Supplementary info.

Appendix A Gene ontology analysis of locust eggs omics.

Appendix B Pathway enrichment analysis of differentially expressed genes and proteins.

Appendix C Differentially expressed genes within metabolism pathways in response to diapauses and development.

Appendix D Differentially expressed peptides identified by LC-ESI-MS/MS.

Appendix E Differentially the sametrend correlation and oppositetrend correlation between mRNAs and proteins.

Appendix A Gene ontology analysis of locust eggs omics.

Gene ontology analysis of locust eggs transcriptome.

N2 vs D2 up	**N2 vs D2 down**
Cellular Component:	**Cellular Component:**
34 (4.3) GO:0005576 extracellular region	**63 (1.1) GO:0005576** extracellular region
17 (2.1) GO:0044421 extracellular region part	**32 (0.6) GO:0044421** extracellular region part
381 (48.2) GO:0005623 cell	**3000 (53.2) GO:0005623** cell
381 (48.2) GO:0044464 cell part	**2999 (53.2) GO:0044464** cell part
44 (5.6) GO:0031974 membrane-enclosed lumen	**465 (8.2) GO:0031974** membrane-enclosed lumen
27 (3.4) GO:0031975 envelope	**188 (3.3) GO:0031975** envelope
123 (15.5) GO:0032991 macromolecular complex	**1242 (22.0) GO:0032991** macromolecular complex
236 (29.8) GO:0043226 organelle	**2044 (36.2) GO:0043226** organelle
145 (18.3) GO:0044422 organelle part	**1177 (20.9) GO:0044422** organelle part
17 (2.1) GO:0044421 extracellular region part	**32 (0.6) GO:0044421** extracellular region part
145 (18.3) GO:0044422 organelle part	**1177 (20.9) GO:0044422** organelle part
12 (1.5) GO:0044456 synapse part	**30 (0.5) GO:0044456** synapse part
381 (48.2) GO:0044464 cell part	**2999 (53.2) GO:0044464** cell part
16 (2.0) GO:0045202 synapse	**42 (0.7) GO:0045202** synapse
12 (1.5) GO:0044456 synapse part	**30 (0.5) GO:0044456** synapse part
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Total: 15	**Total:** 15
Biological Process:	**Biological Process:**
42 (5.3) GO:0000003 reproduction	**461 (8.2) GO:0000003** reproduction
64 (8.1) GO:0044085 cellular component biogenesis	**408 (7.2) GO:0044085** cellular component biogenesis
162 (20.5) GO:0032502 developmental process	**1076 (19.1) GO:0032502** developmental process
142 (18.0) GO:0016043 cellular component organization	**839 (14.9) GO:0016043** cellular component organization
31 (3.9) GO:0016265 death	**251 (4.5) GO:0016265** death

39 (4.9) **GO:0022414** reproductive process 26 (3.3) **GO:0002376** immune system process 109 (13.8) **GO:0050896** response to stimulus 182 (23.0) **GO:0032501** multicellular organismal process 63 (8.0) **GO:0010926** anatomical structure formation 25 (3.2) **GO:0051704** multi\-organism process 102 (12.9) **GO:0051234** establishment of localization 15 (1.9) **GO:0022610** biological adhesion 377 (47.7) **GO:0008152** metabolic process 3 (0.4) **GO:0016032** viral reproduction 6 (0.8) **GO:0048511** rhythmic process 164 (20.7) **GO:0043473** pigmentation 22 (2.8) **GO:0040011** locomotion 132 (16.7) **GO:0051179** localization 425 (53.7) **GO:0009987** cellular process 16 (2.0) **GO:0040007** growth 187 (23.6) **GO:0065007** biological regulation ------------------------------------ **Total:** 22	379 (6.7) **GO:0022414** reproductive process 158 (2.8) **GO:0002376** immune system process 616 (10.9) **GO:0050896** response to stimulus 1159 (20.6) **GO:0032501** multicellular organismal process 350 (6.2) **GO:0010926** anatomical structure formation 101 (1.8) **GO:0051704** multi\-organism process 787 (14.0) **GO:0051234** establishment of localization 56 (1.0) **GO:0022610** biological adhesion 3329 (59.0) **GO:0008152** metabolic process 147 (2.6) **GO:0016032** viral reproduction 24 (0.4) **GO:0048511** rhythmic process 1072 (19.0) **GO:0043473** pigmentation 169 (3.0) **GO:0040011** locomotion 904 (16.0) **GO:0051179** localization 256 (4.5) **GO:0040007** growth 3638 (64.5) **GO:0009987** cellular process 1202 (21.3) **GO:0065007** biological regulation ------------------------------------ **Total:** 22
Molecular Function: 4 (0.5) **GO:0009055** electron carrier activity 27 (3.4) **GO:0060089** molecular transducer activity 22 (2.8) **GO:0030528** transcription regulator activity 16 (2.0) **GO:0030234** enzyme regulator activity 409 (51.7) **GO:0003824** catalytic activity 351 (44.4) **GO:0005488** binding 1 (0.1) **GO:0016209** antioxidant activity 1 (0.1) **GO:0015457** auxiliary transport protein activity 7 (0.9) **GO:0045182** translation regulator activity 35 (4.4) **GO:0005198** structural molecule activity 52 (6.6) **GO:0005215** transporter activity ------------------------------------ **Total:** 11 ======================================= **Total GO terms in three ontologies:** 48	**Molecular Function:** 41 (0.7) **GO:0009055** electron carrier activity 62 (1.1) **GO:0060089** molecular transducer activity 58 (1.0) **GO:0030528** transcription regulator activity 94 (1.7) **GO:0030234** enzyme regulator activity 3220 (57.1) **GO:0003824** catalytic activity 2552 (45.3) **GO:0005488** binding 23 (0.4) **GO:0016209** antioxidant activity 7 (0.1) **GO:0015457** auxiliary transport protein activity 7 (0.1) **GO:0016530** metallochaperone activity 95 (1.7) **GO:0045182** translation regulator activity 395 (7.0) **GO:0005198** structural molecule activity 246 (4.4) **GO:0005215** transporter activity ------------------------------------ **Total:** 12 ======================================= **Total GO terms in three ontologies:** 49
N3 vs D3 up	**N3 vs D3 down**

Cellular Component: **38 (3.6) GO:0005576** extracellular region **18 (1.7) GO:0044421** extracellular region part **502 (47.1) GO:0005623** cell **502 (47.1) GO:0044464** cell part **1 (0.1) GO:0019012** virion **1 (0.1) GO:0044423** virion part **50 (4.7) GO:0031974** membrane-enclosed lumen **25 (2.3) GO:0031975** envelope **188 (17.7) GO:0032991** macromolecular complex **321 (30.1) GO:0043226** organelle **165 (15.5) GO:0044422** organelle part **18 (1.7) GO:0044421** extracellular region part **165 (15.5) GO:0044422** organelle part **1 (0.1) GO:0044423** virion part **5 (0.5) GO:0044456** synapse part **502 (47.1) GO:0044464** cell part **6 (0.6) GO:0045202** synapse **5 (0.5) GO:0044456** synapse part ------------------------------------ **Total:** 18	**Cellular Component:** **139 (3.2) GO:0005576** extracellular region **86 (2.0) GO:0044421** extracellular region part **2310 (53.3) GO:0005623** cell **2310 (53.3) GO:0044464** cell part **229 (5.3) GO:0031974** membrane-enclosed lumen **143 (3.3) GO:0031975** envelope **775 (17.9) GO:0032991** macromolecular complex **1281 (29.5) GO:0043226** organelle **746 (17.2) GO:0044422** organelle part **86 (2.0) GO:0044421** extracellular region part **746 (17.2) GO:0044422** organelle part **86 (2.0) GO:0044456** synapse part **2310 (53.3) GO:0044464** cell part **130 (3.0) GO:0045202** synapse **86 (2.0) GO:0044456** synapse part ------------------------------------ **Total:** 15
Biological Process: **67 (6.3) GO:0000003** reproduction **50 (4.7) GO:0044085** cellular component biogenesis **164 (15.4) GO:0032502** developmental process **119 (11.2) GO:0016043** cellular component organization **33 (3.1) GO:0016265** death **53 (5.0) GO:0022414** reproductive process **39 (3.7) GO:0002376** immune system process **127 (11.9) GO:0050896** response to stimulus **187 (17.6) GO:0032501** multicellular organismal process **44 (4.1) GO:0010926** anatomical structure formation **14 (1.3) GO:0051704** multi\-organism process **102 (9.6) GO:0051234** establishment of localization **11 (1.0) GO:0022610** biological adhesion **551 (51.7) GO:0008152** metabolic process	**Biological Process:** **403 (9.3) GO:0000003** reproduction **391 (9.0) GO:0044085** cellular component biogenesis **1047 (24.1) GO:0032502** developmental process **840 (19.4) GO:0016043** cellular component organization **193 (4.5) GO:0016265** death **371 (8.6) GO:0022414** reproductive process **164 (3.8) GO:0002376** immune system process **585 (13.5) GO:0050896** response to stimulus **1153 (26.6) GO:0032501** multicellular organismal process **392 (9.0) GO:0010926** anatomical structure formation **141 (3.3) GO:0051704** multi\-organism process **728 (16.8) GO:0051234** establishment of localization **110 (2.5) GO:0022610** biological adhesion **2166 (50.0) GO:0008152** metabolic process

4 (0.4) **GO:0048511** rhythmic process 14 (1.3) **GO:0016032** viral reproduction 186 (17.5) **GO:0043473** pigmentation 19 (1.8) **GO:0040011** locomotion 125 (11.7) **GO:0051179** localization 573 (53.8) **GO:0009987** cellular process 29 (2.7) **GO:0040007** growth 205 (19.2) **GO:0065007** biological regulation ------------------------------------ **Total:** 22	71 (1.6) **GO:0016032** viral reproduction 52 (1.2) **GO:0048511** rhythmic process 1018 (23.5) **GO:0043473** pigmentation 194 (4.5) **GO:0040011** locomotion 875 (20.2) **GO:0051179** localization 197 (4.5) **GO:0040007** growth 2700 (62.3) **GO:0009987** cellular process 1155 (26.6) **GO:0065007** biological regulation ------------------------------------ **Total:** 22
Molecular Function: 8 (0.8) **GO:0009055** electron carrier activity 13 (1.2) **GO:0060089** molecular transducer activity 16 (1.5) **GO:0030528** transcription regulator activity 30 (2.8) **GO:0030234** enzyme regulator activity 514 (48.3) **GO:0003824** catalytic activity 453 (42.5) **GO:0005488** binding 4 (0.4) **GO:0016209** antioxidant activity 21 (2.0) **GO:0045182** translation regulator activity 82 (7.7) **GO:0005198** structural molecule activity 54 (5.1) **GO:0005215** transporter activity ------------------------------------ **Total:** 10 == **Total GO terms in three ontologies:** 50	**Molecular Function:** 25 (0.6) **GO:0009055** electron carrier activity 173 (4.0) **GO:0060089** molecular transducer activity 72 (1.7) **GO:0030528** transcription regulator activity 118 (2.7) **GO:0030234** enzyme regulator activity 2165 (49.9) **GO:0003824** catalytic activity 1940 (44.7) **GO:0005488** binding 10 (0.2) **GO:0016209** antioxidant activity 8 (0.2) **GO:0015457** auxiliary transport protein activity 1 (0.0) **GO:0016530** metallochaperone activity 45 (1.0) **GO:0045182** translation regulator activity 335 (7.7) **GO:0005198** structural molecule activity 363 (8.4) **GO:0005215** transporter activity ------------------------------------ **Total:** 12 == **Total GO terms in three ontologies:** 49
Gene ontology analysis of locust eggs itraq.	
N2 vs D2 up	**N2 vs D2 down**
Cellular Component: 3 (2.8) **GO:0005576** extracellular region 1 (0.9) **GO:0044421** extracellular region part 65 (60.7) **GO:0005623** cell 65 (60.7) **GO:0044464** cell part 7 (6.5) **GO:0031974** membrane-enclosed lumen 4 (3.7) **GO:0031975** envelope 37 (34.6) **GO:0032991** macromolecular complex 49 (45.8) **GO:0043226** organelle	**Cellular Component:** 3 (3.3) **GO:0005576** extracellular region 1 (1.1) **GO:0044421** extracellular region part 48 (53.3) **GO:0005623** cell 48 (53.3) **GO:0044464** cell part 5 (5.6) **GO:0031974** membrane-enclosed lumen 3 (3.3) **GO:0031975** envelope 23 (25.6) **GO:0032991** macromolecular complex 34 (37.8) **GO:0043226** organelle

27 (25.2) GO:0044422 organelle part	**20 (22.2) GO:0044422** organelle part
1 (0.9) GO:0044421 extracellular region part	**1 (1.1) GO:0044421** extracellular region part
27 (25.2) GO:0044422 organelle part	**20 (22.2) GO:0044422** organelle part
2 (1.9) GO:0044456 synapse part	**2 (2.2) GO:0044456** synapse part
65 (60.7) GO:0044464 cell part	**48 (53.3) GO:0044464** cell part
2 (1.9) GO:0045202 synapse	**2 (2.2) GO:0045202** synapse
2 (1.9) GO:0044456 synapse part	**2 (2.2) GO:0044456** synapse part
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Total: 15	**Total:** 15
Biological Process:	**Biological Process:**
25 (23.4) GO:0032502 developmental process	**7 (7.8) GO:0044085** cellular component biogenesis
10 (9.3) GO:0044085 cellular component biogenesis	**18 (20.0) GO:0032502** developmental process
7 (6.5) GO:0000003 reproduction	**8 (8.9) GO:0000003** reproduction
22 (20.6) GO:0016043 cellular component organization	**16 (17.8) GO:0016043** cellular component organization
3 (2.8) GO:0016265 death	**4 (4.4) GO:0016265** death
7 (6.5) GO:0022414 reproductive process	**7 (7.8) GO:0022414** reproductive process
6 (5.6) GO:0002376 immune system process	**3 (3.3) GO:0002376** immune system process
16 (15.0) GO:0050896 response to stimulus	**12 (13.3) GO:0050896** response to stimulus
26 (24.3) GO:0032501 multicellular organismal process	**23 (25.6) GO:0032501** multicellular organismal process
11 (10.3) GO:0010926 anatomical structure formation	**7 (7.8) GO:0010926** anatomical structure formation
4 (3.7) GO:0051704 multi\-organism process	**2 (2.2) GO:0051704** multi\-organism process
20 (18.7) GO:0051234 establishment of localization	**18 (20.0) GO:0051234** establishment of localization
3 (2.8) GO:0022610 biological adhesion	**2 (2.2) GO:0022610** biological adhesion
62 (57.9) GO:0008152 metabolic process	**53 (58.9) GO:0008152** metabolic process
3 (2.8) GO:0016032 viral reproduction	**0 (0.0) GO:0048511** rhythmic process
1 (0.9) GO:0048511 rhythmic process	**2 (2.2) GO:0016032** viral reproduction
23 (21.5) GO:0043473 pigmentation	**18 (20.0) GO:0043473** pigmentation
4 (3.7) GO:0040011 locomotion	**2 (2.2) GO:0040011** locomotion
23 (21.5) GO:0051179 localization	**21 (23.3) GO:0051179** localization
69 (64.5) GO:0009987 cellular process	**54 (60.0) GO:0009987** cellular process
3 (2.8) GO:0040007 growth	**3 (3.3) GO:0040007** growth
26 (24.3) GO:0065007 biological regulation	**23 (25.6) GO:0065007** biological regulation
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Total: 22	**Total:** 22
Molecular Function:	**Molecular Function:**
1 (0.9) GO:0009055 electron carrier activity	**1 (1.1) GO:0009055** electron carrier activity
1 (0.9) GO:0060089 molecular transducer activity	**3 (3.3) GO:0060089** molecular transducer activity

1 (0.9) GO:0030528 transcription regulator activity **4 (3.7) GO:0030234** enzyme regulator activity **59 (55.1) GO:0003824** catalytic activity **51 (47.7) GO:0005488** binding **2 (1.9) GO:0016209** antioxidant activity **1 (0.9) GO:0045182** translation regulator activity **17 (15.9) GO:0005198** structural molecule activity **8 (7.5) GO:0005215** transporter activity ------------------------------------ **Total:** 10 == **Total GO terms in three ontologies:** 47	**1 (1.1) GO:0030528** transcription regulator activity **3 (3.3) GO:0030234** enzyme regulator activity **51 (56.7) GO:0003824** catalytic activity **49 (54.4) GO:0005488** binding **2 (2.2) GO:0016209** antioxidant activity **5 (5.6) GO:0045182** translation regulator activity **5 (5.6) GO:0005198** structural molecule activity **6 (6.7) GO:0005215** transporter activity ------------------------------------ **Total:** 10 == **Total GO terms in three ontologies:** 47
N3 vs D3 up	**N3 vs D3 down**
Cellular Component: **4 (6.1) GO:0005576** extracellular region **1 (1.5) GO:0044421** extracellular region part **40 (60.6) GO:0005623** cell **40 (60.6) GO:0044464** cell part **5 (7.6) GO:0031974** membrane-enclosed lumen **1 (1.5) GO:0031975** envelope **24 (36.4) GO:0032991** macromolecular complex **30 (45.5) GO:0043226** organelle **20 (30.3) GO:0044422** organelle part **1 (1.5) GO:0044421** extracellular region part **20 (30.3) GO:0044422** organelle part **2 (3.0) GO:0044456** synapse part **40 (60.6) GO:0044464** cell part **2 (3.0) GO:0045202** synapse **2 (3.0) GO:0044456** synapse part ------------------------------------ **Total:** 15	**Cellular Component:** **3 (1.4) GO:0005576** extracellular region **1 (0.5) GO:0044421** extracellular region part **115 (53.5) GO:0005623** cell **115 (53.5) GO:0044464** cell part **8 (3.7) GO:0031974** membrane-enclosed lumen **5 (2.3) GO:0031975** envelope **61 (28.4) GO:0032991** macromolecular complex **71 (33.0) GO:0043226** organelle **44 (20.5) GO:0044422** organelle part **1 (0.5) GO:0044421** extracellular region part **44 (20.5) GO:0044422** organelle part **2 (0.9) GO:0044456** synapse part **115 (53.5) GO:0044464** cell part **2 (0.9) GO:0045202** synapse **2 (0.9) GO:0044456** synapse part ------------------------------------ **Total:** 15
Biological Process: **11 (16.7) GO:0044085** cellular component biogenesis **15 (22.7) GO:0032502** developmental process **10 (15.2) GO:0000003** reproduction **15 (22.7) GO:0016043** cellular component organization **4 (6.1) GO:0016265** death **10 (15.2) GO:0022414** reproductive process	**Biological Process:** **9 (4.2) GO:0044085** cellular component biogenesis **41 (19.1) GO:0032502** developmental process **9 (4.2) GO:0000003** reproduction **30 (14.0) GO:0016043** cellular component organization **8 (3.7) GO:0016265** death **8 (3.7) GO:0022414** reproductive process

4 (6.1) GO:0002376 immune system process **10 (15.2) GO:0050896** response to stimulus **19 (28.8) GO:0032501** multicellular organismal process **12 (18.2) GO:0010926** anatomical structure formation **3 (4.5) GO:0051704** multi\-organism process **10 (15.2) GO:0051234** establishment of localization **37 (56.1) GO:0008152** metabolic process **1 (1.5) GO:0016032** viral reproduction **14 (21.2) GO:0043473** pigmentation **6 (9.1) GO:0040011** locomotion **14 (21.2) GO:0051179** localization **40 (60.6) GO:0009987** cellular process **3 (4.5) GO:0040007** growth **17 (25.8) GO:0065007** biological regulation ------------------------------------ **Total:** 20	**5 (2.3) GO:0002376** immune system process **17 (7.9) GO:0050896** response to stimulus **44 (20.5) GO:0032501** multicellular organismal process **11 (5.1) GO:0010926** anatomical structure formation **2 (0.9) GO:0051704** multi\-organism process **37 (17.2) GO:0051234** establishment of localization **5 (2.3) GO:0022610** biological adhesion **128 (59.5) GO:0008152** metabolic process **1 (0.5) GO:0016032** viral reproduction **2 (0.9) GO:0048511** rhythmic process **39 (18.1) GO:0043473** pigmentation **3 (1.4) GO:0040011** locomotion **40 (18.6) GO:0051179** localization **1 (0.5) GO:0001906** cell killing **129 (60.0) GO:0009987** cellular process **2 (0.9) GO:0040007** growth **45 (20.9) GO:0065007** biological regulation ------------------------------------ **Total:** 23
Molecular Function: **1 (1.5) GO:0060089** molecular transducer activity **4 (6.1) GO:0045182** translation regulator activity **5 (7.6) GO:0030234** enzyme regulator activity **5 (7.6) GO:0005198** structural molecule activity **36 (54.5) GO:0003824** catalytic activity **38 (57.6) GO:0005488** binding **3 (4.5) GO:0005215** transporter activity ------------------------------------ **Total:** 7 == **Total GO terms in three ontologies:** 42	**Molecular Function:** **1 (0.5) GO:0009055** electron carrier activity **4 (1.9) GO:0060089** molecular transducer activity **1 (0.5) GO:0030528** transcription regulator activity **4 (1.9) GO:0030234** enzyme regulator activity **126 (58.6) GO:0003824** catalytic activity **115 (53.5) GO:0005488** binding **3 (1.4) GO:0016209** antioxidant activity **9 (4.2) GO:0045182** translation regulator activity **18 (8.4) GO:0005198** structural molecule activity **16 (7.4) GO:0005215** transporter activity ------------------------------------ **Total:** 10 == **Total GO terms in three ontologies:** 48

Gene ontology analysis of locust eggs diapause related genes and proteins. (N2 vs D2 ∩ N3 vs D3)

Diapause related genes up	Diapause related genes down
Cellular Component:	**Cellular Component:**

12 (4.2) GO:0005576 extracellular region **151 (53.0) GO:0005623** cell **17 (6.0) GO:0031974** membrane-enclosed lumen **4 (1.4) GO:0031975** envelope **60 (21.1) GO:0032991** macromolecular complex **100 (35.1) GO:0043226** organelle **8 (2.8) GO:0044421** extracellular region part **56 (19.6) GO:0044422** organelle part **4 (1.4) GO:0044456** synapse part **151 (53.0) GO:0044464** cell part **9 (3.2) GO:0045202** synapse ------------------------------------ **Total:** 11	**10 (1.4) GO:0005576** extracellular region **431 (59.0) GO:0005623** cell **53 (7.3) GO:0031974** membrane-enclosed lumen **31 (4.2) GO:0031975** envelope **238 (32.6) GO:0032991** macromolecular complex **318 (43.6) GO:0043226** organelle **3 (0.4) GO:0044421** extracellular region part **197 (27.0) GO:0044422** organelle part **2 (0.3) GO:0044456** synapse part **431 (59.0) GO:0044464** cell part **3 (0.4) GO:0045202** synapse ------------------------------------ **Total:** 11
Biological Process: **23 (8.1) GO:0000003** reproduction **65 (22.8) GO:0032502** developmental process **35 (12.3) GO:0044085** cellular component biogenesis **59 (20.7) GO:0016043** cellular component organization **15 (5.3) GO:0016265** death **20 (7.0) GO:0022414** reproductive process **9 (3.2) GO:0002376** immune system process **38 (13.3) GO:0050896** response to stimulus **69 (24.2) GO:0032501** multicellular organismal process **28 (9.8) GO:0010926** anatomical structure formation **5 (1.8) GO:0051704** multi\-organism process **29 (10.2) GO:0051234** establishment of localization **6 (2.1) GO:0022610** biological adhesion **151 (53.0) GO:0008152** metabolic process **1 (0.4) GO:0016032** viral reproduction **3 (1.1) GO:0048511** rhythmic process **59 (20.7) GO:0043473** pigmentation **11 (3.9) GO:0040011** locomotion **40 (14.0) GO:0051179** localization **13 (4.6) GO:0040007** growth **179 (62.8) GO:0009987** cellular process **73 (25.6) GO:0065007** biological regulation	**Biological Process:** **89 (12.2) GO:0000003** reproduction **65 (8.9) GO:0044085** cellular component biogenesis **129 (17.7) GO:0032502** developmental process **129 (17.7) GO:0016043** cellular component organization **42 (5.8) GO:0016265** death **73 (10.0) GO:0022414** reproductive process **15 (2.1) GO:0002376** immune system process **66 (9.0) GO:0050896** response to stimulus **141 (19.3) GO:0032501** multicellular organismal process **50 (6.8) GO:0010926** anatomical structure formation **9 (1.2) GO:0051704** multi\-organism process **104 (14.2) GO:0051234** establishment of localization **9 (1.2) GO:0022610** biological adhesion **475 (65.1) GO:0008152** metabolic process **47 (6.4) GO:0016032** viral reproduction **6 (0.8) GO:0048511** rhythmic process **125 (17.1) GO:0043473** pigmentation **19 (2.6) GO:0040011** locomotion **118 (16.2) GO:0051179** localization **39 (5.3) GO:0040007** growth **531 (72.7) GO:0009987** cellular process **138 (18.9) GO:0065007** biological regulation

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Molecular Function: 1 (0.4) **GO:0009055** electron carrier activity 3 (1.1) **GO:0060089** molecular transducer activity 4 (1.4) **GO:0045182** translation regulator activity 6 (2.1) **GO:0030528** transcription regulator activity 6 (2.1) **GO:0030234** enzyme regulator activity 12 (4.2) **GO:0005198** structural molecule activity 144 (50.5) **GO:0003824** catalytic activity 139 (48.8) **GO:0005488** binding 12 (4.2) **GO:0005215** transporter activity ------------------------------------ **Total:** 9 == **Total GO terms in three ontologies:** 42	**Molecular Function:** 4 (0.5) **GO:0009055** electron carrier activity 7 (1.0) **GO:0060089** molecular transducer activity 6 (0.8) **GO:0030528** transcription regulator activity 6 (0.8) **GO:0030234** enzyme regulator activity 349 (47.8) **GO:0003824** catalytic activity 292 (40.0) **GO:0005488** binding 1 (0.1) **GO:0016209** antioxidant activity 1 (0.1) **GO:0015457** auxiliary transport protein activity 25 (3.4) **GO:0045182** translation regulator activity 151 (20.7) **GO:0005198** structural molecule activity 26 (3.6) **GO:0005215** transporter activity ------------------------------------ **Total:** 11 == **Total GO terms in three ontologies:** 44
Diapause related proteins up	**Diapause related proteins down**
Cellular Component: 2 (40.0) **GO:0005623** cell 1 (20.0) **GO:0031974** membrane-enclosed lumen 1 (20.0) **GO:0032991** macromolecular complex 1 (20.0) **GO:0043226** organelle 1 (20.0) **GO:0044422** organelle part 2 (40.0) **GO:0044464** cell part ------------------------------------ **Total:** 6	**Cellular Component:** 1 (10.0) **GO:0005576** extracellular region 5 (50.0) **GO:0005623** cell 3 (30.0) **GO:0032991** macromolecular complex 2 (20.0) **GO:0043226** organelle 1 (10.0) **GO:0044422** organelle part 5 (50.0) **GO:0044464** cell part ------------------------------------ **Total:** 6
Biological Process: 1 (20.0) **GO:0032502** developmental process 1 (20.0) **GO:0044085** cellular component biogenesis 1 (20.0) **GO:0000003** reproduction 1 (20.0) **GO:0016043** cellular component organization 1 (20.0) **GO:0016265** death 1 (20.0) **GO:0022414** reproductive process 1 (20.0) **GO:0002376** immune system process 1 (20.0) **GO:0050896** response to stimulus 2 (40.0) **GO:0032501** multicellular organismal process 1 (20.0) **GO:0010926** anatomical structure formation	**Biological Process:** 4 (40.0) **GO:0032502** developmental process 3 (30.0) **GO:0016043** cellular component organization 1 (10.0) **GO:0022610** biological adhesion 7 (70.0) **GO:0008152** metabolic process 1 (10.0) **GO:0016265** death 3 (30.0) **GO:0043473** pigmentation 1 (10.0) **GO:0050896** response to stimulus 3 (30.0) **GO:0051179** localization 4 (40.0) **GO:0032501** multicellular organismal process 5 (50.0) **GO:0009987** cellular process

1 **(20.0)** **GO:0051234** establishment of localization **4** **(80.0)** **GO:0008152** metabolic process **1** **(20.0)** **GO:0016032** viral reproduction **2** **(40.0)** **GO:0043473** pigmentation **1** **(20.0)** **GO:0040011** locomotion **1** **(20.0)** **GO:0051179** localization **3** **(60.0)** **GO:0009987** cellular process **1** **(20.0)** **GO:0040007** growth **2** **(40.0)** **GO:0065007** biological regulation ----------------------------------- **Total:** 19	**1** **(10.0)** **GO:0010926** anatomical structure formation **4** **(40.0)** **GO:0065007** biological regulation **2** **(20.0)** **GO:0051234** establishment of localization ----------------------------------- **Total:** 13
Molecular Function: **1** **(20.0)** **GO:0030234** enzyme regulator activity **4** **(80.0)** **GO:0003824** catalytic activity **1** **(20.0)** **GO:0005488** binding ----------------------------------- **Total:** 3 == **Total GO terms in three ontologies:** 28	**Molecular Function:** **1** **(10.0)** **GO:0030234** enzyme regulator activity **1** **(10.0)** **GO:0045182** translation regulator activity **5** **(50.0)** **GO:0003824** catalytic activity **8** **(80.0)** **GO:0005488** binding ----------------------------------- **Total:** 4 == **Total GO terms in three ontologies:** 23
Gene ontology analysis of locust eggs development related genes and proteins. (N2 vs N3 ∩ D2 vs D3)	
Development related genes up	**Development related genes down**
Cellular Component: **36** **(6.2)** **GO:0005576** extracellular region **9** **(1.6)** **GO:0044421** extracellular region part **265** **(45.8)** **GO:0005623** cell **265** **(45.8)** **GO:0044464** cell part **8** **(1.4)** **GO:0031974** membrane-enclosed lumen **11** **(1.9)** **GO:0031975** envelope **57** **(9.9)** **GO:0032991** macromolecular complex **111** **(19.2)** **GO:0043226** organelle **64** **(11.1)** **GO:0044422** organelle part **9** **(1.6)** **GO:0044421** extracellular region part **64** **(11.1)** **GO:0044422** organelle part **20** **(3.5)** **GO:0044456** synapse part **265** **(45.8)** **GO:0044464** cell part **23** **(4.0)** **GO:0045202** synapse **20** **(3.5)** **GO:0044456** synapse part	**Cellular Component:** **20** **(3.4)** **GO:0005576** extracellular region **297** **(50.6)** **GO:0005623** cell **22** **(3.7)** **GO:0031974** membrane-enclosed lumen **14** **(2.4)** **GO:0031975** envelope **91** **(15.5)** **GO:0032991** macromolecular complex **165** **(28.1)** **GO:0043226** organelle **12** **(2.0)** **GO:0044421** extracellular region part **90** **(15.3)** **GO:0044422** organelle part **7** **(1.2)** **GO:0044456** synapse part **297** **(50.6)** **GO:0044464** cell part **10** **(1.7)** **GO:0045202** synapse ----------------------------------- **Total:** 11

------------------------------------ **Total:** 15	
Biological Process: **136 (23.5) GO:0032502** developmental process **24 (4.2) GO:0000003** reproduction **42 (7.3) GO:0044085** cellular component biogenesis **107 (18.5) GO:0016043** cellular component organization **16 (2.8) GO:0016265** death **23 (4.0) GO:0022414** reproductive process **17 (2.9) GO:0002376** immune system process **72 (12.5) GO:0050896** response to stimulus **149 (25.8) GO:0032501** multicellular organismal process **46 (8.0) GO:0010926** anatomical structure formation **16 (2.8) GO:0051704** multi\-organism process **91 (15.7) GO:0051234** establishment of localization **22 (3.8) GO:0022610** biological adhesion **214 (37.0) GO:0008152** metabolic process **4 (0.7) GO:0048511** rhythmic process **113 (19.6) GO:0043473** pigmentation **13 (2.2) GO:0040011** locomotion **108 (18.7) GO:0051179** localization **280 (48.4) GO:0009987** cellular process **8 (1.4) GO:0040007** growth **127 (22.0) GO:0065007** biological regulation ------------------------------------ **Total:** 21	**Biological Process:** **45 (7.7) GO:0044085** cellular component biogenesis **128 (21.8) GO:0032502** developmental process **54 (9.2) GO:0000003** reproduction **100 (17.0) GO:0016043** cellular component organization **23 (3.9) GO:0016265** death **50 (8.5) GO:0022414** reproductive process **21 (3.6) GO:0002376** immune system process **84 (14.3) GO:0050896** response to stimulus **155 (26.4) GO:0032501** multicellular organismal process **55 (9.4) GO:0010926** anatomical structure formation **14 (2.4) GO:0051704** multi\-organism process **91 (15.5) GO:0051234** establishment of localization **8 (1.4) GO:0022610** biological adhesion **258 (44.0) GO:0008152** metabolic process **2 (0.3) GO:0016032** viral reproduction **5 (0.9) GO:0048511** rhythmic process **142 (24.2) GO:0043473** pigmentation **18 (3.1) GO:0040011** locomotion **117 (19.9) GO:0051179** localization **320 (54.5) GO:0009987** cellular process **16 (2.7) GO:0040007** growth **155 (26.4) GO:0065007** biological regulation ------------------------------------ **Total:** 22
Molecular Function: **3 (0.5) GO:0009055** electron carrier activity **37 (6.4) GO:0060089** molecular transducer activity **8 (1.4) GO:0030528** transcription regulator activity **13 (2.2) GO:0030234** enzyme regulator activity **261 (45.2) GO:0003824** catalytic activity **256 (44.3) GO:0005488** binding **9 (1.6) GO:0016209** antioxidant activity **2 (0.3) GO:0015457** auxiliary transport protein activity	**Molecular Function:** **2 (0.3) GO:0009055** electron carrier activity **20 (3.4) GO:0060089** molecular transducer activity **13 (2.2) GO:0030528** transcription regulator activity **18 (3.1) GO:0030234** enzyme regulator activity **287 (48.9) GO:0003824** catalytic activity **234 (39.9) GO:0005488** binding **4 (0.7) GO:0016209** antioxidant activity **1 (0.2) GO:0015457** auxiliary transport protein activity

50 (8.7) **GO:0005198** structural molecule activity 65 (11.2) **GO:0005215** transporter activity ------------------------------------ **Total:** 10 == **Total GO terms in three ontologies:** 46	3 (0.5) **GO:0045182** translation regulator activity 24 (4.1) **GO:0005198** structural molecule activity 65 (11.1) **GO:0005215** transporter activity ------------------------------------ **Total:** 11 == **Total GO terms in three ontologies:** 44
Development related proteins up	**Development related proteins down**
Cellular Component: 1 (8.3) **GO:0005576** extracellular region 6 (50.0) **GO:0005623** cell 1 (8.3) **GO:0031974** membrane-enclosed lumen 5 (41.7) **GO:0032991** macromolecular complex 5 (41.7) **GO:0043226** organelle 1 (8.3) **GO:0044421** extracellular region part 2 (16.7) **GO:0044422** organelle part 6 (50.0) **GO:0044464** cell part ------------------------------------ **Total:** 8	**Cellular Component:** 2 (9.1) **GO:0005576** extracellular region 12 (54.5) **GO:0005623** cell 2 (9.1) **GO:0031974** membrane-enclosed lumen 2 (9.1) **GO:0031975** envelope 11 (50.0) **GO:0032991** macromolecular complex 10 (45.5) **GO:0043226** organelle 1 (4.5) **GO:0044421** extracellular region part 7 (31.8) **GO:0044422** organelle part 12 (54.5) **GO:0044464** cell part ------------------------------------ **Total:** 9
Biological Process: 2 (16.7) **GO:0044085** cellular component biogenesis 2 (16.7) **GO:0032502** developmental process 1 (8.3) **GO:0000003** reproduction 2 (16.7) **GO:0016043** cellular component organization 6 (50.0) **GO:0008152** metabolic process 1 (8.3) **GO:0016265** death 1 (8.3) **GO:0022414** reproductive process 3 (25.0) **GO:0043473** pigmentation 2 (16.7) **GO:0051179** localization 2 (16.7) **GO:0050896** response to stimulus 7 (58.3) **GO:0009987** cellular process 3 (25.0) **GO:0032501** multicellular organismal process 2 (16.7) **GO:0010926** anatomical structure formation 2 (16.7) **GO:0051234** establishment of localization 3 (25.0) **GO:0065007** biological regulation ------------------------------------ **Total:** 15	**Biological Process:** 3 (13.6) **GO:0032502** developmental process 2 (9.1) **GO:0044085** cellular component biogenesis 1 (4.5) **GO:0000003** reproduction 4 (18.2) **GO:0016043** cellular component organization 1 (4.5) **GO:0016265** death 1 (4.5) **GO:0002376** immune system process 1 (4.5) **GO:0050896** response to stimulus 3 (13.6) **GO:0032501** multicellular organismal process 2 (9.1) **GO:0010926** anatomical structure formation 3 (13.6) **GO:0051234** establishment of localization 13 (59.1) **GO:0008152** metabolic process 1 (4.5) **GO:0016032** viral reproduction 2 (9.1) **GO:0043473** pigmentation 3 (13.6) **GO:0051179** localization 15 (68.2) **GO:0009987** cellular process 1 (4.5) **GO:0040007** growth 3 (13.6) **GO:0065007** biological regulation

	------------------------------------ **Total:** 17
Molecular Function: 1 (8.3) **GO:0030234** enzyme regulator activity 2 (16.7) **GO:0005198** structural molecule activity 3 (25.0) **GO:0003824** catalytic activity 6 (50.0) **GO:0005488** binding 1 (8.3) **GO:0005215** transporter activity ------------------------------------ **Total:** 5 == **Total GO terms in three ontologies:** 28	**Molecular Function:** 1 (4.5) **GO:0030234** enzyme regulator activity 7 (31.8) **GO:0005198** structural molecule activity 6 (27.3) **GO:0003824** catalytic activity 9 (40.9) **GO:0005488** binding 2 (9.1) **GO:0005215** transporter activity ------------------------------------ **Total:** 5 == **Total GO terms in three ontologies:** 31

Appendix B Pathway enrichment analysis of differentially expressed genes and proteins.

Pathway	**N2 vs D2**	**All unigenes**	**P-value**
Peroxisome	175	448	4.34E-06
Phagosome	192	517	5.60E-05
Ribosome	523	838	1.83E-90
Proteasome	129	181	1.29E-31
Aminoacyl-tRNA biosynthesis	146	258	3.67E-20
RNA transport	665	1833	1.14E-11
mRNA surveillance pathway	505	1415	4.45E-08
Protein processing in endoplasmic reticulum	328	878	8.74E-08
Protein export	38	72	2.33E-05
Ribosome biogenesis in eukaryotes	197	528	3.31E-05
Metabolic pathways	2048	5285	1.45E-59
Oxidative phosphorylation	258	483	3.85E-29
Alanine, aspartate and glutamate metabolism	123	184	4.16E-26
Arginine and proline metabolism	161	282	1.26E-22
Pyruvate metabolism	163	294	4.30E-21
Valine, leucine and isoleucine degradation	162	298	7.98E-20
Glyoxylate and dicarboxylate metabolism	94	144	3.22E-19
Glycolysis / Gluconeogenesis	171	363	3.70E-13
Citrate cycle (TCA cycle)	167	353	4.42E-13
Butanoate metabolism	88	157	1.97E-12
Tryptophan metabolism	99	194	1.36E-10
Glycine, serine and threonine metabolism	106	218	1.13E-09
Propanoate metabolism	99	200	1.17E-09
Fatty acid metabolism	110	229	1.35E-09
beta-Alanine metabolism	97	199	4.76E-09

Valine, leucine and isoleucine biosynthesis	39	59	4.86E-09
Pentose phosphate pathway	80	162	4.97E-08
Synthesis and degradation of ketone bodies	27	39	2.74E-07
Cysteine and methionine metabolism	96	211	3.75E-07
Histidine metabolism	53	101	7.92E-07
Pantothenate and CoA biosynthesis	37	64	1.73E-06
Tyrosine metabolism	94	219	1.03E-05
Fructose and mannose metabolism	88	205	1.93E-05
One carbon pool by folate	38	75	7.53E-05
Amino sugar and nucleotide sugar metabolism	107	270	0.000149
Glutathione metabolism	85	210	0.000303
Vitamin B6 metabolism	12	18	0.001099
Biosynthesis of unsaturated fatty acids	56	135	0.001533
Phenylalanine metabolism	48	113	0.001785
Fatty acid biosynthesis	24	48	0.001927
Phenylalanine, tyrosine and tryptophan biosynthesis	17	31	0.002478
Selenocompound metabolism	32	70	0.00249
Glycerolipid metabolism	94	259	0.008052
Sphingolipid metabolism	34	85	0.021349
Retinol metabolism	70	194	0.022661
Ascorbate and aldarate metabolism	62	170	0.024323
Arachidonic acid metabolism	42	110	0.026655
alpha-Linolenic acid metabolism	42	113	0.041468
Primary bile acid biosynthesis	31	80	0.042174
Fatty acid elongation	38	101	0.042187
Salivary secretion	293	645	1.08E-18
Antigen processing and presentation	98	206	1.92E-08
Collecting duct acid secretion	49	96	5.67E-06
PPAR signaling pathway	115	279	1.15E-05
Synaptic vesicle cycle	113	280	4.07E-05
Dopaminergic synapse	135	370	0.001437
Endocrine and other factor-regulated calcium reabsorption	65	169	0.006007
GnRH signaling pathway	89	245	0.00944
Phototransduction	35	85	0.012141
Insulin signaling pathway	183	544	0.013268
Adipocytokine signaling pathway	65	176	0.016242
Total	9430	22088	

Pathway	**N3 vs D3**	**All unigenes**	**P-value**
Ribosome	364	838	9.63E-26
ECM-receptor interaction	191	398	1.22E-19
Salivary secretion	273	645	8.32E-18

Protein digestion and absorption	175	390	1.23E-14
Tyrosine metabolism	103	219	1.22E-10
Pancreatic secretion	161	394	9.83E-10
Circadian rhythm - fly	57	111	3.55E-08
GABAergic synapse	103	248	3.73E-07
Phototransduction - fly	64	144	4.09E-06
Glycine, serine and threonine metabolism	89	218	5.13E-06
Cardiac muscle contraction	133	353	5.29E-06
mRNA surveillance pathway	449	1415	1.80E-05
Insect hormone biosynthesis	56	127	2.10E-05
Pentose phosphate pathway	67	162	4.37E-05
Gastric acid secretion	121	331	6.52E-05
Circadian rhythm - mammal	54	126	7.50E-05
Glyoxylate and dicarboxylate metabolism	60	144	8.26E-05
Steroid hormone biosynthesis	64	156	8.49E-05
Melanogenesis	117	322	0.000114
RNA transport	559	1833	0.000194
Citrate cycle (TCA cycle)	125	353	0.000238
Glycolysis / Gluconeogenesis	128	363	0.000247
Glycerophospholipid metabolism	108	299	0.000262
Antigen processing and presentation	78	206	0.000353
Cytosolic DNA-sensing pathway	64	163	0.00037
Complement and coagulation cascades	50	121	0.00039
Phenylalanine metabolism	47	113	0.000482
Hematopoietic cell lineage	77	207	0.000705
Cell adhesion molecules (CAMs)	152	458	0.001499
Olfactory transduction	48	124	0.002623
Phenylalanine, tyrosine and tryptophan biosynthesis	16	31	0.002908
Riboflavin metabolism	25	56	0.003119
Linoleic acid metabolism	24	54	0.004012
Tryptophan metabolism	69	194	0.004654
Proximal tubule bicarbonate reclamation	26	61	0.00558
Oxidative phosphorylation	155	483	0.005799
Arginine and proline metabolism	95	282	0.006502
Regulation of actin cytoskeleton	448	1515	0.008402
Drug metabolism - cytochrome P450	71	206	0.009532
Phagosome	163	517	0.009794
Retrograde endocannabinoid signaling	84	250	0.010709
Renin-angiotensin system	20	46	0.010977
Hedgehog signaling pathway	76	225	0.012766
Pyruvate metabolism	96	294	0.015668

Neurotrophin signaling pathway	113	352	0.016116
D-Glutamine and D-glutamate metabolism	5	7	0.017708
Neuroactive ligand-receptor interaction	217	714	0.018227
Phototransduction	32	85	0.019156
Taurine and hypotaurine metabolism	17	40	0.02334
Sulfur metabolism	21	52	0.02346
Focal adhesion	301	1018	0.026643
Adherens junction	245	821	0.028747
Drug metabolism - other enzymes	80	249	0.03672
Glutamatergic synapse	94	297	0.037039
MAPK signaling pathway	229	771	0.040028
Ubiquinone and other terpenoid-quinone biosynthesis	19	49	0.04607
Glycerolipid metabolism	82	259	0.048132
Caffeine metabolism	11	25	0.048368
Total	6971	19934	
Pathway	**N2 vs N3**	**All unigenes**	**P-value**
Metabolic pathways	2329	5285	2.60E-24
Salivary secretion	363	645	7.14E-22
Oxidative phosphorylation	283	483	1.10E-20
Proteasome	130	181	1.42E-20
Protein digestion and absorption	233	390	1.04E-18
Glycine, serine and threonine metabolism	142	218	2.48E-16
Pancreatic secretion	221	394	1.13E-13
RNA transport	835	1833	2.18E-12
Ribosome	410	838	2.26E-11
Pyruvate metabolism	167	294	2.76E-11
Synaptic vesicle cycle	160	280	3.78E-11
ECM-receptor interaction	214	398	6.15E-11
Citrate cycle (TCA cycle)	191	353	3.22E-10
Alanine, aspartate and glutamate metabolism	111	184	4.83E-10
Cardiac muscle contraction	188	353	2.36E-09
mRNA surveillance pathway	640	1415	3.61E-09
Valine, leucine and isoleucine biosynthesis	44	59	1.02E-08
Arginine and proline metabolism	152	282	2.73E-08
Antigen processing and presentation	116	206	5.23E-08
Tyrosine metabolism	121	219	1.15E-07
Glyoxylate and dicarboxylate metabolism	85	144	1.94E-07
Phototransduction	54	85	1.37E-06
Aminoacyl-tRNA biosynthesis	135	258	1.42E-06
Melanogenesis	162	322	3.10E-06
Glutathione metabolism	112	210	3.35E-06

Endocrine and other factor-regulated calcium reabsorption	93	169	3.98E-06
Riboflavin metabolism	38	56	4.98E-06
Valine, leucine and isoleucine degradation	148	298	1.92E-05
Phototransduction - fly	79	144	2.36E-05
Glycerolipid metabolism	130	259	3.17E-05
Collecting duct acid secretion	56	96	3.58E-05
Renin-angiotensin system	31	46	4.55E-05
Proximal tubule bicarbonate reclamation	38	61	9.14E-05
Histidine metabolism	57	101	0.00011
Phagosome	236	517	0.00015
Butanoate metabolism	82	157	0.000163
Fatty acid biosynthesis	30	48	0.000454
Pentose phosphate pathway	82	162	0.000599
Synthesis and degradation of ketone bodies	25	39	0.000782
Insect hormone biosynthesis	66	127	0.000803
Glutamatergic synapse	138	297	0.001377
Retrograde endocannabinoid signaling	118	250	0.001485
Tryptophan metabolism	94	194	0.001576
Olfactory transduction	63	124	0.002151
Phenylalanine metabolism	58	113	0.002338
Adherens junction	350	821	0.002379
PPAR signaling pathway	129	279	0.0024
Arachidonic acid metabolism	56	110	0.003467
Dopaminergic synapse	165	370	0.00432
GABAergic synapse	114	248	0.005156
Amino sugar and nucleotide sugar metabolism	123	270	0.005462
Drug metabolism - other enzymes	114	249	0.00601
Phenylalanine, tyrosine and tryptophan biosynthesis	19	31	0.006785
One carbon pool by folate	39	75	0.008577
Pantothenate and CoA biosynthesis	34	64	0.009023
Metabolism of xenobiotics by cytochrome P450	101	221	0.009816
Cholinergic synapse	103	226	0.010098
Peroxisome	193	448	0.012294
Vitamin B6 metabolism	12	18	0.012414
Cysteine and methionine metabolism	96	211	0.013325
Glycolysis / Gluconeogenesis	158	363	0.014453
Gastric acid secretion	145	331	0.014454
Complement and coagulation cascades	58	121	0.014573
Fatty acid elongation	49	101	0.018098
Glycerophospholipid metabolism	131	299	0.01912
Protein export	36	72	0.023316

Steroid hormone biosynthesis	71	156	0.029477
Calcium signaling pathway	208	496	0.032244
Long-term depression	97	220	0.032696
Aldosterone-regulated sodium reabsorption	43	90	0.033983
Fat digestion and absorption	73	162	0.035062
Lysosome	190	452	0.03567
Retinol metabolism	86	194	0.036787
Chemokine signaling pathway	363	893	0.042138
Starch and sucrose metabolism	126	295	0.047285
Drug metabolism - cytochrome P450	90	206	0.048342
Total	12832	26679	

Pathway	**D2 vs D3**	**All unigenes**	**P-value**
Cell adhesion molecules (CAMs)	170	458	2.64E-20
Hematopoietic cell lineage	91	207	9.95E-17
Protein digestion and absorption	131	390	2.90E-12
Tyrosine metabolism	82	219	8.85E-11
Insect hormone biosynthesis	54	127	7.03E-10
T cell receptor signaling pathway	150	501	1.20E-09
Fatty acid biosynthesis	28	48	1.54E-09
Neuroactive ligand-receptor interaction	193	714	4.55E-08
Cytosolic DNA-sensing pathway	58	163	3.55E-07
B cell receptor signaling pathway	80	252	6.47E-07
Cardiac muscle contraction	103	353	1.64E-06
Bile secretion	220	886	5.28E-06
Calcium signaling pathway	133	496	8.12E-06
Gastric acid secretion	95	331	8.60E-06
RNA polymerase	159	620	1.70E-05
ECM-receptor interaction	107	398	5.24E-05
Complement and coagulation cascades	40	121	0.000142
Vitamin digestion and absorption	48	157	0.000277
Glycosphingolipid biosynthesis - ganglio series	12	23	0.000339
Pancreatic secretion	102	394	0.000349
Fc gamma R-mediated phagocytosis	228	986	0.00041
Drug metabolism - other enzymes	69	249	0.000412
Purine metabolism	253	1114	0.000628
ABC transporters	173	732	0.000686
Other glycan degradation	20	52	0.00077
Salivary secretion	151	645	0.002138
Lysine degradation	191	838	0.002287
Vascular smooth muscle contraction	153	656	0.002346
Steroid hormone biosynthesis	44	156	0.002894

Drug metabolism - cytochrome P450	55	206	0.003595
Pyrimidine metabolism	194	862	0.003798
Focal adhesion	225	1018	0.004759
Phenylalanine metabolism	33	113	0.005101
Fat digestion and absorption	44	162	0.006134
Taste transduction	26	87	0.008732
Cytokine-cytokine receptor interaction	48	184	0.009752
Glycerophospholipid metabolism	73	299	0.010026
Riboflavin metabolism	18	56	0.012304
Olfactory transduction	34	124	0.012623
Proximal tubule bicarbonate reclamation	19	61	0.014634
Jak-STAT signaling pathway	45	176	0.017109
Regulation of actin cytoskeleton	318	1515	0.01768
Renin-angiotensin system	15	46	0.018568
Glycosphingolipid biosynthesis - globo series	9	23	0.019076
Metabolism of xenobiotics by cytochrome P450	54	221	0.023463
mRNA surveillance pathway	296	1415	0.024986
Antigen processing and presentation	50	206	0.031646
Fatty acid elongation	27	101	0.03293
Intestinal immune network for IgA production	2	2	0.0356
Glycosaminoglycan degradation	17	58	0.036023
Melanogenesis	74	322	0.036476
Circadian rhythm - fly	29	111	0.037019
Vasopressin-regulated water reabsorption	112	508	0.038831
Starch and sucrose metabolism	68	295	0.040926
Lysosome	100	452	0.044741
Total	5323	20909	

Appendix C Differentially expressed genes within metabolism pathways in response to diapauses and development.	
Up-regulated genes related to diapause	
geneID	Swissprot-annotation
CL10099.Contig1_All	Rho-related GTP-binding protein RhoU OS=Mus musculus GN=Rhou PE=2 SV=1
CL10174.Contig1_All	Calcium/calmodulin-dependent protein kinase type II alpha chain OS=Drosophila melanogaster GN=CaMKII PE=1 SV=1
CL1018.Contig19_All	Protein pellino OS=Drosophila melanogaster GN=Pli PE=1 SV=1
CL10183.Contig2_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL10252.Contig1_All	N-glycosylase/DNA lyase OS=Drosophila melanogaster GN=Ogg1 PE=2 SV=2

CL10322.Contig1_All	40S ribosomal protein S29 OS=Scarabaeus laticollis GN=RpS29 PE=3 SV=1
CL10353.Contig2_All	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Oryctolagus cuniculus GN=MGAT1 PE=1 SV=1
CL10397.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL10397.Contig2_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL10565.Contig4_All	Protein numb OS=Drosophila melanogaster GN=numb PE=1 SV=2
CL10605.Contig2_All	--
CL10633.Contig2_All	Cystathionine beta-synthase OS=Oryctolagus cuniculus GN=CBS PE=2 SV=3
CL10834.Contig1_All	NADP-dependent malic enzyme OS=Dictyostelium discoideum GN=malA PE=2 SV=1
CL10834.Contig2_All	NADP-dependent malic enzyme OS=Dictyostelium discoideum GN=malA PE=2 SV=1
CL1094.Contig2_All	Triple functional domain protein OS=Homo sapiens GN=TRIO PE=1 SV=2
CL11039.Contig3_All	Ragulator complex protein LAMTOR4 OS=Xenopus tropicalis GN=lamtor4 PE=3 SV=1
CL11107.Contig2_All	40S ribosomal protein S30 OS=Rattus norvegicus GN=Fau PE=1 SV=1
CL11299.Contig1_All	Plasma membrane calcium-transporting ATPase 3 OS=Rattus norvegicus GN=Atp2b3 PE=2 SV=2
CL11436.Contig1_All	Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=2
CL11459.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
CL11643.Contig2_All	Alcohol dehydrogenase 1 OS=Caenorhabditis elegans GN=sodh-1 PE=1 SV=2
CL11663.Contig2_All	--
CL11757.Contig3_All	--
CL11955.Contig1_All	--
CL12092.Contig1_All	Histone H2A OS=Cairina moschata PE=3 SV=2
CL12127.Contig1_All	Mannose-1-phosphate guanyltransferase beta-A OS=Xenopus laevis GN=gmppb-a PE=2 SV=1
CL12127.Contig2_All	Mannose-1-phosphate guanyltransferase beta OS=Drosophila pseudoobscura pseudoobscura GN=GA10892 PE=3 SV=1
CL12193.Contig2_All	--
CL12208.Contig1_All	--
CL1221.Contig1_All	--
CL12211.Contig2_All	Histone H2A, sperm (Fragment) OS=Lytechinus pictus PE=3 SV=1

CL12521.Contig1_All	Metal-response element-binding transcription factor 2 OS=Mus musculus GN=Mtf2 PE=1 SV=2
CL1256.Contig14_All	RNA-binding protein fusilli OS=Drosophila melanogaster GN=fus PE=2 SV=1
CL12582.Contig2_All	Mannose-binding protein C OS=Bos taurus GN=MBL PE=2 SV=1
CL12622.Contig2_All	--
CL12673.Contig1_All	--
CL12744.Contig2_All	--
CL12802.Contig2_All	Septin-7 OS=Pongo abelii GN=SEPT7 PE=2 SV=2
CL12839.Contig1_All	Peroxisomal membrane protein PMP34 OS=Mus musculus GN=Slc25a17 PE=2 SV=1
CL12996.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL1302.Contig2_All	S-adenosylmethionine synthase OS=Drosophila melanogaster GN=Sam-S PE=2 SV=2
CL1308.Contig5_All	Uncharacterized protein B0495.8 OS=Caenorhabditis elegans GN=B0495.8 PE=2 SV=1
CL13089.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL1318.Contig2_All	--
CL13322.Contig1_All	--
CL13335.Contig3_All	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4
CL13534.Contig1_All	--
CL13568.Contig1_All	Atrial natriuretic peptide-converting enzyme OS=Mus musculus GN=Corin PE=2 SV=2
CL13593.Contig3_All	Dihydropyrimidine dehydrogenase [NADP(+)] OS=Caenorhabditis elegans GN=dpyd-1 PE=3 SV=2
CL1360.Contig2_All	--
CL1369.Contig2_All	Disintegrin and metalloproteinase domain-containing protein 10 OS=Bos taurus GN=ADAM10 PE=1 SV=1
CL13747.Contig1_All	--
CL13830.Contig2_All	Spectrin beta chain OS=Drosophila melanogaster GN=beta-Spec PE=1 SV=2
CL13845.Contig1_All	--
CL1403.Contig1_All	Zinc finger protein 675 OS=Homo sapiens GN=ZNF675 PE=1 SV=3
CL1406.Contig2_All	UDP-galactose translocator OS=Bos taurus GN=SLC35A2 PE=2 SV=1
CL14077.Contig1_All	--
CL14116.Contig4_All	Heat shock cognate 70 kDa protein 2 OS=Dictyostelium discoideum GN=hspE-1 PE=1 SV=1
CL14126.Contig1_All	C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2

CL14317.Contig1_All	Hepatitis A virus cellular receptor 1 OS=Chlorocebus aethiops GN=HAVCR1 PE=1 SV=2
CL14464.Contig1_All	Synaptophysin OS=Rattus norvegicus GN=Syp PE=1 SV=1
CL14736.Contig1_All	Eukaryotic translation initiation factor 5A OS=Spodoptera frugiperda GN=eIF-5A PE=2 SV=1
CL14857.Contig1_All	Protein MON2 homolog OS=Drosophila pseudoobscura pseudoobscura GN=mon2 PE=3 SV=2
CL15114.Contig1_All	E3 ubiquitin-protein ligase TRIM71 OS=Danio rerio GN=trim71 PE=2 SV=1
CL15168.Contig1_All	--
CL15372.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL15400.Contig1_All	--
CL15406.Contig2_All	39S ribosomal protein L4, mitochondrial OS=Bos taurus GN=MRPL4 PE=1 SV=1
CL15410.Contig2_All	--
CL15504.Contig1_All	--
CL15512.Contig1_All	--
CL15528.Contig1_All	--
CL15528.Contig2_All	--
CL1554.Contig1_All	Peroxisomal multifunctional enzyme A OS=Dictyostelium discoideum GN=mfeA PE=2 SV=1
CL1554.Contig2_All	Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3
CL1555.Contig1_All	G1/S-specific cyclin-E OS=Hemicentrotus pulcherrimus GN=CYCE PE=2 SV=1
CL15593.Contig1_All	NADP-specific glutamate dehydrogenase OS=Giardia intestinalis PE=2 SV=1
CL1578.Contig8_All	--
CL1583.Contig5_All	Probable malate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=mdh-1 PE=3 SV=1
CL15972.Contig4_All	Homeotic protein Sex combs reduced OS=Drosophila melanogaster GN=Scr PE=1 SV=5
CL16005.Contig6_All	--
CL16005.Contig8_All	--
CL16033.Contig2_All	--
CL16144.Contig13_All	--
CL16144.Contig8_All	--
CL16181.Contig1_All	--
CL16189.Contig13_All	--
CL16189.Contig2_All	--
CL1635.Contig1_All	Protein rtoA OS=Dictyostelium discoideum GN=rtoA PE=2 SV=2

CL16445.Contig2_All	--
CL1673.Contig1_All	Casein kinase I isoform delta OS=Rattus norvegicus GN=Csnk1d PE=1 SV=2
CL16839.Contig1_All	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2
CL1684.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL16878.Contig2_All	--
CL1694.Contig1_All	--
CL17016.Contig1_All	Serine dehydratase-like OS=Mus musculus GN=Sdsl PE=2 SV=1
CL17073.Contig1_All	--
CL17110.Contig3_All	--
CL172.Contig3_All	Molybdenum cofactor biosynthesis protein 1 OS=Bos taurus GN=MOCS1 PE=2 SV=2
CL1721.Contig4_All	--
CL1724.Contig3_All	Ankyrin repeat and SAM domain-containing protein 1A OS=Homo sapiens GN=ANKS1A PE=1 SV=4
CL17274.Contig1_All	Peptidyl-prolyl cis-trans isomerase B OS=Dictyostelium discoideum GN=cypB PE=1 SV=1
CL17335.Contig1_All	Estradiol 17-beta-dehydrogenase 8 OS=Rattus norvegicus GN=Hsd17b8 PE=3 SV=1
CL17574.Contig3_All	--
CL17609.Contig2_All	--
CL17646.Contig1_All	--
CL17682.Contig1_All	--
CL17740.Contig3_All	--
CL17836.Contig2_All	--
CL17918.Contig3_All	--
CL17918.Contig5_All	--
CL1804.Contig1_All	--
CL1925.Contig1_All	--
CL2167.Contig2_All	Mevalonate kinase OS=Bos taurus GN=MVK PE=2 SV=1
CL2363.Contig1_All	Protein DJ-1 OS=Dictyostelium discoideum GN=DDB_G0285969 PE=3 SV=1
CL2363.Contig2_All	Protein DJ-1 OS=Dictyostelium discoideum GN=DDB_G0285969 PE=3 SV=1
CL2363.Contig3_All	--
CL2453.Contig2_All	Protein argonaute-2 OS=Drosophila melanogaster GN=AGO2 PE=1 SV=3
CL2514.Contig1_All	Nucleic-acid-binding protein from transposon X-element OS=Drosophila melanogaster GN=ORF1 PE=4 SV=1
CL2532.Contig4_All	Transcription factor Dp-1 OS=Bos taurus GN=TFDP1 PE=2 SV=1
CL2687.Contig2_All	--

CL2689.Contig1_All	Dynein beta chain, ciliary OS=Tripneustes gratilla PE=1 SV=1
CL2741.Contig2_All	--
CL2791.Contig4_All	--
CL2950.Contig5_All	Cadherin-related tumor suppressor OS=Drosophila melanogaster GN=ft PE=1 SV=3
CL2950.Contig6_All	Cadherin-related tumor suppressor OS=Drosophila melanogaster GN=ft PE=1 SV=3
CL2959.Contig3_All	--
CL2992.Contig9_All	Ankyrin-3 OS=Mus musculus GN=Ank3 PE=1 SV=1
CL3043.Contig1_All	Retinol dehydrogenase 13 OS=Homo sapiens GN=RDH13 PE=1 SV=2
CL3104.Contig4_All	Nuclear factor 1 A-type OS=Mus musculus GN=Nfia PE=1 SV=1
CL3210.Contig1_All	Serine/threonine-protein kinase MARK2 OS=Mus musculus GN=Mark2 PE=1 SV=3
CL3210.Contig2_All	Serine/threonine-protein kinase MARK1 OS=Homo sapiens GN=MARK1 PE=1 SV=2
CL3266.Contig1_All	Holotricin-3 OS=Holotrichia diomphalia PE=1 SV=2
CL3436.Contig1_All	--
CL354.Contig1_All	--
CL3706.Contig1_All	--
CL3706.Contig6_All	--
CL3774.Contig1_All	60S ribosomal protein L41 OS=Spodoptera frugiperda GN=RpL41 PE=3 SV=1
CL3814.Contig1_All	C-terminal-binding protein 1 OS=Homo sapiens GN=CTBP1 PE=1 SV=2
CL3817.Contig1_All	Transcription factor MafG OS=Mus musculus GN=Mafg PE=1 SV=1
CL3967.Contig2_All	--
CL405.Contig16_All	--
CL4101.Contig2_All	Nicastrin OS=Drosophila melanogaster GN=nct PE=1 SV=3
CL4118.Contig1_All	Voltage-dependent anion-selective channel OS=Drosophila melanogaster GN=porin PE=1 SV=3
CL424.Contig1_All	--
CL4270.Contig3_All	Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3
CL4368.Contig2_All	--
CL4368.Contig3_All	--
CL4396.Contig3_All	Glutamate--cysteine ligase OS=Drosophila melanogaster GN=Gclc PE=2 SV=1
CL4516.Contig10_All	Tyrosine-protein phosphatase Lar OS=Drosophila melanogaster GN=Lar PE=1 SV=2

CL4516.Contig4_All	Tyrosine-protein phosphatase Lar OS=Drosophila melanogaster GN=Lar PE=1 SV=2
CL459.Contig1_All	Rho guanine nucleotide exchange factor 12 OS=Homo sapiens GN=ARHGEF12 PE=1 SV=1
CL4663.Contig1_All	60S ribosomal protein L31 OS=Paralichthys olivaceus GN=rpl31 PE=2 SV=1
CL4712.Contig6_All	--
CL4742.Contig2_All	--
CL4906.Contig2_All	U2 small nuclear ribonucleoprotein A' OS=Mus musculus GN=Snrpa1 PE=1 SV=2
CL4976.Contig1_All	Uncharacterized histidine-rich protein DDB_G0274557 OS=Dictyostelium discoideum GN=DDB_G0274557 PE=4 SV=1
CL4994.Contig1_All	--
CL4994.Contig6_All	Cytochrome P450 6k1 OS=Blattella germanica GN=CYP6K1 PE=2 SV=1
CL4994.Contig8_All	Cytochrome P450 6k1 OS=Blattella germanica GN=CYP6K1 PE=2 SV=1
CL502.Contig1_All	--
CL5177.Contig4_All	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica PE=4 SV=1
CL5192.Contig2_All	60S ribosomal protein L5 OS=Suberites domuncula GN=RPL5 PE=2 SV=1
CL5226.Contig1_All	--
CL5246.Contig1_All	Protein RIC1 homolog OS=Drosophila melanogaster GN=CG9063 PE=1 SV=1
CL5374.Contig2_All	Zinc finger protein 577 OS=Homo sapiens GN=ZNF577 PE=2 SV=3
CL5393.Contig3_All	X-ray repair cross-complementing protein 5 OS=Mus musculus GN=Xrcc5 PE=2 SV=4
CL5396.Contig2_All	--
CL5396.Contig3_All	--
CL5396.Contig4_All	--
CL5396.Contig7_All	--
CL5396.Contig8_All	--
CL5467.Contig1_All	GTP-binding nuclear protein Ran OS=Brugia malayi GN=Bm1_44725 PE=2 SV=2
CL556.Contig5_All	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Danio rerio GN=igf2bp1 PE=1 SV=1
CL5686.Contig1_All	FK506-binding protein 1 OS=Dictyostelium discoideum GN=fkbp1 PE=3 SV=1
CL5689.Contig2_All	Probable proton ATPase 1B OS=Leishmania donovani GN=H1B PE=2 SV=1
CL5706.Contig1_All	--

CL572.Contig2_All	--
CL5733.Contig2_All	Integumentary mucin A.1 OS=Xenopus laevis PE=1 SV=1
CL5739.Contig2_All	--
CL5924.Contig3_All	--
CL6035.Contig1_All	Glyceraldehyde-3-phosphate dehydrogenase OS=Mustela putorius furo GN=GAPDH PE=2 SV=1
CL6037.Contig1_All	--
CL6079.Contig2_All	RNA-binding protein 1 OS=Drosophila melanogaster GN=Rbp1 PE=2 SV=3
CL612.Contig3_All	Histone H2B OS=Anopheles gambiae GN=AGAP012199 PE=2 SV=5
CL6174.Contig2_All	--
CL6189.Contig1_All	--
CL6472.Contig1_All	40S ribosomal protein S3a-A OS=Xenopus laevis GN=rps3a-a PE=2 SV=3
CL6536.Contig1_All	Mitochondrial intermembrane space import and assembly protein 40-B OS=Xenopus laevis GN=chchd4-b PE=2 SV=1
CL6544.Contig2_All	--
CL6583.Contig2_All	Fibropellin-1 OS=Strongylocentrotus purpuratus GN=EGF1 PE=1 SV=2
CL6586.Contig1_All	Protein alan shepard OS=Drosophila willistoni GN=shep PE=3 SV=2
CL6751.Contig1_All	Hexokinase type 2 OS=Drosophila melanogaster GN=Hex-t2 PE=2 SV=4
CL677.Contig1_All	Autophagy-related protein 8 OS=Dictyostelium discoideum GN=atg8 PE=1 SV=1
CL678.Contig2_All	--
CL6873.Contig2_All	Homeotic protein spalt-major OS=Drosophila melanogaster GN=salm PE=1 SV=3
CL7042.Contig1_All	Nuclear pore complex protein Nup214 OS=Drosophila melanogaster GN=Nup214 PE=1 SV=2
CL7112.Contig1_All	--
CL7272.Contig3_All	40S ribosomal protein S4, X isoform OS=Danio rerio GN=rps4x PE=2 SV=3
CL7456.Contig1_All	Uncharacterized histidine-rich protein DDB_G0274557 OS=Dictyostelium discoideum GN=DDB_G0274557 PE=4 SV=1
CL7468.Contig2_All	--
CL747.Contig1_All	--
CL7489.Contig1_All	Protein TsetseEP OS=Glossina palpalis palpalis PE=4 SV=1
CL7489.Contig2_All	Protein TsetseEP OS=Glossina palpalis palpalis PE=4 SV=1

CL7528.Contig1_All	NEDD4-binding protein 2 OS=Homo sapiens GN=N4BP2 PE=1 SV=2
CL7571.Contig1_All	Nucleic-acid-binding protein from transposon X-element OS=Drosophila melanogaster GN=ORF1 PE=4 SV=1
CL7604.Contig1_All	Venom dipeptidyl peptidase 4 OS=Apis mellifera PE=1 SV=1
CL7785.Contig1_All	--
CL8015.Contig1_All	--
CL814.Contig5_All	U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein OS=Homo sapiens GN=SNRNP27 PE=1 SV=1
CL835.Contig1_All	--
CL8486.Contig1_All	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3
CL8615.Contig2_All	--
CL8662.Contig3_All	--
CL8683.Contig4_All	--
CL8784.Contig1_All	Tudor domain-containing protein 1 OS=Oryzias latipes GN=tdrd1 PE=2 SV=1
CL8818.Contig4_All	E3 ubiquitin-protein ligase sina OS=Schistosoma mansoni GN=SINA PE=1 SV=1
CL8832.Contig2_All	--
CL884.Contig1_All	--
CL889.Contig6_All	Histone H3 OS=Urechis caupo PE=1 SV=2
CL8926.Contig2_All	Ubiquitin carboxyl-terminal hydrolase 15 OS=Rattus norvegicus GN=Usp15 PE=1 SV=1
CL9376.Contig2_All	--
CL939.Contig1_All	--
CL9436.Contig2_All	RNA-binding protein 1 OS=Drosophila melanogaster GN=Rbp1 PE=2 SV=3
CL9516.Contig1_All	--
CL9544.Contig1_All	Zinc finger CCHC domain-containing protein 9 OS=Homo sapiens GN=ZCCHC9 PE=2 SV=2
CL9568.Contig1_All	--
CL9608.Contig1_All	Cytoglobin-2 OS=Danio rerio GN=cygb2 PE=2 SV=1
CL9680.Contig1_All	Ubiquitin carboxyl-terminal hydrolase 45 OS=Mus musculus GN=Usp45 PE=2 SV=1
CL9736.Contig3_All	Mucin-4 OS=Mus musculus GN=Muc4 PE=2 SV=1
CL9767.Contig3_All	--
CL9820.Contig1_All	Histone H2B OS=Drosophila sechellia GN=His2B PE=3 SV=3
CL9917.Contig4_All	--
Unigene10488_All	Uncharacterized protein K02A2.6 OS=Caenorhabditis elegans GN=K02A2.6

	PE=2 SV=1
Unigene10929_All	--
Unigene109711_All	--
Unigene109829_All	Aldehyde dehydrogenase X, mitochondrial OS=Rattus norvegicus GN=Aldh1b1 PE=1 SV=1
Unigene109884_All	--
Unigene110048_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene110151_All	--
Unigene11180_All	Mannose-binding protein C OS=Bos taurus GN=MBL PE=2 SV=1
Unigene114389_All	--
Unigene115107_All	--
Unigene116463_All	snRNA-activating protein complex subunit 1 OS=Macaca fascicularis GN=SNAPC1 PE=2 SV=1
Unigene11987_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene123944_All	Meiosis arrest female protein 1 OS=Rattus norvegicus GN=Marf1 PE=1 SV=2
Unigene124511_All	Heat shock 70 kDa protein cognate 4 OS=Manduca sexta PE=2 SV=1
Unigene12604_All	--
Unigene129199_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene131696_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene131945_All	--
Unigene135016_All	--
Unigene135337_All	Spore coat protein SP96 OS=Dictyostelium discoideum GN=cotA PE=4 SV=2
Unigene135529_All	Transaldolase OS=Cricetulus griseus GN=TALDO1 PE=2 SV=1
Unigene135863_All	--
Unigene138279_All	Retrovirus-related Pol polyprotein from transposon 17.6 OS=Drosophila melanogaster GN=pol PE=4 SV=1
Unigene138773_All	WAS/WASL-interacting protein family member 1 OS=Rattus norvegicus GN=Wipf1 PE=1 SV=2
Unigene138867_All	--
Unigene139044_All	--
Unigene140218_All	--
Unigene140450_All	--
Unigene140920_All	--
Unigene140965_All	--
Unigene141092_All	--
Unigene141254_All	--

Unigene14131_All	--
Unigene141590_All	Facilitated trehalose transporter Tret1 OS=Drosophila virilis GN=Tret1 PE=3 SV=2
Unigene141748_All	Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=3
Unigene143171_All	Histone H4 OS=Trichogramma cacoeciae PE=3 SV=3
Unigene143874_All	Ubiquitin-conjugating enzyme E2-17 kDa OS=Drosophila melanogaster GN=eff PE=2 SV=1
Unigene145301_All	--
Unigene14754_All	--
Unigene16097_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene16244_All	--
Unigene1625_All	--
Unigene16634_All	--
Unigene16722_All	--
Unigene16895_All	--
Unigene17242_All	--
Unigene18374_All	--
Unigene18510_All	--
Unigene20209_All	--
Unigene2036_All	--
Unigene20430_All	--
Unigene21009_All	--
Unigene22596_All	--
Unigene23019_All	Uncharacterized protein B0495.8 OS=Caenorhabditis elegans GN=B0495.8 PE=2 SV=1
Unigene23028_All	--
Unigene23473_All	30S ribosomal protein S7, organellar chromatophore OS=Paulinella chromatophora GN=rps7 PE=3 SV=1
Unigene24026_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene24566_All	--
Unigene24568_All	--
Unigene24600_All	--
Unigene24861_All	--
Unigene25023_All	--
Unigene25542_All	--
Unigene26153_All	--
Unigene26519_All	--
Unigene27059_All	Glyceraldehyde-3-phosphate dehydrogenase OS=Oryctolagus cuniculus GN=GAPDH PE=1 SV=3
Unigene27063_All	--

Unigene27472_All	--
Unigene27496_All	--
Unigene2809_All	--
Unigene28972_All	--
Unigene29883_All	--
Unigene32133_All	--
Unigene32240_All	--
Unigene32570_All	Progestin and adipoQ receptor family member 3 OS=Mus musculus GN=Paqr3 PE=2 SV=1
Unigene32684_All	--
Unigene32713_All	--
Unigene32771_All	--
Unigene33232_All	--
Unigene33525_All	--
Unigene33725_All	--
Unigene33772_All	--
Unigene34925_All	--
Unigene34969_All	--
Unigene35415_All	--
Unigene355_All	Nucleic-acid-binding protein from transposon X-element OS=Drosophila melanogaster GN=ORF1 PE=4 SV=1
Unigene36530_All	Formin-2 OS=Homo sapiens GN=FMN2 PE=1 SV=4
Unigene36628_All	--
Unigene37929_All	ATP-dependent RNA helicase DHX8 OS=Mus musculus GN=Dhx8 PE=2 SV=1
Unigene38399_All	--
Unigene39761_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene39767_All	--
Unigene39794_All	--
Unigene39933_All	--
Unigene39968_All	--
Unigene40022_All	--
Unigene41043_All	--
Unigene41616_All	--
Unigene41994_All	--
Unigene43092_All	--
Unigene43965_All	--
Unigene44011_All	--
Unigene44100_All	--
Unigene45287_All	Trypsin-1 OS=Astacus fluviatilis PE=1 SV=1

Unigene46005_All	--
Unigene46412_All	--
Unigene49569_All	--
Unigene50100_All	--
Unigene51301_All	--
Unigene52396_All	--
Unigene53427_All	--
Unigene53661_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene53680_All	--
Unigene54589_All	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 OS=Bos taurus GN=PFKFB2 PE=1 SV=2
Unigene54734_All	--
Unigene54773_All	Collectin-11 OS=Danio rerio GN=colec11 PE=2 SV=1
Unigene54900_All	Vesicular glutamate transporter 2 OS=Rattus norvegicus GN=Slc17a6 PE=1 SV=1
Unigene54910_All	Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1
Unigene55242_All	--
Unigene55308_All	--
Unigene55711_All	--
Unigene56287_All	Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1
Unigene56592_All	--
Unigene56759_All	--
Unigene57005_All	--
Unigene58796_All	--
Unigene58872_All	--
Unigene589_All	--
Unigene59421_All	Histone H3.3 OS=Trichinella pseudospiralis GN=HHT3 PE=2 SV=3
Unigene61252_All	--
Unigene61597_All	Mucin-3A OS=Homo sapiens GN=MUC3A PE=2 SV=2
Unigene62275_All	--
Unigene62384_All	--
Unigene62799_All	--
Unigene64700_All	--
Unigene647_All	2-hydroxyacylsphingosine 1-beta-galactosyltransferase OS=Rattus norvegicus GN=Ugt8 PE=2 SV=1
Unigene65254_All	--
Unigene65815_All	--

Unigene66840_All	--
Unigene68149_All	Superoxide dismutase [Cu-Zn] OS=Danio rerio GN=sod1 PE=2 SV=1
Unigene68889_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene69301_All	--
Unigene69423_All	--
Unigene69424_All	--
Unigene69425_All	--
Unigene69426_All	--
Unigene69429_All	--
Unigene69430_All	--
Unigene69432_All	--
Unigene69516_All	--
Unigene69865_All	--
Unigene70444_All	--
Unigene70819_All	--
Unigene70900_All	--
Unigene71107_All	--
Unigene73401_All	--
Unigene73864_All	--
Unigene74013_All	--
Unigene74593_All	--
Unigene746_All	--
Unigene7472_All	--
Unigene75689_All	--
Unigene76393_All	--
Unigene76713_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene7924_All	Zinc finger E-box-binding homebox protein zag-1 OS=Caenorhabditis elegans GN=zag-1 PE=2 SV=1
Unigene80454_All	--
Unigene8061_All	Venom dipeptidyl peptidase 4 OS=Vespula vulgaris PE=1 SV=1
Unigene8173_All	Tigger transposable element-derived protein 2 OS=Homo sapiens GN=TIGD2 PE=2 SV=1
Unigene8463_All	--
Unigene9009_All	Zinc finger protein 1 OS=Drosophila melanogaster GN=zfh1 PE=1 SV=2
Unigene946_All	--
Unigene9850_All	Retrovirus-related Pol polyprotein from transposon 17.6 OS=Drosophila melanogaster GN=pol PE=4 SV=1
Down-regulated genes related to diapause	
geneID	Swissprot-annotation

CL10249.Contig1_All	--
CL10706.Contig1_All	Armadillo segment polarity protein OS=Drosophila melanogaster GN=arm PE=1 SV=1
CL10925.Contig1_All	Glutamine synthetase, mitochondrial OS=Squalus acanthias PE=2 SV=1
CL1120.Contig2_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL11505.Contig1_All	--
CL11603.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL11672.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL11672.Contig3_All	Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2
CL11733.Contig1_All	Zinc finger protein 768 OS=Mus musculus GN=Znf768 PE=2 SV=1
CL11839.Contig2_All	Alpha/beta hydrolase domain-containing protein 14B OS=Mus musculus GN=Abhd14b PE=2 SV=1
CL11922.Contig1_All	--
CL1199.Contig2_All	--
CL12305.Contig1_All	--
CL12531.Contig1_All	Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 PE=1 SV=2
CL1285.Contig4_All	--
CL1291.Contig1_All	Uncharacterized transmembrane protein DDB_G0289901 OS=Dictyostelium discoideum GN=DDB_G0289901 PE=4 SV=1
CL1291.Contig3_All	--
CL13261.Contig1_All	--
CL13347.Contig1_All	PRADC1-like protein OS=Drosophila melanogaster GN=CG9849 PE=2 SV=1
CL13462.Contig2_All	--
CL13818.Contig8_All	--
CL15277.Contig1_All	--
CL15286.Contig1_All	--
CL15490.Contig1_All	UPF0057 membrane protein T23F2.5 OS=Caenorhabditis elegans GN=T23F2.5 PE=3 SV=1
CL15865.Contig6_All	Polyubiquitin-A OS=Caenorhabditis elegans GN=ubq-1 PE=2 SV=1
CL1643.Contig5_All	--
CL1653.Contig1_All	ADP,ATP carrier protein 1 OS=Anopheles gambiae GN=AGAP006782 PE=2 SV=2
CL1683.Contig1_All	--
CL16874.Contig2_All	--
CL1759.Contig1_All	--

CL17610.Contig1_All	--
CL17610.Contig2_All	--
CL17793.Contig3_All	--
CL17869.Contig1_All	Protein G12 OS=Anopheles gambiae GN=AGAP006187 PE=2 SV=2
CL1996.Contig1_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL2093.Contig1_All	--
CL2118.Contig8_All	Cyclic GMP-AMP synthase OS=Bos taurus GN=MB21D1 PE=3 SV=1
CL2123.Contig2_All	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4
CL2319.Contig1_All	--
CL2319.Contig3_All	--
CL2406.Contig1_All	Ferric-chelate reductase 1 OS=Mus musculus GN=FRRS1 PE=1 SV=1
CL2714.Contig1_All	--
CL3262.Contig10_All	Keratin-associated protein 5-1 OS=Homo sapiens GN=KRTAP5-1 PE=2 SV=1
CL331.Contig2_All	--
CL3541.Contig1_All	--
CL3670.Contig7_All	--
CL3670.Contig8_All	--
CL382.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL3918.Contig2_All	--
CL3999.Contig3_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL405.Contig6_All	--
CL4118.Contig2_All	Voltage-dependent anion-selective channel protein 2 OS=Xenopus laevis GN=vdac2 PE=1 SV=1
CL4359.Contig2_All	--
CL455.Contig1_All	F-box/LRR-repeat protein 7 OS=Mus musculus GN=Fbxl7 PE=1 SV=1
CL4550.Contig1_All	--
CL4740.Contig3_All	--
CL5075.Contig1_All	Headcase protein OS=Drosophila melanogaster GN=hdc PE=1 SV=2
CL5090.Contig1_All	--
CL5090.Contig2_All	--
CL5318.Contig3_All	--
CL5341.Contig2_All	--
CL5372.Contig1_All	Protein FAM13A OS=Bos taurus GN=FAM13A PE=2 SV=1

CL5513.Contig1_All	Cytochrome P450 6k1 OS=Blattella germanica GN=CYP6K1 PE=2 SV=1
CL560.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL5664.Contig1_All	--
CL5696.Contig2_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL5733.Contig3_All	Integumentary mucin A.1 OS=Xenopus laevis PE=1 SV=1
CL5922.Contig1_All	CKLF-like MARVEL transmembrane domain-containing protein 4 OS=Mus musculus GN=Cmtm4 PE=2 SV=1
CL6111.Contig1_All	--
CL6122.Contig3_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
CL6122.Contig4_All	--
CL6451.Contig2_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL6615.Contig2_All	--
CL6660.Contig1_All	--
CL6725.Contig2_All	Zinc finger protein 36, C3H1 type-like 1 OS=Rattus norvegicus GN=Zfp36l1 PE=1 SV=1
CL7058.Contig1_All	--
CL708.Contig5_All	--
CL7447.Contig1_All	Aldehyde dehydrogenase, mitochondrial OS=Pongo abelii GN=ALDH2 PE=2 SV=1
CL7671.Contig2_All	Proprotein convertase subtilisin/kexin type 9 OS=Pan paniscus GN=PCSK9 PE=2 SV=2
CL7971.Contig1_All	Ras-related protein Rab-1A OS=Lymnaea stagnalis GN=RAB1A PE=2 SV=1
CL7974.Contig1_All	--
CL8085.Contig1_All	40S ribosomal protein S13 OS=Rattus norvegicus GN=Rps13 PE=1 SV=2
CL821.Contig10_All	--
CL821.Contig1_All	Serine/arginine repetitive matrix protein 1 OS=Pongo abelii GN=SRRM1 PE=2 SV=1
CL821.Contig3_All	--
CL8670.Contig2_All	PiggyBac transposable element-derived protein 1 OS=Homo sapiens GN=PGBD1 PE=1 SV=1
CL8789.Contig3_All	Synaptic vesicle membrane protein VAT-1 homolog OS=Danio rerio GN=vat1 PE=2 SV=1
CL8835.Contig7_All	--
CL8888.Contig2_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL9063.Contig3_All	--
CL9393.Contig1_All	RNA-binding protein FUS OS=Bos taurus GN=FUS PE=2 SV=2

CL9587.Contig3_All	Hexamerin OS=Blaberus discoidalis PE=2 SV=1
CL9984.Contig1_All	--
Unigene10193_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene10260_All	--
Unigene11657_All	Chitinase-like protein Idgf4 OS=Glossina morsitans morsitans GN=Idgf4 PE=2 SV=1
Unigene12078_All	Calcium-binding protein P OS=Dictyostelium discoideum GN=cbpP PE=2 SV=2
Unigene12127_All	--
Unigene12721_All	26S proteasome non-ATPase regulatory subunit 6 OS=Mus musculus GN=Psmd6 PE=1 SV=1
Unigene13215_All	--
Unigene13440_All	--
Unigene13806_All	--
Unigene13851_All	Transmembrane protein DDB_G0269096 OS=Dictyostelium discoideum GN=DDB_G0269096 PE=4 SV=1
Unigene13942_All	40S ribosomal protein S27 OS=Xenopus laevis GN=rps27 PE=3 SV=2
Unigene14673_All	--
Unigene15210_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene15234_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene1527_All	Methylsterol monooxygenase 1 OS=Rattus norvegicus GN=Msmo1 PE=2 SV=1
Unigene17555_All	--
Unigene1783_All	--
Unigene18195_All	--
Unigene19141_All	--
Unigene20399_All	Trypsin V-A OS=Rattus norvegicus PE=2 SV=1
Unigene21372_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene22072_All	Heat shock protein DDB_G0280215 OS=Dictyostelium discoideum GN=DDB_G0280215 PE=3 SV=1
Unigene22595_All	Location of vulva defective 1 OS=Caenorhabditis elegans GN=lov-1 PE=1 SV=4
Unigene22930_All	Mucin-6 OS=Homo sapiens GN=MUC6 PE=1 SV=3
Unigene24038_All	--
Unigene24575_All	--
Unigene25020_All	--
Unigene25285_All	--
Unigene25534_All	--
Unigene26069_All	--
Unigene26338_All	--

