1901           | 1.06237 |
| DB915434 | <b>Positive selection</b> gi 62879067 gb DN894304.1 DN894304 | 0        | 195  | hydroxyacyl-coenzyme a dehydrogenase 3-ketoacyl-coenzyme a thiolase enoyl-coenzyme a hydratase (trifunctional protein) beta subunit | C:GO:0005743,P:GO:0006631,F:GO:0003988 | Thiolase_N,Thiolase_N | 2.54372 |
| DB915444 | gi 5210701 gb AI764766.1 AI764766                            | 3.00E-21 | 84.9 | ---NA---                                                                                                                            |                                        | Pfam-B_4326,Na_Ca_ex  |         |
| DB915489 | gi 27167682 gb BY742285.1 BY742285                           | 1.00E-10 | 68   | ceramide kinase-like protein                                                                                                        |                                        | DAGK_cat              |         |
| DB915490 | gi 22695415 gb BU181431.1 BU181431                           | 0.0007   | 48.1 |                                                                                                                                     |                                        |                       |         |
| DB915494 | gi 22667226 gb BU153704.1 BU153704                           | 0        | 361  | exosome component isoform cra_a                                                                                                     |                                        | RNase_PH_C, RNase_PH  | 0.10495 |
| DB915500 | gi 54446259 gb CV559043.1 CV559043                           | 8.00E-16 | 84.9 | kinesin-73 cg8183-pb                                                                                                                |                                        | CAP_GLY               |         |
| DB915516 | gi 83528675 gb DB294632.1 DB294632                           | 0.009    | 44.1 |                                                                                                                                     |                                        |                       |         |
| DB915518 | BY799694                                                     | 0.004    | 40.1 |                                                                                                                                     |                                        |                       |         |
| DB915531 | gi 9122948 gb BE252803.1 BE252803                            | 0        | 215  | trafficking protein particle complex 2                                                                                              | P:GO:0006888,C:GO:0005622              | Sedlin_N              |         |

|          |                                    |          |      |                                                    |                                                                  |                  |         |
|----------|------------------------------------|----------|------|----------------------------------------------------|------------------------------------------------------------------|------------------|---------|
| DB915536 | gi 18516245 gb BM467203.1 BM467203 | 2.00E-14 | 50.6 | n-acetylglucosaminyltransferase v                  | F:GO:0016740,C:GO:0005575                                        |                  |         |
| DB915540 | gi 24726160 gb CA392957.1 CA392957 | 1.00E-08 | 61.1 | sodium-iodide related cotransporter                |                                                                  |                  | 1.33033 |
| DB915561 | GS013876                           | 0.001    | 34.2 |                                                    |                                                                  |                  |         |
| DB915569 | GS008202                           | 0.0004   | 38.2 | reverse transcriptase                              | F:GO:0003723,P:GO:0006278,F:GO:0003964                           |                  | 0.63493 |
| DB915570 | gi 46816392 gb CN503768.1 CN503768 | 0        | 176  | rna binding motif protein 8a                       | C:GO:0044424,F:GO:0005488                                        | RRM_1            | 0.27304 |
| DB915574 | gi 32180984 gb CD679253.1 CD679253 | 0.009    | 44.1 |                                                    |                                                                  |                  |         |
| DB915596 | gi 50134954 gb CO469865.1 CO469865 | 3.00E-26 | 118  | ntf2-related export protein 2                      |                                                                  | Pfam-B_5119,NTF2 | 0.78157 |
| DB915607 | gi 62033613 gb DN685351.1 DN685351 | 0        | 264  | novel proteintransmembrane protein 111 (zgc:86609) | F:GO:0003674,C:GO:0005575                                        | DUF106           | 0.13216 |
| DB915615 | GS020607                           | 0.005    | 34.2 |                                                    |                                                                  |                  |         |
| DB915617 | GS014020                           | 0.005    | 34.2 |                                                    |                                                                  |                  |         |
| DB915644 | GS004966                           | 0.006    | 34.2 |                                                    |                                                                  |                  |         |
| DB915667 | GS020551                           | 0.003    | 31.8 |                                                    |                                                                  |                  |         |
| DB915668 | gi 37629295 gb CF732962.1 CF732962 | 4.00E-15 | 82.6 | pb1 protein                                        |                                                                  | BAH              |         |
| DB915670 | gi 46855352 gb CN527196.1 CN527196 | 5.00E-06 | 51.9 | rab11 family interacting protein 2 (class i)       |                                                                  | RBD-FIP          |         |
| DB915675 | gi 54441692 gb CV556796.1 CV556796 | 0        | 286  | basic leucine zipper and w2 domains 1              | P:GO:0006353,F:GO:0005488,P:GO:0045449,P:GO:0032268,P:GO:0051128 | W2               | 0.70233 |
| DB915689 | gi 10666276 gb BE989171.1 BE989171 | 0.01     | 44.1 |                                                    |                                                                  |                  |         |

|          |                                    |          |      |                                          |                                                                                            |                        |         |
|----------|------------------------------------|----------|------|------------------------------------------|--------------------------------------------------------------------------------------------|------------------------|---------|
| DB915691 | gi 24723586 gb CA391579.1 CA391579 | 2.00E-07 | 49.6 | g protein gamma subunit                  |                                                                                            | G-gamma                | 0.92647 |
| DB915693 | gi 58060845 gb CX734009.1 CX734009 | 3.00E-37 | 155  | protein kinasedelta                      | F:GO:0005488,F:GO:0016301                                                                  | Pfam-B_9526,C1_1,C1_1  |         |
| DB915719 | BY796848                           | 0.006    | 36.2 |                                          |                                                                                            |                        |         |
| DB915750 | gi 19001128 gb BM687870.1 BM687870 | 5.61E-45 | 181  | chromosome 14 open reading frame 135     | C:GO:0016021                                                                               | Pecanex_C              |         |
| DB915757 | gi 62871793 gb DN887030.1 DN887030 | 2.00E-06 | 43.7 | prothoracicostatic peptide precursor     | P:GO:0006355,F:GO:0005179,F:GO:0003674,F:GO:0000166,C:GO:0005615,P:GO:0002168,C:GO:0005576 |                        |         |
| DB915761 | gi 19018444 gb BM705186.1 BM705186 | 8.00E-11 | 38.6 | phospholipase a2                         | F:GO:0046872,F:GO:0004623,F:GO:0005509,F:GO:0016787,P:GO:0016042,C:GO:0005576,P:GO:0006644 | Phospholip_A2_1        | 0.77686 |
| DB915763 | gi 22667808 gb BU154276.1 BU154276 | 0        | 362  | glyceraldehyde-3-phosphate dehydrogenase | C:GO:0005737,F:GO:0051287,P:GO:0006096,F:GO:0004365                                        | Gp_dh_C,Gp_dh_N        | 0.10068 |
| DB915774 | gi 75846277 gb DT876537.1 DT876537 | 5.00E-40 | 165  | light-inducedbrain protein 44            |                                                                                            | UPF0041                | 1.14919 |
| DB915776 | gi 62826866 gb DN857217.1 DN857217 | 0        | 445  | casein kinasebeta polypeptide isoform 2  | P:GO:0030177,P:GO:0007249,F:GO:0005515,C:GO:0005956,F:GO:0004682,F:GO:0008605              | CK_II_beta,Pfam-B_5275 | 1.3143  |
| DB915789 | GS013908                           | 0.005    | 34.2 |                                          |                                                                                            |                        |         |
| DB915807 | gi 41349257 gb CK628371.1 CK628371 | 0.001    | 46.1 |                                          |                                                                                            |                        |         |
| DB915812 | GS020701                           | 0.002    | 32.2 |                                          |                                                                                            |                        |         |

|          |                                            |          |      |                                                                            |                                            |                          |
|----------|--------------------------------------------|----------|------|----------------------------------------------------------------------------|--------------------------------------------|--------------------------|
| DB915822 | BY798436                                   | 0.007    | 36.3 |                                                                            |                                            |                          |
| DB915832 | gi 16086844 gb <br>BI879573.1 BI879573     | 0.0001   | 47.8 | ---NA---                                                                   |                                            |                          |
| DB915848 | GS014157                                   | 0.005    | 34.2 |                                                                            |                                            |                          |
| DB915849 | gi 22679229 gb <br>BU165277.1 <br>BU165277 | 3.00E-32 | 139  | translocated promoter<br>region (to activated<br>met oncogene)             | F:GO:0003674,C:GO:<br>0005635              | Cortex-I_coil<br>0.90314 |
| DB915858 | BY797553                                   | 0.0009   | 39.1 |                                                                            |                                            |                          |
| DB915864 | gi 14064158 gb <br>BG753505.1 <br>BG753505 | 0.009    | 31.3 |                                                                            |                                            |                          |
| DB915866 | gi 18510625 gb <br>BM461585.1 <br>BM461585 | 0        | 456  | histone deacetylase 3                                                      |                                            | Hist_deacetyl<br>2.44999 |
| DB915868 | gi 22355575 gb <br>BQ940097.1 <br>BQ940097 | 5.00E-05 | 45   | pleckstrin homology<br>domainfamily m (with<br>run domain) member 2        |                                            |                          |
| DB915882 | gi 85165194 gb <br>DW593133.1 <br>DW593133 | 3.00E-09 | 51.3 | phd finger protein 8                                                       |                                            |                          |
| DB915883 | gi 15959381 gb <br>BI846858.1 BI846858     | 4.00E-07 | 55.8 | map microtubule<br>affinity-regulating<br>kinase 1                         | P:GO:0009987,F:GO:<br>0016740,C:GO:0044424 | 1.96025                  |
| DB915891 | gi 49672802 gb <br>CO426508.1 <br>CO426508 | 5.00E-39 | 161  | ---NA---                                                                   |                                            | Sdh5<br>0.84475          |
| DB915905 | gi 37599559 gb <br>CF725391.1 CF725391     | 0.003    | 46.1 |                                                                            |                                            |                          |
| DB915914 | gi 46824907 gb <br>CN512283.1 <br>CN512283 | 0        | 96.9 | phosphatidylinositol<br>transfer protein retinal<br>degeneration b protein |                                            | IP_trans                 |
| DB915917 | BY797191                                   | 0.004    | 36.2 |                                                                            |                                            |                          |
| DB915922 | gi 22803777 gb <br>BU501356.1 <br>BU501356 | 8.00E-14 | 57.4 | ras and ef-hand<br>domain containing                                       | P:GO:0009987,P:GO:<br>0006810              | PglZ, Ras<br>0.3492      |

|          |                                            |          |      |                                                                           |                                                                                                                |                                    |         |
|----------|--------------------------------------------|----------|------|---------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------|------------------------------------|---------|
| DB915936 | gi 54445268 gb <br>CV558564.1 <br>CV558564 | 5.00E-20 | 47.8 | pentatricopeptide<br>repeat domain 3                                      |                                                                                                                |                                    |         |
| DB915948 | GS008053                                   | 0.006    | 32.2 |                                                                           |                                                                                                                |                                    |         |
| DB915966 | gi 49673531 gb <br>CO427237.1 <br>CO427237 | 2.00E-28 | 126  | propionyl-coenzyme<br>aalpha polypeptide                                  | F:GO:0005524,F:GO:<br>0016874,P:GO:<br>0009102,P:GO:<br>0008152,F:GO:<br>0003824,F:GO:<br>0009374,C:GO:0005575 | Biotin_carb_C                      |         |
| DB915971 | gi 85185754 gb <br>DW600651.1 <br>DW600651 | 0        | 131  | mtp18_danreame:<br>full=mitochondrial 18<br>kda proteiname:<br>full=mtp18 | P:GO:0006915,C:GO:<br>0005739,F:GO:<br>0008270,F:GO:<br>0004089,P:GO:0015976                                   | MTP18                              |         |
| DB915990 | gi 75841529 gb <br>DT871789.1 DT871789     | 0        | 212  | nuclear transcription<br>factorbeta                                       | C:GO:0005622                                                                                                   | CBFD_NFYB_<br>HMF, Pfam-<br>B_5136 | 0.08562 |
| DB915991 | gi 22803689 gb <br>BU501318.1 <br>BU501318 | 4.00E-12 | 72.5 | cg12393 cg12393-pa                                                        |                                                                                                                | PH                                 |         |
| DB915994 | GS008140                                   | 0.006    | 34.2 |                                                                           |                                                                                                                |                                    |         |
| DB916009 | gi 85168246 gb <br>DW594662.1 <br>DW594662 | 3.00E-22 | 103  | sulfide:quinone<br>oxidoreductase                                         |                                                                                                                |                                    |         |
| DB916010 | gi 62839787 gb <br>DN869846.1 <br>DN869846 | 0.0002   | 50.1 |                                                                           |                                                                                                                |                                    |         |
| DB916027 | GS020504                                   | 0.006    | 34.2 |                                                                           |                                                                                                                |                                    |         |
| DB916040 | GS014173                                   | 0.005    | 34.2 |                                                                           |                                                                                                                |                                    |         |
| DB916042 | gi 46820184 gb <br>CN507560.1 <br>CN507560 | 0        | 361  | dehydrodolichyl<br>diphosphate synthase                                   | F:GO:0016740,C:GO:<br>0005575                                                                                  | Prenyltransf                       | 0.8832  |
| DB916052 | GS020629                                   | 0.001    | 36.2 |                                                                           |                                                                                                                |                                    |         |
| DB916059 | gi 46815093 gb <br>CN502469.1 <br>CN502469 | 0        | 342  | isocitrate<br>dehydrogenase 2<br>(nadp+)mitochondrial                     | P:GO:0008152,F:GO:<br>0004450                                                                                  | Iso_dh                             | 1.35172 |