Unigene26896_All	--
Unigene26897_All	--
Unigene27686_All	40S ribosomal protein S27 OS=Rattus norvegicus GN=Rps27 PE=2 SV=3
Unigene27714_All	Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2
Unigene28977_All	--
Unigene29624_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene29786_All	--
Unigene30008_All	Eukaryotic translation initiation factor 1 OS=Pongo abelii GN=EIF1 PE=3 SV=1
Unigene30180_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene30400_All	Translationally-controlled tumor protein homolog OS=Bombyx mori GN=Tctp PE=2 SV=1
Unigene30466_All	Probable proton ATPase 1B OS=Leishmania donovani GN=H1B PE=2 SV=1
Unigene30468_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene32893_All	Retinal Mueller cells isomerohydrolase OS=Danio rerio GN=rpe65c PE=1 SV=1
Unigene32916_All	Scavenger receptor class B member 1 OS=Bos taurus GN=SCARB1 PE=2 SV=1
Unigene32983_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene33066_All	Integumentary mucin C.1 (Fragment) OS=Xenopus laevis PE=2 SV=1
Unigene34085_All	--
Unigene34248_All	--
Unigene34616_All	--
Unigene34892_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene36361_All	--
Unigene36373_All	Trypsin-1 OS=Anopheles gambiae GN=TRYP1 PE=2 SV=3
Unigene36397_All	--
Unigene36643_All	Endothelial differentiation-related factor 1 homolog OS=Xenopus laevis GN=edf1 PE=2 SV=1
Unigene37149_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene37973_All	Peroxiredoxin-5, mitochondrial OS=Rattus norvegicus GN=Prdx5 PE=1 SV=1
Unigene380_All	ATP-binding cassette sub-family F member 1 OS=Mus musculus GN=Abcf1 PE=1 SV=1
Unigene38355_All	40S ribosomal protein S30 OS=Rattus norvegicus GN=Fau PE=1 SV=1
Unigene3894_All	--
Unigene3926_All	Prisilkin-39 OS=Pinctada fucata PE=1 SV=1

Unigene39661_All	--
Unigene39665_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene39940_All	Potassium channel subfamily K member 1 OS=Cavia porcellus GN=KCNK1 PE=2 SV=1
Unigene40121_All	ATP-binding cassette sub-family G member 1 OS=Homo sapiens GN=ABCG1 PE=2 SV=3
Unigene4034_All	2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1
Unigene40668_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene40682_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene40697_All	--
Unigene41767_All	--
Unigene42070_All	--
Unigene42115_All	--
Unigene42161_All	--
Unigene42363_All	--
Unigene4288_All	Probable pyridoxine biosynthesis protein pdx1 OS=Dictyostelium discoideum GN=pdx1 PE=1 SV=1
Unigene43772_All	--
Unigene44387_All	Flavohemoprotein A OS=Dictyostelium discoideum GN=fhbA PE=2 SV=1
Unigene4438_All	--
Unigene44714_All	Rhodopsin OS=Sepia officinalis GN=RHO PE=2 SV=1
Unigene44987_All	Keratin, type I cytoskeletal 9 OS=Canis familiaris GN=KRT9 PE=3 SV=1
Unigene45320_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene45691_All	40S ribosomal protein S25 OS=Spodoptera frugiperda GN=RpS25 PE=3 SV=1
Unigene47509_All	--
Unigene47813_All	--
Unigene48046_All	--
Unigene48050_All	Locomotion-related protein Hikaru genki OS=Drosophila melanogaster GN=hig PE=1 SV=2
Unigene48143_All	--
Unigene48201_All	--
Unigene48285_All	--
Unigene49179_All	--
Unigene50133_All	--
Unigene50348_All	--
Unigene50772_All	--

Unigene51572_All	--
Unigene52047_All	Mucin-17 OS=Homo sapiens GN=MUC17 PE=1 SV=2
Unigene52057_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene52134_All	40S ribosomal protein S16 OS=Drosophila melanogaster GN=RpS16 PE=2 SV=1
Unigene52172_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene52630_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene54474_All	60S ribosomal protein L19 OS=Ictalurus punctatus GN=rpl19 PE=2 SV=1
Unigene55200_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene55233_All	--
Unigene55774_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene56907_All	--
Unigene56922_All	--
Unigene57372_All	--
Unigene57474_All	Venom carboxylesterase-6 OS=Apis mellifera PE=2 SV=1
Unigene57763_All	Protein takeout OS=Drosophila melanogaster GN=to PE=2 SV=1
Unigene58870_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene59041_All	--
Unigene59077_All	Ras-related protein Rab-11B OS=Rattus norvegicus GN=Rab11b PE=2 SV=4
Unigene59121_All	--
Unigene60378_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene61568_All	--
Unigene61626_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene62033_All	ATP synthase lipid-binding protein, mitochondrial OS=Rattus norvegicus GN=Atp5g2 PE=2 SV=1
Unigene62120_All	Protein charybde OS=Drosophila melanogaster GN=chrb PE=2 SV=2
Unigene62192_All	Collagen alpha-2(IV) chain OS=Caenorhabditis elegans GN=let-2 PE=1 SV=2
Unigene62233_All	--
Unigene63252_All	Mediator of DNA damage checkpoint protein 1 OS=Sus scrofa GN=MDC1 PE=3 SV=1
Unigene637_All	Keratin-associated protein 5-1 OS=Homo sapiens GN=KRTAP5-1 PE=2 SV=1
Unigene64288_All	--

Unigene64435_All	--
Unigene65052_All	60S ribosomal protein L24 OS=Pagrus major GN=rpl24 PE=2 SV=1
Unigene65439_All	--
Unigene66473_All	Histone H3.3 OS=Trichinella pseudospiralis GN=HHT3 PE=2 SV=3
Unigene67234_All	--
Unigene68653_All	--
Unigene69069_All	--
Unigene70166_All	--
Unigene70244_All	Keratin-associated protein 5-1 OS=Homo sapiens GN=KRTAP5-1 PE=2 SV=1
Unigene70245_All	Keratin-associated protein 5-1 OS=Homo sapiens GN=KRTAP5-1 PE=2 SV=1
Unigene7119_All	--
Unigene71291_All	--
Unigene71397_All	--
Unigene72323_All	--
Unigene73667_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene73975_All	Glutathione S-transferase OS=Blattella germanica PE=1 SV=3
Unigene74304_All	Membrane transporter D1 OS=Leishmania donovani PE=3 SV=1
Unigene7555_All	--
Unigene75664_All	--
Unigene76720_All	Pro-neuropeptide Y OS=Aplysia californica GN=NPY PE=1 SV=1
Unigene7696_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
Unigene77208_All	60S ribosomal protein L10a OS=Macaca fascicularis GN=RPL10A PE=2 SV=3
Unigene80778_All	--
Unigene80959_All	--
Unigene80976_All	--
Unigene8790_All	--
Unigene9084_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene9146_All	--
Unigene9526_All	--
Up-regulated genes related to development	
geneID	Swissprot-annotation
CL1.Contig4_All	--
CL10016.Contig1_All	Protein takeout OS=Drosophila melanogaster GN=to PE=2 SV=1
CL10026.Contig2_All	Tubby-related protein 4 OS=Homo sapiens GN=TULP4 PE=2 SV=2

CL10064.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL10071.Contig1_All	--
CL10077.Contig1_All	--
CL10088.Contig2_All	--
CL10105.Contig1_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL10109.Contig2_All	--
CL10139.Contig1_All	--
CL10167.Contig1_All	--
CL1023.Contig1_All	Late cornified envelope-like proline-rich protein 1 OS=Bos taurus GN=LELP1 PE=3 SV=1
CL10233.Contig1_All	Endocuticle structural glycoprotein SgAbd-8 OS=Schistocerca gregaria PE=1 SV=1
CL10247.Contig1_All	--
CL10298.Contig1_All	Synaptotagmin-2 OS=Mus musculus GN=Syt2 PE=1 SV=1
CL10395.Contig1_All	--
CL10400.Contig1_All	Atherin OS=Homo sapiens GN=SAMD1 PE=1 SV=1
CL10433.Contig2_All	--
CL1046.Contig1_All	--
CL10489.Contig2_All	Dapper homolog 3 OS=Mus musculus GN=Dact3 PE=1 SV=1
CL10511.Contig2_All	Balbiani ring protein 3 OS=Chironomus tentans GN=BR3 PE=2 SV=1
CL10536.Contig1_All	--
CL10536.Contig2_All	--
CL10565.Contig3_All	Protein numb OS=Drosophila melanogaster GN=numb PE=1 SV=2
CL10572.Contig1_All	Transforming growth factor-beta-induced protein ig-h3 OS=Mus musculus GN=Tgfbi PE=2 SV=1
CL10572.Contig2_All	Transforming growth factor-beta-induced protein ig-h3 OS=Mus musculus GN=Tgfbi PE=2 SV=1
CL10613.Contig1_All	--
CL10675.Contig2_All	--
CL10692.Contig2_All	--
CL10694.Contig2_All	--
CL10735.Contig1_All	--
CL10787.Contig3_All	--
CL10802.Contig1_All	Cuticle protein 65 OS=Locusta migratoria PE=1 SV=1
CL10802.Contig2_All	Cuticle protein 65 OS=Locusta migratoria PE=1 SV=1
CL1081.Contig11_All	--
CL1081.Contig4_All	--

CL10831.Contig1_All	--
CL10831.Contig2_All	--
CL10890.Contig1_All	Solute carrier family 2, facilitated glucose transporter member 1 OS=Bos taurus GN=SLC2A1 PE=2 SV=1
CL10909.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL10926.Contig1_All	--
CL10961.Contig1_All	1-acylglycerophosphocholine O-acyltransferase 1 OS=Drosophila melanogaster GN=CG32699 PE=2 SV=1
CL10970.Contig1_All	--
CL1099.Contig1_All	Putative uncharacterized transposon-derived protein F52C9.6 OS=Caenorhabditis elegans GN=F52C9.6 PE=5 SV=1
CL11019.Contig2_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
CL11030.Contig1_All	--
CL11032.Contig1_All	--
CL11049.Contig2_All	Mediator of RNA polymerase II transcription subunit 15 OS=Mus musculus GN=Med15 PE=2 SV=2
CL11154.Contig1_All	--
CL11183.Contig1_All	Collagen alpha-3(IX) chain OS=Gallus gallus GN=COL9A3 PE=2 SV=1
CL11183.Contig3_All	Cuticle collagen 2C (Fragment) OS=Haemonchus contortus GN=2C PE=2 SV=1
CL11184.Contig1_All	--
CL11201.Contig1_All	--
CL11213.Contig1_All	--
CL11222.Contig1_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3
CL11222.Contig2_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3
CL11235.Contig1_All	--
CL11235.Contig2_All	--
CL11243.Contig1_All	Probable nuclear hormone receptor HR3 OS=Galleria mellonella GN=HR3 PE=2 SV=1
CL11243.Contig2_All	Probable nuclear hormone receptor HR3 OS=Manduca sexta GN=HR3 PE=2 SV=1
CL11288.Contig1_All	--
CL11302.Contig2_All	Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2
CL11310.Contig1_All	--
CL11374.Contig2_All	--
CL11419.Contig6_All	--

CL11469.Contig1_All	--
CL11473.Contig2_All	--
CL11480.Contig2_All	--
CL11500.Contig1_All	Carboxypeptidase B OS=Astacus fluviatilis PE=1 SV=1
CL11511.Contig6_All	--
CL11514.Contig1_All	--
CL11514.Contig2_All	--
CL11522.Contig1_All	--
CL11547.Contig1_All	Trinucleotide repeat-containing gene 18 protein OS=Homo sapiens GN=TNRC18 PE=1 SV=3
CL11612.Contig1_All	--
CL11629.Contig1_All	Dehydrogenase/reductase SDR family member 11 OS=Mus musculus GN=Dhrs11 PE=2 SV=1
CL11629.Contig2_All	Dehydrogenase/reductase SDR family member 11 OS=Mus musculus GN=Dhrs11 PE=2 SV=1
CL11632.Contig1_All	Hemolymph lipopolysaccharide-binding protein OS=Periplaneta americana PE=1 SV=1
CL11632.Contig2_All	Hemolymph lipopolysaccharide-binding protein OS=Periplaneta americana PE=1 SV=1
CL11638.Contig2_All	--
CL11648.Contig2_All	Ninjurin-2 OS=Homo sapiens GN=NINJ2 PE=2 SV=1
CL11658.Contig1_All	--
CL11700.Contig2_All	AMMECR1-like protein OS=Pongo abelii GN=AMMECR1L PE=2 SV=1
CL1171.Contig1_All	--
CL11743.Contig1_All	Down syndrome cell adhesion molecule-like protein Dscam2 OS=Drosophila melanogaster GN=Dscam2 PE=2 SV=3
CL11787.Contig2_All	--
CL11812.Contig1_All	Putative fatty acyl-CoA reductase CG5065 OS=Drosophila melanogaster GN=CG5065 PE=3 SV=1
CL11837.Contig3_All	--
CL11875.Contig2_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL11888.Contig1_All	Atherin OS=Oryctolagus cuniculus GN=SAMD1 PE=2 SV=1
CL11888.Contig2_All	Atherin OS=Oryctolagus cuniculus GN=SAMD1 PE=2 SV=1
CL11892.Contig1_All	Salivary glue protein Sgs-3 OS=Drosophila erecta GN=Sgs3 PE=2 SV=3
CL11895.Contig1_All	--
CL1190.Contig2_All	--
CL11905.Contig1_All	Mucin-22 OS=Homo sapiens GN=MUC22 PE=1 SV=2

CL11907.Contig1_All	--
CL1191.Contig3_All	--
CL11916.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
CL11925.Contig1_All	--
CL11928.Contig2_All	--
CL1193.Contig3_All	--
CL11936.Contig1_All	--
CL1194.Contig2_All	--
CL1197.Contig1_All	DNA-directed RNA polymerase III subunit RPC10 OS=Homo sapiens GN=POLR3K PE=1 SV=2
CL11985.Contig1_All	--
CL12.Contig2_All	--
CL1202.Contig4_All	Ubiquinone biosynthesis protein COQ7 homolog OS=Mus musculus GN=Coq7 PE=2 SV=3
CL12058.Contig2_All	--
CL12095.Contig1_All	Allatostatins OS=Diploptera punctata PE=1 SV=2
CL12096.Contig1_All	Putative nuclease HARBI1 OS=Homo sapiens GN=HARBI1 PE=1 SV=1
CL12120.Contig2_All	--
CL12137.Contig2_All	GA-binding protein subunit beta-1 OS=Homo sapiens GN=GABPB1 PE=1 SV=2
CL12144.Contig4_All	Fatty acid-binding protein, muscle OS=Schistocerca gregaria PE=1 SV=2
CL12158.Contig1_All	--
CL12173.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL12212.Contig2_All	Visual pigment-like receptor peropsin OS=Mus musculus GN=Rrh PE=1 SV=1
CL12226.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL12226.Contig2_All	--
CL12226.Contig3_All	--
CL12344.Contig2_All	--
CL12359.Contig2_All	--
CL12370.Contig2_All	--
CL12371.Contig1_All	--
CL12386.Contig1_All	--
CL12442.Contig1_All	Another transcription unit protein OS=Drosophila melanogaster GN=Atu PE=1 SV=2
CL12442.Contig2_All	Another transcription unit protein OS=Drosophila melanogaster GN=Atu PE=1 SV=2
CL12443.Contig1_All	--
CL12470.Contig2_All	--

CL12496.Contig2_All	Synaptotagmin 1 OS=Drosophila melanogaster GN=Syt1 PE=1 SV=2
CL12529.Contig1_All	Period circadian protein (Fragments) OS=Drosophila mauritiana GN=per PE=3 SV=2
CL12532.Contig1_All	Calponin homology domain-containing protein DDB_G0272472 OS=Dictyostelium discoideum GN=DDB_G0272472 PE=4 SV=1
CL12545.Contig1_All	Tropomyosin-1 OS=Bombyx mori PE=1 SV=1
CL12545.Contig2_All	Tropomyosin-1 OS=Bombyx mori PE=1 SV=1
CL12545.Contig3_All	Tropomyosin-1 OS=Bombyx mori PE=1 SV=1
CL12545.Contig4_All	Tropomyosin-1 OS=Bombyx mori PE=1 SV=1
CL12575.Contig1_All	--
CL12622.Contig1_All	--
CL12629.Contig1_All	--
CL12629.Contig2_All	--
CL12707.Contig2_All	--
CL1273.Contig4_All	Superoxide dismutase [Cu-Zn] OS=Prionace glauca GN=sod1 PE=1 SV=1
CL1279.Contig2_All	--
CL12795.Contig1_All	Down syndrome cell adhesion molecule homolog OS=Rattus norvegicus GN=Dscam PE=1 SV=1
CL12809.Contig1_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL12809.Contig2_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL12811.Contig2_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL12817.Contig2_All	--
CL12844.Contig2_All	Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1
CL1286.Contig3_All	--
CL12881.Contig1_All	--
CL12891.Contig2_All	--
CL12933.Contig1_All	--
CL12933.Contig2_All	--
CL130.Contig2_All	Esterase FE4 OS=Myzus persicae PE=1 SV=1
CL13029.Contig1_All	Paxillin OS=Mus musculus GN=Pxn PE=1 SV=1
CL13032.Contig2_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL13034.Contig2_All	--
CL13041.Contig1_All	--
CL13104.Contig1_All	Oligoribonuclease, mitochondrial OS=Rattus norvegicus GN=Rexo2 PE=2 SV=1

CL13114.Contig2_All	--
CL13115.Contig2_All	Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=2
CL13116.Contig3_All	--
CL13120.Contig1_All	Keratin-associated protein 5-5 OS=Mus musculus GN=Krtap5-5 PE=2 SV=1
CL13120.Contig2_All	Keratin-associated protein 5-1 OS=Homo sapiens GN=KRTAP5-1 PE=2 SV=1
CL13128.Contig2_All	DBF4-type zinc finger-containing protein 2 homolog OS=Mus musculus GN=Zdbf2 PE=2 SV=1
CL13197.Contig1_All	Ras-related protein Rab-32 OS=Homo sapiens GN=RAB32 PE=1 SV=3
CL13238.Contig2_All	--
CL13272.Contig1_All	--
CL13283.Contig1_All	Prohormone-3 OS=Apis mellifera PE=1 SV=1
CL13283.Contig2_All	Prohormone-3 OS=Apis mellifera PE=1 SV=1
CL1330.Contig1_All	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3
CL1330.Contig2_All	Fatty acid synthase OS=Rattus norvegicus GN=Fasn PE=1 SV=3
CL1330.Contig4_All	Fatty acid synthase OS=Rattus norvegicus GN=Fasn PE=1 SV=3
CL1330.Contig5_All	Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2
CL13314.Contig2_All	--
CL13333.Contig2_All	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3
CL13356.Contig2_All	--
CL13368.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
CL13434.Contig2_All	--
CL13479.Contig1_All	--
CL13501.Contig2_All	--
CL1351.Contig4_All	--
CL1352.Contig1_All	Tetra-peptide repeat homeobox protein 1 OS=Homo sapiens GN=TPRX1 PE=2 SV=3
CL1352.Contig2_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL1352.Contig3_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL1352.Contig4_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL1352.Contig5_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4

CL1352.Contig6_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL1352.Contig7_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
CL13608.Contig1_All	--
CL13694.Contig1_All	--
CL13695.Contig1_All	--
CL13713.Contig1_All	--
CL13713.Contig2_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL13727.Contig1_All	--
CL13739.Contig2_All	Probable serine/threonine-protein kinase DDB_G0282963 OS=Dictyostelium discoideum GN=DDB_G0282963 PE=3 SV=1
CL1374.Contig1_All	--
CL1379.Contig1_All	Progestin and adipoQ receptor family member 3 OS=Mus musculus GN=Paqr3 PE=2 SV=1
CL13824.Contig2_All	Glutamate receptor 1 OS=Drosophila melanogaster GN=Glu-RI PE=2 SV=2
CL13869.Contig2_All	DBF4-type zinc finger-containing protein 2 homolog OS=Mus musculus GN=Zdbf2 PE=2 SV=1
CL1389.Contig1_All	--
CL13903.Contig3_All	--
CL13909.Contig1_All	Elongation of very long chain fatty acids protein AAEL008004 OS=Aedes aegypti GN=AAEL008004 PE=2 SV=2
CL13909.Contig2_All	Elongation of very long chain fatty acids protein AAEL008004 OS=Aedes aegypti GN=AAEL008004 PE=2 SV=2
CL13927.Contig2_All	Gamma-interferon-inducible lysosomal thiol reductase OS=Bos taurus GN=IFI30 PE=2 SV=1
CL1396.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL1396.Contig2_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL1396.Contig3_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL1396.Contig4_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL1396.Contig5_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL13963.Contig1_All	Septin-4 OS=Pongo abelii GN=SEPT4 PE=2 SV=1
CL13972.Contig2_All	--
CL14003.Contig2_All	--
CL14021.Contig1_All	--
CL14042.Contig1_All	--
CL14047.Contig2_All	--
CL14056.Contig1_All	--
CL14060.Contig1_All	--

CL14112.Contig1_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
CL14112.Contig2_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
CL14120.Contig2_All	Uncharacterized protein C10orf95 OS=Homo sapiens GN=C10orf95 PE=2 SV=1
CL14159.Contig2_All	Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1
CL1416.Contig3_All	--
CL14198.Contig2_All	--
CL14280.Contig1_All	--
CL14298.Contig1_All	Mastermind-like domain-containing protein 1 OS=Mus musculus GN=Mamld1 PE=2 SV=1
CL14305.Contig1_All	--
CL1432.Contig6_All	--
CL14335.Contig1_All	Discoidin domain-containing receptor 2 OS=Homo sapiens GN=DDR2 PE=1 SV=2
CL14339.Contig1_All	Regucalcin OS=Danio rerio GN=rgn PE=2 SV=1
CL14354.Contig1_All	--
CL14391.Contig1_All	Protein lethal(2)essential for life OS=Drosophila melanogaster GN=l(2)efl PE=1 SV=1
CL14404.Contig1_All	--
CL14404.Contig2_All	--
CL14472.Contig2_All	--
CL14491.Contig2_All	Acylphosphatase-1 OS=Sus scrofa GN=ACYP1 PE=1 SV=2
CL14503.Contig3_All	Ras-GEF domain-containing family member 1B-A OS=Danio rerio GN=rasgef1ba PE=2 SV=2
CL14548.Contig1_All	--
CL14552.Contig2_All	--
CL14585.Contig2_All	Glutamate receptor ionotropic, kainate 2 OS=Homo sapiens GN=GRIK2 PE=1 SV=1
CL14593.Contig1_All	--
CL14593.Contig2_All	Endocuticle structural glycoprotein SgAbd-8 OS=Schistocerca gregaria PE=1 SV=1
CL14593.Contig3_All	Endocuticle structural glycoprotein SgAbd-8 OS=Schistocerca gregaria PE=1 SV=1
CL14594.Contig1_All	--
CL14598.Contig1_All	--
CL14629.Contig1_All	Carboxypeptidase E OS=Lophius americanus GN=cpe PE=2 SV=1
CL14634.Contig1_All	SH3 and multiple ankyrin repeat domains protein 3 OS=Rattus norvegicus

	GN=Shank3 PE=1 SV=2
CL14649.Contig1_All	--
CL14650.Contig1_All	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
CL14650.Contig2_All	Acanthoscurrin-1 OS=Acanthoscurria gomesiana GN=acantho1 PE=1 SV=1
CL14699.Contig1_All	--
CL14700.Contig1_All	--
CL14766.Contig1_All	--
CL14839.Contig2_All	ATP-binding cassette sub-family G member 1 OS=Homo sapiens GN=ABCG1 PE=2 SV=3
CL14854.Contig2_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL14913.Contig1_All	--
CL14919.Contig2_All	Wiskott-Aldrich syndrome protein homolog OS=Mus musculus GN=Was PE=1 SV=1
CL14919.Contig3_All	Wiskott-Aldrich syndrome protein homolog OS=Mus musculus GN=Was PE=1 SV=1
CL14947.Contig1_All	Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1 SV=5
CL1495.Contig1_All	Histone-lysine N-methyltransferase, H3 lysine-79 specific OS=Dictyostelium discoideum GN=dotA PE=2 SV=2
CL14952.Contig1_All	Heparan sulfate 2-O-sulfotransferase pipe OS=Drosophila melanogaster GN=pip PE=1 SV=1
CL14952.Contig2_All	Heparan sulfate 2-O-sulfotransferase pipe OS=Drosophila melanogaster GN=pip PE=1 SV=1
CL1496.Contig2_All	Inositol oxygenase OS=Pongo abelii GN=MIOX PE=2 SV=1
CL14980.Contig2_All	--
CL14984.Contig1_All	--
CL15010.Contig1_All	--
CL15035.Contig2_All	--
CL15039.Contig1_All	Fatty acyl-CoA reductase 1 OS=Rattus norvegicus GN=Far1 PE=2 SV=1
CL15061.Contig1_All	--
CL15095.Contig1_All	--
CL15124.Contig1_All	--
CL15124.Contig2_All	--
CL15158.Contig1_All	Endocuticle structural glycoprotein ABD-4 OS=Locusta migratoria PE=1 SV=3
CL15158.Contig2_All	Endocuticle structural glycoprotein ABD-4 OS=Locusta migratoria PE=1 SV=3
CL15172.Contig2_All	--

CL15184.Contig1_All	--
CL15205.Contig1_All	--
CL15214.Contig1_All	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2
CL15218.Contig1_All	--
CL15218.Contig2_All	--
CL15222.Contig1_All	--
CL15239.Contig1_All	--
CL15275.Contig1_All	Apolipoprotein D OS=Cavia porcellus GN=APOD PE=2 SV=1
CL15275.Contig2_All	--
CL15275.Contig3_All	Apolipoprotein D OS=Cavia porcellus GN=APOD PE=2 SV=1
CL15281.Contig2_All	--
CL15295.Contig2_All	--
CL15300.Contig2_All	--
CL15307.Contig4_All	--
CL15324.Contig1_All	--
CL15324.Contig2_All	--
CL15332.Contig1_All	Sulfotransferase family cytosolic 1B member 1 OS=Gallus gallus GN=SULT1B1 PE=2 SV=1
CL15361.Contig1_All	--
CL15387.Contig1_All	--
CL154.Contig3_All	Retrovirus-related Pol polyprotein from transposon 17.6 OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL15430.Contig2_All	--
CL15451.Contig1_All	Prohormone-1 OS=Apis mellifera PE=1 SV=1
CL15451.Contig2_All	Prohormone-1 OS=Apis mellifera PE=1 SV=1
CL15467.Contig2_All	F-box/LRR-repeat protein 16 OS=Mus musculus GN=Fbxl16 PE=2 SV=1
CL15475.Contig1_All	--
CL15488.Contig1_All	--
CL155.Contig2_All	Cuticlin-1 OS=Caenorhabditis elegans GN=cut-1 PE=2 SV=2
CL15522.Contig1_All	--
CL15524.Contig1_All	--
CL1557.Contig2_All	Fatty acyl-CoA reductase 1 OS=Rattus norvegicus GN=Far1 PE=2 SV=1
CL1557.Contig4_All	--
CL15579.Contig1_All	--
CL15579.Contig2_All	--
CL15604.Contig1_All	--
CL15626.Contig2_All	--

CL15684.Contig1_All	SH2 domain-containing protein 4B OS=Mus musculus GN=Sh2d4b PE=2 SV=1
CL15709.Contig1_All	--
CL15772.Contig1_All	--
CL15836.Contig2_All	--
CL15860.Contig1_All	--
CL15896.Contig2_All	--
CL15898.Contig2_All	--
CL1590.Contig1_All	--
CL15939.Contig1_All	Prothoracicostatic peptide OS=Bombyx mori PE=1 SV=2
CL15939.Contig2_All	Prothoracicostatic peptide OS=Bombyx mori PE=1 SV=2
CL15986.Contig2_All	--
CL16001.Contig2_All	--
CL16004.Contig5_All	--
CL16019.Contig2_All	RanBP-type and C3HC4-type zinc finger-containing protein 1 OS=Dicentrarchus labrax GN=rbck1 PE=3 SV=1
CL16025.Contig1_All	--
CL16025.Contig2_All	--
CL16050.Contig1_All	--
CL16051.Contig4_All	--
CL16066.Contig1_All	--
CL16068.Contig1_All	Dual specificity protein phosphatase 23 OS=Homo sapiens GN=DUSP23 PE=1 SV=1
CL16101.Contig2_All	Probable cytochrome P450 4aa1 OS=Drosophila melanogaster GN=Cyp4aa1 PE=2 SV=2
CL16107.Contig1_All	--
CL16114.Contig2_All	--
CL16115.Contig2_All	Craniofacial development protein 2 OS=Bos taurus GN=CFDP2 PE=1 SV=2
CL16133.Contig1_All	--
CL16141.Contig1_All	--
CL16202.Contig1_All	Atherin OS=Homo sapiens GN=SAMD1 PE=1 SV=1
CL16218.Contig1_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL16232.Contig1_All	--
CL16279.Contig2_All	--
CL16295.Contig2_All	--
CL16319.Contig2_All	--
CL16335.Contig1_All	Troponin C, isoform 1 OS=Drosophila melanogaster GN=TpnC41C PE=2 SV=2

CL16354.Contig1_All	RNA-binding protein 39 OS=Pongo abelii GN=RBM39 PE=2 SV=1
CL16360.Contig1_All	Protein unc-13 homolog D OS=Homo sapiens GN=UNC13D PE=1 SV=1
CL16363.Contig1_All	--
CL16419.Contig7_All	--
CL165.Contig3_All	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Rattus norvegicus GN=Mgat2 PE=1 SV=1
CL16529.Contig1_All	--
CL16529.Contig2_All	--
CL16533.Contig1_All	--
CL16577.Contig1_All	15-hydroxyprostaglandin dehydrogenase [NAD(+)] OS=Mus musculus GN=Hpgd PE=2 SV=1
CL16630.Contig1_All	Toll-like receptor 2 OS=Ovis aries GN=TLR2 PE=2 SV=1
CL16631.Contig1_All	--
CL16634.Contig1_All	--
CL16662.Contig1_All	--
CL1668.Contig1_All	Titin OS=Homo sapiens GN=TTN PE=1 SV=4
CL16681.Contig2_All	--
CL16701.Contig1_All	--
CL16710.Contig8_All	--
CL16714.Contig1_All	Paramyosin, long form OS=Drosophila melanogaster GN=Prm PE=1 SV=1
CL16714.Contig2_All	Paramyosin, long form OS=Drosophila melanogaster GN=Prm PE=1 SV=1
CL16764.Contig1_All	--
CL16785.Contig2_All	--
CL16787.Contig1_All	--
CL16809.Contig2_All	--
CL16878.Contig11_All	--
CL16878.Contig4_All	Transposable element Tc3 transposase OS=Caenorhabditis elegans GN=tc3a PE=1 SV=1
CL1689.Contig2_All	--
CL1694.Contig3_All	--
CL16963.Contig1_All	--
CL16971.Contig1_All	--
CL17000.Contig1_All	--
CL17014.Contig1_All	--
CL17014.Contig2_All	--
CL17085.Contig1_All	Copia protein OS=Drosophila melanogaster GN=GIP PE=1 SV=3
CL17090.Contig2_All	--

CL17096.Contig1_All	--
CL1715.Contig1_All	--
CL17175.Contig1_All	--
CL17179.Contig4_All	--
CL17190.Contig2_All	Endoplasmic reticulum metallopeptidase 1 OS=Mus musculus GN=Ermp1 PE=1 SV=2
CL17207.Contig6_All	--
CL17295.Contig1_All	--
CL17295.Contig2_All	--
CL173.Contig1_All	Nucleolysin TIA-1 isoform p40 OS=Homo sapiens GN=TIA1 PE=1 SV=3
CL17344.Contig3_All	Retrovirus-related Pol polyprotein from transposon opus OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL17364.Contig1_All	--
CL17371.Contig1_All	--
CL17380.Contig1_All	Keratin, type I cytoskeletal 10 OS=Canis familiaris GN=KRT10 PE=2 SV=1
CL17380.Contig2_All	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2
CL17436.Contig2_All	Lysine-specific demethylase 6A OS=Mus musculus GN=Kdm6a PE=1 SV=2
CL17462.Contig1_All	--
CL17470.Contig2_All	--
CL17543.Contig1_All	--
CL17591.Contig2_All	Uncharacterized protein K02A2.6 OS=Caenorhabditis elegans GN=K02A2.6 PE=2 SV=1
CL17591.Contig3_All	Uncharacterized protein K02A2.6 OS=Caenorhabditis elegans GN=K02A2.6 PE=2 SV=1
CL17595.Contig2_All	--
CL17632.Contig4_All	--
CL17649.Contig1_All	--
CL17673.Contig1_All	--
CL17677.Contig5_All	--
CL17682.Contig3_All	--
CL17716.Contig1_All	--
CL17717.Contig2_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL17717.Contig3_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL17732.Contig2_All	--
CL17751.Contig3_All	Farnesyl pyrophosphate synthase OS=Gallus gallus GN=FDPS PE=1 SV=2
CL17755.Contig1_All	--
CL17771.Contig1_All	--

CL17799.Contig1_All	Transposable element Tc1 transposase OS=Caenorhabditis elegans GN=tc1a PE=3 SV=1
CL17805.Contig1_All	--
CL17813.Contig8_All	--
CL17828.Contig1_All	--
CL17913.Contig1_All	--
CL17972.Contig1_All	--
CL17972.Contig2_All	Uncharacterized protein DDB_G0274915 OS=Dictyostelium discoideum GN=DDB_G0274915 PE=4 SV=2
CL17976.Contig1_All	--
CL17976.Contig2_All	--
CL17976.Contig4_All	Leucine-rich repeats and immunoglobulin-like domains protein 2 OS=Mus musculus GN=Lrig2 PE=2 SV=1
CL18.Contig14_All	--
CL18.Contig6_All	Transposable element Tcb2 transposase OS=Caenorhabditis briggsae PE=3 SV=1
CL1847.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL1861.Contig3_All	--
CL1864.Contig2_All	--
CL1893.Contig1_All	--
CL1893.Contig2_All	--
CL1903.Contig1_All	--
CL194.Contig2_All	--
CL1958.Contig1_All	--
CL1969.Contig2_All	Leucine-rich repeat-containing protein 15 OS=Mus musculus GN=Lrrc15 PE=2 SV=1
CL1984.Contig1_All	Protein croquemort OS=Drosophila melanogaster GN=crq PE=1 SV=2
CL1998.Contig1_All	--
CL2008.Contig1_All	--
CL2063.Contig1_All	--
CL2116.Contig1_All	Jerky protein homolog-like OS=Mus musculus GN=Jrkl PE=2 SV=1
CL213.Contig1_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
CL213.Contig2_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
CL2175.Contig1_All	--
CL2179.Contig2_All	--
CL2186.Contig2_All	Serine/arginine repetitive matrix protein 1 OS=Gallus gallus GN=SRRM1 PE=2 SV=1

CL2195.Contig1_All	--
CL2195.Contig2_All	--
CL2206.Contig2_All	--
CL2226.Contig1_All	--
CL2233.Contig11_All	--
CL2233.Contig1_All	Uncharacterized protein PF11_0207 OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0207 PE=4 SV=2
CL2233.Contig2_All	Uncharacterized protein PF11_0207 OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0207 PE=4 SV=2
CL2233.Contig3_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL2233.Contig4_All	Transcriptional regulator ATRX homolog OS=Caenorhabditis elegans GN=xnp-1 PE=1 SV=1
CL2233.Contig5_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL2233.Contig6_All	Titin OS=Mus musculus GN=Ttn PE=1 SV=1
CL2233.Contig7_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL2233.Contig8_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL2233.Contig9_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL2237.Contig2_All	--
CL2240.Contig3_All	Solute carrier family 2, facilitated glucose transporter member 8 OS=Homo sapiens GN=SLC2A8 PE=1 SV=3
CL2244.Contig1_All	--
CL229.Contig2_All	Zinc finger homeobox protein 4 OS=Gallus gallus GN=ZFHX4 PE=2 SV=2
CL2314.Contig1_All	--
CL2324.Contig5_All	Organic cation transporter protein OS=Drosophila melanogaster GN=Orct PE=1 SV=1
CL2335.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL2340.Contig1_All	--
CL2361.Contig1_All	Espin OS=Rattus norvegicus GN=Espn PE=1 SV=2
CL2387.Contig1_All	--
CL2387.Contig2_All	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2
CL239.Contig2_All	--
CL2406.Contig2_All	--
CL2415.Contig5_All	--
CL2441.Contig1_All	--
CL2454.Contig1_All	--
CL2454.Contig2_All	--
CL2454.Contig3_All	--
CL2462.Contig1_All	--
CL247.Contig2_All	--

CL2517.Contig2_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL252.Contig5_All	--
CL2553.Contig1_All	--
CL2559.Contig1_All	--
CL2593.Contig1_All	--
CL2600.Contig2_All	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4
CL2601.Contig1_All	Wiskott-Aldrich syndrome protein homolog OS=Mus musculus GN=Was PE=1 SV=1
CL2601.Contig3_All	Wiskott-Aldrich syndrome protein homolog OS=Mus musculus GN=Was PE=1 SV=1
CL2611.Contig3_All	Transcription factor AP-2-beta OS=Mus musculus GN=Tfap2b PE=1 SV=2
CL2611.Contig5_All	--
CL2618.Contig1_All	Pro-resilin OS=Drosophila melanogaster GN=resilin PE=1 SV=1
CL2661.Contig1_All	--
CL2664.Contig2_All	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3
CL2671.Contig2_All	BTB/POZ domain-containing protein KCTD15 OS=Mus musculus GN=Kctd15 PE=1 SV=1
CL2701.Contig9_All	--
CL2720.Contig2_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL2728.Contig1_All	--
CL2740.Contig2_All	--
CL2771.Contig2_All	Probable cytochrome P450 6a20 OS=Drosophila melanogaster GN=Cyp6a20 PE=2 SV=2
CL282.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL282.Contig2_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL284.Contig2_All	--
CL2865.Contig1_All	--
CL2865.Contig2_All	--
CL2945.Contig1_All	--
CL2958.Contig1_All	Glucose dehydrogenase [acceptor] OS=Drosophila pseudoobscura pseudoobscura GN=Gld PE=3 SV=4
CL2964.Contig2_All	--
CL2964.Contig3_All	--
CL2964.Contig4_All	--
CL2964.Contig5_All	--
CL297.Contig1_All	--

CL2993.Contig2_All	B-cell linker protein OS=Gallus gallus GN=BLNK PE=1 SV=1
CL2993.Contig3_All	B-cell linker protein OS=Gallus gallus GN=BLNK PE=1 SV=1
CL2996.Contig1_All	Cuticle collagen 1 OS=Caenorhabditis elegans GN=sqt-3 PE=3 SV=2
CL2996.Contig2_All	Collagen alpha-2(IV) chain OS=Caenorhabditis elegans GN=let-2 PE=1 SV=2
CL3030.Contig1_All	--
CL3040.Contig1_All	Putative uncharacterized transposon-derived protein F52C9.6 OS=Caenorhabditis elegans GN=F52C9.6 PE=5 SV=1
CL3048.Contig1_All	Loricrin OS=Mus musculus GN=Lor PE=2 SV=2
CL3048.Contig2_All	Loricrin OS=Mus musculus GN=Lor PE=2 SV=2
CL3073.Contig1_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
CL3073.Contig2_All	--
CL3093.Contig2_All	--
CL3093.Contig3_All	--
CL3108.Contig1_All	Cuticle protein 18.6, isoform A OS=Locusta migratoria PE=1 SV=1
CL3108.Contig2_All	Cuticle protein 18.6, isoform A OS=Locusta migratoria PE=1 SV=1
CL3109.Contig2_All	--
CL311.Contig5_All	--
CL3203.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL3203.Contig2_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL3203.Contig3_All	Adenylate cyclase, terminal-differentiation specific OS=Dictyostelium discoideum GN=acrA PE=1 SV=1
CL3275.Contig1_All	Calmodulin OS=Dictyostelium discoideum GN=calA PE=1 SV=3
CL3290.Contig2_All	--
CL3336.Contig1_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
CL3384.Contig1_All	SH3-containing GRB2-like protein 3-interacting protein 1 OS=Psammomys obesus GN=SGIP1 PE=1 SV=1
CL3386.Contig1_All	Adenylate cyclase, terminal-differentiation specific OS=Dictyostelium discoideum GN=acrA PE=1 SV=1
CL3386.Contig2_All	UPF0746 protein DDB_G0281095 OS=Dictyostelium discoideum GN=DDB_G0281095 PE=3 SV=1
CL3393.Contig2_All	--
CL3393.Contig5_All	--

CL3393.Contig8_All	--
CL3410.Contig1_All	Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=2
CL3410.Contig2_All	--
CL3468.Contig1_All	--
CL3476.Contig1_All	Aquaporin-12 OS=Mus musculus GN=Aqp12 PE=2 SV=1
CL3476.Contig2_All	Aquaporin-12 OS=Mus musculus GN=Aqp12 PE=2 SV=1
CL3476.Contig3_All	Aquaporin-12 OS=Mus musculus GN=Aqp12 PE=2 SV=1
CL3476.Contig4_All	--
CL3497.Contig2_All	--
CL3503.Contig4_All	--
CL3519.Contig1_All	--
CL3521.Contig2_All	--
CL3525.Contig1_All	--
CL3528.Contig5_All	--
CL3553.Contig1_All	--
CL3560.Contig3_All	--
CL3567.Contig11_All	--
CL3583.Contig1_All	--
CL3646.Contig1_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3
CL3660.Contig2_All	Dorsal-ventral patterning protein Sog OS=Drosophila melanogaster GN=sog PE=1 SV=1
CL3680.Contig1_All	--
CL3720.Contig1_All	Larval cuticle protein LCP-17 OS=Bombyx mori GN=LCP17 PE=2 SV=1
CL3750.Contig1_All	Arylsulfatase B OS=Mus musculus GN=Arsb PE=2 SV=3
CL3763.Contig3_All	--
CL3764.Contig2_All	--
CL3809.Contig2_All	--
CL3837.Contig1_All	--
CL3871.Contig1_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL39.Contig2_All	Collectin-46 OS=Bos taurus GN=CL46 PE=2 SV=1
CL39.Contig4_All	Serine/arginine repetitive matrix protein 1 OS=Gallus gallus GN=SRRM1 PE=2 SV=1
CL3912.Contig1_All	Troponin T OS=Periplaneta americana GN=TNT PE=2 SV=1
CL3912.Contig2_All	Troponin T OS=Periplaneta americana GN=TNT PE=2 SV=1
CL3912.Contig3_All	Troponin T OS=Periplaneta americana GN=TNT PE=2 SV=1
CL3916.Contig2_All	--
CL3917.Contig1_All	--

CL392.Contig5_All	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ivd PE=1 SV=2
CL392.Contig6_All	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ivd PE=1 SV=2
CL392.Contig7_All	--
CL392.Contig8_All	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ivd PE=1 SV=2
CL392.Contig9_All	PDZ and LIM domain protein Zasp OS=Drosophila melanogaster GN=Zasp52 PE=1 SV=2
CL3932.Contig1_All	Four and a half LIM domains protein 2 OS=Bos taurus GN=FHL2 PE=2 SV=1
CL3932.Contig6_All	Four and a half LIM domains protein 2 OS=Bos taurus GN=FHL2 PE=2 SV=1
CL3945.Contig2_All	--
CL3954.Contig1_All	Prohormone-2 OS=Apis mellifera PE=1 SV=1
CL3954.Contig2_All	Prohormone-2 OS=Apis mellifera PE=1 SV=1
CL3974.Contig1_All	--
CL3983.Contig1_All	Venom carboxylesterase-6 OS=Apis mellifera PE=2 SV=1
CL399.Contig4_All	--
CL4010.Contig1_All	--
CL4027.Contig1_All	Ice-structuring glycoprotein (Fragment) OS=Notothenia coriiceps neglecta GN=afgp8 PE=1 SV=2
CL404.Contig2_All	Actin, muscle OS=Manduca sexta PE=2 SV=1
CL404.Contig4_All	Actin, muscle OS=Manduca sexta PE=2 SV=1
CL404.Contig7_All	Actin, cytoplasmic A3a OS=Helicoverpa armigera GN=actA3a PE=2 SV=1
CL404.Contig8_All	Actin, muscle OS=Manduca sexta PE=2 SV=1
CL4040.Contig1_All	--
CL4047.Contig1_All	--
CL405.Contig10_All	--
CL405.Contig15_All	--
CL405.Contig8_All	--
CL4161.Contig3_All	Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2
CL4199.Contig1_All	--
CL4199.Contig2_All	--
CL4204.Contig2_All	Lysozyme E OS=Drosophila melanogaster GN=LysE PE=2 SV=2
CL4269.Contig1_All	--
CL4278.Contig3_All	Glycogenin-1 OS=Mus musculus GN=Gyg1 PE=2 SV=3
CL4296.Contig1_All	F-box only protein 32 OS=Mus musculus GN=Fbxo32 PE=2 SV=1
CL4319.Contig1_All	--

CL4323.Contig1_All	--
CL4326.Contig1_All	--
CL433.Contig3_All	--
CL433.Contig4_All	--
CL4333.Contig2_All	--
CL4344.Contig2_All	Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2
CL4361.Contig5_All	--
CL4380.Contig1_All	--
CL44.Contig2_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
CL4445.Contig2_All	--
CL4445.Contig3_All	--
CL4487.Contig3_All	--
CL4487.Contig4_All	--
CL4490.Contig2_All	Pre-mRNA-processing factor 39 OS=Drosophila melanogaster GN=CG1646 PE=1 SV=1
CL4492.Contig4_All	E3 ubiquitin-protein ligase RNF31 OS=Mus musculus GN=Rnf31 PE=1 SV=2
CL4492.Contig6_All	E3 ubiquitin-protein ligase RNF31 OS=Mus musculus GN=Rnf31 PE=1 SV=2
CL4505.Contig1_All	--
CL4514.Contig11_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL4514.Contig2_All	Protein anoxia up-regulated OS=Drosophila melanogaster GN=fau PE=1 SV=3
CL4514.Contig7_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL4517.Contig1_All	Synaptic vesicle glycoprotein 2B OS=Mus musculus GN=Sv2b PE=1 SV=1
CL4530.Contig1_All	--
CL4530.Contig2_All	--
CL459.Contig8_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL4591.Contig1_All	--
CL4605.Contig1_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL461.Contig13_All	Myosin heavy chain, muscle OS=Drosophila melanogaster GN=Mhc PE=1 SV=4
CL461.Contig3_All	Myosin heavy chain, muscle OS=Drosophila melanogaster GN=Mhc PE=1 SV=4
CL461.Contig4_All	Myosin heavy chain, muscle OS=Drosophila melanogaster GN=Mhc PE=1 SV=4
CL461.Contig8_All	Myosin heavy chain, muscle OS=Drosophila melanogaster GN=Mhc PE=1 SV=4

CL4637.Contig2_All	Slit homolog 1 protein OS=Rattus norvegicus GN=Slit1 PE=1 SV=1
CL466.Contig1_All	--
CL466.Contig2_All	--
CL4683.Contig1_All	--
CL4719.Contig1_All	--
CL4743.Contig1_All	Protein yellow OS=Drosophila yakuba GN=y PE=3 SV=1
CL4797.Contig1_All	--
CL4797.Contig2_All	--
CL48.Contig4_All	--
CL4815.Contig1_All	Glutamate-gated chloride channel OS=Drosophila melanogaster GN=GluClalpha PE=1 SV=2
CL4837.Contig2_All	--
CL4883.Contig5_All	--
CL489.Contig2_All	--
CL4900.Contig1_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
CL4902.Contig1_All	--
CL4902.Contig2_All	--
CL4902.Contig3_All	--
CL4902.Contig4_All	--
CL4902.Contig5_All	--
CL4902.Contig6_All	--
CL4911.Contig1_All	--
CL4916.Contig1_All	26S proteasome non-ATPase regulatory subunit 1 OS=Drosophila melanogaster GN=Rpn2 PE=1 SV=1
CL4958.Contig2_All	--
CL4984.Contig2_All	--
CL4994.Contig2_All	Cytochrome P450 6k1 OS=Blattella germanica GN=CYP6K1 PE=2 SV=1
CL5007.Contig1_All	--
CL501.Contig2_All	--
CL5065.Contig1_All	--
CL5065.Contig2_All	--
CL5071.Contig2_All	Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3
CL5086.Contig1_All	--
CL5087.Contig2_All	--
CL5115.Contig2_All	Down syndrome cell adhesion molecule-like protein Dscam2 OS=Drosophila melanogaster GN=Dscam2 PE=2 SV=3

CL5141.Contig2_All	Acetylcholine receptor subunit alpha-L1 OS=Schistocerca gregaria PE=2 SV=1
CL5153.Contig1_All	--
CL5172.Contig1_All	Endocuticle structural glycoprotein SgAbd-8 OS=Schistocerca gregaria PE=1 SV=1
CL5172.Contig2_All	Endocuticle structural glycoprotein SgAbd-8 OS=Schistocerca gregaria PE=1 SV=1
CL5194.Contig1_All	Aromatic-L-amino-acid decarboxylase OS=Mus musculus GN=Ddc PE=2 SV=1
CL5194.Contig2_All	Aromatic-L-amino-acid decarboxylase OS=Mus musculus GN=Ddc PE=2 SV=1
CL5205.Contig4_All	--
CL5251.Contig2_All	Transmembrane protein 181 OS=Homo sapiens GN=TMEM181 PE=1 SV=2
CL5253.Contig1_All	Neural Wiskott-Aldrich syndrome protein OS=Bos taurus GN=WASL PE=1 SV=1
CL5253.Contig2_All	Neural Wiskott-Aldrich syndrome protein OS=Bos taurus GN=WASL PE=1 SV=1
CL5287.Contig3_All	Transposable element Hobo transposase OS=Drosophila melanogaster GN=T PE=4 SV=1
CL5300.Contig2_All	RING finger protein nhl-1 OS=Caenorhabditis elegans GN=nhl-1 PE=1 SV=2
CL5343.Contig1_All	--
CL5343.Contig2_All	--
CL5366.Contig1_All	--
CL5407.Contig1_All	Down syndrome cell adhesion molecule-like protein Dscam2 OS=Drosophila melanogaster GN=Dscam2 PE=2 SV=3
CL5438.Contig2_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
CL5442.Contig1_All	--
CL5464.Contig1_All	--
CL5483.Contig3_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2
CL5488.Contig2_All	ATP-binding cassette sub-family A member 1 OS=Mus musculus GN=Abca1 PE=1 SV=4
CL5489.Contig1_All	--
CL5531.Contig1_All	--
CL5552.Contig1_All	Muscle LIM protein Mlp84B OS=Drosophila melanogaster GN=Mlp84B PE=1 SV=1
CL5552.Contig2_All	Muscle LIM protein Mlp84B OS=Drosophila melanogaster GN=Mlp84B PE=1 SV=1
CL5552.Contig4_All	Muscle LIM protein Mlp84B OS=Drosophila melanogaster GN=Mlp84B PE=1

	SV=1
CL5556.Contig1_All	Mitochondrial coenzyme A transporter SLC25A42 OS=Xenopus laevis GN=slc25a42 PE=2 SV=1
CL5562.Contig2_All	--
CL5562.Contig3_All	--
CL5591.Contig2_All	Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2
CL5594.Contig1_All	--
CL5653.Contig1_All	Androgen-induced gene 1 protein OS=Homo sapiens GN=AIG1 PE=1 SV=2
CL5688.Contig2_All	--
CL5699.Contig1_All	--
CL5699.Contig2_All	--
CL57.Contig1_All	--
CL573.Contig1_All	--
CL5736.Contig1_All	--
CL5787.Contig1_All	Retrovirus-related Pol polyprotein from transposon opus OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL5836.Contig8_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL5848.Contig2_All	Atrial natriuretic peptide receptor 1 OS=Rattus norvegicus GN=Npr1 PE=1 SV=1
CL5895.Contig1_All	--
CL5904.Contig2_All	--
CL5911.Contig2_All	Putative uncharacterized transposon-derived protein F52C9.6 OS=Caenorhabditis elegans GN=F52C9.6 PE=5 SV=1
CL5911.Contig3_All	Putative uncharacterized transposon-derived protein F52C9.6 OS=Caenorhabditis elegans GN=F52C9.6 PE=5 SV=1
CL5913.Contig2_All	--
CL5929.Contig1_All	--
CL5932.Contig2_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
CL594.Contig3_All	--
CL5950.Contig3_All	--
CL5981.Contig2_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL600.Contig4_All	--
CL6014.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
CL6034.Contig2_All	Nocturnin OS=Homo sapiens GN=CCRN4L PE=2 SV=2
CL6046.Contig1_All	Phosphoenolpyruvate phosphomutase OS=Mytilus edulis PE=1 SV=3

CL6046.Contig3_All	Phosphoenolpyruvate phosphomutase OS=Mytilus edulis PE=1 SV=3
CL6052.Contig1_All	Microtubule-associated protein Jupiter OS=Drosophila melanogaster GN=Jupiter PE=1 SV=2
CL6084.Contig2_All	Alpha-tocopherol transfer protein-like OS=Pongo abelii GN=TTPAL PE=2 SV=1
CL6100.Contig2_All	Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 PE=1 SV=3
CL6137.Contig1_All	--
CL6140.Contig1_All	Myosin light chain alkali OS=Drosophila virilis GN=Mlc1 PE=4 SV=1
CL6140.Contig2_All	Myosin light chain alkali OS=Drosophila virilis GN=Mlc1 PE=4 SV=1
CL6187.Contig1_All	Caspase OS=Drosophila melanogaster GN=Ice PE=1 SV=2
CL6201.Contig1_All	Myosin regulatory light chain 2 OS=Bombyx mori PE=1 SV=1
CL621.Contig5_All	--
CL6213.Contig3_All	Complement factor H OS=Bos taurus GN=CFH PE=1 SV=3
CL6214.Contig1_All	--
CL6232.Contig1_All	--
CL6235.Contig1_All	--
CL6235.Contig2_All	--
CL6235.Contig3_All	--
CL6236.Contig2_All	Cuticle protein 63 OS=Locusta migratoria PE=1 SV=1
CL6242.Contig2_All	UDP-glucuronosyltransferase 1-1 OS=Rattus norvegicus GN=Ugt1a1 PE=1 SV=1
CL6244.Contig1_All	Reticulon-1 OS=Xenopus tropicalis GN=rtn1 PE=2 SV=2
CL6285.Contig1_All	--
CL6303.Contig1_All	Complexin OS=Drosophila melanogaster GN=cpx PE=2 SV=1
CL6322.Contig2_All	--
CL6331.Contig3_All	--
CL6332.Contig1_All	--
CL6400.Contig1_All	--
CL6400.Contig2_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL6424.Contig3_All	--
CL645.Contig3_All	--
CL6461.Contig1_All	--
CL6461.Contig2_All	--
CL6468.Contig2_All	--

CL6471.Contig2_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL648.Contig3_All	Troponin I OS=Drosophila melanogaster GN=wupA PE=2 SV=3
CL648.Contig4_All	Troponin I OS=Drosophila melanogaster GN=wupA PE=2 SV=3
CL648.Contig5_All	Troponin I OS=Drosophila melanogaster GN=wupA PE=2 SV=3
CL6491.Contig2_All	--
CL6535.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
CL6619.Contig2_All	--
CL6627.Contig1_All	--
CL6627.Contig2_All	--
CL6627.Contig3_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
CL6636.Contig1_All	--
CL6636.Contig2_All	--
CL6643.Contig1_All	--
CL669.Contig1_All	--
CL675.Contig1_All	--
CL6760.Contig1_All	Elongation of very long chain fatty acids protein AAEL008004 OS=Aedes aegypti GN=AAEL008004 PE=2 SV=2
CL6775.Contig3_All	Retrovirus-related Pol polyprotein from transposon opus OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL6783.Contig2_All	--
CL6787.Contig1_All	--
CL6787.Contig3_All	--
CL6823.Contig1_All	--
CL6838.Contig1_All	--
CL6857.Contig2_All	Retrovirus-related Pol polyprotein from transposon 17.6 OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL688.Contig1_All	--
CL688.Contig2_All	--
CL6893.Contig1_All	--
CL6921.Contig1_All	--
CL698.Contig1_All	DNA repair protein complementing XP-A cells homolog OS=Drosophila melanogaster GN=Xpac PE=2 SV=3
CL699.Contig2_All	--
CL7006.Contig1_All	--

CL7006.Contig2_All	--
CL7053.Contig2_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL7054.Contig1_All	TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1
CL7088.Contig1_All	--
CL7102.Contig1_All	Aquaporin AQPAe.a OS=Aedes aegypti GN=AAEL003512 PE=2 SV=2
CL7102.Contig2_All	--
CL7145.Contig1_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
CL7150.Contig1_All	Sulfotransferase 1C4 OS=Homo sapiens GN=SULT1C4 PE=1 SV=2
CL7151.Contig3_All	PHD finger and CXXC domain-containing protein CG17446 OS=Drosophila melanogaster GN=CG17446 PE=1 SV=1
CL7220.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL7220.Contig2_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL7250.Contig2_All	--
CL7296.Contig1_All	--
CL7296.Contig2_All	--
CL7309.Contig1_All	PDF receptor OS=Drosophila melanogaster GN=Pdfr PE=1 SV=2
CL7310.Contig3_All	Epithelial discoidin domain-containing receptor 1 OS=Rattus norvegicus GN=Ddr1 PE=2 SV=1
CL7348.Contig1_All	Glutathione S-transferase 1, isoform D OS=Anopheles gambiae GN=GstD1 PE=1 SV=1
CL7348.Contig2_All	Glutathione S-transferase 1, isoform D OS=Anopheles gambiae GN=GstD1 PE=1 SV=1
CL7366.Contig2_All	--
CL7372.Contig1_All	--
CL7432.Contig1_All	--
CL7448.Contig1_All	Uncharacterized protein DDB_G0279979 OS=Dictyostelium discoideum GN=DDB_G0279979 PE=4 SV=1
CL7448.Contig2_All	Microtubule-associated protein futsch OS=Drosophila melanogaster GN=futsch PE=1 SV=4
CL7480.Contig1_All	--
CL7480.Contig2_All	--
CL7495.Contig2_All	Neprilysin OS=Oryctolagus cuniculus GN=MME PE=1 SV=2
CL7500.Contig2_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2

CL7501.Contig2_All	--
CL7530.Contig1_All	Peroxiredoxin-6 OS=Gallus gallus GN=PRDX6 PE=2 SV=3
CL7530.Contig2_All	Peroxiredoxin-6 OS=Gallus gallus GN=PRDX6 PE=2 SV=3
CL7530.Contig3_All	Peroxiredoxin-6 OS=Gallus gallus GN=PRDX6 PE=2 SV=3
CL7530.Contig4_All	Peroxiredoxin-6 OS=Gallus gallus GN=PRDX6 PE=2 SV=3
CL7530.Contig5_All	Peroxiredoxin-6 OS=Gallus gallus GN=PRDX6 PE=2 SV=3
CL758.Contig2_All	Glutamate receptor 1 OS=Drosophila melanogaster GN=Glu-RI PE=2 SV=2
CL7609.Contig1_All	--
CL7631.Contig2_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2
CL7642.Contig2_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2
CL7674.Contig3_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL7718.Contig1_All	Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2
CL772.Contig1_All	Pupal cuticle protein 36 OS=Manduca sexta GN=PCP36 PE=1 SV=1
CL772.Contig2_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL772.Contig3_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL778.Contig2_All	Tropomyosin-1, isoforms 33/34 OS=Drosophila melanogaster GN=Tm1 PE=2 SV=2
CL7797.Contig1_All	Collagen alpha-5(IV) chain OS=Homo sapiens GN=COL4A5 PE=1 SV=2
CL7797.Contig3_All	--
CL7803.Contig3_All	Poly(rC)-binding protein 3 OS=Mus musculus GN=Pcbp3 PE=2 SV=3
CL7830.Contig2_All	--
CL7871.Contig1_All	Glutathione S-transferase D7 OS=Anopheles gambiae GN=GstD7 PE=2 SV=1
CL7871.Contig2_All	Glutathione S-transferase D7 OS=Anopheles gambiae GN=GstD7 PE=2 SV=1
CL7876.Contig2_All	--
CL7934.Contig1_All	--
CL7934.Contig2_All	--
CL7942.Contig1_All	--
CL7951.Contig2_All	--
CL7986.Contig2_All	--
CL8017.Contig1_All	--

CL8041.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL8041.Contig2_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL8079.Contig1_All	--
CL8116.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL8116.Contig3_All	Homeobox protein Hox-A4 OS=Gallus gallus GN=HOXA4 PE=2 SV=1
CL8116.Contig4_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL8129.Contig1_All	--
CL8129.Contig2_All	--
CL8162.Contig1_All	Cathelicidin-3 OS=Bos taurus GN=CATHL3 PE=1 SV=2
CL8162.Contig2_All	--
CL8162.Contig3_All	Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 PE=1 SV=1
CL8163.Contig1_All	--
CL8190.Contig1_All	--
CL8287.Contig2_All	--
CL8315.Contig1_All	--
CL8320.Contig1_All	--
CL8320.Contig2_All	--
CL8334.Contig1_All	--
CL8346.Contig1_All	Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1
CL8362.Contig1_All	--
CL8375.Contig1_All	--
CL8385.Contig3_All	Ferric-chelate reductase 1 OS=Mus musculus GN=FRRS1 PE=1 SV=1
CL8409.Contig1_All	Serine/arginine repetitive matrix protein 1 OS=Gallus gallus GN=SRRM1 PE=2 SV=1
CL8419.Contig2_All	--
CL842.Contig2_All	--
CL8437.Contig2_All	--
CL8439.Contig2_All	Retrovirus-related Pol polyprotein from type-2 retrotransposable element R2DM OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL8469.Contig2_All	--
CL8497.Contig1_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL8580.Contig1_All	--
CL8597.Contig2_All	ATP synthase subunit epsilon, mitochondrial OS=Bos taurus GN=ATP5E PE=1 SV=4
CL8629.Contig2_All	Flexible cuticle protein 12 OS=Hyalophora cecropia GN=CP12 PE=2 SV=1

CL8629.Contig3_All	Flexible cuticle protein 12 OS=Hyalophora cecropia GN=CP12 PE=2 SV=1
CL8653.Contig1_All	--
CL867.Contig1_All	Probable multidrug resistance-associated protein lethal(2)03659 OS=Drosophila melanogaster GN=l(2)03659 PE=2 SV=3
CL8689.Contig2_All	--
CL8692.Contig1_All	--
CL8692.Contig2_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL8692.Contig3_All	--
CL8692.Contig4_All	--
CL8728.Contig1_All	--
CL8736.Contig2_All	--
CL8753.Contig2_All	Fatty-acid amide hydrolase 2 OS=Homo sapiens GN=FAAH2 PE=2 SV=1
CL8783.Contig1_All	--
CL8808.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL886.Contig2_All	LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1
CL889.Contig7_All	Protein kinase C iota type OS=Rattus norvegicus GN=Prkci PE=1 SV=1
CL8899.Contig1_All	--
CL8943.Contig3_All	--
CL8956.Contig1_All	rRNA 2'-O-methyltransferase fibrillarin OS=Drosophila melanogaster GN=Fib PE=2 SV=1
CL8956.Contig2_All	Keratin, type I cytoskeletal 9 OS=Canis familiaris GN=KRT9 PE=3 SV=1
CL8994.Contig1_All	--
CL9028.Contig2_All	Zinc finger X-linked protein ZXDA/ZXDB OS=Mus musculus GN=Zxda PE=2 SV=1
CL9046.Contig2_All	Zinc finger homeobox protein 4 OS=Homo sapiens GN=ZFHX4 PE=1 SV=1
CL9104.Contig3_All	--
CL9110.Contig1_All	Mucin-1 OS=Mesocricetus auratus GN=MUC1 PE=2 SV=1
CL9152.Contig1_All	Uncharacterized protein K02A2.6 OS=Caenorhabditis elegans GN=K02A2.6 PE=2 SV=1
CL9163.Contig2_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL9171.Contig2_All	--
CL9184.Contig1_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL9190.Contig1_All	--
CL92.Contig1_All	--

CL9211.Contig1_All	Alkylglycerol monooxygenase OS=Xenopus tropicalis GN=agmo PE=2 SV=1
CL9217.Contig1_All	--
CL9261.Contig1_All	NADH-ubiquinone oxidoreductase chain 6 OS=Locusta migratoria GN=ND6 PE=3 SV=1
CL9268.Contig1_All	Glutathione S-transferase omega-1 OS=Rattus norvegicus GN=Gsto1 PE=1 SV=2
CL9275.Contig1_All	--
CL9275.Contig2_All	Period circadian protein (Fragments) OS=Drosophila simulans GN=per PE=3 SV=2
CL9314.Contig2_All	--
CL9339.Contig2_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL9342.Contig1_All	--
CL9342.Contig2_All	--
CL9359.Contig1_All	Guanylate cyclase soluble subunit beta-1 OS=Rattus norvegicus GN=Gucy1b3 PE=1 SV=2
CL9379.Contig1_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
CL9379.Contig2_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
CL9386.Contig1_All	Histone-lysine N-methyltransferase MLL2 OS=Homo sapiens GN=MLL2 PE=1 SV=2
CL9394.Contig1_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
CL9395.Contig1_All	Cuticle protein 65 OS=Locusta migratoria PE=1 SV=1
CL9395.Contig2_All	Cuticle protein 65 OS=Locusta migratoria PE=1 SV=1
CL9396.Contig3_All	--
CL9396.Contig4_All	--
CL9396.Contig5_All	--
CL9438.Contig2_All	Guanine nucleotide exchange factor for Rab-3A OS=Bos taurus GN=RAB3IL1 PE=2 SV=1
CL9452.Contig1_All	--
CL9463.Contig1_All	--
CL9472.Contig1_All	BarH-like 1 homeobox protein OS=Homo sapiens GN=BARHL1 PE=2 SV=1
CL9474.Contig1_All	--
CL9474.Contig2_All	--
CL9506.Contig3_All	Keratin-associated protein 5-5 OS=Mus musculus GN=Krtap5-5 PE=2 SV=1
CL9506.Contig4_All	Keratin-associated protein 5-5 OS=Mus musculus GN=Krtap5-5 PE=2 SV=1
CL9572.Contig2_All	--
CL9611.Contig1_All	--
CL9611.Contig2_All	--

CL9613.Contig3_All	--
CL9643.Contig1_All	Krueppel homologous protein 1 OS=Drosophila melanogaster GN=Kr-h1 PE=2 SV=2
CL9643.Contig2_All	Krueppel homologous protein 1 OS=Drosophila melanogaster GN=Kr-h1 PE=2 SV=2
CL9647.Contig1_All	Lachesin OS=Schistocerca americana GN=LAC PE=1 SV=1
CL9647.Contig2_All	Lachesin OS=Schistocerca americana GN=LAC PE=1 SV=1
CL9647.Contig3_All	Lachesin OS=Schistocerca americana GN=LAC PE=1 SV=1
CL9691.Contig1_All	Zinc finger protein GLIS2 homolog OS=Drosophila melanogaster GN=sug PE=2 SV=1
CL9698.Contig1_All	Glucose dehydrogenase [acceptor] OS=Drosophila melanogaster GN=Gld PE=3 SV=3
CL9699.Contig1_All	--
CL9703.Contig1_All	General transcription factor II-I repeat domain-containing protein 2 OS=Mus musculus GN=Gtf2ird2 PE=2 SV=1
CL9755.Contig1_All	--
CL9758.Contig2_All	--
CL9792.Contig2_All	--
CL9852.Contig1_All	Tubulin alpha chain, testis-specific OS=Oncorhynchus mykiss PE=2 SV=1
CL9852.Contig2_All	Tubulin alpha chain OS=Bombyx mori PE=2 SV=1
CL9853.Contig2_All	--
CL9881.Contig1_All	Cytochrome P450 4C1 OS=Blaberus discoidalis GN=CYP4C1 PE=2 SV=1
CL9900.Contig1_All	--
CL9908.Contig2_All	Histidine-rich glycoprotein OS=Plasmodium lophurae PE=4 SV=1
CL9919.Contig1_All	--
CL994.Contig2_All	--
CL9957.Contig1_All	--
CL9957.Contig2_All	--
CL9972.Contig2_All	--
Unigene10030_All	--
Unigene10094_All	Vesicle-associated membrane protein 2 OS=Macaca mulatta GN=VAMP2 PE=3 SV=3
Unigene10095_All	--
Unigene101038_All	--
Unigene101065_All	--
Unigene10106_All	Unconventional myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Unigene10111_All	--
Unigene10113_All	--
Unigene101309_All	--
Unigene101569_All	--
Unigene101661_All	--
Unigene10175_All	--
Unigene101773_All	--
Unigene10179_All	--
Unigene101833_All	--
Unigene10213_All	--
Unigene10214_All	--
Unigene10215_All	--
Unigene10242_All	--
Unigene10254_All	Myosin-M heavy chain OS=Dictyostelium discoideum GN=myoM PE=1 SV=1
Unigene102551_All	--
Unigene102587_All	--
Unigene10261_All	--
Unigene102626_All	--
Unigene102744_All	--
Unigene102946_All	--
Unigene103023_All	--
Unigene10305_All	Protein Skeletor, isoforms D/E OS=Drosophila melanogaster GN=Skeletor PE=1 SV=3
Unigene103131_All	--
Unigene103240_All	--
Unigene10325_All	--
Unigene103261_All	--
Unigene10326_All	SET and MYND domain-containing protein 4 OS=Pongo abelii GN=SMYD4 PE=2 SV=1
Unigene103302_All	--
Unigene103376_All	--
Unigene10345_All	--
Unigene103501_All	--
Unigene10354_All	--
Unigene103636_All	--
Unigene103665_All	--
Unigene103673_All	--
Unigene103732_All	--
Unigene10375_All	Putative SCAN domain-containing protein SCAND2P OS=Homo sapiens GN=SCAND2P PE=5 SV=2
Unigene103847_All	--

Unigene10390_All	General transcription factor II-I repeat domain-containing protein 2B OS=Homo sapiens GN=GTF2IRD2B PE=1 SV=1
Unigene103929_All	--
Unigene103934_All	--
Unigene103943_All	--
Unigene103985_All	--
Unigene104016_All	--
Unigene10408_All	--
Unigene10413_All	--
Unigene104172_All	--
Unigene104225_All	--
Unigene104365_All	--
Unigene104393_All	--
Unigene10444_All	Arrestin homolog OS=Locusta migratoria PE=2 SV=1
Unigene10449_All	Neural-cadherin OS=Drosophila melanogaster GN=CadN PE=1 SV=2
Unigene104509_All	--
Unigene10455_All	--
Unigene104589_All	--
Unigene104637_All	Dehydrogenase/reductase SDR family member 11 OS=Gallus gallus GN=DHRS11 PE=2 SV=1
Unigene104643_All	--
Unigene104705_All	--
Unigene104819_All	Pro-resilin OS=Drosophila melanogaster GN=resilin PE=1 SV=1
Unigene104821_All	--
Unigene10482_All	--
Unigene104848_All	--
Unigene104856_All	--
Unigene104865_All	--
Unigene104915_All	--
Unigene104938_All	--
Unigene104952_All	--
Unigene10496_All	--
Unigene104981_All	--
Unigene10499_All	Ankyrin repeat and death domain-containing protein 1A OS=Homo sapiens GN=ANKDD1A PE=2 SV=2
Unigene105092_All	Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2
Unigene105097_All	--
Unigene10511_All	DNA-directed RNA polymerase II subunit RPB1 OS=Drosophila melanogaster GN=RpII215 PE=3 SV=4

Unigene10530_All	--
Unigene105314_All	--
Unigene105323_All	--
Unigene105332_All	--
Unigene105451_All	--
Unigene10545_All	--
Unigene10555_All	--
Unigene1055_All	--
Unigene105768_All	--
Unigene10598_All	--
Unigene1060_All	--
Unigene10639_All	--
Unigene10645_All	--
Unigene10654_All	--
Unigene10655_All	--
Unigene10665_All	--
Unigene10668_All	--
Unigene1066_All	--
Unigene10694_All	Colorectal mutant cancer protein OS=Homo sapiens GN=MCC PE=1 SV=2
Unigene10697_All	--
Unigene106_All	Prolyl 3-hydroxylase 1 OS=Gallus gallus GN=LEPRE1 PE=1 SV=1
Unigene10702_All	--
Unigene107077_All	--
Unigene10707_All	--
Unigene10732_All	Polypeptide N-acetylgalactosaminyltransferase 14 OS=Homo sapiens GN=GALNT14 PE=2 SV=1
Unigene1074_All	--
Unigene10758_All	--
Unigene107599_All	Pro-resilin OS=Drosophila melanogaster GN=resilin PE=1 SV=1
Unigene10761_All	--
Unigene10767_All	--
Unigene10793_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene10802_All	Slit homolog 1 protein OS=Rattus norvegicus GN=Slit1 PE=1 SV=1
Unigene1083_All	Serine/arginine repetitive matrix protein 1 OS=Gallus gallus GN=SRRM1 PE=2 SV=1
Unigene10940_All	--
Unigene109461_All	--
Unigene109528_All	--

Unigene10956_All	--
Unigene10967_All	Lysosome-associated membrane glycoprotein 5 OS=Xenopus tropicalis GN=lamp5 PE=2 SV=1
Unigene109843_All	Collagen alpha-5(IV) chain OS=Homo sapiens GN=COL4A5 PE=1 SV=2
Unigene11029_All	--
Unigene11032_All	Craniofacial development protein 2 OS=Bos taurus GN=CFDP2 PE=1 SV=2
Unigene11033_All	--
Unigene110363_All	--
Unigene11036_All	--
Unigene11043_All	Ketohexokinase OS=Homo sapiens GN=KHK PE=1 SV=1
Unigene11060_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene11061_All	--
Unigene11064_All	--
Unigene1107_All	--
Unigene11151_All	Acid sphingomyelinase-like phosphodiesterase 3a OS=Rattus norvegicus GN=Smpdl3a PE=2 SV=1
Unigene11184_All	--
Unigene11214_All	--
Unigene11216_All	--
Unigene11217_All	--
Unigene11223_All	--
Unigene11229_All	--
Unigene1124_All	Defense protein l(2)34Fc OS=Drosophila melanogaster GN=l(2)34Fc PE=2 SV=1
Unigene11252_All	--
Unigene11298_All	Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1
Unigene1130_All	--
Unigene11315_All	--
Unigene11326_All	Endocuticle structural glycoprotein SgAbd-2 OS=Schistocerca gregaria PE=1 SV=1
Unigene11345_All	--
Unigene11366_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene11375_All	--
Unigene11395_All	--
Unigene11448_All	Forkhead box protein G1 OS=Cercopithecus pygerythrus GN=FOXG1 PE=3 SV=1
Unigene11454_All	--

Unigene11461_All	Serine/arginine repetitive matrix protein 5 OS=Homo sapiens GN=SRRM5 PE=1 SV=3
Unigene11468_All	--
Unigene11509_All	--
Unigene115171_All	--
Unigene1152_All	Spore coat protein SP96 OS=Dictyostelium discoideum GN=cotA PE=4 SV=2
Unigene11530_All	--
Unigene115488_All	--
Unigene11575_All	--
Unigene11595_All	--
Unigene11606_All	--
Unigene11614_All	--
Unigene11632_All	--
Unigene11691_All	--
Unigene11713_All	--
Unigene11717_All	--
Unigene11729_All	--
Unigene11734_All	--
Unigene11746_All	--
Unigene11749_All	--
Unigene1179_All	--
Unigene11823_All	--
Unigene1182_All	--
Unigene11856_All	--
Unigene11892_All	--
Unigene1189_All	--
Unigene11906_All	--
Unigene11926_All	--
Unigene11953_All	--
Unigene11973_All	--
Unigene11975_All	--
Unigene12008_All	--
Unigene12054_All	--
Unigene120_All	Dorsal-ventral patterning protein Sog OS=Drosophila melanogaster GN=sog PE=1 SV=1
Unigene12152_All	--
Unigene12168_All	--
Unigene1217_All	--
Unigene12240_All	--
Unigene12256_All	--
Unigene12260_All	--

Unigene122730_All	--
Unigene122951_All	--
Unigene123102_All	Fatty acid synthase OS=Gallus gallus GN=FASN PE=1 SV=5
Unigene123155_All	--
Unigene123164_All	--
Unigene123244_All	--
Unigene12334_All	--
Unigene123403_All	--
Unigene123428_All	--
Unigene12346_All	Endocuticle structural glycoprotein SgAbd-9 OS=Schistocerca gregaria PE=1 SV=1
Unigene123659_All	--
Unigene123660_All	--
Unigene123691_All	--
Unigene123878_All	--
Unigene123990_All	--
Unigene124182_All	--
Unigene1241_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene124210_All	--
Unigene12435_All	--
Unigene124653_All	--
Unigene124742_All	--
Unigene12481_All	--
Unigene124857_All	--
Unigene12485_All	--
Unigene124912_All	--
Unigene124936_All	--
Unigene124995_All	--
Unigene125145_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
Unigene125149_All	--
Unigene125217_All	--
Unigene125267_All	Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4
Unigene125316_All	--
Unigene12536_All	--
Unigene125567_All	--
Unigene125617_All	Cuticle protein 8 OS=Locusta migratoria PE=1 SV=1
Unigene125652_All	--
Unigene125684_All	--
Unigene12569_All	--

Unigene12614_All	--
Unigene12623_All	--
Unigene12625_All	--
Unigene12649_All	--
Unigene12658_All	--
Unigene12697_All	--
Unigene1269_All	--
Unigene12705_All	Microtubule-associated protein 9 OS=Mus musculus GN=Map9 PE=2 SV=2
Unigene12722_All	--
Unigene1276_All	--
Unigene12796_All	--
Unigene12802_All	--
Unigene128323_All	--
Unigene128426_All	--
Unigene1284_All	Loricrin OS=Mus musculus GN=Lor PE=2 SV=2
Unigene12853_All	--
Unigene1285_All	Keratin, type I cytoskeletal 9 OS=Mus musculus GN=Krt9 PE=1 SV=2
Unigene128630_All	Cuticle protein 18.7 OS=Locusta migratoria PE=1 SV=1
Unigene128728_All	--
Unigene12875_All	--
Unigene128818_All	--
Unigene128903_All	--
Unigene12897_All	--
Unigene129119_All	--
Unigene129290_All	--
Unigene129344_All	--
Unigene12935_All	Down syndrome cell adhesion molecule-like protein Dscam2 OS=Drosophila melanogaster GN=Dscam2 PE=2 SV=3
Unigene129575_All	--
Unigene129578_All	--
Unigene12977_All	Keratin-3, type I cytoskeletal 51 kDa OS=Xenopus laevis PE=2 SV=1
Unigene12980_All	Sodium/potassium-transporting ATPase subunit beta-2 OS=Drosophila melanogaster GN=nrv2 PE=1 SV=2
Unigene130042_All	--
Unigene13033_All	--
Unigene13039_All	--
Unigene1304_All	--
Unigene130607_All	--

Unigene13069_All	--
Unigene131402_All	--
Unigene1314_All	--
Unigene131821_All	--
Unigene131934_All	--
Unigene132087_All	--
Unigene13225_All	--
Unigene1322_All	Serine/arginine repetitive matrix protein 3 OS=Homo sapiens GN=SRRM3 PE=2 SV=4
Unigene132541_All	--
Unigene132562_All	--
Unigene132609_All	--
Unigene132770_All	--
Unigene133019_All	--
Unigene133111_All	--
Unigene133901_All	--
Unigene13410_All	--
Unigene134176_All	Formin-like protein 2 OS=Mus musculus GN=Fmnl2 PE=2 SV=2
Unigene13422_All	--
Unigene134271_All	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3
Unigene134273_All	--
Unigene134425_All	--
Unigene13449_All	--
Unigene134798_All	--
Unigene134822_All	--
Unigene134841_All	--
Unigene1348_All	--
Unigene135178_All	--
Unigene135340_All	--
Unigene13537_All	--
Unigene135488_All	--
Unigene136234_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene136366_All	--
Unigene136595_All	--
Unigene136605_All	--
Unigene136634_All	--
Unigene136734_All	--
Unigene136831_All	--
Unigene137017_All	--

Unigene137039_All	--
Unigene137298_All	--
Unigene137355_All	--
Unigene137416_All	--
Unigene137539_All	--
Unigene13753_All	--
Unigene137552_All	--
Unigene137727_All	--
Unigene137762_All	--
Unigene137773_All	--
Unigene13787_All	--
Unigene13807_All	--
Unigene138264_All	--
Unigene138276_All	--
Unigene138515_All	--
Unigene13852_All	Transmembrane protein 198 OS=Homo sapiens GN=TMEM198 PE=2 SV=1
Unigene138554_All	--
Unigene13858_All	--
Unigene13864_All	--
Unigene138679_All	--
Unigene13874_All	--
Unigene13880_All	Homeobox protein aristaless OS=Drosophila melanogaster GN=al PE=1 SV=2
Unigene13885_All	--
Unigene138893_All	Neural Wiskott-Aldrich syndrome protein OS=Mus musculus GN=Wasl PE=1 SV=1
Unigene138995_All	--
Unigene1389_All	--
Unigene138_All	Vitellogenin-1 OS=Gallus gallus GN=VTG1 PE=1 SV=1
Unigene139035_All	--
Unigene13903_All	Innexin shaking-B OS=Aedes aegypti GN=shakB PE=3 SV=1
Unigene13910_All	--
Unigene139124_All	--
Unigene139125_All	--
Unigene139188_All	--
Unigene13920_All	--
Unigene13926_All	--
Unigene139457_All	--
Unigene139480_All	--
Unigene13951_All	--

Unigene1395_All	Fatty acid synthase OS=Gallus gallus GN=FASN PE=1 SV=5
Unigene139636_All	--
Unigene13966_All	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2
Unigene139755_All	Probable cytochrome P450 313a5 OS=Drosophila melanogaster GN=Cyp313a5 PE=1 SV=2
Unigene13976_All	--
Unigene139899_All	--
Unigene139953_All	Serine/arginine repetitive matrix protein 1 OS=Gallus gallus GN=SRRM1 PE=2 SV=1
Unigene14019_All	--
Unigene140254_All	--
Unigene14031_All	--
Unigene140374_All	--
Unigene140382_All	--
Unigene140387_All	Activating signal cointegrator 1 complex subunit 2 homolog OS=Dictyostelium discoideum GN=ascc2 PE=3 SV=2
Unigene140532_All	--
Unigene140534_All	Retrotransposon-like protein 1 OS=Mus musculus GN=Rtl1 PE=2 SV=1
Unigene140545_All	--
Unigene140661_All	--
Unigene140675_All	--
Unigene140682_All	--
Unigene140701_All	--
Unigene140764_All	Krueppel-like factor 2 OS=Mus musculus GN=Klf2 PE=1 SV=2
Unigene140872_All	--
Unigene14094_All	--
Unigene141014_All	--
Unigene141021_All	--
Unigene141034_All	--
Unigene141042_All	--
Unigene14107_All	--
Unigene14109_All	Period circadian protein (Fragments) OS=Drosophila mauritiana GN=per PE=3 SV=2
Unigene141107_All	--
Unigene14118_All	--
Unigene14139_All	--
Unigene141450_All	--
Unigene14146_All	--

Unigene14153_All	--
Unigene14164_All	--
Unigene14172_All	--
Unigene14177_All	--
Unigene14178_All	--
Unigene141940_All	--
Unigene14202_All	--
Unigene14208_All	--
Unigene14217_All	--
Unigene14221_All	--
Unigene142430_All	--
Unigene142486_All	--
Unigene14253_All	--
Unigene14261_All	--
Unigene142640_All	--
Unigene142661_All	--
Unigene14274_All	--
Unigene1427_All	--
Unigene142855_All	--
Unigene14287_All	--
Unigene1428_All	UDP-glucuronosyltransferase 2B30 OS=Macaca fascicularis GN=UGT2B30 PE=1 SV=1
Unigene1429_All	--
Unigene14307_All	--
Unigene14337_All	--
Unigene1433_All	--
Unigene14413_All	--
Unigene144145_All	--
Unigene1443_All	Multiple coagulation factor deficiency protein 2 homolog OS=Mus musculus GN=Mcfd2 PE=2 SV=1
Unigene14519_All	--
Unigene1454_All	--
Unigene145858_All	--
Unigene1458_All	--
Unigene146316_All	--
Unigene1466_All	--
Unigene14700_All	--
Unigene14701_All	--
Unigene14704_All	--
Unigene14723_All	--
Unigene14724_All	--
Unigene147308_All	--

Unigene14772_All	Solute carrier family 2, facilitated glucose transporter member 5 OS=Equus caballus GN=SLC2A5 PE=2 SV=1
Unigene147866_All	--
Unigene147913_All	--
Unigene147_All	--
Unigene1480_All	--
Unigene14937_All	--
Unigene14965_All	--
Unigene1497_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
Unigene1498_All	--
Unigene14_All	Krueppel homologous protein 1 OS=Drosophila melanogaster GN=Kr-h1 PE=2 SV=2
Unigene15000_All	Formin-1 OS=Homo sapiens GN=FMN1 PE=2 SV=3
Unigene15028_All	--
Unigene15084_All	--
Unigene15113_All	--
Unigene15117_All	Down syndrome cell adhesion molecule-like protein Dscam2 OS=Drosophila melanogaster GN=Dscam2 PE=2 SV=3
Unigene15138_All	Fatty acyl-CoA reductase 1 OS=Xenopus laevis GN=far1 PE=2 SV=1
Unigene1515_All	--
Unigene15162_All	--
Unigene15166_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene15213_All	--
Unigene15301_All	--
Unigene15311_All	--
Unigene15315_All	Uronyl 2-sulfotransferase OS=Mus musculus GN=Ust PE=2 SV=3
Unigene1531_All	--
Unigene1535_All	--
Unigene15399_All	Cytochrome P450 4C1 OS=Blaberus discoidalis GN=CYP4C1 PE=2 SV=1
Unigene15432_All	Nuclear hormone receptor E75 OS=Metapenaeus ensis GN=E75 PE=2 SV=1
Unigene1547_All	--
Unigene15486_All	--
Unigene15570_All	Homeobox protein Mohawk OS=Mus musculus GN=Mkx PE=2 SV=1
Unigene15573_All	--
Unigene15581_All	--

Unigene15585_All	--
Unigene15610_All	--
Unigene15685_All	--
Unigene15704_All	--
Unigene15707_All	--
Unigene1571_All	Venom protease OS=Megabombus pennsylvanicus PE=1 SV=1
Unigene15776_All	--
Unigene15795_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene15835_All	--
Unigene15875_All	--
Unigene1587_All	--
Unigene1588_All	--
Unigene1593_All	Muscleblind-like protein 3 OS=Mus musculus GN=Mbnl3 PE=2 SV=1
Unigene15970_All	--
Unigene15992_All	--
Unigene15999_All	--
Unigene1600_All	Calexcitin-2 OS=Caenorhabditis elegans GN=cex-2 PE=2 SV=3
Unigene16039_All	--
Unigene16050_All	--
Unigene16063_All	--
Unigene16069_All	--
Unigene1607_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene16092_All	--
Unigene160_All	--
Unigene16131_All	--
Unigene16142_All	--
Unigene16176_All	--
Unigene16187_All	--
Unigene16192_All	--
Unigene16196_All	--
Unigene16202_All	--
Unigene16214_All	--
Unigene16215_All	--
Unigene16255_All	--
Unigene16274_All	--
Unigene16275_All	--
Unigene16302_All	--
Unigene16306_All	--

Unigene16339_All	--
Unigene16355_All	--
Unigene16382_All	--
Unigene16390_All	--
Unigene16391_All	--
Unigene16418_All	--
Unigene16419_All	--
Unigene16429_All	--
Unigene16432_All	Dehydrogenase/reductase SDR family member 11 OS=Bos taurus GN=DHRS11 PE=2 SV=1
Unigene16449_All	--
Unigene16465_All	--
Unigene16486_All	--
Unigene16491_All	Serine/arginine repetitive matrix protein 1 OS=Gallus gallus GN=SRRM1 PE=2 SV=1
Unigene16526_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene16551_All	--
Unigene16575_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene16611_All	--
Unigene16625_All	Salivary glue protein Sgs-3 OS=Drosophila erecta GN=Sgs3 PE=2 SV=3
Unigene16641_All	--
Unigene16654_All	Cuticle protein 18.6, isoform A OS=Locusta migratoria PE=1 SV=1
Unigene16655_All	--
Unigene16656_All	--
Unigene16686_All	Orcokinin peptides type B OS=Procambarus clarkii PE=1 SV=1
Unigene1671_All	--
Unigene16728_All	--
Unigene16736_All	--
Unigene16738_All	--
Unigene16743_All	--
Unigene1675_All	--
Unigene16762_All	--
Unigene16799_All	--
Unigene16818_All	--
Unigene16845_All	Forkhead box protein F2 OS=Homo sapiens GN=FOXF2 PE=1 SV=2
Unigene16849_All	--
Unigene16862_All	--

Unigene16879_All	Pickpocket protein 28 OS=Drosophila melanogaster GN=ppk28 PE=1 SV=1
Unigene16893_All	--
Unigene16896_All	--
Unigene16939_All	--
Unigene16978_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene17044_All	--
Unigene17049_All	--
Unigene17084_All	Down syndrome cell adhesion molecule-like protein Dscam2 OS=Drosophila melanogaster GN=Dscam2 PE=2 SV=3
Unigene17088_All	--
Unigene17133_All	--
Unigene17148_All	--
Unigene17188_All	--
Unigene17231_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene17247_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
Unigene17251_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene17271_All	--
Unigene1727_All	--
Unigene17288_All	Probable cytochrome P450 301a1, mitochondrial OS=Drosophila melanogaster GN=Cyp301a1 PE=2 SV=1
Unigene17335_All	--
Unigene17336_All	--
Unigene17337_All	--
Unigene17349_All	Aminopeptidase N OS=Rattus norvegicus GN=Anpep PE=1 SV=2
Unigene17354_All	Aquaporin AQPAe.a OS=Aedes aegypti GN=AAEL003512 PE=2 SV=2
Unigene1738_All	--
Unigene17418_All	--
Unigene17431_All	F-box/LRR-repeat protein 2 OS=Mus musculus GN=Fbxl2 PE=1 SV=1
Unigene17437_All	Extracellular domains-containing protein CG31004 OS=Drosophila melanogaster GN=CG31004 PE=1 SV=1
Unigene17457_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
Unigene17468_All	Atrial natriuretic peptide-converting enzyme OS=Mus musculus GN=Corin PE=2 SV=2
Unigene17471_All	Cadherin-89D OS=Drosophila melanogaster GN=Cad89D PE=2 SV=3

Unigene17505_All	--
Unigene17544_All	Protein Skeletor, isoforms D/E OS=Drosophila melanogaster GN=Skeletor PE=1 SV=3
Unigene17553_All	--
Unigene17554_All	Sterile alpha and TIR motif-containing protein 1 OS=Drosophila melanogaster GN=Ect4 PE=2 SV=1
Unigene17575_All	--
Unigene17606_All	--
Unigene17613_All	--
Unigene17621_All	Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=2
Unigene1763_All	Myosin-11 OS=Gallus gallus GN=MYH11 PE=1 SV=4
Unigene17674_All	cGMP-dependent protein kinase, isozyme 1 OS=Drosophila melanogaster GN=Pkg21D PE=1 SV=2
Unigene17704_All	Long-chain-fatty-acid--CoA ligase ACSBG2 OS=Xenopus laevis GN=acsbg2 PE=2 SV=1
Unigene17710_All	Uncharacterized family 31 glucosidase KIAA1161 OS=Homo sapiens GN=KIAA1161 PE=1 SV=2
Unigene17712_All	--
Unigene17721_All	Alanine--glyoxylate aminotransferase 2, mitochondrial OS=Bos taurus GN=AGXT2 PE=2 SV=1
Unigene17730_All	--
Unigene17738_All	Peroxidase OS=Drosophila melanogaster GN=Pxd PE=2 SV=2
Unigene17739_All	Peroxidasin homolog OS=Caenorhabditis briggsae GN=pxn-1 PE=3 SV=1
Unigene17740_All	--
Unigene17756_All	--
Unigene17765_All	--
Unigene1776_All	--
Unigene17770_All	--
Unigene17775_All	--
Unigene17807_All	--
Unigene17818_All	--
Unigene17841_All	Homeobox protein Hox-A13 OS=Mus musculus GN=Hoxa13 PE=1 SV=1
Unigene17861_All	--
Unigene17868_All	Peroxidasin OS=Xenopus tropicalis GN=pxdn PE=2 SV=1
Unigene17876_All	--
Unigene17893_All	Protein Shroom3 OS=Xenopus laevis GN=shroom3 PE=2 SV=1
Unigene17913_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3

Unigene17919_All	--
Unigene17923_All	Bromodomain and WD repeat-containing DDB_G0285837 OS=Dictyostelium discoideum GN=DDB_G0285837 PE=4 SV=1
Unigene17937_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene17942_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene17984_All	Sodium-coupled neutral amino acid transporter 2 OS=Gallus gallus GN=SLC38A2 PE=2 SV=2
Unigene17988_All	--
Unigene17998_All	--
Unigene18006_All	--
Unigene18035_All	--
Unigene18044_All	Cytochrome P450 307a1 OS=Drosophila melanogaster GN=spo PE=1 SV=3
Unigene18052_All	--
Unigene18057_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene18064_All	--
Unigene18089_All	--
Unigene18097_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene18111_All	Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3
Unigene18130_All	--
Unigene18141_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
Unigene18157_All	SPARC OS=Caenorhabditis elegans GN=ost-1 PE=1 SV=1
Unigene18158_All	--
Unigene18167_All	--
Unigene18207_All	--
Unigene18211_All	--
Unigene18213_All	--
Unigene18214_All	--
Unigene18244_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene18265_All	--
Unigene18310_All	--
Unigene18322_All	Alpha-tocopherol transfer protein OS=Rattus norvegicus GN=Ttpa PE=1 SV=1
Unigene18347_All	--

Unigene18360_All	Protein henna OS=Drosophila melanogaster GN=Hn PE=2 SV=3
Unigene18375_All	--
Unigene18380_All	Muscle-specific protein 20 OS=Drosophila melanogaster GN=Mp20 PE=2 SV=2
Unigene18408_All	--
Unigene18409_All	--
Unigene18410_All	--
Unigene18414_All	--
Unigene18446_All	--
Unigene18448_All	MD-2-related lipid-recognition protein OS=Manduca sexta PE=1 SV=1
Unigene18477_All	--
Unigene18480_All	--
Unigene18504_All	--
Unigene18549_All	--
Unigene18580_All	--
Unigene18601_All	von Willebrand factor D and EGF domain-containing protein OS=Homo sapiens GN=VWDE PE=2 SV=4
Unigene18606_All	--
Unigene18623_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene18636_All	--
Unigene18639_All	--
Unigene18641_All	--
Unigene18648_All	--
Unigene18650_All	Leucine-rich repeat-containing protein 20 OS=Mus musculus GN=Lrrc20 PE=2 SV=1
Unigene18669_All	--
Unigene18685_All	--
Unigene18703_All	--
Unigene18720_All	Down syndrome cell adhesion molecule-like protein Dscam2 OS=Drosophila melanogaster GN=Dscam2 PE=2 SV=3
Unigene18721_All	--
Unigene18739_All	Excitatory amino acid transporter 1 OS=Ambystoma tigrinum GN=SLC1A3 PE=2 SV=1
Unigene18805_All	--
Unigene18821_All	Chaperone activity of bc1 complex-like, mitochondrial OS=Danio rerio GN=adck3 PE=2 SV=1
Unigene18838_All	--
Unigene18864_All	--
Unigene18872_All	--

Unigene1888_All	--
Unigene18908_All	--
Unigene1896_All	--
Unigene19030_All	--
Unigene19039_All	--
Unigene19043_All	--
Unigene19060_All	--
Unigene19091_All	--
Unigene19106_All	--
Unigene19107_All	--
Unigene19128_All	--
Unigene19177_All	--
Unigene1921_All	--
Unigene19295_All	--
Unigene19362_All	--
Unigene19423_All	--
Unigene19445_All	Corticotropin-releasing factor-binding protein OS=Mus musculus GN=Crhbp PE=2 SV=1
Unigene1944_All	--
Unigene19452_All	Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2
Unigene19493_All	--
Unigene19518_All	--
Unigene1952_All	--
Unigene19560_All	--
Unigene19621_All	--
Unigene19635_All	Glucose dehydrogenase [acceptor] OS=Drosophila melanogaster GN=Gld PE=3 SV=3
Unigene19664_All	TANK-binding kinase 1-binding protein 1 OS=Homo sapiens GN=TBKBP1 PE=1 SV=1
Unigene19678_All	--
Unigene19707_All	--
Unigene19726_All	Cardioactive peptide OS=Periplaneta americana GN=CCAP PE=2 SV=1
Unigene19756_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene19788_All	--
Unigene19794_All	--
Unigene19798_All	--
Unigene19800_All	--
Unigene19811_All	--
Unigene19913_All	Putative protein TPRXL OS=Homo sapiens GN=TPRXL PE=5 SV=2

Unigene19933_All	--
Unigene19_All	--
Unigene20040_All	--
Unigene20063_All	--
Unigene20071_All	--
Unigene20112_All	--
Unigene20121_All	--
Unigene20122_All	--
Unigene20141_All	--
Unigene2014_All	Endocuticle structural glycoprotein SgAbd-8 OS=Schistocerca gregaria PE=1 SV=1
Unigene2015_All	--
Unigene20175_All	--
Unigene20225_All	Probable G-protein coupled receptor 52 OS=Mus musculus GN=Gpr52 PE=3 SV=1
Unigene20245_All	Pro-resilin OS=Drosophila melanogaster GN=resilin PE=1 SV=1
Unigene20251_All	Atherin OS=Oryctolagus cuniculus GN=SAMD1 PE=2 SV=1
Unigene20266_All	--
Unigene20274_All	--
Unigene20295_All	--
Unigene20328_All	--
Unigene20352_All	--
Unigene20397_All	--
Unigene20407_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene20432_All	--
Unigene20434_All	--
Unigene20481_All	--
Unigene20531_All	--
Unigene20566_All	Furin-like protease 2 OS=Drosophila melanogaster GN=Fur2 PE=2 SV=2
Unigene20740_All	--
Unigene20789_All	--
Unigene20791_All	--
Unigene207_All	--
Unigene20872_All	--
Unigene20898_All	--
Unigene208_All	--
Unigene20918_All	--
Unigene20959_All	--
Unigene21059_All	Keratin-associated protein 4-6 OS=Homo sapiens GN=KRTAP4-6 PE=2 SV=3

Unigene21074_All	--
Unigene21092_All	--
Unigene21226_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene21269_All	--
Unigene21311_All	Mucin-13 OS=Rattus norvegicus GN=Muc13 PE=2 SV=1
Unigene21313_All	--
Unigene21320_All	--
Unigene21340_All	--
Unigene21379_All	--
Unigene21390_All	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
Unigene21395_All	--
Unigene2140_All	--
Unigene21440_All	--
Unigene21479_All	--
Unigene21525_All	--
Unigene21535_All	--
Unigene21536_All	--
Unigene21544_All	--
Unigene21558_All	--
Unigene21560_All	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial OS=Homo sapiens GN=DHTKD1 PE=2 SV=2
Unigene21565_All	--
Unigene21577_All	--
Unigene21580_All	--
Unigene21581_All	--
Unigene21592_All	--
Unigene21593_All	--
Unigene21610_All	Regulating synaptic membrane exocytosis protein 2 OS=Rattus norvegicus GN=Rims2 PE=1 SV=1
Unigene21613_All	--
Unigene21621_All	--
Unigene21624_All	--
Unigene21635_All	--
Unigene21641_All	Tubulin alpha chain OS=Bombyx mori PE=2 SV=1
Unigene21644_All	--
Unigene21645_All	--
Unigene21650_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene21662_All	--
Unigene21664_All	--
Unigene21665_All	--

Unigene21668_All	--
Unigene21669_All	--
Unigene21674_All	--
Unigene21675_All	Potassium voltage-gated channel protein Shaw OS=Drosophila melanogaster GN=Shaw PE=2 SV=1
Unigene21676_All	Discoidin domain-containing receptor 2 OS=Homo sapiens GN=DDR2 PE=1 SV=2
Unigene2167_All	--
Unigene21687_All	Esterase FE4 OS=Myzus persicae PE=1 SV=1
Unigene21691_All	Uncharacterized protein F12A10.7 OS=Caenorhabditis elegans GN=F12A10.7 PE=4 SV=2
Unigene21698_All	--
Unigene21701_All	--
Unigene21708_All	--
Unigene21713_All	--
Unigene21717_All	--
Unigene21731_All	--
Unigene21736_All	--
Unigene21750_All	--
Unigene21767_All	--
Unigene21824_All	--
Unigene21831_All	--
Unigene21848_All	--
Unigene21858_All	--
Unigene21910_All	--
Unigene21972_All	--
Unigene21997_All	--
Unigene22022_All	Integrin alpha-PS2 OS=Drosophila melanogaster GN=if PE=1 SV=2
Unigene22056_All	--
Unigene22113_All	--
Unigene2211_All	--
Unigene22122_All	Uncharacterized protein C10orf95 OS=Homo sapiens GN=C10orf95 PE=2 SV=1
Unigene22187_All	--
Unigene22195_All	--
Unigene22225_All	--
Unigene22296_All	--
Unigene2232_All	--
Unigene22337_All	--
Unigene22352_All	--
Unigene22373_All	--

Unigene22374_All	--
Unigene2244_All	--
Unigene22468_All	Vasodilator-stimulated phosphoprotein OS=Mus musculus GN=Vasp PE=1 SV=4
Unigene22485_All	Neprilysin-1 OS=Caenorhabditis elegans GN=nep-1 PE=1 SV=3
Unigene22491_All	--
Unigene22493_All	Lysine-specific demethylase 6B OS=Mus musculus GN=Kdm6b PE=1 SV=1
Unigene22547_All	--
Unigene22602_All	--
Unigene22650_All	--
Unigene22680_All	Cytochrome P450 4g1 OS=Drosophila melanogaster GN=Cyp4g1 PE=2 SV=1
Unigene22710_All	--
Unigene22744_All	--
Unigene22813_All	--
Unigene2288_All	--
Unigene2290_All	--
Unigene23023_All	--
Unigene23047_All	--
Unigene23049_All	--
Unigene23064_All	--
Unigene23143_All	--
Unigene23162_All	--
Unigene23212_All	--
Unigene23238_All	--
Unigene23269_All	--
Unigene23284_All	--
Unigene23301_All	--
Unigene23336_All	--
Unigene23351_All	--
Unigene23360_All	--
Unigene23361_All	--
Unigene23368_All	--
Unigene23373_All	--
Unigene23377_All	--
Unigene23402_All	Formin-1 OS=Mus musculus GN=Fmn1 PE=1 SV=2
Unigene23425_All	Atherin OS=Homo sapiens GN=SAMD1 PE=1 SV=1
Unigene23431_All	Keratin, type I cytoskeletal 10 OS=Bos taurus GN=KRT10 PE=3 SV=1
Unigene23476_All	--
Unigene23488_All	--

Unigene23506_All	--
Unigene23510_All	--
Unigene23524_All	--
Unigene23529_All	--
Unigene23554_All	--
Unigene23556_All	--
Unigene23609_All	--
Unigene23610_All	--
Unigene23642_All	Craniofacial development protein 2 OS=Bos taurus GN=CFDP2 PE=1 SV=2
Unigene23678_All	--
Unigene2370_All	--
Unigene23724_All	--
Unigene23749_All	--
Unigene23764_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene23772_All	--
Unigene23794_All	Nostrin OS=Rattus norvegicus GN=Nostrin PE=2 SV=1
Unigene23800_All	--
Unigene23801_All	--
Unigene23831_All	--
Unigene23847_All	--
Unigene23877_All	--
Unigene23917_All	--
Unigene23964_All	--
Unigene24021_All	--
Unigene24089_All	--
Unigene24096_All	--
Unigene2409_All	--
Unigene240_All	--
Unigene24111_All	--
Unigene24114_All	--
Unigene24121_All	--
Unigene24128_All	--
Unigene24161_All	--
Unigene24201_All	--
Unigene24213_All	--
Unigene24241_All	--
Unigene24286_All	--
Unigene242_All	--
Unigene24304_All	--
Unigene24322_All	--

Unigene24326_All	--
Unigene24328_All	--
Unigene24344_All	--
Unigene2436_All	--
Unigene24377_All	--
Unigene24387_All	Endocuticle structural glycoprotein SgAbd-2 OS=Schistocerca gregaria PE=1 SV=1
Unigene24392_All	--
Unigene24393_All	--
Unigene243_All	Head-specific guanylate cyclase OS=Drosophila melanogaster GN=Gycalpha99B PE=2 SV=2
Unigene24410_All	--
Unigene24444_All	--
Unigene2444_All	--
Unigene24455_All	--
Unigene24457_All	--
Unigene24464_All	Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1
Unigene24471_All	--
Unigene24482_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene24483_All	Cuticle protein 19 OS=Locusta migratoria PE=1 SV=1
Unigene24511_All	--
Unigene24570_All	--
Unigene24592_All	--
Unigene24593_All	--
Unigene24630_All	--
Unigene24656_All	--
Unigene24660_All	--
Unigene24692_All	Probable cytochrome P450 303a1 OS=Drosophila melanogaster GN=Cyp303a1 PE=2 SV=1
Unigene2469_All	Dehydrogenase/reductase SDR family member 11 OS=Gallus gallus GN=DHRS11 PE=2 SV=1
Unigene24759_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene24781_All	--
Unigene24794_All	--
Unigene24827_All	--
Unigene24833_All	--
Unigene24834_All	--

Unigene2483_All	Circadian clock-controlled protein OS=Drosophila yakuba GN=anon-3B1.2 PE=3 SV=1
Unigene24842_All	Loricrin OS=Mus musculus GN=Lor PE=2 SV=2
Unigene24849_All	--
Unigene24856_All	--
Unigene24862_All	--
Unigene24885_All	--
Unigene24888_All	Astakine OS=Penaeus monodon PE=2 SV=1
Unigene24936_All	Inactive rhomboid protein 1 OS=Drosophila melanogaster GN=rho-5 PE=2 SV=1
Unigene24962_All	Chaoptin OS=Drosophila melanogaster GN=chp PE=1 SV=2
Unigene24995_All	--
Unigene2501_All	--
Unigene25033_All	Transcription initiation factor TFIID subunit 4 OS=Homo sapiens GN=TAF4 PE=1 SV=2
Unigene25036_All	--
Unigene25041_All	--
Unigene25042_All	--
Unigene25048_All	--
Unigene25050_All	--
Unigene25051_All	--
Unigene25079_All	Mucin-22 OS=Homo sapiens GN=MUC22 PE=1 SV=2
Unigene25102_All	Prolactin-releasing peptide receptor OS=Mus musculus GN=Prlhr PE=2 SV=2
Unigene25108_All	--
Unigene25123_All	Transposon TX1 uncharacterized 149 kDa protein OS=Xenopus laevis PE=4 SV=1
Unigene25132_All	--
Unigene25146_All	--
Unigene25162_All	--
Unigene25198_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene25200_All	--
Unigene25208_All	--
Unigene25211_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
Unigene2522_All	--
Unigene25230_All	Venom dipeptidyl peptidase 4 OS=Apis mellifera PE=1 SV=1
Unigene25238_All	--
Unigene2525_All	--
Unigene25276_All	Ethanolamine-phosphate phospho-lyase OS=Homo sapiens GN=AGXT2L1 PE=1 SV=1

Unigene25287_All	--
Unigene2530_All	Neuropeptide F OS=Locusta migratoria PE=1 SV=1
Unigene25311_All	--
Unigene25318_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene25342_All	--
Unigene25349_All	--
Unigene25446_All	Fucolectin OS=Anguilla anguilla PE=1 SV=1
Unigene25481_All	--
Unigene25501_All	--
Unigene25508_All	Sarcalumenin OS=Oryctolagus cuniculus GN=SRL PE=2 SV=1
Unigene2550_All	--
Unigene25522_All	Protein NPC2 homolog OS=Drosophila melanogaster GN=Npc2a PE=1 SV=1
Unigene25540_All	--
Unigene25550_All	CUB and sushi domain-containing protein 3 OS=Homo sapiens GN=CSMD3 PE=2 SV=3
Unigene25582_All	BTB/POZ domain-containing protein 6 OS=Homo sapiens GN=BTBD6 PE=1 SV=3
Unigene2558_All	Atherin OS=Oryctolagus cuniculus GN=SAMD1 PE=2 SV=1
Unigene25593_All	--
Unigene25602_All	--
Unigene25606_All	Histidine-rich glycoprotein OS=Plasmodium lophurae PE=4 SV=1
Unigene25607_All	--
Unigene25616_All	--
Unigene25639_All	--
Unigene25641_All	--
Unigene25642_All	--
Unigene25676_All	--
Unigene25730_All	Serine/arginine repetitive matrix protein 3 OS=Homo sapiens GN=SRRM3 PE=2 SV=4
Unigene25740_All	--
Unigene25756_All	--
Unigene25763_All	Ecto-NOX disulfide-thiol exchanger 2 OS=Homo sapiens GN=ENOX2 PE=1 SV=2
Unigene25765_All	--
Unigene25782_All	--
Unigene25824_All	--
Unigene25846_All	--
Unigene25872_All	Zinc finger protein jing homolog OS=Aedes aegypti GN=AAEL000263 PE=3

	SV=1
Unigene25886_All	Muscle LIM protein 1 OS=Drosophila melanogaster GN=Mlp60A PE=2 SV=1
Unigene25916_All	Glucose dehydrogenase [acceptor] OS=Drosophila melanogaster GN=Gld PE=3 SV=3
Unigene25926_All	--
Unigene25931_All	PH domain-containing protein DDB_G0275795 OS=Dictyostelium discoideum GN=DDB_G0275795 PE=4 SV=1
Unigene25954_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene25961_All	--
Unigene25968_All	SH3 and cysteine-rich domain-containing protein 3 OS=Xenopus tropicalis GN=stac3 PE=2 SV=1
Unigene25992_All	--
Unigene26015_All	Cytosolic carboxypeptidase NnaD OS=Drosophila melanogaster GN=NnaD PE=2 SV=2
Unigene26029_All	--
Unigene26046_All	--
Unigene26059_All	Thyroid transcription factor 1 OS=Canis familiaris GN=TITF1 PE=2 SV=1
Unigene26067_All	--
Unigene2606_All	Protein takeout OS=Drosophila melanogaster GN=to PE=2 SV=1
Unigene2608_All	--
Unigene26118_All	--
Unigene26143_All	--
Unigene26180_All	--
Unigene26197_All	Irregular chiasm C-roughest protein OS=Drosophila melanogaster GN=rst PE=2 SV=2
Unigene26202_All	--
Unigene26230_All	Rho GTPase-activating protein 18 OS=Homo sapiens GN=ARHGAP18 PE=1 SV=3
Unigene26233_All	Protein kinase C-binding protein NELL1 OS=Homo sapiens GN=NELL1 PE=1 SV=4
Unigene26246_All	--
Unigene26251_All	--
Unigene26311_All	--
Unigene26332_All	--
Unigene26355_All	Protein tipE OS=Drosophila melanogaster GN=tipE PE=2 SV=1
Unigene26358_All	--

Unigene26365_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene26386_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene26418_All	26S proteasome non-ATPase regulatory subunit 1 OS=Drosophila melanogaster GN=Rpn2 PE=1 SV=1
Unigene26430_All	--
Unigene26443_All	PDZ domain-containing protein 2 OS=Rattus norvegicus GN=Pdzd2 PE=1 SV=1
Unigene26447_All	--
Unigene26465_All	--
Unigene26469_All	--
Unigene26502_All	--
Unigene26535_All	--
Unigene26542_All	--
Unigene26546_All	--
Unigene26559_All	--
Unigene26592_All	--
Unigene26600_All	--
Unigene26604_All	Ryanodine receptor 44F OS=Drosophila melanogaster GN=Rya-r44F PE=1 SV=3
Unigene26618_All	--
Unigene26647_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene2665_All	--
Unigene26692_All	--
Unigene26698_All	Luciferin 4-monooxygenase OS=Luciola cruciata PE=1 SV=1
Unigene26708_All	--
Unigene2670_All	Lysine-specific demethylase 6B OS=Homo sapiens GN=KDM6B PE=1 SV=4
Unigene2675_All	Clavesin-2 OS=Mus musculus GN=Clvs2 PE=2 SV=1
Unigene26772_All	--
Unigene26784_All	--
Unigene26798_All	--
Unigene26835_All	--
Unigene26864_All	--
Unigene26880_All	Guanine nucleotide-binding protein subunit beta-like protein OS=Dictyostelium discoideum GN=gpbB PE=1 SV=2
Unigene2690_All	Protein scarlet OS=Drosophila melanogaster GN=st PE=1 SV=3
Unigene26914_All	--

Unigene2691_All	--
Unigene26932_All	--
Unigene2702_All	--
Unigene27058_All	--
Unigene27086_All	--
Unigene27132_All	--
Unigene27188_All	--
Unigene271_All	--
Unigene27278_All	--
Unigene27314_All	--
Unigene27324_All	Zinc finger homeobox protein 4 OS=Gallus gallus GN=ZFHX4 PE=2 SV=2
Unigene27328_All	Venom carboxylesterase-6 OS=Apis mellifera PE=2 SV=1
Unigene27344_All	Multiple epidermal growth factor-like domains protein 11 OS=Homo sapiens GN=MEGF11 PE=2 SV=3
Unigene27347_All	--
Unigene27357_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene27371_All	--
Unigene27400_All	Centrosomal protein of 104 kDa OS=Homo sapiens GN=CEP104 PE=1 SV=1
Unigene27401_All	--
Unigene27416_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
Unigene27437_All	--
Unigene27453_All	Serine/threonine-protein phosphatase 1 regulatory subunit 10 OS=Macaca mulatta GN=PPP1R10 PE=3 SV=1
Unigene2748_All	--
Unigene27509_All	Neprilysin OS=Oryctolagus cuniculus GN=MME PE=1 SV=2
Unigene27532_All	--
Unigene27536_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene27538_All	--
Unigene27544_All	--
Unigene27559_All	Endocuticle structural glycoprotein ABD-5 OS=Locusta migratoria PE=1 SV=1
Unigene27649_All	Chitinase-like protein Idgf4 OS=Glossina morsitans morsitans GN=Idgf4 PE=2 SV=1
Unigene27656_All	--
Unigene27674_All	--
Unigene27699_All	Salivary glue protein Sgs-3 OS=Drosophila melanogaster GN=Sgs3 PE=2 SV=1

Unigene2770_All	--
Unigene27715_All	--
Unigene27725_All	--
Unigene27750_All	--
Unigene27787_All	--
Unigene27796_All	--
Unigene27817_All	--
Unigene27830_All	--
Unigene2783_All	Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2
Unigene27857_All	Serpin B12 OS=Mus musculus GN=Serpinb12 PE=2 SV=1
Unigene27864_All	TLR4 interactor with leucine rich repeats OS=Homo sapiens GN=TRIL PE=1 SV=2
Unigene27881_All	--
Unigene27882_All	--
Unigene27893_All	--
Unigene27896_All	--
Unigene27932_All	--
Unigene27947_All	--
Unigene27957_All	--
Unigene27965_All	--
Unigene2798_All	--
Unigene28013_All	--
Unigene2802_All	Cuticle protein 3 OS=Lonomia obliqua PE=1 SV=2
Unigene28061_All	--
Unigene2812_All	--
Unigene28130_All	--
Unigene28142_All	--
Unigene28178_All	--
Unigene28210_All	--
Unigene28272_All	--
Unigene2829_All	ATP-binding cassette sub-family C member Sur OS=Drosophila melanogaster GN=Sur PE=1 SV=4
Unigene28300_All	--
Unigene28322_All	--
Unigene2832_All	--
Unigene28394_All	--
Unigene28407_All	--
Unigene28469_All	--
Unigene285_All	Glycoprotein 3-alpha-L-fucosyltransferase A OS=Drosophila melanogaster GN=FucTA PE=1 SV=2
Unigene28677_All	--

Unigene28695_All	--
Unigene28698_All	--
Unigene28748_All	--
Unigene28794_All	--
Unigene28827_All	Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=2
Unigene28870_All	--
Unigene2887_All	--
Unigene28901_All	--
Unigene28912_All	--
Unigene28915_All	--
Unigene28924_All	--
Unigene2892_All	--
Unigene28949_All	--
Unigene28962_All	--
Unigene28971_All	--
Unigene28973_All	--
Unigene28980_All	--
Unigene28986_All	--
Unigene29007_All	--
Unigene29013_All	--
Unigene29014_All	--
Unigene29019_All	--
Unigene29021_All	--
Unigene29023_All	--
Unigene29057_All	--
Unigene29066_All	--
Unigene29074_All	--
Unigene29087_All	Cytochrome b5 type B OS=Mus musculus GN=Cyb5b PE=1 SV=1
Unigene29102_All	--
Unigene29106_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene29107_All	--
Unigene29108_All	--
Unigene29122_All	--
Unigene29125_All	--
Unigene29127_All	--
Unigene29139_All	--
Unigene29142_All	--
Unigene29149_All	--
Unigene29157_All	--

Unigene2915_All	PI-PLC X domain-containing protein 1 OS=Mus musculus GN=Plcxd1 PE=2 SV=1
Unigene29162_All	--
Unigene29167_All	--
Unigene29170_All	--
Unigene29174_All	--
Unigene29178_All	--
Unigene29183_All	--
Unigene29191_All	Transcription factor SPT20 homolog OS=Dictyostelium discoideum GN=DDB_G0280065 PE=3 SV=1
Unigene29196_All	--
Unigene29203_All	--
Unigene29212_All	Forkhead box protein G1 OS=Epomophorus gambianus GN=FOXG1 PE=3 SV=1
Unigene29216_All	--
Unigene29223_All	Chaperone activity of bc1 complex-like, mitochondrial OS=Danio rerio GN=adck3 PE=2 SV=1
Unigene29254_All	H/ACA ribonucleoprotein complex subunit 1 OS=Danio rerio GN=gar1 PE=2 SV=1
Unigene29256_All	--
Unigene29263_All	--
Unigene29269_All	--
Unigene29272_All	--
Unigene29293_All	--
Unigene2929_All	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3
Unigene29303_All	Cytochrome P450 4C1 OS=Blaberus discoidalis GN=CYP4C1 PE=2 SV=1
Unigene29306_All	Tubby-related protein 4 OS=Mus musculus GN=Tulp4 PE=2 SV=1
Unigene29307_All	--
Unigene29308_All	--
Unigene29312_All	Putative uncharacterized protein FLJ37770 OS=Homo sapiens PE=5 SV=1
Unigene29327_All	--
Unigene29355_All	--
Unigene2935_All	--
Unigene29364_All	--
Unigene29376_All	--
Unigene29421_All	EGF-like domain-containing protein 2 OS=Lottia gigantea PE=1 SV=1
Unigene29438_All	--
Unigene29446_All	--

Unigene29448_All	--
Unigene29477_All	--
Unigene29478_All	--
Unigene29499_All	--
Unigene29513_All	--
Unigene29553_All	--
Unigene29572_All	Endocuticle structural glycoprotein SgAbd-5 OS=Schistocerca gregaria PE=1 SV=1
Unigene29586_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene29602_All	Dopamine N-acetyltransferase OS=Drosophila melanogaster GN=Dat PE=1 SV=1
Unigene29662_All	--
Unigene29672_All	Probable phospholipase A1 magnifin OS=Vespa magnifica PE=1 SV=1
Unigene29738_All	--
Unigene29756_All	--
Unigene29758_All	--
Unigene29762_All	Dehydrogenase/reductase SDR family member 11 OS=Gallus gallus GN=DHRS11 PE=2 SV=1
Unigene29830_All	--
Unigene29911_All	--
Unigene29927_All	--
Unigene29930_All	--
Unigene29983_All	--
Unigene30005_All	--
Unigene3000_All	--
Unigene30061_All	--
Unigene30111_All	Uncharacterized protein KIAA1586 OS=Homo sapiens GN=KIAA1586 PE=2 SV=2
Unigene30112_All	--
Unigene30168_All	--
Unigene3017_All	--
Unigene30240_All	--
Unigene30288_All	--
Unigene30296_All	--
Unigene30372_All	Serine/arginine repetitive matrix protein 3 OS=Homo sapiens GN=SRRM3 PE=2 SV=4
Unigene30377_All	--
Unigene30425_All	--
Unigene30482_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4

Unigene30561_All	--
Unigene30570_All	--
Unigene30585_All	--
Unigene30603_All	--
Unigene30618_All	--
Unigene30700_All	--
Unigene30707_All	--
Unigene30714_All	--
Unigene30738_All	--
Unigene3076_All	NADH-ubiquinone oxidoreductase chain 4 OS=Locusta migratoria GN=ND4 PE=3 SV=1
Unigene30771_All	--
Unigene30778_All	--
Unigene3078_All	--
Unigene30802_All	--
Unigene30843_All	--
Unigene30860_All	--
Unigene30921_All	--
Unigene30948_All	--
Unigene30976_All	--
Unigene30980_All	--
Unigene31062_All	--
Unigene31063_All	--
Unigene31111_All	--
Unigene31169_All	--
Unigene31228_All	--
Unigene31240_All	--
Unigene31300_All	--
Unigene31307_All	--
Unigene31346_All	--
Unigene31351_All	--
Unigene31368_All	--
Unigene31382_All	--
Unigene31387_All	--
Unigene31400_All	Growth hormone secretagogue receptor type 1 OS=Homo sapiens GN=GHSR PE=1 SV=1
Unigene31402_All	--
Unigene31422_All	--
Unigene31460_All	--
Unigene31466_All	--
Unigene31470_All	--
Unigene31471_All	--

Unigene31475_All	--
Unigene31515_All	--
Unigene31518_All	--
Unigene31555_All	--
Unigene31566_All	--
Unigene31576_All	--
Unigene31632_All	Fatty acyl-CoA reductase 2 OS=Mus musculus GN=Far2 PE=2 SV=1
Unigene31717_All	--
Unigene31729_All	--
Unigene31762_All	--
Unigene31768_All	--
Unigene31777_All	--
Unigene31781_All	--
Unigene31790_All	--
Unigene31801_All	--
Unigene31805_All	--
Unigene3181_All	--
Unigene31824_All	--
Unigene31843_All	--
Unigene3184_All	--
Unigene31860_All	--
Unigene31889_All	--
Unigene31895_All	--
Unigene31909_All	--
Unigene31979_All	--
Unigene319_All	--
Unigene32001_All	--
Unigene32011_All	--
Unigene3202_All	--
Unigene32059_All	--
Unigene32073_All	--
Unigene32091_All	--
Unigene32098_All	--
Unigene32100_All	--
Unigene32117_All	--
Unigene32227_All	--
Unigene32237_All	Retrovirus-related Pol polyprotein from transposon 297 OS=Drosophila melanogaster GN=pol PE=4 SV=1
Unigene32275_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2

Unigene32283_All	Salivary glue protein Sgs-3 OS=Drosophila yakuba GN=Sgs3 PE=2 SV=3
Unigene32323_All	--
Unigene32326_All	--
Unigene32339_All	--
Unigene32395_All	--
Unigene32402_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene32413_All	--
Unigene32492_All	Disintegrin and metalloproteinase domain-containing protein 22 OS=Homo sapiens GN=ADAM22 PE=1 SV=1
Unigene32560_All	Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2
Unigene32568_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2
Unigene3256_All	--
Unigene32598_All	Cuticle protein 19 OS=Locusta migratoria PE=1 SV=1
Unigene32600_All	--
Unigene32610_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene32619_All	Protein sprouty OS=Drosophila melanogaster GN=sty PE=2 SV=2
Unigene32636_All	Probable serine/threonine-protein kinase DDB_G0284491 OS=Dictyostelium discoideum GN=DDB_G0284491 PE=3 SV=1
Unigene32645_All	--
Unigene32660_All	--
Unigene32672_All	--
Unigene32691_All	Sodium channel protein para OS=Drosophila melanogaster GN=para PE=2 SV=3
Unigene32694_All	--
Unigene32706_All	--
Unigene32738_All	--
Unigene32752_All	--
Unigene32760_All	--
Unigene32770_All	--
Unigene32814_All	--
Unigene32826_All	--
Unigene32832_All	--
Unigene32839_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene32841_All	--
Unigene32876_All	--

Unigene32883_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
Unigene3288_All	--
Unigene32894_All	--
Unigene32899_All	--
Unigene32903_All	--
Unigene32957_All	--
Unigene32965_All	--
Unigene33028_All	--
Unigene33050_All	--
Unigene33070_All	--
Unigene33079_All	--
Unigene33088_All	Centrosomal protein of 104 kDa OS=Mus musculus GN=Cep104 PE=1 SV=1
Unigene33119_All	--
Unigene33145_All	--
Unigene33169_All	Cubilin OS=Rattus norvegicus GN=Cubn PE=1 SV=2
Unigene3317_All	--
Unigene33188_All	--
Unigene33196_All	--
Unigene33200_All	--
Unigene33266_All	--
Unigene33274_All	--
Unigene33286_All	--
Unigene33298_All	--
Unigene33317_All	--
Unigene33338_All	--
Unigene33346_All	--
Unigene33365_All	--
Unigene33371_All	--
Unigene33397_All	--
Unigene33402_All	--
Unigene33405_All	--
Unigene33412_All	Atherin OS=Homo sapiens GN=SAMD1 PE=1 SV=1
Unigene33449_All	--
Unigene33457_All	--
Unigene33489_All	--
Unigene33497_All	--
Unigene33543_All	--
Unigene33552_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene33573_All	--
Unigene3357_All	--

Unigene33595_All	--
Unigene335_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene33604_All	--
Unigene33609_All	--
Unigene33632_All	--
Unigene33637_All	--
Unigene33645_All	--
Unigene33658_All	--
Unigene33667_All	--
Unigene33683_All	Regulator of G-protein signaling 20 OS=Homo sapiens GN=RGS20 PE=1 SV=4
Unigene33705_All	--
Unigene33707_All	--
Unigene33711_All	--
Unigene33757_All	--
Unigene33796_All	--
Unigene33807_All	--
Unigene33812_All	--
Unigene33821_All	--
Unigene33822_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene33825_All	--
Unigene33862_All	Muscle-specific protein 20 OS=Drosophila melanogaster GN=Mp20 PE=2 SV=2
Unigene33888_All	--
Unigene33917_All	--
Unigene33922_All	Heparan sulfate 2-O-sulfotransferase pipe OS=Drosophila melanogaster GN=pip PE=1 SV=1
Unigene33933_All	Inhibin beta chain OS=Drosophila melanogaster GN=Actbeta PE=2 SV=2
Unigene33936_All	Paramyosin (Fragment) OS=Dermatophagoides farinae PE=1 SV=1
Unigene34057_All	--
Unigene34072_All	--
Unigene34076_All	Uncharacterized protein K02A2.6 OS=Caenorhabditis elegans GN=K02A2.6 PE=2 SV=1
Unigene34107_All	--
Unigene34151_All	--
Unigene34173_All	--
Unigene34214_All	Choline dehydrogenase, mitochondrial OS=Homo sapiens GN=CHDH PE=2 SV=2
Unigene34216_All	--

Unigene34250_All	--
Unigene34299_All	Suppressor of tumorigenicity 14 protein OS=Homo sapiens GN=ST14 PE=1 SV=2
Unigene34317_All	--
Unigene34365_All	--
Unigene34396_All	--
Unigene34412_All	--
Unigene34448_All	--
Unigene34526_All	--
Unigene34614_All	--
Unigene34655_All	--
Unigene34748_All	--
Unigene34750_All	Cuticle protein 19 OS=Locusta migratoria PE=1 SV=1
Unigene34755_All	--
Unigene34797_All	--
Unigene34801_All	Regucalcin OS=Mus musculus GN=Rgn PE=1 SV=1
Unigene34819_All	--
Unigene34839_All	--
Unigene34890_All	--
Unigene34898_All	--
Unigene34913_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene34916_All	--
Unigene34921_All	Salivary glue protein Sgs-3 OS=Drosophila erecta GN=Sgs3 PE=2 SV=3
Unigene34944_All	--
Unigene34964_All	--
Unigene34993_All	--
Unigene34994_All	--
Unigene35005_All	Uncharacterized protein C10orf95 OS=Homo sapiens GN=C10orf95 PE=2 SV=1
Unigene35011_All	--
Unigene35031_All	--
Unigene35037_All	--
Unigene35054_All	--
Unigene35127_All	--
Unigene35165_All	--
Unigene35166_All	--
Unigene35171_All	--
Unigene35177_All	Flexible cuticle protein 12 OS=Hyalophora cecropia GN=CP12 PE=2 SV=1
Unigene35209_All	--

Unigene35221_All	--
Unigene35263_All	Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2
Unigene35278_All	--
Unigene35409_All	Vascular endothelial growth factor A OS=Mesocricetus auratus GN=VEGFA PE=2 SV=1
Unigene35411_All	--
Unigene35439_All	--
Unigene35444_All	--
Unigene35452_All	--
Unigene3546_All	--
Unigene35516_All	--
Unigene35557_All	--
Unigene35567_All	--
Unigene35580_All	--
Unigene35586_All	--
Unigene35676_All	--
Unigene35710_All	--
Unigene35724_All	--
Unigene35836_All	--
Unigene35864_All	--
Unigene36180_All	--
Unigene36183_All	Actin, muscle OS=Manduca sexta PE=2 SV=1
Unigene36189_All	--
Unigene36195_All	Protein 4.1 homolog OS=Drosophila melanogaster GN=cora PE=1 SV=1
Unigene36231_All	--
Unigene36278_All	--
Unigene36283_All	--
Unigene36328_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene36330_All	--
Unigene36354_All	--
Unigene36378_All	--
Unigene36410_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene36435_All	Glutamate receptor 4 OS=Mus musculus GN=Gria4 PE=1 SV=2
Unigene36469_All	--
Unigene36510_All	--
Unigene36547_All	Uncharacterized protein C10orf95 OS=Homo sapiens GN=C10orf95 PE=2 SV=1
Unigene36555_All	--
Unigene36576_All	--

Unigene36583_All	--
Unigene36599_All	--
Unigene36600_All	--
Unigene36610_All	--
Unigene36612_All	--
Unigene36619_All	Cytochrome P450 4C1 OS=Blaberus discoidalis GN=CYP4C1 PE=2 SV=1
Unigene36627_All	--
Unigene36633_All	--
Unigene36638_All	--
Unigene36648_All	--
Unigene36658_All	--
Unigene36706_All	Protein scarlet OS=Drosophila melanogaster GN=st PE=1 SV=3
Unigene36713_All	--
Unigene36714_All	--
Unigene36739_All	Tetraspanin-17 OS=Caenorhabditis elegans GN=tsp-17 PE=2 SV=3
Unigene36741_All	--
Unigene36743_All	--
Unigene36748_All	--
Unigene36756_All	Neprilysin OS=Oryctolagus cuniculus GN=MME PE=1 SV=2
Unigene36760_All	--
Unigene36771_All	--
Unigene36776_All	Keratin-associated protein 19-2 OS=Mus musculus GN=Krtap19-2 PE=2 SV=1
Unigene36781_All	--
Unigene36788_All	Serine--pyruvate aminotransferase, mitochondrial OS=Mus musculus GN=Agxt PE=1 SV=2
Unigene36816_All	Ras-related protein Rab-28 OS=Mus musculus GN=Rab28 PE=2 SV=1
Unigene36840_All	--
Unigene36871_All	--
Unigene36876_All	Myosin heavy chain, skeletal muscle, adult OS=Gallus gallus PE=1 SV=4
Unigene36884_All	--
Unigene36905_All	--
Unigene36910_All	--
Unigene36927_All	--
Unigene36965_All	--
Unigene37023_All	--
Unigene3703_All	--
Unigene37074_All	--

Unigene3708_All	--
Unigene37145_All	--
Unigene37182_All	Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3
Unigene37204_All	--
Unigene37211_All	--
Unigene37319_All	--
Unigene37336_All	--
Unigene37392_All	--
Unigene37447_All	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma suspectum PE=1 SV=3
Unigene37464_All	--
Unigene37580_All	Cuticle protein 21.3 OS=Locusta migratoria PE=1 SV=1
Unigene37581_All	--
Unigene37634_All	--
Unigene37647_All	--
Unigene37675_All	--
Unigene3768_All	--
Unigene37733_All	--
Unigene37792_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene37794_All	--
Unigene37882_All	--
Unigene37954_All	--
Unigene37_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene38002_All	--
Unigene38014_All	--
Unigene38023_All	--
Unigene38033_All	--
Unigene38051_All	--
Unigene38058_All	--
Unigene38087_All	--
Unigene38184_All	--
Unigene38241_All	--
Unigene38244_All	--
Unigene38246_All	--
Unigene38257_All	--
Unigene38271_All	--
Unigene38291_All	--
Unigene38302_All	--
Unigene38330_All	--

Unigene38385_All	--
Unigene38433_All	--
Unigene38434_All	--
Unigene38454_All	--
Unigene38465_All	--
Unigene38499_All	--
Unigene38509_All	--
Unigene38522_All	--
Unigene38541_All	--
Unigene38562_All	--
Unigene38579_All	--
Unigene38585_All	--
Unigene38606_All	--
Unigene38613_All	--
Unigene38644_All	--
Unigene38661_All	--
Unigene38719_All	--
Unigene38765_All	--
Unigene38856_All	--
Unigene38914_All	--
Unigene38920_All	--
Unigene38928_All	--
Unigene38965_All	--
Unigene38988_All	--
Unigene38995_All	--
Unigene38999_All	--
Unigene39000_All	Cuticle protein 6.4 OS=Locusta migratoria PE=1 SV=1
Unigene39003_All	--
Unigene39004_All	--
Unigene39046_All	Potassium voltage-gated channel protein Shal OS=Drosophila melanogaster GN=Shal PE=1 SV=2
Unigene39080_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene39085_All	--
Unigene39099_All	--
Unigene39124_All	--
Unigene39143_All	--
Unigene3914_All	--
Unigene39151_All	--
Unigene3916_All	--
Unigene39185_All	--

Unigene39194_All	--
Unigene39199_All	--
Unigene3922_All	--
Unigene39253_All	--
Unigene39275_All	--
Unigene39288_All	--
Unigene39304_All	--
Unigene39341_All	--
Unigene39352_All	--
Unigene39367_All	--
Unigene39392_All	--
Unigene39407_All	--
Unigene39459_All	--
Unigene39462_All	--
Unigene39467_All	--
Unigene3947_All	--
Unigene39505_All	--
Unigene39514_All	--
Unigene39526_All	--
Unigene39555_All	Larval cuticle protein F1 OS=Tenebrio molitor PE=1 SV=1
Unigene39572_All	Spidroin-2 (Fragment) OS=Nephila clavipes PE=2 SV=1
Unigene39597_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
Unigene39598_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
Unigene39635_All	--
Unigene39660_All	--
Unigene39688_All	--
Unigene39691_All	--
Unigene39734_All	--
Unigene39759_All	Fatty acid synthase OS=Gallus gallus GN=FASN PE=1 SV=5
Unigene39760_All	Fatty acid synthase OS=Gallus gallus GN=FASN PE=1 SV=5
Unigene3980_All	--
Unigene39815_All	--
Unigene39880_All	--
Unigene39958_All	--
Unigene39966_All	--
Unigene39980_All	Matrix metalloproteinase-24 OS=Homo sapiens GN=MMP24 PE=2 SV=1
Unigene40004_All	--

Unigene40012_All	Microtubule-associated protein futsch OS=Drosophila melanogaster GN=futsch PE=1 SV=4
Unigene40050_All	--
Unigene40064_All	TPPP family protein CG4893 OS=Drosophila melanogaster GN=CG4893 PE=2 SV=1
Unigene40071_All	Lachesin OS=Drosophila melanogaster GN=Lac PE=2 SV=2
Unigene40075_All	Ubiquitin-conjugating enzyme E2Q-like protein CG4502 OS=Drosophila melanogaster GN=CG4502 PE=2 SV=1
Unigene40080_All	--
Unigene40101_All	--
Unigene40112_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
Unigene40113_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
Unigene40119_All	--
Unigene40137_All	C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8 OS=Homo sapiens GN=CPAMD8 PE=1 SV=2
Unigene40148_All	--
Unigene40153_All	--
Unigene40159_All	--
Unigene4022_All	--
Unigene40232_All	Sarcosine dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Sardh PE=1 SV=2
Unigene40243_All	--
Unigene40246_All	Lysocardiolipin acyltransferase 1 OS=Homo sapiens GN=LCLAT1 PE=1 SV=1
Unigene40322_All	--
Unigene40330_All	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2
Unigene40338_All	--
Unigene40342_All	--
Unigene40347_All	Protein piccolo OS=Mus musculus GN=Pclo PE=1 SV=4
Unigene40351_All	Major facilitator superfamily domain-containing protein 6-A OS=Danio rerio GN=mfsd6a PE=3 SV=1
Unigene40354_All	--
Unigene40355_All	Organic cation transporter protein OS=Drosophila melanogaster GN=Orct PE=1 SV=1
Unigene4036_All	Espin OS=Mus musculus GN=Espn PE=1 SV=2
Unigene40387_All	--
Unigene40391_All	--
Unigene40395_All	Fatty acid-binding protein, muscle OS=Locusta migratoria PE=1 SV=2

Unigene40405_All	Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2
Unigene40409_All	Probable serine/threonine-protein kinase clkA OS=Dictyostelium discoideum GN=clkA PE=3 SV=1
Unigene40422_All	Pro-resilin OS=Drosophila melanogaster GN=resilin PE=1 SV=1
Unigene40438_All	Organic solute transporter alpha-like protein OS=Drosophila melanogaster GN=CG6836 PE=2 SV=1
Unigene40439_All	--
Unigene40456_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene40464_All	--
Unigene4046_All	--
Unigene4048_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene40500_All	Dihydrodiol dehydrogenase 3 OS=Bos taurus PE=2 SV=1
Unigene40530_All	Acetylcholine receptor subunit alpha-L1 OS=Schistocerca gregaria PE=2 SV=1
Unigene40536_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene40560_All	Protein shisa-4 OS=Homo sapiens GN=SHISA4 PE=2 SV=3
Unigene40590_All	--
Unigene40596_All	--
Unigene40614_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene40628_All	--
Unigene40637_All	--
Unigene40686_All	--
Unigene40689_All	Carbonic anhydrase-related protein 10 OS=Pongo abelii GN=CA10 PE=2 SV=1
Unigene40693_All	--
Unigene40706_All	--
Unigene40710_All	Homeobox protein prospero OS=Drosophila melanogaster GN=pros PE=1 SV=3
Unigene40726_All	--
Unigene4073_All	B-cell receptor CD22 OS=Mus musculus GN=Cd22 PE=1 SV=1
Unigene40762_All	--
Unigene40777_All	--
Unigene40785_All	--
Unigene4080_All	--
Unigene4081_All	--

Unigene40825_All	Dipeptidase 2 OS=Rattus norvegicus GN=Dpep2 PE=2 SV=1
Unigene40830_All	General transcription factor II-I repeat domain-containing protein 2A OS=Homo sapiens GN=GTF2IRD2 PE=2 SV=2
Unigene40841_All	--
Unigene40843_All	--
Unigene40846_All	Neural cell adhesion molecule 1-B OS=Xenopus laevis GN=ncam1-b PE=2 SV=1
Unigene4084_All	--
Unigene40852_All	--
Unigene40866_All	--
Unigene408_All	Scavenger receptor class B member 1 OS=Rattus norvegicus GN=Scarb1 PE=1 SV=1
Unigene40910_All	--
Unigene40920_All	Splicing factor 3A subunit 2 OS=Mus musculus GN=Sf3a2 PE=2 SV=2
Unigene40971_All	--
Unigene40984_All	--
Unigene4099_All	--
Unigene41004_All	--
Unigene41027_All	--
Unigene41031_All	--
Unigene41046_All	--
Unigene41052_All	--
Unigene41059_All	--
Unigene41086_All	ETS domain-containing protein Elk-3 OS=Homo sapiens GN=ELK3 PE=1 SV=2
Unigene41089_All	--
Unigene4108_All	--
Unigene41096_All	--
Unigene41130_All	--
Unigene41131_All	--
Unigene41133_All	--
Unigene41141_All	--
Unigene41152_All	--
Unigene4115_All	--
Unigene41161_All	Inactive pancreatic lipase-related protein 1 OS=Homo sapiens GN=PNLIPRP1 PE=1 SV=1
Unigene4117_All	--
Unigene41228_All	--
Unigene41236_All	Cytochrome P450 4g15 OS=Drosophila melanogaster GN=Cyp4g15 PE=2 SV=1

Unigene41238_All	Prohormone-4 OS=Apis mellifera PE=1 SV=1
Unigene4123_All	Neprilysin-2 OS=Caenorhabditis elegans GN=nep-2 PE=1 SV=2
Unigene41256_All	Neurotrimin OS=Rattus norvegicus GN=Ntm PE=1 SV=1
Unigene41298_All	--
Unigene41311_All	--
Unigene41315_All	--
Unigene41408_All	--
Unigene41420_All	--
Unigene41435_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene41441_All	--
Unigene41462_All	--
Unigene41485_All	--
Unigene41500_All	--
Unigene41556_All	--
Unigene41579_All	Adenylate cyclase, terminal-differentiation specific OS=Dictyostelium discoideum GN=acrA PE=1 SV=1
Unigene41586_All	--
Unigene41606_All	--
Unigene41617_All	ATP-binding cassette sub-family G member 1 OS=Homo sapiens GN=ABCG1 PE=2 SV=3
Unigene4161_All	--
Unigene41633_All	--
Unigene41660_All	--
Unigene41673_All	--
Unigene4171_All	--
Unigene417_All	Band 7 protein AGAP004871 OS=Anopheles gambiae GN=AGAP004871 PE=3 SV=3
Unigene41808_All	--
Unigene41821_All	Transcription initiation factor TFIID subunit 4 OS=Homo sapiens GN=TAF4 PE=1 SV=2
Unigene41874_All	--
Unigene41900_All	--
Unigene41976_All	--
Unigene41995_All	--
Unigene42022_All	--
Unigene42109_All	--
Unigene42123_All	--
Unigene42124_All	--
Unigene42159_All	--
Unigene42165_All	--

Unigene42171_All	--
Unigene42187_All	--
Unigene42215_All	Cuticle protein 8 OS=Locusta migratoria PE=1 SV=1
Unigene4223_All	--
Unigene42271_All	--
Unigene42272_All	Ankyrin repeat and death domain-containing protein 1A OS=Homo sapiens GN=ANKDD1A PE=2 SV=2
Unigene42292_All	--
Unigene42296_All	--
Unigene42308_All	--
Unigene42311_All	Protein yellow OS=Drosophila subobscura GN=y PE=3 SV=1
Unigene42325_All	--
Unigene42330_All	Rhomboid-like protease 5 OS=Toxoplasma gondii GN=ROM5 PE=1 SV=1
Unigene42342_All	--
Unigene42352_All	--
Unigene42399_All	--
Unigene42420_All	Tyrosine-protein phosphatase non-receptor type 23 (Fragment) OS=Rattus norvegicus GN=Ptpn23 PE=1 SV=2
Unigene42423_All	--
Unigene4242_All	--
Unigene42447_All	Techylectin-5B OS=Tachypleus tridentatus PE=1 SV=1
Unigene42517_All	--
Unigene42535_All	Neuroblastoma suppressor of tumorigenicity 1 OS=Danio rerio GN=nbl1 PE=2 SV=1
Unigene4253_All	--
Unigene42564_All	--
Unigene42603_All	ADP,ATP carrier protein 2 OS=Anopheles gambiae GN=AGAP002358 PE=3 SV=2
Unigene42604_All	--
Unigene42613_All	Salivary glue protein Sgs-3 OS=Drosophila erecta GN=Sgs3 PE=2 SV=3
Unigene42651_All	--
Unigene42655_All	--
Unigene42661_All	--
Unigene42671_All	--
Unigene42679_All	--
Unigene42688_All	--
Unigene42705_All	--
Unigene42718_All	--

Unigene4271_All	--
Unigene4272_All	YLP motif-containing protein 1 OS=Mus musculus GN=Ylpm1 PE=2 SV=2
Unigene4274_All	--
Unigene42755_All	--
Unigene42769_All	Cytochrome P450 4g15 OS=Drosophila melanogaster GN=Cyp4g15 PE=2 SV=1
Unigene42790_All	--
Unigene4280_All	--
Unigene42829_All	--
Unigene4282_All	--
Unigene42842_All	--
Unigene4284_All	Loricrin OS=Homo sapiens GN=LOR PE=1 SV=2
Unigene4286_All	--
Unigene42876_All	--
Unigene42890_All	Mariner Mos1 transposase OS=Drosophila mauritiana GN=mariner\T PE=1 SV=1
Unigene42899_All	--
Unigene42905_All	--
Unigene4291_All	--
Unigene4293_All	Protease inhibitors OS=Locusta migratoria PE=1 SV=2
Unigene42990_All	--
Unigene4302_All	--
Unigene43032_All	--
Unigene43048_All	--
Unigene430_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene4310_All	--
Unigene4313_All	--
Unigene4316_All	--
Unigene43170_All	--
Unigene43176_All	--
Unigene4319_All	--
Unigene43221_All	--
Unigene4328_All	--
Unigene43298_All	--
Unigene4329_All	--
Unigene43303_All	Proto-oncogene tyrosine-protein kinase receptor Ret OS=Mus musculus GN=Ret PE=1 SV=2
Unigene4331_All	--
Unigene4332_All	--

Unigene4341_All	--
Unigene43432_All	--
Unigene4350_All	Eclosion hormone OS=Bombyx mori PE=1 SV=2
Unigene43529_All	--
Unigene43540_All	--
Unigene4359_All	--
Unigene43607_All	--
Unigene43634_All	--
Unigene4365_All	Pro-resilin OS=Drosophila melanogaster GN=resilin PE=1 SV=1
Unigene4370_All	--
Unigene43720_All	Uncharacterized protein PF11_0207 OS=Plasmodium falciparum (isolate 3D7) GN=PF11_0207 PE=4 SV=2
Unigene43769_All	--
Unigene43770_All	--
Unigene43775_All	--
Unigene43789_All	--
Unigene43793_All	--
Unigene43822_All	--
Unigene43832_All	--
Unigene43847_All	--
Unigene4384_All	--
Unigene43852_All	Lysyl oxidase homolog 2B OS=Danio rerio GN=loxl2b PE=2 SV=1
Unigene43916_All	Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=1 SV=3
Unigene43919_All	--
Unigene4394_All	--
Unigene43950_All	--
Unigene43964_All	--
Unigene43997_All	--
Unigene4399_All	--
Unigene44000_All	--
Unigene4401_All	--
Unigene44020_All	--
Unigene44022_All	Adenosine deaminase OS=Xenopus laevis GN=ada PE=2 SV=1
Unigene44023_All	--
Unigene4402_All	--
Unigene44052_All	--
Unigene44055_All	--
Unigene44061_All	--

Unigene44070_All	Excitatory amino acid transporter 2 OS=Rattus norvegicus GN=Slc1a2 PE=1 SV=2
Unigene4407_All	WNT1-inducible-signaling pathway protein 1 OS=Homo sapiens GN=WISP1 PE=1 SV=1
Unigene44081_All	Excitatory amino acid transporter 2 OS=Homo sapiens GN=SLC1A2 PE=1 SV=2
Unigene44085_All	--
Unigene44086_All	--
Unigene44090_All	--
Unigene44103_All	--
Unigene44116_All	--
Unigene44122_All	--
Unigene4412_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2
Unigene44137_All	--
Unigene44145_All	--
Unigene44149_All	--
Unigene44150_All	--
Unigene44158_All	--
Unigene44166_All	--
Unigene44174_All	--
Unigene44177_All	--
Unigene44179_All	--
Unigene44184_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene44193_All	--
Unigene44194_All	--
Unigene44209_All	--
Unigene4421_All	--
Unigene44226_All	--
Unigene4424_All	--
Unigene442_All	Mucin-22 OS=Homo sapiens GN=MUC22 PE=1 SV=2
Unigene44317_All	--
Unigene4432_All	--
Unigene4436_All	--
Unigene44378_All	--
Unigene4441_All	--
Unigene44438_All	--
Unigene44465_All	--
Unigene44468_All	--
Unigene44564_All	--
Unigene44737_All	--

Unigene44782_All	--
Unigene44788_All	--
Unigene447_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene44843_All	--
Unigene44848_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
Unigene44857_All	--
Unigene44882_All	--
Unigene44941_All	--
Unigene44968_All	--
Unigene449_All	--
Unigene45059_All	--
Unigene45110_All	--
Unigene45124_All	--
Unigene45187_All	--
Unigene45188_All	Dehydrogenase/reductase SDR family member 11 OS=Mus musculus GN=Dhrs11 PE=2 SV=1
Unigene45219_All	Period circadian protein (Fragment) OS=Drosophila ananassae GN=per PE=3 SV=1
Unigene4523_All	--
Unigene45271_All	--
Unigene45346_All	--
Unigene45364_All	--
Unigene45373_All	--
Unigene45404_All	--
Unigene45429_All	--
Unigene4542_All	--
Unigene45472_All	--
Unigene45499_All	--
Unigene45524_All	--
Unigene45533_All	--
Unigene45555_All	--
Unigene45577_All	--
Unigene45581_All	--
Unigene45627_All	--
Unigene45628_All	Keratin-3, type I cytoskeletal 51 kDa OS=Xenopus laevis PE=2 SV=1
Unigene45680_All	--
Unigene45687_All	--
Unigene45699_All	Atherin OS=Oryctolagus cuniculus GN=SAMD1 PE=2 SV=1
Unigene45711_All	--

Unigene45718_All	--
Unigene45766_All	--
Unigene45789_All	Zinc finger protein 526 OS=Homo sapiens GN=ZNF526 PE=2 SV=2
Unigene45807_All	--
Unigene45832_All	Inverted formin-2 OS=Mus musculus GN=Inf2 PE=1 SV=1
Unigene45833_All	--
Unigene45841_All	--
Unigene45866_All	--
Unigene45891_All	--
Unigene45906_All	--
Unigene45907_All	--
Unigene45913_All	--
Unigene45914_All	--
Unigene45918_All	--
Unigene45952_All	--
Unigene45988_All	--
Unigene4598_All	Protein abrupt OS=Drosophila melanogaster GN=ab PE=1 SV=2
Unigene45991_All	--
Unigene46012_All	--
Unigene46041_All	--
Unigene46051_All	--
Unigene46073_All	--
Unigene46108_All	--
Unigene46135_All	--
Unigene46157_All	--
Unigene46181_All	--
Unigene46183_All	--
Unigene46193_All	--
Unigene46196_All	--
Unigene46206_All	--
Unigene46309_All	--
Unigene46311_All	--
Unigene4632_All	--
Unigene46331_All	--
Unigene46351_All	--
Unigene46415_All	--
Unigene46419_All	--
Unigene4646_All	--
Unigene46509_All	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3

Unigene4651_All	--
Unigene46530_All	--
Unigene46587_All	--
Unigene46627_All	--
Unigene46637_All	--
Unigene46644_All	--
Unigene46779_All	Putative SCAN domain-containing protein SCAND2P OS=Homo sapiens GN=SCAND2P PE=5 SV=2
Unigene46815_All	--
Unigene46856_All	--
Unigene46888_All	--
Unigene46906_All	--
Unigene46923_All	--
Unigene46995_All	--
Unigene47021_All	--
Unigene4702_All	--
Unigene47039_All	--
Unigene47046_All	--
Unigene47086_All	--
Unigene47093_All	--
Unigene47122_All	--
Unigene47200_All	--
Unigene47223_All	--
Unigene47288_All	Glutamate-gated chloride channel OS=Drosophila melanogaster GN=GluClalpha PE=1 SV=2
Unigene47295_All	Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1
Unigene472_All	Acetylcholine receptor subunit alpha-type acr-16 OS=Caenorhabditis elegans GN=acr-16 PE=2 SV=1
Unigene47354_All	Neuroendocrine convertase 2 OS=Sus scrofa GN=PCSK2 PE=2 SV=1
Unigene47372_All	--
Unigene47423_All	--
Unigene47428_All	Pikachurin OS=Bos taurus GN=EGFLAM PE=2 SV=1
Unigene4742_All	--
Unigene47484_All	LIRP OS=Locusta migratoria PE=1 SV=2
Unigene47490_All	MATH and LRR domain-containing protein PFE0570w OS=Plasmodium falciparum (isolate 3D7) GN=PFE0570w PE=2 SV=1
Unigene47492_All	Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4
Unigene47496_All	Myb-like protein X OS=Dictyostelium discoideum GN=mybX PE=3 SV=1

Unigene47498_All	Dopamine N-acetyltransferase OS=Drosophila melanogaster GN=Dat PE=1 SV=1
Unigene47499_All	--
Unigene47529_All	--
Unigene47557_All	Multiple epidermal growth factor-like domains protein 6 OS=Mus musculus GN=Megf6 PE=2 SV=3
Unigene47560_All	Calbindin-32 OS=Drosophila melanogaster GN=Cbp53E PE=2 SV=1
Unigene47568_All	Bromodomain-containing protein DDB_G0280777 OS=Dictyostelium discoideum GN=DDB_G0280777 PE=4 SV=1
Unigene47573_All	--
Unigene47574_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene47575_All	Large neutral amino acids transporter small subunit 2 OS=Rattus norvegicus GN=Slc7a8 PE=1 SV=1
Unigene47584_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene47599_All	Protein rhomboid OS=Drosophila melanogaster GN=rho PE=1 SV=2
Unigene47602_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene47605_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene47620_All	--
Unigene47639_All	--
Unigene47641_All	--
Unigene47643_All	--
Unigene47682_All	--
Unigene47693_All	--
Unigene47743_All	--
Unigene47745_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene47748_All	--
Unigene47760_All	--
Unigene47788_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene47833_All	Sodium/potassium-transporting ATPase subunit alpha-4 OS=Mus musculus GN=Atp1a4 PE=1 SV=3
Unigene47843_All	L-lactate dehydrogenase OS=Drosophila melanogaster GN=ImpL3 PE=2 SV=1
Unigene47845_All	--
Unigene47883_All	--
Unigene47942_All	--

Unigene47986_All	--
Unigene48001_All	Synaptic vesicular amine transporter OS=Bos taurus GN=SLC18A2 PE=1 SV=1
Unigene48004_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene48008_All	--
Unigene48068_All	Adenylate cyclase, terminal-differentiation specific OS=Dictyostelium discoideum GN=acrA PE=1 SV=1
Unigene48094_All	Acetylcholine receptor subunit alpha-like 1 OS=Drosophila melanogaster GN=nAcRalpha-96Aa PE=2 SV=2
Unigene48097_All	--
Unigene48102_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3
Unigene48113_All	Endochitinase OS=Manduca sexta PE=2 SV=1
Unigene48126_All	Hemocyte protein-glutamine gamma-glutamyltransferase OS=Tachypleus tridentatus PE=1 SV=1
Unigene48188_All	Mediator of RNA polymerase II transcription subunit 15 OS=Xenopus laevis GN=med15 PE=1 SV=1
Unigene48196_All	--
Unigene48199_All	--
Unigene48203_All	Acetylcholine receptor subunit beta-like 1 OS=Drosophila melanogaster GN=nAcRbeta-64B PE=2 SV=1
Unigene48205_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene48212_All	--
Unigene48213_All	--
Unigene48228_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene48289_All	--
Unigene48291_All	--
Unigene48309_All	--
Unigene48333_All	Neural-cadherin OS=Drosophila melanogaster GN=CadN PE=1 SV=2
Unigene48344_All	--
Unigene48366_All	--
Unigene48380_All	--
Unigene48382_All	--
Unigene48387_All	--
Unigene48389_All	Potassium voltage-gated channel protein Shab OS=Drosophila melanogaster GN=Shab PE=1 SV=2
Unigene48391_All	--

Unigene48395_All	--
Unigene483_All	--
Unigene48404_All	--
Unigene4842_All	--
Unigene48434_All	--
Unigene48449_All	Zinc finger protein 782 OS=Homo sapiens GN=ZNF782 PE=2 SV=1
Unigene48453_All	--
Unigene48470_All	Katanin p60 ATPase-containing subunit A-like 1 OS=Homo sapiens GN=KATNAL1 PE=1 SV=1
Unigene48488_All	--
Unigene48530_All	--
Unigene48566_All	--
Unigene48585_All	Low-density lipoprotein receptor-related protein 4 OS=Homo sapiens GN=LRP4 PE=1 SV=4
Unigene48590_All	--
Unigene48600_All	--
Unigene48602_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene48630_All	--
Unigene48636_All	Keratin-associated protein 4-4 OS=Homo sapiens GN=KRTAP4-4 PE=2 SV=1
Unigene48641_All	--
Unigene48652_All	DBF4-type zinc finger-containing protein 2 homolog OS=Mus musculus GN=Zdbf2 PE=2 SV=1
Unigene48680_All	--
Unigene48692_All	--
Unigene48722_All	--
Unigene48729_All	--
Unigene48763_All	--
Unigene48786_All	Putative protein TPRXL OS=Homo sapiens GN=TPRXL PE=5 SV=2
Unigene48792_All	--
Unigene48824_All	--
Unigene48837_All	--
Unigene48839_All	--
Unigene48840_All	Uncharacterized protein C10orf95 OS=Homo sapiens GN=C10orf95 PE=2 SV=1
Unigene48889_All	--
Unigene48943_All	--
Unigene48976_All	--
Unigene49039_All	--
Unigene49080_All	--

Unigene4908_All	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2 OS=Homo sapiens GN=HCN2 PE=1 SV=3
Unigene49117_All	--
Unigene49135_All	--
Unigene49156_All	--
Unigene49188_All	--
Unigene49201_All	--
Unigene49256_All	--
Unigene49345_All	--
Unigene49356_All	--
Unigene493_All	Gamma-aminobutyric acid receptor subunit beta OS=Musca domestica GN=Rdl PE=1 SV=2
Unigene49416_All	--
Unigene49426_All	--
Unigene49441_All	Glutathione S-transferase OS=Blattella germanica PE=1 SV=3
Unigene49454_All	--
Unigene49473_All	--
Unigene49502_All	--
Unigene49506_All	--
Unigene49535_All	--
Unigene49554_All	--
Unigene4960_All	--
Unigene49683_All	--
Unigene49719_All	--
Unigene49725_All	--
Unigene49762_All	--
Unigene4977_All	--
Unigene49796_All	--
Unigene49801_All	--
Unigene49872_All	--
Unigene49896_All	--
Unigene49920_All	Nucleolar protein 58 OS=Dictyostelium discoideum GN=nop58 PE=3 SV=1
Unigene49928_All	Heterogeneous nuclear ribonucleoprotein A3 OS=Rattus norvegicus GN=Hnrnpa3 PE=1 SV=1
Unigene49990_All	--
Unigene49999_All	--
Unigene4_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene50001_All	--

Unigene50013_All	Keratin, type I cytoskeletal 9 OS=Mus musculus GN=Krt9 PE=1 SV=2
Unigene50022_All	--
Unigene50038_All	--
Unigene50054_All	--
Unigene50064_All	--
Unigene50075_All	Protein lethal(2)essential for life OS=Drosophila melanogaster GN=l(2)efl PE=1 SV=1
Unigene50096_All	Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3 PE=1 SV=2
Unigene50104_All	UPF0746 protein DDB_G0281095 OS=Dictyostelium discoideum GN=DDB_G0281095 PE=3 SV=1
Unigene50106_All	--
Unigene50113_All	--
Unigene50116_All	--
Unigene50175_All	--
Unigene50179_All	--
Unigene5017_All	--
Unigene50184_All	--
Unigene5019_All	--
Unigene50208_All	--
Unigene50243_All	--
Unigene5028_All	--
Unigene50324_All	Ras-associated and pleckstrin homology domains-containing protein 1 OS=Homo sapiens GN=RAPH1 PE=1 SV=3
Unigene50361_All	--
Unigene50363_All	--
Unigene50371_All	--
Unigene50385_All	--
Unigene50386_All	--
Unigene50422_All	--
Unigene50426_All	--
Unigene50441_All	--
Unigene50469_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene50495_All	--
Unigene50528_All	--
Unigene505_All	--
Unigene50743_All	--
Unigene50750_All	--
Unigene50753_All	--
Unigene50786_All	--

Unigene5081_All	--
Unigene5082_All	--
Unigene50907_All	--
Unigene50911_All	--
Unigene5092_All	--
Unigene50932_All	--
Unigene51102_All	--
Unigene51287_All	--
Unigene51309_All	--
Unigene51366_All	--
Unigene51374_All	--
Unigene51408_All	--
Unigene51464_All	Serine/arginine repetitive matrix protein 3 OS=Homo sapiens GN=SRRM3 PE=2 SV=4
Unigene51465_All	Ankyrin repeat domain-containing protein 6 OS=Mus musculus GN=Ankrd6 PE=1 SV=2
Unigene51477_All	--
Unigene5147_All	--
Unigene51482_All	--
Unigene51497_All	--
Unigene51515_All	--
Unigene51535_All	--
Unigene51561_All	--
Unigene51566_All	--
Unigene51584_All	--
Unigene51590_All	--
Unigene51611_All	--
Unigene51614_All	Acanthoscurrin-1 OS=Acanthoscurria gomesiana GN=acantho1 PE=1 SV=1
Unigene51618_All	--
Unigene51625_All	Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=2
Unigene51630_All	--
Unigene51632_All	Paramyosin, short form OS=Drosophila melanogaster GN=Prm PE=2 SV=2
Unigene51640_All	--
Unigene51652_All	--
Unigene51656_All	--
Unigene51673_All	--
Unigene51680_All	--
Unigene51690_All	--
Unigene51701_All	--

Unigene51702_All	--
Unigene51720_All	--
Unigene51730_All	--
Unigene51731_All	--
Unigene51734_All	Formin-1 OS=Mus musculus GN=Fmn1 PE=1 SV=2
Unigene51756_All	--
Unigene51768_All	--
Unigene517_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene51881_All	--
Unigene5193_All	--
Unigene52009_All	--
Unigene52020_All	--
Unigene52037_All	--
Unigene5210_All	ATP-dependent RNA helicase ddx46 OS=Dictyostelium discoideum GN=helB1 PE=2 SV=1
Unigene52117_All	--
Unigene52194_All	Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1
Unigene52230_All	--
Unigene52281_All	--
Unigene52306_All	--
Unigene52309_All	--
Unigene52358_All	--
Unigene52366_All	--
Unigene52388_All	--
Unigene52439_All	--
Unigene5254_All	--
Unigene52596_All	--
Unigene52609_All	Fatty acid synthase OS=Rattus norvegicus GN=Fasn PE=1 SV=3
Unigene52700_All	--
Unigene52712_All	--
Unigene52749_All	Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2
Unigene52755_All	--
Unigene52807_All	--
Unigene52808_All	--
Unigene52852_All	--
Unigene52879_All	--
Unigene52921_All	Paxillin OS=Mus musculus GN=Pxn PE=1 SV=1
Unigene52937_All	--

Unigene52987_All	Period circadian protein (Fragments) OS=Drosophila simulans GN=per PE=3 SV=2
Unigene53028_All	--
Unigene53052_All	--
Unigene53058_All	--
Unigene53072_All	--
Unigene53100_All	--
Unigene53121_All	--
Unigene53135_All	--
Unigene53147_All	--
Unigene53164_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene531_All	--
Unigene53209_All	--
Unigene53211_All	--
Unigene53224_All	--
Unigene5322_All	--
Unigene53236_All	--
Unigene53240_All	--
Unigene53264_All	Cuticle protein 63 OS=Locusta migratoria PE=1 SV=1
Unigene53296_All	Chromosome alignment-maintaining phosphoprotein 1 OS=Mus musculus GN=Champ1 PE=1 SV=1
Unigene53331_All	--
Unigene53345_All	--
Unigene53368_All	--
Unigene53408_All	--
Unigene53409_All	--
Unigene53410_All	--
Unigene53438_All	--
Unigene53452_All	--
Unigene53470_All	--
Unigene53494_All	--
Unigene53502_All	--
Unigene53503_All	--
Unigene53509_All	--
Unigene53520_All	--
Unigene53539_All	--
Unigene53549_All	--
Unigene53584_All	--
Unigene53618_All	--
Unigene53623_All	--

Unigene53635_All	--
Unigene53678_All	--
Unigene53683_All	--
Unigene5368_All	--
Unigene53690_All	--
Unigene53694_All	--
Unigene53697_All	--
Unigene53721_All	--
Unigene53748_All	--
Unigene53759_All	--
Unigene53770_All	--
Unigene5377_All	--
Unigene53841_All	Splicing factor, arginine/serine-rich 19 OS=Homo sapiens GN=SCAF1 PE=1 SV=3
Unigene53864_All	--
Unigene53869_All	--
Unigene53875_All	--
Unigene53896_All	--
Unigene53921_All	--
Unigene53927_All	--
Unigene53928_All	--
Unigene53931_All	--
Unigene53955_All	--
Unigene53987_All	--
Unigene54013_All	Dopamine N-acetyltransferase OS=Drosophila melanogaster GN=Dat PE=1 SV=1
Unigene54083_All	--
Unigene54154_All	--
Unigene54185_All	--
Unigene54192_All	--
Unigene54228_All	Down syndrome cell adhesion molecule-like protein Dscam2 OS=Drosophila melanogaster GN=Dscam2 PE=2 SV=3
Unigene54266_All	--
Unigene54280_All	--
Unigene54300_All	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3
Unigene54328_All	Lachesin OS=Schistocerca americana GN=LAC PE=1 SV=1
Unigene54336_All	--
Unigene54366_All	--
Unigene54369_All	--
Unigene54410_All	--

Unigene54412_All	--
Unigene54417_All	--
Unigene54458_All	--
Unigene54465_All	--
Unigene54487_All	--
Unigene54511_All	Inverted formin-2 OS=Mus musculus GN=Inf2 PE=1 SV=1
Unigene54530_All	--
Unigene54585_All	--
Unigene5459_All	Serine/arginine repetitive matrix protein 3 OS=Homo sapiens GN=SRRM3 PE=2 SV=4
Unigene54656_All	Transmembrane protein fend OS=Drosophila melanogaster GN=fend PE=2 SV=1
Unigene54697_All	Salivary glue protein Sgs-3 OS=Drosophila yakuba GN=Sgs3 PE=2 SV=3
Unigene54698_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene54723_All	Cadherin-23 OS=Rattus norvegicus GN=Cdh23 PE=2 SV=1
Unigene54742_All	Sodium/potassium-transporting ATPase subunit alpha OS=Drosophila melanogaster GN=Atpalpha PE=1 SV=3
Unigene54744_All	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Bufo marinus GN=ATP1A1 PE=1 SV=2
Unigene5477_All	--
Unigene54800_All	--
Unigene54809_All	Potassium channel subfamily K member 18 OS=Mus musculus GN=Kcnk18 PE=1 SV=1
Unigene54817_All	--
Unigene54852_All	--
Unigene54854_All	Mucin-17 OS=Homo sapiens GN=MUC17 PE=1 SV=2
Unigene54855_All	Muscle LIM protein Mlp84B OS=Drosophila melanogaster GN=Mlp84B PE=1 SV=1
Unigene5487_All	--
Unigene54907_All	--
Unigene5497_All	--
Unigene54987_All	--
Unigene54990_All	--
Unigene55036_All	--
Unigene55040_All	--
Unigene55070_All	Regulator of G-protein signaling 11 OS=Homo sapiens GN=RGS11 PE=1 SV=2
Unigene55077_All	--

Unigene55109_All	Glutamate [NMDA] receptor subunit 1 OS=Drosophila ananassae GN=Nmdar1 PE=3 SV=1
Unigene55115_All	Protein Skeletor, isoforms D/E OS=Drosophila melanogaster GN=Skeletor PE=1 SV=3
Unigene55179_All	Protein still life, isoforms C/SIF type 2 OS=Drosophila melanogaster GN=sif PE=2 SV=2
Unigene55225_All	--
Unigene55229_All	--
Unigene55241_All	JNK-interacting protein 1 OS=Drosophila melanogaster GN=Aplip1 PE=1 SV=2
Unigene55278_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene552_All	--
Unigene55307_All	--
Unigene55313_All	--
Unigene5537_All	Techylectin-5B OS=Tachypleus tridentatus PE=1 SV=1
Unigene55383_All	--
Unigene55421_All	Lachesin OS=Schistocerca americana GN=LAC PE=1 SV=1
Unigene55448_All	Kallikrein-14 OS=Mus musculus GN=Klk14 PE=2 SV=1
Unigene55470_All	--
Unigene55476_All	--
Unigene55507_All	--
Unigene55525_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2
Unigene55582_All	--
Unigene55621_All	--
Unigene55664_All	Serine/arginine repetitive matrix protein 1 OS=Gallus gallus GN=SRRM1 PE=2 SV=1
Unigene55691_All	--
Unigene55735_All	Phenoloxidase subunit A3 OS=Drosophila melanogaster GN=proPo-A3 PE=1 SV=1
Unigene55743_All	Aminopeptidase N OS=Sus scrofa GN=ANPEP PE=1 SV=4
Unigene55745_All	--
Unigene55756_All	--
Unigene55785_All	--
Unigene55791_All	cGMP-specific 3',5'-cyclic phosphodiesterase OS=Drosophila pseudoobscura pseudoobscura GN=Pde6 PE=3 SV=3
Unigene55812_All	--
Unigene55836_All	--
Unigene55842_All	--
Unigene55860_All	--

Unigene55887_All	PiggyBac transposable element-derived protein 4 OS=Homo sapiens GN=PGBD4 PE=2 SV=3
Unigene55922_All	--
Unigene5594_All	--
Unigene55955_All	--
Unigene55961_All	ALK tyrosine kinase receptor OS=Mus musculus GN=Alk PE=1 SV=2
Unigene55980_All	GTP-binding protein Di-Ras2 OS=Macaca fascicularis GN=DIRAS2 PE=2 SV=1
Unigene55992_All	--
Unigene55993_All	--
Unigene56012_All	Down syndrome cell adhesion molecule-like protein Dscam2 OS=Drosophila melanogaster GN=Dscam2 PE=2 SV=3
Unigene56029_All	--
Unigene56060_All	--
Unigene56073_All	--
Unigene56075_All	Histone-lysine N-methyltransferase, H3 lysine-79 specific OS=Dictyostelium discoideum GN=dotA PE=2 SV=2
Unigene56076_All	--
Unigene56077_All	--
Unigene56082_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene56087_All	cGMP-dependent protein kinase, isozyme 1 OS=Drosophila melanogaster GN=Pkg21D PE=1 SV=2
Unigene56096_All	--
Unigene56097_All	--
Unigene56104_All	--
Unigene56139_All	Juxtaposed with another zinc finger protein 1 OS=Pongo abelii GN=JAZF1 PE=2 SV=1
Unigene56148_All	--
Unigene56153_All	--
Unigene56163_All	--
Unigene56171_All	Guanine nucleotide-binding protein subunit gamma-e OS=Drosophila melanogaster GN=Ggamma30A PE=1 SV=1
Unigene56175_All	--
Unigene56183_All	--
Unigene5619_All	--
Unigene56203_All	--
Unigene56230_All	Nuclear transcription factor Y subunit beta OS=Dictyostelium discoideum GN=nfyB PE=3 SV=1