|          |                                            |          |      |                             |                                                             |                                                  |         |
|----------|--------------------------------------------|----------|------|-----------------------------|-------------------------------------------------------------|--------------------------------------------------|---------|
| DB916069 | gi 40542491 gb <br>BU694178.1 <br>BU694178 | 0.003    | 46.1 |                             |                                                             |                                                  |         |
| DB916103 | BY798920                                   | 0.0002   | 44.1 |                             |                                                             |                                                  |         |
| DB916106 | BY799441                                   | 0.004    | 40.1 |                             |                                                             |                                                  |         |
| DB916112 | BY795187                                   | 0        | 226  | ribosomal protein l27       |                                                             | Ribosomal_L2<br>7e                               |         |
| DB916114 | gi 19401994 gb <br>BM942131.1 <br>BM942131 | 0.003    | 46.1 |                             |                                                             | Pfam-B_9429,<br>Pfam-<br>B_2280,Pfam-<br>B_19169 |         |
| DB916138 | gi 62889609 gb <br>DN904846.1 <br>DN904846 | 0.009    | 40.1 |                             |                                                             |                                                  |         |
| DB916143 | gi 40318253 gb <br>CK352366.1 <br>CK352366 | 0.003    | 46.1 |                             |                                                             |                                                  |         |
| DB916147 | GS004664                                   | 0.002    | 36.2 |                             |                                                             |                                                  |         |
| DB916154 | gi 37635939 gb <br>CF739601.1 CF739601     | 0        | 201  | histone h2b-3               | C:GO:0000786,F:GO:<br>0003677,P:GO:<br>0006334,C:GO:0005634 | Histone                                          | 1.67955 |
| DB916156 | gi 40319267 gb <br>CK353380.1 <br>CK353380 | 0.009    | 37.3 |                             |                                                             |                                                  |         |
| DB916160 | gi 19399078 gb <br>BM939926.1 <br>BM939926 | 0.005    | 42.3 |                             |                                                             |                                                  |         |
| DB916166 | gi 23650882 gb <br>BU728721.1 <br>BU728721 | 0.003    | 46.1 |                             |                                                             |                                                  |         |
| DB916182 | GS013860                                   | 0.006    | 34.2 |                             |                                                             |                                                  |         |
| DB916190 | gi 62041668 gb <br>DN689395.1 <br>DN689395 | 4.00E-29 | 107  | lmbr1 domain-<br>containing |                                                             |                                                  | 0.9933  |

|          |                                    |          |                                                       |                                                                  |                                                   |         |
|----------|------------------------------------|----------|-------------------------------------------------------|------------------------------------------------------------------|---------------------------------------------------|---------|
| DB916201 | gi 62832587 gb DN862938.1 DN862938 | 4.00E-37 | 155 ring finger protein 115                           | F:GO:0046872,F:GO:0008270,F:GO:0005515                           | Pfam-B_13390,Pfam-B_2600,Pfam-B_14559,Pfam-B_9059 | 1.1331  |
| DB916209 | gi 62853764 gb DN883809.1 DN883809 | 0.004    | 42.8                                                  |                                                                  |                                                   |         |
| DB916211 | GS004800                           | 0.002    | 36.2                                                  |                                                                  |                                                   |         |
| DB916225 | GS004616                           | 0.006    | 34.2                                                  |                                                                  |                                                   |         |
| DB916242 | gi 57593145 gb CX566116.1 CX566116 | 0        | 111 meningioma expressed antigen 5                    | F:GO:0016787,F:GO:0016740                                        | Pfam-B_600,Pfam-B_600                             | 0.37438 |
| DB916251 | GS008258                           | 0.006    | 34.2                                                  |                                                                  |                                                   |         |
| DB916276 | gi 62032998 gb DN685038.1 DN685038 | 0.004    | 37.7                                                  |                                                                  |                                                   |         |
| DB916277 | gi 54439969 gb CV555940.1 CV555940 | 5.00E-06 | 52.4 ---NA---                                         |                                                                  | Pfam-B_4326,Pfam-B_4326                           |         |
| DB916280 | gi 54447646 gb CV559734.1 CV559734 | 4.00E-31 | 112 kelch domain containing 10                        | F:GO:0003674,P:GO:0008150                                        | Kelch_1,Kelch_2                                   |         |
| DB916283 | gi 62872736 gb DN887973.1 DN887973 | 0        | 355 chaperonin containingsubunit 7                    | P:GO:0006457,F:GO:0051082,F:GO:0005524,F:GO:0042802,C:GO:0005832 | Cpn60_TCP1                                        | 2.6597  |
| DB916293 | gi 24025296 gb BU840896.1 BU840896 | 0.004    | 38.6                                                  |                                                                  |                                                   |         |
| DB916298 | BY800055                           | 0.0009   | 42.1                                                  |                                                                  |                                                   |         |
| DB916304 | gi 62883081 gb DN898318.1 DN898318 | 1.00E-09 | 64.3 organic cation transporter family member (oct-1) | F:GO:0015101,P:GO:0015695,C:GO:0016021                           | Sugar_tr                                          | 1.1984  |
| DB916307 | gi 24721459 gb CA390418.1 CA390418 | 7.00E-05 | 48.7 neuroendocrine protein 7b2                       |                                                                  | Secretogranin_V                                   | 1.3485  |

|          |                                                           |          |      |                                                   |                                                     |                            |        |
|----------|-----------------------------------------------------------|----------|------|---------------------------------------------------|-----------------------------------------------------|----------------------------|--------|
| DB916330 | gi 13148998 gb BG342560.1 BG342560                        | 1.00E-06 | 53.8 | cell adhesion molecule                            |                                                     | Pfam-B_2000,fn3            | 1.6787 |
| DB916334 | gi 62884905 gb DN900142.1 DN900142                        | 0.002    | 30.4 |                                                   |                                                     |                            |        |
| DB916350 | gi 18973569 gb BM666120.1 BM666120                        | 0.0003   | 44.6 |                                                   |                                                     | Pfam-B_4326                |        |
| DB916353 | gi 15715666 gb BI738653.1 BI738653                        | 2.00E-42 | 158  | progesterone receptor membrane component 1        |                                                     | Pfam-B_3152,Cyt-b5         |        |
| DB916355 | gi 32274839 gb CD723985.1 CD723985                        | 0.003    | 46.1 |                                                   |                                                     |                            |        |
| DB916366 | gi 16779712 gb BM050445.1 BM050445                        | 8.00E-08 | 44.6 | multisynthetase complex p38 auxiliary component   |                                                     | HPC2,Pfam-B_18106,GST_C    |        |
| DB916367 | gi 14960856 gb BI296435.1 BI296435                        | 0.003    | 46.1 |                                                   |                                                     |                            |        |
| DB916376 | gi 21120176 gb BQ424861.1 BQ424861                        | 7.00E-19 | 66.3 | ephrin receptor                                   | F:GO:0016740                                        | fn3, fn3, Pfam-B_2000, WSC |        |
| DB916378 | gi 24719633 gb CA389458.1 CA389458                        | 5.00E-06 | 52.4 | zinc transporter                                  | P:GO:0006829,F:GO:0005385                           | Zip                        |        |
| DB916388 | gi 15707388 gb BI730375.1 BI730375                        | 0.006    | 28.6 |                                                   |                                                     |                            |        |
| DB916409 | gi 77501868 gb DV214183.1 DV214183                        | 6.00E-12 | 72.1 | mitochondrial phosphate carrier protein cg4994-pa | C:GO:0005743,C:GO:0016021,F:GO:0005488,P:GO:0006810 | Mito_carr                  |        |
| DB916428 | <b>Embryo specific</b> gi 42746200 gb CK780522.1 CK780522 | 3.00E-25 | 69.2 | ded protein                                       |                                                     | Pfam-B_2199                |        |
| DB916446 | gi 37635569 gb CF739232.1 CF739232                        | 0.001    | 44.1 |                                                   |                                                     |                            |        |
| DB916454 | BY799681                                                  | 8.00E-14 | 50.1 | ---NA---                                          |                                                     | Pkinase                    |        |

|          |                                    |          |      |                                                               |                                                     |                   |
|----------|------------------------------------|----------|------|---------------------------------------------------------------|-----------------------------------------------------|-------------------|
| DB916465 | gi 49672835 gb CO426541.1 CO426541 | 2.00E-35 | 148  | brefeldin a-inhibited guanine nucleotide-exchange protein 1   |                                                     | 1.0219            |
| DB916467 | BY799112                           | 0.004    | 40.1 |                                                               |                                                     |                   |
| DB916469 | gi 62023664 gb DN680663.1 DN680663 | 4.00E-19 | 95.9 | prp38 pre-mrna processing factor 38domain                     | PRP38                                               | 0.55547           |
| DB916481 | gi 15713843 gb BI736830.1 BI736830 | 5.00E-42 | 128  | subfamilymember 9                                             | DnaJ,Pfam-B_4588, Pfam-B_19269,Pfam-B_9394          | 0.39313           |
| DB916512 | gi 62827568 gb DN857919.1 DN857919 | 7.00E-13 | 40.9 | resistance to inhibitors of cholinesterase 8 homolog a        | C:GO:0005737 Ric8                                   |                   |
| DB916514 | gi 15713384 gb BI736371.1 BI736371 | 6.00E-24 | 87.2 | dopamine receptor-1                                           | 7tm_1                                               | 0.60642           |
| DB916520 | gi 41341993 gb CK621107.1 CK621107 | 6.00E-22 | 105  | short chain dehydrogenase                                     | F:GO:0005488,F:GO:0016491,P:GO:0008152,F:GO:0003824 | adh_short 2.12755 |
| DB916529 | BY799434                           | 0.0009   | 42.1 | neighbor of brca1 gene 1                                      |                                                     |                   |
| DB916541 | gi 9382869 gb BB465680.1 BB465680  | 0.01     | 44.1 |                                                               |                                                     |                   |
| DB916545 | gi 85184210 gb DW600145.1 DW600145 | 3.00E-30 | 98.2 | ---NA---                                                      | CSD                                                 | 1.86407           |
| DB916546 | gi 32464111 gb CD805285.1 CD805285 | 0        | 246  | mitogen-activated protein kinase kinase 1                     | P:GO:0006468,F:GO:0005524,F:GO:0004674,F:GO:0004713 | Pkinase           |
| DB916547 | gi 1088214 gb H92636.1 H92636      | 0.0006   | 48.1 | ---NA---                                                      |                                                     |                   |
| DB916552 | GS013863                           | 0.0004   | 38.2 |                                                               |                                                     |                   |
| DB916575 | gi 19042248 gb BM721984.1 BM721984 | 2.00E-25 | 104  | pleckstrin homology domainfamily m (with run domain) member 2 | C:GO:0016020 PH                                     |                   |