Unigene56242_All	Tubulin alpha-1 chain OS=Drosophila melanogaster GN=alphaTub84B PE=2 SV=1
Unigene56274_All	--
Unigene56293_All	--
Unigene56323_All	--
Unigene56324_All	--
Unigene56329_All	Skin secretory protein xP2 OS=Xenopus laevis GN=p2 PE=2 SV=2
Unigene56330_All	SPRY domain-containing SOCS box protein 3 OS=Bos taurus GN=SPSB3 PE=2 SV=1
Unigene56350_All	--
Unigene5641_All	--
Unigene56424_All	--
Unigene56426_All	Hemolymph lipopolysaccharide-binding protein OS=Periplaneta americana PE=1 SV=1
Unigene56437_All	--
Unigene56439_All	--
Unigene5643_All	--
Unigene56462_All	--
Unigene56463_All	--
Unigene56467_All	--
Unigene56533_All	--
Unigene56538_All	--
Unigene56594_All	--
Unigene56602_All	--
Unigene56607_All	--
Unigene56617_All	Nuclear transcription factor Y subunit beta OS=Dictyostelium discoideum GN=nfyB PE=3 SV=1
Unigene56637_All	--
Unigene56643_All	--
Unigene56651_All	--
Unigene56670_All	--
Unigene56746_All	--
Unigene56809_All	--
Unigene56816_All	Microtubule-associated protein RP/EB family member 1 OS=Xenopus tropicalis GN=mapre1 PE=2 SV=1
Unigene56866_All	--
Unigene56898_All	Protein cappuccino OS=Drosophila melanogaster GN=capu PE=1 SV=2
Unigene5690_All	--
Unigene56915_All	--
Unigene56920_All	--

Unigene56927_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene56998_All	--
Unigene57010_All	--
Unigene57033_All	Cuticle protein 16.5, isoform A OS=Locusta migratoria PE=1 SV=1
Unigene57072_All	--
Unigene57090_All	--
Unigene57128_All	--
Unigene57161_All	--
Unigene57252_All	--
Unigene57258_All	--
Unigene57259_All	--
Unigene57271_All	--
Unigene57283_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene57302_All	--
Unigene57317_All	--
Unigene57322_All	--
Unigene57323_All	--
Unigene57342_All	--
Unigene5734_All	--
Unigene57380_All	--
Unigene57382_All	--
Unigene57392_All	--
Unigene57412_All	Acetylcholine receptor subunit beta-like 1 OS=Drosophila melanogaster GN=nAcRbeta-64B PE=2 SV=1
Unigene57432_All	Endocuticle structural glycoprotein SgAbd-8 OS=Schistocerca gregaria PE=1 SV=1
Unigene57512_All	Kazal-type serine protease inhibitor domain-containing protein 1 OS=Mus musculus GN=Kazald1 PE=1 SV=2
Unigene57520_All	--
Unigene57534_All	--
Unigene57538_All	Neurotrimin OS=Rattus norvegicus GN=Ntm PE=1 SV=1
Unigene57558_All	--
Unigene57569_All	Transcription initiation factor TFIID subunit 4 OS=Homo sapiens GN=TAF4 PE=1 SV=2
Unigene57582_All	--
Unigene57590_All	--
Unigene5759_All	--
Unigene57600_All	--
Unigene57623_All	--
Unigene57629_All	--

Unigene57647_All	--
Unigene57658_All	--
Unigene57669_All	Protein takeout OS=Drosophila melanogaster GN=to PE=2 SV=1
Unigene57682_All	--
Unigene57808_All	--
Unigene57842_All	--
Unigene57858_All	--
Unigene57876_All	--
Unigene57897_All	--
Unigene58091_All	--
Unigene58176_All	--
Unigene58188_All	--
Unigene58264_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene58330_All	--
Unigene58332_All	--
Unigene5834_All	--
Unigene58359_All	--
Unigene5835_All	--
Unigene58515_All	--
Unigene58576_All	--
Unigene58597_All	--
Unigene58616_All	--
Unigene58760_All	--
Unigene58784_All	--
Unigene58790_All	--
Unigene58800_All	--
Unigene58831_All	Angiopoietin-related protein 1 OS=Homo sapiens GN=ANGPTL1 PE=2 SV=1
Unigene58847_All	--
Unigene58850_All	--
Unigene58858_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
Unigene58866_All	--
Unigene58889_All	--
Unigene58905_All	--
Unigene58908_All	--
Unigene58919_All	--
Unigene58952_All	--
Unigene58955_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene58971_All	--

Unigene58976_All	--
Unigene58981_All	--
Unigene58991_All	--
Unigene58992_All	--
Unigene59003_All	--
Unigene5900_All	--
Unigene59013_All	Transmembrane protein 198-B OS=Danio rerio GN=tmem198b PE=2 SV=1
Unigene59024_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene59027_All	--
Unigene59043_All	Fatty acid synthase OS=Rattus norvegicus GN=Fasn PE=1 SV=3
Unigene59046_All	--
Unigene59057_All	Iodotyrosine dehalogenase 1 OS=Homo sapiens GN=IYD PE=1 SV=2
Unigene59070_All	--
Unigene59075_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
Unigene59083_All	--
Unigene59091_All	--
Unigene59095_All	--
Unigene59114_All	Zinc finger protein 474 OS=Mus musculus GN=Znf474 PE=2 SV=2
Unigene59130_All	--
Unigene59132_All	--
Unigene59138_All	--
Unigene5915_All	Neural Wiskott-Aldrich syndrome protein OS=Rattus norvegicus GN=Wasl PE=1 SV=2
Unigene59164_All	--
Unigene59168_All	--
Unigene59169_All	--
Unigene59186_All	--
Unigene59193_All	--
Unigene59206_All	Bile salt-activated lipase OS=Homo sapiens GN=CEL PE=1 SV=3
Unigene59209_All	--
Unigene59211_All	--
Unigene59218_All	--
Unigene59221_All	--
Unigene59232_All	--
Unigene59241_All	--
Unigene5925_All	--
Unigene59293_All	--

Unigene5929_All	--
Unigene59335_All	Cytochrome P450 4C1 OS=Blaberus discoidalis GN=CYP4C1 PE=2 SV=1
Unigene59381_All	--
Unigene59386_All	--
Unigene59399_All	--
Unigene59403_All	--
Unigene59405_All	--
Unigene59434_All	--
Unigene59491_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3
Unigene59536_All	--
Unigene59587_All	--
Unigene59652_All	--
Unigene59685_All	--
Unigene5974_All	--
Unigene59755_All	--
Unigene5977_All	--
Unigene59860_All	Atherin OS=Mus musculus GN=Samd1 PE=3 SV=1
Unigene59881_All	--
Unigene59896_All	--
Unigene59901_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene59902_All	--
Unigene59954_All	--
Unigene6010_All	--
Unigene60285_All	Titin OS=Homo sapiens GN=TTN PE=1 SV=4
Unigene60304_All	--
Unigene60356_All	Loricrin OS=Mus musculus GN=Lor PE=2 SV=2
Unigene60402_All	--
Unigene60433_All	--
Unigene6046_All	--
Unigene60495_All	--
Unigene60541_All	--
Unigene60556_All	--
Unigene60574_All	--
Unigene60594_All	--
Unigene60596_All	Zinc finger homeobox protein 4 OS=Homo sapiens GN=ZFHX4 PE=1 SV=1
Unigene6060_All	--
Unigene60657_All	--
Unigene6067_All	--

Unigene6068_All	--
Unigene6072_All	--
Unigene60764_All	--
Unigene6081_All	--
Unigene60831_All	--
Unigene60892_All	Adipokinetic prohormone type 2 OS=Locusta migratoria PE=1 SV=3
Unigene60915_All	--
Unigene60935_All	Transmembrane protease serine 13 OS=Mus musculus GN=Tmprss13 PE=2 SV=2
Unigene60978_All	--
Unigene60997_All	--
Unigene609_All	--
Unigene61005_All	--
Unigene61018_All	--
Unigene61048_All	--
Unigene61127_All	--
Unigene61128_All	--
Unigene61154_All	--
Unigene6115_All	--
Unigene6119_All	--
Unigene61203_All	--
Unigene61236_All	--
Unigene61249_All	Neural Wiskott-Aldrich syndrome protein OS=Homo sapiens GN=WASL PE=1 SV=2
Unigene61289_All	--
Unigene61313_All	--
Unigene61324_All	--
Unigene61336_All	--
Unigene61373_All	--
Unigene6137_All	--
Unigene61407_All	--
Unigene61409_All	--
Unigene61419_All	--
Unigene6142_All	--
Unigene61451_All	--
Unigene61460_All	--
Unigene61469_All	--
Unigene61490_All	--
Unigene61496_All	--
Unigene61510_All	--
Unigene61512_All	--

Unigene61518_All	--
Unigene61547_All	--
Unigene61552_All	--
Unigene61566_All	--
Unigene61577_All	--
Unigene61620_All	--
Unigene6162_All	--
Unigene61633_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene61648_All	--
Unigene61688_All	--
Unigene61704_All	--
Unigene61720_All	--
Unigene61751_All	--
Unigene61784_All	--
Unigene61785_All	--
Unigene61800_All	--
Unigene61811_All	--
Unigene61826_All	--
Unigene61834_All	--
Unigene61886_All	Multidrug resistance-associated protein 4 OS=Homo sapiens GN=ABCC4 PE=1 SV=3
Unigene61889_All	--
Unigene61891_All	--
Unigene61896_All	--
Unigene61902_All	--
Unigene61942_All	--
Unigene61954_All	--
Unigene62004_All	--
Unigene62010_All	--
Unigene62024_All	--
Unigene62029_All	--
Unigene6202_All	--
Unigene62030_All	--
Unigene62046_All	--
Unigene62059_All	--
Unigene62064_All	--
Unigene62065_All	--
Unigene62066_All	--
Unigene62081_All	--
Unigene62082_All	--

Unigene62091_All	Carbonic anhydrase-related protein 10 OS=Pongo abelii GN=CA10 PE=2 SV=1
Unigene62116_All	--
Unigene62137_All	Cuticle protein 67, isoform B OS=Locusta migratoria PE=1 SV=1
Unigene6214_All	--
Unigene62171_All	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
Unigene62189_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene62190_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
Unigene62198_All	Muscle M-line assembly protein unc-89 OS=Caenorhabditis elegans GN=unc-89 PE=1 SV=3
Unigene6224_All	--
Unigene62265_All	N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1
Unigene6226_All	--
Unigene6234_All	--
Unigene62351_All	--
Unigene62364_All	--
Unigene62390_All	Leucine-rich repeat neuronal protein 1 OS=Bos taurus GN=LRRN1 PE=3 SV=1
Unigene62417_All	Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=2
Unigene6241_All	--
Unigene62421_All	--
Unigene6244_All	--
Unigene62470_All	Regucalcin OS=Xenopus tropicalis GN=rgn PE=2 SV=1
Unigene62542_All	--
Unigene62544_All	--
Unigene62551_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene62566_All	--
Unigene62587_All	--
Unigene62595_All	Prostaglandin reductase 1 OS=Oryctolagus cuniculus GN=PTGR1 PE=2 SV=1
Unigene62597_All	Gamma-1-syntrophin OS=Homo sapiens GN=SNTG1 PE=1 SV=1
Unigene6264_All	--
Unigene62659_All	--
Unigene62661_All	Lachesin OS=Schistocerca americana GN=LAC PE=1 SV=1
Unigene62672_All	Wnt inhibitory factor 1 OS=Xenopus laevis GN=wif1 PE=2 SV=1
Unigene62733_All	--

Unigene62747_All	--
Unigene62750_All	Atherin OS=Homo sapiens GN=SAMD1 PE=1 SV=1
Unigene62754_All	Atherin OS=Oryctolagus cuniculus GN=SAMD1 PE=2 SV=1
Unigene62784_All	--
Unigene62812_All	--
Unigene62814_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene62838_All	--
Unigene62855_All	--
Unigene6287_All	--
Unigene62881_All	--
Unigene62889_All	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase P OS=Drosophila melanogaster GN=GlcAT-P PE=2 SV=1
Unigene62891_All	--
Unigene62897_All	Plectin (Fragment) OS=Cricetulus griseus GN=PLEC PE=1 SV=1
Unigene62935_All	Myb-like protein P OS=Dictyostelium discoideum GN=mybP PE=3 SV=1
Unigene62936_All	--
Unigene62945_All	--
Unigene62966_All	Sodium channel protein para OS=Drosophila melanogaster GN=para PE=2 SV=3
Unigene62982_All	--
Unigene62985_All	--
Unigene63016_All	--
Unigene63024_All	--
Unigene63027_All	--
Unigene63035_All	--
Unigene63040_All	Prespore protein Dp87 OS=Dictyostelium discoideum GN=cotD PE=2 SV=2
Unigene63054_All	--
Unigene63065_All	--
Unigene63068_All	--
Unigene63089_All	--
Unigene63138_All	--
Unigene63140_All	--
Unigene63166_All	--
Unigene63168_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene63211_All	--
Unigene63238_All	--
Unigene63336_All	--

Unigene63356_All	--
Unigene63362_All	--
Unigene633_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene63420_All	--
Unigene63469_All	--
Unigene634_All	Low density lipoprotein receptor adapter protein 1-B OS=Xenopus laevis GN=ldlrap1-b PE=1 SV=1
Unigene63500_All	--
Unigene63514_All	--
Unigene63535_All	--
Unigene63581_All	--
Unigene63586_All	Brachyury protein OS=Canis familiaris GN=T PE=2 SV=1
Unigene63589_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene63646_All	Cytochrome P450 6a2 OS=Drosophila melanogaster GN=Cyp6a2 PE=2 SV=2
Unigene63655_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene63662_All	--
Unigene63691_All	--
Unigene63708_All	Transcription factor SOX-30 OS=Mus musculus GN=Sox30 PE=2 SV=1
Unigene63731_All	--
Unigene63735_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene63745_All	--
Unigene63753_All	Salivary glue protein Sgs-3 OS=Drosophila simulans GN=Sgs3 PE=2 SV=2
Unigene63755_All	--
Unigene63838_All	--
Unigene63859_All	Protease inhibitors OS=Locusta migratoria PE=1 SV=2
Unigene638_All	--
Unigene63908_All	--
Unigene6392_All	--
Unigene63940_All	--
Unigene63983_All	--
Unigene64010_All	--
Unigene64015_All	--
Unigene64024_All	--
Unigene64066_All	--

Unigene64094_All	--
Unigene640_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene64126_All	--
Unigene64209_All	--
Unigene64233_All	--
Unigene64234_All	--
Unigene64266_All	--
Unigene64314_All	--
Unigene64346_All	--
Unigene64363_All	--
Unigene64373_All	--
Unigene64414_All	--
Unigene64419_All	--
Unigene6441_All	--
Unigene64468_All	--
Unigene64498_All	--
Unigene6449_All	--
Unigene64542_All	--
Unigene64560_All	--
Unigene64565_All	--
Unigene64568_All	--
Unigene64591_All	--
Unigene64596_All	--
Unigene64615_All	--
Unigene64627_All	--
Unigene64630_All	--
Unigene64631_All	--
Unigene64709_All	--
Unigene64760_All	--
Unigene64800_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene64808_All	Circadian clock-controlled protein OS=Drosophila melanogaster GN=anon-3B1.2 PE=2 SV=2
Unigene64848_All	--
Unigene64855_All	--
Unigene64870_All	--
Unigene64887_All	--
Unigene64910_All	--
Unigene64924_All	Probable sodium/potassium/calcium exchanger CG1090 OS=Drosophila melanogaster GN=CG1090 PE=2 SV=3

Unigene64970_All	--
Unigene64997_All	--
Unigene65030_All	--
Unigene65047_All	--
Unigene65049_All	--
Unigene65064_All	--
Unigene65120_All	--
Unigene65137_All	--
Unigene65169_All	Multiple inositol polyphosphate phosphatase 1 OS=Pongo abelii GN=MINPP1 PE=2 SV=1
Unigene6516_All	--
Unigene65173_All	--
Unigene65190_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene65193_All	--
Unigene65195_All	--
Unigene65205_All	--
Unigene65248_All	--
Unigene6526_All	--
Unigene65284_All	--
Unigene65298_All	--
Unigene6531_All	--
Unigene6538_All	--
Unigene65447_All	--
Unigene65505_All	--
Unigene65617_All	--
Unigene65661_All	--
Unigene6566_All	--
Unigene65674_All	--
Unigene65729_All	--
Unigene6574_All	--
Unigene6580_All	--
Unigene6584_All	--
Unigene66009_All	--
Unigene66029_All	--
Unigene6605_All	--
Unigene66097_All	--
Unigene66121_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene66122_All	--
Unigene66180_All	Calbindin-32 OS=Drosophila melanogaster GN=Cbp53E PE=2 SV=1

Unigene66212_All	Synapsin OS=Drosophila melanogaster GN=Syn PE=1 SV=2
Unigene66214_All	Adipokinetic prohormone type 1 OS=Locusta migratoria PE=1 SV=1
Unigene66216_All	--
Unigene6630_All	--
Unigene66312_All	--
Unigene66324_All	--
Unigene66341_All	--
Unigene66348_All	--
Unigene66350_All	Sulfotransferase 1C4 OS=Homo sapiens GN=SULT1C4 PE=1 SV=2
Unigene66354_All	Dachshund homolog 1 OS=Mus musculus GN=Dach1 PE=1 SV=1
Unigene66356_All	--
Unigene66359_All	Fatty acid synthase OS=Rattus norvegicus GN=Fasn PE=1 SV=3
Unigene66365_All	Cytochrome P450 4g15 OS=Drosophila melanogaster GN=Cyp4g15 PE=2 SV=1
Unigene66379_All	Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3
Unigene66386_All	ALK tyrosine kinase receptor OS=Homo sapiens GN=ALK PE=1 SV=3
Unigene66405_All	--
Unigene66407_All	Atherin OS=Oryctolagus cuniculus GN=SAMD1 PE=2 SV=1
Unigene66431_All	--
Unigene66446_All	Dehydrogenase/reductase SDR family member 11 OS=Gallus gallus GN=DHRS11 PE=2 SV=1
Unigene66447_All	--
Unigene66522_All	Frequenin-1 OS=Drosophila melanogaster GN=Frq1 PE=2 SV=2
Unigene66524_All	--
Unigene66528_All	--
Unigene66529_All	--
Unigene66531_All	--
Unigene66537_All	--
Unigene66549_All	Potassium voltage-gated channel protein Shaw OS=Drosophila melanogaster GN=Shaw PE=2 SV=1
Unigene66562_All	--
Unigene66565_All	--
Unigene66569_All	--
Unigene66570_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene66608_All	--

Unigene6660_All	--
Unigene66621_All	--
Unigene66634_All	--
Unigene66720_All	--
Unigene66733_All	--
Unigene66746_All	Period circadian protein (Fragment) OS=Drosophila serrata GN=per PE=3 SV=1
Unigene66757_All	--
Unigene66775_All	--
Unigene66780_All	Furin-like protease 2 OS=Drosophila melanogaster GN=Fur2 PE=2 SV=2
Unigene66801_All	--
Unigene6684_All	--
Unigene66898_All	--
Unigene66948_All	--
Unigene6694_All	--
Unigene66955_All	--
Unigene6699_All	--
Unigene66_All	--
Unigene67018_All	Keratin, type I cytoskeletal 10 OS=Rattus norvegicus GN=Krt10 PE=2 SV=1
Unigene67023_All	--
Unigene67024_All	Clathrin coat assembly protein AP180 OS=Rattus norvegicus GN=Snap91 PE=1 SV=1
Unigene67046_All	Putative beta-carotene-binding protein OS=Schistocerca gregaria PE=1 SV=1
Unigene67052_All	--
Unigene67066_All	--
Unigene67067_All	--
Unigene67073_All	--
Unigene67138_All	Neurexin-2-beta OS=Rattus norvegicus GN=Nrxn2 PE=1 SV=1
Unigene67142_All	--
Unigene6714_All	--
Unigene67174_All	--
Unigene6717_All	--
Unigene67211_All	--
Unigene67244_All	--
Unigene67262_All	--
Unigene67264_All	--
Unigene67296_All	--
Unigene67298_All	--
Unigene67315_All	--

Unigene6731_All	--
Unigene6744_All	--
Unigene67457_All	--
Unigene67465_All	--
Unigene6749_All	--
Unigene67528_All	--
Unigene67623_All	--
Unigene67626_All	--
Unigene67642_All	--
Unigene67645_All	--
Unigene67666_All	--
Unigene6768_All	--
Unigene676_All	Cyclin-L1 OS=Homo sapiens GN=CCNL1 PE=1 SV=1
Unigene67749_All	Probable serine/threonine-protein kinase pkgA OS=Dictyostelium discoideum GN=pkgA PE=3 SV=1
Unigene67792_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene6779_All	Putative beta-carotene-binding protein OS=Schistocerca gregaria PE=1 SV=1
Unigene67837_All	--
Unigene67862_All	--
Unigene67868_All	--
Unigene67889_All	--
Unigene67896_All	Circadian clock-controlled protein OS=Drosophila yakuba GN=anon-3B1.2 PE=3 SV=1
Unigene67977_All	--
Unigene68012_All	--
Unigene68021_All	--
Unigene68053_All	--
Unigene68060_All	--
Unigene68077_All	--
Unigene68087_All	Formin-G OS=Dictyostelium discoideum GN=forG PE=1 SV=1
Unigene68114_All	--
Unigene68155_All	--
Unigene68162_All	--
Unigene68217_All	--
Unigene68226_All	--
Unigene68336_All	--
Unigene68429_All	UDP-N-acetylglucosamine transferase subunit ALG13 homolog OS=Homo sapiens GN=ALG13 PE=1 SV=2
Unigene68442_All	--

Unigene68481_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene68503_All	--
Unigene68505_All	Glutathione S-transferase OS=Blattella germanica PE=1 SV=3
Unigene68553_All	--
Unigene68584_All	--
Unigene68619_All	--
Unigene68631_All	--
Unigene68727_All	--
Unigene68742_All	--
Unigene68770_All	--
Unigene68826_All	--
Unigene68837_All	Leucine-rich repeat-containing G-protein coupled receptor 6 OS=Mus musculus GN=Lgr6 PE=2 SV=1
Unigene68863_All	--
Unigene68887_All	--
Unigene68896_All	--
Unigene6890_All	--
Unigene68970_All	--
Unigene68983_All	--
Unigene69013_All	Glycine-rich protein 3 OS=Pinctada maxima PE=1 SV=1
Unigene69036_All	--
Unigene69065_All	--
Unigene69066_All	--
Unigene6910_All	--
Unigene69119_All	--
Unigene69141_All	--
Unigene69158_All	--
Unigene69181_All	--
Unigene6919_All	Follistatin-related protein 4 OS=Mus musculus GN=Fstl4 PE=2 SV=1
Unigene69231_All	--
Unigene69265_All	--
Unigene69292_All	--
Unigene69302_All	--
Unigene69317_All	--
Unigene69359_All	--
Unigene69360_All	--
Unigene69418_All	Glutamic acid-rich protein OS=Plasmodium falciparum (isolate FC27 / Papua New Guinea) GN=GARP PE=4 SV=1

Unigene69431_All	--
Unigene69452_All	Fatty acyl-CoA reductase 1 OS=Gallus gallus GN=FAR1 PE=2 SV=1
Unigene69455_All	Fatty acyl-CoA reductase 1 OS=Xenopus laevis GN=far1 PE=2 SV=1
Unigene69461_All	--
Unigene69503_All	Protein roadkill OS=Drosophila melanogaster GN=rdx PE=1 SV=2
Unigene69561_All	Protein spire OS=Drosophila melanogaster GN=spir PE=1 SV=1
Unigene69581_All	--
Unigene69585_All	--
Unigene69597_All	--
Unigene69609_All	--
Unigene69648_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene69650_All	R3H and coiled-coil domain-containing protein 1-like OS=Mus musculus GN=R3hcc1l PE=2 SV=1
Unigene69652_All	--
Unigene69657_All	--
Unigene69658_All	--
Unigene69687_All	--
Unigene69688_All	Uncharacterized protein CG3556 OS=Drosophila melanogaster GN=CG3556 PE=2 SV=1
Unigene69693_All	Ryanodine receptor 44F OS=Drosophila melanogaster GN=Rya-r44F PE=1 SV=3
Unigene69700_All	--
Unigene69744_All	--
Unigene69749_All	Collagen alpha-1(II) chain OS=Bos taurus GN=COL2A1 PE=1 SV=4
Unigene6974_All	--
Unigene69751_All	--
Unigene69752_All	--
Unigene69772_All	--
Unigene6983_All	--
Unigene69841_All	--
Unigene69863_All	Synaptotagmin-11 OS=Mus musculus GN=Syt11 PE=2 SV=2
Unigene69873_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene69893_All	--
Unigene69899_All	--
Unigene69908_All	--

Unigene69911_All	Zinc finger protein 526 OS=Bos taurus GN=ZNF526 PE=2 SV=1
Unigene69965_All	Major facilitator superfamily domain-containing protein 6 OS=Mus musculus GN=Mfsd6 PE=1 SV=1
Unigene69966_All	Transposable element Tc3 transposase OS=Caenorhabditis elegans GN=tc3a PE=1 SV=1
Unigene69980_All	Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2
Unigene7000_All	--
Unigene70014_All	CD151 antigen OS=Bos taurus GN=CD151 PE=2 SV=1
Unigene7001_All	--
Unigene70023_All	--
Unigene70029_All	--
Unigene7003_All	--
Unigene70061_All	--
Unigene70085_All	--
Unigene70093_All	--
Unigene70110_All	--
Unigene70197_All	--
Unigene70214_All	Neuroendocrine convertase 2 OS=Pongo abelii GN=PCSK2 PE=2 SV=1
Unigene70236_All	--
Unigene70247_All	--
Unigene70263_All	Protein scarlet OS=Drosophila melanogaster GN=st PE=1 SV=3
Unigene70271_All	--
Unigene70279_All	--
Unigene70289_All	--
Unigene70305_All	--
Unigene70317_All	Formin-like protein 2 OS=Homo sapiens GN=FMNL2 PE=1 SV=3
Unigene70319_All	--
Unigene7032_All	--
Unigene70356_All	--
Unigene70365_All	--
Unigene70368_All	Homeobox protein Mohawk OS=Mus musculus GN=Mkx PE=2 SV=1
Unigene70372_All	--
Unigene70383_All	--
Unigene70440_All	--
Unigene70442_All	Integumentary mucin C.1 (Fragment) OS=Xenopus laevis PE=2 SV=1
Unigene70446_All	Transmembrane and TPR repeat-containing protein 1 OS=Mus musculus GN=Tmtc1 PE=2 SV=2
Unigene70482_All	--

Unigene70485_All	--
Unigene70496_All	--
Unigene7050_All	--
Unigene70512_All	--
Unigene70539_All	--
Unigene70563_All	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2 OS=Homo sapiens GN=HCN2 PE=1 SV=3
Unigene70570_All	--
Unigene70575_All	--
Unigene70576_All	--
Unigene70586_All	--
Unigene70640_All	--
Unigene70657_All	Longitudinals lacking protein, isoforms A/B/D/L OS=Drosophila melanogaster GN=lola PE=1 SV=1
Unigene70690_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene70694_All	--
Unigene70714_All	--
Unigene70719_All	--
Unigene70725_All	Discoidin domain-containing receptor 2 OS=Homo sapiens GN=DDR2 PE=1 SV=2
Unigene70739_All	--
Unigene7073_All	--
Unigene70741_All	--
Unigene70743_All	--
Unigene70753_All	--
Unigene70784_All	--
Unigene70805_All	--
Unigene70812_All	--
Unigene70847_All	--
Unigene7085_All	--
Unigene70874_All	--
Unigene70876_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene70901_All	--
Unigene70933_All	Endocuticle structural glycoprotein SgAbd-3 OS=Schistocerca gregaria PE=1 SV=1
Unigene70959_All	--
Unigene70963_All	Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2
Unigene70987_All	--

Unigene70990_All	--
Unigene70994_All	--
Unigene71005_All	--
Unigene71038_All	--
Unigene71051_All	--
Unigene71052_All	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Xenopus laevis GN=atp1a1 PE=2 SV=1
Unigene71055_All	--
Unigene71083_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene71098_All	Hemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2
Unigene71100_All	--
Unigene7110_All	--
Unigene71118_All	--
Unigene71193_All	--
Unigene71203_All	Serine/arginine repetitive matrix protein 3 OS=Homo sapiens GN=SRRM3 PE=2 SV=4
Unigene71257_All	--
Unigene71267_All	--
Unigene71305_All	--
Unigene71399_All	--
Unigene71417_All	--
Unigene71424_All	--
Unigene71426_All	--
Unigene71453_All	--
Unigene71473_All	--
Unigene71482_All	--
Unigene71508_All	--
Unigene71509_All	--
Unigene7155_All	--
Unigene71598_All	--
Unigene71617_All	--
Unigene71631_All	--
Unigene71740_All	--
Unigene71778_All	--
Unigene71822_All	--
Unigene71867_All	--
Unigene71884_All	--
Unigene71892_All	--
Unigene71990_All	--
Unigene72003_All	--
Unigene72006_All	--

Unigene72013_All	--
Unigene72025_All	--
Unigene7202_All	--
Unigene72046_All	--
Unigene72061_All	--
Unigene72075_All	--
Unigene72077_All	--
Unigene72096_All	--
Unigene72105_All	Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=3
Unigene72112_All	--
Unigene72124_All	Short neuropeptide F OS=Aedes aegypti GN=sNPF PE=2 SV=2
Unigene72128_All	--
Unigene72133_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene72194_All	--
Unigene72197_All	--
Unigene72201_All	--
Unigene72229_All	--
Unigene72244_All	--
Unigene72254_All	--
Unigene7226_All	--
Unigene72295_All	--
Unigene72304_All	--
Unigene72317_All	--
Unigene72326_All	--
Unigene72367_All	--
Unigene72379_All	Sodium/potassium-transporting ATPase subunit alpha-4 OS=Homo sapiens GN=ATP1A4 PE=1 SV=3
Unigene72397_All	--
Unigene72456_All	--
Unigene72487_All	--
Unigene72489_All	--
Unigene72516_All	ALK tyrosine kinase receptor OS=Homo sapiens GN=ALK PE=1 SV=3
Unigene72540_All	--
Unigene72541_All	--
Unigene72550_All	--
Unigene72552_All	--
Unigene72559_All	--
Unigene72566_All	--
Unigene72579_All	--

Unigene72590_All	--
Unigene72613_All	--
Unigene72614_All	--
Unigene72629_All	--
Unigene72661_All	--
Unigene72695_All	--
Unigene72716_All	--
Unigene72736_All	--
Unigene7283_All	--
Unigene72861_All	--
Unigene72887_All	--
Unigene72942_All	--
Unigene72970_All	--
Unigene729_All	SH2 domain-containing adapter protein F OS=Homo sapiens GN=SHF PE=1 SV=2
Unigene73008_All	--
Unigene73068_All	--
Unigene73084_All	--
Unigene73098_All	--
Unigene7315_All	--
Unigene7320_All	General transcription factor II-I repeat domain-containing protein 2 OS=Bos taurus GN=GTF2IRD2 PE=2 SV=1
Unigene73247_All	--
Unigene7327_All	--
Unigene73320_All	--
Unigene7340_All	--
Unigene73410_All	--
Unigene73435_All	--
Unigene73468_All	--
Unigene73470_All	--
Unigene73522_All	--
Unigene73545_All	--
Unigene7362_All	--
Unigene73661_All	--
Unigene73687_All	--
Unigene73710_All	Zinc finger CCCH domain-containing protein 15 homolog OS=Dictyostelium discoideum GN=DDB_G0292410 PE=3 SV=1
Unigene73747_All	--
Unigene7375_All	--
Unigene73767_All	--

Unigene73794_All	FMRFamide-related neuropeptides OS=Procambarus clarkii PE=1 SV=1
Unigene73816_All	--
Unigene73824_All	--
Unigene73877_All	--
Unigene73882_All	--
Unigene73885_All	Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2
Unigene73928_All	--
Unigene73933_All	--
Unigene73934_All	--
Unigene73935_All	--
Unigene73938_All	--
Unigene73943_All	--
Unigene73948_All	--
Unigene73952_All	--
Unigene73957_All	--
Unigene73958_All	--
Unigene73963_All	--
Unigene73971_All	--
Unigene7397_All	--
Unigene73_All	Salivary glue protein Sgs-3 OS=Drosophila melanogaster GN=Sgs3 PE=2 SV=1
Unigene74008_All	--
Unigene74009_All	--
Unigene7400_All	--
Unigene74015_All	--
Unigene74028_All	--
Unigene74031_All	--
Unigene74046_All	--
Unigene7404_All	--
Unigene74050_All	--
Unigene74053_All	--
Unigene74070_All	Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2
Unigene74080_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene74091_All	--
Unigene74097_All	Neurogenic locus protein delta OS=Drosophila melanogaster GN=Dl PE=1 SV=2
Unigene74105_All	--
Unigene74125_All	--
Unigene74136_All	--

Unigene74172_All	--
Unigene74201_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene7421_All	--
Unigene74252_All	--
Unigene74284_All	--
Unigene74303_All	--
Unigene7437_All	--
Unigene7440_All	--
Unigene74410_All	--
Unigene7442_All	--
Unigene74519_All	--
Unigene74562_All	--
Unigene74627_All	--
Unigene74640_All	--
Unigene74671_All	--
Unigene74708_All	--
Unigene7470_All	--
Unigene74736_All	--
Unigene74769_All	--
Unigene74775_All	Circadian clock-controlled protein OS=Drosophila yakuba GN=anon-3B1.2 PE=3 SV=1
Unigene7477_All	--
Unigene74794_All	--
Unigene74822_All	F-box/WD repeat-containing protein sel-10 OS=Caenorhabditis elegans GN=sel-10 PE=1 SV=3
Unigene74844_All	--
Unigene74862_All	--
Unigene7486_All	--
Unigene75003_All	--
Unigene75076_All	--
Unigene75309_All	--
Unigene7531_All	--
Unigene75326_All	--
Unigene75358_All	--
Unigene75369_All	--
Unigene75378_All	--
Unigene753_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
Unigene75402_All	--
Unigene75406_All	--
Unigene7540_All	--

Unigene75413_All	--
Unigene7541_All	--
Unigene75482_All	--
Unigene75490_All	--
Unigene75680_All	--
Unigene75682_All	--
Unigene75753_All	Transmembrane protease serine 13 OS=Mus musculus GN=Tmprss13 PE=2 SV=2
Unigene75772_All	--
Unigene75786_All	--
Unigene75791_All	--
Unigene75820_All	--
Unigene75842_All	Probable sodium/potassium/calcium exchanger CG1090 OS=Drosophila melanogaster GN=CG1090 PE=2 SV=3
Unigene75863_All	--
Unigene75907_All	--
Unigene75993_All	--
Unigene76013_All	--
Unigene76025_All	--
Unigene76055_All	--
Unigene76104_All	--
Unigene76108_All	--
Unigene76122_All	--
Unigene76171_All	--
Unigene76182_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
Unigene76222_All	--
Unigene76227_All	Fatty acyl-CoA reductase 1 OS=Xenopus laevis GN=far1 PE=2 SV=1
Unigene76265_All	--
Unigene76273_All	--
Unigene76279_All	--
Unigene76283_All	--
Unigene76289_All	--
Unigene76307_All	--
Unigene76334_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
Unigene76339_All	--
Unigene76359_All	--
Unigene76400_All	--
Unigene76402_All	--

Unigene76426_All	--
Unigene76436_All	--
Unigene76478_All	--
Unigene76488_All	--
Unigene76513_All	--
Unigene7653_All	--
Unigene76543_All	--
Unigene76559_All	--
Unigene76566_All	--
Unigene7657_All	--
Unigene76622_All	--
Unigene76641_All	Diuretic hormone OS=Locusta migratoria PE=1 SV=1
Unigene76648_All	--
Unigene76703_All	--
Unigene76714_All	--
Unigene76725_All	--
Unigene7673_All	--
Unigene76754_All	--
Unigene76758_All	--
Unigene76784_All	--
Unigene76788_All	--
Unigene76795_All	--
Unigene76810_All	--
Unigene7742_All	--
Unigene7781_All	--
Unigene778_All	--
Unigene77974_All	--
Unigene7838_All	--
Unigene7840_All	--
Unigene7858_All	--
Unigene7864_All	--
Unigene7878_All	Tigger transposable element-derived protein 4 OS=Homo sapiens GN=TIGD4 PE=2 SV=2
Unigene7890_All	--
Unigene7916_All	--
Unigene7986_All	--
Unigene7992_All	--
Unigene79_All	Allergen Cr-PI OS=Periplaneta americana PE=1 SV=1
Unigene7_All	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1
Unigene8015_All	--
Unigene8029_All	--

Unigene8055_All	--
Unigene8057_All	--
Unigene8065_All	--
Unigene8140_All	--
Unigene8145_All	--
Unigene8209_All	--
Unigene8228_All	--
Unigene822_All	--
Unigene8246_All	--
Unigene8248_All	--
Unigene8253_All	--
Unigene8260_All	--
Unigene826_All	--
Unigene8272_All	--
Unigene82_All	Allergen Cr-PI OS=Periplaneta americana PE=1 SV=1
Unigene8327_All	--
Unigene834_All	--
Unigene840_All	--
Unigene8428_All	--
Unigene8439_All	--
Unigene8454_All	--
Unigene8479_All	--
Unigene8492_All	--
Unigene8547_All	Tigger transposable element-derived protein 1 OS=Homo sapiens GN=TIGD1 PE=1 SV=1
Unigene8568_All	Vanin-like protein 3 OS=Drosophila melanogaster GN=CG32750 PE=3 SV=1
Unigene8624_All	--
Unigene863_All	--
Unigene864_All	Endothelin-converting enzyme 1 OS=Homo sapiens GN=ECE1 PE=1 SV=2
Unigene865_All	Troponin C, isoform 3 OS=Drosophila melanogaster GN=TpnC73F PE=2 SV=2
Unigene8666_All	--
Unigene8669_All	--
Unigene8674_All	--
Unigene8697_All	--
Unigene8704_All	--
Unigene8809_All	--
Unigene8815_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene8874_All	--
Unigene8893_All	--

Unigene8914_All	Glucose dehydrogenase [acceptor] OS=Drosophila melanogaster GN=Gld PE=3 SV=3
Unigene8978_All	--
Unigene8986_All	--
Unigene8988_All	--
Unigene9012_All	--
Unigene9038_All	--
Unigene9103_All	--
Unigene9123_All	--
Unigene9133_All	--
Unigene915_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene9164_All	--
Unigene9181_All	--
Unigene9247_All	--
Unigene9282_All	Craniofacial development protein 2 OS=Bos taurus GN=CFDP2 PE=1 SV=2
Unigene9287_All	--
Unigene9293_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene9304_All	--
Unigene9333_All	--
Unigene9364_All	--
Unigene9366_All	--
Unigene9381_All	--
Unigene9401_All	--
Unigene9403_All	--
Unigene9416_All	--
Unigene9447_All	--
Unigene9461_All	Spindle pole body component 97 OS=Dictyostelium discoideum GN=spc97 PE=2 SV=2
Unigene947_All	TWiK family of potassium channels protein 7 OS=Caenorhabditis elegans GN=twk-7 PE=3 SV=3
Unigene9488_All	--
Unigene952_All	--
Unigene9547_All	--
Unigene9594_All	Inactive pancreatic lipase-related protein 1 OS=Homo sapiens GN=PNLIPRP1 PE=1 SV=1
Unigene9646_All	--
Unigene964_All	--
Unigene9663_All	--
Unigene9666_All	--

Unigene9676_All	--
Unigene9677_All	--
Unigene9684_All	--
Unigene96933_All	--
Unigene97086_All	--
Unigene97124_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
Unigene97147_All	--
Unigene9720_All	--
Unigene97292_All	--
Unigene97400_All	--
Unigene9748_All	Heat shock protein 68 OS=Drosophila melanogaster GN=Hsp68 PE=1 SV=1
Unigene974_All	--
Unigene97516_All	Chorion peroxidase OS=Drosophila melanogaster GN=Pxt PE=2 SV=3
Unigene9759_All	--
Unigene97605_All	--
Unigene97664_All	--
Unigene97707_All	--
Unigene97720_All	--
Unigene97731_All	--
Unigene97823_All	--
Unigene97930_All	--
Unigene9794_All	--
Unigene9798_All	--
Unigene98003_All	--
Unigene98037_All	--
Unigene9804_All	--
Unigene98066_All	--
Unigene98122_All	--
Unigene98130_All	--
Unigene98140_All	Glutamate receptor ionotropic, kainate 5 OS=Homo sapiens GN=GRIK5 PE=2 SV=2
Unigene98150_All	--
Unigene9829_All	PAX-interacting protein 1 OS=Xenopus laevis GN=paxip1 PE=1 SV=1
Unigene9845_All	Desumoylating isopeptidase 1 OS=Homo sapiens GN=DESI1 PE=1 SV=1
Unigene987_All	--
Unigene9907_All	Myosin heavy chain, muscle OS=Drosophila melanogaster GN=Mhc PE=1 SV=4
Unigene9922_All	PIH1 domain-containing protein 1 OS=Xenopus laevis GN=pih1d1 PE=2 SV=1

Unigene99415_All	--
Unigene9947_All	Fatty acid synthase OS=Rattus norvegicus GN=Fasn PE=1 SV=3
Unigene99579_All	--
Unigene99587_All	--
Unigene99628_All	--
Unigene99687_All	--
Unigene9969_All	Muscle M-line assembly protein unc-89 OS=Caenorhabditis elegans GN=unc-89 PE=1 SV=3
Unigene9990_All	Fatty acyl-CoA reductase 1 OS=Xenopus laevis GN=far1 PE=2 SV=1
Unigene9995_All	--
Unigene99960_All	--
Unigene999_All	--
Down-regulated genes related to development	
geneID	Swissprot-annotation
CL10001.Contig1_All	--
CL10043.Contig2_All	--
CL10054.Contig2_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3
CL10106.Contig2_All	--
CL10110.Contig1_All	--
CL10118.Contig1_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
CL10135.Contig1_All	--
CL1014.Contig2_All	F-box only protein 28 OS=Homo sapiens GN=FBXO28 PE=1 SV=1
CL10147.Contig1_All	Mucin-22 OS=Homo sapiens GN=MUC22 PE=1 SV=2
CL10154.Contig1_All	--
CL10188.Contig1_All	Phosphoserine aminotransferase OS=Mus musculus GN=Psat1 PE=1 SV=1
CL10190.Contig2_All	Facilitated trehalose transporter Tret1 OS=Aedes aegypti GN=Tret1 PE=3 SV=1
CL102.Contig1_All	--
CL102.Contig5_All	--
CL102.Contig6_All	--
CL10200.Contig2_All	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] A OS=Dictyostelium discoideum GN=tpsA PE=2 SV=1
CL10217.Contig10_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
CL10217.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2

CL10217.Contig2_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
CL10217.Contig4_All	Probable RNA-directed DNA polymerase from transposon X-element OS=Drosophila melanogaster GN=X-element\ORF2 PE=3 SV=1
CL10217.Contig7_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL10220.Contig1_All	SprT-like domain-containing protein Spartan OS=Rattus norvegicus GN=Sprtn PE=2 SV=1
CL10242.Contig2_All	Mitochondrial sodium/hydrogen exchanger 9B2 OS=Homo sapiens GN=SLC9B2 PE=1 SV=2
CL10255.Contig1_All	--
CL10264.Contig1_All	--
CL10264.Contig2_All	--
CL10264.Contig3_All	--
CL10264.Contig4_All	--
CL10266.Contig2_All	--
CL10282.Contig1_All	Argininosuccinate lyase OS=Lithobates catesbeiana GN=ASL PE=3 SV=1
CL10282.Contig2_All	Argininosuccinate lyase OS=Lithobates catesbeiana GN=ASL PE=3 SV=1
CL10303.Contig1_All	Retrovirus-related Pol polyprotein from type-2 retrotransposable element R2DM OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL10304.Contig1_All	--
CL1033.Contig2_All	Folliculin OS=Xenopus tropicalis GN=flcn PE=2 SV=1
CL10341.Contig1_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL10341.Contig2_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL10341.Contig3_All	Loricrin OS=Mus musculus GN=Lor PE=2 SV=2
CL10341.Contig4_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL10341.Contig5_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
CL10369.Contig5_All	Alpha-taxilin OS=Mus musculus GN=Txlna PE=2 SV=1
CL10384.Contig1_All	Spidroin-2 (Fragment) OS=Nephila clavipes PE=2 SV=1
CL10389.Contig1_All	--
CL10389.Contig2_All	--
CL10392.Contig2_All	Peroxisome proliferator-activated receptor gamma coactivator-related protein 1 OS=Homo sapiens GN=PPRC1 PE=1 SV=1
CL10429.Contig1_All	--
CL10429.Contig2_All	--

CL1045.Contig3_All	--
CL10456.Contig5_All	Salivary glue protein Sgs-3 OS=Drosophila yakuba GN=Sgs3 PE=2 SV=3
CL10468.Contig1_All	--
CL10469.Contig2_All	Nesprin-1 OS=Mus musculus GN=Syne1 PE=1 SV=2
CL10469.Contig3_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL10469.Contig4_All	Nesprin-1 OS=Mus musculus GN=Syne1 PE=1 SV=2
CL10469.Contig5_All	Nesprin-1 OS=Mus musculus GN=Syne1 PE=1 SV=2
CL10469.Contig6_All	Nesprin-1 OS=Mus musculus GN=Syne1 PE=1 SV=2
CL10508.Contig2_All	--
CL10516.Contig1_All	--
CL10548.Contig2_All	5'-3' exoribonuclease 1 OS=Mus musculus GN=Xrn1 PE=1 SV=1
CL10548.Contig3_All	Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2
CL1055.Contig1_All	--
CL1056.Contig1_All	--
CL10561.Contig1_All	--
CL10579.Contig2_All	--
CL10603.Contig1_All	--
CL10622.Contig1_All	--
CL10622.Contig2_All	--
CL10630.Contig2_All	--
CL10635.Contig1_All	--
CL1064.Contig1_All	--
CL10659.Contig1_All	--
CL10683.Contig1_All	--
CL10683.Contig2_All	--
CL10721.Contig1_All	--
CL10734.Contig1_All	NFX1-type zinc finger-containing protein 1 OS=Mus musculus GN=Znfx1 PE=2 SV=3
CL10755.Contig1_All	--
CL10762.Contig1_All	Formin-like protein 2 OS=Homo sapiens GN=FMNL2 PE=1 SV=3
CL10770.Contig2_All	--
CL10794.Contig1_All	Facilitated trehalose transporter Tret1 OS=Drosophila yakuba GN=Tret1 PE=3 SV=1
CL10823.Contig1_All	--
CL10823.Contig2_All	--
CL10825.Contig1_All	--
CL10848.Contig1_All	Sterol O-acyltransferase 2 OS=Mus musculus GN=Soat2 PE=2 SV=2
CL10864.Contig1_All	--

CL10887.Contig2_All	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Microtus ochrogaster GN=IDH1 PE=3 SV=1
CL1093.Contig3_All	--
CL1095.Contig1_All	Mariner Mos1 transposase OS=Drosophila mauritiana GN=mariner\T PE=1 SV=1
CL10956.Contig3_All	Glutamine and serine-rich protein 1 OS=Xenopus laevis GN=qser1 PE=2 SV=2
CL1097.Contig2_All	--
CL10987.Contig6_All	Twitchin OS=Caenorhabditis elegans GN=unc-22 PE=1 SV=3
CL1099.Contig12_All	--
CL10994.Contig2_All	Solute carrier family 35 member G1 OS=Mus musculus GN=Slc35g1 PE=2 SV=1
CL11005.Contig1_All	--
CL1103.Contig3_All	--
CL11057.Contig2_All	Zinc finger protein 34 OS=Bos taurus GN=ZNF34 PE=2 SV=1
CL11074.Contig2_All	Venom dipeptidyl peptidase 4 OS=Apis mellifera PE=1 SV=1
CL11088.Contig1_All	--
CL11089.Contig1_All	Transcription elongation regulator 1 OS=Mus musculus GN=Tcerg1 PE=1 SV=2
CL11089.Contig4_All	Protein lin-10 OS=Caenorhabditis elegans GN=lin-10 PE=1 SV=1
CL1109.Contig5_All	--
CL11090.Contig2_All	Octapeptide-repeat protein T2 OS=Mus musculus GN=Srst PE=2 SV=1
CL11092.Contig1_All	Probable polyketide synthase 45 OS=Dictyostelium discoideum GN=pks45 PE=3 SV=2
CL11107.Contig1_All	40S ribosomal protein S30 OS=Rattus norvegicus GN=Fau PE=1 SV=1
CL11125.Contig3_All	--
CL11129.Contig1_All	Elongation of very long chain fatty acids protein AAEL008004 OS=Aedes aegypti GN=AAEL008004 PE=2 SV=2
CL11133.Contig1_All	40S ribosomal protein S25 OS=Spodoptera frugiperda GN=RpS25 PE=3 SV=1
CL11177.Contig2_All	Vesicular glutamate transporter 2 OS=Rattus norvegicus GN=Slc17a6 PE=1 SV=1
CL11177.Contig3_All	Vesicular glutamate transporter 2 OS=Bos taurus GN=SLC17A6 PE=2 SV=1
CL11188.Contig1_All	--
CL11209.Contig1_All	--
CL11222.Contig3_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3

CL11230.Contig1_All	--
CL11258.Contig3_All	Zinc transporter 1 OS=Macaca fascicularis GN=SLC30A1 PE=2 SV=1
CL1126.Contig1_All	--
CL1128.Contig3_All	Protein yellow OS=Drosophila erecta GN=y PE=3 SV=1
CL1128.Contig5_All	Protein yellow OS=Drosophila pseudoobscura pseudoobscura GN=y PE=3 SV=2
CL1128.Contig6_All	Protein yellow OS=Drosophila pseudoobscura pseudoobscura GN=y PE=3 SV=2
CL11304.Contig1_All	--
CL1131.Contig2_All	--
CL1135.Contig1_All	--
CL11383.Contig1_All	--
CL11416.Contig2_All	--
CL11423.Contig2_All	Tensin-1 OS=Bos taurus GN=TNS1 PE=2 SV=1
CL11459.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
CL11466.Contig1_All	--
CL11466.Contig2_All	--
CL11475.Contig1_All	Microtubule-associated protein futsch OS=Drosophila melanogaster GN=futsch PE=1 SV=4
CL1150.Contig1_All	Beclin-1-like protein OS=Drosophila melanogaster GN=Atg6 PE=2 SV=1
CL11511.Contig19_All	--
CL11529.Contig1_All	--
CL11567.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
CL11578.Contig1_All	Phospholipase B1, membrane-associated OS=Monodelphis domestica GN=PLB1 PE=2 SV=1
CL11587.Contig2_All	--
CL11589.Contig1_All	Steroid hormone receptor ERR1 OS=Canis familiaris GN=ESRRA PE=2 SV=1
CL11591.Contig1_All	--
CL11591.Contig3_All	--
CL11645.Contig1_All	--
CL11671.Contig1_All	Tyrosine 3-monooxygenase OS=Drosophila melanogaster GN=ple PE=2 SV=2
CL11694.Contig2_All	Neuroserpin OS=Homo sapiens GN=SERPINI1 PE=1 SV=1
CL11696.Contig2_All	--
CL11697.Contig2_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL11708.Contig2_All	Transposable element Tcb1 transposase OS=Caenorhabditis briggsae PE=3 SV=1

CL11719.Contig2_All	Protein diaphanous OS=Drosophila melanogaster GN=dia PE=2 SV=2
CL11723.Contig4_All	ABC transporter G family member 20 OS=Dictyostelium discoideum GN=abcG20 PE=3 SV=1
CL11738.Contig2_All	--
CL11742.Contig2_All	--
CL11755.Contig2_All	--
CL11771.Contig1_All	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus GN=Acat1 PE=1 SV=1
CL11771.Contig2_All	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus GN=Acat1 PE=1 SV=1
CL11772.Contig2_All	--
CL11773.Contig1_All	--
CL11773.Contig2_All	--
CL11787.Contig1_All	--
CL1180.Contig2_All	Syntaxin-1A OS=Rattus norvegicus GN=Stx1a PE=1 SV=1
CL11833.Contig1_All	Fatty acyl-CoA reductase 1 OS=Xenopus laevis GN=far1 PE=2 SV=1
CL11844.Contig1_All	Myosin light chain kinase, smooth muscle OS=Mus musculus GN=Mylk PE=1 SV=3
CL11864.Contig4_All	Protein will die slowly OS=Drosophila melanogaster GN=wds PE=2 SV=1
CL11890.Contig2_All	Protein bric-a-brac 1 OS=Drosophila melanogaster GN=bab1 PE=2 SV=2
CL11909.Contig2_All	Protein distal antenna OS=Drosophila melanogaster GN=dan PE=1 SV=2
CL11929.Contig1_All	--
CL11939.Contig2_All	Programmed cell death 6-interacting protein OS=Mus musculus GN=Pdcd6ip PE=1 SV=3
CL11975.Contig1_All	--
CL11982.Contig1_All	--
CL11990.Contig2_All	--
CL12049.Contig2_All	--
CL12076.Contig2_All	--
CL12078.Contig1_All	--
CL12110.Contig2_All	--
CL12118.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL12119.Contig1_All	Neurexin-4 OS=Drosophila melanogaster GN=Nrx-IV PE=1 SV=2
CL12119.Contig2_All	Neurexin-4 OS=Drosophila melanogaster GN=Nrx-IV PE=1 SV=2
CL12119.Contig3_All	Neurexin-4 OS=Drosophila melanogaster GN=Nrx-IV PE=1 SV=2

CL12134.Contig1_All	--
CL12167.Contig10_All	--
CL12167.Contig2_All	--
CL12167.Contig9_All	--
CL12184.Contig2_All	--
CL1221.Contig1_All	--
CL12232.Contig1_All	--
CL12238.Contig2_All	--
CL12246.Contig1_All	--
CL12249.Contig2_All	--
CL1225.Contig2_All	Otopetrin-2 OS=Mus musculus GN=Otop2 PE=2 SV=1
CL1225.Contig3_All	Otopetrin-2 OS=Mus musculus GN=Otop2 PE=2 SV=1
CL1225.Contig5_All	Otopetrin-2 OS=Mus musculus GN=Otop2 PE=2 SV=1
CL12255.Contig1_All	--
CL12262.Contig1_All	--
CL12262.Contig3_All	--
CL12265.Contig2_All	Solute carrier family 25 member 40 OS=Xenopus tropicalis GN=slc25a40 PE=2 SV=1
CL12269.Contig1_All	--
CL12272.Contig1_All	--
CL1229.Contig1_All	Vasotab OS=Hybomitra bimaculata PE=1 SV=1
CL1229.Contig2_All	Vasotab OS=Hybomitra bimaculata PE=1 SV=1
CL1229.Contig3_All	--
CL12303.Contig4_All	Voltage-dependent calcium channel subunit alpha-2/delta-3 OS=Rattus norvegicus GN=Cacna2d3 PE=2 SV=1
CL12311.Contig1_All	Anterior pharynx in excess protein 1 OS=Caenorhabditis elegans GN=apx-1 PE=2 SV=1
CL12311.Contig2_All	von Willebrand factor D and EGF domain-containing protein OS=Homo sapiens GN=VWDE PE=2 SV=4
CL12313.Contig1_All	--
CL12319.Contig2_All	--
CL1232.Contig2_All	--
CL1233.Contig1_All	--
CL12335.Contig4_All	--
CL12340.Contig1_All	--
CL12340.Contig3_All	--
CL12351.Contig2_All	--
CL1236.Contig2_All	--
CL12369.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL1239.Contig2_All	--
CL1239.Contig3_All	--

CL1239.Contig4_All	--
CL12396.Contig1_All	Tryptase OS=Sus scrofa GN=MCT7 PE=2 SV=1
CL1240.Contig2_All	--
CL12416.Contig1_All	Scavenger receptor class F member 2 OS=Homo sapiens GN=SCARF2 PE=1 SV=4
CL12437.Contig1_All	--
CL12441.Contig1_All	Inositol-3-phosphate synthase 1-B OS=Xenopus laevis GN=isyna1-b PE=2 SV=2
CL12441.Contig2_All	Inositol-3-phosphate synthase 1-B OS=Xenopus laevis GN=isyna1-b PE=2 SV=2
CL12451.Contig1_All	--
CL12451.Contig2_All	--
CL12466.Contig1_All	--
CL12466.Contig2_All	--
CL12466.Contig3_All	--
CL12473.Contig1_All	--
CL12473.Contig2_All	--
CL12474.Contig2_All	--
CL12479.Contig1_All	Sulfhydryl oxidase 1 OS=Gallus gallus GN=QSOX1 PE=1 SV=1
CL12490.Contig1_All	--
CL12492.Contig1_All	Copia protein OS=Drosophila melanogaster GN=GIP PE=1 SV=3
CL12501.Contig2_All	Dentin sialophosphoprotein OS=Mus musculus GN=Dspp PE=1 SV=2
CL12501.Contig4_All	Dentin sialophosphoprotein OS=Mus musculus GN=Dspp PE=1 SV=2
CL12530.Contig3_All	Nuclear receptor coactivator 2 OS=Mus musculus GN=Ncoa2 PE=1 SV=3
CL1256.Contig14_All	RNA-binding protein fusilli OS=Drosophila melanogaster GN=fus PE=2 SV=1
CL12568.Contig2_All	Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 PE=1 SV=3
CL12579.Contig1_All	Phospholipase D1 OS=Rattus norvegicus GN=Pld1 PE=1 SV=3
CL12588.Contig3_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
CL1260.Contig10_All	--
CL1260.Contig15_All	--
CL1260.Contig1_All	--
CL1260.Contig6_All	--
CL12602.Contig4_All	E3 ubiquitin-protein ligase TRIP12 OS=Bos taurus GN=TRIP12 PE=2 SV=2
CL12634.Contig1_All	--
CL12639.Contig1_All	--

CL12645.Contig1_All	Coiled-coil domain-containing protein 74B OS=Homo sapiens GN=CCDC74B PE=2 SV=1
CL12660.Contig2_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL12687.Contig1_All	Thrombospondin type-1 domain-containing protein 7B OS=Homo sapiens GN=THSD7B PE=2 SV=2
CL12687.Contig2_All	Thrombospondin type-1 domain-containing protein 7B OS=Homo sapiens GN=THSD7B PE=2 SV=2
CL12690.Contig1_All	--
CL12734.Contig2_All	Transcriptional repressor p66-beta OS=Homo sapiens GN=GATAD2B PE=1 SV=1
CL12737.Contig1_All	Sodium-coupled monocarboxylate transporter 1 OS=Homo sapiens GN=SLC5A8 PE=1 SV=2
CL12738.Contig1_All	--
CL12744.Contig3_All	S-adenosylmethionine decarboxylase proenzyme OS=Drosophila melanogaster GN=SamDC PE=2 SV=1
CL12753.Contig1_All	--
CL12758.Contig1_All	--
CL12769.Contig1_All	--
CL12769.Contig2_All	--
CL12796.Contig1_All	--
CL12811.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL12842.Contig1_All	--
CL12849.Contig1_All	--
CL12857.Contig1_All	Solute carrier family 2, facilitated glucose transporter member 1 OS=Oryctolagus cuniculus GN=SLC2A1 PE=2 SV=1
CL12860.Contig2_All	--
CL12877.Contig1_All	Long-chain fatty acid transport protein 1 OS=Homo sapiens GN=SLC27A1 PE=2 SV=1
CL12892.Contig1_All	--
CL12907.Contig3_All	Sialin OS=Mus musculus GN=Slc17a5 PE=2 SV=2
CL12918.Contig2_All	Acetylcholine receptor subunit alpha-like OS=Manduca sexta GN=ARA1 PE=2 SV=1
CL1292.Contig1_All	--
CL12949.Contig1_All	--
CL12990.Contig4_All	--
CL130.Contig1_All	Esterase FE4 OS=Myzus persicae PE=1 SV=1
CL13033.Contig2_All	--
CL13042.Contig1_All	--
CL13042.Contig2_All	--
CL13042.Contig3_All	--

CL13052.Contig1_All	--
CL13053.Contig2_All	Interaptin OS=Dictyostelium discoideum GN=abpD PE=1 SV=1
CL13053.Contig3_All	Transcription factor SPT20 homolog OS=Dictyostelium discoideum GN=DDB_G0280065 PE=3 SV=1
CL13066.Contig1_All	--
CL13112.Contig1_All	Carboxypeptidase D OS=Drosophila melanogaster GN=svr PE=1 SV=2
CL13112.Contig2_All	Carboxypeptidase D OS=Drosophila melanogaster GN=svr PE=1 SV=2
CL13112.Contig3_All	Carboxypeptidase D OS=Anas platyrhynchos GN=CPD PE=1 SV=1
CL1312.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL1312.Contig2_All	Protein takeout OS=Drosophila melanogaster GN=to PE=2 SV=1
CL1312.Contig3_All	Protein takeout OS=Drosophila melanogaster GN=to PE=2 SV=1
CL13135.Contig1_All	--
CL13135.Contig3_All	--
CL13135.Contig4_All	--
CL1318.Contig2_All	--
CL13191.Contig2_All	Antigen WC1.1 OS=Bos taurus PE=2 SV=1
CL13194.Contig1_All	--
CL13200.Contig2_All	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1
CL13200.Contig3_All	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1
CL13274.Contig2_All	--
CL1328.Contig2_All	--
CL13292.Contig1_All	--
CL13298.Contig1_All	Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1
CL13298.Contig2_All	Leukocyte elastase inhibitor OS=Bos taurus GN=SERPINB1 PE=2 SV=2
CL13298.Contig3_All	Leukocyte elastase inhibitor OS=Bos taurus GN=SERPINB1 PE=2 SV=2
CL13298.Contig4_All	Leukocyte elastase inhibitor OS=Bos taurus GN=SERPINB1 PE=2 SV=2
CL13305.Contig1_All	--
CL13331.Contig1_All	--
CL13363.Contig2_All	Spondin-1 OS=Gallus gallus GN=SPON1 PE=2 SV=1
CL13380.Contig1_All	--
CL1341.Contig2_All	--
CL13432.Contig1_All	Protein yellow OS=Drosophila erecta GN=y PE=3 SV=1

CL13440.Contig2_All	Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3
CL1345.Contig1_All	--
CL1345.Contig3_All	--
CL13526.Contig2_All	--
CL13535.Contig2_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL1355.Contig3_All	Vesicular glutamate transporter 3 OS=Danio rerio GN=slc17a8 PE=3 SV=2
CL13561.Contig4_All	--
CL13561.Contig6_All	--
CL13561.Contig7_All	Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3
CL13561.Contig8_All	Leucine-rich repeat-containing protein 15 OS=Rattus norvegicus GN=Lrrc15 PE=2 SV=1
CL13565.Contig1_All	Lysosome membrane protein 2 OS=Mus musculus GN=Scarb2 PE=1 SV=3
CL13565.Contig2_All	Lysosome membrane protein 2 OS=Mus musculus GN=Scarb2 PE=1 SV=3
CL13568.Contig1_All	Atrial natriuretic peptide-converting enzyme OS=Mus musculus GN=Corin PE=2 SV=2
CL13581.Contig1_All	--
CL13581.Contig2_All	Probable aminopeptidase NPEPL1 OS=Pongo abelii GN=NPEPL1 PE=3 SV=2
CL13584.Contig1_All	Alpha-amylase 2 OS=Drosophila ananassae GN=Amy58 PE=3 SV=2
CL13599.Contig1_All	--
CL1360.Contig2_All	--
CL13607.Contig1_All	Sulfatase-modifying factor 1 OS=Bos taurus GN=SUMF1 PE=2 SV=1
CL13631.Contig1_All	Short-chain dehydrogenase/reductase family 9C member 7 OS=Homo sapiens GN=SDR9C7 PE=2 SV=1
CL13640.Contig1_All	--
CL13677.Contig1_All	--
CL13677.Contig2_All	--
CL13678.Contig2_All	Retinoid-inducible serine carboxypeptidase OS=Rattus norvegicus GN=Scpep1 PE=2 SV=1
CL13685.Contig2_All	--
CL137.Contig1_All	--
CL137.Contig2_All	--
CL137.Contig3_All	--
CL137.Contig4_All	--
CL137.Contig5_All	--
CL137.Contig6_All	--

CL13723.Contig2_All	Insulin-like growth factor-binding protein complex acid labile subunit OS=Papio hamadryas GN=IGFALS PE=2 SV=1
CL13729.Contig3_All	Protein-methionine sulfoxide oxidase MICAL3 OS=Homo sapiens GN=MICAL3 PE=1 SV=2
CL13741.Contig2_All	--
CL13778.Contig2_All	--
CL13790.Contig1_All	WD repeat-containing protein 74 OS=Bos taurus GN=WDR74 PE=2 SV=1
CL1380.Contig4_All	Translation initiation factor IF-2, mitochondrial OS=Bos taurus GN=MTIF2 PE=1 SV=1
CL13804.Contig1_All	--
CL13804.Contig2_All	--
CL13818.Contig6_All	--
CL13836.Contig1_All	Protein krueppel OS=Drosophila melanogaster GN=Kr PE=1 SV=2
CL13836.Contig2_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL1384.Contig1_All	MD-2-related lipid-recognition protein OS=Manduca sexta PE=1 SV=1
CL13847.Contig1_All	--
CL13860.Contig2_All	--
CL13893.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL13893.Contig2_All	--
CL13921.Contig2_All	--
CL13948.Contig1_All	--
CL13956.Contig1_All	--
CL13957.Contig1_All	Coiled-coil domain-containing protein 177 OS=Mus musculus GN=Ccdc177 PE=1 SV=1
CL13973.Contig1_All	--
CL14017.Contig1_All	--
CL14024.Contig1_All	Myosin-J heavy chain OS=Dictyostelium discoideum GN=myoJ PE=4 SV=2
CL14032.Contig1_All	Clavesin-2 OS=Macaca fascicularis GN=CLVS2 PE=2 SV=2
CL14032.Contig2_All	Clavesin-2 OS=Macaca fascicularis GN=CLVS2 PE=2 SV=2
CL14033.Contig2_All	Retrovirus-related Pol polyprotein from transposon 17.6 OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL14052.Contig1_All	Fatty acyl-CoA reductase 1 OS=Rattus norvegicus GN=Far1 PE=2 SV=1
CL14055.Contig1_All	--
CL14055.Contig2_All	--
CL14055.Contig3_All	--

CL14065.Contig1_All	--
CL14073.Contig2_All	--
CL14089.Contig1_All	PiggyBac transposable element-derived protein 4 OS=Homo sapiens GN=PGBD4 PE=2 SV=3
CL14115.Contig1_All	--
CL1412.Contig2_All	--
CL14124.Contig1_All	--
CL14126.Contig1_All	C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2
CL14136.Contig2_All	Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1
CL14137.Contig2_All	Endoribonuclease Dcr-1 OS=Drosophila melanogaster GN=Dcr-1 PE=1 SV=1
CL14141.Contig1_All	--
CL14156.Contig1_All	--
CL14180.Contig1_All	--
CL14208.Contig2_All	--
CL14225.Contig2_All	--
CL14237.Contig1_All	DNA-directed RNA polymerase II subunit RPB1 OS=Mus musculus GN=Polr2a PE=1 SV=3
CL14270.Contig1_All	--
CL1428.Contig2_All	Copper-transporting ATPase 1 OS=Homo sapiens GN=ATP7A PE=1 SV=3
CL1428.Contig3_All	Copper-transporting ATPase 1 OS=Rattus norvegicus GN=Atp7a PE=1 SV=1
CL14333.Contig1_All	Protein bowel OS=Drosophila melanogaster GN=bowl PE=1 SV=1
CL14344.Contig3_All	Bridging integrator 3 OS=Rattus norvegicus GN=Bin3 PE=2 SV=1
CL14358.Contig1_All	--
CL14358.Contig2_All	--
CL14358.Contig3_All	--
CL14362.Contig1_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
CL14362.Contig2_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL14362.Contig3_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL14398.Contig1_All	--
CL14399.Contig1_All	WD repeat-containing protein 67 OS=Homo sapiens GN=WDR67 PE=2 SV=2
CL14403.Contig1_All	Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2
CL14437.Contig1_All	--
CL14437.Contig2_All	--
CL14477.Contig1_All	--

CL14485.Contig1_All	--
CL14508.Contig2_All	--
CL1451.Contig1_All	--
CL14533.Contig3_All	Glutathione synthetase OS=Xenopus laevis GN=gss PE=2 SV=1
CL14539.Contig1_All	--
CL14544.Contig1_All	--
CL14544.Contig2_All	--
CL14550.Contig1_All	--
CL14586.Contig2_All	--
CL1459.Contig2_All	Thymic stromal cotransporter protein OS=Mus musculus GN=Slc46a2 PE=1 SV=2
CL14590.Contig3_All	Cytosolic purine 5'-nucleotidase OS=Pongo abelii GN=NT5C2 PE=2 SV=1
CL14603.Contig1_All	--
CL14612.Contig2_All	--
CL14624.Contig1_All	--
CL14626.Contig1_All	--
CL14627.Contig1_All	--
CL14635.Contig1_All	Lactase-like protein OS=Mus musculus GN=Lctl PE=2 SV=1
CL14656.Contig2_All	Low-density lipoprotein receptor OS=Rattus norvegicus GN=Ldlr PE=2 SV=1
CL14659.Contig1_All	Sensory neuron membrane protein 1 OS=Apis mellifera PE=3 SV=1
CL14659.Contig2_All	Sensory neuron membrane protein 1 OS=Apis mellifera PE=3 SV=1
CL14709.Contig2_All	Myotubularin-related protein 14 OS=Homo sapiens GN=MTMR14 PE=1 SV=2
CL1471.Contig2_All	Protein phosphatase 1 regulatory subunit 14C OS=Homo sapiens GN=PPP1R14C PE=1 SV=3
CL14716.Contig3_All	ARL14 effector protein OS=Rattus norvegicus GN=Arl14ep PE=2 SV=1
CL14727.Contig1_All	Synaptotagmin-like protein 5 OS=Homo sapiens GN=SYTL5 PE=1 SV=1
CL14738.Contig2_All	--
CL1474.Contig1_All	--
CL14783.Contig1_All	DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5
CL14785.Contig1_All	Esterase FE4 OS=Myzus persicae PE=1 SV=1
CL14803.Contig1_All	--
CL14806.Contig2_All	Protein yellow OS=Drosophila subobscura GN=y PE=3 SV=1
CL14806.Contig3_All	--
CL14892.Contig1_All	--

CL14945.Contig1_All	--
CL14968.Contig1_All	--
CL14968.Contig2_All	--
CL14985.Contig1_All	Superoxide dismutase [Cu-Zn] OS=Drosophila willistoni GN=Sod PE=3 SV=2
CL1500.Contig1_All	--
CL15041.Contig2_All	--
CL15069.Contig1_All	Ras-related protein Rab-7L1 OS=Pongo abelii GN=RAB7L1 PE=2 SV=1
CL15092.Contig1_All	--
CL15108.Contig3_All	Calpain-A OS=Drosophila melanogaster GN=CalpA PE=1 SV=2
CL15114.Contig1_All	E3 ubiquitin-protein ligase TRIM71 OS=Danio rerio GN=trim71 PE=2 SV=1
CL15114.Contig2_All	E3 ubiquitin-protein ligase TRIM71 OS=Danio rerio GN=trim71 PE=2 SV=1
CL15114.Contig3_All	E3 ubiquitin-protein ligase TRIM71 OS=Danio rerio GN=trim71 PE=2 SV=1
CL15125.Contig1_All	--
CL1515.Contig2_All	Uncharacterized protein CG10915 OS=Drosophila melanogaster GN=CG10915 PE=1 SV=1
CL15163.Contig1_All	--
CL15167.Contig2_All	Selenium-binding protein 1 OS=Xenopus tropicalis GN=selenbp1 PE=2 SV=1
CL1517.Contig2_All	--
CL1517.Contig3_All	--
CL15175.Contig3_All	Astakine OS=Penaeus monodon PE=2 SV=1
CL15197.Contig1_All	--
CL152.Contig3_All	--
CL15222.Contig2_All	--
CL15223.Contig1_All	--
CL15270.Contig2_All	Arylsulfatase I OS=Canis familiaris GN=ARSI PE=2 SV=2
CL15287.Contig1_All	Uncharacterized protein R102.4 OS=Caenorhabditis elegans GN=R102.4 PE=2 SV=3
CL15287.Contig2_All	Uncharacterized protein R102.4 OS=Caenorhabditis elegans GN=R102.4 PE=2 SV=3
CL15299.Contig1_All	--
CL153.Contig1_All	--
CL15301.Contig1_All	Spondin-2 OS=Homo sapiens GN=SPON2 PE=1 SV=3
CL15301.Contig2_All	Spondin-2 OS=Homo sapiens GN=SPON2 PE=1 SV=3
CL15305.Contig1_All	--
CL15325.Contig3_All	TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1

CL15369.Contig2_All	--
CL15406.Contig2_All	39S ribosomal protein L4, mitochondrial OS=Bos taurus GN=MRPL4 PE=1 SV=1
CL15409.Contig1_All	Prolargin OS=Rattus norvegicus GN=Prelp PE=2 SV=1
CL15409.Contig2_All	PH domain leucine-rich repeat-containing protein phosphatase 1 OS=Homo sapiens GN=PHLPP1 PE=1 SV=3
CL15410.Contig2_All	--
CL15413.Contig1_All	Ecdysone-induced protein 74EF isoform B OS=Drosophila melanogaster GN=Eip74EF PE=2 SV=2
CL15413.Contig3_All	Ecdysone-induced protein 74EF isoform B OS=Drosophila melanogaster GN=Eip74EF PE=2 SV=2
CL15415.Contig1_All	--
CL15415.Contig2_All	--
CL15420.Contig2_All	--
CL15426.Contig8_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
CL1546.Contig2_All	GATA-binding factor A OS=Drosophila melanogaster GN=pnr PE=1 SV=1
CL1549.Contig3_All	--
CL15496.Contig2_All	--
CL15499.Contig1_All	--
CL1550.Contig1_All	Acrosin OS=Oryctolagus cuniculus GN=ACR PE=2 SV=1
CL1550.Contig2_All	Acrosin OS=Oryctolagus cuniculus GN=ACR PE=2 SV=1
CL1550.Contig3_All	--
CL1555.Contig1_All	G1/S-specific cyclin-E OS=Hemicentrotus pulcherrimus GN=CYCE PE=2 SV=1
CL15551.Contig1_All	Protein rtoA OS=Dictyostelium discoideum GN=rtoA PE=2 SV=2
CL15557.Contig1_All	--
CL15563.Contig1_All	--
CL15578.Contig1_All	--
CL15578.Contig2_All	--
CL1563.Contig1_All	A-kinase anchor protein 1, mitochondrial OS=Mus musculus GN=Akap1 PE=1 SV=4
CL15645.Contig1_All	Bromodomain-containing protein DDB_G0280777 OS=Dictyostelium discoideum GN=DDB_G0280777 PE=4 SV=1
CL15701.Contig1_All	--
CL15728.Contig2_All	Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Rattus norvegicus GN=Ppp4r1 PE=2 SV=1
CL1577.Contig1_All	--
CL1577.Contig2_All	--

CL15869.Contig2_All	Dentin sialophosphoprotein OS=Homo sapiens GN=DSPP PE=1 SV=2
CL15881.Contig1_All	--
CL15881.Contig2_All	--
CL15882.Contig2_All	Syntaxin-12 OS=Mus musculus GN=Stx12 PE=1 SV=1
CL15886.Contig1_All	--
CL15886.Contig2_All	--
CL15901.Contig2_All	--
CL15908.Contig1_All	UPF0544 protein C5orf45 homolog OS=Danio rerio GN=zgc:123335 PE=2 SV=1
CL1591.Contig2_All	--
CL15912.Contig2_All	--
CL15919.Contig6_All	--
CL15925.Contig1_All	--
CL15925.Contig2_All	--
CL15949.Contig1_All	--
CL15949.Contig3_All	--
CL15957.Contig1_All	Solute carrier family 41 member 1 OS=Pongo abelii GN=SLC41A1 PE=2 SV=1
CL15992.Contig1_All	--
CL16019.Contig1_All	RanBP-type and C3HC4-type zinc finger-containing protein 1 OS=Dicentrarchus labrax GN=rbck1 PE=3 SV=1
CL16030.Contig2_All	Reticulon-4-interacting protein 1 homolog, mitochondrial OS=Danio rerio GN=rtn4ip1 PE=2 SV=2
CL1605.Contig2_All	Rho GTPase-activating protein 19 OS=Xenopus laevis GN=arhgap19 PE=2 SV=1
CL16081.Contig1_All	Stearoyl-CoA desaturase 5 OS=Bos taurus GN=SCD5 PE=2 SV=1
CL16081.Contig2_All	Stearoyl-CoA desaturase 5 OS=Homo sapiens GN=SCD5 PE=2 SV=2
CL16081.Contig4_All	Stearoyl-CoA desaturase 5 OS=Bos taurus GN=SCD5 PE=2 SV=1
CL16112.Contig1_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL16112.Contig2_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL16129.Contig1_All	--
CL1614.Contig15_All	Prolyl 4-hydroxylase subunit alpha-1 OS=Pongo abelii GN=P4HA1 PE=2 SV=1
CL16169.Contig1_All	--
CL16169.Contig2_All	--
CL16191.Contig1_All	--
CL16194.Contig1_All	--
CL16194.Contig2_All	--

CL16221.Contig1_All	--
CL16227.Contig2_All	--
CL1623.Contig1_All	--
CL1624.Contig1_All	Fatty acyl-CoA reductase 1 OS=Rattus norvegicus GN=Far1 PE=2 SV=1
CL16288.Contig1_All	--
CL1629.Contig1_All	--
CL16309.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL1632.Contig2_All	LIM and SH3 domain protein F42H10.3 OS=Caenorhabditis elegans GN=F42H10.3 PE=4 SV=3
CL16321.Contig2_All	--
CL16364.Contig1_All	Thymus-specific serine protease OS=Mus musculus GN=Prss16 PE=2 SV=1
CL16373.Contig3_All	--
CL1638.Contig1_All	--
CL16387.Contig5_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL16407.Contig1_All	--
CL16408.Contig1_All	--
CL16410.Contig2_All	--
CL16456.Contig2_All	--
CL16467.Contig1_All	--
CL16467.Contig2_All	--
CL16467.Contig3_All	--
CL16476.Contig1_All	--
CL16480.Contig2_All	--
CL16482.Contig2_All	Carbonic anhydrase 7 OS=Homo sapiens GN=CA7 PE=1 SV=1
CL16491.Contig1_All	--
CL16495.Contig1_All	--
CL1651.Contig5_All	Apoptosis 1 inhibitor OS=Drosophila melanogaster GN=th PE=1 SV=2
CL16511.Contig4_All	Probable RNA-directed DNA polymerase from transposon X-element OS=Drosophila melanogaster GN=X-element\ORF2 PE=3 SV=1
CL16514.Contig2_All	--
CL16543.Contig1_All	--
CL16561.Contig1_All	--
CL16561.Contig2_All	--
CL16567.Contig3_All	--
CL16610.Contig1_All	Serine/threonine-protein kinase BRSK2 OS=Homo sapiens GN=BRSK2 PE=1 SV=3

CL16648.Contig1_All	NFX1-type zinc finger-containing protein 1 OS=Homo sapiens GN=ZNFX1 PE=1 SV=2
CL16648.Contig2_All	NFX1-type zinc finger-containing protein 1 OS=Homo sapiens GN=ZNFX1 PE=1 SV=2
CL16659.Contig2_All	--
CL167.Contig1_All	--
CL167.Contig2_All	--
CL167.Contig3_All	--
CL1670.Contig3_All	Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Rattus norvegicus GN=Baiap2 PE=1 SV=1
CL16711.Contig1_All	--
CL16738.Contig2_All	--
CL16744.Contig1_All	Mite allergen Der p 7 OS=Dermatophagoides pteronyssinus GN=DERP7 PE=1 SV=1
CL16744.Contig2_All	Mite allergen Der p 7 OS=Dermatophagoides pteronyssinus GN=DERP7 PE=1 SV=1
CL16753.Contig1_All	--
CL16769.Contig3_All	--
CL16771.Contig4_All	Retrovirus-related Pol polyprotein from transposon 297 OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL16775.Contig1_All	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2
CL16775.Contig2_All	Dipeptidyl peptidase 1 OS=Mus musculus GN=Ctsc PE=2 SV=1
CL16784.Contig2_All	--
CL16810.Contig1_All	--
CL16830.Contig1_All	UDP-glucuronosyltransferase 1-8 OS=Homo sapiens GN=UGT1A8 PE=1 SV=1
CL16830.Contig2_All	UDP-glucuronosyltransferase 2C1 (Fragment) OS=Oryctolagus cuniculus GN=UGT2C1 PE=2 SV=1
CL16840.Contig2_All	Large neutral amino acids transporter small subunit 2 OS=Mus musculus GN=Slc7a8 PE=1 SV=1
CL16847.Contig1_All	--
CL16847.Contig2_All	--
CL1686.Contig5_All	Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3
CL16872.Contig2_All	--
CL16876.Contig1_All	--
CL16903.Contig1_All	--
CL16907.Contig2_All	--
CL16943.Contig1_All	--
CL16948.Contig1_All	--

CL16972.Contig1_All	--
CL16976.Contig2_All	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3
CL17004.Contig1_All	UDP-glucuronosyltransferase 2B15 OS=Rattus norvegicus GN=Ugt2b15 PE=1 SV=1
CL17004.Contig2_All	UDP-glucuronosyltransferase 1-3 OS=Rattus norvegicus GN=Ugt1a3 PE=2 SV=1
CL17027.Contig2_All	--
CL1703.Contig3_All	--
CL17038.Contig1_All	--
CL17038.Contig2_All	--
CL17055.Contig1_All	--
CL1707.Contig3_All	--
CL17106.Contig1_All	Nuclear RNA export factor 1 OS=Coturnix coturnix japonica GN=NXF1 PE=1 SV=1
CL17121.Contig3_All	--
CL17127.Contig1_All	--
CL17138.Contig1_All	--
CL17147.Contig2_All	Gamma-interferon-inducible lysosomal thiol reductase OS=Homo sapiens GN=IFI30 PE=1 SV=3
CL17179.Contig1_All	--
CL17202.Contig1_All	--
CL17205.Contig1_All	--
CL17205.Contig3_All	--
CL1723.Contig2_All	Glycosyltransferase 25 family member OS=Aedes aegypti GN=AAEL003481 PE=3 SV=1
CL17233.Contig9_All	--
CL1724.Contig2_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL17247.Contig1_All	--
CL17248.Contig2_All	Tigger transposable element-derived protein 2 OS=Homo sapiens GN=TIGD2 PE=2 SV=1
CL17261.Contig3_All	--
CL17297.Contig3_All	--
CL17297.Contig4_All	--
CL17297.Contig6_All	--
CL173.Contig2_All	Nucleolysin TIA-1 isoform p40 OS=Homo sapiens GN=TIA1 PE=1 SV=3
CL17330.Contig1_All	--
CL17332.Contig1_All	--
CL17332.Contig3_All	--
CL17365.Contig1_All	--
CL17412.Contig1_All	--

CL17459.Contig5_All	--
CL17462.Contig2_All	--
CL17462.Contig4_All	--
CL17468.Contig13_All	THAP domain-containing protein 9 OS=Homo sapiens GN=THAP9 PE=2 SV=2
CL17475.Contig1_All	--
CL17475.Contig2_All	--
CL17498.Contig1_All	Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1
CL175.Contig3_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
CL17503.Contig1_All	Tigger transposable element-derived protein 6 OS=Homo sapiens GN=TIGD6 PE=2 SV=2
CL1751.Contig3_All	Retrovirus-related Pol polyprotein from transposon opus OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL17518.Contig3_All	Phenoloxidase subunit A3 OS=Drosophila melanogaster GN=proPo-A3 PE=1 SV=1
CL17524.Contig1_All	Transmembrane protein adipocyte-associated 1 homolog OS=Danio rerio GN=tpra1 PE=2 SV=1
CL17541.Contig2_All	--
CL17546.Contig3_All	1,5-anhydro-D-fructose reductase OS=Sus scrofa GN=AKR1E2 PE=1 SV=2
CL17564.Contig1_All	--
CL17582.Contig2_All	Protein brambleberry OS=Danio rerio GN=bmb PE=2 SV=1
CL17584.Contig1_All	General transcription factor II-I repeat domain-containing protein 2 OS=Bos taurus GN=GTF2IRD2 PE=2 SV=1
CL17592.Contig1_All	--
CL17592.Contig2_All	--
CL17592.Contig3_All	--
CL17592.Contig4_All	--
CL17592.Contig5_All	--
CL17600.Contig1_All	--
CL17607.Contig3_All	--
CL17631.Contig1_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL17631.Contig2_All	--
CL17632.Contig1_All	--
CL17645.Contig1_All	--
CL17651.Contig1_All	--

CL17700.Contig3_All	--
CL17711.Contig1_All	--
CL17711.Contig2_All	--
CL1773.Contig3_All	Acyl-CoA synthetase family member 2, mitochondrial OS=Danio rerio GN=acsf2 PE=2 SV=1
CL17747.Contig4_All	Probable RNA-directed DNA polymerase from transposon X-element OS=Drosophila melanogaster GN=X-element\ORF2 PE=3 SV=1
CL17751.Contig1_All	--
CL17765.Contig3_All	--
CL17789.Contig1_All	SCAN domain-containing protein 3 OS=Homo sapiens GN=SCAND3 PE=2 SV=1
CL17797.Contig1_All	--
CL17810.Contig7_All	--
CL17811.Contig4_All	Transposon TX1 uncharacterized 149 kDa protein OS=Xenopus laevis PE=4 SV=1
CL17811.Contig7_All	--
CL17813.Contig10_All	--
CL17837.Contig2_All	PiggyBac transposable element-derived protein 4 OS=Homo sapiens GN=PGBD4 PE=2 SV=3
CL17840.Contig2_All	--
CL17840.Contig3_All	Protein piccolo OS=Mus musculus GN=Pclo PE=1 SV=4
CL17844.Contig2_All	Transposable element Tcb1 transposase OS=Caenorhabditis briggsae PE=3 SV=1
CL17851.Contig1_All	Zinc finger protein 865 OS=Homo sapiens GN=ZNF865 PE=3 SV=1
CL17864.Contig9_All	--
CL17872.Contig1_All	--
CL17887.Contig5_All	--
CL1792.Contig1_All	--
CL1792.Contig3_All	--
CL17920.Contig1_All	Putative uncharacterized protein FLJ37770 OS=Homo sapiens PE=5 SV=1
CL17959.Contig1_All	--
CL17966.Contig2_All	--
CL1810.Contig2_All	Protein ovo OS=Drosophila melanogaster GN=ovo PE=1 SV=2
CL1816.Contig2_All	--
CL1822.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL1822.Contig2_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL1850.Contig2_All	--
CL1850.Contig3_All	--