|          |                                                              |          |      |                                                               |                                                                  |                    |         |
|----------|--------------------------------------------------------------|----------|------|---------------------------------------------------------------|------------------------------------------------------------------|--------------------|---------|
| DB916580 | gi 13287696 gb BG394248.1 BG394248                           | 7.00E-34 | 131  | cug tripletrna binding protein 1                              | F:GO:0003723,C:GO:0005737,F:GO:0000166,P:GO:0006397,C:GO:0005634 | Pfam-B_9954, RRM_1 |         |
| DB916581 | gi 13298115 gb BG404667.1 BG404667                           | 0        | 197  | trap1 protein                                                 | C:GO:0005615,C:GO:0005739,F:GO:0000166                           | HSP90              | 0.97455 |
| DB916589 | BY799992                                                     | 0.003    | 40.1 |                                                               |                                                                  |                    |         |
| DB916598 | gi 62040511 gb DN688828.1 DN688828                           | 0.009    | 44.1 |                                                               |                                                                  |                    |         |
| DB916602 | gi 62828226 gb DN858577.1 DN858577                           | 1.00E-22 | 97.7 | mitochondrial ribosomal protein s31                           | F:GO:0003677,C:GO:0005634,C:GO:0005739,P:GO:0006355              |                    | 1.06517 |
| DB916610 | gi 15713449 gb BI736436.1 BI736436                           | 0        | 199  | ryanodine receptorbrain                                       |                                                                  |                    |         |
| DB916621 | gi 24025046 gb BU840646.1 BU840646                           | 0        | 260  | flj10081 protein                                              |                                                                  |                    |         |
| DB916638 | <b>Positive selection</b> gi 62841191 gb DN871250.1 DN871250 | 0        | 443  | glucose-6-phosphate isomerase                                 |                                                                  | PGI                | 2.77942 |
| DB916649 | <b>Embryo specific</b> gi 46565340 gb CN483836.1 CN483836    | 9.81E-45 | 180  |                                                               |                                                                  | DUF618             | 0.46992 |
| DB916691 | gi 23679586 gb BU740243.1 BU740243                           | 0.003    | 46.1 |                                                               |                                                                  |                    |         |
| DB916696 | gi 22368572 gb BQ953094.1 BQ953094                           | 0        | 430  | septin-1 (diff6 protein homolog) (protein innocent bystander) |                                                                  | Septin             | 0.64062 |
| DB916698 | GS014086                                                     | 0.005    | 34.2 |                                                               |                                                                  |                    |         |
| DB916705 | gi 16779962 gb BM050695.1 BM050695                           | 0.0002   | 46.9 | isoform cra_a                                                 | P:GO:0007067,F:GO:0005085,C:GO:0005634,F:GO:0003677              |                    |         |

|          |                                                              |          |      |                                                                              |                                                                  |                                 |         |
|----------|--------------------------------------------------------------|----------|------|------------------------------------------------------------------------------|------------------------------------------------------------------|---------------------------------|---------|
| DB916708 | gi 22810996 gb BU504763.1 BU504763                           | 0.003    | 46.1 |                                                                              |                                                                  |                                 |         |
| DB916710 | gi 22677816 gb BU163864.1 BU163864                           | 0        | 424  | ---NA---                                                                     |                                                                  | AdoHcyase_N AD, AdoHcyase       | 0.61617 |
| DB916716 | gi 21119271 gb BQ423947.1 BQ423947                           | 0        | 444  | solute carrier family 25 member 3 isoform b precursor isoform 5              | C:GO:0005743,F:GO:0015317,P:GO:0006810,C:GO:0016021              | Mito_carr, Mito_carr, Mito_carr | 0.3872  |
| DB916728 | gi 49677532 gb CO431238.1 CO431238                           | 0        | 345  | retinoic acid induced 17                                                     |                                                                  | zf-MIZ                          | 3.2364  |
| DB916730 | gi 45305774 gb CK876143.1 CK876143                           | 4.00E-08 | 53.3 | transposable element tcb1 transposase                                        | F:GO:0004803,P:GO:0015074,P:GO:0006313,F:GO:0003677,C:GO:0005634 | Pfam-B_261,Transposase_5        |         |
| DB916731 | <b>Positive selection</b> gi 85209685 gb DW609023.1 DW609023 | 0        | 594  | splicing factorpartial                                                       |                                                                  | Mov34,PROCT                     | 2.29367 |
| DB916737 | gi 85186909 gb DW601057.1 DW601057                           | 2.00E-13 | 77.1 | cell growth regulator with ring finger domain 1                              |                                                                  | Pfam-B_14559                    |         |
| DB916738 | gi 46867777 gb CN539621.1 CN539621                           | 0        | 477  | protein phosphatase 2 (formerly 2a)regulatory subunit a (pr 65)alpha isoform | F:GO:0005515,C:GO:0005829                                        | HEAT,HEAT,H EAT,HEAT,HEAT       | 1.53838 |
| DB916747 | gi 16498433 gb BB664679.1 BB664679                           | 1.00E-05 | 51   | limbic system-associated membrane protein                                    |                                                                  | I-set,I-set                     |         |
| DB916749 | gi 37600524 gb CF726356.1 CF726356                           | 0.0006   | 36.8 | group ii plp decarboxylase                                                   |                                                                  |                                 |         |
| DB916750 | gi 18511152 gb BM462112.1 BM462112                           | 4.00E-16 | 86.1 | neurofilament protein                                                        | C:GO:0005882,F:GO:0005198                                        | Filament,Pfam-B_9207, IncA      | 0.14146 |
| DB916759 | <b>Embryo specific</b> GS013851                              | 0.006    | 34.2 |                                                                              |                                                                  |                                 |         |

|          |                                                           |          |      |                                     |                                                     |                                    |         |
|----------|-----------------------------------------------------------|----------|------|-------------------------------------|-----------------------------------------------------|------------------------------------|---------|
| DB916787 | gi 21761396 gb BQ636937.1 BQ636937                        | 3.00E-32 | 138  | briggsae cbr-kpc-1 protein          | P:GO:0006508,F:GO:0004289                           | P_proprotein                       | 1.35643 |
| DB916797 | GS020737                                                  | 0.006    | 24.9 |                                     |                                                     | Toxin_9                            |         |
| DB916803 | gi 5034953 gb AI717649.1 AI717649                         | 0.01     | 44.1 |                                     |                                                     |                                    |         |
| DB916806 | <b>Embryo specific</b> gi 18511097 gb BM462057.1 BM462057 | 7.01E-45 | 156  | lipaselysosomalcholesterol esterase | F:GO:0003824                                        | Abhydro_lipase,Abhydrolase_1       |         |
| DB916826 | gi 62840200 gb DN870259.1 DN870259                        | 1.00E-28 | 127  | aspartyl-trna synthetase 2          | F:GO:0016874,C:GO:0005739,F:GO:0000166              | tRNA-synt_2, tRNA-synt_2,tRNA_anti |         |
| DB916834 | gi 119789939 gb EH282497.1 EH282497                       | 0.009    | 44.1 |                                     |                                                     |                                    |         |
| DB916841 | GS020607                                                  | 0.003    | 31.8 |                                     |                                                     |                                    |         |
| DB916855 | gi 19038856 gb BM719944.1 BM719944                        | 0.009    | 44.1 |                                     |                                                     |                                    |         |
| DB916864 | gi 62834106 gb DN864457.1 DN864457                        | 5.00E-11 | 68.9 | transmembrane protein 68            | F:GO:0008415,P:GO:0008152,C:GO:0016021,C:GO:0016020 |                                    |         |
| DB916866 | gi 46823056 gb CN510432.1 CN510432                        | 4.00E-27 | 122  | ras-related protein rab-2           |                                                     |                                    | 1.18766 |
| DB916884 | gi 55687774 gb CV782834.1 CV782834                        | 7.00E-11 | 68.4 | neuroligin 2                        | F:GO:0004104,F:GO:0016787                           | COesterase                         |         |
| DB916892 | gi 21762757 gb BQ638298.1 BQ638298                        | 0.003    | 46.1 |                                     |                                                     |                                    |         |
| DB916896 | gi 46867496 gb CN539340.1 CN539340                        | 6.00E-43 | 174  | cg32486 cg32486-pd                  |                                                     |                                    | 1.59183 |

|          |                                                              |          |      |                                                                       |                                                                  |                                          |         |
|----------|--------------------------------------------------------------|----------|------|-----------------------------------------------------------------------|------------------------------------------------------------------|------------------------------------------|---------|
| DB916905 | gi 19043030 gb BM722448.1 BM722448                           | 1.00E-42 | 159  | myosin heavy chain v                                                  | C:GO:0016459,F:GO:0005524,F:GO:0003774                           | Pfam-B_7363                              |         |
| DB916916 | gi 54449541 gb CV560673.1 CV560673                           | 0        | 385  | pyruvate kinase                                                       | F:GO:0004743,F:GO:0030955,F:GO:0000287,P:GO:0006096              | PK_C,PK                                  | 3.11525 |
| DB916921 | <b>Positive selection</b> gi 62886183 gb DN901420.1 DN901420 | 5.00E-40 | 163  | 14-3-3 zeta                                                           |                                                                  | 2014/03/03                               | 3.81437 |
| DB916930 | gi 57592233 gb CX565204.1 CX565204                           | 0        | 346  | cop9 (constitutive photomorphogenic) subunit 4 (arabidopsis thaliana) | F:GO:0005515,C:GO:0008180                                        | LppC,RPN7                                | 0.88055 |
| DB916931 | gi 24718100 gb CA388673.1 CA388673                           | 0.001    | 43.7 |                                                                       |                                                                  |                                          |         |
| DB916935 | gi 62879685 gb DN894922.1 DN894922                           | 0        | 213  | cathepsin b                                                           |                                                                  | Propeptide_C1,Peptidase_C1               | 1.5871  |
| DB916953 | gi 49673021 gb CO426727.1 CO426727                           | 6.00E-07 | 55.2 | sh2-domain-containing inositol 5-phosphatase 2a                       | C:GO:0044464                                                     | Pfam-B_1233                              |         |
| DB916959 | gi 85205875 gb DW607560.1 DW607560                           | 3.00E-26 | 77.6 | solute carrier family 7 member 9+at                                   |                                                                  | AA_permease                              | 0.71213 |
| DB916961 | GS020727                                                     | 0.005    | 32.2 |                                                                       |                                                                  |                                          |         |
| DB916997 | gi 85194217 gb DW603108.1 DW603108                           | 1.00E-11 | 49.6 | ---NA---                                                              |                                                                  |                                          | 0.8545  |
| DB917015 | gi 10202485 gb BE781287.1 BE781287                           | 0        | 308  | glycyl-trna synthetase                                                | P:GO:0006426,P:GO:0045055,F:GO:0005524,C:GO:0030141,F:GO:0004820 | HGTP_anticonodon,Pfam-B_5084,Pfam-B_8963 | 1.65772 |
| DB917032 | <b>Embryo specific</b> gi 37599680 gb CF725512.1 CF725512    | 0        | 236  | cullin-associated and neddylation-dissociated 1                       | C:GO:0005575                                                     |                                          | 0.5603  |

|          |                                     |          |      |                                                                                        |                                                                                                                                                |                              |         |
|----------|-------------------------------------|----------|------|----------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------|---------|
| DB917065 | gi 11974693 gb BF689285.1 BF689285  | 2.00E-27 | 123  | poly a bindingcytoplasmic 1 b                                                          | F:GO:0005488                                                                                                                                   | PABP                         | 1.63415 |
| DB917078 | BY795896                            | 2.00E-25 | 111  | arystal structure of the habc domain of neuronal syntaxin from the squid loligo pealei | C:GO:0016020,F:GO:0005484,P:GO:0016192,P:GO:0006886                                                                                            | Syntaxin                     | 0.92096 |
| DB917115 | gi 46463206 gb CN457480.1 CN457480  | 0        | 522  | ribonucleotide reductase m1                                                            | C:GO:0005971,P:GO:0009263,P:GO:0006260,F:GO:0005515,P:GO:0051259,F:GO:0017076,F:GO:0004748                                                     | Ribonuc_red_l gC             |         |
| DB917131 | gi 62021326 gb DN679488.1 DN679488  | 7.00E-32 | 86.8 | acetyl-coenzyme a carboxylase beta                                                     |                                                                                                                                                | CPSase_L_D2, CPSase_L_cha in | 0.65265 |
| DB917133 | gi 119782557 gb EH279172.1 EH279172 | 2.00E-12 | 53.8 | selenoprotein w2a                                                                      | F:GO:0008430                                                                                                                                   | Rdx                          |         |
| DB917141 | BY795054                            | 2.00E-14 | 74.8 | af454399_1fasciclin-like protein                                                       |                                                                                                                                                | Fasciclin,Fasci clin         |         |
| DB917148 | gi 50138719 gb CO471579.1 CO471579  | 7.00E-15 | 81.7 | glutaredoxin-mitochondrial precursor                                                   | F:GO:0009055,F:GO:0015035,C:GO:0005575                                                                                                         | Glutaredoxin                 |         |
| DB917152 | gi 54449072 gb CV560438.1 CV560438  | 0.003    | 46.1 |                                                                                        |                                                                                                                                                |                              |         |
| DB917159 | gi 15713204 gb BI736191.1 BI736191  | 0.0001   | 33.6 | fras1 related extracellular matrix protein 1                                           | F:GO:0005529,P:GO:0007275,C:GO:0005578,C:GO:0005576,C:GO:0005575,F:GO:0005515,P:GO:0007160,F:GO:0046872,F:GO:0005509,P:GO:0007155,F:GO:0005488 | Lectin_C                     | 0.7063  |

|          |                                            |          |      |                                                                        |                                                                                                                                                                                                                                       |                   |
|----------|--------------------------------------------|----------|------|------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------|
| DB917161 | gi 18987264 gb <br>BM677368.1 <br>BM677368 | 5.00E-05 | 49.2 |                                                                        |                                                                                                                                                                                                                                       |                   |
| DB917181 | gi 15708863 gb <br>BI731850.1 BI731850     | 0        | 436  | heat shock protein 90                                                  | HSP90                                                                                                                                                                                                                                 | 1.35662           |
| DB917183 | gi 23657488 gb <br>BU732018.1 <br>BU732018 | 0.0001   | 47.8 |                                                                        |                                                                                                                                                                                                                                       |                   |
| DB917231 | gi 62880192 gb <br>DN895429.1 <br>DN895429 | 9.00E-15 | 81.3 | nuclear receptor<br>subfamilygroupmemb<br>er 5                         | F:GO:0043565,F:GO:<br>0003700,C:GO:<br>0005634,F:GO:<br>0004879,F:GO:<br>0008270,P:GO:<br>0006829,P:GO:<br>0006355,F:GO:<br>0004872,P:GO:<br>0006353,F:GO:<br>0046872,P:GO:<br>0031564,P:GO:<br>0006350,P:GO:<br>0007601,F:GO:0003707 | Hormone_rece<br>p |
| DB917250 | gi 15715211 gb <br>BI738198.1 BI738198     | 1.00E-06 | 41   | kinesin-like protein<br>unc-104 (protein<br>immaculate<br>connections) |                                                                                                                                                                                                                                       |                   |
| DB917271 | gi 32181141 gb <br>CD679410.1 <br>CD679410 | 0.0004   | 35.9 | ---NA---                                                               |                                                                                                                                                                                                                                       |                   |
| DB917289 | BY799577                                   | 0.004    | 40.1 |                                                                        |                                                                                                                                                                                                                                       |                   |
| DB917384 | gi 37604110 gb <br>CF729942.1 CF729942     | 7.00E-10 | 65.1 | still life type 1                                                      |                                                                                                                                                                                                                                       | 0.77972           |
| DB917386 | BY795966                                   | 0.003    | 40.1 |                                                                        |                                                                                                                                                                                                                                       |                   |
| DB917419 | gi 32179217 gb <br>CD677486.1 <br>CD677486 | 3.00E-29 | 117  | nudix hydrolase 6                                                      |                                                                                                                                                                                                                                       |                   |
| DB917433 | BY796191                                   | 3.00E-06 | 33.1 |                                                                        |                                                                                                                                                                                                                                       |                   |

|          |                                                       |          |      |                                                |                                        |                         |
|----------|-------------------------------------------------------|----------|------|------------------------------------------------|----------------------------------------|-------------------------|
| DB917443 | gi 22681209 gb BU167225.1 BU167225                    | 0.003    | 46.1 |                                                | Pfam-B_16856                           |                         |
| DB917452 | gi 24731857 gb CA395939.1 CA395939                    | 3.00E-07 | 56.5 | ---NA---                                       | Pkinase                                | 1.93198                 |
| DB917494 | gi 22803240 gb BU501159.1 BU501159                    | 2.00E-32 | 108  | elongation factor ts                           | EF_TS,EF_TS                            | 0.72332                 |
| DB917518 | BY795051                                              | 0        | 242  | ribosomal protein l15                          | C:GO:0005840,F:GO:0003735,P:GO:0006412 | Ribosomal_L1 5e 1.73916 |
| DB917523 | BY795432                                              | 0.009    | 31.3 |                                                |                                        |                         |
| DB917532 | gi 15707842 gb BI730829.1 BI730829                    | 3.00E-40 | 163  | protein tyrosinereceptorm                      | F:GO:0016791,F:GO:0004872,P:GO:0006470 | Y_phosphatase           |
| DB917535 | gi 19017737 gb BM704479.1 BM704479                    | 5.04E-44 | 143  | basket cg5680-partial                          | F:GO:0004707,P:GO:0006468,F:GO:0005524 | Pkinase 1.8378          |
| DB917590 | BY796013                                              | 0.006    | 36.8 |                                                |                                        |                         |
| DB917593 | gi 85208787 gb DW608631.1 DW608631                    | 0.006    | 41.4 |                                                | SH3_1                                  |                         |
| DB917622 | gi 46462290 gb CN456564.1 CN456564                    | 0.009    | 44.1 | ---NA---                                       |                                        |                         |
| DB917660 | GS004604                                              | 0.006    | 34.2 |                                                | UIM                                    |                         |
| DB917670 | GS013969                                              | 0.005    | 34.2 |                                                |                                        |                         |
| DB917672 | Embryo specific gi 75844134 gb DT874394.1 DT874394    | 1.00E-07 | 53.5 | trafficking protein particle complex subunit 3 |                                        |                         |
| DB917693 | gi 119789608 gb EH282167.1 EH282167                   | 3.00E-26 | 119  | ---NA---                                       |                                        | 0.55793                 |
| DB917697 | Positive selection gi 62830261 gb DN860612.1 DN860612 | 5.04E-44 | 178  | lethals1921 cg2245-pa                          |                                        | 2.54494                 |
| DB917703 | BY799323                                              | 0.004    | 40.1 |                                                |                                        |                         |

|          |                    |                                            |          |      |                                                                                                                                                                                                                                                               |                                            |                                       |         |
|----------|--------------------|--------------------------------------------|----------|------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------|---------------------------------------|---------|
| DB917713 |                    | gi 10592574 gb <br>BE952277.1 BE952277     | 5.00E-40 | 165  | atp-bindingsub-family<br>fmember 2                                                                                                                                                                                                                            | F:GO:0005524,F:GO:<br>0016887              | Pfam-B_11162                          |         |
| DB917724 |                    | GS019928                                   | 0.002    | 36.2 |                                                                                                                                                                                                                                                               |                                            |                                       |         |
| DB917726 | Positive selection | gi 85203147 gb <br>DW606219.1 <br>DW606219 | 0        | 357  | homolog 1                                                                                                                                                                                                                                                     | P:GO:0008150,C:GO:<br>0005575              | FtsJ,Pfam-<br>B_40                    | 5.43052 |
| DB917728 |                    | gi 46815915 gb <br>CN503291.1 <br>CN503291 | 1.00E-05 | 44   | pleiotrophin(heparin-<br>binding growth-<br>associated molecule)<br>(hb-gam) (heparin-<br>binding growth factor<br>8) (hbgf-8)<br>(osteoblast-specific<br>factor 1) (osf-1)<br>(heparin-binding<br>neutrophilic factor)<br>(heparin-binding brain<br>mitogen) |                                            | PTN_MK_C,PT<br>N_MK_C,PTN_<br>MK_C    | 0.91517 |
| DB917766 | Embryo specific    | gi 37601458 gb <br>CF727290.1 CF727290     | 1.00E-12 | 48.3 | lunapark b isoform 1                                                                                                                                                                                                                                          |                                            | 7tm_6,Pfam-<br>B_7282,Pfam-<br>B_8566 |         |
| DB917773 |                    | gi 85183291 gb <br>DW599817.1 <br>DW599817 | 0        | 269  | dna topoisomerase<br>type i                                                                                                                                                                                                                                   | F:GO:0003677,P:GO:<br>0006259              | Topoisom_I_N                          | 0.786   |
| DB917775 |                    | gi 22703862 gb <br>BU189878.1 <br>BU189878 | 0.01     | 44.1 |                                                                                                                                                                                                                                                               |                                            |                                       |         |
| DB917777 |                    | GS013936                                   | 9.00E-05 | 40.1 |                                                                                                                                                                                                                                                               |                                            |                                       |         |
| DB917780 |                    | gi 22810959 gb <br>BU504726.1 <br>BU504726 | 6.00E-37 | 99.6 | death-associated<br>protein 6                                                                                                                                                                                                                                 | C:GO:0016605,F:GO:<br>0005515,F:GO:0016564 | Daxx                                  |         |
| DB917797 |                    | BY795427                                   | 1.00E-14 | 70.7 | cofi_schpoame:<br>full=cofilin<br>full=actin-<br>depolymerizing factor<br>1                                                                                                                                                                                   | C:GO:0044424                               | Cofilin_ADF,Pf<br>am-B_8155           | 1.5354  |

|          |                                            |          |      |                                                                  |                                                             |              |
|----------|--------------------------------------------|----------|------|------------------------------------------------------------------|-------------------------------------------------------------|--------------|
| DB917800 | gi 49677444 gb <br>CO431150.1 <br>CO431150 | 0        | 164  | btb poz domain-<br>containing protein 7                          |                                                             | BACK         |
| DB917801 | gi 62052542 gb <br>DN694838.1 <br>DN694838 | 0.01     | 41.4 |                                                                  |                                                             | Pfam-B_13263 |
| DB917810 | gi 12042305 gb <br>BF726394.1 BF726394     | 0.0007   | 48.1 |                                                                  |                                                             |              |
| DB917850 | GS020606                                   | 0.006    | 34.2 |                                                                  |                                                             |              |
| DB917867 | gi 57591534 gb <br>CX564505.1 <br>CX564505 | 0        | 410  | btb poz domain-<br>containing protein<br>kctd3                   |                                                             |              |
| DB917874 | gi 85170412 gb <br>DW595532.1 <br>DW595532 | 1.00E-16 | 87.7 | leukotriene a-4<br>hydrolase                                     | F:GO:0016787                                                |              |
| DB917876 | gi 19019757 gb <br>BM706499.1 <br>BM706499 | 6.00E-36 | 121  | cp072_xenlaame:<br>full=upf0472 protein<br>c16orf72 homolog      |                                                             | 1.40699      |
| DB917901 | GS014081                                   | 0.006    | 34.2 |                                                                  |                                                             |              |
| DB917919 | gi 49670130 gb <br>CO424003.1 <br>CO424003 | 4.00E-23 | 109  | sorting nexin 4                                                  | F:GO:0035091,P:GO:<br>0007154,F:GO:<br>0005515,P:GO:0015031 | Vps5         |
| DB917932 | gi 15709733 gb <br>BI732720.1 BI732720     | 0.0002   | 46.9 | ---NA---                                                         |                                                             | Pfam-B_1587  |
| DB917946 | GS020744                                   | 0.0003   | 38.2 | ---NA---                                                         |                                                             |              |
| DB917957 | GS020498                                   | 0.005    | 34.2 |                                                                  |                                                             |              |
| DB917972 | GS004859                                   | 0.001    | 36.2 |                                                                  |                                                             |              |
| DB917999 | gi 62879485 gb <br>DN894722.1 <br>DN894722 | 0        | 251  | thioredoxin domain<br>containing 4<br>(endoplasmic<br>reticulum) |                                                             |              |
| DB918001 | gi 85178073 gb <br>DW598188.1 <br>DW598188 | 0        | 248  | solute carrier<br>family member e2                               | TPT,TPT,EamA                                                | 0.5436       |
| DB918016 | gi 37597892 gb <br>CF723724.1 CF723724     | 0.0001   | 47.8 | ---NA---                                                         |                                                             |              |