CL1852.Contig1_All	Vitamin K epoxide reductase complex subunit 1 OS=Mus musculus GN=Vkorc1 PE=2 SV=1
CL1852.Contig2_All	Vitamin K epoxide reductase complex subunit 1 OS=Mus musculus GN=Vkorc1 PE=2 SV=1
CL1867.Contig1_All	Sorting nexin-27 OS=Mus musculus GN=Snx27 PE=1 SV=2
CL19.Contig3_All	--
CL1904.Contig3_All	28S ribosomal protein S18c, mitochondrial OS=Homo sapiens GN=MRPS18C PE=1 SV=1
CL1904.Contig4_All	28S ribosomal protein S18c, mitochondrial OS=Homo sapiens GN=MRPS18C PE=1 SV=1
CL191.Contig5_All	Protein turtle OS=Drosophila melanogaster GN=tutl PE=2 SV=2
CL1913.Contig1_All	--
CL1913.Contig2_All	--
CL1925.Contig2_All	Platelet glycoprotein Ib alpha chain OS=Mus musculus GN=Gp1ba PE=2 SV=2
CL1925.Contig3_All	Platelet glycoprotein Ib alpha chain OS=Mus musculus GN=Gp1ba PE=2 SV=2
CL193.Contig4_All	Lysosomal Pro-X carboxypeptidase OS=Bos taurus GN=PRCP PE=2 SV=1
CL1932.Contig2_All	--
CL1944.Contig1_All	--
CL1945.Contig1_All	--
CL1951.Contig1_All	--
CL1952.Contig3_All	Sulfotransferase family cytosolic 1B member 1 OS=Gallus gallus GN=SULT1B1 PE=2 SV=1
CL1967.Contig3_All	--
CL1974.Contig10_All	Tropomyosin-1, isoforms 9A/A/B OS=Drosophila melanogaster GN=Tm1 PE=1 SV=2
CL1974.Contig11_All	Tropomyosin OS=Locusta migratoria PE=3 SV=1
CL1974.Contig12_All	Tropomyosin-1, isoforms 9A/A/B OS=Drosophila melanogaster GN=Tm1 PE=1 SV=2
CL1974.Contig14_All	Tropomyosin OS=Locusta migratoria PE=3 SV=1
CL1974.Contig15_All	Tropomyosin OS=Locusta migratoria PE=3 SV=1
CL1974.Contig16_All	Tropomyosin OS=Locusta migratoria PE=3 SV=1
CL1974.Contig17_All	Tropomyosin OS=Locusta migratoria PE=3 SV=1
CL1974.Contig18_All	Tropomyosin-1, isoforms 9A/A/B OS=Drosophila melanogaster GN=Tm1 PE=1 SV=2
CL1974.Contig1_All	Tropomyosin-1, isoforms 9A/A/B OS=Drosophila melanogaster GN=Tm1 PE=1 SV=2
CL1974.Contig20_All	Tropomyosin-1, isoforms 9A/A/B OS=Drosophila melanogaster GN=Tm1 PE=1 SV=2
CL1974.Contig21_All	Tropomyosin OS=Locusta migratoria PE=3 SV=1

CL1974.Contig2_All	Tropomyosin OS=Locusta migratoria PE=3 SV=1
CL1974.Contig4_All	Tropomyosin-1, isoforms 9A/A/B OS=Drosophila melanogaster GN=Tm1 PE=1 SV=2
CL1974.Contig5_All	Tropomyosin OS=Locusta migratoria PE=3 SV=1
CL1974.Contig6_All	Tropomyosin OS=Locusta migratoria PE=3 SV=1
CL1974.Contig8_All	Tropomyosin OS=Locusta migratoria PE=3 SV=1
CL1974.Contig9_All	Tropomyosin-2 OS=Bombyx mori PE=1 SV=1
CL1975.Contig2_All	--
CL1975.Contig3_All	--
CL1990.Contig1_All	Histone H1-II OS=Glyptotendipes barbipes PE=3 SV=1
CL2014.Contig2_All	Homeobox protein abdominal-A OS=Drosophila melanogaster GN=abd-A PE=2 SV=2
CL2032.Contig6_All	Pyruvate carboxylase, mitochondrial OS=Bos taurus GN=PC PE=2 SV=2
CL2045.Contig3_All	Sodium/potassium-transporting ATPase subunit alpha OS=Drosophila melanogaster GN=Atpalpha PE=1 SV=3
CL2045.Contig4_All	Sodium/potassium-transporting ATPase subunit alpha OS=Drosophila melanogaster GN=Atpalpha PE=1 SV=3
CL2045.Contig5_All	Sodium/potassium-transporting ATPase subunit alpha OS=Drosophila melanogaster GN=Atpalpha PE=1 SV=3
CL2074.Contig3_All	Epoxide hydrolase 1 OS=Oryctolagus cuniculus GN=EPHX1 PE=1 SV=2
CL2083.Contig1_All	--
CL2090.Contig4_All	Calcium release-activated calcium channel protein 1 OS=Drosophila melanogaster GN=olf186-F PE=1 SV=1
CL212.Contig2_All	Phenoloxidase subunit A3 OS=Drosophila melanogaster GN=proPo-A3 PE=1 SV=1
CL212.Contig3_All	Phenoloxidase subunit A3 OS=Drosophila melanogaster GN=proPo-A3 PE=1 SV=1
CL2123.Contig1_All	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4
CL2123.Contig3_All	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4
CL2123.Contig4_All	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4
CL2132.Contig19_All	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4
CL2140.Contig1_All	Integrin alpha-PS1 OS=Drosophila melanogaster GN=mew PE=1 SV=2

CL2140.Contig2_All	Integrin alpha-PS1 OS=Drosophila melanogaster GN=mew PE=1 SV=2
CL2146.Contig1_All	Sialin OS=Mus musculus GN=Slc17a5 PE=2 SV=2
CL2146.Contig2_All	Uncharacterized transporter C38C10.2 OS=Caenorhabditis elegans GN=C38C10.2 PE=1 SV=2
CL2151.Contig1_All	--
CL2151.Contig2_All	--
CL2152.Contig2_All	Fumarate hydratase, mitochondrial OS=Danio rerio GN=fh PE=2 SV=1
CL2159.Contig4_All	--
CL2168.Contig2_All	--
CL2173.Contig4_All	--
CL2199.Contig1_All	--
CL220.Contig1_All	--
CL220.Contig3_All	--
CL2217.Contig1_All	--
CL222.Contig12_All	PDZ and LIM domain protein Zasp OS=Drosophila melanogaster GN=Zasp52 PE=1 SV=2
CL2260.Contig2_All	--
CL227.Contig11_All	--
CL227.Contig12_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL227.Contig2_All	--
CL227.Contig6_All	Mariner Mos1 transposase OS=Drosophila mauritiana GN=mariner\T PE=1 SV=1
CL2272.Contig1_All	--
CL2294.Contig4_All	PiggyBac transposable element-derived protein 4 OS=Homo sapiens GN=PGBD4 PE=2 SV=3
CL23.Contig2_All	RNA-directed DNA polymerase from mobile element jockey OS=Drosophila melanogaster GN=pol PE=1 SV=1
CL2307.Contig1_All	Peptidoglycan-recognition protein SB1 OS=Drosophila melanogaster GN=PGRP-SB1 PE=2 SV=2
CL2319.Contig4_All	--
CL232.Contig2_All	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1
CL2324.Contig2_All	Organic cation transporter protein OS=Drosophila melanogaster GN=Orct PE=1 SV=1
CL2324.Contig6_All	Organic cation transporter protein OS=Drosophila melanogaster GN=Orct PE=1 SV=1
CL2324.Contig9_All	Organic cation transporter protein OS=Drosophila melanogaster GN=Orct PE=1 SV=1
CL2332.Contig1_All	--
CL2345.Contig2_All	--

CL2361.Contig4_All	Espin OS=Mus musculus GN=Espn PE=1 SV=2
CL2383.Contig2_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
CL2384.Contig2_All	--
CL2385.Contig1_All	--
CL2390.Contig2_All	Cytochrome P450 6j1 OS=Blattella germanica GN=CYP6J1 PE=2 SV=1
CL2399.Contig27_All	--
CL2399.Contig51_All	Serine/threonine-protein kinase PRP4 homolog OS=Rattus norvegicus GN=Prpf4b PE=2 SV=1
CL2407.Contig1_All	Vacuolar protein sorting-associated protein 35 OS=Bos taurus GN=VPS35 PE=2 SV=1
CL2428.Contig1_All	--
CL2437.Contig3_All	--
CL2452.Contig1_All	--
CL2453.Contig3_All	Protein argonaute-2 OS=Drosophila melanogaster GN=AGO2 PE=1 SV=3
CL2454.Contig4_All	--
CL2467.Contig2_All	--
CL2470.Contig1_All	--
CL2482.Contig2_All	Zinc finger protein castor homolog 1 OS=Mus musculus GN=Casz1 PE=2 SV=3
CL2482.Contig3_All	Homeobox protein abdominal-A homolog OS=Tribolium castaneum GN=ABD-A PE=2 SV=2
CL2497.Contig3_All	--
CL250.Contig2_All	--
CL2502.Contig11_All	--
CL251.Contig2_All	--
CL251.Contig9_All	--
CL2512.Contig3_All	--
CL2517.Contig1_All	--
CL2520.Contig2_All	--
CL2529.Contig3_All	DnaJ homolog subfamily B member 6-B OS=Xenopus laevis GN=dnajb6-b PE=2 SV=1
CL2532.Contig1_All	Transcription factor Dp-1 OS=Bos taurus GN=TFDP1 PE=2 SV=1
CL2535.Contig2_All	--
CL2536.Contig10_All	Uncharacterized protein DDB_G0286299 OS=Dictyostelium discoideum GN=DDB_G0286299 PE=4 SV=1
CL2536.Contig9_All	Uncharacterized protein DDB_G0286299 OS=Dictyostelium discoideum GN=DDB_G0286299 PE=4 SV=1

CL2542.Contig1_All	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2 OS=Homo sapiens GN=HCN2 PE=1 SV=3
CL2542.Contig2_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL2548.Contig1_All	Hormone receptor 4 OS=Drosophila melanogaster GN=Hr4 PE=1 SV=4
CL2550.Contig3_All	--
CL2560.Contig2_All	--
CL2577.Contig2_All	Neuronal acetylcholine receptor subunit alpha-7 OS=Rattus norvegicus GN=Chrna7 PE=1 SV=2
CL2584.Contig2_All	Xanthine dehydrogenase OS=Dictyostelium discoideum GN=xdh PE=3 SV=1
CL2596.Contig1_All	Probable UDP-glucose 4-epimerase OS=Drosophila melanogaster GN=Gale PE=2 SV=1
CL2599.Contig1_All	--
CL2599.Contig4_All	--
CL260.Contig2_All	NF-kappa-B inhibitor epsilon OS=Mus musculus GN=Nfkbie PE=2 SV=2
CL2606.Contig1_All	Myosin light chain kinase, smooth muscle OS=Bos taurus GN=MYLK PE=1 SV=1
CL2606.Contig2_All	Titin OS=Homo sapiens GN=TTN PE=1 SV=4
CL2606.Contig3_All	Titin OS=Homo sapiens GN=TTN PE=1 SV=4
CL261.Contig3_All	--
CL2611.Contig1_All	--
CL2611.Contig2_All	--
CL2621.Contig1_All	--
CL2623.Contig1_All	--
CL2623.Contig2_All	--
CL2631.Contig2_All	--
CL2633.Contig1_All	--
CL2633.Contig2_All	RNA-directed DNA polymerase from mobile element jockey OS=Drosophila melanogaster GN=pol PE=1 SV=1
CL2633.Contig3_All	RNA-directed DNA polymerase from mobile element jockey OS=Drosophila melanogaster GN=pol PE=1 SV=1
CL2635.Contig1_All	--
CL2635.Contig2_All	--
CL2635.Contig3_All	--
CL2646.Contig1_All	Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=2
CL2646.Contig2_All	Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=2
CL2662.Contig1_All	--

CL2665.Contig1_All	--
CL2666.Contig1_All	--
CL2667.Contig1_All	Retinal dehydrogenase 1 OS=Gallus gallus GN=ALDH1A1 PE=2 SV=1
CL267.Contig7_All	--
CL2685.Contig3_All	Dynactin subunit 5 OS=Pongo abelii GN=DCTN5 PE=2 SV=1
CL2695.Contig2_All	--
CL2698.Contig1_All	--
CL2718.Contig2_All	--
CL2739.Contig1_All	--
CL2750.Contig1_All	--
CL2756.Contig2_All	--
CL2764.Contig2_All	Papilin OS=Drosophila melanogaster GN=Ppn PE=1 SV=2
CL2774.Contig2_All	Protein kinase shaggy OS=Drosophila melanogaster GN=sgg PE=1 SV=3
CL2800.Contig1_All	--
CL281.Contig1_All	--
CL281.Contig2_All	--
CL2818.Contig1_All	Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3
CL2819.Contig2_All	--
CL2823.Contig1_All	Sterol regulatory element-binding protein 1 OS=Mus musculus GN=Srebf1 PE=1 SV=4
CL284.Contig3_All	--
CL2844.Contig12_All	Liprin-beta-1 OS=Mus musculus GN=Ppfibp1 PE=1 SV=3
CL2845.Contig1_All	--
CL2861.Contig1_All	--
CL2876.Contig1_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL2876.Contig2_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL2876.Contig4_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL2876.Contig5_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
CL2882.Contig1_All	--
CL2888.Contig1_All	Loricrin OS=Mus musculus GN=Lor PE=2 SV=2
CL289.Contig2_All	--
CL2906.Contig7_All	Maternal protein tudor OS=Drosophila melanogaster GN=tud PE=1 SV=2
CL2907.Contig2_All	--

CL292.Contig1_All	Nuclear factor of activated T-cells 5 OS=Homo sapiens GN=NFAT5 PE=1 SV=1
CL2934.Contig3_All	--
CL294.Contig2_All	--
CL2968.Contig4_All	--
CL2992.Contig4_All	Ankyrin-3 OS=Mus musculus GN=Ank3 PE=1 SV=1
CL2999.Contig2_All	--
CL3032.Contig2_All	Methyltransferase-like protein 2-A OS=Danio rerio GN=mettl2a PE=2 SV=1
CL306.Contig2_All	--
CL306.Contig3_All	--
CL3061.Contig2_All	Regulating synaptic membrane exocytosis protein 2 OS=Homo sapiens GN=RIMS2 PE=1 SV=2
CL3062.Contig2_All	Serine protease snake OS=Drosophila melanogaster GN=snk PE=1 SV=2
CL3063.Contig2_All	Kinase D-interacting substrate of 220 kDa OS=Rattus norvegicus GN=Kidins220 PE=1 SV=2
CL3063.Contig4_All	Kinase D-interacting substrate of 220 kDa OS=Homo sapiens GN=KIDINS220 PE=1 SV=3
CL3079.Contig1_All	Hexamerin OS=Blaberus discoidalis PE=2 SV=1
CL3079.Contig2_All	Hexamerin OS=Blaberus discoidalis PE=2 SV=1
CL3079.Contig3_All	Hexamerin OS=Blaberus discoidalis PE=2 SV=1
CL313.Contig1_All	--
CL313.Contig3_All	--
CL3142.Contig1_All	--
CL3146.Contig1_All	Uncharacterized aarF domain-containing protein kinase 2 OS=Mus musculus GN=Adck2 PE=2 SV=1
CL3149.Contig1_All	--
CL3149.Contig2_All	--
CL3163.Contig4_All	Elongator complex protein 6 OS=Xenopus laevis GN=elp6 PE=2 SV=1
CL3180.Contig2_All	Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2
CL3181.Contig4_All	--
CL3192.Contig1_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
CL3192.Contig2_All	Collectin-11 OS=Mus musculus GN=Colec11 PE=2 SV=2
CL3196.Contig1_All	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2
CL3202.Contig1_All	--
CL322.Contig1_All	--
CL3226.Contig4_All	RNA-directed DNA polymerase from mobile element jockey OS=Drosophila melanogaster GN=pol PE=1 SV=1

CL3233.Contig1_All	--
CL3243.Contig1_All	TBC1 domain family member 20 OS=Homo sapiens GN=TBC1D20 PE=1 SV=1
CL3243.Contig2_All	TBC1 domain family member 20 OS=Homo sapiens GN=TBC1D20 PE=1 SV=1
CL3245.Contig1_All	--
CL3248.Contig2_All	Equilibrative nucleoside transporter 3 OS=Bos taurus GN=SLC29A3 PE=2 SV=1
CL331.Contig10_All	--
CL3313.Contig2_All	UPF0609 protein C4orf27 OS=Homo sapiens GN=C4orf27 PE=1 SV=2
CL3333.Contig4_All	Solute carrier family 35 member C2 OS=Homo sapiens GN=SLC35C2 PE=1 SV=2
CL3337.Contig1_All	Calcium-binding protein P OS=Dictyostelium discoideum GN=cbpP PE=2 SV=2
CL3337.Contig2_All	Calcium-binding protein P OS=Dictyostelium discoideum GN=cbpP PE=2 SV=2
CL3337.Contig3_All	Calcium-binding protein P OS=Dictyostelium discoideum GN=cbpP PE=2 SV=2
CL3337.Contig4_All	Calcium-binding protein P OS=Dictyostelium discoideum GN=cbpP PE=2 SV=2
CL3337.Contig5_All	Calcium-binding protein P OS=Dictyostelium discoideum GN=cbpP PE=2 SV=2
CL3337.Contig6_All	Calcium-binding protein P OS=Dictyostelium discoideum GN=cbpP PE=2 SV=2
CL3338.Contig9_All	--
CL3346.Contig1_All	--
CL3370.Contig2_All	--
CL3378.Contig1_All	--
CL3391.Contig6_All	Kelch-like protein 26 OS=Homo sapiens GN=KLHL26 PE=2 SV=2
CL3393.Contig1_All	--
CL3404.Contig1_All	--
CL3459.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL3467.Contig1_All	--
CL347.Contig1_All	--
CL3474.Contig1_All	--
CL3483.Contig1_All	--
CL3506.Contig1_All	--
CL3530.Contig1_All	Putative helicase MOV-10 OS=Gallus gallus GN=MOV10 PE=2 SV=1
CL3530.Contig3_All	Putative helicase MOV-10 OS=Gallus gallus GN=MOV10 PE=2 SV=1

CL3548.Contig1_All	--
CL3575.Contig3_All	--
CL3581.Contig2_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL3591.Contig2_All	Peroxidasin homolog OS=Mus musculus GN=Pxdn PE=2 SV=2
CL3600.Contig2_All	Run domain Beclin-1 interacting and cystein-rich containing protein OS=Mus musculus GN=Kiaa0226 PE=1 SV=2
CL3618.Contig1_All	Carboxylesterase 4A OS=Mus musculus GN=Ces4a PE=2 SV=1
CL3619.Contig1_All	--
CL3646.Contig4_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3
CL3664.Contig1_All	--
CL3664.Contig2_All	--
CL3664.Contig3_All	--
CL3673.Contig1_All	ATP-binding cassette sub-family G member 1 OS=Mus musculus GN=Abcg1 PE=2 SV=1
CL3682.Contig2_All	Serine/arginine repetitive matrix protein 3 OS=Homo sapiens GN=SRRM3 PE=2 SV=4
CL3682.Contig3_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
CL3692.Contig1_All	--
CL3709.Contig1_All	--
CL3709.Contig2_All	--
CL3716.Contig2_All	Probable RNA-binding protein orb2 OS=Drosophila melanogaster GN=orb2 PE=1 SV=1
CL3735.Contig1_All	Multidrug resistance-associated protein 4 OS=Homo sapiens GN=ABCC4 PE=1 SV=3
CL3745.Contig7_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
CL3748.Contig1_All	--
CL3768.Contig2_All	--
CL3774.Contig2_All	60S ribosomal protein L41 OS=Spodoptera frugiperda GN=RpL41 PE=3 SV=1
CL3811.Contig3_All	--
CL3812.Contig5_All	Serine/threonine-protein kinase TAO1 OS=Rattus norvegicus GN=Taok1 PE=1 SV=1
CL3825.Contig3_All	XK-related protein 4 OS=Homo sapiens GN=XKR4 PE=2 SV=1
CL3855.Contig2_All	Kinesin-like protein KIF13A OS=Mus musculus GN=Kif13a PE=1 SV=1
CL3889.Contig1_All	--
CL389.Contig1_All	--

CL389.Contig2_All	--
CL3893.Contig1_All	--
CL3897.Contig3_All	Protein AF-9 OS=Mus musculus GN=Mllt3 PE=1 SV=1
CL3905.Contig1_All	--
CL3907.Contig2_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL3907.Contig3_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
CL3917.Contig2_All	--
CL3920.Contig1_All	Speckle-type POZ protein OS=Pongo abelii GN=SPOP PE=1 SV=1
CL3932.Contig2_All	--
CL3932.Contig4_All	Four and a half LIM domains protein 2 OS=Bos taurus GN=FHL2 PE=2 SV=1
CL3944.Contig7_All	--
CL3951.Contig1_All	--
CL3951.Contig2_All	Multiple epidermal growth factor-like domains protein 11 OS=Homo sapiens GN=MEGF11 PE=2 SV=3
CL3955.Contig1_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3
CL4.Contig1_All	E3 ubiquitin-protein ligase HECW2 OS=Mus musculus GN=Hecw2 PE=2 SV=1
CL4.Contig6_All	E3 ubiquitin-protein ligase HECW2 OS=Mus musculus GN=Hecw2 PE=2 SV=1
CL4015.Contig2_All	5-aminolevulinate synthase, erythroid-specific, mitochondrial OS=Bos taurus GN=ALAS2 PE=2 SV=1
CL4019.Contig1_All	--
CL4020.Contig4_All	Adenylate cyclase type 9 OS=Xenopus laevis GN=adcy9 PE=2 SV=2
CL406.Contig2_All	--
CL4067.Contig1_All	Actin-binding protein anillin OS=Drosophila melanogaster GN=scra PE=1 SV=3
CL4081.Contig2_All	--
CL4081.Contig3_All	--
CL4084.Contig2_All	General transcription factor IIH subunit 1 OS=Drosophila melanogaster GN=Tfb1 PE=2 SV=1
CL4089.Contig1_All	--
CL4094.Contig1_All	Cytochrome P450 6k1 OS=Blattella germanica GN=CYP6K1 PE=2 SV=1
CL4109.Contig3_All	Probable RNA helicase armi OS=Drosophila melanogaster GN=armi PE=2 SV=3
CL414.Contig1_All	--
CL415.Contig10_All	--

CL4153.Contig1_All	--
CL417.Contig1_All	Neurexin-1a OS=Danio rerio GN=nrxn1a PE=2 SV=1
CL4173.Contig2_All	DNA replication complex GINS protein PSF1 OS=Mus musculus GN=Gins1 PE=2 SV=1
CL4197.Contig1_All	--
CL4203.Contig1_All	D-3-phosphoglycerate dehydrogenase OS=Rattus norvegicus GN=Phgdh PE=1 SV=3
CL4203.Contig2_All	D-3-phosphoglycerate dehydrogenase OS=Rattus norvegicus GN=Phgdh PE=1 SV=3
CL4211.Contig1_All	Toll-like receptor 2 OS=Ovis aries GN=TLR2 PE=2 SV=1
CL4214.Contig10_All	--
CL4214.Contig9_All	--
CL4228.Contig2_All	--
CL4255.Contig2_All	--
CL4257.Contig1_All	--
CL4285.Contig3_All	--
CL4293.Contig1_All	--
CL4293.Contig2_All	--
CL4311.Contig1_All	--
CL4331.Contig3_All	--
CL4336.Contig1_All	--
CL4341.Contig1_All	Lysosomal protein NCU-G1 OS=Salmo salar PE=2 SV=1
CL4353.Contig1_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
CL4353.Contig2_All	Putative protein TPRXL OS=Homo sapiens GN=TPRXL PE=5 SV=2
CL4356.Contig1_All	--
CL4368.Contig3_All	--
CL437.Contig3_All	--
CL4404.Contig2_All	Phosphatase and actin regulator 2 OS=Homo sapiens GN=PHACTR2 PE=1 SV=2
CL4407.Contig2_All	--
CL4429.Contig1_All	--
CL4437.Contig1_All	--
CL444.Contig3_All	--
CL444.Contig4_All	--
CL4448.Contig1_All	--
CL4450.Contig1_All	--
CL4450.Contig2_All	--
CL4450.Contig3_All	--
CL4450.Contig4_All	--

CL4450.Contig5_All	--
CL4481.Contig1_All	--
CL4492.Contig3_All	E3 ubiquitin-protein ligase RNF31 OS=Homo sapiens GN=RNF31 PE=1 SV=1
CL451.Contig1_All	Proton-coupled amino acid transporter 4 OS=Xenopus laevis GN=slc36a4 PE=2 SV=1
CL4514.Contig9_All	Salivary glue protein Sgs-3 OS=Drosophila yakuba GN=Sgs3 PE=2 SV=3
CL4517.Contig2_All	Synaptic vesicle glycoprotein 2C OS=Rattus norvegicus GN=Sv2c PE=1 SV=1
CL4521.Contig2_All	--
CL4524.Contig5_All	tRNA wybutosine-synthesizing protein 3 homolog OS=Homo sapiens GN=TYW3 PE=2 SV=2
CL4528.Contig4_All	--
CL4529.Contig2_All	--
CL4536.Contig1_All	--
CL454.Contig3_All	Phospholipid scramblase 1 OS=Mus musculus GN=Plscr1 PE=2 SV=1
CL4544.Contig2_All	Low-density lipoprotein receptor-related protein 2 OS=Rattus norvegicus GN=Lrp2 PE=1 SV=1
CL457.Contig1_All	--
CL4585.Contig1_All	Fatty-acid amide hydrolase 2-A OS=Danio rerio GN=faah2a PE=2 SV=1
CL459.Contig1_All	Rho guanine nucleotide exchange factor 12 OS=Homo sapiens GN=ARHGEF12 PE=1 SV=1
CL4598.Contig1_All	UDP-glucuronosyltransferase 2B1 OS=Rattus norvegicus GN=Ugt2b1 PE=2 SV=1
CL4646.Contig2_All	Protein bric-a-brac 1 OS=Drosophila melanogaster GN=bab1 PE=2 SV=2
CL4666.Contig1_All	--
CL4675.Contig1_All	--
CL4678.Contig1_All	Voltage-dependent calcium channel type D subunit alpha-1 OS=Drosophila melanogaster GN=Ca-alpha1D PE=1 SV=2
CL4683.Contig2_All	--
CL4687.Contig1_All	--
CL4689.Contig1_All	--
CL4689.Contig2_All	--
CL4718.Contig1_All	Prostaglandin E2 receptor EP2 subtype OS=Homo sapiens GN=PTGER2 PE=2 SV=2
CL4720.Contig2_All	--
CL4722.Contig2_All	--
CL4722.Contig3_All	--
CL4727.Contig2_All	--

CL4741.Contig2_All	--
CL4756.Contig2_All	--
CL4770.Contig1_All	Atherin OS=Homo sapiens GN=SAMD1 PE=1 SV=1
CL4791.Contig3_All	DNA topoisomerase 2-alpha OS=Sus scrofa GN=TOP2A PE=2 SV=1
CL4791.Contig4_All	DNA topoisomerase 2-alpha OS=Gallus gallus GN=TOP2A PE=2 SV=2
CL4801.Contig2_All	Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13 PE=1 SV=2
CL4807.Contig2_All	--
CL4811.Contig3_All	Spidroin-1 (Fragment) OS=Nephila clavipes PE=1 SV=3
CL4812.Contig1_All	--
CL4812.Contig2_All	--
CL4826.Contig2_All	--
CL4833.Contig1_All	--
CL4833.Contig2_All	--
CL4862.Contig2_All	Juvenile hormone esterase OS=Heliothis virescens PE=1 SV=2
CL4876.Contig2_All	Diacylglycerol kinase theta OS=Mus musculus GN=Dgkq PE=1 SV=1
CL4877.Contig1_All	--
CL4878.Contig1_All	Lipase member M OS=Homo sapiens GN=LIPM PE=2 SV=2
CL4882.Contig1_All	--
CL4883.Contig6_All	--
CL4898.Contig3_All	--
CL4898.Contig4_All	--
CL4913.Contig2_All	General transcriptional corepressor trfA OS=Dictyostelium discoideum GN=trfA PE=2 SV=1
CL4916.Contig4_All	26S proteasome non-ATPase regulatory subunit 1 OS=Drosophila melanogaster GN=Rpn2 PE=1 SV=1
CL4929.Contig2_All	--
CL4936.Contig1_All	Probable cytochrome P450 304a1 OS=Drosophila melanogaster GN=Cyp304a1 PE=2 SV=2
CL4950.Contig3_All	Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1
CL4950.Contig4_All	--
CL4971.Contig2_All	LINE-1 reverse transcriptase homolog OS=Nycticebus coucang PE=1 SV=1
CL4981.Contig2_All	Peptidoglycan recognition protein 1 OS=Mus musculus GN=Pglyrp1 PE=2 SV=1
CL4989.Contig1_All	Glutamate receptor-interacting protein 1 OS=Rattus norvegicus GN=Grip1 PE=1 SV=1

CL4989.Contig2_All	Glutamate receptor-interacting protein 1 OS=Rattus norvegicus GN=Grip1 PE=1 SV=1
CL4994.Contig1_All	--
CL4994.Contig6_All	Cytochrome P450 6k1 OS=Blattella germanica GN=CYP6K1 PE=2 SV=1
CL4994.Contig8_All	Cytochrome P450 6k1 OS=Blattella germanica GN=CYP6K1 PE=2 SV=1
CL5014.Contig2_All	--
CL502.Contig1_All	--
CL5023.Contig1_All	--
CL5023.Contig3_All	--
CL5026.Contig2_All	Facilitated trehalose transporter Tret1 OS=Drosophila willistoni GN=Tret1 PE=3 SV=1
CL5027.Contig2_All	Fibrous sheath CABYR-binding protein OS=Mus musculus GN=Fscb PE=1 SV=1
CL5027.Contig4_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
CL5027.Contig5_All	Fibrous sheath CABYR-binding protein OS=Mus musculus GN=Fscb PE=1 SV=1
CL5027.Contig6_All	--
CL5027.Contig7_All	--
CL5041.Contig2_All	--
CL5046.Contig3_All	--
CL5048.Contig3_All	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2
CL5058.Contig2_All	Tigger transposable element-derived protein 4 OS=Mus musculus GN=Tigd4 PE=2 SV=1
CL5062.Contig1_All	--
CL5073.Contig3_All	--
CL508.Contig7_All	Elongation factor 1-alpha, somatic form OS=Xenopus laevis GN=eef1as PE=2 SV=1
CL5082.Contig1_All	--
CL5125.Contig1_All	--
CL5142.Contig3_All	Trehalase OS=Pimpla hypochondriaca GN=tre1 PE=1 SV=1
CL5144.Contig1_All	Solute carrier organic anion transporter family member 5A1 OS=Homo sapiens GN=SLCO5A1 PE=2 SV=2
CL5144.Contig2_All	Solute carrier organic anion transporter family member 5A1 OS=Homo sapiens GN=SLCO5A1 PE=2 SV=2
CL5144.Contig3_All	Solute carrier organic anion transporter family member 5A1 OS=Homo sapiens GN=SLCO5A1 PE=2 SV=2
CL5159.Contig3_All	Peroxidase OS=Drosophila melanogaster GN=Pxd PE=2 SV=2
CL5159.Contig4_All	Peroxidase OS=Drosophila melanogaster GN=Pxd PE=2 SV=2

CL5159.Contig5_All	Peroxidase OS=Drosophila melanogaster GN=Pxd PE=2 SV=2
CL5159.Contig6_All	Peroxidase OS=Drosophila melanogaster GN=Pxd PE=2 SV=2
CL5178.Contig1_All	--
CL5198.Contig1_All	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2
CL5199.Contig1_All	--
CL5200.Contig1_All	--
CL5207.Contig1_All	Serine protease easter OS=Drosophila melanogaster GN=ea PE=1 SV=3
CL5219.Contig1_All	--
CL5221.Contig1_All	--
CL5246.Contig1_All	Protein RIC1 homolog OS=Drosophila melanogaster GN=CG9063 PE=1 SV=1
CL5255.Contig2_All	--
CL5267.Contig1_All	Solute carrier family 23 member 2 OS=Mus musculus GN=Slc23a2 PE=1 SV=2
CL5304.Contig2_All	--
CL5311.Contig3_All	--
CL5314.Contig3_All	Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2
CL533.Contig2_All	pre-rRNA processing protein FTSJ3 OS=Gallus gallus GN=FTSJ3 PE=2 SV=2
CL5332.Contig2_All	Prickle-like protein 2 OS=Homo sapiens GN=PRICKLE2 PE=1 SV=2
CL5354.Contig1_All	--
CL5354.Contig2_All	--
CL5361.Contig1_All	--
CL5376.Contig2_All	Serine protease inhibitor I/II OS=Schistocerca gregaria PE=1 SV=1
CL5376.Contig3_All	Serine protease inhibitor I/II OS=Schistocerca gregaria PE=1 SV=1
CL5376.Contig4_All	Serine protease inhibitor I/II OS=Schistocerca gregaria PE=1 SV=1
CL5378.Contig3_All	--
CL5378.Contig4_All	--
CL5388.Contig1_All	Probable cytochrome P450 4aa1 OS=Drosophila melanogaster GN=Cyp4aa1 PE=2 SV=2
CL5388.Contig2_All	--
CL5388.Contig3_All	Probable cytochrome P450 4aa1 OS=Drosophila melanogaster GN=Cyp4aa1 PE=2 SV=2
CL5393.Contig6_All	X-ray repair cross-complementing protein 5 OS=Mus musculus GN=Xrcc5 PE=2 SV=4
CL5396.Contig2_All	--

CL5396.Contig7_All	--
CL5409.Contig1_All	--
CL5410.Contig2_All	Sodium/calcium exchanger 3 OS=Rattus norvegicus GN=Slc8a3 PE=2 SV=1
CL5411.Contig3_All	--
CL543.Contig2_All	--
CL5439.Contig1_All	Dipeptidase 1 OS=Sus scrofa GN=DPEP1 PE=1 SV=1
CL5444.Contig6_All	--
CL5446.Contig1_All	Venom carboxylesterase-6 OS=Apis mellifera PE=2 SV=1
CL5460.Contig1_All	--
CL5465.Contig2_All	--
CL5476.Contig1_All	--
CL5483.Contig1_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2
CL5483.Contig2_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2
CL5491.Contig1_All	--
CL550.Contig1_All	Sorting nexin-6 OS=Pongo abelii GN=SNX6 PE=2 SV=1
CL5535.Contig4_All	Zinc transporter 9 OS=Danio rerio GN=slc30a9 PE=2 SV=1
CL5548.Contig1_All	--
CL5553.Contig2_All	Plectin (Fragment) OS=Cricetulus griseus GN=PLEC PE=1 SV=1
CL5553.Contig3_All	Trichohyalin OS=Homo sapiens GN=TCHH PE=1 SV=2
CL556.Contig4_All	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Danio rerio GN=igf2bp1 PE=1 SV=1
CL5580.Contig3_All	--
CL559.Contig1_All	Leucine-rich repeat-containing protein 15 OS=Rattus norvegicus GN=Lrrc15 PE=2 SV=1
CL559.Contig4_All	Carboxypeptidase N subunit 2 OS=Mus musculus GN=Cpn2 PE=1 SV=2
CL56.Contig1_All	Retrovirus-related Pol polyprotein from transposon opus OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL5608.Contig2_All	Lymphocyte-specific helicase OS=Mus musculus GN=Hells PE=1 SV=2
CL5622.Contig1_All	--
CL5628.Contig1_All	Multivesicular body subunit 12B OS=Mus musculus GN=Mvb12b PE=2 SV=2
CL563.Contig1_All	CCR4-NOT transcription complex subunit 7 OS=Homo sapiens GN=CNOT7 PE=1 SV=3
CL5654.Contig2_All	--
CL5666.Contig1_All	Dentin sialophosphoprotein OS=Homo sapiens GN=DSPP PE=1 SV=2

CL567.Contig2_All	--
CL5687.Contig2_All	--
CL5706.Contig1_All	--
CL5707.Contig1_All	Glutathione S-transferase OS=Blattella germanica PE=1 SV=3
CL5711.Contig1_All	--
CL5714.Contig1_All	Serine protease easter OS=Drosophila melanogaster GN=ea PE=1 SV=3
CL5714.Contig2_All	Serine protease easter OS=Drosophila melanogaster GN=ea PE=1 SV=3
CL5714.Contig6_All	Serine protease easter OS=Drosophila melanogaster GN=ea PE=1 SV=3
CL5732.Contig1_All	Receptor-binding cancer antigen expressed on SiSo cells OS=Mus musculus GN=Ebag9 PE=1 SV=2
CL5745.Contig3_All	--
CL5745.Contig5_All	--
CL5764.Contig1_All	Larval cuticle protein 16/17 OS=Manduca sexta GN=LCP16/17 PE=2 SV=1
CL5764.Contig2_All	Larval cuticle protein 1 OS=Helicoverpa armigera GN=LCP1 PE=4 SV=1
CL5772.Contig1_All	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase OS=Danio rerio GN=dhdh PE=2 SV=2
CL5785.Contig2_All	--
CL5791.Contig2_All	Uncharacterized protein C10orf95 OS=Homo sapiens GN=C10orf95 PE=2 SV=1
CL5791.Contig3_All	Protein furry OS=Drosophila melanogaster GN=fry PE=1 SV=2
CL5806.Contig2_All	--
CL5813.Contig1_All	--
CL5826.Contig2_All	15-hydroxyprostaglandin dehydrogenase [NAD(+)] OS=Bos taurus GN=HPGD PE=2 SV=1
CL5836.Contig1_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL5836.Contig2_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL5836.Contig5_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL5836.Contig6_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL5836.Contig7_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
CL5862.Contig1_All	Homeobox protein prospero OS=Drosophila melanogaster GN=pros PE=1 SV=3
CL5880.Contig2_All	Feline leukemia virus subgroup C receptor-related protein 2 OS=Mus musculus GN=Flvcr2 PE=1 SV=2
CL59.Contig3_All	Mitochondrial ribonuclease P protein 3 OS=Homo sapiens GN=KIAA0391 PE=1 SV=2
CL5908.Contig4_All	WD repeat domain phosphoinositide-interacting protein 2 OS=Gallus gallus GN=WIPI2 PE=2 SV=1

CL5912.Contig2_All	Ferric-chelate reductase 1 OS=Mus musculus GN=FRRS1 PE=1 SV=1
CL5934.Contig1_All	Carboxypeptidase N subunit 2 OS=Mus musculus GN=Cpn2 PE=1 SV=2
CL5934.Contig2_All	Carboxypeptidase N subunit 2 OS=Mus musculus GN=Cpn2 PE=1 SV=2
CL5934.Contig3_All	--
CL5934.Contig4_All	--
CL5939.Contig2_All	--
CL5946.Contig3_All	Down syndrome cell adhesion molecule-like protein Dscam2 OS=Drosophila melanogaster GN=Dscam2 PE=2 SV=3
CL5988.Contig3_All	ATP-binding cassette sub-family G member 4 OS=Homo sapiens GN=ABCG4 PE=2 SV=2
CL5996.Contig1_All	Aryl hydrocarbon receptor nuclear translocator 2 OS=Danio rerio GN=arnt2 PE=1 SV=2
CL5997.Contig2_All	Facilitated trehalose transporter Tret1 OS=Aedes aegypti GN=Tret1 PE=3 SV=1
CL6008.Contig1_All	--
CL6008.Contig2_All	--
CL6012.Contig2_All	--
CL6025.Contig1_All	--
CL6034.Contig1_All	Nocturnin OS=Homo sapiens GN=CCRN4L PE=2 SV=2
CL6036.Contig1_All	Leucine-rich repeat-containing protein 15 OS=Mus musculus GN=Lrrc15 PE=2 SV=1
CL6036.Contig2_All	Protein toll OS=Drosophila melanogaster GN=Tl PE=1 SV=1
CL6047.Contig1_All	H/ACA ribonucleoprotein complex subunit 3 OS=Danio rerio GN=nop10 PE=3 SV=1
CL6065.Contig3_All	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3
CL6066.Contig1_All	--
CL6070.Contig2_All	Autophagy-related protein 16-1 OS=Mus musculus GN=Atg16l1 PE=1 SV=1
CL6097.Contig1_All	Spore coat protein SP96 OS=Dictyostelium discoideum GN=cotA PE=4 SV=2
CL6112.Contig1_All	--
CL6122.Contig1_All	Salivary glue protein Sgs-3 OS=Drosophila yakuba GN=Sgs3 PE=2 SV=3
CL6122.Contig2_All	--
CL6124.Contig1_All	--
CL6124.Contig2_All	--
CL6129.Contig1_All	--
CL6129.Contig2_All	--

CL613.Contig1_All	Tigger transposable element-derived protein 1 OS=Homo sapiens GN=TIGD1 PE=1 SV=1
CL6137.Contig2_All	--
CL6137.Contig3_All	--
CL6151.Contig1_All	60S ribosomal protein L37a OS=Drosophila melanogaster GN=RpL37A PE=1 SV=3
CL6161.Contig2_All	Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2
CL6166.Contig2_All	Putative uncharacterized transposon-derived protein F52C9.6 OS=Caenorhabditis elegans GN=F52C9.6 PE=5 SV=1
CL6199.Contig2_All	Synaptic vesicle membrane protein VAT-1 homolog OS=Danio rerio GN=vat1 PE=2 SV=1
CL620.Contig15_All	--
CL625.Contig1_All	Tafazzin homolog OS=Drosophila melanogaster GN=Taz PE=2 SV=2
CL63.Contig4_All	--
CL6318.Contig2_All	CAD protein OS=Drosophila melanogaster GN=r PE=1 SV=3
CL6336.Contig1_All	Regucalcin OS=Xenopus laevis GN=rgn PE=2 SV=1
CL6337.Contig1_All	--
CL6363.Contig2_All	--
CL6383.Contig7_All	Histone deacetylase 4 OS=Rattus norvegicus GN=Hdac4 PE=1 SV=2
CL6397.Contig2_All	--
CL640.Contig2_All	Exportin-4 OS=Xenopus laevis GN=xpo4 PE=2 SV=1
CL6423.Contig1_All	--
CL6484.Contig2_All	--
CL6485.Contig1_All	--
CL6487.Contig1_All	--
CL65.Contig10_All	Dentin sialophosphoprotein OS=Homo sapiens GN=DSPP PE=1 SV=2
CL65.Contig4_All	Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3
CL6510.Contig1_All	Leukocyte elastase inhibitor OS=Sus scrofa GN=SERPINB1 PE=1 SV=1
CL6511.Contig1_All	Serpin B4 OS=Homo sapiens GN=SERPINB4 PE=1 SV=2
CL652.Contig2_All	--
CL6531.Contig1_All	Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3
CL6531.Contig2_All	Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3
CL6549.Contig3_All	Acyl-CoA synthetase family member 4 OS=Mus musculus GN=Aasdh PE=2 SV=1
CL6555.Contig2_All	--

CL6555.Contig3_All	--
CL659.Contig1_All	--
CL659.Contig2_All	--
CL659.Contig3_All	--
CL659.Contig4_All	--
CL6609.Contig1_All	--
CL6611.Contig2_All	--
CL6628.Contig2_All	--
CL664.Contig1_All	--
CL6647.Contig2_All	Irregular chiasm C-roughest protein OS=Drosophila melanogaster GN=rst PE=2 SV=2
CL6660.Contig2_All	--
CL6662.Contig1_All	--
CL6697.Contig2_All	Poly(ADP-ribose) glycohydrolase OS=Mus musculus GN=Parg PE=1 SV=2
CL6697.Contig3_All	Poly(ADP-ribose) glycohydrolase OS=Mus musculus GN=Parg PE=1 SV=2
CL6700.Contig1_All	--
CL6725.Contig1_All	Zinc finger protein 36, C3H1 type-like 1 OS=Rattus norvegicus GN=Zfp36l1 PE=1 SV=1
CL6748.Contig3_All	--
CL6751.Contig3_All	Hexokinase type 2 OS=Drosophila melanogaster GN=Hex-t2 PE=2 SV=4
CL6753.Contig3_All	Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1
CL6754.Contig1_All	Solute carrier organic anion transporter family member 4C1 OS=Homo sapiens GN=SLCO4C1 PE=1 SV=1
CL6754.Contig2_All	Solute carrier organic anion transporter family member 4C1 OS=Homo sapiens GN=SLCO4C1 PE=1 SV=1
CL6782.Contig3_All	--
CL6788.Contig1_All	F-box/LRR-repeat protein 13 OS=Homo sapiens GN=FBXL13 PE=2 SV=3
CL6797.Contig1_All	3-hydroxy-3-methylglutaryl-coenzyme A reductase OS=Blattella germanica PE=2 SV=1
CL6797.Contig3_All	3-hydroxy-3-methylglutaryl-coenzyme A reductase OS=Blattella germanica PE=2 SV=1
CL68.Contig1_All	--
CL68.Contig7_All	Homeotic protein ultrabithorax OS=Junonia coenia GN=Ubx PE=2 SV=1
CL6801.Contig1_All	UPF0466 protein AGAP011291, mitochondrial OS=Anopheles gambiae GN=AGAP011291 PE=3 SV=2
CL6804.Contig2_All	Vacuolar protein sorting-associated protein 37A OS=Homo sapiens GN=VPS37A PE=1 SV=1

CL6815.Contig4_All	--
CL6818.Contig4_All	Polycomb protein Sfmbt OS=Drosophila melanogaster GN=Sfmbt PE=1 SV=2
CL6822.Contig1_All	Mitochondrial inner membrane protease subunit 1 OS=Mus musculus GN=Immp1l PE=2 SV=1
CL6836.Contig1_All	--
CL6866.Contig1_All	--
CL6866.Contig2_All	--
CL6866.Contig3_All	--
CL6885.Contig1_All	--
CL6907.Contig2_All	--
CL6909.Contig4_All	Ubiquitin carboxyl-terminal hydrolase 51 OS=Homo sapiens GN=USP51 PE=2 SV=1
CL6919.Contig3_All	Pyrroline-5-carboxylate reductase 3 OS=Xenopus laevis GN=pycrl PE=2 SV=2
CL6953.Contig2_All	--
CL6963.Contig2_All	Rap1 GTPase-activating protein 1 OS=Homo sapiens GN=RAP1GAP PE=1 SV=2
CL6975.Contig1_All	--
CL6977.Contig1_All	Elongation of very long chain fatty acids protein AAEL008004 OS=Aedes aegypti GN=AAEL008004 PE=2 SV=2
CL6983.Contig3_All	Legumain OS=Bos taurus GN=LGMN PE=1 SV=1
CL6999.Contig1_All	--
CL7027.Contig1_All	--
CL7027.Contig4_All	--
CL7029.Contig1_All	Innexin inx7 OS=Drosophila melanogaster GN=inx7 PE=1 SV=1
CL7032.Contig4_All	60S acidic ribosomal protein P2 OS=Bos taurus GN=RPLP2 PE=2 SV=1
CL7072.Contig1_All	Long-chain fatty acid transport protein 1 OS=Mus musculus GN=Slc27a1 PE=1 SV=1
CL7076.Contig1_All	--
CL7080.Contig2_All	BAI1-associated protein 3 OS=Mus musculus GN=Baiap3 PE=2 SV=3
CL7082.Contig3_All	Podocan-like protein 1 OS=Mus musculus GN=Podnl1 PE=2 SV=2
CL7085.Contig1_All	--
CL7085.Contig2_All	--
CL7097.Contig1_All	--
CL7097.Contig2_All	Myosin heavy chain IB OS=Acanthamoeba castellanii GN=MIB PE=1 SV=2
CL7113.Contig1_All	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R1 4 (Fragment) OS=Nasonia vitripennis PE=4 SV=1

CL7119.Contig2_All	--
CL7126.Contig3_All	--
CL7137.Contig3_All	Sphingomyelin phosphodiesterase OS=Bos taurus GN=SMPD1 PE=2 SV=1
CL7181.Contig2_All	--
CL7193.Contig1_All	--
CL7193.Contig2_All	--
CL7193.Contig3_All	Integumentary mucin C.1 (Fragment) OS=Xenopus laevis PE=2 SV=1
CL72.Contig4_All	--
CL7200.Contig1_All	Folliculin-interacting protein 2 OS=Mus musculus GN=Fnip2 PE=2 SV=2
CL7213.Contig2_All	--
CL7219.Contig1_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL7219.Contig2_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
CL7229.Contig7_All	Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1
CL7256.Contig2_All	--
CL7293.Contig3_All	Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4
CL7318.Contig1_All	Probable cytochrome P450 6a13 OS=Drosophila melanogaster GN=Cyp6a13 PE=2 SV=1
CL7319.Contig1_All	Solute carrier organic anion transporter family member 4C1 OS=Mus musculus GN=Slco4c1 PE=2 SV=1
CL7329.Contig1_All	Mucin-19 OS=Homo sapiens GN=MUC19 PE=1 SV=2
CL7329.Contig3_All	Keratinocyte proline-rich protein OS=Rattus norvegicus GN=Kprp PE=2 SV=1
CL7331.Contig1_All	--
CL7335.Contig1_All	--
CL7335.Contig2_All	--
CL7335.Contig5_All	--
CL7345.Contig1_All	UNC93-like protein OS=Drosophila melanogaster GN=CG4928 PE=2 SV=1
CL7345.Contig2_All	UNC93-like protein OS=Drosophila melanogaster GN=CG4928 PE=2 SV=1
CL7354.Contig1_All	F-box only protein 28 OS=Homo sapiens GN=FBXO28 PE=1 SV=1
CL7354.Contig2_All	F-box only protein 28 OS=Homo sapiens GN=FBXO28 PE=1 SV=1
CL7354.Contig3_All	F-box only protein 28 OS=Homo sapiens GN=FBXO28 PE=1 SV=1
CL7354.Contig4_All	F-box only protein 28 OS=Homo sapiens GN=FBXO28 PE=1 SV=1
CL7354.Contig6_All	F-box only protein 28 OS=Homo sapiens GN=FBXO28 PE=1 SV=1

CL7354.Contig7_All	F-box only protein 28 OS=Homo sapiens GN=FBXO28 PE=1 SV=1
CL7354.Contig8_All	F-box only protein 28 OS=Homo sapiens GN=FBXO28 PE=1 SV=1
CL7357.Contig1_All	Probable cytochrome P450 301a1, mitochondrial OS=Drosophila melanogaster GN=Cyp301a1 PE=2 SV=1
CL7357.Contig2_All	Probable cytochrome P450 301a1, mitochondrial OS=Drosophila melanogaster GN=Cyp301a1 PE=2 SV=1
CL7385.Contig2_All	Fibrillin-2 OS=Mus musculus GN=Fbn2 PE=1 SV=2
CL7393.Contig2_All	Mucin-22 OS=Homo sapiens GN=MUC22 PE=1 SV=2
CL7409.Contig1_All	--
CL7409.Contig2_All	--
CL741.Contig1_All	--
CL741.Contig3_All	--
CL741.Contig5_All	--
CL7438.Contig2_All	Band 7 protein CG42540 OS=Drosophila melanogaster GN=CG42540 PE=2 SV=2
CL7456.Contig1_All	Uncharacterized histidine-rich protein DDB_G0274557 OS=Dictyostelium discoideum GN=DDB_G0274557 PE=4 SV=1
CL7456.Contig2_All	Probable cytochrome P450 305a1 OS=Drosophila melanogaster GN=Cyp305a1 PE=2 SV=1
CL7470.Contig2_All	Glutathione S-transferase OS=Blattella germanica PE=1 SV=3
CL7491.Contig1_All	Fatty acid-binding protein, muscle OS=Schistocerca gregaria PE=1 SV=2
CL7495.Contig1_All	Membrane metallo-endopeptidase-like 1 OS=Homo sapiens GN=MMEL1 PE=1 SV=2
CL7520.Contig1_All	--
CL7520.Contig2_All	--
CL7532.Contig1_All	--
CL7559.Contig1_All	--
CL7584.Contig1_All	--
CL7590.Contig1_All	--
CL7604.Contig1_All	Venom dipeptidyl peptidase 4 OS=Apis mellifera PE=1 SV=1
CL7615.Contig2_All	Transcriptional repressor scratch 1 OS=Mus musculus GN=Scrt1 PE=1 SV=1
CL7618.Contig2_All	Ubiquitin carboxyl-terminal hydrolase 2 OS=Mus musculus GN=Usp2 PE=1 SV=2
CL7629.Contig1_All	--
CL7646.Contig1_All	Androgen-dependent TFPI-regulating protein OS=Mesocricetus auratus GN=ADTRP PE=2 SV=1
CL7646.Contig2_All	Androgen-dependent TFPI-regulating protein OS=Mesocricetus auratus

	GN=ADTRP PE=2 SV=1
CL7657.Contig2_All	Pre-mRNA-splicing factor 38B OS=Danio rerio GN=prpf38b PE=2 SV=1
CL7668.Contig1_All	--
CL7674.Contig1_All	--
CL7676.Contig3_All	UPF0415 protein C7orf25 homolog OS=Danio rerio GN=zgc:55781 PE=2 SV=1
CL7700.Contig1_All	--
CL771.Contig4_All	Metabotropic glutamate receptor 4 OS=Macaca fascicularis GN=GRM4 PE=2 SV=1
CL7733.Contig1_All	--
CL7737.Contig3_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
CL774.Contig2_All	--
CL7753.Contig2_All	--
CL7790.Contig1_All	Dolichol kinase OS=Mus musculus GN=Dolk PE=2 SV=1
CL7791.Contig1_All	Serine protease easter OS=Drosophila melanogaster GN=ea PE=1 SV=3
CL7791.Contig2_All	Serine protease easter OS=Drosophila melanogaster GN=ea PE=1 SV=3
CL7792.Contig1_All	--
CL7804.Contig3_All	--
CL7820.Contig1_All	--
CL7833.Contig1_All	--
CL7838.Contig2_All	Protein Dok-7 OS=Homo sapiens GN=DOK7 PE=1 SV=1
CL7854.Contig2_All	--
CL7869.Contig2_All	Phosphoserine phosphatase OS=Bos taurus GN=PSPH PE=2 SV=1
CL7878.Contig2_All	Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1 PE=1 SV=3
CL7882.Contig1_All	Uncharacterized proline-rich protein (Fragment) OS=Owenia fusiformis PE=4 SV=1
CL789.Contig2_All	Rho GTPase-activating protein 21 OS=Xenopus tropicalis GN=arhgap21 PE=2 SV=1
CL7926.Contig1_All	P protein OS=Sus scrofa GN=Oca2 PE=2 SV=3
CL7933.Contig2_All	--
CL7944.Contig2_All	Cytochrome P450 9e2 OS=Blattella germanica GN=CYP9E2 PE=2 SV=1
CL7992.Contig2_All	--
CL7997.Contig2_All	--
CL7997.Contig4_All	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1
CL7997.Contig5_All	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1

CL802.Contig2_All	--
CL8022.Contig1_All	--
CL8062.Contig6_All	--
CL8080.Contig1_All	--
CL8082.Contig2_All	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Drosophila melanogaster GN=Gpdh PE=1 SV=3
CL8091.Contig2_All	--
CL8108.Contig2_All	--
CL8118.Contig1_All	--
CL8118.Contig2_All	--
CL8140.Contig1_All	Carboxypeptidase N subunit 2 OS=Mus musculus GN=Cpn2 PE=1 SV=2
CL8140.Contig2_All	--
CL8140.Contig3_All	Carboxypeptidase N subunit 2 OS=Mus musculus GN=Cpn2 PE=1 SV=2
CL8140.Contig4_All	Carboxypeptidase N subunit 2 OS=Mus musculus GN=Cpn2 PE=1 SV=2
CL8147.Contig1_All	--
CL8152.Contig3_All	40S ribosomal protein S26 OS=Rattus norvegicus GN=Rps26 PE=3 SV=3
CL8154.Contig2_All	Retrovirus-related Pol polyprotein from transposon opus OS=Drosophila melanogaster GN=pol PE=4 SV=1
CL8170.Contig2_All	--
CL8174.Contig3_All	--
CL8176.Contig2_All	Polypyrimidine tract-binding protein 1 OS=Rattus norvegicus GN=Ptbp1 PE=1 SV=1
CL8176.Contig3_All	Polypyrimidine tract-binding protein 1 OS=Rattus norvegicus GN=Ptbp1 PE=1 SV=1
CL8177.Contig5_All	--
CL8201.Contig2_All	Serpin B4 OS=Homo sapiens GN=SERPINB4 PE=1 SV=2
CL8209.Contig2_All	PTB domain-containing adapter protein ced-6 OS=Drosophila melanogaster GN=ced-6 PE=1 SV=1
CL8211.Contig2_All	--
CL8216.Contig1_All	--
CL8224.Contig2_All	Venom carboxylesterase-6 OS=Apis mellifera PE=2 SV=1
CL8224.Contig3_All	Venom carboxylesterase-6 OS=Apis mellifera PE=2 SV=1
CL823.Contig9_All	Serine/threonine-protein kinase hippo OS=Drosophila melanogaster GN=hpo PE=1 SV=1
CL8282.Contig3_All	--
CL8292.Contig1_All	--
CL8296.Contig1_All	--

CL8303.Contig1_All	--
CL8303.Contig2_All	--
CL832.Contig1_All	--
CL8324.Contig1_All	Zinc transporter 2 OS=Rattus norvegicus GN=Slc30a2 PE=2 SV=1
CL8324.Contig6_All	Zinc transporter 2 OS=Rattus norvegicus GN=Slc30a2 PE=2 SV=1
CL8352.Contig2_All	Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3
CL8365.Contig1_All	--
CL8434.Contig2_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL8459.Contig2_All	--
CL8473.Contig2_All	Sulfotransferase 1 family member D1 OS=Rattus norvegicus GN=Sult1d1 PE=2 SV=1
CL8495.Contig1_All	--
CL8515.Contig2_All	--
CL8515.Contig3_All	--
CL8520.Contig2_All	--
CL8522.Contig2_All	Sugar phosphate exchanger 2 OS=Danio rerio GN=slc37a2 PE=2 SV=1
CL8553.Contig4_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
CL8554.Contig1_All	--
CL8564.Contig2_All	--
CL8571.Contig1_All	--
CL8571.Contig3_All	--
CL8586.Contig2_All	--
CL8641.Contig1_All	--
CL8642.Contig2_All	--
CL8657.Contig1_All	--
CL8662.Contig2_All	--
CL8691.Contig2_All	Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1
CL8717.Contig2_All	--
CL8732.Contig1_All	--
CL8741.Contig2_All	Kinesin-like protein KIF19 OS=Homo sapiens GN=KIF19 PE=2 SV=2
CL8760.Contig1_All	--
CL8779.Contig1_All	--
CL8789.Contig2_All	Synaptic vesicle membrane protein VAT-1 homolog OS=Danio rerio GN=vat1 PE=2 SV=1
CL8801.Contig1_All	--
CL8801.Contig2_All	--

CL8803.Contig1_All	Carnitine O-palmitoyltransferase 1, liver isoform OS=Rattus norvegicus GN=Cpt1a PE=1 SV=2
CL881.Contig7_All	Arylsulfatase B OS=Felis catus GN=ARSB PE=2 SV=1
CL8838.Contig1_All	Uncharacterized protein KIAA1467 homolog OS=Gallus gallus GN=RCJMB04_14d19 PE=2 SV=1
CL8845.Contig1_All	--
CL8848.Contig2_All	--
CL8870.Contig1_All	--
CL8930.Contig4_All	Major facilitator superfamily domain-containing protein 6 OS=Mus musculus GN=Mfsd6 PE=1 SV=1
CL894.Contig1_All	--
CL8959.Contig1_All	--
CL896.Contig2_All	RNA-directed DNA polymerase from mobile element jockey OS=Drosophila melanogaster GN=pol PE=1 SV=1
CL8977.Contig1_All	--
CL8977.Contig2_All	--
CL9005.Contig3_All	--
CL9008.Contig1_All	--
CL9067.Contig1_All	--
CL9067.Contig2_All	--
CL9091.Contig3_All	--
CL9103.Contig1_All	60S ribosomal protein L13a OS=Bos taurus GN=RPL13A PE=2 SV=3
CL9105.Contig2_All	--
CL9115.Contig2_All	Leucine-rich repeat-containing protein 24 OS=Mus musculus GN=Lrrc24 PE=2 SV=1
CL9122.Contig1_All	--
CL9122.Contig4_All	--
CL9122.Contig5_All	--
CL9136.Contig1_All	--
CL919.Contig1_All	Zinc finger protein rotund OS=Drosophila melanogaster GN=rn PE=1 SV=2
CL9209.Contig2_All	--
CL9212.Contig1_All	--
CL9218.Contig1_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL9218.Contig2_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
CL9238.Contig3_All	Elongation of very long chain fatty acids protein AAEL008004 OS=Aedes aegypti GN=AAEL008004 PE=2 SV=2
CL9256.Contig1_All	Cytochrome P450 4c3 OS=Drosophila melanogaster GN=Cyp4c3 PE=2 SV=1

CL9256.Contig2_All	Cytochrome P450 4C1 OS=Blaberus discoidalis GN=CYP4C1 PE=2 SV=1
CL927.Contig5_All	--
CL9296.Contig2_All	--
CL9300.Contig1_All	PRA1 family protein 3 OS=Macaca fascicularis GN=ARL6IP5 PE=2 SV=1
CL9309.Contig3_All	Activating signal cointegrator 1 complex subunit 3 OS=Gallus gallus GN=ascc3 PE=3 SV=2
CL9312.Contig3_All	--
CL9314.Contig1_All	--
CL9320.Contig2_All	--
CL9337.Contig1_All	--
CL934.Contig2_All	C-1-tetrahydrofolate synthase, cytoplasmic OS=Spodoptera frugiperda PE=2 SV=3
CL9358.Contig1_All	Chitooligosaccharidolytic beta-N-acetylglucosaminidase OS=Bombyx mori PE=1 SV=1
CL9358.Contig2_All	Chitooligosaccharidolytic beta-N-acetylglucosaminidase OS=Bombyx mori PE=1 SV=1
CL9358.Contig3_All	Chitooligosaccharidolytic beta-N-acetylglucosaminidase OS=Bombyx mori PE=1 SV=1
CL9368.Contig1_All	--
CL9390.Contig4_All	Irregular chiasm C-roughest protein OS=Drosophila melanogaster GN=rst PE=2 SV=2
CL9418.Contig3_All	Single-stranded DNA-binding protein 3 OS=Rattus norvegicus GN=Ssbp3 PE=2 SV=1
CL9424.Contig1_All	--
CL9424.Contig3_All	--
CL9433.Contig2_All	--
CL9451.Contig2_All	--
CL9454.Contig1_All	--
CL9482.Contig1_All	Formin-2 OS=Homo sapiens GN=FMN2 PE=1 SV=4
CL9482.Contig2_All	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2
CL9514.Contig3_All	Zinc finger SWIM domain-containing protein 8 OS=Mus musculus GN=Zswim8 PE=1 SV=1
CL953.Contig1_All	--
CL9568.Contig1_All	--
CL9594.Contig1_All	--
CL960.Contig7_All	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial OS=Mus musculus GN=Coq3 PE=2 SV=1
CL9604.Contig3_All	Protein yippee-like 2 OS=Pongo abelii GN=YPEL2 PE=3 SV=1
CL9604.Contig4_All	Protein yippee-like 2 OS=Pongo abelii GN=YPEL2 PE=3 SV=1

CL9623.Contig2_All	--
CL9640.Contig1_All	Carboxypeptidase Q OS=Rattus norvegicus GN=Cpq PE=1 SV=1
CL9640.Contig2_All	Carboxypeptidase Q OS=Rattus norvegicus GN=Cpq PE=1 SV=1
CL971.Contig2_All	UDP-glucuronosyltransferase 1-8 OS=Homo sapiens GN=UGT1A8 PE=1 SV=1
CL9724.Contig2_All	Mannose-P-dolichol utilization defect 1 protein homolog OS=Drosophila melanogaster GN=CG3792 PE=1 SV=2
CL9728.Contig1_All	--
CL9749.Contig3_All	--
CL976.Contig3_All	--
CL9763.Contig2_All	--
CL9773.Contig1_All	60S ribosomal protein L29 OS=Rattus norvegicus GN=Rpl29 PE=1 SV=3
CL979.Contig2_All	Hypoxia-inducible factor 1-alpha OS=Gallus gallus GN=HIF1A PE=2 SV=2
CL9804.Contig1_All	--
CL981.Contig1_All	--
CL981.Contig2_All	--
CL9819.Contig2_All	MKI67 FHA domain-interacting nucleolar phosphoprotein-like OS=Xenopus tropicalis GN=mki67ipl PE=2 SV=1
CL9839.Contig1_All	--
CL9894.Contig2_All	--
CL9898.Contig2_All	--
CL9899.Contig1_All	--
CL99.Contig7_All	--
CL9925.Contig1_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
CL9928.Contig1_All	--
CL9928.Contig2_All	--
CL9948.Contig1_All	Serine/threonine-protein kinase 32C OS=Homo sapiens GN=STK32C PE=1 SV=1
CL9948.Contig2_All	Serine/threonine-protein kinase 32C OS=Homo sapiens GN=STK32C PE=1 SV=1
CL997.Contig2_All	RNA-directed DNA polymerase from mobile element jockey OS=Drosophila funebris GN=jockey\pol PE=1 SV=1
CL9972.Contig1_All	--
CL9977.Contig1_All	Nuclear transcription factor Y subunit alpha OS=Dictyostelium discoideum GN=nfyA PE=3 SV=1
Unigene10064_All	Protein I'm not dead yet OS=Drosophila melanogaster GN=Indy PE=1 SV=2
Unigene10069_All	--

Unigene10087_All	--
Unigene100_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene10123_All	--
Unigene101302_All	--
Unigene10137_All	Cyclin-J OS=Mus musculus GN=Ccnj PE=2 SV=2
Unigene101_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene102024_All	--
Unigene10238_All	--
Unigene102917_All	--
Unigene10296_All	Protein I'm not dead yet OS=Drosophila melanogaster GN=Indy PE=1 SV=2
Unigene10337_All	--
Unigene103394_All	--
Unigene10374_All	--
Unigene103833_All	--
Unigene10402_All	Growth/differentiation factor 11 OS=Mus musculus GN=Gdf11 PE=2 SV=1
Unigene104219_All	--
Unigene10422_All	Retrovirus-related Pol polyprotein from transposon gypsy OS=Drosophila melanogaster GN=pol PE=4 SV=1
Unigene10424_All	--
Unigene10432_All	--
Unigene1044_All	--
Unigene104878_All	--
Unigene105003_All	--
Unigene105030_All	--
Unigene105214_All	--
Unigene10524_All	Protein bicaudal C OS=Drosophila melanogaster GN=BicC PE=1 SV=2
Unigene1053_All	--
Unigene10540_All	Fatty-acid amide hydrolase 2 OS=Homo sapiens GN=FAAH2 PE=2 SV=1
Unigene105_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene10605_All	--
Unigene10616_All	--
Unigene1061_All	--
Unigene106495_All	--
Unigene106819_All	--
Unigene106856_All	--
Unigene107265_All	--

Unigene10728_All	--
Unigene10730_All	Acyl-CoA synthetase family member 2, mitochondrial OS=Macaca fascicularis GN=ACSF2 PE=2 SV=1
Unigene107418_All	--
Unigene10745_All	Wee1-like protein kinase OS=Homo sapiens GN=WEE1 PE=1 SV=2
Unigene107838_All	--
Unigene10785_All	--
Unigene108023_All	--
Unigene10816_All	Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2
Unigene10824_All	Synaptic vesicle glycoprotein 2C OS=Rattus norvegicus GN=Sv2c PE=1 SV=1
Unigene10905_All	--
Unigene10915_All	--
Unigene10918_All	--
Unigene109402_All	--
Unigene109571_All	--
Unigene109574_All	--
Unigene109652_All	--
Unigene109751_All	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R1 (Fragment) OS=Popillia japonica PE=4 SV=1
Unigene109761_All	--
Unigene109776_All	--
Unigene109803_All	--
Unigene109823_All	--
Unigene109898_All	--
Unigene109902_All	--
Unigene109957_All	Beta-galactosidase-1-like protein 3 OS=Rattus norvegicus GN=Glb1l3 PE=2 SV=1
Unigene110023_All	--
Unigene11011_All	--
Unigene110146_All	--
Unigene110163_All	--
Unigene110206_All	--
Unigene110217_All	--
Unigene110283_All	--
Unigene110306_All	--
Unigene110319_All	--
Unigene110328_All	--
Unigene110373_All	--

Unigene110481_All	--
Unigene110502_All	--
Unigene110508_All	--
Unigene110518_All	--
Unigene110551_All	--
Unigene110568_All	Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1
Unigene110608_All	--
Unigene110615_All	--
Unigene110616_All	Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4
Unigene11069_All	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R1 (Fragment) OS=Sciara coprophila PE=4 SV=1
Unigene11078_All	PiggyBac transposable element-derived protein 4 OS=Homo sapiens GN=PGBD4 PE=2 SV=3
Unigene11079_All	--
Unigene111954_All	--
Unigene111969_All	--
Unigene11199_All	--
Unigene11200_All	--
Unigene112019_All	--
Unigene11204_All	--
Unigene112081_All	--
Unigene112125_All	--
Unigene11219_All	--
Unigene112205_All	--
Unigene112255_All	--
Unigene11227_All	--
Unigene11243_All	--
Unigene112458_All	--
Unigene11256_All	--
Unigene11280_All	--
Unigene112949_All	--
Unigene11296_All	--
Unigene113300_All	--
Unigene113367_All	--
Unigene113373_All	--
Unigene113391_All	--
Unigene113414_All	--
Unigene113443_All	--
Unigene113614_All	--

Unigene113615_All	--
Unigene113627_All	--
Unigene113637_All	--
Unigene113659_All	--
Unigene113710_All	--
Unigene11372_All	--
Unigene113759_All	--
Unigene113808_All	--
Unigene113884_All	--
Unigene113897_All	--
Unigene11392_All	--
Unigene114041_All	--
Unigene114099_All	--
Unigene114100_All	--
Unigene114150_All	--
Unigene114196_All	--
Unigene114229_All	--
Unigene114258_All	--
Unigene114299_All	--
Unigene114603_All	--
Unigene114638_All	Transposable element Tcb1 transposase OS=Caenorhabditis briggsae PE=3 SV=1
Unigene114667_All	--
Unigene114687_All	--
Unigene114760_All	--
Unigene114776_All	--
Unigene11479_All	--
Unigene114885_All	--
Unigene114907_All	--
Unigene114941_All	--
Unigene114978_All	--
Unigene115021_All	--
Unigene115049_All	--
Unigene115064_All	--
Unigene115069_All	--
Unigene115080_All	--
Unigene115095_All	--
Unigene115135_All	--
Unigene115156_All	--
Unigene115187_All	--
Unigene115218_All	--
Unigene115240_All	--

Unigene115286_All	--
Unigene115317_All	--
Unigene115441_All	--
Unigene115447_All	--
Unigene11545_All	--
Unigene115462_All	--
Unigene115492_All	DNA-directed RNA polymerase II subunit RPB1 OS=Mus musculus GN=Polr2a PE=1 SV=3
Unigene115494_All	--
Unigene115511_All	--
Unigene11554_All	--
Unigene115566_All	--
Unigene115583_All	--
Unigene115610_All	--
Unigene115658_All	--
Unigene115660_All	--
Unigene115671_All	--
Unigene115681_All	--
Unigene115691_All	--
Unigene115726_All	--
Unigene115734_All	--
Unigene115832_All	--
Unigene115872_All	--
Unigene11591_All	--
Unigene116151_All	--
Unigene116220_All	--
Unigene116224_All	--
Unigene116253_All	--
Unigene116356_All	--
Unigene11647_All	--
Unigene116822_All	--
Unigene11711_All	--
Unigene117278_All	--
Unigene11735_All	--
Unigene117856_All	--
Unigene117_All	Influenza virus NS1A-binding protein homolog OS=Mus musculus GN=Ivns1abp PE=1 SV=2
Unigene11828_All	--
Unigene11840_All	--
Unigene11844_All	--
Unigene1187_All	--

Unigene11923_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene12019_All	Myosin IC heavy chain OS=Acanthamoeba castellanii GN=MIC PE=1 SV=1
Unigene120388_All	--
Unigene12052_All	--
Unigene12186_All	--
Unigene122771_All	--
Unigene12349_All	Heat shock 70 kDa protein cognate 3 OS=Drosophila melanogaster GN=Hsc70-3 PE=2 SV=2
Unigene12350_All	Aquaporin AQPAn.G OS=Anopheles gambiae GN=AGAP008842 PE=3 SV=4
Unigene123825_All	--
Unigene123944_All	Meiosis arrest female protein 1 OS=Rattus norvegicus GN=Marf1 PE=1 SV=2
Unigene124297_All	--
Unigene124346_All	--
Unigene12482_All	Synaptic vesicle membrane protein VAT-1 homolog OS=Danio rerio GN=vat1 PE=2 SV=1
Unigene125152_All	--
Unigene125170_All	Platelet glycoprotein V OS=Rattus norvegicus GN=Gp5 PE=3 SV=1
Unigene125259_All	--
Unigene12558_All	--
Unigene125615_All	--
Unigene12637_All	--
Unigene1263_All	--
Unigene12666_All	Lysosomal aspartic protease OS=Aedes aegypti GN=AAEL006169 PE=1 SV=2
Unigene12699_All	--
Unigene12737_All	--
Unigene12745_All	Sialin OS=Ovis aries GN=SLC17A5 PE=2 SV=1
Unigene12754_All	DNA topoisomerase 2-beta OS=Gallus gallus GN=TOP2B PE=2 SV=1
Unigene12854_All	Selenoprotein N OS=Homo sapiens GN=SEPN1 PE=1 SV=5
Unigene12860_All	Ribonuclease 3 OS=Mus musculus GN=Drosha PE=1 SV=1
Unigene12862_All	Exportin-2 OS=Xenopus laevis GN=cse1l PE=2 SV=1
Unigene12957_All	Cylicin-1 OS=Homo sapiens GN=CYLC1 PE=2 SV=2
Unigene12974_All	--
Unigene13078_All	--
Unigene13142_All	--
Unigene132019_All	--

Unigene133675_All	--
Unigene13372_All	--
Unigene13393_All	--
Unigene13424_All	--
Unigene13432_All	--
Unigene13440_All	--
Unigene13462_All	--
Unigene13494_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
Unigene1351_All	--
Unigene13595_All	--
Unigene13597_All	--
Unigene13646_All	--
Unigene137011_All	--
Unigene13734_All	--
Unigene13736_All	--
Unigene13740_All	--
Unigene13741_All	--
Unigene137456_All	WAP, Kazal, immunoglobulin, Kunitz and NTR domain-containing protein 1 OS=Mus musculus GN=Wfikkn1 PE=2 SV=2
Unigene13828_All	--
Unigene138429_All	--
Unigene13871_All	--
Unigene13943_All	--
Unigene139474_All	--
Unigene13965_All	Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1
Unigene139709_All	--
Unigene13977_All	--
Unigene13981_All	--
Unigene140265_All	--
Unigene140560_All	Triple functional domain protein OS=Homo sapiens GN=TRIO PE=1 SV=2
Unigene140704_All	--
Unigene140912_All	Peroxidasin OS=Xenopus tropicalis GN=pxdn PE=2 SV=1
Unigene14098_All	--
Unigene141019_All	--
Unigene14101_All	--
Unigene14173_All	--
Unigene14176_All	--

Unigene14185_All	--
Unigene14191_All	--
Unigene14228_All	--
Unigene14241_All	--
Unigene14242_All	--
Unigene14244_All	--
Unigene14254_All	--
Unigene14293_All	--
Unigene14443_All	--
Unigene14463_All	--
Unigene144_All	Homeobox protein 2 OS=Dictyostelium discoideum GN=hbx2 PE=2 SV=1
Unigene145586_All	--
Unigene1456_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene145881_All	--
Unigene14590_All	--
Unigene147280_All	--
Unigene14748_All	--
Unigene14769_All	--
Unigene14778_All	--
Unigene148582_All	--
Unigene14908_All	--
Unigene14914_All	--
Unigene14917_All	--
Unigene14927_All	--
Unigene149760_All	--
Unigene15004_All	--
Unigene15013_All	--
Unigene150255_All	--
Unigene15055_All	--
Unigene15063_All	--
Unigene15112_All	--
Unigene15159_All	--
Unigene152111_All	--
Unigene1522_All	--
Unigene15260_All	--
Unigene15348_All	--
Unigene15349_All	--
Unigene1536_All	--
Unigene15412_All	--
Unigene15467_All	--

Unigene15487_All	--
Unigene1548_All	Superoxide dismutase [Cu-Zn] OS=Halocynthia roretzi PE=1 SV=2
Unigene15540_All	--
Unigene15599_All	--
Unigene15600_All	--
Unigene15648_All	--
Unigene15725_All	--
Unigene15731_All	--
Unigene15732_All	--
Unigene15740_All	--
Unigene15766_All	--
Unigene15827_All	--
Unigene15855_All	--
Unigene15883_All	--
Unigene15891_All	--
Unigene15947_All	--
Unigene15959_All	--
Unigene16013_All	--
Unigene16055_All	Regucalcin OS=Xenopus laevis GN=rgn PE=2 SV=1
Unigene16066_All	--
Unigene16078_All	26S proteasome non-ATPase regulatory subunit 10 OS=Dictyostelium discoideum GN=psmD10 PE=2 SV=1
Unigene16100_All	--
Unigene16101_All	--
Unigene16168_All	--
Unigene16266_All	--
Unigene16300_All	--
Unigene16338_All	--
Unigene16343_All	--
Unigene16409_All	--
Unigene16488_All	--
Unigene16527_All	Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=1 SV=2
Unigene16578_All	--
Unigene16586_All	--
Unigene16726_All	--
Unigene16727_All	--
Unigene16804_All	--
Unigene16821_All	--
Unigene16938_All	--
Unigene17016_All	--

Unigene17130_All	--
Unigene17145_All	--
Unigene17181_All	--
Unigene17432_All	Solute carrier family 25 member 38 OS=Rattus norvegicus GN=Slc25a38 PE=2 SV=1
Unigene17448_All	--
Unigene17484_All	Nicotinamide mononucleotide adenylyltransferase 1 OS=Bos taurus GN=NMNAT1 PE=2 SV=1
Unigene17508_All	--
Unigene17515_All	--
Unigene17517_All	Solute carrier family 25 member 38 OS=Homo sapiens GN=SLC25A38 PE=1 SV=1
Unigene17537_All	Aminoacylase-1 OS=Pongo abelii GN=ACY1 PE=2 SV=2
Unigene17655_All	Homeobox protein abdominal-A homolog (Fragment) OS=Schistocerca gregaria GN=ABD-A PE=3 SV=1
Unigene17666_All	Bumetanide-sensitive sodium-(potassium)-chloride cotransporter OS=Manduca sexta PE=2 SV=1
Unigene17671_All	--
Unigene17699_All	--
Unigene17702_All	--
Unigene17716_All	Dynein heavy chain 10, axonemal OS=Homo sapiens GN=DNAH10 PE=1 SV=4
Unigene17741_All	--
Unigene17784_All	--
Unigene17836_All	--
Unigene17843_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene17957_All	--
Unigene18060_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
Unigene18083_All	--
Unigene18084_All	Keratin, type I cytoskeletal 9 OS=Mus musculus GN=Krt9 PE=1 SV=2
Unigene18152_All	--
Unigene18160_All	Clavesin-1 OS=Homo sapiens GN=CLVS1 PE=1 SV=1
Unigene18198_All	--
Unigene18264_All	Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Mus musculus GN=Pycr1 PE=1 SV=1
Unigene18270_All	--
Unigene18281_All	--
Unigene18289_All	--
Unigene1835_All	--
Unigene18374_All	--

Unigene18475_All	--
Unigene18492_All	Tigger transposable element-derived protein 4 OS=Homo sapiens GN=TIGD4 PE=2 SV=2
Unigene18494_All	Rootletin OS=Homo sapiens GN=CROCC PE=1 SV=1
Unigene184_All	--
Unigene18556_All	Protein enabled OS=Drosophila melanogaster GN=ena PE=1 SV=4
Unigene18560_All	--
Unigene18576_All	--
Unigene18655_All	Nuclear protein MDM1 OS=Gallus gallus GN=MDM1 PE=2 SV=1
Unigene18664_All	--
Unigene18673_All	--
Unigene18698_All	--
Unigene18783_All	--
Unigene18797_All	--
Unigene18802_All	Glutathione peroxidase OS=Schistosoma mansoni GN=GPX1 PE=1 SV=2
Unigene1881_All	--
Unigene18834_All	--
Unigene18885_All	Salivary glue protein Sgs-3 OS=Drosophila yakuba GN=Sgs3 PE=2 SV=3
Unigene18904_All	--
Unigene1892_All	--
Unigene1895_All	Putative nuclease HARBI1 OS=Xenopus laevis GN=harbi1 PE=2 SV=1
Unigene1897_All	--
Unigene19049_All	Solute carrier family 15 member 4 OS=Bos taurus GN=SLC15A4 PE=2 SV=2
Unigene1907_All	--
Unigene1909_All	--
Unigene19243_All	--
Unigene19310_All	--
Unigene19340_All	Elongation factor 1-gamma-A OS=Xenopus laevis GN=eef1g-a PE=1 SV=1
Unigene19368_All	--
Unigene19443_All	--
Unigene19495_All	--
Unigene19739_All	--
Unigene19751_All	--
Unigene19784_All	--
Unigene19872_All	Angiotensin-converting enzyme OS=Drosophila melanogaster GN=Ance PE=1 SV=3
Unigene19987_All	--

Unigene19997_All	--
Unigene19999_All	--
Unigene20007_All	Sodium-dependent multivitamin transporter OS=Rattus norvegicus GN=Slc5a6 PE=2 SV=1
Unigene20045_All	Protein hunchback OS=Drosophila sechellia GN=hb PE=3 SV=1
Unigene20047_All	--
Unigene20158_All	--
Unigene20163_All	--
Unigene20186_All	Protein FAM76A OS=Homo sapiens GN=FAM76A PE=2 SV=1
Unigene20220_All	Lipase 3 OS=Drosophila melanogaster GN=Lip3 PE=2 SV=1
Unigene20267_All	--
Unigene20324_All	Mitochondrial folate transporter/carrier OS=Mus musculus GN=Slc25a32 PE=2 SV=1
Unigene20415_All	Granulins OS=Homo sapiens GN=GRN PE=1 SV=2
Unigene20438_All	23 kDa integral membrane protein OS=Schistosoma japonicum PE=2 SV=1
Unigene20482_All	--
Unigene20488_All	--
Unigene20560_All	--
Unigene20591_All	--
Unigene20661_All	--
Unigene20664_All	--
Unigene20729_All	--
Unigene20851_All	--
Unigene20879_All	--
Unigene20902_All	--
Unigene20972_All	--
Unigene21179_All	--
Unigene2122_All	Multidrug resistance-associated protein 4 OS=Homo sapiens GN=ABCC4 PE=1 SV=3
Unigene21271_All	--
Unigene21341_All	--
Unigene21344_All	--
Unigene21422_All	--
Unigene21469_All	--
Unigene21475_All	--
Unigene21518_All	--
Unigene21554_All	--
Unigene21556_All	--

Unigene21579_All	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1
Unigene21590_All	--
Unigene21604_All	Fanconi anemia group J protein homolog OS=Gallus gallus GN=BRIP1 PE=2 SV=1
Unigene21614_All	--
Unigene21631_All	--
Unigene21654_All	--
Unigene21695_All	--
Unigene21721_All	--
Unigene21726_All	Synaptic vesicle membrane protein VAT-1 homolog OS=Danio rerio GN=vat1 PE=2 SV=1
Unigene217_All	--
Unigene21862_All	--
Unigene2191_All	--
Unigene21998_All	--
Unigene22000_All	NFX1-type zinc finger-containing protein 1 OS=Mus musculus GN=Znfx1 PE=2 SV=3
Unigene22023_All	--
Unigene22049_All	--
Unigene22080_All	--
Unigene22085_All	--
Unigene2215_All	Regulator of G-protein signaling 7 OS=Rattus norvegicus GN=Rgs7 PE=2 SV=2
Unigene22177_All	--
Unigene221_All	--
Unigene22323_All	--
Unigene22346_All	--
Unigene22520_All	--
Unigene22522_All	--
Unigene22524_All	--
Unigene22678_All	--
Unigene22788_All	--
Unigene22836_All	--
Unigene22872_All	--
Unigene22894_All	--
Unigene23016_All	--
Unigene23039_All	--
Unigene23165_All	--
Unigene23167_All	--
Unigene23181_All	--
Unigene23226_All	--

Unigene23275_All	--
Unigene23277_All	--
Unigene23293_All	--
Unigene23406_All	--
Unigene23432_All	--
Unigene23433_All	--
Unigene23492_All	--
Unigene2349_All	--
Unigene23523_All	--
Unigene23527_All	--
Unigene23576_All	--
Unigene23606_All	--
Unigene23611_All	--
Unigene23617_All	--
Unigene23633_All	--
Unigene23685_All	--
Unigene23686_All	--
Unigene2372_All	--
Unigene23743_All	--
Unigene23808_All	--
Unigene23814_All	--
Unigene23823_All	--
Unigene23834_All	--
Unigene23842_All	--
Unigene23902_All	Serine/arginine repetitive matrix protein 1 OS=Pongo abelii GN=SRRM1 PE=2 SV=1
Unigene23929_All	--
Unigene23987_All	--
Unigene2398_All	Transferrin OS=Blaberus discoidalis PE=1 SV=1
Unigene2399_All	--
Unigene2402_All	--
Unigene24054_All	--
Unigene24055_All	--
Unigene24104_All	--
Unigene2411_All	--
Unigene24216_All	--
Unigene24295_All	--
Unigene24313_All	--
Unigene24401_All	--
Unigene24405_All	--
Unigene24443_All	--
Unigene24484_All	--