|          |                                            |          |      |                                   |                                                             |                                   |         |
|----------|--------------------------------------------|----------|------|-----------------------------------|-------------------------------------------------------------|-----------------------------------|---------|
| DB918019 | gi 32173232 gb <br>CD671492.1 <br>CD671492 | 7.00E-34 | 144  | src family kinase                 | F:GO:0016301,F:GO:<br>0005488                               | Pkinase_Tyr,S<br>H2               | 0.6104  |
| DB918022 | BY800189                                   | 0.01     | 29.9 |                                   |                                                             |                                   |         |
| DB918029 | gi 22692856 gb <br>BU178872.1 <br>BU178872 | 0        | 240  | heat shock 70 kda<br>protein      |                                                             | HSP70                             | 0.03556 |
| DB918034 | gi 20364661 gb <br>BQ189110.1 <br>BQ189110 | 0.0008   | 44.6 | rna-binding protein               |                                                             |                                   |         |
| DB918076 | Embryo specific GS014107                   | 0.008    | 32.2 |                                   |                                                             |                                   |         |
| DB918077 | gi 55687958 gb <br>CV783018.1 <br>CV783018 | 0        | 223  | electrogenic nbc-like<br>protein  | C:GO:0016020,F:GO:<br>0015380,P:GO:0006810                  | HCO3_cotrans<br>p,Pfam-<br>B_1083 | 0.53722 |
| DB918082 | gi 23655294 gb <br>BU730919.1 <br>BU730919 | 4.00E-09 | 50.1 | thymidine<br>phosphorylase        |                                                             | PYNP_C                            |         |
| DB918083 | gi 32180506 gb <br>CD678775.1 <br>CD678775 | 0.003    | 46.1 |                                   |                                                             |                                   |         |
| DB918107 | gi 54450569 gb <br>CV561175.1 <br>CV561175 | 0        | 258  | atp gtp-binding<br>protein        | F:GO:0005525,P:GO:<br>0006397,F:GO:<br>0005524,C:GO:0005634 | MobB,Clp1,Pf<br>am-B_896          | 0.99895 |
| DB918132 | gi 10664305 gb <br>BE988186.1 BE988186     | 0.009    | 42.1 |                                   |                                                             |                                   |         |
| DB918141 | gi 62886101 gb <br>DN901338.1 <br>DN901338 | 0.0008   | 44.1 |                                   |                                                             |                                   |         |
| DB918147 | gi 24720222 gb <br>CA389757.1 <br>CA389757 | 0.003    | 46.1 |                                   |                                                             |                                   |         |
| DB918152 | gi 55688758 gb <br>CV783818.1 <br>CV783818 | 0        | 114  | neprilysin 4 cg4058-<br>isoform a |                                                             | Peptidase_M1<br>3                 | 0.32307 |
| DB918153 | BY796415                                   | 0        | 188  |                                   |                                                             | TRAP_alpha                        |         |

|          |                                    |          |      |                                                                                                                                                                                        |                                        |                                  |         |
|----------|------------------------------------|----------|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------|----------------------------------|---------|
| DB918158 | gi 58031981 gb CX729524.1 CX729524 | 9.00E-10 | 64.9 | novel proteinmurine pdz domain containing 3                                                                                                                                            |                                        | PDZ                              |         |
| DB918181 | gi 62875748 gb DN890985.1 DN890985 | 3.00E-38 | 120  | mgc82665 protein                                                                                                                                                                       | P:GO:0006506,F:GO:0017176,C:GO:0016021 | Gpi1                             |         |
| DB918182 | BY800356                           | 0.002    | 38.2 |                                                                                                                                                                                        |                                        |                                  |         |
| DB918185 | gi 58061096 gb CX734260.1 CX734260 | 0        | 159  | l-isoaspartyl protein carboxyllike                                                                                                                                                     | C:GO:0005737,F:GO:0008168              | PCMT                             | 0.87122 |
| DB918190 | gi 62879490 gb DN894727.1 DN894727 | 1.00E-12 | 74.4 | titin isoform n2-a                                                                                                                                                                     |                                        | fn3 ,fn3,Pfam-B_5281,Pfam-B_2000 | 0.52188 |
| DB918209 | gi 55688982 gb CV784042.1 CV784042 | 0.0008   | 45.1 |                                                                                                                                                                                        |                                        |                                  |         |
| DB918210 | GS014040                           | 0.006    | 34.2 |                                                                                                                                                                                        |                                        |                                  |         |
| DB918213 | gi 16427361 gb BB467415.2 BB467415 | 0.0002   | 50.1 |                                                                                                                                                                                        |                                        |                                  |         |
| DB918219 | gi 62044604 gb DN690834.1 DN690834 | 0.01     | 44.1 |                                                                                                                                                                                        |                                        |                                  |         |
| DB918241 | GS004743                           | 0.005    | 34.2 |                                                                                                                                                                                        |                                        |                                  |         |
| DB918248 | BY798038                           | 1.00E-38 | 154  | zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein dp) (znf-dp) |                                        |                                  | 0.99741 |
| DB918257 | gi 37636248 gb CF739910.1 CF739910 | 1.00E-19 | 48.3 | hippocampus abundant transcript 1                                                                                                                                                      |                                        |                                  |         |

|          |                                                           |          |      |                                                               |                                                                  |                            |         |
|----------|-----------------------------------------------------------|----------|------|---------------------------------------------------------------|------------------------------------------------------------------|----------------------------|---------|
| DB918271 | gi 40319267 gb CK353380.1 CK353380                        | 0.0005   | 27.6 |                                                               |                                                                  |                            |         |
| DB918277 | BY796836                                                  | 0.006    | 35.9 |                                                               |                                                                  | fn3                        |         |
| DB918284 | gi 50139187 gb CO471789.1 CO471789                        | 0        | 258  | transcription elongation regulator 1                          |                                                                  | FF,FF,FF                   |         |
| DB918309 | gi 45305225 gb CK875594.1 CK875594                        | 0.005    | 44.1 | formate dehydrogenase alpha chain                             |                                                                  |                            |         |
| DB918338 | GS020767                                                  | 0.006    | 34.2 |                                                               |                                                                  |                            |         |
| DB918339 | gi 62849576 gb DN879621.1 DN879621                        | 5.04E-44 | 178  | glutamine synthetase                                          | F:GO:0004356,P:GO:0006542                                        | Gln-synt_C                 | 1.71448 |
| DB918345 | gi 50136337 gb CO470468.1 CO470468                        | 1.00E-21 | 103  | ribosomal protein l31                                         | F:GO:0003735,P:GO:0006412,C:GO:0005840,C:GO:0005622              | Ribosomal_L3 1e            | 1.42388 |
| DB918350 | GS020769                                                  | 0.001    | 36.2 |                                                               |                                                                  |                            |         |
| DB918351 | gi 46813993 gb CN501369.1 CN501369                        | 0.002    | 43.7 |                                                               |                                                                  |                            |         |
| DB918355 | BY799695                                                  | 0.003    | 37.7 |                                                               |                                                                  |                            |         |
| DB918369 | gi 85203913 gb DW606597.1 DW606597                        | 0        | 394  | dolichyl-diphosphooligosaccharide-protein glycosyltransferase | C:GO:0005789,F:GO:0005515,C:GO:0016021,F:GO:0004579,P:GO:0018279 | DDOST_48kD                 | 0.10024 |
| DB918380 | <b>Embryo specific</b> gi 49670267 gb CO424140.1 CO424140 | 0        | 296  | tubulin tyrosine ligase-like member 1                         |                                                                  | Pfam-B_195,TTL,Pfam-B_3648 |         |
| DB918384 | GS014081                                                  | 0.006    | 34.2 |                                                               |                                                                  |                            |         |
| DB918385 | gi 62854718 gb DN884763.1 DN884763                        | 5.00E-17 | 88.1 | cytochrome c oxidase subunit vic                              | C:GO:0016020                                                     | COX9,COX6C                 |         |

|          |                                            |          |      |                                      |                                                             |                                                                                           |        |
|----------|--------------------------------------------|----------|------|--------------------------------------|-------------------------------------------------------------|-------------------------------------------------------------------------------------------|--------|
| DB918388 | gi 18511277 gb <br>BM462237.1 <br>BM462237 | 0        | 171  | secreted protein                     | F:GO:0005488                                                | Pfam-<br>B_7013,TPR_1<br>,Pfam-<br>B_3120,TPR_1<br>,Pfam-<br>B_2967,TPR_1<br>,Pfam-B_7103 | 2.0678 |
| DB918400 | gi 49672982 gb <br>CO426688.1 <br>CO426688 | 1.40E-45 | 182  | myst histone<br>acetyltransferase 2  | F:GO:0003700,C:GO:<br>0005634,F:GO:<br>0008270,P:GO:0006355 | MOZ_SAS                                                                                   | 0.4232 |
| DB918405 | gi 75840928 gb <br>DT871188.1 DT871188     | 2.00E-05 | 50.1 | ---NA---                             |                                                             | Pfam-<br>B_423,zf-<br>C2H2                                                                |        |
| DB918409 | BY797271                                   | 9.00E-21 | 95.9 | formin binding protein<br>1          | F:GO:0005515                                                | SH3_1                                                                                     |        |
| DB918410 | gi 32180832 gb <br>CD679101.1 <br>CD679101 | 0.0005   | 48.1 |                                      |                                                             |                                                                                           |        |
| DB918413 | BY797408                                   | 0.009    | 35.9 | armadillo protein                    | F:GO:0005488                                                | Pfam-B_8871                                                                               |        |
| DB918414 | GS020519                                   | 0.006    | 34.2 |                                      |                                                             |                                                                                           |        |
| DB918417 | gi 24723747 gb <br>CA391663.1 <br>CA391663 | 1.00E-09 | 64.8 | ef hand calcium<br>binding protein 1 |                                                             |                                                                                           |        |
| DB918441 | gi 75847670 gb <br>DT877930.1 DT877930     | 0.008    | 37.7 |                                      |                                                             |                                                                                           |        |
| DB918451 | GS020635                                   | 0.006    | 30.9 |                                      |                                                             |                                                                                           |        |
| DB918461 | gi 85205029 gb <br>DW607145.1 <br>DW607145 | 0        | 392  | chaperonin isoform 1                 |                                                             | Cpn60_TCP1                                                                                | 1.5818 |
| DB918463 | gi 49672068 gb <br>CO425774.1 <br>CO425774 | 2.00E-26 | 119  | glucose transporter                  | F:GO:0005215                                                | Sugar_tr,Sugar<br>_tr                                                                     | 0.7429 |
| DB918464 | gi 85184852 gb <br>DW600369.1 <br>DW600369 | 0        | 427  | fructose-bisphosphate<br>aldolase    | P:GO:0006096,F:GO:<br>0004332                               | Glycolytic                                                                                |        |
| DB918479 | BY796495                                   | 0.004    | 40.1 |                                      |                                                             |                                                                                           |        |

|          |                                                              |          |      |                                                           |                                      |         |
|----------|--------------------------------------------------------------|----------|------|-----------------------------------------------------------|--------------------------------------|---------|
| DB918481 | BY796140                                                     | 2.00E-22 | 101  | uncharacterized protein kiaa0406                          | Pfam-B_3076,Pfam-B_5532,Pfam-B_3077  |         |
| DB918504 | BY795509                                                     | 0.003    | 40.1 |                                                           | Pfam-B_10701,Pfam-B_6449,Pfam-B_6449 |         |
| DB918507 | gi 85164073 gb DW592560.1 DW592560                           | 1.00E-13 | 77.1 | elegans proteinpartially confirmed by transcript evidence | BACK                                 |         |
| DB918515 | gi 9124116 gb BE253696.1 BE253696                            | 3.00E-23 | 92.6 | novel proteinglutamate receptor interacting protein 1     |                                      |         |
| DB918517 | GS020551                                                     | 0.001    | 25.4 |                                                           |                                      |         |
| DB918529 | gi 37598652 gb CF724484.1 CF724484                           | 0        | 177  | ring canal kelch protein                                  | Kelch_1,Kelch_1,Kelch_1,Kelch_1      |         |
| DB918534 | <b>Positive selection</b> gi 58033858 gb CX731384.1 CX731384 | 3.00E-31 | 136  | regulator of g protein signaling                          | DEP,Pfam-B_771                       | 2.50617 |
| DB918535 | gi 19030296 gb BM717038.1 BM717038                           | 2.00E-07 | 57   | aminophospholipid transporter-classstypemember 2          | Pfam-B_7818                          |         |
| DB918540 | gi 62020487 gb DN679079.1 DN679079                           | 2.00E-07 | 46.9 | heme-binding protein                                      | SOUL                                 |         |
| DB918553 | gi 46821839 gb CN509215.1 CN509215                           | 6.00E-20 | 75.3 | isoform c                                                 | Elf1                                 | 1.10808 |
| DB918557 | gi 62844013 gb DN874072.1 DN874072                           | 0.003    | 46.1 |                                                           |                                      |         |
| DB918577 | GS020592                                                     | 0.006    | 34.2 |                                                           |                                      |         |

|          |                                                              |          |      |                                          |                                                     |                                     |         |
|----------|--------------------------------------------------------------|----------|------|------------------------------------------|-----------------------------------------------------|-------------------------------------|---------|
| DB918581 | gi 15708687 gb BI731674.1 BI731674                           | 9.00E-22 | 99.6 | nadh dehydrogenase subunit 5             | C:GO:0044464                                        | NADH5_C,Oxidored_q1                 | 0.8204  |
| DB918585 | gi 13059708 gb BG296747.1 BG296747                           | 0.003    | 46.1 |                                          |                                                     |                                     |         |
| DB918587 | gi 13057929 gb BG295866.1 BG295866                           | 5.00E-43 | 78.4 | chromosome 9 open reading frame 78       |                                                     | Hep_59                              | 0.37597 |
| DB918596 | gi 57592505 gb CX565476.1 CX565476                           | 0        | 248  | pkm2a protein                            | F:GO:0030955,F:GO:0004743,F:GO:0000287              | PK                                  | 3.1316  |
| DB918612 | BY797401                                                     | 0.001    | 42.1 |                                          |                                                     |                                     |         |
| DB918617 | gi 40318338 gb CK352451.1 CK352451                           | 2.00E-12 | 73.9 | zinc finger protein 533                  |                                                     | zf-C2H2_jaz,zf-C2H2_jaz             |         |
| DB918626 | gi 15706647 gb BI729634.1 BI729634                           | 6.00E-20 | 78.5 | calponin-like protein                    | P:GO:0031032,F:GO:0003779                           | Calponin,Calponin,Calponin,Calponin | 1.7782  |
| DB918643 | gi 10681185 gb BE996337.1 BE996337                           | 6.00E-08 | 58.8 | ---NA---                                 |                                                     |                                     |         |
| DB918671 | BY796301                                                     | 0.004    | 38.2 |                                          |                                                     |                                     |         |
| DB918674 | gi 37598756 gb CF724588.1 CF724588                           | 0        | 352  | septin 5a                                | C:GO:0031105,P:GO:0007049,F:GO:0005515,F:GO:0005525 | Septin                              | 0.3854  |
| DB918677 | <b>Positive selection</b> gi 37626470 gb CF730140.1 CF730140 | 0        | 355  | mitochondrial citrate synthase precursor | P:GO:0044262,C:GO:0005759,F:GO:0004108,P:GO:0006099 | Citrate_synt                        | 4.08072 |
| DB918693 | gi 62832182 gb DN862533.1 DN862533                           | 0        | 224  | annexin a7                               |                                                     | Annexin,Annexin                     |         |
| DB918696 | gi 23661204 gb BU733868.1 BU733868                           | 1.00E-11 | 71.2 | microrchidia 2a                          | F:GO:0008270,C:GO:0005575                           | Pfam-B_12816                        |         |
| DB918710 | gi 18500023 gb BM450983.1 BM450983                           | 6.00E-33 | 141  | ies6-similar protein                     |                                                     | YL1_C                               | 0.9255  |

|          |                                                              |          |      |                                                |                                                     |                       |         |
|----------|--------------------------------------------------------------|----------|------|------------------------------------------------|-----------------------------------------------------|-----------------------|---------|
| DB918718 | gi 54444263 gb CV558070.1 CV558070                           | 0        | 306  | myeloid lymphoid or mixed-lineage leukemia     |                                                     | FYRC,SET              | 1.23405 |
| DB918727 | gi 16491547 gb BB657721.1 BB657721                           | 4.00E-19 | 95.9 | riken cdna d230014k01                          |                                                     | Glyco_hydro_85        |         |
| DB918730 | GS008232                                                     | 0.006    | 34.2 |                                                |                                                     |                       |         |
| DB918733 | GS013972                                                     | 0.006    | 34.2 |                                                |                                                     |                       |         |
| DB918739 | <b>Positive selection</b> gi 18524537 gb BM475495.1 BM475495 | 0        | 208  | glia maturation factor gamma                   | F:GO:0005515                                        | Cofilin_ADF           | 2.17042 |
| DB918749 | BY800356                                                     | 0.007    | 36.3 |                                                |                                                     | Pfam-B_13263          |         |
| DB918788 | GS013783                                                     | 0.006    | 34.2 |                                                |                                                     |                       |         |
| DB918821 | gi 54474538 gb CV572201.1 CV572201                           | 0.01     | 44.1 |                                                |                                                     |                       |         |
| DB918823 | BY795432                                                     | 0.006    | 36.8 | ---NA---                                       |                                                     |                       |         |
| DB918827 | gi 85172829 gb DW596553.1 DW596553                           | 0.0004   | 46   | lobe cg10109-pa                                |                                                     | Pfam-B_13617          |         |
| DB918837 | GS013989                                                     | 0.002    | 36.2 | ---NA---                                       |                                                     |                       |         |
| DB918840 | BY798672                                                     | 0.007    | 32.2 |                                                |                                                     |                       |         |
| DB918850 | gi 19354133 gb BM904029.1 BM904029                           | 0        | 297  | leukotriene a4 hydrolase                       | F:GO:0005488,P:GO:0044237,P:GO:0044238,F:GO:0008237 | Peptidase_M1          | 0.6401  |
| DB918855 | GS004626                                                     | 3.00E-05 | 42.1 |                                                |                                                     |                       |         |
| DB918861 | gi 49672294 gb CO426000.1 CO426000                           | 0.002    | 43.7 | cg17233-isoform a isoform 2                    |                                                     | Pfam-B_897,Pfam-B_897 |         |
| DB918862 | gi 85204396 gb DW606834.1 DW606834                           | 1.00E-34 | 140  | cg7154 cg7154-partial                          |                                                     | DUF3512               |         |
| DB918888 | gi 62048371 gb DN692705.1 DN692705                           | 2.00E-33 | 143  | succinyl-ligase subunitmitochondrial precursor |                                                     | Ligase_CoA            | 0.6879  |

|          |                                    |          |      |                                                                                                |                                                                                                         |                              |         |
|----------|------------------------------------|----------|------|------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|------------------------------|---------|
| DB918892 | gi 14063502 gb BG752849.1 BG752849 | 0        | 227  | k6pf_schmaame: full=6-phosphofructokinase short=phosphofructokinaseame: full=phosphohexokinase | F:GO:0003824                                                                                            | PFK                          | 0.81777 |
| DB918895 | gi 37635709 gb CF739372.1 CF739372 | 5.00E-07 | 51.5 | tpa: sco-spondin protein                                                                       | F:GO:0005179,F:GO:0003674,F:GO:0005509,F:GO:0030414,P:GO:0007155,P:GO:0008150,C:GO:0005576,F:GO:0005515 | TSP_1,Pacifast in_I,Cys_knot |         |
| DB918908 | gi 32178072 gb CD676341.1 CD676341 | 0        | 215  | eh-domain containing 3                                                                         | F:GO:0003924,F:GO:0005509                                                                               | efhand                       |         |
| DB918911 | GS013783                           | 0.005    | 31.3 |                                                                                                |                                                                                                         |                              |         |
| DB918916 | BY794962                           | 6.00E-27 | 116  | atp synthetase subunit 6                                                                       | C:GO:0005743,C:GO:0045263,P:GO:0015992,F:GO:0015078,C:GO:0016021,F:GO:0016820                           | ATP-synt_A                   |         |

|          |                                    |          |                                                        |                                                                                                                                                                                                                                                                                  |                     |         |
|----------|------------------------------------|----------|--------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------|---------|
| DB918920 | gi 37598985 gb CF724817.1 CF724817 | 2.00E-42 | 130 myosin vi                                          | P:GO:0051046,C:GO:0031941,P:GO:0030048,C:GO:0031965,F:GO:0043531,P:GO:0050974,C:GO:0005794,P:GO:0006886,C:GO:0005905,C:GO:0001726,F:GO:0003774,P:GO:0006897,F:GO:0051015,P:GO:0030330,C:GO:0016591,P:GO:0045944,C:GO:0048471,F:GO:0005516,P:GO:0042491,C:GO:0005938,C:GO:0045334 |                     |         |
| DB918922 | gi 62045111 gb DN691085.1 DN691085 | 3.00E-43 | 101 synaptophysin (major synaptic vesicle protein p38) | C:GO:0016021,C:GO:0030672,C:GO:0042734,F:GO:0015485,C:GO:0019717,P:GO:0006897                                                                                                                                                                                                    | MARVEL              | 0.3569  |
| DB918923 | gi 62883019 gb DN898256.1 DN898256 | 8.00E-39 | 107 sb:cb283 protein                                   | P:GO:0006508,C:GO:0005622                                                                                                                                                                                                                                                        | Pfam-B_1295         | 0.39108 |
| DB918928 | gi 85176339 gb DW597844.1 DW597844 | 0        | 256 elongation factor gmitochondrial                   | F:GO:0003746,C:GO:0005622,F:GO:0000166,P:GO:0006414,F:GO:0003924                                                                                                                                                                                                                 | EFG_IV,GTP_E FTU_D2 | 0.25377 |
| DB918945 | gi 49679974 gb CO433680.1 CO433680 | 2.80E-45 | 182 cg17766-pa isoform 1                               |                                                                                                                                                                                                                                                                                  | Pfam-B_9841         |         |
| DB918958 | gi 75847792 gb DT878052.1 DT878052 | 4.00E-19 | 60.2 ---NA---                                          |                                                                                                                                                                                                                                                                                  | Pfam-B_5923         |         |