Unigene24552_All	--
Unigene24559_All	--
Unigene2458_All	--
Unigene24622_All	Protein bunched, class 2/F/G isoform OS=Drosophila melanogaster GN=bun PE=2 SV=4
Unigene24678_All	--
Unigene2472_All	--
Unigene24739_All	--
Unigene24753_All	Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=1 SV=2
Unigene24763_All	Skin secretory protein xP2 OS=Xenopus laevis GN=p2 PE=2 SV=2
Unigene24765_All	Tetraspanin-31-B OS=Xenopus laevis GN=tspan31-b PE=2 SV=1
Unigene24776_All	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2
Unigene2477_All	--
Unigene24789_All	--
Unigene24805_All	E3 ubiquitin-protein ligase RNF31 OS=Homo sapiens GN=RNF31 PE=1 SV=1
Unigene24818_All	--
Unigene24822_All	--
Unigene24840_All	Collagen alpha-1(IX) chain OS=Gallus gallus GN=COL9A1 PE=1 SV=4
Unigene24866_All	--
Unigene24883_All	--
Unigene24903_All	Transposable element Tc3 transposase OS=Caenorhabditis elegans GN=tc3a PE=1 SV=1
Unigene24904_All	Transposable element Tc3 transposase OS=Caenorhabditis elegans GN=tc3a PE=1 SV=1
Unigene24958_All	Probable serine hydrolase OS=Drosophila melanogaster GN=kraken PE=2 SV=1
Unigene25109_All	--
Unigene25156_All	--
Unigene25160_All	Putative uncharacterized protein FLJ37770 OS=Homo sapiens PE=5 SV=1
Unigene25174_All	--
Unigene25212_All	--
Unigene25251_All	--
Unigene25262_All	--
Unigene25292_All	--
Unigene25366_All	--
Unigene25471_All	--
Unigene25483_All	--

Unigene25498_All	Iron/zinc purple acid phosphatase-like protein OS=Danio rerio GN=papl PE=2 SV=1
Unigene25511_All	Probable beta-hexosaminidase fdl OS=Drosophila melanogaster GN=fdl PE=1 SV=1
Unigene25524_All	--
Unigene25526_All	--
Unigene25534_All	--
Unigene25586_All	--
Unigene25587_All	Alkaline phosphatase 4 OS=Drosophila melanogaster GN=Aph-4 PE=2 SV=3
Unigene25604_All	--
Unigene25672_All	--
Unigene256_All	--
Unigene25721_All	--
Unigene25725_All	--
Unigene25737_All	Retrovirus-related Pol polyprotein from transposon 17.6 OS=Drosophila melanogaster GN=pol PE=4 SV=1
Unigene25755_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene25761_All	--
Unigene25842_All	Luciferin 4-monooxygenase OS=Luciola cruciata PE=1 SV=1
Unigene2586_All	Innexin inx7 OS=Drosophila melanogaster GN=inx7 PE=1 SV=1
Unigene25882_All	--
Unigene25891_All	--
Unigene2589_All	Retrovirus-related Pol polyprotein from transposon opus OS=Drosophila melanogaster GN=pol PE=4 SV=1
Unigene25903_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
Unigene25971_All	--
Unigene26027_All	--
Unigene26054_All	--
Unigene26170_All	--
Unigene26210_All	Leukocyte elastase inhibitor OS=Xenopus tropicalis GN=serpinb1 PE=2 SV=1
Unigene26214_All	--
Unigene2625_All	--
Unigene26298_All	--
Unigene26310_All	--
Unigene2632_All	Lipase 3 OS=Drosophila melanogaster GN=Lip3 PE=2 SV=1

Unigene2637_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene26385_All	--
Unigene26388_All	--
Unigene26391_All	Alpha-tocopherol transfer protein-like OS=Mus musculus GN=Ttpal PE=2 SV=3
Unigene26394_All	--
Unigene26480_All	--
Unigene2648_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene26520_All	--
Unigene26597_All	--
Unigene26608_All	--
Unigene26666_All	--
Unigene26703_All	--
Unigene26832_All	Probable dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase OS=Drosophila melanogaster GN=CG5091 PE=2 SV=2
Unigene26881_All	--
Unigene26991_All	Uncharacterized protein CG13380 OS=Drosophila melanogaster GN=CG13380 PE=1 SV=2
Unigene27060_All	--
Unigene27068_All	--
Unigene2708_All	--
Unigene27106_All	--
Unigene27159_All	--
Unigene27166_All	--
Unigene27234_All	--
Unigene27235_All	--
Unigene27279_All	--
Unigene272_All	--
Unigene27359_All	Enolase-phosphatase E1 OS=Aedes aegypti GN=AAEL000109 PE=3 SV=1
Unigene27386_All	Myrosinase 1 OS=Brevicoryne brassicae PE=1 SV=1
Unigene273_All	--
Unigene27429_All	--
Unigene27430_All	--
Unigene27493_All	Lysozyme 1 OS=Crassostrea virginica GN=lysoz1 PE=1 SV=3
Unigene27505_All	--
Unigene27521_All	Probable G-protein coupled receptor Mth-like 1 OS=Drosophila melanogaster GN=mthl1 PE=2 SV=1
Unigene27689_All	Pancreatic lipase-related protein 3 OS=Homo sapiens GN=PNLIPRP3 PE=2

	SV=2
Unigene27730_All	--
Unigene2776_All	Apolipophorins OS=Locusta migratoria PE=1 SV=2
Unigene27775_All	Ankyrin repeat domain-containing protein 50 OS=Homo sapiens GN=ANKRD50 PE=1 SV=4
Unigene278_All	--
Unigene27938_All	Programmed cell death 6-interacting protein OS=Xenopus laevis GN=pdcd6ip PE=1 SV=1
Unigene27990_All	--
Unigene28057_All	--
Unigene28136_All	--
Unigene28297_All	--
Unigene28429_All	--
Unigene28449_All	--
Unigene2854_All	--
Unigene28578_All	--
Unigene28615_All	--
Unigene28688_All	Synaptic vesicle glycoprotein 2A OS=Rattus norvegicus GN=Sv2a PE=1 SV=2
Unigene286_All	--
Unigene28812_All	--
Unigene28891_All	--
Unigene28902_All	Atherin OS=Oryctolagus cuniculus GN=SAMD1 PE=2 SV=1
Unigene28908_All	--
Unigene28936_All	--
Unigene28984_All	--
Unigene29065_All	--
Unigene29077_All	--
Unigene29083_All	Myb-like protein I OS=Dictyostelium discoideum GN=mybI PE=3 SV=1
Unigene29097_All	Aminopeptidase N OS=Plutella xylostella GN=APN1 PE=1 SV=1
Unigene29113_All	Venom carboxylesterase-6 OS=Apis mellifera PE=2 SV=1
Unigene2912_All	--
Unigene29138_All	--
Unigene29148_All	--
Unigene29155_All	--
Unigene29171_All	--
Unigene29182_All	--
Unigene29186_All	--

Unigene29213_All	--
Unigene29217_All	Ankyrin repeat and SAM domain-containing protein 6 OS=Mus musculus GN=Anks6 PE=2 SV=2
Unigene29267_All	Homeotic protein antennapedia OS=Drosophila subobscura GN=Antp PE=3 SV=1
Unigene29368_All	--
Unigene29423_All	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R1 (Fragment) OS=Sciara coprophila PE=4 SV=1
Unigene29440_All	--
Unigene29490_All	--
Unigene29492_All	--
Unigene29527_All	--
Unigene29560_All	--
Unigene2960_All	--
Unigene296_All	--
Unigene29763_All	--
Unigene29937_All	--
Unigene29994_All	--
Unigene29_All	--
Unigene30048_All	--
Unigene30068_All	--
Unigene3020_All	Endoplasmic reticulum resident protein 29 OS=Rattus norvegicus GN=Erp29 PE=1 SV=2
Unigene30254_All	--
Unigene30358_All	--
Unigene3040_All	--
Unigene3044_All	--
Unigene30457_All	--
Unigene30460_All	--
Unigene3050_All	--
Unigene30511_All	--
Unigene30522_All	--
Unigene30591_All	PAX-interacting protein 1 OS=Xenopus laevis GN=paxip1 PE=1 SV=1
Unigene30663_All	--
Unigene30671_All	--
Unigene30754_All	--
Unigene30796_All	--
Unigene30804_All	--
Unigene30808_All	--
Unigene30819_All	--

Unigene30822_All	--
Unigene30886_All	--
Unigene30950_All	--
Unigene30957_All	UDP-glucuronosyltransferase 1-9 OS=Mus musculus GN=Ugt1a9 PE=1 SV=3
Unigene30970_All	--
Unigene30988_All	--
Unigene3099_All	PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1
Unigene31025_All	--
Unigene31027_All	--
Unigene31069_All	--
Unigene31116_All	--
Unigene3111_All	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2
Unigene31124_All	--
Unigene31143_All	--
Unigene31206_All	--
Unigene31283_All	--
Unigene31288_All	--
Unigene31301_All	--
Unigene31360_All	--
Unigene31365_All	--
Unigene31394_All	--
Unigene31397_All	--
Unigene31410_All	--
Unigene31446_All	--
Unigene31447_All	--
Unigene31492_All	--
Unigene31510_All	--
Unigene31652_All	Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1
Unigene31697_All	--
Unigene3170_All	--
Unigene31747_All	--
Unigene31780_All	--
Unigene31815_All	--
Unigene31911_All	--
Unigene31946_All	--
Unigene31966_All	--
Unigene32019_All	--
Unigene3201_All	--

Unigene32189_All	--
Unigene32252_All	--
Unigene32253_All	Mariner Mos1 transposase OS=Drosophila mauritiana GN=mariner\T PE=1 SV=1
Unigene32259_All	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Nasonia vitripennis PE=4 SV=2
Unigene32271_All	--
Unigene32299_All	Hexamerin OS=Blaberus discoidalis PE=2 SV=1
Unigene32300_All	Hexamerin OS=Blaberus discoidalis PE=2 SV=1
Unigene32301_All	Hexamerin OS=Blaberus discoidalis PE=2 SV=1
Unigene32302_All	Hexamerin OS=Blaberus discoidalis PE=2 SV=1
Unigene32425_All	--
Unigene32458_All	Angiotensin-converting enzyme (Fragment) OS=Gallus gallus GN=ACE PE=2 SV=1
Unigene32514_All	Protein dopey-1 homolog OS=Drosophila pseudoobscura pseudoobscura GN=GA13490 PE=3 SV=1
Unigene32519_All	Transcription factor E2F8 OS=Rattus norvegicus GN=E2f8 PE=2 SV=2
Unigene32522_All	Zinc finger protein 253 OS=Homo sapiens GN=ZNF253 PE=2 SV=2
Unigene32541_All	--
Unigene32544_All	PC-esterase domain-containing protein 1A OS=Mus musculus GN=Pced1a PE=2 SV=2
Unigene3255_All	--
Unigene32656_All	ER degradation-enhancing alpha-mannosidase-like protein 2 OS=Homo sapiens GN=EDEM2 PE=1 SV=2
Unigene32673_All	Acetyl-CoA carboxylase OS=Gallus gallus GN=ACAC PE=1 SV=1
Unigene32674_All	Uncharacterized histidine-rich protein DDB_G0274557 OS=Dictyostelium discoideum GN=DDB_G0274557 PE=4 SV=1
Unigene32688_All	--
Unigene32689_All	--
Unigene32703_All	--
Unigene32713_All	--
Unigene32724_All	--
Unigene32747_All	2-hydroxyacylsphingosine 1-beta-galactosyltransferase OS=Homo sapiens GN=UGT8 PE=2 SV=2
Unigene32783_All	--
Unigene32791_All	--
Unigene32845_All	--
Unigene32848_All	Protein roadkill OS=Drosophila melanogaster GN=rdx PE=1 SV=2

Unigene32859_All	--
Unigene32887_All	--
Unigene32892_All	Glycine-rich protein 3 OS=Pinctada maxima PE=1 SV=1
Unigene32911_All	UDP-glucose:glycoprotein glucosyltransferase OS=Drosophila melanogaster GN=Ugt PE=1 SV=2
Unigene32939_All	--
Unigene32956_All	Multiple coagulation factor deficiency protein 2 homolog OS=Pongo abelii GN=MCFD2 PE=2 SV=1
Unigene32991_All	--
Unigene32995_All	Vesicle-associated membrane protein 7 OS=Pongo abelii GN=VAMP7 PE=2 SV=3
Unigene33011_All	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1
Unigene33012_All	Programmed cell death 6-interacting protein OS=Xenopus laevis GN=pdcd6ip PE=1 SV=1
Unigene33086_All	--
Unigene33112_All	Protein takeout OS=Drosophila melanogaster GN=to PE=2 SV=1
Unigene33141_All	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial OS=Xenopus laevis GN=echdc3 PE=2 SV=1
Unigene33149_All	Deoxyribonuclease-2-beta OS=Homo sapiens GN=DNASE2B PE=2 SV=1
Unigene33201_All	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2
Unigene3321_All	--
Unigene33272_All	Four-jointed box protein 1 OS=Homo sapiens GN=FJX1 PE=2 SV=1
Unigene33319_All	Leucine-rich repeat-containing protein 15 OS=Mus musculus GN=Lrrc15 PE=2 SV=1
Unigene33325_All	--
Unigene33341_All	--
Unigene33356_All	--
Unigene33432_All	Membrane-bound alkaline phosphatase OS=Bombyx mori GN=Alp-m PE=1 SV=3
Unigene33462_All	Coiled-coil domain-containing protein 111 homolog OS=Danio rerio GN=ccdc111 PE=2 SV=1
Unigene33496_All	--
Unigene33505_All	--
Unigene33517_All	--
Unigene3351_All	--
Unigene33527_All	RNA-binding protein Musashi homolog Rbp6 OS=Drosophila melanogaster GN=Rbp6 PE=2 SV=3

Unigene33536_All	--
Unigene33569_All	--
Unigene33631_All	--
Unigene33692_All	--
Unigene33718_All	--
Unigene33726_All	--
Unigene33766_All	--
Unigene33769_All	--
Unigene33838_All	Transcription initiation factor TFIID subunit 4 OS=Homo sapiens GN=TAF4 PE=1 SV=2
Unigene33849_All	--
Unigene33850_All	--
Unigene33905_All	--
Unigene33959_All	--
Unigene33978_All	--
Unigene34123_All	--
Unigene34234_All	--
Unigene34389_All	Signal recognition particle receptor subunit alpha OS=Mus musculus GN=Srpr PE=1 SV=1
Unigene343_All	Protein yellow OS=Drosophila erecta GN=y PE=3 SV=1
Unigene34421_All	--
Unigene34493_All	--
Unigene34530_All	Hexamerin OS=Blaberus discoidalis PE=2 SV=1
Unigene34577_All	--
Unigene34604_All	--
Unigene34645_All	Lysosomal alpha-mannosidase OS=Cavia porcellus GN=MAN2B1 PE=1 SV=1
Unigene34835_All	--
Unigene34861_All	--
Unigene3489_All	--
Unigene34937_All	--
Unigene34952_All	Synaptic vesicle membrane protein VAT-1 homolog OS=Danio rerio GN=vat1 PE=2 SV=1
Unigene35035_All	--
Unigene35098_All	Protein bicaudal C homolog 1 OS=Mus musculus GN=Bicc1 PE=2 SV=1
Unigene35149_All	--
Unigene35202_All	CCR4-NOT transcription complex subunit 2 OS=Mus musculus GN=Cnot2 PE=2 SV=2
Unigene35217_All	Serine protease snake OS=Drosophila melanogaster GN=snk PE=1 SV=2

Unigene35234_All	Alpha-tocopherol transfer protein-like OS=Pongo abelii GN=TTPAL PE=2 SV=1
Unigene35256_All	--
Unigene35272_All	6-phosphogluconolactonase OS=Bos taurus GN=PGLS PE=2 SV=1
Unigene35277_All	Argininosuccinate synthase OS=Danio rerio GN=ass1 PE=2 SV=1
Unigene35284_All	--
Unigene35297_All	--
Unigene352_All	--
Unigene35305_All	--
Unigene35324_All	--
Unigene35325_All	Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2
Unigene35346_All	--
Unigene35358_All	--
Unigene35363_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene35387_All	--
Unigene35401_All	--
Unigene35524_All	--
Unigene35633_All	--
Unigene35673_All	--
Unigene35766_All	--
Unigene3577_All	--
Unigene35786_All	Kallikrein-14 OS=Mus musculus GN=Klk14 PE=2 SV=1
Unigene35805_All	--
Unigene35846_All	--
Unigene35929_All	--
Unigene36025_All	--
Unigene36245_All	--
Unigene3629_All	--
Unigene36320_All	--
Unigene36326_All	--
Unigene36333_All	--
Unigene36401_All	--
Unigene36508_All	--
Unigene36521_All	--
Unigene36532_All	--
Unigene36570_All	--
Unigene36579_All	--
Unigene36618_All	--

Unigene36639_All	--
Unigene36662_All	--
Unigene36664_All	--
Unigene36668_All	--
Unigene36670_All	--
Unigene36685_All	--
Unigene36708_All	--
Unigene36751_All	--
Unigene36770_All	--
Unigene36808_All	Lipase member H OS=Homo sapiens GN=LIPH PE=1 SV=1
Unigene36827_All	--
Unigene36860_All	--
Unigene36880_All	--
Unigene3693_All	Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1
Unigene36966_All	--
Unigene36987_All	NADH-ubiquinone oxidoreductase chain 5 OS=Locusta migratoria GN=ND5 PE=3 SV=1
Unigene37120_All	Probable adenosine deaminase OS=Dictyostelium discoideum GN=ada PE=3 SV=1
Unigene37257_All	--
Unigene37340_All	--
Unigene37390_All	--
Unigene37397_All	--
Unigene37428_All	--
Unigene37490_All	--
Unigene3762_All	--
Unigene37723_All	--
Unigene37726_All	--
Unigene37802_All	--
Unigene37809_All	--
Unigene37845_All	--
Unigene37877_All	--
Unigene378_All	Feline leukemia virus subgroup C receptor-related protein 2 OS=Mus musculus GN=Flvcr2 PE=1 SV=2
Unigene37929_All	ATP-dependent RNA helicase DHX8 OS=Mus musculus GN=Dhx8 PE=2 SV=1
Unigene38001_All	--
Unigene38007_All	--
Unigene38081_All	--

Unigene38128_All	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT2 PE=1 SV=1
Unigene38191_All	--
Unigene38222_All	--
Unigene38230_All	--
Unigene38255_All	--
Unigene3826_All	--
Unigene38270_All	--
Unigene38281_All	--
Unigene38380_All	--
Unigene3839_All	--
Unigene38556_All	--
Unigene38679_All	--
Unigene38691_All	--
Unigene38723_All	--
Unigene38741_All	--
Unigene38777_All	--
Unigene38819_All	--
Unigene38820_All	--
Unigene38878_All	--
Unigene38882_All	--
Unigene38910_All	--
Unigene38944_All	--
Unigene38962_All	--
Unigene38975_All	--
Unigene3898_All	--
Unigene38991_All	--
Unigene39063_All	--
Unigene39081_All	Uncharacterized protein KIAA1841 homolog OS=Xenopus laevis PE=2 SV=1
Unigene390_All	--
Unigene39138_All	--
Unigene39171_All	--
Unigene39232_All	--
Unigene39246_All	--
Unigene39270_All	--
Unigene39325_All	--
Unigene39362_All	--
Unigene39390_All	--
Unigene39428_All	--
Unigene39434_All	--

Unigene39450_All	--
Unigene39484_All	--
Unigene39523_All	--
Unigene39557_All	--
Unigene39595_All	Ankyrin-3 OS=Mus musculus GN=Ank3 PE=1 SV=1
Unigene39599_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
Unigene39600_All	Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3
Unigene39601_All	G-protein coupled receptor moody OS=Drosophila pseudoobscura pseudoobscura GN=moody PE=3 SV=2
Unigene39606_All	--
Unigene39609_All	G-protein coupled receptor moody OS=Drosophila pseudoobscura pseudoobscura GN=moody PE=3 SV=2
Unigene39664_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene39740_All	--
Unigene39773_All	Protein dopey-1 homolog OS=Drosophila pseudoobscura pseudoobscura GN=GA13490 PE=3 SV=1
Unigene39796_All	--
Unigene39823_All	Aminomethyltransferase, mitochondrial OS=Gallus gallus GN=AMT PE=2 SV=2
Unigene39824_All	Aminomethyltransferase, mitochondrial OS=Gallus gallus GN=AMT PE=2 SV=2
Unigene39839_All	--
Unigene39845_All	Zinc finger MYM-type protein 1 OS=Homo sapiens GN=ZMYM1 PE=2 SV=1
Unigene39879_All	--
Unigene39905_All	Ras-related GTP-binding protein C OS=Mus musculus GN=Rragc PE=2 SV=1
Unigene39906_All	--
Unigene39939_All	--
Unigene39942_All	--
Unigene40039_All	--
Unigene40078_All	WD repeat, SAM and U-box domain-containing protein 1 OS=Homo sapiens GN=WDSUB1 PE=1 SV=3
Unigene40136_All	Probable G-protein coupled receptor Mth-like 10 OS=Drosophila melanogaster GN=mthl10 PE=3 SV=3
Unigene40279_All	--
Unigene40292_All	Uncharacterized protein DDB_G0283357 OS=Dictyostelium discoideum GN=DDB_G0283357 PE=4 SV=1
Unigene40315_All	--
Unigene40325_All	--
Unigene40326_All	--

Unigene40328_All	--
Unigene40358_All	Sphingosine kinase 2 OS=Mus musculus GN=Sphk2 PE=1 SV=2
Unigene40392_All	Synaptic vesicle membrane protein VAT-1 homolog OS=Danio rerio GN=vat1 PE=2 SV=1
Unigene40413_All	Protein split ends OS=Drosophila melanogaster GN=spen PE=1 SV=2
Unigene40457_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene40490_All	Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase OS=Homo sapiens GN=ALG6 PE=1 SV=1
Unigene40604_All	--
Unigene40606_All	RalBP1-associated Eps domain-containing protein 1 OS=Mus musculus GN=Reps1 PE=1 SV=2
Unigene40648_All	--
Unigene40698_All	--
Unigene40724_All	--
Unigene40751_All	--
Unigene40810_All	Protein canopy homolog 1 OS=Xenopus laevis GN=cnpy1 PE=2 SV=1
Unigene40827_All	Ribonucleoside-diphosphate reductase large subunit OS=Mus musculus GN=Rrm1 PE=1 SV=2
Unigene40869_All	--
Unigene40957_All	Prothrombin OS=Pongo abelii GN=F2 PE=2 SV=1
Unigene40999_All	--
Unigene41048_All	--
Unigene41126_All	--
Unigene41150_All	--
Unigene41157_All	--
Unigene41164_All	--
Unigene41246_All	--
Unigene41254_All	--
Unigene41258_All	Lysozyme OS=Meretrix lusoria PE=1 SV=1
Unigene41291_All	--
Unigene41295_All	Epoxide hydrolase 4 OS=Homo sapiens GN=EPHX4 PE=2 SV=2
Unigene41299_All	--
Unigene41343_All	--
Unigene41421_All	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Rattus norvegicus GN=Gapdhs PE=1 SV=1
Unigene41443_All	Transforming growth factor-beta-induced protein ig-h3 OS=Mus musculus GN=Tgfbi PE=2 SV=1
Unigene41491_All	--

Unigene41562_All	--
Unigene41596_All	--
Unigene41621_All	Proactivator polypeptide OS=Bos taurus GN=PSAP PE=1 SV=3
Unigene41637_All	--
Unigene41674_All	--
Unigene41675_All	--
Unigene4167_All	--
Unigene41716_All	--
Unigene41967_All	--
Unigene41968_All	--
Unigene42015_All	--
Unigene42118_All	--
Unigene4215_All	--
Unigene42208_All	Solute carrier family 22 member 6-B OS=Xenopus laevis GN=slc22a6-b PE=2 SV=1
Unigene42213_All	--
Unigene42265_All	Probable RNA helicase armi OS=Drosophila melanogaster GN=armi PE=2 SV=3
Unigene42298_All	--
Unigene42306_All	--
Unigene4231_All	--
Unigene42359_All	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3
Unigene42370_All	Uncharacterized protein DDB_G0282077 OS=Dictyostelium discoideum GN=DDB_G0282077 PE=4 SV=2
Unigene42382_All	Ankyrin repeat domain-containing protein 6 OS=Mus musculus GN=Ankrd6 PE=1 SV=2
Unigene42417_All	--
Unigene4241_All	--
Unigene42426_All	--
Unigene42441_All	--
Unigene42445_All	--
Unigene42449_All	--
Unigene42457_All	--
Unigene42484_All	--
Unigene42653_All	--
Unigene42878_All	--
Unigene42882_All	--
Unigene4292_All	--
Unigene42964_All	--
Unigene43016_All	--

Unigene43097_All	--
Unigene43117_All	--
Unigene43246_All	--
Unigene4324_All	--
Unigene43405_All	--
Unigene43450_All	--
Unigene43463_All	Nuclear factor of activated T-cells 5 OS=Homo sapiens GN=NFAT5 PE=1 SV=1
Unigene43525_All	--
Unigene4360_All	--
Unigene43631_All	--
Unigene4371_All	--
Unigene43761_All	--
Unigene43791_All	--
Unigene4387_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene43892_All	--
Unigene4390_All	--
Unigene43929_All	--
Unigene43942_All	--
Unigene43991_All	--
Unigene43_All	--
Unigene44009_All	--
Unigene4400_All	--
Unigene44011_All	--
Unigene44016_All	--
Unigene44028_All	--
Unigene44037_All	--
Unigene44079_All	ELKS/Rab6-interacting/CAST family member 1 OS=Homo sapiens GN=ERC1 PE=1 SV=1
Unigene44096_All	--
Unigene44109_All	--
Unigene44187_All	--
Unigene44188_All	--
Unigene44202_All	--
Unigene4420_All	--
Unigene4426_All	--
Unigene44319_All	Putative protein TPRXL OS=Homo sapiens GN=TPRXL PE=5 SV=2
Unigene44337_All	--
Unigene44347_All	--
Unigene4435_All	--

Unigene44362_All	--
Unigene44401_All	--
Unigene4443_All	--
Unigene4446_All	--
Unigene44493_All	--
Unigene444_All	Sodium-independent sulfate anion transporter OS=Bos taurus GN=SLC26A11 PE=2 SV=1
Unigene44650_All	--
Unigene44663_All	--
Unigene44706_All	--
Unigene44789_All	--
Unigene44825_All	--
Unigene44874_All	60S ribosomal protein L39 OS=Drosophila melanogaster GN=RpL39 PE=3 SV=2
Unigene44965_All	--
Unigene45033_All	--
Unigene45107_All	--
Unigene4515_All	--
Unigene45234_All	--
Unigene4526_All	--
Unigene45311_All	--
Unigene45314_All	--
Unigene45350_All	Probable G-protein coupled receptor Mth-like 1 OS=Drosophila melanogaster GN=mthl1 PE=2 SV=1
Unigene4551_All	--
Unigene45530_All	--
Unigene45619_All	--
Unigene45640_All	--
Unigene4572_All	--
Unigene45749_All	--
Unigene45782_All	--
Unigene45795_All	--
Unigene45813_All	--
Unigene45835_All	--
Unigene45965_All	--
Unigene45972_All	--
Unigene45973_All	Probable 60S ribosomal protein L37-A OS=Drosophila melanogaster GN=RpL37a PE=3 SV=1
Unigene45977_All	Uncharacterized protein K02A2.6 OS=Caenorhabditis elegans GN=K02A2.6 PE=2 SV=1
Unigene4597_All	--

Unigene459_All	Myotubularin-related protein 14 OS=Homo sapiens GN=MTMR14 PE=1 SV=2
Unigene46017_All	--
Unigene46018_All	--
Unigene46037_All	--
Unigene46099_All	--
Unigene46182_All	--
Unigene46231_All	--
Unigene46295_All	--
Unigene46451_All	--
Unigene46457_All	Probable cytochrome P450 9f2 OS=Drosophila melanogaster GN=Cyp9f2 PE=2 SV=1
Unigene46475_All	--
Unigene46515_All	--
Unigene46552_All	--
Unigene46554_All	--
Unigene46569_All	--
Unigene46601_All	--
Unigene46658_All	--
Unigene46678_All	--
Unigene46692_All	Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3
Unigene46732_All	--
Unigene46837_All	--
Unigene46868_All	--
Unigene46891_All	--
Unigene46916_All	--
Unigene46953_All	--
Unigene46970_All	--
Unigene47088_All	--
Unigene47098_All	--
Unigene47119_All	--
Unigene47135_All	--
Unigene47177_All	--
Unigene47203_All	--
Unigene47215_All	--
Unigene47220_All	--
Unigene47241_All	Voltage-dependent L-type calcium channel subunit beta-2 OS=Oryctolagus cuniculus GN=CACNB2 PE=1 SV=1
Unigene47242_All	Voltage-dependent L-type calcium channel subunit beta-2 OS=Oryctolagus cuniculus GN=CACNB2 PE=1 SV=1

Unigene47243_All	Voltage-dependent L-type calcium channel subunit beta-2 OS=Oryctolagus cuniculus GN=CACNB2 PE=1 SV=1
Unigene47249_All	Protein muscleblind OS=Drosophila melanogaster GN=mbl PE=2 SV=2
Unigene47335_All	--
Unigene47404_All	--
Unigene47464_All	Probable RNA helicase armi OS=Drosophila melanogaster GN=armi PE=2 SV=3
Unigene47479_All	--
Unigene47506_All	F-box only protein 33 OS=Homo sapiens GN=FBXO33 PE=2 SV=1
Unigene47514_All	--
Unigene47548_All	--
Unigene47549_All	--
Unigene47559_All	--
Unigene47601_All	Clavesin-2 OS=Danio rerio GN=clvs2 PE=2 SV=1
Unigene47640_All	DNA polymerase alpha subunit B OS=Rattus norvegicus GN=Pola2 PE=2 SV=2
Unigene4765_All	--
Unigene47701_All	Facilitated trehalose transporter Tret1 OS=Polypedilum vanderplanki GN=Tret1 PE=1 SV=1
Unigene47717_All	--
Unigene47724_All	Sodium-coupled neutral amino acid transporter 1 OS=Pongo abelii GN=SLC38A1 PE=2 SV=1
Unigene47726_All	--
Unigene47747_All	Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3
Unigene47762_All	--
Unigene47764_All	--
Unigene47780_All	--
Unigene47783_All	--
Unigene47846_All	Cysteine-rich hydrophobic domain 2 protein OS=Homo sapiens GN=CHIC2 PE=1 SV=1
Unigene47945_All	Bumetanide-sensitive sodium-(potassium)-chloride cotransporter OS=Manduca sexta PE=2 SV=1
Unigene47946_All	--
Unigene47971_All	Double-strand break repair protein MRE11 OS=Xenopus laevis GN=mre11 PE=2 SV=1
Unigene47987_All	--
Unigene48007_All	Histone-lysine N-methyltransferase MLL4 OS=Mus musculus GN=Wbp7 PE=1 SV=3
Unigene48010_All	--

Unigene48015_All	--
Unigene48060_All	--
Unigene48095_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene48098_All	Zinc finger SWIM domain-containing protein 7 OS=Homo sapiens GN=ZSWIM7 PE=1 SV=1
Unigene48114_All	--
Unigene48125_All	--
Unigene4812_All	--
Unigene48237_All	--
Unigene48263_All	--
Unigene48297_All	Sphingosine-1-phosphate lyase OS=Drosophila melanogaster GN=Sply PE=2 SV=1
Unigene4829_All	--
Unigene48336_All	Salivary glue protein Sgs-3 OS=Drosophila erecta GN=Sgs3 PE=2 SV=3
Unigene48340_All	--
Unigene48357_All	--
Unigene48417_All	--
Unigene48422_All	Uricase OS=Drosophila pseudoobscura pseudoobscura GN=Uro PE=2 SV=2
Unigene48452_All	--
Unigene48461_All	--
Unigene48466_All	UDP-glucuronosyltransferase 2B15 OS=Rattus norvegicus GN=Ugt2b15 PE=1 SV=1
Unigene4846_All	--
Unigene48500_All	--
Unigene48506_All	--
Unigene48572_All	--
Unigene48577_All	Adenosine receptor A2b OS=Homo sapiens GN=ADORA2B PE=2 SV=1
Unigene48610_All	Histidine-rich glycoprotein OS=Plasmodium lophurae PE=4 SV=1
Unigene48611_All	--
Unigene48642_All	--
Unigene48664_All	--
Unigene48679_All	Uncharacterized protein K02A2.6 OS=Caenorhabditis elegans GN=K02A2.6 PE=2 SV=1
Unigene48720_All	--
Unigene48721_All	--
Unigene48746_All	--
Unigene48767_All	--
Unigene48849_All	--

Unigene48955_All	BMP and activin membrane-bound inhibitor homolog OS=Mus musculus GN=Bambi PE=2 SV=1
Unigene49162_All	--
Unigene49308_All	Probable serine/threonine-protein kinase tsuA OS=Dictyostelium discoideum GN=tsuA PE=1 SV=1
Unigene49505_All	--
Unigene4952_All	--
Unigene49576_All	--
Unigene49602_All	--
Unigene49628_All	--
Unigene49640_All	--
Unigene49770_All	--
Unigene49800_All	--
Unigene49823_All	--
Unigene49827_All	--
Unigene49879_All	--
Unigene49905_All	--
Unigene49957_All	--
Unigene50069_All	--
Unigene50143_All	--
Unigene50218_All	--
Unigene50224_All	--
Unigene50231_All	--
Unigene50326_All	--
Unigene50330_All	--
Unigene50353_All	Ankyrin repeat and BTB/POZ domain-containing protein 1 OS=Mus musculus GN=Abtb1 PE=2 SV=1
Unigene50360_All	--
Unigene50477_All	Ras-related GTP-binding protein A OS=Rattus norvegicus GN=Rraga PE=1 SV=1
Unigene50490_All	Aquaporin AQPAe.a OS=Aedes aegypti GN=AAEL003512 PE=2 SV=2
Unigene50562_All	--
Unigene50595_All	--
Unigene50649_All	--
Unigene50697_All	--
Unigene50723_All	Uncharacterized protein K02A2.6 OS=Caenorhabditis elegans GN=K02A2.6 PE=2 SV=1
Unigene50771_All	--
Unigene50848_All	--
Unigene50871_All	--
Unigene50914_All	--

Unigene51099_All	Retrovirus-related Pol polyprotein from transposon 297 OS=Drosophila melanogaster GN=pol PE=4 SV=1
Unigene51218_All	--
Unigene51222_All	--
Unigene51371_All	--
Unigene51407_All	--
Unigene51411_All	--
Unigene51418_All	--
Unigene51457_All	--
Unigene51529_All	--
Unigene51612_All	--
Unigene51624_All	--
Unigene51626_All	--
Unigene51659_All	--
Unigene51682_All	--
Unigene51684_All	--
Unigene51715_All	--
Unigene51722_All	--
Unigene51735_All	--
Unigene51736_All	--
Unigene51744_All	--
Unigene51750_All	--
Unigene51758_All	--
Unigene51786_All	--
Unigene51865_All	--
Unigene51915_All	--
Unigene51968_All	--
Unigene51971_All	--
Unigene52038_All	--
Unigene52044_All	--
Unigene52176_All	--
Unigene52195_All	--
Unigene52197_All	--
Unigene52199_All	--
Unigene52223_All	--
Unigene52307_All	--
Unigene52312_All	--
Unigene52353_All	--
Unigene52354_All	--
Unigene52411_All	Rho GTPase-activating protein gacV OS=Dictyostelium discoideum GN=gacV PE=3 SV=1

Unigene52474_All	--
Unigene52537_All	Probable E3 ubiquitin-protein ligase RNF144A OS=Homo sapiens GN=RNF144A PE=1 SV=2
Unigene52583_All	--
Unigene52640_All	--
Unigene5266_All	--
Unigene52754_All	--
Unigene52778_All	--
Unigene52827_All	--
Unigene52872_All	--
Unigene52885_All	Beta-galactosidase-1-like protein OS=Mus musculus GN=Glb1l PE=2 SV=1
Unigene53033_All	--
Unigene53068_All	--
Unigene53073_All	--
Unigene53079_All	--
Unigene53116_All	--
Unigene53156_All	--
Unigene53185_All	--
Unigene53245_All	--
Unigene53257_All	--
Unigene53270_All	--
Unigene53330_All	Synaptic vesicle membrane protein VAT-1 homolog OS=Mus musculus GN=Vat1 PE=1 SV=3
Unigene53354_All	--
Unigene53422_All	--
Unigene53498_All	--
Unigene53499_All	--
Unigene53507_All	--
Unigene53646_All	--
Unigene53673_All	--
Unigene53689_All	--
Unigene53691_All	--
Unigene53699_All	--
Unigene53766_All	--
Unigene53819_All	--
Unigene5390_All	--
Unigene53964_All	--
Unigene54012_All	--
Unigene54050_All	--
Unigene54076_All	--
Unigene54081_All	--

Unigene54138_All	--
Unigene54145_All	--
Unigene54207_All	--
Unigene54236_All	--
Unigene54259_All	--
Unigene54288_All	Metal regulatory transcription factor 1 OS=Mus musculus GN=Mtf1 PE=2 SV=2
Unigene54527_All	--
Unigene54528_All	--
Unigene54546_All	WAS/WASL-interacting protein family member 2 OS=Homo sapiens GN=WIPF2 PE=1 SV=1
Unigene54578_All	Mariner Mos1 transposase OS=Drosophila mauritiana GN=mariner\T PE=1 SV=1
Unigene54593_All	Serine/arginine repetitive matrix protein 1 OS=Pongo abelii GN=SRRM1 PE=2 SV=1
Unigene54601_All	Serine/arginine repetitive matrix protein 1 OS=Pongo abelii GN=SRRM1 PE=2 SV=1
Unigene54603_All	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 OS=Bos taurus GN=PFKFB2 PE=1 SV=2
Unigene54622_All	--
Unigene5468_All	--
Unigene54743_All	Sodium/potassium-transporting ATPase subunit alpha OS=Drosophila melanogaster GN=Atpalpha PE=1 SV=3
Unigene54766_All	Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2
Unigene54814_All	--
Unigene54838_All	Esterase SG1 (Fragment) OS=Schizaphis graminum GN=SG1 PE=1 SV=1
Unigene54841_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene54876_All	--
Unigene54930_All	--
Unigene54955_All	--
Unigene54956_All	--
Unigene54994_All	G-protein coupled receptor moody OS=Drosophila melanogaster GN=moody PE=2 SV=2
Unigene55005_All	Zinc finger protein weckle OS=Drosophila melanogaster GN=wek PE=1 SV=1
Unigene55075_All	--
Unigene55083_All	Superoxide dismutase [Cu-Zn] OS=Halocynthia roretzi PE=1 SV=2
Unigene55085_All	--

Unigene55162_All	Sodium-coupled monocarboxylate transporter 2 OS=Homo sapiens GN=SLC5A12 PE=2 SV=2
Unigene55236_All	--
Unigene55247_All	Dol-P-Glc:Glc(2)Man(9)GlcNAc(2)-PP-Dol alpha-1,2-glucosyltransferase OS=Homo sapiens GN=ALG10 PE=2 SV=1
Unigene55379_All	--
Unigene55385_All	Protein spinster OS=Drosophila melanogaster GN=spin PE=1 SV=1
Unigene55391_All	--
Unigene55455_All	Homeodomain-only protein OS=Danio rerio GN=hopx PE=3 SV=1
Unigene55518_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2
Unigene55617_All	--
Unigene55640_All	--
Unigene55663_All	Facilitated trehalose transporter Tret1 OS=Polypedilum vanderplanki GN=Tret1 PE=1 SV=1
Unigene55713_All	--
Unigene55730_All	--
Unigene55770_All	--
Unigene55855_All	--
Unigene55918_All	Fatty acid-binding protein, muscle OS=Schistocerca gregaria PE=1 SV=2
Unigene55938_All	--
Unigene5595_All	--
Unigene55960_All	Rap guanine nucleotide exchange factor 4 OS=Homo sapiens GN=RAPGEF4 PE=1 SV=1
Unigene55983_All	--
Unigene56042_All	Transposon TX1 uncharacterized 149 kDa protein OS=Xenopus laevis PE=4 SV=1
Unigene56115_All	--
Unigene56136_All	--
Unigene56205_All	--
Unigene56240_All	--
Unigene5631_All	--
Unigene56410_All	--
Unigene56601_All	--
Unigene5664_All	--
Unigene56673_All	Putative uncharacterized transposon-derived protein F52C9.6 OS=Caenorhabditis elegans GN=F52C9.6 PE=5 SV=1
Unigene56689_All	--
Unigene56698_All	--

Unigene56759_All	--
Unigene56804_All	Uncharacterized transmembrane protein DDB_G0289901 OS=Dictyostelium discoideum GN=DDB_G0289901 PE=4 SV=1
Unigene56844_All	--
Unigene56933_All	--
Unigene56936_All	--
Unigene57035_All	--
Unigene57047_All	--
Unigene5711_All	--
Unigene57126_All	--
Unigene5712_All	--
Unigene57280_All	--
Unigene57350_All	--
Unigene57351_All	Serine proteinase stubble OS=Drosophila melanogaster GN=Sb PE=2 SV=2
Unigene57367_All	--
Unigene57398_All	--
Unigene57418_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene57441_All	Fatty acid-binding protein, muscle OS=Schistocerca gregaria PE=1 SV=2
Unigene57444_All	--
Unigene57471_All	--
Unigene574_All	--
Unigene57523_All	MFS-type transporter SLC18B1 OS=Homo sapiens GN=SLC18B1 PE=2 SV=1
Unigene57547_All	--
Unigene57660_All	--
Unigene57679_All	--
Unigene57871_All	Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2
Unigene578_All	--
Unigene57901_All	Serine/threonine-protein kinase WNK4 OS=Mus musculus GN=Wnk4 PE=1 SV=1
Unigene57949_All	--
Unigene58045_All	--
Unigene58098_All	--
Unigene5811_All	--
Unigene58190_All	--
Unigene58237_All	--
Unigene58238_All	--
Unigene58241_All	--

Unigene58292_All	--
Unigene58389_All	--
Unigene58447_All	Neural-cadherin OS=Drosophila melanogaster GN=CadN PE=1 SV=2
Unigene58460_All	--
Unigene58489_All	Transposon TX1 uncharacterized 149 kDa protein OS=Xenopus laevis PE=4 SV=1
Unigene5848_All	--
Unigene5863_All	--
Unigene58674_All	--
Unigene58801_All	--
Unigene5880_All	Zinc finger BED domain-containing protein 4 OS=Homo sapiens GN=ZBED4 PE=1 SV=2
Unigene58812_All	--
Unigene58890_All	--
Unigene58900_All	--
Unigene58907_All	--
Unigene58_All	Probable RNA helicase armi OS=Drosophila melanogaster GN=armi PE=2 SV=3
Unigene59009_All	--
Unigene59080_All	--
Unigene59098_All	Facilitated trehalose transporter Tret1 OS=Bombyx mori GN=Tret1 PE=1 SV=1
Unigene59113_All	--
Unigene5911_All	--
Unigene59129_All	Retrovirus-related Pol polyprotein from transposon 17.6 OS=Drosophila melanogaster GN=pol PE=4 SV=1
Unigene59134_All	--
Unigene59140_All	--
Unigene59160_All	--
Unigene59188_All	--
Unigene59192_All	--
Unigene59207_All	--
Unigene59214_All	DBF4-type zinc finger-containing protein 2 homolog OS=Mus musculus GN=Zdbf2 PE=2 SV=1
Unigene5922_All	--
Unigene59248_All	--
Unigene59249_All	--
Unigene59250_All	--
Unigene59251_All	--
Unigene59297_All	--
Unigene592_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2

Unigene59318_All	--
Unigene59324_All	--
Unigene59640_All	--
Unigene59693_All	--
Unigene59758_All	--
Unigene59909_All	--
Unigene59920_All	Rho guanine nucleotide exchange factor 7 OS=Rattus norvegicus GN=Arhgef7 PE=1 SV=1
Unigene59943_All	--
Unigene60006_All	--
Unigene60009_All	--
Unigene60101_All	--
Unigene60145_All	--
Unigene60156_All	--
Unigene60189_All	--
Unigene60253_All	--
Unigene60333_All	--
Unigene60337_All	Nuclear hormone receptor E75 OS=Metapenaeus ensis GN=E75 PE=2 SV=1
Unigene60471_All	--
Unigene60554_All	--
Unigene60572_All	Copper-transporting ATPase 2 OS=Rattus norvegicus GN=Atp7b PE=2 SV=1
Unigene60575_All	--
Unigene60591_All	--
Unigene6062_All	--
Unigene60719_All	--
Unigene60757_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
Unigene60786_All	--
Unigene60804_All	--
Unigene60813_All	--
Unigene60833_All	--
Unigene60836_All	--
Unigene60912_All	--
Unigene60973_All	--
Unigene61057_All	--
Unigene6106_All	--
Unigene61097_All	--
Unigene61121_All	--
Unigene61155_All	--
Unigene61170_All	--

Unigene61183_All	--
Unigene61201_All	--
Unigene61209_All	--
Unigene61252_All	--
Unigene61265_All	--
Unigene61314_All	--
Unigene61322_All	--
Unigene61355_All	--
Unigene61394_All	--
Unigene61399_All	--
Unigene6141_All	--
Unigene61442_All	--
Unigene6144_All	--
Unigene6147_All	--
Unigene61583_All	--
Unigene61595_All	--
Unigene6159_All	--
Unigene61643_All	--
Unigene61687_All	--
Unigene61818_All	--
Unigene61821_All	--
Unigene61849_All	--
Unigene61856_All	--
Unigene61861_All	--
Unigene61872_All	--
Unigene61939_All	--
Unigene61981_All	--
Unigene62022_All	--
Unigene62044_All	--
Unigene62049_All	--
Unigene62100_All	--
Unigene62160_All	--
Unigene62176_All	--
Unigene62199_All	--
Unigene62201_All	--
Unigene62245_All	--
Unigene62254_All	Transmembrane protein 104 homolog OS=Drosophila melanogaster GN=CG5262 PE=2 SV=2
Unigene6232_All	--
Unigene62340_All	Uncharacterized aarF domain-containing protein kinase 2 OS=Mus musculus GN=Adck2 PE=2 SV=1

Unigene62377_All	Low-density lipoprotein receptor-related protein 2 OS=Mus musculus GN=Lrp2 PE=1 SV=1
Unigene62412_All	Uncharacterized protein C10orf95 OS=Homo sapiens GN=C10orf95 PE=2 SV=1
Unigene62472_All	Protein spaetzle OS=Drosophila melanogaster GN=spz PE=1 SV=3
Unigene62478_All	Large neutral amino acids transporter small subunit 2 OS=Mus musculus GN=Slc7a8 PE=1 SV=1
Unigene62481_All	Sphingosine kinase 2 OS=Homo sapiens GN=SPHK2 PE=1 SV=2
Unigene62485_All	--
Unigene62514_All	--
Unigene62547_All	--
Unigene62588_All	Facilitated trehalose transporter Tret1 OS=Drosophila virilis GN=Tret1 PE=3 SV=2
Unigene62607_All	--
Unigene62634_All	--
Unigene62703_All	--
Unigene62783_All	--
Unigene62820_All	Acyl-CoA synthetase family member 2, mitochondrial OS=Danio rerio GN=acsf2 PE=2 SV=1
Unigene62928_All	Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3
Unigene62944_All	--
Unigene62994_All	--
Unigene63006_All	--
Unigene63029_All	--
Unigene63038_All	--
Unigene63075_All	--
Unigene63091_All	--
Unigene63163_All	Venom carboxylesterase-6 OS=Apis mellifera PE=2 SV=1
Unigene63181_All	Uncharacterized protein DDB_G0271670 OS=Dictyostelium discoideum GN=DDB_G0271670 PE=4 SV=1
Unigene63224_All	--
Unigene63281_All	--
Unigene63305_All	--
Unigene63307_All	--
Unigene63358_All	--
Unigene6344_All	--
Unigene63465_All	--
Unigene63468_All	--

Unigene6353_All	--
Unigene63540_All	--
Unigene63545_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene63562_All	Histidine-rich glycoprotein OS=Plasmodium lophurae PE=4 SV=1
Unigene63563_All	Histidine-rich glycoprotein OS=Plasmodium lophurae PE=4 SV=1
Unigene63580_All	Uracil-DNA glycosylase OS=Mus musculus GN=Ung PE=2 SV=3
Unigene63640_All	--
Unigene63680_All	--
Unigene63726_All	Lipase member H OS=Homo sapiens GN=LIPH PE=1 SV=1
Unigene63746_All	Myrosinase 1 OS=Brevicoryne brassicae PE=1 SV=1
Unigene63752_All	--
Unigene63807_All	--
Unigene63874_All	--
Unigene64007_All	--
Unigene6405_All	--
Unigene64101_All	--
Unigene64122_All	--
Unigene64142_All	--
Unigene64153_All	--
Unigene64258_All	--
Unigene64269_All	--
Unigene6431_All	--
Unigene64409_All	--
Unigene64481_All	--
Unigene6456_All	--
Unigene64681_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene64683_All	Protein SOGA2 OS=Homo sapiens GN=SOGA2 PE=1 SV=5
Unigene64699_All	--
Unigene64706_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene64721_All	Phenoloxidase subunit A3 OS=Drosophila melanogaster GN=proPo-A3 PE=1 SV=1
Unigene64789_All	Serine protease 44 OS=Mus musculus GN=Prss44 PE=2 SV=1
Unigene64809_All	--
Unigene64903_All	--
Unigene64907_All	--
Unigene64936_All	Carboxypeptidase B OS=Astacus fluviatilis PE=1 SV=1

Unigene64988_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene65038_All	Sialin OS=Homo sapiens GN=SLC17A5 PE=1 SV=2
Unigene65117_All	--
Unigene65225_All	--
Unigene65231_All	--
Unigene65274_All	--
Unigene65306_All	--
Unigene6550_All	--
Unigene65520_All	--
Unigene65540_All	--
Unigene6569_All	--
Unigene65989_All	Serine/threonine-protein phosphatase 4 regulatory subunit 3 OS=Drosophila melanogaster GN=flfl PE=1 SV=4
Unigene6600_All	--
Unigene66050_All	--
Unigene66163_All	--
Unigene66227_All	--
Unigene66258_All	--
Unigene662_All	Facilitated trehalose transporter Tret1 OS=Culex quinquefasciatus GN=Tret1 PE=3 SV=1
Unigene66337_All	--
Unigene66399_All	--
Unigene66413_All	--
Unigene66417_All	--
Unigene66425_All	--
Unigene66438_All	--
Unigene66452_All	--
Unigene66461_All	--
Unigene6647_All	--
Unigene66486_All	--
Unigene66495_All	--
Unigene66508_All	--
Unigene66521_All	--
Unigene66641_All	--
Unigene670_All	--
Unigene67209_All	--
Unigene67213_All	--
Unigene6733_All	--
Unigene67390_All	--
Unigene67405_All	--

Unigene67459_All	--
Unigene67475_All	--
Unigene6754_All	--
Unigene67592_All	Mucin-3A OS=Homo sapiens GN=MUC3A PE=2 SV=2
Unigene6767_All	--
Unigene67760_All	--
Unigene67823_All	--
Unigene67854_All	--
Unigene67944_All	--
Unigene67963_All	--
Unigene67979_All	--
Unigene68044_All	--
Unigene68062_All	--
Unigene68067_All	--
Unigene68080_All	Hypodermin-B OS=Hypoderma lineatum PE=1 SV=1
Unigene68181_All	--
Unigene68228_All	--
Unigene68283_All	--
Unigene68299_All	--
Unigene68318_All	--
Unigene68351_All	--
Unigene68414_All	--
Unigene68418_All	--
Unigene68449_All	--
Unigene68576_All	--
Unigene68580_All	--
Unigene68600_All	--
Unigene68620_All	--
Unigene68623_All	--
Unigene6863_All	--
Unigene68655_All	--
Unigene68682_All	--
Unigene68704_All	--
Unigene68715_All	--
Unigene68729_All	--
Unigene6873_All	--
Unigene68782_All	--
Unigene68828_All	--
Unigene68850_All	--
Unigene68878_All	--
Unigene68907_All	--

Unigene68934_All	--
Unigene68941_All	--
Unigene68986_All	--
Unigene68991_All	--
Unigene68998_All	--
Unigene69042_All	--
Unigene69053_All	--
Unigene69135_All	--
Unigene69227_All	--
Unigene69234_All	--
Unigene69254_All	--
Unigene69285_All	--
Unigene69301_All	--
Unigene69341_All	--
Unigene69376_All	--
Unigene69397_All	Retrovirus-related Pol polyprotein from transposon 17.6 OS=Drosophila melanogaster GN=pol PE=4 SV=1
Unigene69400_All	Uncharacterized protein K02A2.6 OS=Caenorhabditis elegans GN=K02A2.6 PE=2 SV=1
Unigene69402_All	Retrovirus-related Pol polyprotein from transposon 412 OS=Drosophila melanogaster GN=POL PE=4 SV=1
Unigene69403_All	--
Unigene69419_All	Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3
Unigene69513_All	PDZ and LIM domain protein Zasp OS=Drosophila melanogaster GN=Zasp52 PE=1 SV=2
Unigene69514_All	Dystrophin, isoforms A/C/F/G/H OS=Drosophila melanogaster GN=Dys PE=1 SV=3
Unigene69553_All	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3
Unigene69557_All	--
Unigene69568_All	Ecdysone-induced protein 75B, isoform B OS=Drosophila melanogaster GN=Eip75B PE=2 SV=2
Unigene69571_All	Ecdysone-inducible protein E75 OS=Galleria mellonella GN=E75 PE=2 SV=1
Unigene69626_All	--
Unigene69627_All	--
Unigene69697_All	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B OS=Gallus gallus GN=ANKRD44 PE=2 SV=1
Unigene69701_All	Probable cytochrome P450 305a1 OS=Drosophila melanogaster GN=Cyp305a1 PE=2 SV=1

Unigene69708_All	UDP-glucuronosyltransferase 2B15 OS=Rattus norvegicus GN=Ugt2b15 PE=1 SV=1
Unigene69746_All	--
Unigene69755_All	Uncharacterized protein K02A2.6 OS=Caenorhabditis elegans GN=K02A2.6 PE=2 SV=1
Unigene69785_All	Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2
Unigene69850_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene69851_All	--
Unigene69858_All	--
Unigene69865_All	--
Unigene69889_All	--
Unigene69894_All	--
Unigene69922_All	--
Unigene69939_All	--
Unigene7004_All	--
Unigene70076_All	Phosphofurin acidic cluster sorting protein 1 OS=Rattus norvegicus GN=Pacs1 PE=2 SV=1
Unigene7012_All	--
Unigene70130_All	--
Unigene70183_All	--
Unigene70198_All	--
Unigene70299_All	--
Unigene70378_All	Zinc finger protein 845 OS=Homo sapiens GN=ZNF845 PE=2 SV=3
Unigene7039_All	--
Unigene70435_All	--
Unigene70497_All	--
Unigene70500_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1
Unigene70543_All	--
Unigene70544_All	Niemann-Pick C1 protein OS=Sus scrofa GN=NPC1 PE=2 SV=1
Unigene70545_All	--
Unigene7054_All	--
Unigene70557_All	--
Unigene70605_All	--
Unigene70611_All	S-phase kinase-associated protein 2 OS=Mus musculus GN=Skp2 PE=1 SV=1
Unigene7062_All	--
Unigene70646_All	--
Unigene70669_All	--

Unigene70697_All	--
Unigene70704_All	--
Unigene70709_All	Basic proline-rich protein OS=Sus scrofa PE=1 SV=2
Unigene70710_All	--
Unigene70711_All	--
Unigene70717_All	Fibroin heavy chain OS=Bombyx mori GN=FIBH PE=1 SV=4
Unigene7075_All	--
Unigene70770_All	Solute carrier organic anion transporter family member 4A1 OS=Rattus norvegicus GN=Slco4a1 PE=2 SV=1
Unigene70773_All	--
Unigene70780_All	Ferredoxin-fold anticodon-binding domain-containing protein 1 OS=Homo sapiens GN=FDXACB1 PE=2 SV=3
Unigene70804_All	--
Unigene70879_All	Speckle-type POZ protein OS=Pongo abelii GN=SPOP PE=1 SV=1
Unigene70912_All	--
Unigene70950_All	Protein disulfide-isomerase A3 OS=Bos taurus GN=PDIA3 PE=2 SV=1
Unigene71080_All	--
Unigene71084_All	Leukocyte elastase inhibitor OS=Bos taurus GN=SERPINB1 PE=2 SV=2
Unigene71114_All	--
Unigene71162_All	--
Unigene71180_All	--
Unigene7121_All	--
Unigene71238_All	Chondroitin proteoglycan-2 OS=Caenorhabditis elegans GN=cpg-2 PE=1 SV=3
Unigene71254_All	--
Unigene7131_All	--
Unigene71442_All	--
Unigene71446_All	--
Unigene71467_All	--
Unigene71501_All	--
Unigene7157_All	--
Unigene71698_All	--
Unigene71703_All	--
Unigene71769_All	--
Unigene71773_All	--
Unigene71798_All	--
Unigene71815_All	--

Unigene71840_All	--
Unigene71888_All	--
Unigene71948_All	Protease inhibitors OS=Locusta migratoria PE=1 SV=2
Unigene72151_All	--
Unigene72157_All	Splicing factor 3B subunit 3 OS=Mus musculus GN=Sf3b3 PE=2 SV=1
Unigene72159_All	--
Unigene72173_All	--
Unigene72185_All	--
Unigene72227_All	Salivary glue protein Sgs-3 OS=Drosophila melanogaster GN=Sgs3 PE=2 SV=1
Unigene72268_All	--
Unigene72285_All	--
Unigene72324_All	--
Unigene72334_All	Membrane-associated progesterone receptor component 1 OS=Gallus gallus GN=PGRMC1 PE=2 SV=3
Unigene72416_All	Keratin, type I cytoskeletal 9 OS=Canis familiaris GN=KRT9 PE=3 SV=1
Unigene72527_All	Protein takeout OS=Drosophila melanogaster GN=to PE=2 SV=1
Unigene72545_All	--
Unigene72549_All	Venom serine carboxypeptidase OS=Apis mellifera PE=2 SV=1
Unigene72580_All	--
Unigene72589_All	--
Unigene72594_All	Protein dachsous OS=Drosophila melanogaster GN=ds PE=1 SV=3
Unigene72615_All	--
Unigene72622_All	Putative uncharacterized protein DDB_G0291608 OS=Dictyostelium discoideum GN=DDB_G0291608 PE=4 SV=1
Unigene72626_All	--
Unigene72637_All	--
Unigene72640_All	UDP-glucuronosyltransferase 2B14 OS=Oryctolagus cuniculus GN=UGT2B14 PE=2 SV=1
Unigene7267_All	--
Unigene72810_All	--
Unigene72820_All	--
Unigene72916_All	--
Unigene7296_All	--
Unigene72980_All	--
Unigene73040_All	--
Unigene73173_All	--

Unigene7319_All	--
Unigene7321_All	--
Unigene73246_All	--
Unigene73292_All	Nuclear factor of activated T-cells 5 OS=Homo sapiens GN=NFAT5 PE=1 SV=1
Unigene7335_All	--
Unigene73523_All	--
Unigene73570_All	--
Unigene73584_All	--
Unigene73615_All	--
Unigene7369_All	--
Unigene736_All	--
Unigene73716_All	--
Unigene73773_All	--
Unigene7379_All	--
Unigene73826_All	--
Unigene73827_All	--
Unigene7382_All	Phospholipase B-like protein B OS=Dictyostelium discoideum GN=plbB PE=3 SV=1
Unigene73860_All	--
Unigene73875_All	--
Unigene73968_All	--
Unigene7399_All	--
Unigene74057_All	Serine/threonine-protein kinase 3 OS=Mus musculus GN=Stk3 PE=1 SV=1
Unigene74069_All	--
Unigene74095_All	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2
Unigene74108_All	--
Unigene74202_All	--
Unigene7423_All	--
Unigene74251_All	--
Unigene7432_All	--
Unigene7435_All	--
Unigene74380_All	--
Unigene74540_All	--
Unigene7458_All	Acetylcholinesterase (Fragment) OS=Oryctolagus cuniculus GN=ACHE PE=2 SV=1
Unigene7459_All	--
Unigene745_All	--
Unigene7461_All	--

Unigene7462_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
Unigene74670_All	--
Unigene7472_All	--
Unigene74744_All	--
Unigene7481_All	Neural Wiskott-Aldrich syndrome protein OS=Rattus norvegicus GN=Wasl PE=1 SV=2
Unigene74827_All	--
Unigene7485_All	--
Unigene74912_All	--
Unigene74923_All	--
Unigene7494_All	Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3
Unigene74958_All	--
Unigene750_All	--
Unigene75160_All	--
Unigene7516_All	--
Unigene75194_All	--
Unigene75196_All	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
Unigene75308_All	--
Unigene75325_All	--
Unigene75362_All	--
Unigene7539_All	--
Unigene75419_All	--
Unigene75474_All	--
Unigene75514_All	--
Unigene75554_All	--
Unigene75599_All	--
Unigene75625_All	--
Unigene75642_All	--
Unigene75741_All	--
Unigene75756_All	--
Unigene7578_All	--
Unigene75792_All	--
Unigene75808_All	--
Unigene7580_All	--
Unigene75812_All	--
Unigene7581_All	--
Unigene75828_All	--
Unigene7588_All	--

Unigene75912_All	--
Unigene75937_All	--
Unigene75939_All	--
Unigene75942_All	--
Unigene75976_All	--
Unigene7598_All	--
Unigene76036_All	Probable cation-transporting ATPase 13A5 OS=Homo sapiens GN=ATP13A5 PE=2 SV=1
Unigene76041_All	--
Unigene76059_All	--
Unigene7608_All	--
Unigene76109_All	--
Unigene76124_All	--
Unigene76132_All	--
Unigene76138_All	--
Unigene76197_All	--
Unigene76233_All	--
Unigene76295_All	--
Unigene76428_All	--
Unigene76431_All	--
Unigene76445_All	--
Unigene76470_All	--
Unigene76504_All	--
Unigene7650_All	--
Unigene76572_All	--
Unigene76606_All	--
Unigene7660_All	--
Unigene76658_All	--
Unigene76678_All	--
Unigene76698_All	--
Unigene7676_All	--
Unigene767_All	--
Unigene76849_All	--
Unigene7685_All	--
Unigene76861_All	--
Unigene76866_All	--
Unigene76916_All	--
Unigene76943_All	Serine/arginine repetitive matrix protein 1 OS=Pongo abelii GN=SRRM1 PE=2 SV=1
Unigene76965_All	--
Unigene76993_All	--

Unigene77135_All	Transposable element Tcb2 transposase OS=Caenorhabditis briggsae PE=3 SV=1
Unigene77157_All	--
Unigene77168_All	--
Unigene77189_All	--
Unigene77191_All	--
Unigene7719_All	Retrotransposon-like protein 1 OS=Mus musculus GN=Rtl1 PE=2 SV=1
Unigene77216_All	--
Unigene77263_All	--
Unigene77365_All	--
Unigene773_All	--
Unigene77400_All	--
Unigene77461_All	--
Unigene77474_All	--
Unigene77502_All	--
Unigene77526_All	--
Unigene77566_All	--
Unigene77634_All	--
Unigene7765_All	--
Unigene7769_All	--
Unigene77787_All	--
Unigene77802_All	Wnt inhibitory factor 1 OS=Xenopus laevis GN=wif1 PE=2 SV=1
Unigene77851_All	--
Unigene77879_All	--
Unigene77914_All	Transposable element Tc3 transposase OS=Caenorhabditis elegans GN=tc3a PE=1 SV=1
Unigene77922_All	--
Unigene77926_All	--
Unigene77970_All	--
Unigene78039_All	--
Unigene78103_All	--
Unigene78140_All	--
Unigene7814_All	--
Unigene7815_All	--
Unigene78164_All	--
Unigene78175_All	--
Unigene78196_All	--
Unigene78211_All	--
Unigene782_All	--
Unigene7846_All	--

Unigene7848_All	--
Unigene7877_All	--
Unigene7883_All	--
Unigene7956_All	--
Unigene7957_All	--
Unigene7960_All	--
Unigene7982_All	--
Unigene8006_All	--
Unigene8009_All	--
Unigene8010_All	Serine/arginine repetitive matrix protein 1 OS=Pongo abelii GN=SRRM1 PE=2 SV=1
Unigene8018_All	--
Unigene8027_All	--
Unigene8035_All	--
Unigene8042_All	--
Unigene80454_All	--
Unigene80551_All	--
Unigene8086_All	--
Unigene80932_All	--
Unigene80938_All	--
Unigene80952_All	--
Unigene80975_All	--
Unigene81047_All	--
Unigene81080_All	--
Unigene8109_All	--
Unigene8115_All	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2
Unigene8118_All	--
Unigene8129_All	--
Unigene81355_All	--
Unigene8136_All	--
Unigene8172_All	--
Unigene8181_All	--
Unigene81849_All	Tigger transposable element-derived protein 6 OS=Homo sapiens GN=TIGD6 PE=2 SV=2
Unigene8184_All	--
Unigene8189_All	--
Unigene8210_All	--
Unigene82171_All	--
Unigene8226_All	--
Unigene8239_All	--
Unigene8251_All	--

Unigene82550_All	--
Unigene8262_All	--
Unigene83095_All	--
Unigene8309_All	Histone-lysine N-methyltransferase SETMAR OS=Homo sapiens GN=SETMAR PE=1 SV=1
Unigene8331_All	Lactosylceramide 4-alpha-galactosyltransferase OS=Rattus norvegicus GN=A4galt PE=1 SV=1
Unigene83339_All	--
Unigene83410_All	--
Unigene8372_All	Transmembrane and coiled-coil domains protein 1 OS=Rattus norvegicus GN=Tmco1 PE=2 SV=1
Unigene8386_All	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase OS=Danio rerio GN=dhdh PE=2 SV=2
Unigene83888_All	Probable adenosine deaminase OS=Dictyostelium discoideum GN=ada PE=3 SV=1
Unigene83924_All	--
Unigene8394_All	--
Unigene84255_All	--
Unigene844_All	Probable RNA-directed DNA polymerase from transposon BS OS=Drosophila melanogaster GN=RTase PE=2 SV=1
Unigene84724_All	--
Unigene8523_All	--
Unigene8532_All	--
Unigene8546_All	--
Unigene8549_All	--
Unigene8564_All	--
Unigene85715_All	--
Unigene8595_All	--
Unigene8599_All	--
Unigene8636_All	--
Unigene86600_All	--
Unigene868_All	UPF0764 protein C16orf89 homolog OS=Mus musculus PE=2 SV=2
Unigene8707_All	--
Unigene8710_All	Mariner Mos1 transposase OS=Drosophila mauritiana GN=mariner\T PE=1 SV=1
Unigene87206_All	--
Unigene8728_All	--
Unigene8751_All	--
Unigene87522_All	--
Unigene87605_All	--

Unigene8793_All	Craniofacial development protein 2 OS=Bos taurus GN=CFDP2 PE=1 SV=2
Unigene87977_All	--
Unigene8801_All	--
Unigene88052_All	--
Unigene8817_All	--
Unigene88247_All	--
Unigene88292_All	--
Unigene8834_All	--
Unigene88459_All	--
Unigene8845_All	--
Unigene8853_All	--
Unigene8870_All	--
Unigene88736_All	--
Unigene88940_All	--
Unigene88958_All	--
Unigene89050_All	--
Unigene89229_All	--
Unigene8931_All	--
Unigene8941_All	--
Unigene89532_All	--
Unigene89732_All	--
Unigene89733_All	--
Unigene897_All	--
Unigene89885_All	--
Unigene8990_All	--
Unigene90052_All	--
Unigene90082_All	--
Unigene90101_All	--
Unigene90384_All	--
Unigene90497_All	--
Unigene90529_All	--
Unigene9052_All	--
Unigene90598_All	--
Unigene90615_All	--
Unigene90627_All	--
Unigene90629_All	--
Unigene90640_All	--
Unigene90670_All	--
Unigene90730_All	--
Unigene90733_All	--

Unigene90742_All	Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2
Unigene90776_All	--
Unigene90795_All	--
Unigene90821_All	Fatty-acid amide hydrolase 2-B OS=Danio rerio GN=faah2b PE=2 SV=1
Unigene90833_All	--
Unigene90862_All	--
Unigene90882_All	--
Unigene9089_All	--
Unigene90916_All	--
Unigene90930_All	--
Unigene9094_All	--
Unigene90950_All	--
Unigene90997_All	--
Unigene90998_All	--
Unigene9099_All	--
Unigene91004_All	--
Unigene91048_All	--
Unigene91127_All	--
Unigene9114_All	Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=2
Unigene9117_All	--
Unigene9120_All	--
Unigene91228_All	--
Unigene91247_All	--
Unigene9128_All	--
Unigene91294_All	--
Unigene9152_All	--
Unigene9154_All	--
Unigene91581_All	60S ribosomal protein L32 OS=Drosophila yakuba GN=RpL32 PE=2 SV=1
Unigene91629_All	--
Unigene91731_All	--
Unigene9184_All	--
Unigene92005_All	--
Unigene9213_All	--
Unigene9215_All	--
Unigene92198_All	--
Unigene92526_All	--
Unigene9252_All	--
Unigene92617_All	--

Unigene9264_All	Alpha-tocopherol transfer protein-like OS=Pongo abelii GN=TTPAL PE=2 SV=1
Unigene9295_All	--
Unigene9341_All	--
Unigene93536_All	--
Unigene93574_All	--
Unigene935_All	--
Unigene936_All	Neural Wiskott-Aldrich syndrome protein OS=Bos taurus GN=WASL PE=1 SV=1
Unigene9395_All	--
Unigene9405_All	--
Unigene9479_All	--
Unigene9484_All	--
Unigene9502_All	--
Unigene9519_All	--
Unigene9521_All	--
Unigene9522_All	--
Unigene9553_All	--
Unigene9557_All	--
Unigene9561_All	--
Unigene9569_All	--
Unigene9595_All	--
Unigene9597_All	Transmembrane and coiled-coil domains protein 1 OS=Rattus norvegicus GN=Tmco1 PE=2 SV=1
Unigene961_All	--
Unigene9620_All	--
Unigene9621_All	Mariner Mos1 transposase OS=Drosophila mauritiana GN=mariner\T PE=1 SV=1
Unigene9668_All	--
Unigene966_All	--
Unigene9680_All	--
Unigene9689_All	--
Unigene97035_All	--
Unigene97130_All	Beta-1,4-galactosyltransferase 7 OS=Mus musculus GN=B4galt7 PE=2 SV=1
Unigene9715_All	--
Unigene9719_All	--
Unigene9740_All	--
Unigene97465_All	Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=2
Unigene9765_All	Keratinocyte proline-rich protein OS=Rattus norvegicus GN=Kprp PE=2 SV=1

Unigene9768_All	Group XV phospholipase A2 OS=Homo sapiens GN=PLA2G15 PE=1 SV=2
Unigene97783_All	--
Unigene97784_All	--
Unigene97899_All	--
Unigene98054_All	--
Unigene9811_All	--
Unigene9820_All	--
Unigene9821_All	--
Unigene9825_All	--
Unigene9827_All	--
Unigene9833_All	--
Unigene9854_All	--
Unigene9877_All	PH domain-containing protein DDB_G0287875 OS=Dictyostelium discoideum GN=DDB_G0287875 PE=2 SV=1
Unigene9890_All	--
Unigene9920_All	Synaptotagmin 1 OS=Drosophila melanogaster GN=Syt1 PE=1 SV=2
Unigene9939_All	--
Unigene9978_All	--
Unigene9994_All	--
Unigene99_All	Uncharacterized protein LOC284861 OS=Homo sapiens PE=2 SV=1

Appendix D Differentially expressed peptides identified by LC-ESI-MS/MS.

Group ID	Accession	NCBI nr Description
1	Unigene2776_All	RecName: Full=Apolipophorins; Contains: RecName: Full=Apolipophorin-2; AltName: Full=Apolipophorin II; AltName: Full=apoLp-2; Contains: RecName: Full=Apolipophorin-1; AltName: Full=Apolipophorin I; AltName: Full=apoLp-1; Flags: Precursor
2	CL14708.Contig2_All	hemocyanin subunit type 1 [Locusta migratoria]
3	CL14288.Contig1_All	hemocyanin subunit type 2 [Hierodula membranacea]
4	Unigene64721_All	pro-phenoloxidase 1 [Locusta migratoria]
5	Unigene34645_All	lysosomal alpha-mannosidase [Culex quinquefasciatus] >gi|167879595|gb|EDS42978.1| lysosomal alpha-mannosidase [Culex quinquefasciatus]
6	Unigene50478_All	hemocyanin subunit type 2 precursor [Blaptica dubia]
7	Unigene32302_All	hexamerin-like protein 4 [Locusta migratoria]
8	CL3079.Contig3_All	hexamerin-like protein 4 [Locusta migratoria]
9	Unigene32300_All	hexamerin-like protein 4 [Locusta migratoria]

10	Unigene27649_All	imaginal disc growth factor-like protein [Mamestra brassicae]
11	Unigene3081_All	Chain A, Nmr Structure Of Apolipophorin-Iii From Locusta Migratoria >gi|484000|gb|AAA29282.1| apolipophorin-III [Locusta migratoria]
12	Unigene62387_All	RecName: Full=Tubulin beta-1 chain; AltName: Full=Beta-1-tubulin >gi|2613141|gb|AAB84297.1| beta-1 tubulin [Manduca sexta]
12	Unigene62388_All	
13	CL3807.Contig1_All	elongation factor 1 alpha [Locusta migratoria]
14	CL3079.Contig2_All	hexamerin storage protein 3 [Romalea microptera]
15	Unigene20012_All	arginine kinase [Locusta migratoria manilensis]
16	Unigene63433_All	heat shock protein 90 [Locusta migratoria]
17	CL5764.Contig1_All	AAEL014418-PA [Aedes aegypti]
18	Unigene27613_All	hemocyanin subunit type 2 [Hierodula membranacea]
19	Unigene19900_All	hsp70 family member [Locusta migratoria]
20	Unigene27497_All	transferrin [Romalea microptera]
21	Unigene35174_All	ATP-synthase subunit beta [Schistocerca gregaria]
22	Unigene1828_All	elongation factor 2 [Schistocerca gregaria]
23	CL15167.Contig1_All	Selenium-binding protein 1 [Chelonia mydas]
24	Unigene12349_All	ER protein gp78 [Locusta migratoria]
25	Unigene87945_All	PREDICTED: lipase 3-like [Nasonia vitripennis]
26	Unigene55778_All	protein disulfide isomerase [Litopenaeus vannamei]
27	CL212.Contig3_All	pro-phenoloxidase 1 [Locusta migratoria]
28	CL9852.Contig3_All	tubulin alpha-1 chain [Pediculus humanus corporis] >gi|212513985|gb|EEB16383.1| tubulin alpha-1 chain [Pediculus humanus corporis]
28	CL9852.Contig4_All	
28	CL9852.Contig6_All	
28	CL9852.Contig5_All	
29	Unigene42283_All	peptidyl-prolyl isomerase-1 [Locusta migratoria]
30	Unigene27865_All	PREDICTED: heterogeneous nuclear ribonucleoprotein K-like [Megachile rotundata]
31	Unigene72608_All	glutathione S-transferase delta [Locusta migratoria] >gi|329564865|gb|AEB91971.1| glutathione S-transferase delta 1 [Locusta migratoria]
32	Unigene70950_All	protein disulfide-isomerase [Schistocerca gregaria]
33	CL7368.Contig1_All	ER protein gp78 [Locusta migratoria]
34	Unigene57517_All	basic 19k protein precursor [Locusta migratoria] >gi|226482|prf||1515168A hemolymph protein 19kD
35	CL1271.Contig1_All	fructose 1,6-bisphosphate aldolase [Schistocerca gregaria]
36	CL8020.Contig2_All	Myelin expression factor 2 [Acromyrmex echinatior]
36	CL8020.Contig1_All	

37	CL13310.Contig1_All	mitochondrial H+-transporting ATP synthase F1 complex alpha subunit 1 [Cynopterus sphinx]
38	CL5707.Contig1_All	glutathione S-transferase sigma 1 [Locusta migratoria]
39	Unigene32301_All	hexamerin-like protein 4 [Locusta migratoria]
40	CL1550.Contig1_All	-
41	Unigene25909_All	PREDICTED: similar to AGAP010510-PA [Tribolium castaneum] >gi|270010216|gb|EFA06664.1| hypothetical protein TcasGA2_TC009590 [Tribolium castaneum]
42	Unigene64767_All	enolase [Schistocerca gregaria]
43	Unigene1931_All	hypothetical protein SINV_14312 [Solenopsis invicta]
44	Unigene62710_All	histone 2A [Culex quinquefasciatus] >gi|167878040|gb|EDS41423.1| histone 2A [Culex quinquefasciatus]
45	CL16904.Contig3_All	aldo-keto reductase [Reticulitermes flavipes]
46	Unigene25720_All	PREDICTED: hrp65 protein-like [Acyrthosiphon pisum]
47	CL9820.Contig1_All	histone H2B [Rhynchosciara americana]
48	Unigene42795_All	PREDICTED: histone H2A.V [Apis mellifera] >gi|340729962|ref|XP_003403261.1| PREDICTED: histone H2A.V-like [Bombus terrestris] >gi|345494243|ref|XP_001605065.2| PREDICTED: histone H2A.V-like [Nasonia vitripennis] >gi|350396372|ref|XP_003484532.1| PREDICTED: histone H2A.V-like [Bombus impatiens] >gi|383851127|ref|XP_003701091.1| PREDICTED: histone H2A.V-like [Megachile rotundata]
49	Unigene50112_All	catalase, partial [Schistocerca gregaria]
50	Unigene42359_All	GG22420 [Drosophila erecta] >gi|190658808|gb|EDV56021.1| GG22420 [Drosophila erecta]
51	CL13813.Contig1_All	14-3-3 zeta [Apis florea]
52	CL1506.Contig1_All	hypothetical protein TcasGA2_TC000928 [Tribolium castaneum]
52	CL1506.Contig4_All	
53	CL7976.Contig1_All	LD12501p [Drosophila melanogaster]
54	CL9587.Contig3_All	hexamerin-like protein 2 [Locusta migratoria]
55	CL934.Contig3_All	tetrahydrofolate synthase, partial [Agathiphaga queenslandensis]
56	CL3418.Contig2_All	Filamin-C, putative [Pediculus humanus corporis] >gi|212506381|gb|EEB10613.1| Filamin-C, putative [Pediculus humanus corporis]
57	CL14990.Contig1_All	GAPDH [Locusta migratoria]
58	CL934.Contig5_All	tetrahydrofolate synthase, partial [Agathiphaga queenslandensis]
59	Unigene27359_All	E-1 enzyme, isoform CRA_c [Homo sapiens]

60	CL2438.Contig2_All	heat shock protein 20.5 [Locusta migratoria]
61	Unigene57580_All	unknown [Dendroctonus ponderosae]
62	CL13581.Contig2_All	Putative aminopeptidase W07G4.4 [Crassostrea gigas]
63	Unigene42327_All	TPA_exp: ADP/ATP translocase [Amblyomma variegatum]
64	Unigene57708_All	PREDICTED: malate dehydrogenase, mitochondrial-like, partial [Ornithorhynchus anatinus]
65	Unigene35144_All	PREDICTED: hypothetical protein LOC100643287 [Bombus terrestris]
66	Unigene72143_All	Cytosolic non-specific dipeptidase [Crassostrea gigas]
67	Unigene35099_All	GK13135 [Drosophila willistoni] >gi|194169544|gb|EDW84445.1| GK13135 [Drosophila willistoni]
68	Unigene70455_All	Arginine/serine-rich-splicing factor RSP31, putative [Pediculus humanus corporis] >gi|212507742|gb|EEB11604.1| Arginine/serine-rich-splicing factor RSP31, putative [Pediculus humanus corporis]
69	CL5826.Contig1_All	putative alcohol dehydrogenase [Gryllotalpa orientalis]
70	CL13984.Contig1_All	IP15404p [Drosophila melanogaster]
70	CL13984.Contig2_All	
71	CL12180.Contig1_All	PREDICTED: ATP-dependent RNA helicase eIF4A-like [Nasonia vitripennis]
72	CL212.Contig2_All	pro-phenoloxidase 1 [Locusta migratoria]
73	Unigene2980_All	PREDICTED: T-complex protein 1 subunit theta-like [Cricetulus griseus]
74	Unigene25294_All	nuclear protein [Schistocerca gregaria]
75	Unigene27963_All	endoplasmin [Locusta migratoria]
76	CL2032.Contig1_All	pyruvate carboxylase [Glossina morsitans morsitans]
76	CL2032.Contig4_All	
76	CL2032.Contig3_All	
77	CL12061.Contig1_All	lysosomal alpha-mannosidase [Culex quinquefasciatus] >gi|167879595|gb|EDS42978.1| lysosomal alpha-mannosidase [Culex quinquefasciatus]

78	Unigene77688_All	histone h4 [Ciona intestinalis] >gi|51315695|sp|Q27765.3|H4_STYPL RecName: Full=Histone H4 >gi|74929449|sp|Q8I0Y4.3|H4_OIKDI RecName: Full=Histone H4 >gi|7522682|gb|AAB27670.2| H4 histone [Styela plicata] >gi|26800902|emb|CAD38828.1| histone h4.1 [Oikopleura dioica] >gi|48290307|emb|CAF25048.1| histone H4.2 [Oikopleura dioica] >gi|48290309|emb|CAF25049.1| histone H4.3 [Oikopleura dioica] >gi|48290311|emb|CAF25050.1| histone H4.4 [Oikopleura dioica] >gi|48290313|emb|CAF25051.1| histone H4.5 [Oikopleura dioica]
79	Unigene5655_All	acidic lipase [Helicoverpa armigera]
80	Unigene41044_All	GL26145 [Drosophila persimilis] >gi|194115193|gb|EDW37236.1| GL26145 [Drosophila persimilis]
81	CL2519.Contig3_All	PREDICTED: hypoxia up-regulated protein 1-like isoform 2 [Nasonia vitripennis] >gi|345491534|ref|XP_001606217.2| PREDICTED: hypoxia up-regulated protein 1-like isoform 1 [Nasonia vitripennis] >gi|345491536|ref|XP_003426635.1| PREDICTED: hypoxia up-regulated protein 1-like isoform 3 [Nasonia vitripennis]
82	Unigene11912_All	PREDICTED: staphylococcal nuclease domain-containing protein 1-like [Strongylocentrotus purpuratus]
83	Unigene26392_All	PREDICTED: ubiquitin-like modifier-activating enzyme 1-like [Megachile rotundata]
84	Unigene12562_All	40S ribosomal protein S19, putative [Pediculus humanus corporis] >gi|212517468|gb|EEB19356.1| 40S ribosomal protein S19, putative [Pediculus humanus corporis]
85	Unigene832_All	PREDICTED: polyadenylate-binding protein 1-like isoform 1 [Bombus terrestris]
86	CL9831.Contig1_All	venom protein Ci-80a [Chelonus inanitus]
87	CL9775.Contig1_All	hypothetical protein TcasGA2_TC014680 [Tribolium castaneum]
88	Unigene2780_All	hypothetical protein AND_09543 [Anopheles darlingi]
89	Unigene57231_All	calreticulin [Schistocerca gregaria]

90	CL508.Contig5_All	elongation factor 1-alpha, somatic form [Xenopus laevis] >gi|119132|sp|P13549.1|EF1A0_XENLA RecName: Full=Elongation factor 1-alpha, somatic form; Short=EF-1-alpha-S >gi|64655|emb|CAA39027.1| elongation factor 1-alpha [Xenopus laevis] >gi|214111|gb|AAB00075.1| elongation factor 1-alpha chain [Xenopus laevis] >gi|27735380|gb|AAH41196.1| Eef1a-s protein [Xenopus laevis] >gi|27882620|gb|AAH43843.1| Eef1a-s protein [Xenopus laevis]
91	Unigene12815_All	ribosomal protein S3 [Culex quinquefasciatus] >gi|290349644|dbj|BAI77930.1| ribosomal protein S3 [Culex quinquefasciatus]
92	Unigene71219_All	unnamed protein product [Homo sapiens]
93	CL4203.Contig2_All	GJ14930 [Drosophila virilis] >gi|194147720|gb|EDW63418.1| GJ14930 [Drosophila virilis]
94	CL14985.Contig1_All	superoxide dismutase [Schistocerca gregaria]
95	Unigene87581_All	hypothetical protein SINV_05262 [Solenopsis invicta]
96	Unigene10465_All	annexin IX [Chortoicetes terminifera]
97	CL6511.Contig2_All	proteinase inhibitor serpin, partial [Locusta migratoria]
97	CL6511.Contig4_All	
97	CL6511.Contig5_All	
98	Unigene33040_All	Cys protease
99	CL2438.Contig1_All	heat shock protein 20.5 [Locusta migratoria]
100	Unigene2546_All	60S acidic ribosomal protein P0 [Blaptica dubia]
101	Unigene2706_All	S14e ribosomal protein [Dascillus cervinus]
102	CL5764.Contig2_All	cuticular protein RR-1 motif 46 precursor [Bombyx mori] >gi|90704836|dbj|BAE92300.1| cuticle protein [Bombyx mori]
102	CL5764.Contig3_All	
103	CL1890.Contig1_All	hypothetical protein SINV_16494 [Solenopsis invicta]
103	CL1890.Contig2_All	
103	CL1890.Contig3_All	
103	CL1890.Contig4_All	
104	Unigene35237_All	isocitrate dehydrogenase [Papilio xuthus]
105	Unigene35277_All	PREDICTED: argininosuccinate synthase [Saimiri boliviensis boliviensis]
106	Unigene19746_All	RecName: Full=40S ribosomal protein S3a >gi|57869784|gb|AAW57773.1| Parcxpwex01 [Periplaneta americana]
107	CL8055.Contig1_All	translation elongation factor-1 gamma [Locusta migratoria]