|          |                                            |          |                                                                                        |                                                                                               |                                  |         |
|----------|--------------------------------------------|----------|----------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|----------------------------------|---------|
| DB918963 | gi 11534013 gb <br>BF464830.1 BF464830     | 2.94E-44 | 179 cell death regulator<br>aven                                                       |                                                                                               | Pfam-<br>B_5059,Pfam-<br>B_18304 |         |
| DB918969 | gi 15709785 gb <br>BI732772.1 BI732772     | 0.008    | 41.8 ---NA---                                                                          |                                                                                               | Pfam-B_13263                     |         |
| DB918998 | gi 54447186 gb <br>CV559510.1 <br>CV559510 | 0        | 383 uba and wwe domain<br>containing 1                                                 | C:GO:0005737,P:GO:<br>0006464,F:GO:<br>0003677,P:GO:<br>0051028,F:GO:<br>0004842,C:GO:0005634 | HECT                             | 0.71877 |
| DB919005 | gi 4562379 gb <br>AI578003.1 AI578003      | 0.009    | 41.8                                                                                   |                                                                                               |                                  |         |
| DB919009 | gi 39634652 gb <br>CK228548.1 <br>CK228548 | 0.01     | 44.1                                                                                   |                                                                                               |                                  |         |
| DB919012 | BY800189                                   | 0.001    | 33.1                                                                                   |                                                                                               |                                  |         |
| DB919022 | gi 19391314 gb <br>BM932141.1 <br>BM932141 | 0.002    | 46.1                                                                                   |                                                                                               |                                  |         |
| DB919025 | gi 46855487 gb <br>CN527331.1 <br>CN527331 | 0.002    | 46.1                                                                                   |                                                                                               |                                  |         |
| DB919029 | gi 91744148 gb <br>EB380803.1 EB380803     | 0        | 196 ubiquitin-like modifier<br>activating enzyme 1                                     | F:GO:0008641,P:GO:<br>0006512,F:GO:0005488                                                    | UBACT,UBA_e<br>1_C,UBACT         | 0.42771 |
| DB919034 | gi 77505913 gb <br>DV216272.1 DV216272     | 8.00E-23 | 106 thyroid receptor<br>interacting protein                                            |                                                                                               | Pfam-B_2751                      |         |
| DB919048 | gi 75848952 gb <br>DT879212.1 DT879212     | 2.00E-15 | 83.5 serine threonine-<br>protein phosphatase<br>2a catalytic subunit<br>alpha isoform |                                                                                               |                                  |         |
| DB919053 | gi 57592476 gb <br>CX565447.1 <br>CX565447 | 0.0006   | 48.1 nuclear protein hcc-1                                                             | P:GO:0008150,C:GO:<br>0005575                                                                 |                                  |         |
| DB919086 | gi 62037484 gb <br>DN687305.1 <br>DN687305 | 0        | 211 ---NA---                                                                           |                                                                                               | DUF1394                          | 0.7005  |

|          |                                                                      |          |      |                                                                                 |                                                                                               |                                                                                                                               |         |
|----------|----------------------------------------------------------------------|----------|------|---------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------|---------|
| DB919116 | gi 85179409 gb <br>DW598458.1 <br>DW598458                           | 2.00E-07 | 56.5 | 5-<br>methyltetrahydrofolate<br>-homocysteine<br>methyltransferase<br>reductase |                                                                                               | FAD_binding_1                                                                                                                 |         |
| DB919122 | <b>Embryo specific</b> gi 9123195 gb <br>BE253045.1 BE253045         | 3.00E-19 | 67   | glutaminy-peptide<br>cyclotransferase-like                                      |                                                                                               | Peptidase_M2<br>8                                                                                                             | 0.53552 |
| DB919139 | gi 54469703 gb <br>CV569820.1 <br>CV569820                           | 0.003    | 46.1 | nuclear receptor<br>subfamily 1 def                                             |                                                                                               |                                                                                                                               | 0.8208  |
| DB919144 | GS020600                                                             | 0.002    | 36.2 |                                                                                 |                                                                                               | Pfam-<br>B_11119,Pfam<br>-<br>B_16930,Pfam<br>-<br>B_843,Rifin_S<br>TEVOR,Pfam-<br>B_1037,Pfam-<br>B_470,ASFV_J<br>13L,DUF912 |         |
| DB919161 | gi 62049971 gb <br>DN693543.1 <br>DN693543                           | 0.001    | 40   |                                                                                 |                                                                                               |                                                                                                                               |         |
| DB919164 | <b>Positive selection</b> gi 85209585 gb <br>DW608973.1 <br>DW608973 | 0        | 412  | signal recognition<br>particle 54                                               | F:GO:0005525,P:GO:<br>0006614,F:GO:<br>0017111,C:GO:<br>0016020,C:GO:<br>0048500,F:GO:0008312 | SRP54_N,VirE,<br>SRP54                                                                                                        | 2.44455 |
| DB919194 | gi 55687965 gb <br>CV783025.1 <br>CV783025                           | 8.00E-23 | 90   | phosphodiesterase<br>11a                                                        | F:GO:0003824                                                                                  | GAF                                                                                                                           | 0.77045 |
| DB919217 | gi 10650927 gb <br>BE981627.1 BE981627                               | 0.009    | 44.1 |                                                                                 |                                                                                               |                                                                                                                               |         |
| DB919218 | gi 19039147 gb <br>BM720115.1 <br>BM720115                           | 2.00E-27 | 86.3 | cytokine induced<br>apoptosis inhibitor 1                                       | F:GO:0003674,C:GO:<br>0005575                                                                 | CIAPIN1,CIAP1<br>N1                                                                                                           | 0.39746 |

|          |                                         |                                            |          |      |                            |                                                     |                                                 |         |
|----------|-----------------------------------------|--------------------------------------------|----------|------|----------------------------|-----------------------------------------------------|-------------------------------------------------|---------|
| DB919224 |                                         | gi 14062542 gb <br>BG751889.1 <br>BG751889 | 1.00E-12 | 55.6 | cg32486 cg32486-pd         |                                                     |                                                 |         |
| DB919232 |                                         | gi 1483757 gb <br>AA019950.1 AA019950      | 2.00E-05 | 46   | ---NA---                   |                                                     |                                                 |         |
| DB919247 |                                         | gi 40321099 gb <br>CK355167.1 <br>CK355167 | 0.0007   | 45.1 |                            |                                                     |                                                 |         |
| DB919252 |                                         | GS020699                                   | 0.007    | 30.2 |                            |                                                     |                                                 |         |
| DB919264 |                                         | GS004826                                   | 0.006    | 34.2 |                            |                                                     |                                                 |         |
| DB919265 |                                         | gi 58061010 gb <br>CX734174.1 <br>CX734174 | 6.00E-07 | 46.4 | ---NA---                   |                                                     | TUDOR                                           |         |
| DB919269 |                                         | gi 24719522 gb <br>CA389401.1 <br>CA389401 | 0.005    | 35.9 |                            |                                                     | Pfam-<br>B_6449,Pfam-<br>B_4561,Pfam-<br>B_6449 |         |
| DB919285 | GO annotation                           | gi 57592033 gb <br>CX565004.1 <br>CX565004 | 0        | 179  | member ras oncogene family | P:GO:0015031,F:GO:0005525,P:GO:0007264              | Ras                                             | 0.66686 |
| DB919294 |                                         | gi 21171127 gb <br>BQ432051.1 <br>BQ432051 | 0        | 412  | xpa binding protein 1      | F:GO:0017111,C:GO:0005737,F:GO:0005524,F:GO:0005525 | ATP_bind_1                                      | 0.6069  |
| DB919298 | GO annotation,<br>Positive<br>selection | gi 32178315 gb <br>CD676584.1 <br>CD676584 | 1.00E-36 | 153  | cornichon homolog 4        | P:GO:0007242,C:GO:0016021,C:GO:0016020              | Cornichon                                       | 2.32818 |
| DB919300 |                                         | GS004638                                   | 0.006    | 34.2 |                            |                                                     |                                                 |         |
| DB919303 |                                         | BY798085                                   | 0.007    | 36.3 | ---NA---                   |                                                     | Pfam-<br>B_8589,Pfam-<br>B_8589                 |         |
| DB919304 |                                         | gi 16427590 gb <br>BB469110.2 <br>BB469110 | 0.003    | 46.1 |                            |                                                     |                                                 |         |
| DB919318 |                                         | gi 62885542 gb <br>DN900779.1 <br>DN900779 | 0.003    | 42.8 | ---NA---                   |                                                     |                                                 |         |

|          |                                                              |          |      |                                                                           |                                                                                                                                   |                     |         |
|----------|--------------------------------------------------------------|----------|------|---------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|---------------------|---------|
| DB919327 | gi 22684448 gb BU170464.1 BU170464                           | 0        | 331  | kdel (lys-asp-glu-leu) endoplasmic reticulum protein retention receptor 2 | F:GO:0004872,C:GO:0005789,C:GO:0005794,F:GO:0005515,F:GO:0005046,F:GO:0008565,P:GO:0016192,P:GO:0006886,C:GO:0016021,P:GO:0006621 | ER_lumen_rec<br>ept | 1.8471  |
| DB919337 | gi 75842330 gb DT872590.1 DT872590                           | 2.00E-13 | 76.7 | cg11699 cg11699-pa                                                        |                                                                                                                                   | Pfam-B_9283,DUF1358 |         |
| DB919351 | gi 37638635 gb CF742296.1 CF742296                           | 0.01     | 32.7 |                                                                           |                                                                                                                                   |                     |         |
| DB919363 | gi 14974340 gb BI298060.1 BI298060                           | 0.0004   | 46.1 |                                                                           |                                                                                                                                   |                     |         |
| DB919370 | gi 58034682 gb CX732208.1 CX732208                           | 2.00E-17 | 90   | glypican 5                                                                |                                                                                                                                   | Glypican            |         |
| DB919378 | <b>Embryo specific</b> gi 6515768 gb AW209828.1 AW209828     | 0.002    | 40   |                                                                           |                                                                                                                                   |                     |         |
| DB919382 | gi 54443693 gb CV557783.1 CV557783                           | 1.00E-41 | 97.7 | neprilysin 1 isoform a isoform 1                                          |                                                                                                                                   | Peptidase_M13_N     | 0.53162 |
| DB919385 | BY795432                                                     | 3.00E-06 | 42.3 | ---NA---                                                                  |                                                                                                                                   |                     |         |
| DB919388 | gi 19048616 gb BM727283.1 BM727283                           | 1.00E-21 | 103  | hermansky-pudlak syndrome protein                                         |                                                                                                                                   |                     |         |
| DB919402 | gi 85207147 gb DW608127.1 DW608127                           | 0.004    | 44.1 |                                                                           |                                                                                                                                   |                     |         |
|          | <b>Positive selection</b> gi 19029446 gb BM716188.1 BM716188 | 8.97E-44 | 87.7 | cat eye syndrome chromosome candidate 5                                   | F:GO:0016787                                                                                                                      |                     | 2.00032 |
| DB919423 | gi 85196593 gb DW603940.1 DW603940                           | 2.00E-22 | 106  | chromosome 20 open reading frame 116                                      |                                                                                                                                   | DUF2042,DDR GK      | 0.92749 |

|          |                                                              |          |      |                                                                   |                                                                                                                      |               |         |
|----------|--------------------------------------------------------------|----------|------|-------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|---------------|---------|
| DB919428 | gi 58034240 gb CX731766.1 CX731766                           | 1.00E-13 | 77   | heterochromatin protein 1                                         |                                                                                                                      | Chromo        | 0.0465  |
| DB919454 | gi 62847739 gb DN877784.1 DN877784                           | 0        | 159  | ---NA---                                                          |                                                                                                                      | Pfam-B_2982   | 0.1956  |
| DB919457 | gi 49672791 gb CO426497.1 CO426497                           | 0        | 253  | calcium calmodulin-dependent serine protein kinase (maguk family) | F:GO:0004672,F:GO:0005488                                                                                            | Guanylate_kin | 0.6048  |
| DB919463 | GS004835                                                     | 0.005    | 34.2 |                                                                   |                                                                                                                      |               |         |
| DB919489 | BY797860                                                     | 0.004    | 40.1 |                                                                   |                                                                                                                      |               |         |
| DB919490 | gi 62881650 gb DN896887.1 DN896887                           | 0        | 270  | 60s ribosomal protein l13a                                        | F:GO:0003735,C:GO:0015934,P:GO:0006412                                                                               | Ribosomal_L13 | 0.84639 |
| DB919493 | gi 46464405 gb CN458679.1 CN458679                           | 0        | 195  | formylglycineamide ribotide amidotransferase                      | F:GO:0003824,C:GO:0009536                                                                                            |               |         |
| DB919497 | GS020551                                                     | 0.005    | 30.9 |                                                                   |                                                                                                                      |               |         |
| DB919499 | gi 85165100 gb DW593084.1 DW593084                           | 1.00E-05 | 51   | cad96ca cg10244-pa                                                | F:GO:0016740,P:GO:0030324,C:GO:0016021,C:GO:0016020,P:GO:0006468,F:GO:0005524,F:GO:0004714,P:GO:0001759,F:GO:0004872 | Pkinase_Tyr   |         |
| DB919502 | GS014086                                                     | 0.006    | 34.2 |                                                                   |                                                                                                                      |               |         |
| DB919504 | <b>Positive selection</b> gi 49672631 gb CO426337.1 CO426337 | 0        | 240  | elav 2-like protein                                               | F:GO:0003676,P:GO:0048255                                                                                            | RRM_1,RRM_1   | 2.3784  |
| DB919512 | gi 54468701 gb CV569322.1 CV569322                           | 0        | 396  | vacuolar protein sorting 26b-                                     |                                                                                                                      | Vps26         | 0.63451 |
| DB919522 | gi 62045742 gb DN691402.1 DN691402                           | 0        | 336  | eukaryotic translation initiation factor 3 subunit                | P:GO:0006413,F:GO:0003743                                                                                            | eIF-3_zeta    | 0.9211  |