108	CL16364.Contig1_All	hypothetical protein TcasGA2_TC003450 [Tribolium castaneum]
109	CL3079.Contig1_All	hexamerin storage protein 3 [Romalea microptera]
110	CL2542.Contig2_All	acid methyltransferase, putative [Ixodes scapularis] >gi|215494165|gb|EEC03806.1| acid methyltransferase, putative [Ixodes scapularis]
111	Unigene27669_All	PREDICTED: T-complex protein 1 subunit gamma-like [Megachile rotundata]
112	Unigene54198_All	-
113	CL15561.Contig1_All	hypothetical protein SINV_12532 [Solenopsis invicta]
113	CL15561.Contig2_All	
114	CL10618.Contig1_All	hypothetical protein KGM_21424 [Danaus plexippus]
114	CL10618.Contig2_All	
115	Unigene42214_All	Heat shock 70 kDa protein cognate 5 [Acromyrmex echinatior]
116	CL15839.Contig1_All	juvenile hormone binding protein [Locusta migratoria]
117	Unigene27861_All	hypothetical protein DAPPUDRAFT_98603 [Daphnia pulex]
118	Unigene34926_All	ribophorin [Danaus plexippus]
119	CL15798.Contig1_All	PREDICTED: nucleosome assembly protein 1-like 4-like [Apis florea]
120	Unigene25922_All	Heat shock 70 kDa protein 4L [Camponotus floridanus]
121	Unigene40379_All	PREDICTED: similar to chaperonin [Tribolium castaneum] >gi|270002664|gb|EEZ99111.1| hypothetical protein TcasGA2_TC005004 [Tribolium castaneum]
122	Unigene27511_All	ribosomal protein L23 [Lysiphlebus testaceipes]
123	Unigene25708_All	NADPH-specific isocitrate dehydrogenase [Danaus plexippus]
124	Unigene19872_All	angiotensin converting enzyme, partial [Locusta migratoria]
125	Unigene41613_All	PREDICTED: transitional endoplasmic reticulum ATPase TER94-like [Bombus terrestris]
126	Unigene72549_All	Vitellogenic carboxypeptidase [Camponotus floridanus]
127	Unigene49127_All	cytochrome P450 [Locusta migratoria manilensis]
128	Unigene19250_All	ATPase [Homo sapiens]
129	CL810.Contig2_All	hypothetical protein EAI_13116 [Harpegnathos saltator]
130	Unigene42791_All	prohibitin protein WPH [Bombyx mori] >gi|87248645|gb|ABD36375.1| prohibitin protein WPH [Bombyx mori]
131	Unigene12420_All	enoyl-CoA hydratase, partial [Schistocerca gregaria]

132	Unigene41443_All	fasciclin-like protein [Gryllus firmus]
133	Unigene57357_All	mitochondrial voltage-dependent anion channel [Locusta migratoria]
134	Unigene34904_All	glutathione S-transferase sigma 3 [Locusta migratoria]
135	CL2563.Contig1_All	PREDICTED: hydroxysteroid dehydrogenase-like protein 2-like isoform 2 [Gallus gallus]
136	Unigene86782_All	-
137	CL2563.Contig2_All	PREDICTED: hydroxysteroid dehydrogenase-like protein 2-like isoform 2 [Oryzias latipes]
138	Unigene55585_All	triosephosphate isomerase [Blattella germanica]
139	Unigene72442_All	twinstar, partial [Spodoptera frugiperda]
140	Unigene65251_All	PREDICTED: peroxiredoxin 1-like [Apis florea]
141	CL13717.Contig1_All	hypothetical protein DAPPUDRAFT_303199 [Daphnia pulex]
142	Unigene2760_All	S2e ribosomal protein [Meladema coriacea]
143	Unigene12634_All	hypothetical protein AND_01236 [Anopheles darlingi]
144	CL12854.Contig3_All	GD15828 [Drosophila simulans] >gi|194204351|gb|EDX17927.1| GD15828 [Drosophila simulans]
145	Unigene1982_All	clathrin heavy chain [Acheta domesticus]
146	Unigene9341_All	hexamerin storage protein 3 [Romalea microptera]
147	Unigene35310_All	14-3-3 protein epsilon [Schistocerca gregaria]
148	CL6336.Contig1_All	unknown [Dendroctonus ponderosae]
149	Unigene34530_All	hexamerin storage protein 3 [Romalea microptera]
150	CL3079.Contig4_All	hexamerin-like protein 4 [Locusta migratoria]
151	Unigene8431_All	AGAP010155-PA [Anopheles gambiae str. PEST] >gi|157014251|gb|EAA13856.5| AGAP010155-PA [Anopheles gambiae str. PEST]
152	CL16668.Contig1_All	PREDICTED: similar to GST [Tribolium castaneum] >gi|270010123|gb|EFA06571.1| hypothetical protein TcasGA2_TC009482 [Tribolium castaneum]
153	CL3272.Contig1_All	KH domain-containing protein, variant [Loa loa]
153	CL3272.Contig4_All	
154	CL5345.Contig1_All	PREDICTED: hypothetical protein LOC100119498 [Nasonia vitripennis]
155	CL7788.Contig2_All	Elongation factor 1-delta [Acromyrmex echinatior]
155	CL7788.Contig4_All	
156	Unigene72156_All	PREDICTED: profilin-like, partial [Apis mellifera]
157	Unigene2635_All	ribosomal protein S10 [Helicoverpa armigera]
158	CL12410.Contig2_All	NADP-dependent malic enzyme-like protein [Locusta migratoria]
159	Unigene18790_All	PREDICTED: chitinase-like protein Idgf4-like [Apis mellifera]
160	CL9358.Contig1_All	beta-N-acetylglucosaminidase [Locusta migratoria]

160	CL9358.Contig2_All	
161	CL556.Contig3_All	GE15370 [Drosophila yakuba] >gi|194189387|gb|EDX02971.1| GE15370 [Drosophila yakuba]
162	CL1990.Contig1_All	PREDICTED: histone H1-like [Nasonia vitripennis]
163	CL5748.Contig1_All	putative kinectin 1 [Danaus plexippus]
163	CL5748.Contig3_All	
164	Unigene65062_All	Hsjcib isoform5 [Hodotermopsis sjostedti]
165	Unigene7395_All	ubiquitin carboxy-terminal hydrolase [Papilio xuthus]
166	CL11771.Contig1_All	hypothetical protein SINV_01114 [Solenopsis invicta]
167	Unigene34902_All	glutathione S-transferase sigma 1 [Locusta migratoria]
168	Unigene57537_All	putative translationally controlled tumor protein [Graphocephala atropunctata]
169	CL1990.Contig2_All	PREDICTED: histone H1-like [Nasonia vitripennis]
170	CL11694.Contig2_All	serine proteinase inhibitor, putative [Pediculus humanus corporis] >gi|212511271|gb|EEB14288.1| serine proteinase inhibitor, putative [Pediculus humanus corporis]
171	Unigene50319_All	chaperonin subunit 6a zeta [Bombyx mori] >gi|87248083|gb|ABD36094.1| chaperonin subunit 6a zeta [Bombyx mori]
172	Unigene12848_All	hypothetical protein SINV_13670 [Solenopsis invicta]
173	Unigene72473_All	elongation factor 1 beta [Antheraea yamamai]
174	Unigene17156_All	GI18726 [Drosophila mojavensis] >gi|193911201|gb|EDW10068.1| GI18726 [Drosophila mojavensis]
175	CL2584.Contig2_All	GD20338 [Drosophila simulans] >gi|194199221|gb|EDX12797.1| GD20338 [Drosophila simulans]
176	Unigene35414_All	GD12262 [Drosophila simulans] >gi|194197530|gb|EDX11106.1| GD12262 [Drosophila simulans]

177	Unigene56242_All	alpha-Tubulin at 84B [Drosophila melanogaster] >gi|125777817|ref|XP_001359737.1| GA15128 [Drosophila pseudoobscura pseudoobscura] >gi|194741456|ref|XP_001953205.1| GF17649 [Drosophila ananassae] >gi|194899185|ref|XP_001979141.1| GG13808 [Drosophila erecta] >gi|195036708|ref|XP_001989810.1| GH19001 [Drosophila grimshawi] >gi|195109779|ref|XP_001999459.1| GI23057 [Drosophila mojavensis] >gi|195344131|ref|XP_002038642.1| GM10931 [Drosophila sechellia] >gi|195391994|ref|XP_002054644.1| GJ24568 [Drosophila virilis] >gi|195454357|ref|XP_002074205.1| GK12743 [Drosophila willistoni] >gi|195498862|ref|XP_002096707.1| alphaTub84B [Drosophila yakuba] >gi|195568870|ref|XP_002102435.1| GD19909 [Drosophila simulans] >gi|135396|sp|P06603.1|TBA1_DROME RecName: Full=Tubulin alpha-1 chain >gi|158731|gb|AAA28985.1| alpha-tubulin 1 [Drosophila melanogaster] >gi|7298859|gb|AAF54067.1| alpha-Tubulin at 84B [Drosophila melanogaster] >gi|46409240|gb|AAS93777.1| AT25469p [Drosophila melanogaster] >gi|54639487|gb|EAL28889.1| GA15128 [Drosophila pseudoobscura pseudoobscura] >gi|190626264|gb|EDV41788.1| GF17649 [Drosophila ananassae] >gi|190650844|gb|EDV48099.1| GG13808 [Drosophila erecta] >gi|193894006|gb|EDV92872.1| GH19001 [Drosophila grimshawi] >gi|193916053|gb|EDW14920.1| GI23057 [Drosophila mojavensis] >gi|194133663|gb|EDW55179.1| GM10931 [Drosophila sechellia] >gi|194152730|gb|EDW68164.1| GJ24568 [Drosophila virilis] >gi|194170290|gb|EDW85191.1| GK12743 [Drosophila willistoni] >gi|194182808|gb|EDW96419.1| alphaTub84B [Drosophila yakuba] >gi|194198362|gb|EDX11938.1| GD19909 [Drosophila simulans] >gi|392601492|gb|AFM80098.1| alpha-tubulin, partial [Sphyracephala beccarii] >gi|392601502|gb|AFM80103.1| alpha-tubulin, partial [Teleopsis quinqueguttata] >gi|392601514|gb|AFM80109.1| alpha-tubulin, partial [Teleopsis dalmanni]
178	CL10078.Contig1_All	annexin IX [Chortoicetes terminifera]
179	CL10148.Contig2_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212506796|gb|EEB10898.1| conserved hypothetical protein [Pediculus humanus corporis]
180	Unigene48218_All	60S acidic ribosomal protein P2 [Plutella xylostella]
181	Unigene2654_All	hypothetical protein [Bactrocera oleae]
182	CL1512.Contig1_All	RNA m5u methyltransferase, partial [Papilio polytes]
183	Unigene49451_All	hypothetical protein AND_22168 [Anopheles darlingi]

184	Unigene27862_All	26S protease regulatory subunit 6A, putative [Pediculus humanus corporis] >gi|212506177|gb|EEB10468.1| 26S protease regulatory subunit 6A, putative [Pediculus humanus corporis]
185	Unigene50433_All	PREDICTED: similar to inter-alpha-trypsin inhibitor family heavy chain-related protein [Tribolium castaneum]
186	Unigene50476_All	proteasome subunit alpha type, putative [Pediculus humanus corporis] >gi|212505501|gb|EEB09941.1| proteasome subunit alpha type, putative [Pediculus humanus corporis]
187	CL8674.Contig3_All	PREDICTED: importin-5 [Megachile rotundata]
188	CL3599.Contig2_All	PREDICTED: probable ATP-dependent RNA helicase DDX17-like [Bombus impatiens]
189	Unigene19859_All	proteasome zeta subunit, partial [Schistocerca gregaria]
190	Unigene55386_All	Ras-related protein Rab-7a [Salmo salar]
191	CL2135.Contig1_All	Spectrin alpha chain, putative [Pediculus humanus corporis] >gi|212515067|gb|EEB17271.1| Spectrin alpha chain, putative [Pediculus humanus corporis]
192	CL2650.Contig2_All	hypothetical protein SINV_06451 [Solenopsis invicta]
193	CL11759.Contig1_All	GL16409 [Drosophila persimilis] >gi|194105062|gb|EDW27105.1| GL16409 [Drosophila persimilis]
194	Unigene70331_All	GA22228 [Drosophila pseudoobscura pseudoobscura] >gi|198145252|gb|EDY71956.1| GA22228 [Drosophila pseudoobscura pseudoobscura]
195	Unigene40395_All	RecName: Full=Fatty acid-binding protein, muscle; AltName: Full=M-FABP >gi|546690|gb|AAB30739.1| M-FABP [Locusta migratoria]
196	Unigene56022_All	acidic ribosomal protein P1 [Culex quinquefasciatus] >gi|167871355|gb|EDS34738.1| acidic ribosomal protein P1 [Culex quinquefasciatus]
197	Unigene40617_All	unknown [Dendroctonus ponderosae]
198	Unigene42223_All	putative ribosomal protein S4e [Graphocephala atropunctata]
199	CL2074.Contig5_All	juvenile hormone epoxide hydrolase-like protein 5 precursor [Tribolium castaneum] >gi|269093690|dbj|BAI49690.1| juvenile hormone epoxide hydrolase-like protein 5 [Tribolium castaneum]
200	CL6335.Contig1_All	PREDICTED: short/branched chain specific acyl-CoA dehydrogenase, mitochondrial-like [Megachile rotundata]

201	Unigene62343_All	PREDICTED: eukaryotic translation initiation factor 5A-like [Apis florea]
202	Unigene26648_All	60S ribosomal protein L30, putative [Pediculus humanus corporis] >gi|212508604|gb|EEB12237.1| 60S ribosomal protein L30, putative [Pediculus humanus corporis]
203	CL2789.Contig1_All	fmr [Gryllus bimaculatus]
203	CL2789.Contig4_All	
203	CL4546.Contig1_All	
204	CL17068.Contig4_All	PREDICTED: similar to mapmodulin-like protein [Tribolium castaneum]
205	CL3196.Contig2_All	RecName: Full=Heterogeneous nuclear ribonucleoprotein A1, A2/B1 homolog >gi|10107|emb|CAA38481.1| mammalian A1, A2 /B1 hnRNP homologue [Schistocerca americana]
205	Unigene32141_All	
205	CL3196.Contig7_All	
206	CL6318.Contig2_All	PREDICTED: CAD protein-like, partial [Strongylocentrotus purpuratus]
207	CL4671.Contig4_All	unnamed protein product [Homo sapiens]
208	CL1081.Contig6_All	peptidyl-prolyl cis-trans isomerase, partial [Schistocerca gregaria]
209	CL1420.Contig1_All	pyruvate kinase [Helicoverpa armigera]
209	CL1420.Contig2_All	
210	Unigene48131_All	hypothetical protein AND_22292 [Anopheles darlingi]
211	Unigene19740_All	GE19075 [Drosophila yakuba] >gi|194175473|gb|EDW89084.1| GE19075 [Drosophila yakuba]
212	CL2667.Contig1_All	PREDICTED: similar to aldehyde dehydrogenase [Tribolium castaneum] >gi|270000922|gb|EEZ97369.1| hypothetical protein TcasGA2_TC011192 [Tribolium castaneum]
213	Unigene98121_All	PREDICTED: similar to GST [Tribolium castaneum] >gi|270010123|gb|EFA06571.1| hypothetical protein TcasGA2_TC009482 [Tribolium castaneum]
214	CL17951.Contig2_All	RecName: Full=Heterogeneous nuclear ribonucleoprotein A1, A2/B1 homolog >gi|10107|emb|CAA38481.1| mammalian A1, A2 /B1 hnRNP homologue [Schistocerca americana]
215	Unigene25843_All	AAEL002861-PB [Aedes aegypti] >gi|108881660|gb|EAT45885.1| AAEL002861-PA [Aedes aegypti]
216	Unigene63706_All	putative Sjogren syndrome antigen B variant 2 [Danaus plexippus]
217	Unigene34105_All	hypothetical protein BRAFLDRAFT_121463 [Branchiostoma floridae] >gi|229276530|gb|EEN47337.1| hypothetical protein BRAFLDRAFT_121463 [Branchiostoma floridae]

218	CL3356.Contig1_All	hypothetical protein DAPPUDRAFT_248000 [Daphnia pulex]
219	Unigene42234_All	UMP synthase [Drosophila melanogaster]
220	CL12258.Contig1_All	PREDICTED: 3-ketoacyl-CoA thiolase, mitochondrial-like [Acyrthosiphon pisum]
221	Unigene50497_All	GA25753 [Drosophila pseudoobscura pseudoobscura] >gi|198138372|gb|EDY70084.1| GA25753 [Drosophila pseudoobscura pseudoobscura]
222	CL7487.Contig1_All	glycinamide ribotide transformylase, partial [Delia radicum]
222	CL7487.Contig2_All	
222	CL7487.Contig5_All	
223	Unigene64920_All	similar to Drosophila melanogaster Rab1, partial [Drosophila yakuba]
224	Unigene20395_All	PREDICTED: eukaryotic translation initiation factor 4B isoform 14 [Canis lupus familiaris]
225	Unigene72662_All	GTP binding protein [Danaus plexippus]
226	Unigene48130_All	ATP-dependent RNA helicase belle [Tribolium castaneum] >gi|270008148|gb|EFA04596.1| belle [Tribolium castaneum]
227	Unigene42270_All	H(+)-ATPase B subunit [Spodoptera littoralis]
228	Unigene20306_All	thioredoxin-2, putative [Pediculus humanus corporis] >gi|212508405|gb|EEB12117.1| thioredoxin-2, putative [Pediculus humanus corporis]
229	Unigene22452_All	hypothetical protein TcasGA2_TC014157 [Tribolium castaneum]
230	CL3557.Contig1_All	PREDICTED: similar to succinyl-CoA synthetase small subunit, putative isoform 1 [Tribolium castaneum] >gi|91076014|ref|XP_975865.1| PREDICTED: similar to succinyl-CoA synthetase small subunit, putative isoform 2 [Tribolium castaneum] >gi|270014681|gb|EFA11129.1| hypothetical protein TcasGA2_TC004730 [Tribolium castaneum]
231	Unigene20337_All	GE25998 [Drosophila yakuba] >gi|194175206|gb|EDW88817.1| GE25998 [Drosophila yakuba]
232	Unigene49381_All	NAD(P) transhydrogenase, partial [Ostrea edulis]
233	Unigene70282_All	40S ribosomal protein S16 [Aplysia californica]
234	Unigene33743_All	putative acyl-CoA dehydrogenase [Culex pipiens pipiens]
235	Unigene2974_All	PREDICTED: alcohol dehydrogenase class-3-like [Nasonia vitripennis]
236	CL16834.Contig2_All	probable 3-hydroxyacyl-CoA dehydrogenase [Trichinella spiralis] >gi|316976705|gb|EFV59939.1| probable 3-hydroxyacyl-CoA dehydrogenase [Trichinella spiralis]
237	Unigene20235_All	fk506-binding protein 1 [Papilio xuthus]

238	Unigene18259_All	hypothetical protein AND_05520 [Anopheles darlingi]
239	CL2939.Contig2_All	Proteasome subunit alpha type-6 [Acromyrmex echinatior]
240	CL3294.Contig10_All	Programmed cell death 6-interacting protein [Camponotus floridanus]
241	Unigene27387_All	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2-like [Nasonia vitripennis]
242	Unigene18777_All	PREDICTED: 60S ribosomal protein L9-like [Megachile rotundata]
243	CL10739.Contig2_All	receptor for activated protein kinase C-like [Blattella germanica]
244	CL8825.Contig1_All	proteasome (prosome, macropain) 26S subunit, ATPase 2, isoform CRA_a [Rattus norvegicus]
245	CL17826.Contig1_All	PREDICTED: aconitate hydratase, mitochondrial-like [Megachile rotundata]
246	Unigene35217_All	PREDICTED: similar to serine protease [Tribolium castaneum]
247	Unigene62934_All	ribosomal protein L23A [Danaus plexippus]
248	CL14543.Contig1_All	hypothetical protein CAPTEDRAFT_79838, partial [Capitella teleta]
249	CL8082.Contig1_All	sn-glycerol-3-phosphate dehydrogenase isoform 3a [Locusta migratoria] >gi|4163995|gb|AAD05302.1| sn-glycerol-3-phosphate dehydrogenase isoform 3b [Locusta migratoria]
249	Unigene17917_All	
250	CL8936.Contig3_All	proteinase inhibitor serpin, partial [Locusta migratoria]
251	Unigene42500_All	proliferating cell nuclear antigen [Aedes albopictus]
252	CL11520.Contig1_All	-
253	Unigene12372_All	PREDICTED: ran-specific GTPase-activating protein-like [Megachile rotundata]
254	Unigene50311_All	PREDICTED: t-complex protein 1 subunit alpha-like isoform 1 [Apis mellifera]
255	Unigene57871_All	GM25064 [Drosophila sechellia] >gi|194118683|gb|EDW40726.1| GM25064 [Drosophila sechellia]
256	Unigene18707_All	PREDICTED: polyubiquitin-A-like isoform 1 [Apis mellifera]
256	Unigene54664_All	
256	CL15865.Contig3_All	
256	Unigene54672_All	
256	CL15865.Contig1_All	
256	Unigene54670_All	
256	Unigene54667_All	
256	Unigene54666_All	

256	CL15865.Contig2_All	
256	CL15865.Contig4_All	
257	Unigene35295_All	aspartate aminotransferase [Coptotermes formosanus]
258	CL7511.Contig1_All	Double-stranded RNA-specific editase Adar [Camponotus floridanus]
259	Unigene2336_All	PREDICTED: vigilin-like, partial [Apis mellifera]
260	Unigene1548_All	hypothetical protein BRAFLDRAFT_264030 [Branchiostoma floridae] >gi|229275528|gb|EEN46347.1| hypothetical protein BRAFLDRAFT_264030 [Branchiostoma floridae]
260	Unigene55083_All	
261	Unigene18228_All	TPA_exp: Rab5-related subfamily protein 480 [Amblyomma variegatum]
262	CL15952.Contig2_All	proteinase inhibitor serpin, partial [Locusta migratoria]
263	Unigene27367_All	-
264	Unigene50488_All	putative trifunctional hydroxyacyl-coenzyme A dehydrogenase/3-ketoacyl-coenzyme A thiolase/enoyl-coenzyme A hydratase, beta subunit [Maconellicoccus hirsutus]
265	Unigene41697_All	Spectrin alpha chain, putative [Pediculus humanus corporis] >gi|212515067|gb|EEB17271.1| Spectrin alpha chain, putative [Pediculus humanus corporis]
266	Unigene27816_All	phosphatidylethanolamine-binding protein 2 [Culex quinquefasciatus] >gi|167870076|gb|EDS33459.1| phosphatidylethanolamine-binding protein 2 [Culex quinquefasciatus]
267	Unigene57757_All	PREDICTED: hypothetical protein LOC100679065 [Nasonia vitripennis]
268	CL193.Contig4_All	Lysosomal Pro-X carboxypeptidase, putative [Pediculus humanus corporis] >gi|212507369|gb|EEB11325.1| Lysosomal Pro-X carboxypeptidase, putative [Pediculus humanus corporis]
269	Unigene50428_All	hypothetical small protein [Lygus lineolaris]
270	Unigene55918_All	GH15313 [Drosophila grimshawi] >gi|193892353|gb|EDV91219.1| GH15313 [Drosophila grimshawi]
271	CL3196.Contig8_All	Nuclear polyadenylated RNA-binding protein, putative [Pediculus humanus corporis] >gi|212506345|gb|EEB10588.1| Nuclear polyadenylated RNA-binding protein, putative [Pediculus humanus corporis]
272	CL9681.Contig1_All	hypothetical protein AND_04792 [Anopheles darlingi]
273	CL5082.Contig2_All	heat shock protein 20 [Schistocerca gregaria]
274	CL7027.Contig3_All	AAEL017368-PA [Aedes aegypti]
275	Unigene33112_All	PREDICTED: hypothetical protein LOC100123404 [Nasonia

		vitripennis]
276	Unigene72546_All	PREDICTED: threonyl-tRNA synthetase, cytoplasmic-like [Acyrthosiphon pisum]
277	CL9587.Contig2_All	hexamerin-like protein 3 [Locusta migratoria]
278	Unigene20423_All	PREDICTED: 10 kDa heat shock protein, mitochondrial-like [Nasonia vitripennis]
279	CL8224.Contig1_All	PREDICTED: similar to putative esterase [Tribolium castaneum] >gi|270008700|gb|EFA05148.1| hypothetical protein TcasGA2_TC015265 [Tribolium castaneum]
280	CL150.Contig5_All	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP4-like [Megachile rotundata]
281	Unigene33568_All	protein singed, putative [Pediculus humanus corporis] >gi|212506942|gb|EEB11002.1| protein singed, putative [Pediculus humanus corporis]
282	CL4916.Contig2_All	proteasome non-ATPase regulatory subunit [Periplaneta americana]
282	CL4916.Contig3_All	
283	CL8298.Contig1_All	AP-1 complex subunit beta-1 [Harpegnathos saltator]
284	CL14391.Contig1_All	heat shock protein 20.6 [Locusta migratoria]
285	Unigene27612_All	heat shock protein [Aedes aegypti] >gi|108884463|gb|EAT48688.1| AAEL000301-PA [Aedes aegypti]
286	CL9375.Contig1_All	PREDICTED: probable aminopeptidase NPEPL1-like, partial [Taeniopygia guttata]
287	Unigene50145_All	40S ribosomal protein S20, putative [Pediculus humanus corporis] >gi|212517174|gb|EEB19104.1| 40S ribosomal protein S20, putative [Pediculus humanus corporis]
288	Unigene25288_All	Selenide, water dikinase [Harpegnathos saltator]
289	CL16177.Contig2_All	ATP-dependent RNA helicase p62 [Tribolium castaneum]
290	Unigene20416_All	putative transaldolase [Maconellicoccus hirsutus]
291	Unigene2533_All	PREDICTED: proteasome subunit alpha type-2-like [Nasonia vitripennis]
292	Unigene7382_All	PREDICTED: putative phospholipase B-like 2-like, partial [Ciona intestinalis]
293	Unigene72701_All	PREDICTED: similar to phosphoenolpyruvate carboxykinase isoform 2 [Tribolium castaneum] >gi|270009775|gb|EFA06223.1| hypothetical protein TcasGA2_TC009072 [Tribolium castaneum]

294	Unigene63619_All	PREDICTED: electron transfer flavoprotein subunit alpha, mitochondrial-like [Pan paniscus] >gi|397496389|ref|XP_003819020.1| PREDICTED: electron transfer flavoprotein subunit alpha, mitochondrial-like [Pan paniscus] >gi|426379884|ref|XP_004056617.1| PREDICTED: electron transfer flavoprotein subunit alpha, mitochondrial-like [Gorilla gorilla gorilla]
295	Unigene34832_All	PREDICTED: hypothetical protein LOC408406 [Apis mellifera]
296	CL5159.Contig3_All	PREDICTED: peroxidase-like [Megachile rotundata]
297	CL1235.Contig1_All	6-phosphogluconate dehydrogenase, decarboxylating [Tupaia chinensis]
298	Unigene72620_All	AGAP011131-PA [Anopheles gambiae str. PEST] >gi|116131730|gb|EAA05107.3| AGAP011131-PA [Anopheles gambiae str. PEST]
299	Unigene63037_All	Neutral alpha-glucosidase AB precursor, putative [Pediculus humanus corporis] >gi|212515157|gb|EEB17338.1| Neutral alpha-glucosidase AB precursor, putative [Pediculus humanus corporis]
300	CL7749.Contig2_All	glucosamine phosphate isomerase [Acheta domesticus]
301	CL568.Contig1_All	4-aminobutyrate aminotransferase, mitochondrial [Culex quinquefasciatus] >gi|167868572|gb|EDS31955.1| 4-aminobutyrate aminotransferase, mitochondrial [Culex quinquefasciatus]
302	Unigene42555_All	proteasome subunit alpha [Schistocerca gregaria]
303	CL3485.Contig1_All	hypothetical protein SINV_11930 [Solenopsis invicta]
303	CL3485.Contig2_All	
304	Unigene2746_All	hypothetical protein AND_07330 [Anopheles darlingi]
305	Unigene63792_All	ubiquitin carboxyl-terminal hydrolase 5 [Danaus plexippus]
306	CL11408.Contig1_All	PREDICTED: retinal dehydrogenase 1-like isoform 1 [Apis mellifera]
307	Unigene64943_All	putative disulfide-isomerase, partial [Ochlerotatus triseriatus]
308	CL1512.Contig2_All	RNA m5u methyltransferase, partial [Papilio polytes]
309	CL3719.Contig3_All	PREDICTED: glucose dehydrogenase [acceptor]-like [Acyrthosiphon pisum]
310	Unigene64634_All	purine biosynthesis protein 6 [Papilio xuthus]
311	CL2541.Contig2_All	Adenosine kinase 2 [Camponotus floridanus]
311	CL2541.Contig3_All	
312	CL13284.Contig1_All	Serine/threonine-protein kinase OSR1 [Acromyrmex echinatior]
312	CL13284.Contig4_All	

313	CL11140.Contig1_All	PREDICTED: similar to eukaryotic translation initiation factor 3, theta subunit [Tribolium castaneum] >gi|270013675|gb|EFA10123.1| hypothetical protein TcasGA2_TC012303 [Tribolium castaneum]
314	Unigene27593_All	ribosomal protein L11 [Triatoma infestans]
315	Unigene64823_All	heat shock protein 60 [Schistocerca gregaria]
316	Unigene10898_All	PREDICTED: lamin Dm0-like isoform 1 [Nasonia vitripennis]
317	Unigene72334_All	membrane-associated progesterone receptor component, putative [Pediculus humanus corporis] >gi|212507012|gb|EEB11058.1| membrane-associated progesterone receptor component, putative [Pediculus humanus corporis]
318	CL14219.Contig1_All	putative AATS-ALA protein [Triops longicaudatus]
319	Unigene35367_All	PREDICTED: prostaglandin reductase 1-like [Nasonia vitripennis]
320	CL14554.Contig1_All	PREDICTED: LOW QUALITY PROTEIN: prostatic acid phosphatase-like [Apis florea]
321	CL15340.Contig1_All	transketolase [Aedes aegypti] >gi|108879967|gb|EAT44192.1| AAEL004434-PA [Aedes aegypti]
322	Unigene12632_All	PREDICTED: long-chain fatty acid transport protein 4-like isoform 2 [Nasonia vitripennis] >gi|345493605|ref|XP_001603871.2| PREDICTED: long-chain fatty acid transport protein 4-like isoform 1 [Nasonia vitripennis]
323	Unigene57566_All	calponin/transgelin [Papilio xuthus]
324	CL4132.Contig1_All	hypothetical protein SINV_00874 [Solenopsis invicta]
324	CL4132.Contig2_All	
324	CL4132.Contig3_All	
325	Unigene50216_All	glutathione S-transferase sigma 3 [Locusta migratoria]
326	CL11015.Contig1_All	GH27411p [Drosophila melanogaster]
327	Unigene49991_All	vesicle amine transport protein [Danaus plexippus]
328	Unigene100401_All	hypothetical protein IscW_ISCW010888 [Ixodes scapularis] >gi|215504615|gb|EEC14109.1| hypothetical protein IscW_ISCW010888 [Ixodes scapularis]
329	CL5772.Contig1_All	Apoptosis regulator BAX [Cricetulus griseus]
330	Unigene49955_All	Signal peptidase complex catalytic subunit SEC11C [Camponotus floridanus]
331	CL1532.Contig1_All	hypothetical protein AND_02632 [Anopheles darlingi] >gi|312384065|gb|EFR28884.1| hypothetical protein AND_02633 [Anopheles darlingi]
332	CL12336.Contig1_All	PREDICTED: filaggrin [Callithrix jacchus]

333	Unigene26150_All	eukaryotic translation initiation factor 3 subunit, putative [Pediculus humanus corporis] >gi|212514234|gb|EEB16593.1| eukaryotic translation initiation factor 3 subunit, putative [Pediculus humanus corporis]
334	CL15224.Contig1_All	ubiquilin [Clonorchis sinensis]
334	CL15224.Contig2_All	
335	CL198.Contig5_All	Apolipoprotein D precursor, putative [Pediculus humanus corporis] >gi|212514217|gb|EEB16576.1| Apolipoprotein D precursor, putative [Pediculus humanus corporis]
336	Unigene18760_All	ACYPI010231 [Acyrthosiphon pisum]
337	Unigene3007_All	Ras-related nuclear protein [Priapulus caudatus]
338	CL4316.Contig7_All	translation initiationfactor eIF-4gamma [Homo sapiens]
339	Unigene628_All	putative accessory gland protein [Gryllus pennsylvanicus]
340	CL7191.Contig3_All	eukaryotic translation termination factor 1 [Sus scrofa]
341	Unigene42812_All	Phosphoglycerate mutase 1 [Camponotus floridanus]
342	CL12144.Contig3_All	fatty acid binding protein [Nylanderia nr. pubens LZ-2010] >gi|334262744|gb|AEG74454.1| fatty acid-binding protein [Nylanderia nr. pubens LZ-2011]
343	CL6072.Contig1_All	PREDICTED: probable hydroxyacid-oxoacid transhydrogenase, mitochondrial-like [Bombus impatiens]
343	CL6072.Contig2_All	
344	Unigene27722_All	interleukin enhancer binding factor [Eriocheir sinensis]
345	CL7739.Contig1_All	putative thioredoxin reductase isoform 2 [Danaus plexippus]
345	CL7739.Contig6_All	
345	CL7739.Contig2_All	
345	CL7739.Contig4_All	
346	Unigene17916_All	putative fructose 1,6-bisphosphate [Hottentotta judaicus]
347	Unigene27624_All	-
348	Unigene42324_All	RNA-binding protein 1 [Acromyrmex echinatior]
349	CL2334.Contig1_All	hypothetical protein TRIADDRAFT_62597 [Trichoplax adhaerens] >gi|190578721|gb|EDV18945.1| hypothetical protein TRIADDRAFT_62597 [Trichoplax adhaerens]
350	CL5714.Contig1_All	GH18317 [Drosophila grimshawi] >gi|193894487|gb|EDV93353.1| GH18317 [Drosophila grimshawi]
350	CL5714.Contig2_All	
350	CL5714.Contig6_All	

351	CL10030.Contig2_All	PREDICTED: uncharacterized protein LOC100878109 [Megachile rotundata]
352	CL14240.Contig1_All	Dihydrolipoyl dehydrogenase, putative [Pediculus humanus corporis] >gi|212512144|gb|EEB14971.1| Dihydrolipoyl dehydrogenase, putative [Pediculus humanus corporis]
353	Unigene50237_All	hypotheical protein [Nasutitermes takasagoensis]
354	CL5172.Contig1_All	Endocuticle structural glycoprotein SgAbd-2, putative [Pediculus humanus corporis] >gi|212518331|gb|EEB20084.1| Endocuticle structural glycoprotein SgAbd-2, putative [Pediculus humanus corporis]
355	Unigene27590_All	hypothetical protein DAPPUDRAFT_98603 [Daphnia pulex]
356	CL12144.Contig4_All	MPA13 allergen [Periplaneta americana]
357	Unigene27781_All	-
358	CL6421.Contig2_All	PREDICTED: similar to Cuticular protein 57A CG18066-PA [Tribolium castaneum] >gi|270008726|gb|EFA05174.1| hypothetical protein TcasGA2_TC015304 [Tribolium castaneum]
359	Unigene62745_All	PREDICTED: THO complex subunit 4-like, partial [Sus scrofa]
360	Unigene2491_All	26S proteasome non-ATPase regulatory subunit 3 [Heterocephalus glaber]
361	CL212.Contig4_All	pro-phenoloxidase 1 [Locusta migratoria]
362	Unigene70717_All	-
363	CL12568.Contig1_All	Proliferation-associated protein 2G4 [Harpegnathos saltator]
364	Unigene19778_All	control protein HCTL035 [Eueides isabella] >gi|358443156|gb|AEU11824.1| control protein HCTL035 [Heliconius ismenius] >gi|358443158|gb|AEU11825.1| control protein HCTL035 [Heliconius hecale] >gi|358443160|gb|AEU11826.1| control protein HCTL035 [Heliconius aoede] >gi|358443164|gb|AEU11828.1| control protein HCTL035 [Heliconius doris] >gi|358443170|gb|AEU11831.1| control protein HCTL035 [Heliconius hortense] >gi|358443172|gb|AEU11832.1| control protein HCTL035 [Heliconius hewitsoni] >gi|358443174|gb|AEU11833.1| control protein HCTL035 [Heliconius sara] >gi|358443176|gb|AEU11834.1| control protein HCTL035 [Heliconius demeter] >gi|358443178|gb|AEU11835.1| control protein HCTL035 [Heliconius charithonia]

365	Unigene2954_All	calmodulin-A [Pediculus humanus corporis] >gi|212512858|gb|EEB15542.1| calmodulin-A [Pediculus humanus corporis]
366	Unigene25194_All	High mobility group protein B2, putative [Pediculus humanus corporis] >gi|212505508|gb|EEB09948.1| High mobility group protein B2, putative [Pediculus humanus corporis]
367	CL12144.Contig1_All	MPA13 allergen [Periplaneta americana]
368	CL5735.Contig1_All	PREDICTED: similar to alpha actinin CG4376-PB [Tribolium castaneum]
369	Unigene9016_All	GM17593 [Drosophila sechellia] >gi|194126754|gb|EDW48797.1| GM17593 [Drosophila sechellia]
370	Unigene12930_All	PREDICTED: adenosylhomocysteinase-like [Bombus impatiens]
371	Unigene35257_All	PREDICTED: hypothetical protein LOC100115805 isoform 2 [Nasonia vitripennis] >gi|345494865|ref|XP_001600427.2| PREDICTED: hypothetical protein LOC100115805 isoform 1 [Nasonia vitripennis]
372	Unigene63651_All	nascent-polypeptide-associated complex alpha polypeptide [Ictalurus punctatus]
373	Unigene55519_All	coagulation factor X [Culex quinquefasciatus] >gi|167874734|gb|EDS38117.1| coagulation factor X [Culex quinquefasciatus]
374	Unigene47794_All	PREDICTED: similar to reticulocalbin [Tribolium castaneum] >gi|270006175|gb|EFA02623.1| hypothetical protein TcasGA2_TC008343 [Tribolium castaneum]
375	CL14635.Contig1_All	PREDICTED: lactase-phlorizin hydrolase-like [Saccoglossus kowalevskii]
376	Unigene63417_All	93 kDa serpin [Tenebrio molitor]
377	Unigene57865_All	AGAP000396-PA [Anopheles gambiae str. PEST] >gi|116130529|gb|EAA06406.3| AGAP000396-PA [Anopheles gambiae str. PEST]
378	CL2869.Contig1_All	hypothetical protein SINV_80769 [Solenopsis invicta]
378	CL2869.Contig2_All	
379	Unigene10403_All	PREDICTED: similar to proteasome subunit beta type 5,8 [Tribolium castaneum]
380	Unigene17353_All	AGAP010495-PA [Anopheles gambiae str. PEST] >gi|157016809|gb|EDO64018.1| AGAP010495-PA [Anopheles gambiae str. PEST]
381	Unigene62958_All	putative ribosomal protein S7e [Graphocephala atropunctata]
382	Unigene14590_All	-

383	Unigene2613_All	putative acyl-CoA dehydrogenase [Culex pipiens pipiens]
383	CL3068.Contig2_All	
384	CL1974.Contig12_All	tropomyosin invertebrate [Aedes aegypti] >gi|108881790|gb|EAT46015.1| AAEL002761-PH [Aedes aegypti]
384	CL1974.Contig1_All	
385	Unigene63746_All	GK16843 [Drosophila willistoni] >gi|194158163|gb|EDW73064.1| GK16843 [Drosophila willistoni]
386	Unigene72527_All	hypothetical protein [Locusta migratoria]
387	Unigene27381_All	40S ribosomal protein SA, putative [Pediculus humanus corporis] >gi|212511928|gb|EEB14788.1| 40S ribosomal protein SA, putative [Pediculus humanus corporis]
388	CL1758.Contig10_All	PREDICTED: uncharacterized protein LOC100878501 [Megachile rotundata]
388	CL1758.Contig11_All	
388	CL1758.Contig2_All	
388	CL1758.Contig1_All	
388	CL1758.Contig8_All	
388	CL1758.Contig5_All	
388	CL1758.Contig3_All	
389	Unigene20103_All	PREDICTED: similar to cathepsin D isoform 1 [Tribolium castaneum] >gi|270002651|gb|EEZ99098.1| hypothetical protein TcasGA2_TC004989 [Tribolium castaneum]
390	CL1167.Contig2_All	PREDICTED: zinc finger RNA-binding protein-like isoform 2 [Nasonia vitripennis]
391	Unigene20100_All	putative accessory gland protein [Gryllus bimaculatus]
392	CL1207.Contig7_All	mitochondrial cytochrome c oxidase subunit IV [Locusta migratoria] >gi|453073540|gb|AGG22608.1| mitochondrial cytochrome c oxidase subunit IV [Locusta migratoria]
393	CL2664.Contig1_All	PREDICTED: similar to AGAP006099-PA isoform 2 [Tribolium castaneum] >gi|270004017|gb|EFA00465.1| hypothetical protein TcasGA2_TC003323 [Tribolium castaneum]
394	Unigene32911_All	PREDICTED: UDP-glucose:glycoprotein glucosyltransferase-like, partial [Apis mellifera]
395	Unigene19918_All	translation initiation factor 2 gamma subunit [Locusta migratoria]
396	Unigene20436_All	proteasome subunit beta type 2 [Xenopus borealis]
397	CL6678.Contig1_All	-
397	CL6678.Contig2_All	

398	CL550.Contig1_All	PREDICTED: sorting nexin-6-like [Megachile rotundata]
398	CL550.Contig2_All	
399	CL14275.Contig1_All	hypothetical protein SINV_15529 [Solenopsis invicta]
400	Unigene64837_All	ribosomal protein S18 [Cryptocercus punctulatus]
401	Unigene71890_All	MCM4 minichromosome maintenance deficient 4, mitotin [Schistosoma japonicum]
402	Unigene34822_All	nascent polypeptide-associated complex subunit alpha isoform 1 [Danio rerio]
403	Unigene48383_All	similar to Drosophila melanogaster CG7461, partial [Drosophila yakuba]
404	Unigene34492_All	Proteasome subunit alpha type-4 [Camponotus floridanus]
405	CL16174.Contig1_All	hypothetical protein PANDA_021998 [Ailuropoda melanoleuca]
406	CL3397.Contig1_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167877718|gb|EDS41101.1| conserved hypothetical protein [Culex quinquefasciatus]
406	CL3397.Contig2_All	
407	Unigene35007_All	GK19989 [Drosophila willistoni] >gi|194161810|gb|EDW76711.1| GK19989 [Drosophila willistoni]
408	CL7959.Contig1_All	beta-NAC-like protein [Reticulitermes flavipes]
409	Unigene65135_All	antioxidant enzyme [Gryllotalpa orientalis]
410	CL4032.Contig1_All	Putative fatty acyl-CoA reductase [Acromyrmex echinatior]
410	CL4032.Contig2_All	
411	Unigene78266_All	hypothetical protein CRE_17774 [Caenorhabditis remanei] >gi|308250191|gb|EFO94143.1| hypothetical protein CRE_17774 [Caenorhabditis remanei]
412	Unigene42826_All	PREDICTED: complement component 1 Q subcomponent-binding protein, mitochondrial-like isoform 2 [Bombus terrestris]
413	Unigene72488_All	PREDICTED: KH domain-containing, RNA-binding, signal transduction-associated protein 3-like isoform 2 [Megachile rotundata]
414	CL9940.Contig1_All	60S ribosomal protein L12 [Harpegnathos saltator]
415	Unigene35272_All	hypothetical protein SINV_15871 [Solenopsis invicta]
416	CL5667.Contig1_All	farnesoic acid methyltransferase [Schistocerca gregaria] >gi|359843268|gb|AEV89769.1| farnesoic acid O-methyltransferase [Schistocerca gregaria]
417	Unigene25498_All	hypothetical protein AND_11271 [Anopheles darlingi]
418	Unigene18737_All	PREDICTED: peroxiredoxin-4-like [Meleagris gallopavo]

419	CL2443.Contig1_All	unknown [Dendroctonus ponderosae]
420	CL12041.Contig2_All	Splicing factor, arginine/serine-rich 2 [Acromyrmex echinatior]
421	Unigene56319_All	Prohibitin-2, putative [Pediculus humanus corporis] >gi|212507492|gb|EEB11424.1| Prohibitin-2, putative [Pediculus humanus corporis]
422	Unigene62863_All	PREDICTED: 26S proteasome non-ATPase regulatory subunit 13-like [Nasonia vitripennis]
423	Unigene50168_All	PREDICTED: putative peroxiredoxin-like [Strongylocentrotus purpuratus]
424	Unigene20220_All	PREDICTED: similar to AGAP003501-PA [Tribolium castaneum] >gi|270005165|gb|EFA01613.1| hypothetical protein TcasGA2_TC007182 [Tribolium castaneum]
425	Unigene48158_All	methylmalonate semialdehyde dehydrogenase [Periplaneta americana]
426	Unigene34888_All	PREDICTED: coatomer subunit delta [Taeniopygia guttata]
427	Unigene12519_All	ribosomal protein S28e [Biphyllus lunatus]
428	Unigene10695_All	hypothetical protein KGM_11399 [Danaus plexippus]
429	CL13335.Contig2_All	rCG43497, isoform CRA_a [Rattus norvegicus]
430	Unigene41123_All	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis), isoform CRA_c [Homo sapiens]
431	CL8176.Contig1_All	putative polypyrimidine tract binding protein [Danaus plexippus]
431	CL8176.Contig3_All	
431	CL8176.Contig5_All	
431	CL8176.Contig2_All	
432	CL11560.Contig1_All	PREDICTED: peroxisomal multifunctional enzyme type 2-like, partial [Apis mellifera]
433	CL889.Contig6_All	histone H3 [Aedes aegypti] >gi|108880810|gb|EAT45035.1| AAEL003685-PA, partial [Aedes aegypti]
434	Unigene65006_All	V-ATPase subunit E, partial [Locusta migratoria]
435	Unigene42572_All	Ecdysteroid-regulated 16 kDa protein [Acromyrmex echinatior]
436	Unigene27615_All	PREDICTED: pontin protein isoform 1 [Apis mellifera]
437	Unigene34880_All	prolyl endopeptidase [Papilio xuthus]
438	CL1856.Contig1_All	hypothetical protein SINV_06119 [Solenopsis invicta]
439	Unigene26472_All	methylthioadenosine phosphorylase, isoform CRA_a [Homo sapiens]
440	Unigene20248_All	PREDICTED: hypothetical protein LOC100679865 [Nasonia vitripennis]
441	CL2123.Contig1_All	PREDICTED: inter-alpha-trypsin inhibitor heavy chain H3-like

		[Strongylocentrotus purpuratus]
441	CL2123.Contig2_All	
441	CL2123.Contig4_All	
441	CL2123.Contig3_All	
442	CL6003.Contig1_All	ATP synthase gamma subunit [Aedes aegypti] >gi|108875130|gb|EAT39355.1| AAEL008848-PA [Aedes aegypti]
443	CL6807.Contig2_All	GH04194p [Drosophila melanogaster]
444	CL13867.Contig1_All	GF17890 [Drosophila ananassae] >gi|190626734|gb|EDV42258.1| GF17890 [Drosophila ananassae]
444	CL13867.Contig2_All	
445	Unigene64145_All	GM12487 [Drosophila sechellia] >gi|194130901|gb|EDW52944.1| GM12487 [Drosophila sechellia]
446	Unigene11787_All	glutathione S-transferase sigma 7 [Locusta migratoria]
447	CL16649.Contig1_All	GI17722 [Drosophila mojavensis] >gi|193913655|gb|EDW12522.1| GI17722 [Drosophila mojavensis]
447	CL16649.Contig2_All	
448	Unigene72220_All	aspartyl-tRNA synthetase [Cherax quadricarinatus]
449	CL9495.Contig1_All	PREDICTED: kynurenine--oxoglutarate transaminase 3-like [Megachile rotundata]
449	CL9495.Contig3_All	
450	Unigene2761_All	putative, partial [Drosophila melanogaster]
451	Unigene57120_All	glu- + pro-tRNA synthetase [Limnadia lenticularis]
452	CL2744.Contig2_All	hypothetical protein AND_09670 [Anopheles darlingi]
453	Unigene56754_All	PREDICTED: importin subunit beta-1-like isoform 2 [Nasonia vitripennis]
454	CL4161.Contig1_All	-
454	CL4161.Contig3_All	
455	CL7791.Contig1_All	hypothetical protein SINV_13001 [Solenopsis invicta]
455	CL7791.Contig2_All	
456	Unigene1085_All	Putative nuclease HARBI1 [Crassostrea gigas]
456	CL5358.Contig1_All	
457	Unigene50296_All	RuvB-like 2 [Harpegnathos saltator]
458	Unigene10802_All	Slit like protein 1 protein [Myotis davidii]
459	Unigene48801_All	GM18141p [Drosophila melanogaster]
460	Unigene57238_All	PARK7, partial [Pterocnemia pennata]
461	CL10282.Contig1_All	unnamed protein product [Macaca fascicularis]
461	CL10282.Contig2_All	
462	CL7803.Contig2_All	hypothetical protein SINV_09712 [Solenopsis invicta]

463	CL8322.Contig1_All	glyoxalase, putative [Ixodes scapularis] >gi|215504587|gb|EEC14081.1| glyoxalase, putative [Ixodes scapularis]
464	CL9473.Contig2_All	Dynein heavy chain, cytoplasmic [Harpegnathos saltator]
465	CL3919.Contig1_All	sarco(endo)plasmic reticulum-type calcium ATPase [Heliothis virescens]
465	CL3919.Contig2_All	
465	CL3919.Contig3_All	
466	CL17084.Contig2_All	PREDICTED: leucine--tRNA ligase, cytoplasmic-like [Hydra magnipapillata]
467	Unigene32747_All	PREDICTED: similar to glucosyl/glucuronosyl transferases [Tribolium castaneum]
468	Unigene65168_All	PREDICTED: clavesin-1-like [Nasonia vitripennis]
469	CL15166.Contig1_All	GNBP3 [Locusta migratoria]
470	CL10350.Contig1_All	PREDICTED: regulator of chromosome condensation-like [Gorilla gorilla gorilla]
471	Unigene32708_All	glycine hydroxylmethyltransferase [Papilio xuthus]
472	CL6511.Contig6_All	proteinase inhibitor serpin, partial [Locusta migratoria]
473	CL2152.Contig1_All	fumarate hydratase, putative [Pediculus humanus corporis] >gi|212509973|gb|EEB13244.1| fumarate hydratase, putative [Pediculus humanus corporis]
474	CL13112.Contig4_All	PREDICTED: Carboxypeptidase D-like [Saccoglossus kowalevskii]
475	CL1475.Contig4_All	40S ribosomal protein S24 [Harpegnathos saltator]
476	Unigene72688_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212512352|gb|EEB15145.1| conserved hypothetical protein [Pediculus humanus corporis]
477	Unigene55538_All	PREDICTED: deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial-like [Macaca mulatta]
478	Unigene48334_All	hypothetical protein TcasGA2_TC016069 [Tribolium castaneum]
479	Unigene12880_All	Stress-induced-phosphoprotein 1 [Camponotus floridanus]
480	Unigene34811_All	electron-transfer-flavoprotein beta polypeptide [Bombyx mori] >gi|87248127|gb|ABD36116.1| electron-transfer-flavoprotein beta polypeptide [Bombyx mori]
481	Unigene55796_All	aubergine protein [Danaus plexippus]
482	Unigene12666_All	PREDICTED: lysosomal aspartic protease-like [Nasonia vitripennis]
483	Unigene57485_All	unnamed protein product [Homo sapiens]

484	CL13759.Contig1_All	proprotein convertase subtilisin/kexin type 4, furin [Culex quinquefasciatus] >gi|167878465|gb|EDS41848.1| proprotein convertase subtilisin/kexin type 4, furin [Culex quinquefasciatus]
485	CL13366.Contig1_All	PREDICTED: coatomer subunit gamma-like [Macaca mulatta]
485	CL13366.Contig2_All	
486	Unigene72312_All	ribosomal protein S17e [Eucinetus sp. APV-2005]
487	Unigene82_All	hexamerin-like protein 1 [Locusta migratoria]
488	Unigene42370_All	-
489	CL1314.Contig1_All	importin-7 [Danaus plexippus]
489	CL1314.Contig2_All	
490	Unigene56314_All	hypothetical protein DAPPUDRAFT_57262 [Daphnia pulex]
491	Unigene56240_All	-
492	CL11089.Contig1_All	PREDICTED: glucose-6-phosphate 1-epimerase-like [Megachile rotundata]
492	CL11089.Contig5_All	
493	CL13067.Contig1_All	unnamed protein product [Tetraodon nigroviridis]
494	Unigene72478_All	homolog of zebrafish ES1 [Rattus norvegicus]
495	Unigene33385_All	Acyl-CoA synthetase family member 3, mitochondrial [Tupaia chinensis]
496	CL6995.Contig2_All	E1b-55kD-associated protein, putative [Pediculus humanus corporis] >gi|212508552|gb|EEB12200.1| E1b-55kD-associated protein, putative [Pediculus humanus corporis]
497	Unigene56407_All	PREDICTED: phosphoglycerate kinase-like [Megachile rotundata]
498	CL4278.Contig1_All	Glycogenin-1 [Acromyrmex echinatior]
499	CL5222.Contig1_All	LP07340p [Drosophila melanogaster]
500	Unigene72651_All	PREDICTED: proteasome subunit beta type-3-like [Apis mellifera]
501	CL12451.Contig1_All	-
502	CL4455.Contig1_All	PREDICTED: 60S ribosomal protein L31-like [Bombus impatiens]
503	Unigene48386_All	hypothetical protein AND_16974 [Anopheles darlingi]
504	CL10609.Contig1_All	Annexin-B9 [Harpegnathos saltator]
505	Unigene12482_All	PREDICTED: synaptic vesicle membrane protein VAT-1 homolog isoform 2 [Acyrthosiphon pisum]
506	Unigene42374_All	PREDICTED: 40S ribosomal protein S9-like [Nasonia vitripennis]
507	Unigene12058_All	GK23319 [Drosophila willistoni] >gi|194170577|gb|EDW85478.1| GK23319 [Drosophila willistoni]
508	Unigene17537_All	PREDICTED: abhydrolase domain-containing protein 14A-like isoform 2 [Gorilla gorilla gorilla]

509	Unigene41326_All	PREDICTED: similar to GA11371-PA [Tribolium castaneum]
510	Unigene40827_All	Ribonucleoside-diphosphate reductase large subunit [Myotis davidii]
511	Unigene21632_All	ADP ribosylation factor 79F, isoform B [Drosophila melanogaster] >gi|24668762|ref|NP_730757.1| ADP ribosylation factor 79F, isoform A [Drosophila melanogaster] >gi|24668769|ref|NP_730758.1| ADP ribosylation factor 79F, isoform C [Drosophila melanogaster] >gi|24668773|ref|NP_730759.1| ADP ribosylation factor 79F, isoform H [Drosophila melanogaster] >gi|24668777|ref|NP_730760.1| ADP ribosylation factor 79F, isoform E [Drosophila melanogaster] >gi|161085839|ref|NP_001097667.1| ADP ribosylation factor 79F, isoform F [Drosophila melanogaster] >gi|221513662|ref|NP_001097668.2| ADP ribosylation factor 79F, isoform I [Drosophila melanogaster] >gi|442634232|ref|NP_001262225.1| ADP ribosylation factor 79F, isoform J [Drosophila melanogaster] >gi|58394100|ref|XP_320516.2| AGAP012014-PA [Anopheles gambiae str. PEST] >gi|125978691|ref|XP_001353378.1| GA21036 [Drosophila pseudoobscura pseudoobscura] >gi|157115009|ref|XP_001652515.1| adp-ribosylation factor, arf [Aedes aegypti] >gi|170035930|ref|XP_001845819.1| ADP-ribosylation factor 1 [Culex quinquefasciatus] >gi|194752565|ref|XP_001958592.1| GF23441 [Drosophila ananassae] >gi|194876431|ref|XP_001973775.1| GG13164 [Drosophila erecta] >gi|195019299|ref|XP_001984951.1| GH14762 [Drosophila grimshawi] >gi|195127774|ref|XP_002008343.1| GI11864 [Drosophila mojavensis] >gi|195160571|ref|XP_002021149.1| GL25178 [Drosophila persimilis] >gi|195348855|ref|XP_002040963.1| GM22073 [Drosophila sechellia] >gi|195377781|ref|XP_002047666.1| GJ13559 [Drosophila virilis] >gi|195441372|ref|XP_002068485.1| GK20496 [Drosophila willistoni] >gi|195496824|ref|XP_002095857.1| GE19486 [Drosophila yakuba] >gi|195592450|ref|XP_002085948.1| GD12049 [Drosophila simulans] >gi|47117660|sp|P61209.2|ARF1_DROME RecName: Full=ADP-ribosylation factor 1 >gi|47117661|sp|P61210.2|ARF1_LOCMI RecName: Full=ADP-ribosylation factor 1; AltName: Full=lARF1 >gi|6648586|gb|AAF21238.1|U90609_1 ADP-ribosylation factor 1 [Locusta migratoria] >gi|385340|gb|AAB27066.1| ADP-ribosylation factor 1 [Drosophila melanogaster] >gi|7296589|gb|AAF51871.1| ADP ribosylation factor 79F, isoform A [Drosophila melanogaster] >gi|7296590|gb|AAF51872.1| ADP ribosylation factor 79F, isoform E [Drosophila melanogaster] >gi|7296591|gb|AAF51873.1| ADP ribosylation factor 79F, isoform C [Drosophila melanogaster]

		>gi|7296592|gb|AAF51874.1| ADP ribosylation factor 79F, isoform B [Drosophila melanogaster] >gi|16648298|gb|AAL25414.1| LD24904p [Drosophila melanogaster] >gi|23094334|gb|AAN12207.1| ADP ribosylation factor 79F, isoform H [Drosophila melanogaster] >gi|54642136|gb|EAL30885.1| GA21036 [Drosophila pseudoobscura pseudoobscura] >gi|55234664|gb|EAA00461.2| AGAP012014-PA [Anopheles gambiae str. PEST] >gi|94468810|gb|ABF18254.1| GTP-binding ADP-ribosylation factor Arf1 [Aedes aegypti] >gi|108877049|gb|EAT41274.1| AAEL007065-PA [Aedes aegypti] >gi|158028609|gb|ABW08583.1| ADP ribosylation factor 79F, isoform F [Drosophila melanogaster] >gi|167878418|gb|EDS41801.1| ADP-ribosylation factor 1 [Culex quinquefasciatus] >gi|190625874|gb|EDV41398.1| GF23441 [Drosophila ananassae] >gi|190655558|gb|EDV52801.1| GG13164 [Drosophila erecta] >gi|193898433|gb|EDV97299.1| GH14762 [Drosophila grimshawi] >gi|193919952|gb|EDW18819.1| GI11864 [Drosophila mojavensis] >gi|194118262|gb|EDW40305.1| GL25178 [Drosophila persimilis] >gi|194122473|gb|EDW44516.1| GM22073 [Drosophila sechellia] >gi|194154824|gb|EDW70008.1| GJ13559 [Drosophila virilis] >gi|194164570|gb|EDW79471.1| GK20496 [Drosophila willistoni] >gi|194181958|gb|EDW95569.1| GE19486 [Drosophila yakuba] >gi|194197957|gb|EDX11533.1| GD12049 [Drosophila simulans] >gi|220902698|gb|ABW08584.2| ADP ribosylation factor 79F, isoform I [Drosophila melanogaster] >gi|440216206|gb|AGB94918.1| ADP ribosylation factor 79F, isoform J [Drosophila melanogaster]
512	CL14590.Contig1_All	hypothetical protein SINV_13764 [Solenopsis invicta]
512	CL14590.Contig3_All	
512	CL14590.Contig2_All	
513	CL12583.Contig1_All	hypothetical protein SINV_01576 [Solenopsis invicta]
513	CL12583.Contig2_All	
514	Unigene72100_All	GM14682p [Drosophila melanogaster]
515	CL9470.Contig1_All	PREDICTED: ras-like GTP-binding protein Rho1 isoform 1 [Nasonia vitripennis] >gi|156544952|ref|XP_001607493.1| PREDICTED: ras-like GTP-binding protein Rho1 isoform 2 [Nasonia vitripennis]
515	Unigene20318_All	
515	CL9470.Contig2_All	
516	Unigene2352_All	hypothetical protein [Bactrocera oleae]
517	CL2238.Contig1_All	female neotenic-specific protein 1 [Cryptotermes secundus]
517	CL2238.Contig2_All	
518	Unigene12542_All	hypothetical protein KGM_20431 [Danaus plexippus]

519	Unigene87758_All	-
520	CL9557.Contig2_All	AGAP001341-PA [Anopheles gambiae str. PEST] >gi|116116516|gb|EAA43211.3| AGAP001341-PA [Anopheles gambiae str. PEST]
521	CL9361.Contig1_All	PREDICTED: ras-related protein Rab-11A isoform 2 [Saimiri boliviensis boliviensis]
521	CL9361.Contig2_All	
522	Unigene7377_All	RAB10, member RAS oncogene family [Xenopus (Silurana) tropicalis] >gi|166796642|gb|AAI59386.1| LOC100145267 protein [Xenopus (Silurana) tropicalis]
523	CL1550.Contig3_All	-
524	CL6510.Contig1_All	proteinase inhibitor serpin, partial [Locusta migratoria]
525	Unigene72524_All	PREDICTED: 3'(2'),5'-bisphosphate nucleotidase 1-like isoform 1 [Nasonia vitripennis] >gi|345489447|ref|XP_003426141.1| PREDICTED: 3'(2'),5'-bisphosphate nucleotidase 1-like isoform 2 [Nasonia vitripennis]
526	CL9942.Contig2_All	PREDICTED: apolipophorins-like, partial [Apis florea]
527	CL16691.Contig2_All	proteasome non-ATPase regulatory subunit, partial [Schistocerca gregaria]
528	Unigene34218_All	putative wd-repeat protein [Danaus plexippus]
529	CL12631.Contig2_All	PREDICTED: protein transport protein Sec24C-like [Apis mellifera]
529	CL12631.Contig4_All	
530	Unigene40566_All	glutathione S-transferase [Locusta migratoria]
531	Unigene12572_All	S31 protein [Anguilla anguilla]
532	CL2935.Contig1_All	nucleoplasmin isoform 1-like protein [Maconellicoccus hirsutus]
532	CL2935.Contig2_All	
533	Unigene27570_All	hypothetical protein SINV_80286 [Solenopsis invicta]
534	CL1852.Contig1_All	PREDICTED: vitamin K epoxide reductase complex subunit 1-like protein 1-like [Megachile rotundata]
535	Unigene19985_All	NSFL1 cofactor p47 [Crassostrea gigas]
536	Unigene65019_All	Probable histone-binding protein Caf1 [Harpegnathos saltator]
537	CL2650.Contig3_All	unknown [Homo sapiens]
538	CL3962.Contig1_All	ribosomal protein L10Ae [Cicindela littoralis]
539	Unigene635_All	PREDICTED: phosphatidylinositol transfer protein alpha isoform-like [Nasonia vitripennis]
540	CL10086.Contig2_All	blackjack [Schistocerca americana]
541	CL14565.Contig1_All	PREDICTED: elongation factor Tu-like, partial [Bombus impatiens]

542	CL6896.Contig1_All	PREDICTED: rRNA 2'-O-methyltransferase fibrillarin [Apis mellifera]
542	CL6896.Contig2_All	
543	CL2132.Contig15_All	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein-like [Strongylocentrotus purpuratus]
544	Unigene64606_All	PREDICTED: n-alpha-acetyltransferase 16, NatA auxiliary subunit-like, partial [Meleagris gallopavo]
545	CL4158.Contig1_All	-
546	Unigene20230_All	aspartate aminotransferase, partial [Allonemobius socius]
547	CL16420.Contig1_All	putative CG5976 [Heliconius melpomene]
548	CL12266.Contig1_All	arg methyltransferase [Periplaneta americana]
548	Unigene20108_All	
549	Unigene63260_All	hypothetical protein BRAFLDRAFT_217668 [Branchiostoma floridae] >gi|229279827|gb|EEN50603.1| hypothetical protein BRAFLDRAFT_217668 [Branchiostoma floridae]
550	Unigene64611_All	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform-like [Nasonia vitripennis]
551	CL1049.Contig1_All	protein transport protein Sec23A, putative [Pediculus humanus corporis] >gi|212516424|gb|EEB18437.1| protein transport protein Sec23A, putative [Pediculus humanus corporis]
551	CL1049.Contig2_All	
552	Unigene12931_All	trypsin [Culex quinquefasciatus] >gi|167879490|gb|EDS42873.1| trypsin [Culex quinquefasciatus]
552	Unigene32561_All	
553	Unigene65224_All	PREDICTED: eukaryotic translation initiation factor 2 subunit 1-like [Apis florea]
554	CL5546.Contig1_All	tyrosyl-tRNA synthetase [Drosophila virilis]
554	CL5546.Contig2_All	
555	CL5924.Contig1_All	PREDICTED: phospholipid hydroperoxide glutathione peroxidase, mitochondrial-like [Megachile rotundata]
556	Unigene12470_All	unknown [Marsupenaeus japonicus]
557	Unigene2786_All	hypothetical protein DAPPUDRAFT_44590 [Daphnia pulex]
558	Unigene70426_All	Serine/threonine-protein phosphatase alpha-1 isoform [Harpegnathos saltator]

559	Unigene3117_All	transformer-2 sex-determining protein, putative [Pediculus humanus corporis] >gi|212510258|gb|EEB13469.1| transformer-2 sex-determining protein, putative [Pediculus humanus corporis]
559	Unigene139774_All	
560	CL2218.Contig1_All	cytochrome c oxidase, subunit Va, isoform CRA_b [Rattus norvegicus]
561	Unigene40759_All	similar to Drosophila melanogaster CG2852, partial [Drosophila yakuba]
562	CL4988.Contig1_All	PREDICTED: similar to carnitine o-acetyltransferase [Tribolium castaneum] >gi|270007434|gb|EFA03882.1| hypothetical protein TcasGA2_TC014006 [Tribolium castaneum]
563	Unigene50248_All	mitochondrial cytochrome c [Locusta migratoria]
564	CL2074.Contig4_All	juvenile hormone epoxide hydrolase-like protein 5 precursor [Tribolium castaneum] >gi|269093690|dbj|BAI49690.1| juvenile hormone epoxide hydrolase-like protein 5 [Tribolium castaneum]
565	Unigene62876_All	60S ribosomal protein L37a [Harpegnathos saltator]
566	Unigene49910_All	peptidase (mitochondrial processing) beta, isoform CRA_d [Rattus norvegicus]
567	CL1582.Contig1_All	PREDICTED: LOW QUALITY PROTEIN: heterogeneous nuclear ribonucleoprotein Q-like [Apis florea]
567	CL1582.Contig3_All	
568	CL6923.Contig1_All	hypothetical protein EAG_07856 [Camponotus floridanus]
568	CL6923.Contig3_All	
568	CL6923.Contig2_All	
568	CL6923.Contig4_All	
569	Unigene2484_All	similar to Drosophila melanogaster yip6, partial [Drosophila yakuba]
570	Unigene72257_All	microsomal glutathione S-transferase-like protein [Scaptomyza flava]
571	Unigene49995_All	PREDICTED: similar to proteasome beta subunit [Tribolium castaneum] >gi|270003046|gb|EEZ99493.1| hypothetical protein TcasGA2_TC000069 [Tribolium castaneum]
572	Unigene27566_All	similar to Drosophila melanogaster CG11024, partial [Drosophila yakuba]
573	CL1639.Contig1_All	PREDICTED: DAZ-associated protein 1-like [Bombus terrestris]
574	Unigene57453_All	GTP-binding protein SAR1B, putative [Pediculus humanus corporis] >gi|212518131|gb|EEB19923.1| GTP-binding protein SAR1B, putative [Pediculus humanus corporis]

575	CL4784.Contig1_All	hypothetical protein SINV_15664 [Solenopsis invicta]
575	CL4784.Contig2_All	
575	CL4784.Contig3_All	
576	Unigene50189_All	PREDICTED: signal recognition particle 68 kDa protein-like [Gorilla gorilla gorilla]
577	CL11266.Contig1_All	Inosine-5'-monophosphate dehydrogenase [Acromyrmex echinatior]
577	CL11266.Contig2_All	
578	Unigene45548_All	-
579	Unigene2398_All	GD11174 [Drosophila simulans] >gi|194193747|gb|EDX07323.1| GD11174 [Drosophila simulans]
580	Unigene26497_All	Rho GDP dissociation inhibitor [Schistocerca gregaria]
581	Unigene72016_All	fattyacid-CoA ligase [Acanthamoeba castellanii str. Neff] >gi|440794653|gb|ELR15810.1| fattyacid-CoA ligase [Acanthamoeba castellanii str. Neff]
582	CL16040.Contig1_All	L-xylulose reductase [Danaus plexippus]
582	CL16040.Contig2_All	
583	CL14815.Contig1_All	PREDICTED: uncharacterized protein LOC101178559, partial [Nomascus leucogenys]
584	Unigene12385_All	AGAP006104-PA [Anopheles gambiae str. PEST] >gi|157015993|gb|EAA11277.4| AGAP006104-PA [Anopheles gambiae str. PEST]
585	Unigene63363_All	PREDICTED: similar to AGAP001827-PA [Tribolium castaneum] >gi|270005695|gb|EFA02143.1| hypothetical protein TcasGA2_TC007793 [Tribolium castaneum]
586	Unigene63022_All	exuperantia [Danaus plexippus]
587	CL3659.Contig1_All	Rm62 [Tribolium castaneum]
588	Unigene20099_All	PREDICTED: similar to secretory carrier-associated membrane protein [Tribolium castaneum] >gi|270015052|gb|EFA11500.1| hypothetical protein TcasGA2_TC014214 [Tribolium castaneum]
589	CL8230.Contig1_All	ACYPI005467 [Acyrthosiphon pisum]
589	CL8230.Contig6_All	
589	CL8230.Contig3_All	
589	CL8230.Contig2_All	
590	Unigene50235_All	putative mitochondrial superoxide dismutase 2 variant 1 [Taeniopygia guttata]
591	Unigene42547_All	PREDICTED: thioredoxin reductase 1, cytoplasmic isoform 3 [Orcinus orca]
592	CL7594.Contig1_All	apoptosis-linked protein 2 [Danaus plexippus]
593	CL17147.Contig1_All	PREDICTED: DNA-directed RNA polymerases I and III subunit RPAC1-like [Bombus impatiens]

593	CL17147.Contig2_All	
594	CL8723.Contig1_All	PREDICTED: nodal modulator 1-like, partial [Pan troglodytes]
595	Unigene42627_All	PREDICTED: similar to fumarylacetoacetate hydrolase [Tribolium castaneum] >gi|270014035|gb|EFA10483.1| hypothetical protein TcasGA2_TC012729 [Tribolium castaneum]
596	Unigene12913_All	Proteasome subunit alpha type-7-1 [Harpegnathos saltator]
597	CL11989.Contig1_All	PREDICTED: similar to eukaryotic translation initiation factor 4H [Tribolium castaneum] >gi|270009076|gb|EFA05524.1| hypothetical protein TcasGA2_TC015711 [Tribolium castaneum]
598	Unigene19954_All	GD19802 [Drosophila simulans] >gi|194198178|gb|EDX11754.1| GD19802 [Drosophila simulans]
599	CL13684.Contig2_All	cystathionine beta-lyase, partial [Schistocerca gregaria]
600	CL17077.Contig2_All	DEAD box ATP-dependent RNA helicase [Danaus plexippus]
601	Unigene42055_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212511745|gb|EEB14638.1| conserved hypothetical protein [Pediculus humanus corporis]
602	CL4069.Contig2_All	Chain A, Crystal Structure Of The Catalytic Domain Of An Adenosine Deaminase That Acts On Rna (hadar2) Bound To Inositol Hexakisphosphate (ihp) >gi|78101144|pdb|1ZY7|B Chain B, Crystal Structure Of The Catalytic Domain Of An Adenosine Deaminase That Acts On Rna (hadar2) Bound To Inositol Hexakisphosphate (ihp)
602	CL4069.Contig3_All	
602	CL4069.Contig6_All	
603	CL11671.Contig1_All	pale, isoform A [Drosophila melanogaster] >gi|433470|emb|CAA53802.1| tyrosine hydroxylase [Drosophila melanogaster] >gi|595801|gb|AAA62877.1| tyrosine hydroxylase type 1, neuronal form [Drosophila melanogaster] >gi|23094058|gb|AAN12080.1| pale, isoform A [Drosophila melanogaster]
603	CL11671.Contig2_All	
604	CL12252.Contig3_All	PREDICTED: 6-phosphofructokinase-like isoform 1 [Acyrthosiphon pisum]
605	Unigene57358_All	PREDICTED: sex-lethal homolog isoform 3 [Nasonia vitripennis]
606	CL9339.Contig1_All	chitin deacetylase 2, partial [Locusta migratoria]
606	CL9339.Contig2_All	
607	Unigene12618_All	translocation protein 1 [Biston betularia]
608	CL12441.Contig1_All	myo-inositol-1-phosphate synthase [Aedes albopictus]

609	Unigene35360_All	unnamed protein product [Homo sapiens]
610	Unigene64675_All	GD15515 [Drosophila simulans] >gi|194204921|gb|EDX18497.1| GD15515 [Drosophila simulans]
611	Unigene19737_All	pre-mRNA-splicing factor, putative [Pediculus humanus corporis] >gi|212505340|gb|EEB09812.1| pre-mRNA-splicing factor, putative [Pediculus humanus corporis]
612	Unigene12447_All	ubiquitin carboxyl-terminal hydrolase isozyme L5, putative [Pediculus humanus corporis] >gi|212517318|gb|EEB19229.1| ubiquitin carboxyl-terminal hydrolase isozyme L5, putative [Pediculus humanus corporis]
613	Unigene62806_All	succinate dehydrogenase, flavoprotein subunit [Pediculus humanus corporis] >gi|212516755|gb|EEB18729.1| succinate dehydrogenase, flavoprotein subunit [Pediculus humanus corporis]
614	CL9227.Contig2_All	GA23745 [Drosophila pseudoobscura pseudoobscura] >gi|198150028|gb|EDY73545.1| GA23745 [Drosophila pseudoobscura pseudoobscura]
615	Unigene35339_All	PREDICTED: importin subunit alpha-3-like [Nasonia vitripennis]
616	CL6919.Contig1_All	Pyrroline-5-carboxylate reductase 2 [Harpegnathos saltator]
616	CL6919.Contig2_All	
617	CL65.Contig1_All	hypothetical protein TcasGA2_TC001594 [Tribolium castaneum]
617	CL65.Contig8_All	
618	CL7878.Contig3_All	PREDICTED: xaa-Pro aminopeptidase 1 [Callithrix jacchus]
619	Unigene42713_All	similar to CG6891 [Papilio xuthus] >gi|389610993|dbj|BAM19107.1| simila to CG6891 [Papilio polytes]
620	Unigene18160_All	PREDICTED: alpha-tocopherol transfer protein-like [Megachile rotundata]
621	CL10036.Contig1_All	ribosomal protein large subunit 12 [Ostrinia nubilalis] >gi|170784002|gb|ACB37449.1| ribosomal protein large subunit 12 [Ostrinia nubilalis]
622	CL9277.Contig3_All	AAEL001806-PA [Aedes aegypti]
622	Unigene21579_All	
623	CL7903.Contig1_All	histone deacetylase 2C, putative [Pediculus humanus corporis] >gi|212511344|gb|EEB14348.1| histone deacetylase 2C, putative [Pediculus humanus corporis]
623	CL7903.Contig2_All	
624	Unigene25324_All	hypothetical protein SINV_06958 [Solenopsis invicta]

625	Unigene26210_All	proteinase inhibitor serpin, partial [Locusta migratoria]
626	Unigene56236_All	PREDICTED: uncharacterized protein C05D11.1-like [Strongylocentrotus purpuratus]
627	Unigene42585_All	FK506-binding protein 8 [Camponotus floridanus]
628	Unigene57735_All	PREDICTED: similar to ras-related protein Rab-8A, putative [Tribolium castaneum]
629	CL10780.Contig1_All	PREDICTED: speckle-type POZ protein-like [Cricetulus griseus]
630	CL1393.Contig1_All	cytochrome c oxidase, subunit VIIA [Culex quinquefasciatus] >gi|167863934|gb|EDS27317.1| cytochrome c oxidase, subunit VIIA [Culex quinquefasciatus]
631	Unigene32891_All	GL15032 [Drosophila persimilis] >gi|194117617|gb|EDW39660.1| GL15032 [Drosophila persimilis]
632	CL8224.Contig2_All	PREDICTED: esterase FE4-like [Acyrthosiphon pisum]
632	CL8224.Contig3_All	
633	Unigene62019_All	PREDICTED: hypothetical protein LOC100160127 [Acyrthosiphon pisum]
634	Unigene48541_All	thioredoxin domain-containing protein 4 precursor, putative [Pediculus humanus corporis] >gi|212508792|gb|EEB12380.1| thioredoxin domain-containing protein 4 precursor, putative [Pediculus humanus corporis]
635	Unigene56246_All	TPA_inf: 26S proteasome [Amblyomma variegatum]
636	CL8363.Contig1_All	PREDICTED: heterogeneous nuclear ribonucleoprotein F-like [Nasonia vitripennis]
637	CL392.Contig5_All	hypothetical protein SINV_00192 [Solenopsis invicta]
638	Unigene47819_All	JAB-MPN domain protein [Danaus plexippus]
639	Unigene34128_All	MCM2, partial [Mus musculus]
640	Unigene644_All	ras-related protein Rab-14, partial [Papilio polytes]
641	Unigene56312_All	heat shock protein 20.7 [Locusta migratoria]
642	Unigene39928_All	PREDICTED: V-type proton ATPase subunit C-like [Nasonia vitripennis]
643	Unigene42522_All	DEAD box ATP-dependent RNA helicase [Culex quinquefasciatus] >gi|167862451|gb|EDS25834.1| DEAD box ATP-dependent RNA helicase [Culex quinquefasciatus]
644	CL14578.Contig1_All	ribose-5-phosphate isomerase [Aedes aegypti] >gi|108872043|gb|EAT36268.1| AAEL011627-PA [Aedes aegypti]
645	CL3968.Contig1_All	hypothetical protein SINV_06119 [Solenopsis invicta]
646	Unigene27815_All	hypothetical protein AND_15699 [Anopheles darlingi]

647	CL9379.Contig1_All	control protein HCTL029 [Heliconius ismenius] >gi|358443074|gb|AEU11783.1| control protein HCTL029 [Heliconius hecale] >gi|358443076|gb|AEU11784.1| control protein HCTL029 [Heliconius aoede] >gi|358443078|gb|AEU11785.1| control protein HCTL029 [Heliconius burneyi] >gi|358443088|gb|AEU11790.1| control protein HCTL029 [Heliconius hewitsoni] >gi|358443090|gb|AEU11791.1| control protein HCTL029 [Heliconius sara]
648	Unigene42506_All	hypothetical protein [Thermobia domestica]
649	Unigene57482_All	clathrin heavy chain [Acheta domesticus] >gi|262304531|gb|ACY44858.1| clathrin heavy chain [Ctenolepisma lineata]
650	CL10731.Contig1_All	GM14873p [Drosophila melanogaster]
651	Unigene72514_All	40S ribosomal protein S25, putative [Pediculus humanus corporis] >gi|212512081|gb|EEB14913.1| 40S ribosomal protein S25, putative [Pediculus humanus corporis]
652	Unigene26407_All	Small ubiquitin-related modifier 3 [Acromyrmex echinatior]
653	Unigene65181_All	hypothetical protein SINV_12523 [Solenopsis invicta]
654	Unigene48988_All	AGAP001138-PA [Anopheles gambiae str. PEST] >gi|157012975|gb|EAA01034.4| AGAP001138-PA [Anopheles gambiae str. PEST]
655	Unigene10066_All	Beta-mannosidase [Crassostrea gigas]
656	Unigene20005_All	PREDICTED: signal recognition particle 72 kDa protein-like isoform 1 [Nasonia vitripennis]
657	Unigene64794_All	PREDICTED: similar to adenosylhomocysteinase [Tribolium castaneum] >gi|270007826|gb|EFA04274.1| hypothetical protein TcasGA2_TC014564 [Tribolium castaneum]
658	CL11216.Contig1_All	glutamine amidotransferase, partial [Schistocerca gregaria]
659	CL5742.Contig2_All	PREDICTED: laminin subunit gamma-1-like isoform 3 [Bombus terrestris]
660	CL11092.Contig1_All	hypothetical protein CAPTEDRAFT_186995 [Capitella teleta]
661	CL16532.Contig2_All	PREDICTED: ankyrin repeat domain-containing protein 39 [Sarcophilus harrisii]
661	Unigene55143_All	
662	CL5772.Contig4_All	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase [Camponotus floridanus]
663	Unigene70251_All	TAR DNA-binding protein 43 [Camponotus floridanus]

664	Unigene762_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167867241|gb|EDS30624.1| conserved hypothetical protein [Culex quinquefasciatus]
665	Unigene49223_All	PREDICTED: lon protease homolog, mitochondrial-like [Apis mellifera]
666	Unigene70114_All	hypothetical protein SINV_01609 [Solenopsis invicta]
667	Unigene19928_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167874638|gb|EDS38021.1| conserved hypothetical protein [Culex quinquefasciatus]
668	Unigene80801_All	thioredoxin-1 [Clonorchis sinensis]
669	Unigene19972_All	PREDICTED: methylcrotonoyl-CoA carboxylase beta chain, mitochondrial-like, partial [Ornithorhynchus anatinus]
670	Unigene1656_All	adenylate kinase 2 [Helicoverpa armigera]
671	CL9036.Contig3_All	PREDICTED: UV excision repair protein RAD23 homolog A isoform 2 [Trichechus manatus latirostris]
672	Unigene56154_All	PREDICTED: uncharacterized protein LOC100880549 [Megachile rotundata]
673	CL9179.Contig1_All	hypothetical protein AND_22302 [Anopheles darlingi]
674	CL4791.Contig1_All	PREDICTED: DNA topoisomerase 2-beta [Xenopus (Silurana) tropicalis]
675	Unigene65048_All	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A, putative [Pediculus humanus corporis] >gi|212506780|gb|EEB10882.1| Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A, putative [Pediculus humanus corporis]
676	Unigene33444_All	hypothetical protein KGM_00826 [Danaus plexippus]
677	Unigene50143_All	-
678	Unigene25205_All	hypothetical protein [Macaca fascicularis]
679	Unigene17948_All	unnamed protein product [Mus musculus]
680	Unigene50213_All	PREDICTED: rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha-like [Oryzias latipes]
681	CL17546.Contig1_All	aldo-keto reductase, partial [Schistocerca gregaria]
682	CL12807.Contig1_All	PREDICTED: CG4420-like [Saccoglossus kowalevskii]
682	CL12807.Contig2_All	
683	Unigene25517_All	PREDICTED: similar to conserved hypothetical protein [Tribolium castaneum] >gi|270005570|gb|EFA02018.1| hypothetical protein TcasGA2_TC007641 [Tribolium castaneum]
684	Unigene48297_All	hypothetical protein AND_13953 [Anopheles darlingi]

685	Unigene55097_All	Basic leucine zipper and W2 domain-containing protein 2 [Acromyrmex echinatior]
686	CL11614.Contig1_All	PREDICTED: 14 kDa phosphohistidine phosphatase-like [Ornithorhynchus anatinus]
687	Unigene34986_All	GI11352 [Drosophila mojavensis] >gi|193920863|gb|EDW19730.1| GI11352 [Drosophila mojavensis]
688	Unigene70486_All	Zygotic DNA replication licensing factor mcm6-B [Crassostrea gigas]
689	Unigene54651_All	AGAP008059-PA [Anopheles gambiae str. PEST] >gi|55237617|gb|EAA12591.2| AGAP008059-PA [Anopheles gambiae str. PEST]
690	CL7819.Contig1_All	Dynein intermediate chain, cytosolic [Camponotus floridanus]
690	CL7819.Contig3_All	
690	CL7819.Contig5_All	
690	CL7819.Contig2_All	
690	CL7819.Contig4_All	
690	CL7819.Contig6_All	
691	Unigene20185_All	PREDICTED: bifunctional aminoacyl-tRNA synthetase-like, partial [Amphimedon queenslandica]
692	Unigene18975_All	26S proteasome non-ATPase regulatory subunit 11 [Acromyrmex echinatior]
693	Unigene2988_All	Nuclear protein NP60-like protein [Camponotus floridanus]
694	Unigene17604_All	unknown [Dendroctonus ponderosae]
695	CL7193.Contig1_All	-
696	CL9620.Contig2_All	PREDICTED: succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial [Macaca mulatta]
697	Unigene26000_All	hypothetical protein DAPPUDRAFT_305547 [Daphnia pulex]
698	Unigene3020_All	Endoplasmic reticulum protein ERp29, putative [Pediculus humanus corporis] >gi|212510717|gb|EEB13839.1| Endoplasmic reticulum protein ERp29, putative [Pediculus humanus corporis]
699	Unigene39823_All	unnamed protein product [Homo sapiens]
700	Unigene57694_All	PREDICTED: eukaryotic translation initiation factor 3 subunit E-like [Strongylocentrotus purpuratus]
701	Unigene34699_All	cellular apoptosis susceptibility protein, partial [Calanus helgolandicus]
702	Unigene72495_All	TPA_exp: carbonyl reductase 3 [Amblyomma variegatum]
703	Unigene35003_All	PREDICTED: 26S proteasome non-ATPase regulatory subunit 8-like, partial [Macaca mulatta]