|          |                                    |          |      |                                                         |                                        |                                                                         |         |  |
|----------|------------------------------------|----------|------|---------------------------------------------------------|----------------------------------------|-------------------------------------------------------------------------|---------|--|
| DB919532 | gi 62889265 gb DN904502.1 DN904502 | 0.003    | 46.1 |                                                         |                                        |                                                                         |         |  |
| DB919535 | gi 58060842 gb CX734006.1 CX734006 | 9.81E-45 | 161  | sec24 related<br>genemember a                           | P:GO:0006810,C:GO:0043231,C:GO:0044444 | Sec23_helical,<br>Sec23_BS                                              | 0.605   |  |
| DB919573 | gi 18502650 gb BM453610.1 BM453610 | 2.00E-29 | 77.6 | 26s proteasome non-<br>atpase regulatory<br>subunit 3   |                                        |                                                                         | 1.47768 |  |
| DB919626 | gi 62025168 gb DN681178.1 DN681178 | 0.002    | 46.1 |                                                         |                                        |                                                                         |         |  |
| DB919632 | GS020635                           | 0.005    | 31.3 |                                                         |                                        |                                                                         |         |  |
| DB919654 | gi 9592429 gb BB536929.1 BB536929  | 0.009    | 44.1 |                                                         |                                        |                                                                         |         |  |
| DB919658 | GS004874                           | 0.006    | 34.2 |                                                         |                                        |                                                                         |         |  |
| DB919673 | gi 49680703 gb CO434409.1 CO434409 | 2.00E-21 | 103  | diras family protein                                    |                                        | Ras                                                                     |         |  |
| DB919678 | gi 85183348 gb DW599836.1 DW599836 | 7.00E-08 | 58.5 | hemagglutinin family<br>protein                         |                                        | Apolipoprotein<br>,Pfam-B_6360                                          |         |  |
| DB919682 | GS004713                           | 0.006    | 34.2 |                                                         |                                        | Pfam-<br>B_13263,Pfam-<br>-<br>B_13263,Pfam-<br>-B_4326,Pfam-<br>B_4326 |         |  |
| DB919689 | gi 22701075 gb BU187091.1 BU187091 | 0        | 323  | loc495086 protein                                       | F:GO:0003824                           | Ligase_CoA                                                              | 0.0164  |  |
| DB919694 | gi 62029256 gb DN683163.1 DN683163 | 0        | 209  | flavoprotein subunit of<br>complex ii<br>isoformpartial | F:GO:0050660,F:GO:0016491,P:GO:0006099 | Succ_DH_flav_<br>C,FAD_binding<br>_2                                    | 0.56633 |  |

|          |                                    |          |      |                                                 |                                        |                     |         |
|----------|------------------------------------|----------|------|-------------------------------------------------|----------------------------------------|---------------------|---------|
| DB919698 | gi 46818729 gb CN506105.1 CN506105 | 0        | 418  | cytochrome c-1                                  | F:GO:0005488                           | Cytochrom_C1        | 2.02743 |
| DB919705 | gi 62025064 gb DN681122.1 DN681122 | 1.00E-14 | 55.1 | pancreatic lipase-related protein               |                                        | Lipase              |         |
| DB919706 | gi 75852061 gb DT882321.1 DT882321 | 0.009    | 44.1 |                                                 |                                        |                     |         |
| DB919709 | GS020584                           | 0.001    | 36.2 |                                                 |                                        |                     |         |
| DB919714 | gi 42746528 gb CK780850.1 CK780850 | 2.00E-36 | 152  | barrier-to-autointegration factor               |                                        | BAF                 | 1.00035 |
| DB919719 | gi 22707068 gb BU193084.1 BU193084 | 3.00E-34 | 76.7 | est1p-like protein b                            |                                        | Tektin              |         |
| DB919746 | gi 20158553 gb BQ108899.1 BQ108899 | 8.00E-15 | 76.2 | ---NA---                                        | F:GO:0015171,C:GO:0016020,P:GO:0006810 | AA_permease, UNC-50 |         |
| DB919748 | gi 13057197 gb BG295500.1 BG295500 | 0.006    | 44.1 |                                                 |                                        |                     |         |
| DB919755 | GS004597                           | 0.0008   | 34.2 |                                                 |                                        |                     |         |
| DB919758 | gi 11531219 gb BF462036.1 BF462036 | 0        | 184  | replication factor c (activator 1) 3            | F:GO:0005524,F:GO:0017111              | RFC-E_C             | 0.64225 |
| DB919760 | gi 22361768 gb BQ946290.1 BQ946290 | 0        | 357  | developmentally regulated gtp binding protein 2 | C:GO:0005622,F:GO:0005525              | MMR_HSR1            | 1.42339 |
| DB919767 | gi 19045615 gb BM724284.1 BM724284 | 2.00E-41 | 154  | rcor3 protein                                   |                                        | Myb_DNA-binding     | 1.2038  |
| DB919770 | GS013833                           | 0.008    | 30.2 |                                                 |                                        |                     |         |
| DB919776 | gi 62831095 gb DN861446.1 DN861446 | 0.008    | 40.9 |                                                 |                                        |                     |         |
| DB919784 | gi 32464087 gb CD805261.1 CD805261 | 0        | 238  | subfamilymember 13                              | F:GO:0003674,P:GO:0008150              | Pfam-B_618          |         |

|          |                                            |          |      |                                         |                                                                                               |             |         |
|----------|--------------------------------------------|----------|------|-----------------------------------------|-----------------------------------------------------------------------------------------------|-------------|---------|
| DB919786 | gi 57592538 gb <br>CX565509.1 <br>CX565509 | 3.00E-28 | 124  | mediator complex<br>subunit 4 cg8609-pa |                                                                                               | Med4        | 0.7867  |
| DB919787 | GS014073                                   | 0.006    | 30.2 |                                         |                                                                                               |             |         |
| DB919798 | GS013784                                   | 0.005    | 34.2 |                                         |                                                                                               |             |         |
| DB919821 | GS014124                                   | 0.008    | 30.4 |                                         |                                                                                               |             |         |
| DB919823 | gi 58032180 gb <br>CX729723.1 <br>CX729723 | 0        | 321  | escrt-ii<br>complexhomolog              | C:GO:0005737,P:GO:<br>0006357,C:GO:<br>0005667,F:GO:<br>0008134,P:GO:0015031                  | EAP30       |         |
| DB919835 | gi 22707271 gb <br>BU193287.1 <br>BU193287 | 0        | 347  | ---NA---                                | C:GO:0045261,F:GO:<br>0046933,P:GO:<br>0015986,F:GO:<br>0046872,F:GO:<br>0005524,F:GO:0046961 | ATP-synt_ab |         |
| DB919848 | gi 40321099 gb <br>CK355167.1 <br>CK355167 | 0.003    | 42.8 | ---NA---                                |                                                                                               |             |         |
| DB919851 | gi 62831095 gb <br>DN861446.1 <br>DN861446 | 0.001    | 44.6 |                                         |                                                                                               |             |         |
| DB919856 | gi 75851478 gb <br>DT881738.1 DT881738     | 2.00E-10 | 65.9 |                                         |                                                                                               |             |         |
| DB919889 | gi 14061048 gb <br>BG750395.1 <br>BG750395 | 2.00E-11 | 70.3 | kiaa1813 protein<br>isoform 2           |                                                                                               |             |         |
| DB919898 | BY795432                                   | 0.006    | 29.5 |                                         |                                                                                               |             |         |
| DB919902 | gi 42747349 gb <br>CK781671.1 <br>CK781671 | 3.00E-18 | 92.7 | ---NA---                                |                                                                                               | FERM_M      | 1.46845 |
| DB919908 | BY797096                                   | 0.0008   | 42.1 |                                         |                                                                                               |             |         |
| DB919918 | gi 46465385 gb <br>CN459659.1 <br>CN459659 | 0.0003   | 46   |                                         |                                                                                               |             |         |
| DB919919 | gi 23662340 gb <br>BU734431.1 <br>BU734431 | 0.002    | 46.1 |                                         |                                                                                               |             |         |

|          |                                            |          |      |                                                    |                                                             |                               |
|----------|--------------------------------------------|----------|------|----------------------------------------------------|-------------------------------------------------------------|-------------------------------|
| DB919927 | gi 20337251 gb <br>BF455627.2 BF455627     | 0.01     | 44.1 |                                                    |                                                             |                               |
| DB919932 | BY795145                                   | 2.00E-27 | 72.5 | 60s ribosomal protein<br>rpl22                     | F:GO:0003735,P:GO:<br>0006412,C:GO:<br>0005840,C:GO:0005622 | Ribosomal_L2<br>2e            |
| DB919941 | gi 12771566 gb <br>BG261750.1 <br>BG261750 | 0.005    | 42.3 |                                                    |                                                             |                               |
| DB919943 | gi 85207821 gb <br>DW608344.1 <br>DW608344 | 4.00E-07 | 56.1 | co-chaperone-curved<br>dna binding protein a       | F:GO:0051082,P:GO:<br>0006457,F:GO:0031072                  | DnaJ                          |
| DB919958 | gi 32177529 gb <br>CD675798.1 <br>CD675798 | 9.00E-31 | 133  | iron-sulfur<br>assemblymitochondria<br>l precursor |                                                             | Fe-S_biosyn 1.07501           |
| DB919968 | gi 22376010 gb <br>BQ960532.1 <br>BQ960532 | 0        | 472  | mgc84682 protein                                   | F:GO:0046872,C:GO:<br>0005737,F:GO:<br>0008237,C:GO:0008180 | Mov34,Pfam-<br>B_8170 2.06522 |
| DB919992 | gi 85170404 gb <br>DW595525.1 <br>DW595525 | 0        | 214  | propionyl coenzyme<br>abeta polypeptide            | F:GO:0016874                                                | Carboxyl_trans                |
| DB920003 | BY798745                                   | 0.0009   | 42.1 | ---NA---                                           |                                                             |                               |
| DB920004 | BY795432                                   | 0.002    | 37.7 |                                                    |                                                             |                               |
| DB920010 | gi 4561003 gb <br>AI576627.1 AI576627      | 4.00E-10 | 65.2 | cytochrome c oxidase<br>copper chaperone           |                                                             | COX17                         |
| DB920013 | gi 46821571 gb <br>CN508947.1 <br>CN508947 | 4.00E-19 | 89.3 | immunoglobulin<br>binding protein 1                | P:GO:0009966,F:GO:<br>0003674,C:GO:0005575                  | TAP42                         |
| DB920032 | GS004683                                   | 0.007    | 32.2 |                                                    |                                                             |                               |
| DB920033 | gi 85170536 gb <br>DW595579.1 <br>DW595579 | 3.00E-08 | 59.3 | skiv2l protein                                     |                                                             |                               |
| DB920054 | BY799424                                   | 0.002    | 38.2 |                                                    |                                                             |                               |