704	Unigene7763_All	GI14054 [Drosophila mojavensis] >gi|193912712|gb|EDW11579.1| GI14054 [Drosophila mojavensis]
705	Unigene35292_All	Phosphate carrier protein, mitochondrial [Cricetulus griseus]
706	Unigene33140_All	juvenile hormone esterase [Bactrocera dorsalis]
707	Unigene64842_All	hypothetical protein SINV_10183 [Solenopsis invicta]
708	CL809.Contig2_All	hypothetical protein SINV_14017 [Solenopsis invicta]
708	Unigene47589_All	
709	CL12077.Contig1_All	vesicle associated protein [Culex quinquefasciatus] >gi|167871448|gb|EDS34831.1| vesicle associated protein [Culex quinquefasciatus]
709	CL12077.Contig3_All	
709	CL12077.Contig2_All	
709	CL12077.Contig4_All	
710	Unigene85985_All	uncharacterized protein LOC449549 [Danio rerio] >gi|51895902|gb|AAH82296.1| Zgc:100918 [Danio rerio]
711	Unigene9943_All	Netrin-4, putative [Ixodes scapularis] >gi|215498522|gb|EEC08016.1| Netrin-4, putative [Ixodes scapularis]
712	CL14656.Contig1_All	AGAP001798-PA [Anopheles gambiae str. PEST] >gi|333469975|gb|EAA01121.5| AGAP001798-PA [Anopheles gambiae str. PEST]
713	Unigene18896_All	Chondroitin proteoglycan-2 [Camponotus floridanus]
714	CL10188.Contig1_All	PREDICTED: phosphoserine aminotransferase-like, partial [Meleagris gallopavo]
714	CL10188.Contig2_All	
715	CL6069.Contig1_All	PREDICTED: c-terminal-binding protein-like, partial [Bombus terrestris]
715	CL6069.Contig4_All	
715	CL6069.Contig3_All	
715	CL6069.Contig2_All	
716	CL5424.Contig2_All	glycogen phosphorylase [Culex quinquefasciatus] >gi|167880093|gb|EDS43476.1| glycogen phosphorylase [Culex quinquefasciatus]
717	Unigene72735_All	60S ribosomal protein L17 [Camponotus floridanus]
718	Unigene19137_All	unnamed protein product [Tetraodon nigroviridis]
719	Unigene342_All	PREDICTED: similar to DNA replication licensing factor MCM3 [Tribolium castaneum] >gi|270015933|gb|EFA12381.1| hypothetical protein TcasGA2_TC002088 [Tribolium castaneum]
720	Unigene56222_All	SEC13 homolog [Salmo salar]

721	Unigene27961_All	AGAP001695-PA [Anopheles gambiae str. PEST] >gi|333470076|gb|EAL38548.3| AGAP001695-PA [Anopheles gambiae str. PEST]
722	Unigene35192_All	effete, isoform A [Drosophila melanogaster] >gi|187117170|ref|NP_001119686.1| effete [Acyrthosiphon pisum] >gi|442619106|ref|NP_001262578.1| effete, isoform B [Drosophila melanogaster] >gi|442619108|ref|NP_001262579.1| effete, isoform C [Drosophila melanogaster] >gi|58381090|ref|XP_310998.2| AGAP000145-PA [Anopheles gambiae str. PEST] >gi|157134117|ref|XP_001663154.1| ubiquitin-conjugating enzyme E2 [Aedes aegypti] >gi|194743322|ref|XP_001954149.1| GF18131 [Drosophila ananassae] >gi|194900836|ref|XP_001979961.1| GG21088 [Drosophila erecta] >gi|195061220|ref|XP_001995948.1| GH14086 [Drosophila grimshawi] >gi|195113175|ref|XP_002001144.1| GI10619 [Drosophila mojavensis] >gi|195143851|ref|XP_002012910.1| GL23670 [Drosophila persimilis] >gi|195328929|ref|XP_002031164.1| GM25828 [Drosophila sechellia] >gi|195390905|ref|XP_002054107.1| GJ22971 [Drosophila virilis] >gi|195444200|ref|XP_002069759.1| GK11688 [Drosophila willistoni] >gi|195501528|ref|XP_002097834.1| eff [Drosophila yakuba] >gi|195570846|ref|XP_002103415.1| GD20402 [Drosophila simulans] >gi|198451027|ref|XP_002137205.1| GA26693 [Drosophila pseudoobscura pseudoobscura] >gi|136643|sp|P25867.1|UBCD1_DROME RecName: Full=Ubiquitin-conjugating enzyme E2-17 kDa; AltName: Full=Protein effete; AltName: Full=Ubiquitin carrier protein; AltName: Full=Ubiquitin-protein ligase >gi|8783|emb|CAA44453.1| ubiquitin-conjugating enzyme [Drosophila melanogaster] >gi|7299919|gb|AAF55093.1| effete, isoform A [Drosophila melanogaster] >gi|16648156|gb|AAL25343.1| GH14739p [Drosophila melanogaster] >gi|55243675|gb|EAA06420.3| AGAP000145-PA [Anopheles gambiae str. PEST] >gi|94468952|gb|ABF18325.1| ubiquitin-conjugating enzyme [Aedes aegypti] >gi|108881406|gb|EAT45631.1| AAEL003103-PA [Aedes aegypti] >gi|190627186|gb|EDV42710.1| GF18131 [Drosophila ananassae] >gi|190651664|gb|EDV48919.1| GG21088 [Drosophila erecta] >gi|193891740|gb|EDV90606.1| GH14086 [Drosophila grimshawi] >gi|193917738|gb|EDW16605.1| GI10619 [Drosophila mojavensis] >gi|194101853|gb|EDW23896.1| GL23670 [Drosophila persimilis] >gi|194120107|gb|EDW42150.1| GM25828 [Drosophila sechellia] >gi|194152193|gb|EDW67627.1| GJ22971 [Drosophila virilis] >gi|194165844|gb|EDW80745.1| GK11688 [Drosophila willistoni] >gi|194183935|gb|EDW97546.1| eff [Drosophila yakuba]

		>gi|194199342|gb|EDX12918.1| GD20402 [Drosophila simulans] >gi|198131302|gb|EDY67763.1| GA26693 [Drosophila pseudoobscura pseudoobscura] >gi|239791033|dbj|BAH72034.1| ACYPI000078 [Acyrthosiphon pisum] >gi|270002752|gb|EEZ99199.1| effete [Tribolium castaneum] >gi|440217433|gb|AGB95959.1| effete, isoform B [Drosophila melanogaster] >gi|440217434|gb|AGB95960.1| effete, isoform C [Drosophila melanogaster]
723	CL16979.Contig1_All	Apolipoprotein A-I-binding protein [Pteropus alecto]
724	CL769.Contig3_All	S5 [Suberites domuncula]
724	CL769.Contig4_All	
724	CL17179.Contig5_All	
725	Unigene12903_All	V-ATPase subunit D [Locusta migratoria]
726	CL11923.Contig1_All	PREDICTED: vacuolar protein sorting-associated protein 4A [Ovis aries]
727	Unigene50498_All	PREDICTED: similar to dodo [Tribolium castaneum] >gi|270004471|gb|EFA00919.1| hypothetical protein TcasGA2_TC003825 [Tribolium castaneum]
728	Unigene10827_All	GK25006 [Drosophila willistoni] >gi|194167780|gb|EDW82681.1| GK25006 [Drosophila willistoni]
729	CL9135.Contig2_All	hypothetical protein SINV_16598 [Solenopsis invicta]
729	CL9135.Contig3_All	
730	Unigene26368_All	PREDICTED: importin subunit alpha-2-like [Megachile rotundata]

731	CL3.Contig1_All	hypothetical protein TcasGA2_TC016051 [Tribolium castaneum]
732	Unigene27968_All	Signal recognition particle 54 kDa protein, putative [Pediculus humanus corporis] >gi|212509171|gb|EEB12639.1| Signal recognition particle 54 kDa protein, putative [Pediculus humanus corporis]
733	CL5326.Contig2_All	GE20837 [Drosophila yakuba] >gi|194179417|gb|EDW93028.1| GE20837 [Drosophila yakuba]
733	CL5326.Contig3_All	
734	CL8430.Contig1_All	AGAP004689-PC [Anopheles gambiae str. PEST] >gi|157014635|gb|EAA13176.4| AGAP004689-PC [Anopheles gambiae str. PEST]
735	Unigene70544_All	Niemann-Pick C1 protein [Camponotus floridanus]
736	CL13631.Contig1_All	hypothetical protein BRAFLDRAFT_209743 [Branchiostoma floridae] >gi|229278428|gb|EEN49215.1| hypothetical protein BRAFLDRAFT_209743 [Branchiostoma floridae]
737	Unigene12369_All	putative acyl-coenzyme A dehydrogenase, short chain [Maconellicoccus hirsutus]
738	Unigene20065_All	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP1A-like [Bombus impatiens]
739	Unigene64985_All	Transcription elongation factor B polypeptide 2 [Acromyrmex echinatior]
740	CL9332.Contig1_All	hypothetical protein BRAFLDRAFT_125113 [Branchiostoma floridae] >gi|229291439|gb|EEN62111.1| hypothetical protein BRAFLDRAFT_125113 [Branchiostoma floridae]
740	CL9332.Contig2_All	
741	Unigene35136_All	26S protease regulatory subunit 6B [Harpegnathos saltator]
742	CL6119.Contig1_All	pterin-4 alpha-carbinolamine dehydratase [Alligator mississippiensis]
742	CL6119.Contig2_All	
743	Unigene27901_All	-
744	CL11193.Contig1_All	PREDICTED: uncharacterized protein LOC100883656 [Megachile rotundata]
744	CL11193.Contig2_All	
745	CL461.Contig14_All	PREDICTED: LOW QUALITY PROTEIN: myosin heavy chain, muscle-like [Apis florea]
745	CL461.Contig1_All	
745	CL461.Contig6_All	
746	Unigene12370_All	unnamed protein product [Tetraodon nigroviridis]
747	Unigene10757_All	hypothetical protein SINV_15529 [Solenopsis invicta]

748	CL13343.Contig2_All	hypothetical protein SINV_80267 [Solenopsis invicta]
749	Unigene9768_All	1-O-acylceramide synthase precursor, putative [Pediculus humanus corporis] >gi|212516277|gb|EEB18310.1| 1-O-acylceramide synthase precursor, putative [Pediculus humanus corporis]
750	CL6983.Contig1_All	Legumain [Chelonia mydas]
751	Unigene20261_All	hypothetical protein TcasGA2_TC009300 [Tribolium castaneum]
752	Unigene142717_All	hypothetical protein CRE_17774 [Caenorhabditis remanei] >gi|308250191|gb|EFO94143.1| hypothetical protein CRE_17774 [Caenorhabditis remanei]
753	Unigene12230_All	AAEL003459-PA [Aedes aegypti]
754	Unigene2768_All	Luciferin 4-monooxygenase [Acromyrmex echinatior]
755	CL9042.Contig2_All	PREDICTED: prefoldin subunit 5-like [Nasonia vitripennis]
755	Unigene21728_All	
756	CL5682.Contig1_All	hypothetical protein SINV_00974 [Solenopsis invicta]
757	CL11676.Contig1_All	PREDICTED: similar to Y-box binding protein isoform 1 [Tribolium castaneum] >gi|270007364|gb|EFA03812.1| hypothetical protein TcasGA2_TC013925 [Tribolium castaneum]
757	CL11676.Contig3_All	
757	CL11676.Contig2_All	
758	Unigene20440_All	PREDICTED: spectrin beta chain-like [Megachile rotundata]
759	Unigene2985_All	RNA-binding protein 1 [Harpegnathos saltator]
760	Unigene27974_All	RecName: Full=Annulin; AltName: Full=Protein-glutamine gamma-glutamyltransferase; AltName: Full=Transglutaminase >gi|160839|gb|AAA29806.1| annulin [Schistocerca americana]
761	CL17733.Contig2_All	PREDICTED: acetyl-coenzyme A synthetase-like [Bombus terrestris]
762	Unigene63726_All	PREDICTED: lipase member H-A-like [Megachile rotundata]
763	Unigene55183_All	RecName: Full=Lachesin; Flags: Precursor >gi|294841|gb|AAC37185.1| lachesin [Schistocerca americana]
764	Unigene27767_All	vesicle-associated membrane protein-associated protein B/C isoform 2 [Homo sapiens] >gi|4240460|gb|AAD13578.1| VAMP-associated protein C [Homo sapiens]
765	Unigene25691_All	Ras-related protein Rab-18 [Pteropus alecto]
766	Unigene72187_All	vacuolar ATPase subunit H [Locusta migratoria manilensis]
767	Unigene35442_All	similar to Hypothetical protein CGI-99, isoform CRA_d [Rattus

		norvegicus]
768	CL1687.Contig1_All	RIKEN cDNA 1810014F10, isoform CRA_h [Mus musculus]
769	CL9646.Contig1_All	hypothetical protein TcasGA2_TC000224 [Tribolium castaneum]
770	CL9127.Contig1_All	hypothetical protein DAPPUDRAFT_306482 [Daphnia pulex]
771	Unigene62300_All	PREDICTED: oligosaccharyltransferase complex subunit ostc-B-like [Nasonia vitripennis]
772	CL6079.Contig1_All	PREDICTED: uncharacterized protein LOC100878663 [Megachile rotundata]
772	CL6079.Contig2_All	
773	Unigene49411_All	Copa protein [Danio rerio]
774	Unigene42468_All	hypothetical protein AND_12480 [Anopheles darlingi]
775	CL13914.Contig2_All	unnamed protein product [Mus musculus]
776	Unigene27713_All	heat shock protein 20.7 [Schistocerca gregaria]
777	Unigene72261_All	ubiquinol-cytochrome c reductase [Locusta migratoria manilensis]
778	CL4506.Contig1_All	vasa-like [Schistocerca gregaria]
779	CL12202.Contig2_All	PREDICTED: 4-trimethylaminobutyraldehyde dehydrogenase-like [Monodelphis domestica]
780	CL1408.Contig1_All	hypothetical protein SINV_02434 [Solenopsis invicta]
781	CL7547.Contig2_All	PREDICTED: malignant T-cell-amplified sequence 1-like [Megachile rotundata]
782	Unigene19364_All	TPA_inf: vesicle coat complex COPI beta' subunit [Amblyomma variegatum]
783	Unigene2536_All	PREDICTED: GDP dissociation inhibitor 2-like [Oryctolagus cuniculus]
784	Unigene25560_All	PREDICTED: similar to dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase [Tribolium castaneum]
785	Unigene27689_All	Ves G 1 allergen precursor, putative [Pediculus humanus corporis] >gi|212507765|gb|EEB11627.1| Ves G 1 allergen precursor, putative [Pediculus humanus corporis]
786	Unigene55897_All	unknown [Tribolium castaneum]
787	Unigene20058_All	eukaryotic translation initiation factor 3 subunit 6 interacting protein, partial [Oryzias melastigma]
788	CL8530.Contig2_All	Anopheles gambiae str. PEST AGAP012474-PA [Anopheles gambiae str. PEST] >gi|116132975|gb|EAA03469.3| AGAP012474-PA [Anopheles gambiae str. PEST]
789	Unigene148533_All	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like [Strongylocentrotus purpuratus]

790	Unigene34913_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212508292|gb|EEB12031.1| conserved hypothetical protein [Pediculus humanus corporis]
791	Unigene32956_All	PREDICTED: uncharacterized protein LOC100875363 [Megachile rotundata]
792	Unigene70653_All	nudix-type motif 5 [Sus scrofa]
793	CL61.Contig1_All	N-alpha-acetyltransferase 38, NatC auxiliary subunit [Chelonia mydas]
794	CL5943.Contig1_All	eukaryotic translation initiation factor 3 subunit F, partial [Papilio polytes]
795	CL5934.Contig1_All	variable lymphocyte receptor A [Eptatretus burgeri]
796	Unigene57320_All	hypothetical protein SINV_08437 [Solenopsis invicta]
797	CL5152.Contig2_All	MIP13670p [Drosophila melanogaster]
797	CL9746.Contig2_All	
797	CL9746.Contig1_All	
798	Unigene2648_All	-
799	Unigene62165_All	60S ribosomal protein L8 [Harpegnathos saltator] >gi|307212337|gb|EFN88141.1| 60S ribosomal protein L8 [Harpegnathos saltator]
800	Unigene12545_All	hypothetical protein SINV_01170 [Solenopsis invicta]
801	Unigene11348_All	hypothetical protein TcasGA2_TC008666 [Tribolium castaneum]
802	Unigene25700_All	hexamerin-like protein 5 [Locusta migratoria]
803	CL11630.Contig1_All	nicotinamide adenine dinucleotide phosphate (NADP[H])-binding protein FX [human, erythrocytes, Peptide Partial, 54 aa, segment 2 of 3]
804	CL7470.Contig2_All	glutathione S-transferase sigma 7 [Locusta migratoria]
805	CL14453.Contig1_All	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial [Camponotus floridanus]
806	CL2876.Contig1_All	chemosensory protein 2 precursor [Tribolium castaneum] >gi|112031657|gb|ABH88176.1| chemosensory protein 2 [Tribolium castaneum] >gi|270004849|gb|EFA01297.1| chemosensory protein 20 [Tribolium castaneum]
806	CL2876.Contig6_All	
807	Unigene12304_All	tar RNA binding protein [Procambarus clarkii]
808	Unigene63926_All	coatomer protein complex subunit beta [Bombyx mori] >gi|284027822|gb|ADB66735.1| coatomer protein complex subunit beta [Bombyx mori]
809	Unigene1040_All	PREDICTED: myosin regulatory light chain sqh-like [Megachile rotundata]

810	Unigene47960_All	arp2/3, putative [Pediculus humanus corporis] >gi|212516742|gb|EEB18716.1| arp2/3, putative [Pediculus humanus corporis]
811	Unigene74153_All	28 kDa heat- and acid-stable phosphoprotein [Camponotus floridanus]
812	Unigene25680_All	Flavin reductase [Harpegnathos saltator]
813	CL2230.Contig2_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212505571|gb|EEB10000.1| conserved hypothetical protein [Pediculus humanus corporis]
813	CL2230.Contig1_All	
813	CL2230.Contig3_All	
814	Unigene35286_All	PREDICTED: dipeptidase 1-like [Nasonia vitripennis]
815	Unigene72525_All	ribosomal protein S6 [Tribolium castaneum]
816	CL488.Contig1_All	PREDICTED: thioredoxin-like 1-like [Saccoglossus kowalevskii]
817	Unigene35402_All	Eukaryotic translation initiation factor 3 subunit K [Camponotus floridanus]
818	Unigene56415_All	PREDICTED: similar to DnaJ homolog subfamily A member 1 [Tribolium castaneum] >gi|270001716|gb|EEZ98163.1| hypothetical protein TcasGA2_TC000590 [Tribolium castaneum]
819	Unigene35063_All	ATP synthase subunit O, mitochondrial [Nasonia vitripennis]
820	CL2045.Contig1_All	Na+,K+ ATPase alpha-subunit 1 [Megacyllene robiniae]
820	CL2045.Contig4_All	
820	CL2045.Contig3_All	
820	CL2045.Contig5_All	
820	CL2045.Contig2_All	
821	CL16060.Contig2_All	hypothetical protein TcasGA2_TC014887 [Tribolium castaneum]
822	Unigene64064_All	Programmed cell death protein 4 [Chelonia mydas]
823	Unigene27503_All	U1 small nuclear ribonucleoprotein A [Bombyx mori] >gi|76496416|gb|ABA43713.1| SNF [Bombyx mori]
824	Unigene20095_All	Annexin-B9 [Acromyrmex echinatior]
825	Unigene27820_All	PREDICTED: protein CDV3 homolog A-like [Megachile rotundata]
826	Unigene11259_All	PREDICTED: 26S proteasome non-ATPase regulatory subunit 7-like [Bombus terrestris]
827	Unigene48478_All	GM23092 [Drosophila sechellia] >gi|194129428|gb|EDW51471.1| GM23092 [Drosophila sechellia]
828	Unigene18177_All	hypothetical protein TcasGA2_TC010770 [Tribolium castaneum]
829	Unigene20078_All	PREDICTED: LOW QUALITY PROTEIN: lipase maturation factor 2, partial [Nomascus leucogenys]

830	CL3.Contig2_All	PREDICTED: similar to B52 CG10851-PA [Tribolium castaneum]
830	Unigene123395_All	
831	CL6511.Contig1_All	proteinase inhibitor serpin, partial [Locusta migratoria]
831	CL6511.Contig3_All	
832	Unigene50317_All	PREDICTED: similar to signal sequence receptor beta subunit [Tribolium castaneum] >gi|270014481|gb|EFA10929.1| hypothetical protein TcasGA2_TC001756 [Tribolium castaneum]
833	Unigene18146_All	cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232759|gb|AFZ38890.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232761|gb|AFZ38891.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232763|gb|AFZ38892.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232765|gb|AFZ38893.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232767|gb|AFZ38894.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232769|gb|AFZ38895.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232771|gb|AFZ38896.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232773|gb|AFZ38897.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232775|gb|AFZ38898.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232777|gb|AFZ38899.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232779|gb|AFZ38900.1| cold shock domain-containing E1 protein, partial [Pterodroma deserta] >gi|428232781|gb|AFZ38901.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232783|gb|AFZ38902.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232785|gb|AFZ38903.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232787|gb|AFZ38904.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232789|gb|AFZ38905.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232791|gb|AFZ38906.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232793|gb|AFZ38907.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232795|gb|AFZ38908.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232797|gb|AFZ38909.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232799|gb|AFZ38910.1|

		cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232801|gb|AFZ38911.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232803|gb|AFZ38912.1| cold shock domain-containing E1 protein, partial [Pterodroma madeira] >gi|428232805|gb|AFZ38913.1| cold shock domain-containing E1 protein, partial [Pterodroma feae] >gi|428232807|gb|AFZ38914.1| cold shock domain-containing E1 protein, partial [Pterodroma feae] >gi|428232809|gb|AFZ38915.1| cold shock domain-containing E1 protein, partial [Pterodroma feae] >gi|428232811|gb|AFZ38916.1| cold shock domain-containing E1 protein, partial [Pterodroma feae] >gi|428232813|gb|AFZ38917.1| cold shock domain-containing E1 protein, partial [Pterodroma feae] >gi|428232815|gb|AFZ38918.1| cold shock domain-containing E1 protein, partial [Pterodroma feae] >gi|428232817|gb|AFZ38919.1| cold shock domain-containing E1 protein, partial [Pterodroma feae] >gi|428232819|gb|AFZ38920.1| cold shock domain-containing E1 protein, partial [Pterodroma feae] >gi|428232821|gb|AFZ38921.1| cold shock domain-containing E1 protein, partial [Pterodroma feae] >gi|428232823|gb|AFZ38922.1| cold shock domain-containing E1 protein, partial [Pterodroma feae]
834	CL15203.Contig1_All	PREDICTED: nidogen-2-like [Nasonia vitripennis]
834	CL15203.Contig2_All	
835	Unigene32148_All	PREDICTED: hypothetical protein LOC100165083 [Acyrthosiphon pisum]
836	Unigene50119_All	60S ribosomal protein L21 [Harpegnathos saltator]
837	Unigene35325_All	PREDICTED: hypothetical protein LOC100116643 [Nasonia vitripennis]
838	CL5898.Contig1_All	Neuroglian precursor, putative [Pediculus humanus corporis] >gi|212515537|gb|EEB17669.1| Neuroglian precursor, putative [Pediculus humanus corporis]
838	CL5898.Contig2_All	
839	CL2317.Contig1_All	GL21588 [Drosophila persimilis] >gi|194112391|gb|EDW34434.1| GL21588 [Drosophila persimilis]
840	Unigene61379_All	-
841	Unigene48022_All	-
842	Unigene44219_All	Chain A, Crystal Structure Of Anopheles Gambiae SerTHR PHOSPHATASE COMPLEXED With Zn2+
843	CL9741.Contig1_All	hypothetical protein SINV_80687 [Solenopsis invicta]
844	CL7643.Contig1_All	PREDICTED: similar to karyopherin alpha 6 [Tribolium castaneum] >gi|270002024|gb|EEZ98471.1| hypothetical protein TcasGA2_TC000963 [Tribolium castaneum]

845	CL6048.Contig1_All	disulfide oxidoreductase [Aedes aegypti] >gi|403183173|gb|EJY57905.1| AAEL011158-PB [Aedes aegypti]
845	CL6048.Contig3_All	
846	Unigene49147_All	RecName: Full=60S ribosomal protein L38 >gi|49532898|dbj|BAD26684.1| Ribosomal protein L38 [Plutella xylostella] >gi|268306456|gb|ACY95349.1| ribosomal protein L38 [Manduca sexta] >gi|308512793|gb|ADO33050.1| ribosomal protein L38 [Biston betularia] >gi|315115463|gb|ADT80704.1| ribosomal protein L38 [Euphydryas aurinia] >gi|342356451|gb|AEL28884.1| ribosomal protein L38 [Heliconius melpomene cythera]
847	CL2864.Contig1_All	hypothetical protein SINV_15420 [Solenopsis invicta]
847	CL2864.Contig4_All	
847	CL2864.Contig2_All	
847	CL2864.Contig3_All	
848	CL14806.Contig2_All	yellow [Culex quinquefasciatus] >gi|167881573|gb|EDS44956.1| yellow [Culex quinquefasciatus]
849	CL1736.Contig3_All	PREDICTED: similar to AGAP000901-PA, partial [Tribolium castaneum]
850	CL6501.Contig1_All	fructose 1,6-bisphosphate aldolase [Schistocerca gregaria]
851	CL15204.Contig2_All	glutamine synthetase [Schistocerca gregaria]
852	Unigene72370_All	PREDICTED: protein BCCIP homolog isoform 1 [Nasonia vitripennis]
853	CL5527.Contig1_All	PREDICTED: inorganic pyrophosphatase-like [Megachile rotundata]
854	Unigene42461_All	FAA [Bos taurus]
855	CL5570.Contig1_All	hypothetical protein AND_22869 [Anopheles darlingi]
855	CL5570.Contig5_All	
855	CL5570.Contig4_All	
855	CL5570.Contig8_All	
855	CL5570.Contig2_All	
856	CL1901.Contig1_All	ATP-binding cassette sub-family E member 1 [Acromyrmex echinatior]
857	Unigene32610_All	PREDICTED: hypothetical protein LOC410581 [Apis mellifera]
858	Unigene12787_All	PREDICTED: transmembrane protein 214-A-like [Apis florea]
859	Unigene39785_All	PREDICTED: eukaryotic translation initiation factor 2A-like [Bombus terrestris]
860	CL15115.Contig1_All	Charged multivesicular body protein 2a [Harpegnathos saltator]

861	CL7300.Contig1_All	GD18485 [Drosophila simulans] >gi|194200286|gb|EDX13862.1| GD18485 [Drosophila simulans]
861	CL7300.Contig2_All	
862	CL4627.Contig1_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167867290|gb|EDS30673.1| conserved hypothetical protein [Culex quinquefasciatus]
862	CL4627.Contig3_All	
862	CL4627.Contig2_All	
863	CL3824.Contig1_All	hypothetical protein [Maconellicoccus hirsutus]
864	Unigene32673_All	GD10202 [Drosophila simulans] >gi|194192535|gb|EDX06111.1| GD10202 [Drosophila simulans]
865	CL2407.Contig1_All	putative vacuolar protein sorting 35 isoform 1 [Danaus plexippus]
865	CL2407.Contig2_All	
866	CL2867.Contig3_All	PREDICTED: importin-9-like [Nasonia vitripennis]
867	Unigene33134_All	Actin-like protein 87C [Camponotus floridanus]
868	CL2119.Contig1_All	reverse transcriptase, partial [Heteropterus morpheus]
869	CL5037.Contig1_All	PREDICTED: similar to AGAP003789-PA [Tribolium castaneum] >gi|270008459|gb|EFA04907.1| hypothetical protein TcasGA2_TC014971 [Tribolium castaneum]
870	CL6097.Contig1_All	hypothetical protein KGM_01982 [Danaus plexippus]
870	CL6097.Contig2_All	
871	Unigene57318_All	putative SUI protein [Cecidostiba fungosa]
872	CL9725.Contig1_All	glutathione S-transferase [Locusta migratoria]
872	CL9725.Contig2_All	
873	Unigene57763_All	hypothetical protein [Locusta migratoria]
874	Unigene71084_All	serine protease inhibitor 11 precursor [Bombyx mori] >gi|195972026|gb|ACG61175.1| serpin-11 [Bombyx mori]
875	Unigene57846_All	26S proteasome non-ATPase regulatory subunit 6 [Harpegnathos saltator]
876	Unigene72534_All	hypothetical protein TcasGA2_TC001043 [Tribolium castaneum]
877	CL13593.Contig1_All	putative glutamate synthase, partial [Laodelphax striatella]
878	CL6701.Contig1_All	hypothetical protein SINV_04490 [Solenopsis invicta]
878	CL6701.Contig2_All	
879	Unigene49950_All	PREDICTED: similar to mitogen-activated protein-binding protein-interacting protein [Tribolium castaneum] >gi|270011751|gb|EFA08199.1| hypothetical protein TcasGA2_TC005826 [Tribolium castaneum]

880	Unigene9559_All	ADP-dependent glucokinase [Camponotus floridanus]
881	Unigene42351_All	glucosyl glucuronosyl transferases [Locusta migratoria]
882	Unigene27952_All	PREDICTED: 40S ribosomal protein S8-like [Megachile rotundata]
883	Unigene42315_All	Soluble NSF attachment protein [Acromyrmex echinatior]
884	CL4897.Contig1_All	gamma-butyrobetaine dioxygenase [Culex quinquefasciatus] >gi|167881772|gb|EDS45155.1| gamma-butyrobetaine dioxygenase [Culex quinquefasciatus]
884	CL4897.Contig4_All	
884	CL4897.Contig6_All	
885	CL4316.Contig8_All	-
886	CL6583.Contig1_All	hypothetical protein SINV_13610 [Solenopsis invicta]
886	CL6583.Contig2_All	
887	Unigene69735_All	multiprotein bridging factor 1 [Papilio xuthus]
888	CL7364.Contig3_All	Chain A, Single Stranded Dna-Binding Domain Of Human Replication Protein A Bound To Single Stranded Dna, Rpa70 Subunit, Residues 183-420
889	Unigene40363_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212505634|gb|EEB10038.1| conserved hypothetical protein [Pediculus humanus corporis]
890	Unigene1926_All	GA17553 [Drosophila affinis]
891	Unigene12497_All	hypothetical protein DAPPUDRAFT_52799 [Daphnia pulex]
892	Unigene25563_All	toll-like receptor [Carcinoscorpius rotundicauda]
893	Unigene27835_All	PREDICTED: developmentally-regulated GTP-binding protein 2-like [Megachile rotundata]
894	Unigene72416_All	-
895	Unigene34919_All	Tyrosyl-tRNA synthetase, cytoplasmic [Harpegnathos saltator]
896	Unigene19904_All	ribosomal protein L19e [Curculio glandium]
897	CL14473.Contig1_All	Chain A, Solution Structure Of The Lipoic Acid-Bearing Domain Of The E2 Component Of Human, Mitochondrial Branched-Chain Alpha- Ketoacid Dehydrogenase >gi|17942551|pdb|1K8M|A Chain A, Solution Structure Of The Lipoic Acid-Bearing Domain Of The E2 Component Of Human, Mitochondrial Branched-Chain Alpha-Ketoacid Dehydrogenase
897	CL14473.Contig2_All	
898	CL11654.Contig1_All	EIP28, putative [Pediculus humanus corporis] >gi|212511056|gb|EEB14105.1| EIP28, putative [Pediculus humanus corporis]
899	CL2774.Contig1_All	shaggy, partial [Biston betularia]
899	CL2774.Contig3_All	

899	CL2774.Contig2_All	
899	CL2774.Contig4_All	
900	CL526.Contig1_All	hypothetical protein SINV_14069 [Solenopsis invicta]
900	CL526.Contig2_All	
900	CL526.Contig4_All	
900	CL526.Contig5_All	
900	CL526.Contig3_All	
901	Unigene49875_All	cactin [Papilio xuthus]
902	Unigene64693_All	UMO-1 activating enzyme [Heliconius numata aurora]
903	Unigene17679_All	glycogen synthase [Locusta migratoria]
904	Unigene57441_All	hypothetical protein DAPPUDRAFT_334837 [Daphnia pulex]
905	Unigene11272_All	RhoA activator C11orf59-like protein [Acromyrmex echinatior]
906	CL5053.Contig2_All	sideroflexin 1,2,3 [Culex quinquefasciatus] >gi|167866826|gb|EDS30209.1| sideroflexin 1,2,3 [Culex quinquefasciatus]
906	CL5053.Contig3_All	
907	Unigene63719_All	hypothetical protein TcasGA2_TC005990 [Tribolium castaneum]
908	Unigene64975_All	PREDICTED: similar to COP9 complex homolog subunit 6 CG6932-PA [Tribolium castaneum] >gi|270016217|gb|EFA12663.1| hypothetical protein TcasGA2_TC002246 [Tribolium castaneum]
909	CL6774.Contig1_All	hypothetical protein TcasGA2_TC001438 [Tribolium castaneum]
909	CL6774.Contig2_All	
910	Unigene41257_All	aprt [Drosophila pseudoobscura pseudoobscura] >gi|198150078|gb|EAL31079.3| aprt [Drosophila pseudoobscura pseudoobscura]
911	CL3844.Contig3_All	Fc receptor, IgE, low affinity II, alpha polypeptide isoform b [Rattus norvegicus] >gi|149015581|gb|EDL74962.1| Fc receptor, IgE, low affinity II, alpha polypeptide, isoform CRA_d [Rattus norvegicus]
912	Unigene64827_All	ribosomal protein L7Ae [Scarabaeus laticollis]
913	CL2564.Contig1_All	DNA damage-binding protein, putative [Pediculus humanus corporis] >gi|212510165|gb|EEB13380.1| DNA damage-binding protein, putative [Pediculus humanus corporis]
914	Unigene63549_All	PREDICTED: actin-related protein 2/3 complex subunit 1A [Papio anubis]
915	CL16271.Contig1_All	hypothetical protein TcasGA2_TC013119 [Tribolium castaneum]
916	Unigene27917_All	PREDICTED: translocon-associated protein subunit delta-like [Bombus impatiens]

917	Unigene34768_All	sorbitol dehydrogenase-2 [Papilio xuthus]
918	CL16491.Contig3_All	hypothetical protein KGM_01561 [Danaus plexippus]
919	Unigene57589_All	rCG60635, isoform CRA_a [Rattus norvegicus]
920	CL17631.Contig1_All	acid methyltransferase, putative [Ixodes scapularis] >gi|215492041|gb|EEC01682.1| acid methyltransferase, putative [Ixodes scapularis]
921	CL8735.Contig2_All	PREDICTED: hypothetical protein LOC726093 [Apis mellifera]
922	CL10086.Contig1_All	blackjack [Schistocerca americana]
922	CL10086.Contig6_All	
922	CL10086.Contig5_All	
923	Unigene49852_All	PREDICTED: similar to MGC107831 protein [Tribolium castaneum] >gi|270011250|gb|EFA07698.1| hypothetical protein TcasGA2_TC002174 [Tribolium castaneum]
924	Unigene53964_All	-
925	Unigene48103_All	unknown [Dendroctonus ponderosae]
926	CL3222.Contig2_All	hypothetical protein DAPPUDRAFT_54753 [Daphnia pulex]
927	Unigene27528_All	S-phase kinase-associated protein 1 [Camponotus floridanus] >gi|307199189|gb|EFN79876.1| S-phase kinase-associated protein 1 [Harpegnathos saltator] >gi|332025844|gb|EGI66000.1| S-phase kinase-associated protein 1 [Acromyrmex echinatior]
928	Unigene2831_All	aldo-keto reductase [Reticulitermes flavipes]
929	CL11352.Contig1_All	hypothetical protein KGM_11297 [Danaus plexippus]
929	CL11352.Contig2_All	
929	CL11352.Contig6_All	
929	CL11352.Contig3_All	
929	CL11352.Contig4_All	
929	CL11352.Contig5_All	
930	CL4177.Contig3_All	hypothetical protein [Trichomonas vaginalis G3] >gi|121902235|gb|EAY07229.1| hypothetical protein TVAG_050450 [Trichomonas vaginalis G3]
930	Unigene115602_All	
931	Unigene11145_All	NADH-ubiquinone oxidoreductase B8 subunit [Loa loa]
932	Unigene39687_All	hypothetical protein WUBG_12878 [Wuchereria bancrofti]
933	Unigene47533_All	hypothetical protein IscW_ISCW007279 [Ixodes scapularis] >gi|215501461|gb|EEC10955.1| hypothetical protein IscW_ISCW007279 [Ixodes scapularis]
934	CL1112.Contig2_All	PREDICTED: serine/threonine-protein phosphatase 5-like [Megachile rotundata]

935	Unigene19390_All	PREDICTED: apoptosis-inducing factor 1, mitochondrial-like, partial [Ornithorhynchus anatinus]
936	Unigene2636_All	PREDICTED: dual specificity mitogen-activated protein kinase kinase 6-like [Bombus terrestris]
937	Unigene35061_All	PRO2242 [Homo sapiens]
938	Unigene27446_All	PREDICTED: uncharacterized protein LOC101243185 [Ciona intestinalis]
939	Unigene64645_All	PREDICTED: 26S proteasome non-ATPase regulatory subunit 5-like [Sus scrofa]
940	CL6794.Contig1_All	PREDICTED: similar to serine protease [Tribolium castaneum]
940	CL6794.Contig2_All	
941	CL419.Contig1_All	hypothetical protein AND_14252 [Anopheles darlingi]
941	CL419.Contig3_All	
942	CL7470.Contig1_All	glutathione S-transferase sigma 6 [Locusta migratoria]
943	CL11195.Contig1_All	hypothetical protein KGM_15670 [Danaus plexippus]
944	Unigene10307_All	AGAP010476-PA [Anopheles gambiae str. PEST] >gi|157018348|gb|EAA07158.4| AGAP010476-PA [Anopheles gambiae str. PEST]
945	Unigene9264_All	PREDICTED: alpha-tocopherol transfer protein-like [Megachile rotundata]
946	Unigene54518_All	-
947	CL9133.Contig1_All	Ras-like protein 3 [Harpegnathos saltator]
948	CL5796.Contig1_All	hypothetical protein AND_22238 [Anopheles darlingi]
949	Unigene12952_All	PREDICTED: sarcoplasmic calcium-binding protein-like [Megachile rotundata]
950	Unigene65145_All	hypothetical protein AND_05592 [Anopheles darlingi]
951	Unigene1457_All	PREDICTED: UBX domain-containing protein 1-like [Acyrthosiphon pisum]
952	CL16099.Contig1_All	hypothetical protein NEMVEDRAFT_v1g153571 [Nematostella vectensis] >gi|156200119|gb|EDO26630.1| predicted protein [Nematostella vectensis]
953	CL15034.Contig1_All	adenylsulphate kinase, partial [Papilio polytes]
953	CL15034.Contig2_All	
954	Unigene77590_All	elongation factor 2 [Salpingoeca sp. ATCC 50818]
955	CL7809.Contig1_All	Aquaporin AQPcic, putative [Pediculus humanus corporis] >gi|212514414|gb|EEB16742.1| Aquaporin AQPcic, putative [Pediculus humanus corporis]
955	CL7809.Contig2_All	
956	CL8167.Contig1_All	hypothetical protein AND_11867 [Anopheles darlingi]
956	CL8167.Contig2_All	
956	CL8167.Contig3_All	

957	Unigene65007_All	hypothetical protein DAPPUDRAFT_187536 [Daphnia pulex]
958	CL8527.Contig1_All	PREDICTED: L-lactate dehydrogenase-like isoform 2 [Bombus impatiens]
958	CL8527.Contig2_All	
959	Unigene51119_All	-
960	Unigene50282_All	THUMP domain containing 1 [Rattus norvegicus]
961	Unigene12331_All	DnaJ-like protein subfamily A member 1 [Harpegnathos saltator]
962	CL2883.Contig1_All	hypothetical protein SINV_10014 [Solenopsis invicta]
962	CL2883.Contig3_All	
963	CL4422.Contig1_All	Threonyl-tRNA synthetase, cytoplasmic, putative [Pediculus humanus corporis] >gi|212518045|gb|EEB19847.1| Threonyl-tRNA synthetase, cytoplasmic, putative [Pediculus humanus corporis]
964	Unigene54773_All	hypothetical protein BRAFLDRAFT_248156 [Branchiostoma floridae] >gi|229273848|gb|EEN44691.1| hypothetical protein BRAFLDRAFT_248156 [Branchiostoma floridae]
965	Unigene42664_All	Cytochrome c oxidase subunit 5B, mitochondrial [Harpegnathos saltator]
966	Unigene69951_All	hypothetical protein SINV_14764 [Solenopsis invicta]
967	Unigene55317_All	Retinol dehydrogenase 14 [Harpegnathos saltator]
968	CL5648.Contig8_All	hypothetical protein DAPPUDRAFT_226211 [Daphnia pulex]
969	Unigene72738_All	Dappu_192333-like protein [Daphnia pulex]
970	CL2801.Contig1_All	PREDICTED: sestrin homolog [Apis florea]
970	CL2801.Contig2_All	
971	Unigene70028_All	PREDICTED: similar to acid alpha-glucosidase [Tribolium castaneum]
972	Unigene20135_All	Mediator of RNA polymerase II transcription subunit 20 [Acromyrmex echinatior]
973	Unigene11590_All	GM14238p [Drosophila melanogaster]
974	CL10185.Contig1_All	Sequestosome-1 [Camponotus floridanus]
974	CL10185.Contig2_All	
975	Unigene42699_All	GD25036 [Drosophila simulans] >gi|194194815|gb|EDX08391.1| GD25036 [Drosophila simulans]
976	Unigene32709_All	GSTO1 [Locusta migratoria]
977	CL15740.Contig1_All	PREDICTED: aminoacylase-1A-like [Acyrthosiphon pisum]
978	CL761.Contig1_All	PREDICTED: echinoderm microtubule-associated protein-like 1-like isoform 2 [Acyrthosiphon pisum]
978	CL761.Contig9_All	

978	CL761.Contig6_All	
978	CL761.Contig8_All	
978	CL761.Contig2_All	
978	CL761.Contig5_All	
978	CL761.Contig3_All	
978	CL761.Contig4_All	
979	CL2642.Contig1_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167868598|gb|EDS31981.1| conserved hypothetical protein [Culex quinquefasciatus]
979	CL2642.Contig2_All	
980	CL13849.Contig2_All	PREDICTED: uncharacterized protein LOC100877842 [Megachile rotundata]
981	Unigene27717_All	mitochondrial ribosomal protein S31-like protein [Scylla paramamosain]
982	Unigene1067_All	regulator of chromosome condensation [Culex quinquefasciatus] >gi|167878220|gb|EDS41603.1| regulator of chromosome condensation [Culex quinquefasciatus]
983	Unigene72464_All	hypothetical protein TcasGA2_TC004962 [Tribolium castaneum]
984	CL1870.Contig2_All	Splicing factor U2AF 50 kDa subunit [Camponotus floridanus]
985	CL822.Contig1_All	NADPH cytochrome b5 reductase [Helicoverpa armigera]
985	CL822.Contig2_All	
986	CL9710.Contig1_All	PREDICTED: similar to glutathione peroxidase [Tribolium castaneum]
986	CL9710.Contig2_All	
987	CL12784.Contig1_All	PREDICTED: similar to GA20113-PA [Tribolium castaneum] >gi|270004043|gb|EFA00491.1| hypothetical protein TcasGA2_TC003351 [Tribolium castaneum]
987	CL12784.Contig2_All	
988	CL5314.Contig2_All	signal recognition particle receptor, alpha subunit, putative [Ixodes scapularis] >gi|215501564|gb|EEC11058.1| signal recognition particle receptor, alpha subunit, putative [Ixodes scapularis]
988	CL5314.Contig3_All	
989	Unigene142143_All	-
990	Unigene26800_All	mCG128607 [Mus musculus]
991	Unigene27928_All	PREDICTED: calcineurin-like phosphoesterase domain-containing protein 1-like, partial [Anolis carolinensis]

992	CL9044.Contig1_All	PREDICTED: hypothetical protein [Tribolium castaneum] >gi|270003229|gb|EEZ99676.1| hypothetical protein TcasGA2_TC002433 [Tribolium castaneum]
992	CL9044.Contig2_All	
993	CL14206.Contig1_All	PREDICTED: uncharacterized protein LOC100881900 [Megachile rotundata]
993	CL14206.Contig2_All	
994	Unigene55164_All	similar to Drosophila melanogaster CG8031, partial [Drosophila yakuba]
995	Unigene19986_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212518590|gb|EEB20336.1| conserved hypothetical protein [Pediculus humanus corporis]
996	Unigene72506_All	SPFH domain-containing protein 1 precursor, putative [Pediculus humanus corporis] >gi|212507835|gb|EEB11697.1| SPFH domain-containing protein 1 precursor, putative [Pediculus humanus corporis]
997	Unigene9493_All	glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651925|emb|CAE51216.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651927|emb|CAE51217.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651929|emb|CAE51218.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651931|emb|CAE51219.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651933|emb|CAE51220.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651935|emb|CAE51221.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651939|emb|CAE51223.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651941|emb|CAE51224.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651943|emb|CAE51225.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651945|emb|CAE51226.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651947|emb|CAE51227.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata] >gi|37651949|emb|CAE51228.1| glucose 6 phosphate dehydrogenase [Adalia bipunctata]
998	Unigene34981_All	cutA divalent cation tolerance homolog (E. coli), isoform CRA_c [Mus musculus]
999	Unigene35139_All	unnamed protein product [Mus musculus]
1000	Unigene32763_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212517061|gb|EEB19008.1| conserved hypothetical protein

		[Pediculus humanus corporis]
1001	CL16646.Contig3_All	PREDICTED: septin-1-like [Bombus impatiens] >gi|380027389|ref|XP_003697408.1| PREDICTED: septin-1-like [Apis florea]
1002	Unigene2816_All	hypothetical protein SINV_01503 [Solenopsis invicta]
1003	Unigene27772_All	protein SET, putative [Pediculus humanus corporis] >gi|212508028|gb|EEB11847.1| protein SET, putative [Pediculus humanus corporis]
1004	Unigene56657_All	Chain A, Solution Structure Of The Pci Domain
1005	Unigene41170_All	aldo-keto reductase [Reticulitermes flavipes]
1006	Unigene57831_All	unknown [Dendroctonus ponderosae]
1007	CL5603.Contig3_All	hypothetical protein EAG_07565 [Camponotus floridanus]
1007	CL5603.Contig5_All	
1007	CL5603.Contig8_All	
1007	CL5603.Contig4_All	
1008	Unigene55095_All	PREDICTED: AMP deaminase 2-like [Apis mellifera]
1009	Unigene56144_All	GI15909 [Drosophila mojavensis] >gi|193908860|gb|EDW07727.1| GI15909 [Drosophila mojavensis]
1010	Unigene50075_All	PREDICTED: similar to heat shock protein 1 [Tribolium castaneum] >gi|270010666|gb|EFA07114.1| hypothetical protein TcasGA2_TC010105 [Tribolium castaneum]
1011	Unigene10125_All	PREDICTED: hypothetical protein LOC100741236 [Bombus impatiens]
1012	CL6817.Contig1_All	PREDICTED: spectrin beta chain [Apis mellifera]
1013	Unigene33343_All	GI21469 [Drosophila mojavensis] >gi|193907666|gb|EDW06533.1| GI21469 [Drosophila mojavensis]
1014	Unigene19877_All	PREDICTED: cullin-associated NEDD8-dissociated protein 1 [Saimiri boliviensis boliviensis]
1015	Unigene41621_All	expressed hypothetical protein [Trichoplax adhaerens] >gi|190580074|gb|EDV20160.1| expressed hypothetical protein [Trichoplax adhaerens]
1016	Unigene64900_All	Sorting nexin-12 [Camponotus floridanus]
1017	Unigene20298_All	PREDICTED: similar to snare protein sec22 [Tribolium castaneum] >gi|270005842|gb|EFA02290.1| hypothetical protein TcasGA2_TC007954 [Tribolium castaneum]

1018	CL15969.Contig1_All	Charged multivesicular body protein 4C, putative [Pediculus humanus corporis] >gi|212506086|gb|EEB10402.1| Charged multivesicular body protein 4C, putative [Pediculus humanus corporis]
1019	Unigene25011_All	hypothetical protein C07A12.7 - Caenorhabditis elegans
1019	Unigene25013_All	
1020	Unigene24757_All	yellow [Tribolium castaneum]
1021	Unigene64701_All	Death-associated protein 1 [Camponotus floridanus]
1022	Unigene63394_All	hypothetical protein AND_11577 [Anopheles darlingi]
1023	CL11384.Contig1_All	Nucleoprotein TPR [Camponotus floridanus]
1023	CL11384.Contig2_All	
1024	CL6244.Contig1_All	Reticulon-1 [Camponotus floridanus]
1024	CL6244.Contig3_All	
1024	CL6244.Contig2_All	
1025	Unigene72384_All	signal recognition particle [Triatoma infestans]
1026	Unigene50234_All	hoip-prov protein isoform A [Lysiphlebus testaceipes]
1027	CL1848.Contig1_All	hypothetical protein DAPPUDRAFT_8978 [Daphnia pulex]
1027	CL1848.Contig2_All	
1028	Unigene20319_All	casein kinase 2, beta polypeptide, isoform CRA_c [Homo sapiens]
1029	Unigene12881_All	ADP-ribosylation factor-like protein 2 [Laodelphax striatella]
1030	Unigene9667_All	PREDICTED: signal recognition particle receptor subunit beta-like [Megachile rotundata]
1031	Unigene42645_All	hypothetical protein EAI_14301 [Harpegnathos saltator]
1032	CL3433.Contig3_All	PREDICTED: serpin B3 [Bos taurus]
1032	CL3433.Contig4_All	
1033	CL15974.Contig1_All	protein ROP, putative [Pediculus humanus corporis] >gi|212515758|gb|EEB17848.1| protein ROP, putative [Pediculus humanus corporis]
1033	CL15974.Contig2_All	
1034	CL7636.Contig1_All	phosphoacetylglucosamine mutase [Trichinella spiralis] >gi|316956870|gb|EFV46946.1| phosphoacetylglucosamine mutase [Trichinella spiralis]
1035	Unigene72519_All	predicted protein [Nematostella vectensis] >gi|156223847|gb|EDO44678.1| predicted protein [Nematostella vectensis]
1036	CL5013.Contig2_All	PREDICTED: similar to mitochondrial oxodicarboxylate carrier [Tribolium castaneum] >gi|270006043|gb|EFA02491.1| hypothetical protein TcasGA2_TC008186 [Tribolium castaneum]

1037	CL15914.Contig1_All	hypothetical protein SINV_13673 [Solenopsis invicta]
1038	Unigene40854_All	UDP-N-acetylglucosamine pyrophosphorylase [Nilaparvata lugens]
1039	CL10977.Contig2_All	SKB1-like [Ictalurus punctatus]
1040	CL2528.Contig4_All	PREDICTED: synaptobrevin homolog YKT6-like isoform 1 [Nasonia vitripennis] >gi|345485320|ref|XP_003425242.1| PREDICTED: synaptobrevin homolog YKT6-like isoform 2 [Nasonia vitripennis]
1041	CL13276.Contig1_All	PREDICTED: valacyclovir hydrolase isoform 3 [Gorilla gorilla gorilla]
1041	CL13276.Contig2_All	
1042	Unigene32940_All	hypothetical protein Phum_PHUM556460 [Pediculus humanus corporis] >gi|212517227|gb|EEB19148.1| hypothetical protein Phum_PHUM556460 [Pediculus humanus corporis]
1043	CL13333.Contig1_All	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2 [Acromyrmex echinatior]
1043	CL13333.Contig2_All	
1044	CL4490.Contig1_All	pre-mRNA-splicing factor clf-1, putative [Pediculus humanus corporis] >gi|212509866|gb|EEB13152.1| pre-mRNA-splicing factor clf-1, putative [Pediculus humanus corporis]
1045	CL5114.Contig1_All	serine/threonine-protein phosphatase 2a catalytic subunit alpha isoform-like protein, partial [Equus caballus]
1046	Unigene49823_All	hypothetical protein [Locusta migratoria]
1047	CL3850.Contig1_All	PREDICTED: 60S ribosomal protein L34-like [Apis florea]
1048	Unigene2778_All	ribosomal protein L22 [Lysiphlebus testaceipes]
1049	CL12862.Contig2_All	Zinc finger protein 207 [Caligus clemensi]
1050	Unigene34918_All	PREDICTED: nicalin-1-like [Nasonia vitripennis]
1051	Unigene49893_All	PREDICTED: 6-pyruvoyl tetrahydrobiopterin synthase-like [Nasonia vitripennis]
1052	CL5418.Contig1_All	hypothetical protein SINV_14360 [Solenopsis invicta]
1052	CL5418.Contig2_All	
1053	Unigene34860_All	hypothetical protein KGM_09507 [Danaus plexippus]
1054	Unigene11939_All	COP9 constitutive photomorphogenic subunit 3-like protein, partial [Spea multiplicata] >gi|388899926|gb|AFJ79014.2| COP9 constitutive photomorphogenic subunit 3-like protein 3, partial [Spea bombifrons]
1055	CL14924.Contig1_All	PREDICTED: similar to glycoprotein 25l [Tribolium castaneum] >gi|270001537|gb|EEZ97984.1| hypothetical protein TcasGA2_TC000379 [Tribolium castaneum]

1056	CL2431.Contig1_All	PREDICTED: hypothetical protein LOC100748178 [Bombus impatiens]
1056	CL2431.Contig3_All	
1056	Unigene125334_All	
1056	Unigene125335_All	
1057	CL14783.Contig1_All	hypothetical protein SINV_15055 [Solenopsis invicta]
1058	Unigene20384_All	PREDICTED: protein catecholamines up [Apis mellifera]
1059	CL2946.Contig4_All	PREDICTED: similar to ATP synthase delta chain, mitochondrial [Tribolium castaneum] >gi|270008191|gb|EFA04639.1| hypothetical protein TcasGA2_TC013931 [Tribolium castaneum]
1060	Unigene40413_All	PREDICTED: similar to AGAP005127-PA [Tribolium castaneum]
1061	Unigene42308_All	hypothetical protein TcasGA2_TC014264 [Tribolium castaneum]
1062	Unigene27433_All	PREDICTED: histone acetyltransferase type B catalytic subunit-like [Nasonia vitripennis]
1063	Unigene64075_All	GM14862p [Drosophila melanogaster]
1064	CL3281.Contig1_All	60S ribosomal protein L15, putative [Pediculus humanus corporis] >gi|212510707|gb|EEB13832.1| 60S ribosomal protein L15, putative [Pediculus humanus corporis]
1065	CL4500.Contig5_All	protein 4.1G, putative [Ixodes scapularis] >gi|215504448|gb|EEC13942.1| protein 4.1G, putative [Ixodes scapularis]
1065	CL4500.Contig8_All	
1065	CL4500.Contig9_All	
1066	Unigene49850_All	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 [Crassostrea gigas]
1067	Unigene32439_All	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial-like [Amphimedon queenslandica]
1068	Unigene49939_All	PREDICTED: LOW QUALITY PROTEIN: interferon-related developmental regulator 1-like [Megachile rotundata]
1069	Unigene48789_All	PREDICTED: 60S ribosomal protein L18-like [Apis florea]
1070	CL559.Contig1_All	PREDICTED: carboxypeptidase N subunit 2 [Taeniopygia guttata]
1071	CL11325.Contig3_All	hypothetical protein SINV_12772 [Solenopsis invicta]
1072	Unigene12750_All	vacuolar H+ ATP synthase 16 kDa proteolipid subunit [Apis mellifera] >gi|33521676|gb|AAQ21381.1| vacuolar H+ ATP synthase 16 kDa proteolipid subunit [Apis mellifera]

1073	Unigene64641_All	PREDICTED: COP9 signalosome complex subunit 8-like [Apis florea]
1074	Unigene55520_All	hypothetical protein SINV_02451 [Solenopsis invicta]
1075	Unigene70248_All	Tryptophanyl-tRNA synthetase, putative [Pediculus humanus corporis] >gi|212516396|gb|EEB18409.1| Tryptophanyl-tRNA synthetase, putative [Pediculus humanus corporis]
1076	Unigene87751_All	PREDICTED: synaptic vesicle membrane protein VAT-1 homolog isoform 1 [Acyrthosiphon pisum]
1077	CL2953.Contig1_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167874806|gb|EDS38189.1| conserved hypothetical protein [Culex quinquefasciatus]
1077	CL2953.Contig2_All	
1078	CL14673.Contig1_All	Chain A, Structural Analysis Of A Cytoplasmic Dynein Light Chain-Intermediate Chain Complex >gi|149243128|pdb|2PG1|B Chain B, Structural Analysis Of A Cytoplasmic Dynein Light Chain-Intermediate Chain Complex >gi|149243129|pdb|2PG1|C Chain C, Structural Analysis Of A Cytoplasmic Dynein Light Chain-Intermediate Chain Complex >gi|149243130|pdb|2PG1|D Chain D, Structural Analysis Of A Cytoplasmic Dynein Light Chain-Intermediate Chain Complex >gi|237640495|pdb|3DVT|A Chain A, Biochemical And Structural Characterization Of The Pak1- Lc8 Interaction >gi|237640496|pdb|3DVT|B Chain B, Biochemical And Structural Characterization Of The Pak1- Lc8 Interaction >gi|237640497|pdb|3DVT|C Chain C, Biochemical And Structural Characterization Of The Pak1- Lc8 Interaction >gi|237640498|pdb|3DVT|D Chain D, Biochemical And Structural Characterization Of The Pak1- Lc8 Interaction >gi|237640499|pdb|3DVT|E Chain E, Biochemical And Structural Characterization Of The Pak1- Lc8 Interaction >gi|237640500|pdb|3DVT|F Chain F, Biochemical And Structural Characterization Of The Pak1- Lc8 Interaction
1079	CL5198.Contig1_All	oxoglutarate/malate carrier protein, putative [Ixodes scapularis] >gi|215496609|gb|EEC06249.1| oxoglutarate/malate carrier protein, putative [Ixodes scapularis]
1080	CL16928.Contig1_All	croquemort [Culex quinquefasciatus] >gi|167873895|gb|EDS37278.1| croquemort [Culex quinquefasciatus]
1081	CL1640.Contig1_All	histone deacetylase [Periplaneta americana]
1081	CL1640.Contig2_All	
1082	Unigene34887_All	PREDICTED: replication factor C subunit 2-like [Taeniopygia

		guttata]
1083	Unigene20026_All	GM20399 [Drosophila sechellia] >gi|194125426|gb|EDW47469.1| GM20399 [Drosophila sechellia]
1084	CL1987.Contig2_All	putative adenylosuccinate synthetase [Danaus plexippus]
1085	CL7859.Contig3_All	RecName: Full=Fasciclin-1; AltName: Full=Fasciclin I; Short=FAS I; Short=FCN; Flags: Precursor >gi|160847|gb|AAA29809.1| FCN I precursor [Schistocerca americana]
1086	CL1317.Contig1_All	hypothetical protein TcasGA2_TC005451 [Tribolium castaneum]
1086	CL1317.Contig2_All	
1087	CL9750.Contig1_All	PREDICTED: general vesicular transport factor p115-like, partial [Ailuropoda melanoleuca]
1087	CL9750.Contig2_All	
1088	Unigene34952_All	PREDICTED: synaptic vesicle membrane protein VAT-1 homolog isoform 2 [Acyrthosiphon pisum]
1089	CL2453.Contig1_All	argonaute-2, partial [Schistocerca gregaria]
1089	Unigene47415_All	
1090	CL9080.Contig1_All	PREDICTED: ATP-dependent RNA helicase DDX42, partial [Ornithorhynchus anatinus]
1090	CL9080.Contig3_All	
1091	Unigene55751_All	PREDICTED: alpha-aminoadipic semialdehyde dehydrogenase [Gorilla gorilla gorilla]
1092	Unigene47897_All	ribosomal protein L28 [Lysiphlebus testaceipes]
1093	CL16830.Contig1_All	PREDICTED: similar to glucosyl/glucuronosyl transferases [Tribolium castaneum]
1094	Unigene72331_All	hypothetical protein TRIADDRAFT_62141 [Trichoplax adhaerens] >gi|190579303|gb|EDV19401.1| hypothetical protein TRIADDRAFT_62141 [Trichoplax adhaerens]
1095	Unigene12698_All	hypothetical protein SINV_15401 [Solenopsis invicta]
1096	Unigene40431_All	Cell division protein kinase 10 [Harpegnathos saltator]
1097	Unigene19946_All	PREDICTED: similar to AGAP005618-PA [Tribolium castaneum] >gi|270002697|gb|EEZ99144.1| hypothetical protein TcasGA2_TC012925 [Tribolium castaneum]
1098	Unigene65104_All	Eukaryotic translation initiation factor 4E [Harpegnathos saltator]
1099	Unigene42186_All	PREDICTED: putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15-like [Megachile rotundata]
1100	CL9990.Contig3_All	hypothetical protein SINV_80414 [Solenopsis invicta]

1100	CL9990.Contig2_All	
1101	CL2568.Contig1_All	hypothetical protein KGM_21235 [Danaus plexippus]
1101	CL2568.Contig3_All	
1102	Unigene64810_All	hypothetical protein AND_22869 [Anopheles darlingi]
1103	CL9608.Contig1_All	PREDICTED: cytoglobin-2-like isoform 1 [Bombus terrestris] >gi|340716700|ref|XP_003396833.1| PREDICTED: cytoglobin-2-like isoform 2 [Bombus terrestris]
1104	Unigene72337_All	PREDICTED: enhancer of yellow 2 transcription factor [Apis mellifera]
1105	CL16830.Contig2_All	PREDICTED: similar to glucosyl/glucuronosyl transferases [Tribolium castaneum]
1106	Unigene69647_All	MAP kinase JNK [Aedes albopictus]
1107	Unigene18802_All	Probable phospholipid hydroperoxide glutathione peroxidase [Harpegnathos saltator]
1108	Unigene11314_All	putative Nucleolar GTP-binding protein [Danaus plexippus]
1109	CL13200.Contig1_All	dihydropyrimidinase [Xenopus laevis] >gi|54311199|gb|AAH84771.1| LOC495311 protein [Xenopus laevis]
1109	CL13200.Contig3_All	
1109	CL13200.Contig2_All	
1109	CL13200.Contig4_All	
1110	Unigene2618_All	hypothetical protein SINV_09190 [Solenopsis invicta]
1111	Unigene35203_All	PREDICTED: GTP-binding protein Rheb homolog [Megachile rotundata]
1112	CL2638.Contig1_All	Protein lingerer [Harpegnathos saltator]
1113	Unigene18098_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167875259|gb|EDS38642.1| conserved hypothetical protein [Culex quinquefasciatus]
1114	Unigene42242_All	RNA-binding protein 8A, putative [Pediculus humanus corporis] >gi|212513184|gb|EEB15812.1| RNA-binding protein 8A, putative [Pediculus humanus corporis]
1115	Unigene21842_All	glyceraldehyde 3-phosphate dehydrogenase [Schistosoma japonicum]
1116	CL2588.Contig2_All	thioredoxin-like protein [Cherax quadricarinatus]
1117	Unigene41187_All	PREDICTED: similar to putative prefoldin [Tribolium castaneum] >gi|270002137|gb|EEZ98584.1| hypothetical protein TcasGA2_TC001098 [Tribolium castaneum]
1118	Unigene41047_All	Serine/threonine-protein phosphatase 6 [Harpegnathos saltator]
1119	Unigene57565_All	GrpE protein-like protein 1, mitochondrial [Harpegnathos saltator]

1120	CL15987.Contig1_All	hypothetical protein TcasGA2_TC011089 [Tribolium castaneum]
1120	CL15987.Contig2_All	
1121	Unigene35204_All	hypothetical protein TcasGA2_TC014551 [Tribolium castaneum]
1122	Unigene56689_All	hypothetical protein AND_16069 [Anopheles darlingi]
1123	Unigene12403_All	GJ13165 [Drosophila virilis] >gi|194154111|gb|EDW69295.1| GJ13165 [Drosophila virilis]
1124	Unigene25569_All	blackjack [Schistocerca americana]
1125	CL7755.Contig1_All	PREDICTED: apoptosis inhibitor 5-like [Megachile rotundata]
1126	Unigene24912_All	-
1126	Unigene24914_All	
1126	Unigene24913_All	
1127	CL682.Contig1_All	hypothetical protein DAPPUDRAFT_64017 [Daphnia pulex]
1127	CL682.Contig3_All	
1127	Unigene28991_All	
1127	CL682.Contig7_All	
1127	CL682.Contig5_All	
1127	CL682.Contig2_All	
1128	CL8562.Contig1_All	hypothetical protein [Monosiga brevicollis MX1] >gi|163775698|gb|EDQ89321.1| predicted protein [Monosiga brevicollis MX1]
1128	CL8562.Contig2_All	
1129	Unigene104155_All	VEGF27Ca [Danaus plexippus]
1130	CL155.Contig1_All	hypothetical protein TcasGA2_TC000163 [Tribolium castaneum]
1130	CL155.Contig2_All	
1131	CL15432.Contig1_All	PREDICTED: transportin-1-like [Bombus terrestris]
1131	CL15432.Contig2_All	
1132	CL2827.Contig1_All	PREDICTED: protein dpy-30 homolog [Megachile rotundata]
1133	Unigene25413_All	ribosomal protein S29 [Chrysomela tremula]
1134	Unigene35253_All	GD11125 [Drosophila simulans] >gi|194193647|gb|EDX07223.1| GD11125 [Drosophila simulans]
1134	Unigene85227_All	
1134	Unigene85375_All	
1135	Unigene64974_All	hypothetical protein TcasGA2_TC010676 [Tribolium castaneum]
1136	Unigene50397_All	Small ubiquitin-related modifier [Camponotus floridanus]

1137	CL4544.Contig2_All	low-density lipoprotein receptor, putative [Pediculus humanus corporis] >gi|212515374|gb|EEB17529.1| low-density lipoprotein receptor, putative [Pediculus humanus corporis]
1138	Unigene47847_All	Eukaryotic translation initiation factor 3 subunit J [Harpegnathos saltator]
1139	CL12118.Contig1_All	hypothetical protein Phum_PHUM515410 [Pediculus humanus corporis] >gi|212516455|gb|EEB18468.1| hypothetical protein Phum_PHUM515410 [Pediculus humanus corporis]
1139	CL12118.Contig2_All	
1140	Unigene64853_All	ribosomal protein L24e [Blattella germanica]
1141	CL2390.Contig2_All	PREDICTED: cytochrome P450 6k1-like [Bombus terrestris]
1142	CL10478.Contig1_All	guanine nucleotide-binding protein Gq alpha subunit [Bemisia tabaci]
1143	CL11246.Contig2_All	hypothetical protein SINV_06331 [Solenopsis invicta]
1144	Unigene34770_All	PREDICTED: alpha-L-fucosidase-like [Strongylocentrotus purpuratus]
1145	CL6013.Contig1_All	unnamed protein product [Tetraodon nigroviridis]
1145	CL6013.Contig2_All	
1146	Unigene35326_All	Leukotriene A-4 hydrolase [Harpegnathos saltator]
1147	CL16011.Contig1_All	GM25731 [Drosophila sechellia] >gi|194119911|gb|EDW41954.1| GM25731 [Drosophila sechellia]
1147	CL16011.Contig2_All	
1148	Unigene27784_All	PREDICTED: similar to Proteasome p44.5 subunit CG10149-PB [Tribolium castaneum]
1149	Unigene72490_All	mitochondrial cysteine desulfurase [Scylla paramamosain]
1150	Unigene62907_All	group II PLP decarboxylase, putative [Ixodes scapularis] >gi|215495432|gb|EEC05073.1| group II PLP decarboxylase, putative [Ixodes scapularis]
1151	CL7789.Contig1_All	GJ22112 [Drosophila virilis] >gi|194145154|gb|EDW61550.1| GJ22112 [Drosophila virilis]
1152	Unigene65001_All	hypothetical protein EAG_09605 [Camponotus floridanus]
1153	CL11715.Contig5_All	beta-N-acetylglucosaminidase NAG2 precursor [Tribolium castaneum] >gi|148611478|gb|ABQ95983.1| beta-N-acetylglucosaminidase NAG2 [Tribolium castaneum]

1154	Unigene42350_All	esterase D [Megaptera novaeangliae] >gi|265679637|gb|ACY76509.1|
		esterase D [Megaptera novaeangliae] >gi|265679639|gb|ACY76510.1|
		esterase D [Megaptera novaeangliae] >gi|265679641|gb|ACY76511.1|
		esterase D [Megaptera novaeangliae] >gi|265679643|gb|ACY76512.1|
		esterase D [Megaptera novaeangliae] >gi|265679645|gb|ACY76513.1|
		esterase D [Megaptera novaeangliae] >gi|265679647|gb|ACY76514.1|
		esterase D [Megaptera novaeangliae] >gi|265679649|gb|ACY76515.1|
		esterase D [Megaptera novaeangliae] >gi|265679651|gb|ACY76516.1|
		esterase D [Megaptera novaeangliae] >gi|265679653|gb|ACY76517.1|
		esterase D [Megaptera novaeangliae] >gi|265679655|gb|ACY76518.1|
		esterase D [Megaptera novaeangliae] >gi|265679657|gb|ACY76519.1|
		esterase D [Megaptera novaeangliae] >gi|265679659|gb|ACY76520.1|
		esterase D [Megaptera novaeangliae] >gi|265679661|gb|ACY76521.1|
		esterase D [Megaptera novaeangliae] >gi|265679663|gb|ACY76522.1|
		esterase D [Megaptera novaeangliae] >gi|265679665|gb|ACY76523.1|
		esterase D [Megaptera novaeangliae] >gi|265679667|gb|ACY76524.1|
		esterase D [Megaptera novaeangliae] >gi|265679669|gb|ACY76525.1|
		esterase D [Megaptera novaeangliae] >gi|265679671|gb|ACY76526.1|
		esterase D [Megaptera novaeangliae] >gi|265679673|gb|ACY76527.1|
		esterase D [Megaptera novaeangliae] >gi|265679675|gb|ACY76528.1|
		esterase D [Megaptera novaeangliae] >gi|265679677|gb|ACY76529.1|
		esterase D [Megaptera novaeangliae] >gi|265679679|gb|ACY76530.1|
		esterase D [Megaptera novaeangliae] >gi|265679681|gb|ACY76531.1|
		esterase D [Megaptera novaeangliae] >gi|265679683|gb|ACY76532.1|
		esterase D [Megaptera novaeangliae] >gi|265679685|gb|ACY76533.1|
		esterase D [Megaptera novaeangliae] >gi|265679687|gb|ACY76534.1|
		esterase D [Megaptera novaeangliae] >gi|265679689|gb|ACY76535.1|
		esterase D [Megaptera novaeangliae] >gi|265679691|gb|ACY76536.1|
		esterase D [Megaptera novaeangliae] >gi|265679693|gb|ACY76537.1|
		esterase D [Megaptera novaeangliae] >gi|265679695|gb|ACY76538.1|
		esterase D [Megaptera novaeangliae] >gi|265679697|gb|ACY76539.1|
		esterase D [Megaptera novaeangliae] >gi|265679699|gb|ACY76540.1|
		esterase D [Megaptera novaeangliae] >gi|265679701|gb|ACY76541.1|
		esterase D [Megaptera novaeangliae] >gi|265679703|gb|ACY76542.1|
		esterase D [Megaptera novaeangliae] >gi|265679705|gb|ACY76543.1|
		esterase D [Megaptera novaeangliae] >gi|265679707|gb|ACY76544.1|
		esterase D [Megaptera novaeangliae] >gi|265679709|gb|ACY76545.1|
		esterase D [Megaptera novaeangliae] >gi|265679711|gb|ACY76546.1|
		esterase D [Megaptera novaeangliae] >gi|265679713|gb|ACY76547.1|
		esterase D [Megaptera novaeangliae] >gi|265679715|gb|ACY76548.1|
		esterase D [Megaptera novaeangliae] >gi|265679717|gb|ACY76549.1|
		esterase D [Megaptera novaeangliae] >gi|265679719|gb|ACY76550.1|
		esterase D [Megaptera novaeangliae] >gi|265679721|gb|ACY76551.1|
		esterase D [Megaptera novaeangliae] >gi|265679723|gb|ACY76552.1|

		esterase D [Megaptera novaeangliae] >gi|265679725|gb|ACY76553.1| esterase D [Megaptera novaeangliae] >gi|265679727|gb|ACY76554.1| esterase D [Megaptera novaeangliae] >gi|265679729|gb|ACY76555.1| esterase D [Megaptera novaeangliae] >gi|265679731|gb|ACY76556.1| esterase D [Megaptera novaeangliae] >gi|265679733|gb|ACY76557.1| esterase D [Megaptera novaeangliae] >gi|265679735|gb|ACY76558.1| esterase D [Megaptera novaeangliae] >gi|265679737|gb|ACY76559.1| esterase D [Megaptera novaeangliae] >gi|265679739|gb|ACY76560.1| esterase D [Megaptera novaeangliae] >gi|265679741|gb|ACY76561.1| esterase D [Megaptera novaeangliae] >gi|265679743|gb|ACY76562.1| esterase D [Megaptera novaeangliae] >gi|265679745|gb|ACY76563.1| esterase D [Megaptera novaeangliae] >gi|265679747|gb|ACY76564.1| esterase D [Megaptera novaeangliae] >gi|265679749|gb|ACY76565.1| esterase D [Megaptera novaeangliae] >gi|265679751|gb|ACY76566.1| esterase D [Megaptera novaeangliae] >gi|265679753|gb|ACY76567.1| esterase D [Megaptera novaeangliae] >gi|265679755|gb|ACY76568.1| esterase D [Megaptera novaeangliae] >gi|265679757|gb|ACY76569.1| esterase D [Megaptera novaeangliae] >gi|265679759|gb|ACY76570.1| esterase D [Megaptera novaeangliae] >gi|265679761|gb|ACY76571.1| esterase D [Megaptera novaeangliae] >gi|265679763|gb|ACY76572.1| esterase D [Megaptera novaeangliae] >gi|265679765|gb|ACY76573.1| esterase D [Megaptera novaeangliae] >gi|265679767|gb|ACY76574.1| esterase D [Megaptera novaeangliae] >gi|265679769|gb|ACY76575.1| esterase D [Megaptera novaeangliae] >gi|265679771|gb|ACY76576.1| esterase D [Megaptera novaeangliae] >gi|265679773|gb|ACY76577.1| esterase D [Megaptera novaeangliae] >gi|265679775|gb|ACY76578.1| esterase D [Megaptera novaeangliae] >gi|265679777|gb|ACY76579.1| esterase D [Eubalaena australis] >gi|265679779|gb|ACY76580.1| esterase D [Eubalaena australis] >gi|265679781|gb|ACY76581.1| esterase D [Eubalaena australis] >gi|265679783|gb|ACY76582.1| esterase D [Eubalaena australis] >gi|265679785|gb|ACY76583.1| esterase D [Eubalaena australis] >gi|265679787|gb|ACY76584.1| esterase D [Eubalaena australis] >gi|265679789|gb|ACY76585.1| esterase D [Eubalaena australis] >gi|265679791|gb|ACY76586.1| esterase D [Eubalaena australis] >gi|265679793|gb|ACY76587.1| esterase D [Eubalaena australis] >gi|265679795|gb|ACY76588.1| esterase D [Eubalaena australis] >gi|265679797|gb|ACY76589.1| esterase D [Eubalaena australis] >gi|265679799|gb|ACY76590.1| esterase D [Eubalaena australis] >gi|265679801|gb|ACY76591.1| esterase D [Eubalaena australis] >gi|265679803|gb|ACY76592.1| esterase D [Eubalaena australis] >gi|265679805|gb|ACY76593.1| esterase D [Eubalaena australis] >gi|265679807|gb|ACY76594.1| esterase D [Eubalaena australis] >gi|265679809|gb|ACY76595.1| esterase D [Eubalaena australis] >gi|265679811|gb|ACY76596.1|

		esterase D [Eubalaena australis] >gi|265679813|gb|ACY76597.1| esterase D [Eubalaena australis] >gi|265679815|gb|ACY76598.1| esterase D [Eubalaena australis] >gi|265679817|gb|ACY76599.1| esterase D [Eubalaena australis] >gi|265679819|gb|ACY76600.1| esterase D [Eubalaena australis] >gi|265679821|gb|ACY76601.1| esterase D [Eubalaena australis] >gi|265679823|gb|ACY76602.1| esterase D [Balaenoptera musculus] >gi|265679825|gb|ACY76603.1| esterase D [Balaenoptera physalus] >gi|265679827|gb|ACY76604.1| esterase D [Balaenoptera physalus] >gi|265679837|gb|ACY76609.1| esterase D [Balaenoptera bonaerensis]
1155	CL4799.Contig1_All	PREDICTED: 50S ribosomal protein L13-like [Bombus impatiens]
1155	CL4799.Contig2_All	
1156	CL16545.Contig1_All	PREDICTED: spectrin beta chain-like isoform 2 [Acyrthosiphon pisum]
1156	Unigene40149_All	
1157	CL11429.Contig1_All	-
1158	CL3260.Contig1_All	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase [Camponotus floridanus]
1158	CL3260.Contig2_All	
1159	Unigene2949_All	-
1160	Unigene1781_All	DNA replication licensing factor Mcm6 [Danaus plexippus]
1161	CL12479.Contig1_All	unnamed protein product [Homo sapiens]
1161	CL12479.Contig2_All	
1161	CL12479.Contig3_All	
1162	CL5940.Contig3_All	hypothetical protein DAPPUDRAFT_62984 [Daphnia pulex]
1162	CL5940.Contig4_All	
1163	Unigene42765_All	PREDICTED: LOW QUALITY PROTEIN: zinc finger protein-like 1 [Papio anubis]

1164	Unigene42475_All	PREDICTED: similar to diazepam binding inhibitor, putative [Tribolium castaneum] >gi|270013948|gb|EFA10396.1| hypothetical protein TcasGA2_TC012627 [Tribolium castaneum]
1165	Unigene19817_All	SUMO-1-conjugating enzyme UBC9, putative [Pediculus humanus corporis] >gi|212510945|gb|EEB14025.1| SUMO-1-conjugating enzyme UBC9, putative [Pediculus humanus corporis]
1166	CL7509.Contig1_All	hypothetical protein TcasGA2_TC008324 [Tribolium castaneum]
1166	CL7509.Contig2_All	
1167	Unigene27956_All	Serine proteinase stubble [Camponotus floridanus]
1168	Unigene42455_All	PREDICTED: similar to ATPase inhibitor-like protein [Tribolium castaneum] >gi|270014813|gb|EFA11261.1| hypothetical protein TcasGA2_TC010795 [Tribolium castaneum]
1169	Unigene72091_All	actin, partial [Cryptocercus punctulatus]
1170	CL4293.Contig2_All	-
1171	CL16174.Contig2_All	hypothetical protein PANDA_021998 [Ailuropoda melanoleuca]
1172	CL3562.Contig1_All	Ras GTPase-activating protein-binding protein 2 [Harpegnathos saltator]
1172	CL3562.Contig2_All	
1173	Unigene63488_All	-
1174	Unigene35156_All	unnamed protein product [Tetraodon nigroviridis]
1175	CL8271.Contig1_All	RecName: Full=Fasciclin-2; AltName: Full=Fasciclin II; Short=FAS II; Flags: Precursor
1175	CL8271.Contig3_All	
1175	CL8271.Contig6_All	
1176	CL8532.Contig1_All	hypothetical protein TcasGA2_TC013859 [Tribolium castaneum]
1177	Unigene70118_All	GE23922 [Drosophila yakuba] >gi|194184580|gb|EDW98191.1| GE23922 [Drosophila yakuba]
1178	Unigene55377_All	Translocation protein SEC63-like protein [Camponotus floridanus]
1179	Unigene50299_All	hypothetical protein AND_13038 [Anopheles darlingi]
1180	Unigene20206_All	Mitochondrial carrier-like protein 1 [Heterocephalus glaber]
1181	Unigene42057_All	PREDICTED: similar to metalloprotease [Tribolium castaneum] >gi|270001475|gb|EEZ97922.1| hypothetical protein TcasGA2_TC000308 [Tribolium castaneum]
1182	CL9640.Contig1_All	hypothetical protein DAPPUDRAFT_189393 [Daphnia pulex]
1183	Unigene57344_All	PREDICTED: pre-rRNA-processing protein TSR1 homolog [Bombus terrestris]

1184	Unigene65031_All	PREDICTED: acetyl-CoA acetyltransferase, cytosolic-like [Nasonia vitripennis]
1185	CL6149.Contig1_All	AGAP006340-PB [Anopheles gambiae str. PEST] >gi|157016159|gb|EDO63851.1| AGAP006340-PB [Anopheles gambiae str. PEST]
1185	CL6149.Contig2_All	
1185	CL6149.Contig3_All	
1185	CL6149.Contig4_All	
1186	Unigene63554_All	mitochondrial ATP-dependent clp protease ATP-binding subunit clpx-like [Perca flavescens]
1187	CL6669.Contig1_All	Putative V-type proton ATPase 116 kDa subunit a [Acromyrmex echinatior]
1187	CL6669.Contig4_All	
1188	Unigene27900_All	hypothetical protein BRAFLDRAFT_214346 [Branchiostoma floridae] >gi|229297901|gb|EEN68533.1| hypothetical protein BRAFLDRAFT_214346 [Branchiostoma floridae]
1189	CL12137.Contig1_All	PREDICTED: hypothetical protein LOC100641148, partial [Amphimedon queenslandica]
1189	CL12137.Contig2_All	
1190	Unigene69907_All	beta-glucuronidase {exon 12} {EC 3.2.1.31} [human, mucopolysaccharidosis type VII hydrops fetalis patient, Peptide Partial Mutant, 63 aa]
1191	CL9567.Contig1_All	hypothetical protein SINV_05985 [Solenopsis invicta]
1192	Unigene12338_All	PREDICTED: similar to hydrogen-transporting ATP synthase, G-subunit, putative [Tribolium castaneum] >gi|270006474|gb|EFA02922.1| hypothetical protein TcasGA2_TC008513 [Tribolium castaneum]
1193	CL14801.Contig1_All	AGAP005418-PA [Anopheles gambiae str. PEST] >gi|157015439|gb|EAA10870.4| AGAP005418-PA [Anopheles gambiae str. PEST]
1193	CL14801.Contig2_All	
1193	CL14801.Contig3_All	
1194	Unigene42329_All	replication factor C subunit 3 [Papilio polytes]
1195	Unigene71801_All	unnamed protein product [Tetraodon nigroviridis]
1196	CL12772.Contig1_All	hypothetical protein TcasGA2_TC006367 [Tribolium castaneum]
1196	CL12772.Contig2_All	
1197	CL494.Contig11_All	hypothetical protein TcasGA2_TC004718 [Tribolium castaneum]
1197	CL494.Contig25_All	
1197	CL494.Contig23_All	
1197	CL494.Contig18_All	
1197	CL494.Contig4_All	

1197	CL494.Contig13_All	
1197	CL494.Contig16_All	
1197	CL494.Contig22_All	
1197	CL494.Contig2_All	
1197	CL494.Contig9_All	
1197	CL494.Contig19_All	
1197	CL494.Contig8_All	
1197	CL494.Contig3_All	
1197	CL494.Contig1_All	
1197	CL494.Contig15_All	
1198	Unigene18363_All	PREDICTED: RNA-binding protein squid-like [Apis florea]
1199	CL16060.Contig1_All	PREDICTED: similar to oxidoreductase [Tribolium castaneum]
1200	Unigene20124_All	GF19326 [Drosophila ananassae] >gi|190622736|gb|EDV38260.1| GF19326 [Drosophila ananassae]
1201	CL10581.Contig1_All	PREDICTED: lambda-crystallin homolog [Megachile rotundata]
1202	CL12963.Contig1_All	hypothetical protein TcasGA2_TC010853 [Tribolium castaneum]
1202	CL12963.Contig3_All	
1203	CL8747.Contig1_All	Zinc finger CCCH domain-containing protein 10 [Acromyrmex echinatior]
1203	CL8747.Contig3_All	
1203	CL8747.Contig2_All	
1204	Unigene26479_All	PREDICTED: probable salivary secreted peptide-like [Megachile rotundata]
1205	CL15578.Contig1_All	-
1205	CL15578.Contig2_All	
1206	CL9264.Contig1_All	hypothetical protein TcasGA2_TC008045 [Tribolium castaneum]
1207	CL11447.Contig1_All	Methylglutaconyl-CoA hydratase, mitochondrial [Columba livia]
1208	Unigene64936_All	carboxypeptidase A [Tribolium castaneum]
1209	CL3949.Contig4_All	PREDICTED: ERI1 exoribonuclease 2 [Gallus gallus]
1210	Unigene55208_All	capping protein beta 3 subunit [Mus musculus]
1211	CL7495.Contig1_All	Membrane metallo-endopeptidase-like 1 [Harpegnathos saltator]
1211	CL7495.Contig6_All	
1211	CL7495.Contig5_All	
1211	CL7495.Contig4_All	
1212	CL8201.Contig1_All	proteinase inhibitor serpin, partial [Locusta migratoria]
1213	CL5273.Contig1_All	bystin, partial [Papilio xuthus]

1214	Unigene5830_All	PREDICTED: splicing factor 3B subunit 3-like, partial [Macaca mulatta]
1214	Unigene34204_All	
1215	CL3881.Contig10_All	Fox-1-like protein A [Camponotus floridanus]
1215	CL3881.Contig5_All	
1215	CL3881.Contig7_All	
1215	CL3881.Contig16_All	
1215	CL3881.Contig21_All	
1215	CL3881.Contig14_All	
1215	CL3881.Contig15_All	
1215	CL3881.Contig6_All	
1215	CL3881.Contig18_All	
1215	CL3881.Contig8_All	
1215	CL3881.Contig20_All	
1215	CL3881.Contig4_All	
1215	CL3881.Contig11_All	
1215	CL3881.Contig9_All	
1215	CL3881.Contig12_All	
1215	CL3881.Contig13_All	
1215	CL3881.Contig17_All	
1215	CL3881.Contig3_All	
1216	CL12602.Contig4_All	PREDICTED: similar to thyroid hormone receptor interactor 12 isoform 1 [Tribolium castaneum]
1216	CL12602.Contig5_All	
1217	Unigene749_All	40S ribosomal protein S23 [Harpegnathos saltator]
1218	CL5149.Contig1_All	pur-alpha [Aedes aegypti] >gi|108871498|gb|EAT35723.1| AAEL012134-PA [Aedes aegypti]
1218	CL5149.Contig2_All	
1218	CL5149.Contig3_All	
1219	CL14035.Contig1_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167865118|gb|EDS28501.1| conserved hypothetical protein [Culex quinquefasciatus]
1219	CL14035.Contig2_All	
1220	Unigene34828_All	hypothetical protein CAPTEDRAFT_154135 [Capitella teleta]
1221	CL4414.Contig2_All	hypothetical protein SINV_16602 [Solenopsis invicta]
1221	CL4414.Contig5_All	
1221	CL4414.Contig3_All	
1222	Unigene11414_All	UDP-glucose pyrophosphorylase 2, isoform CRA_a [Rattus norvegicus]

1223	Unigene27346_All	dihydrolipoamide succinyltransferase, putative [Ixodes scapularis] >gi|215506253|gb|EEC15747.1| dihydrolipoamide succinyltransferase, putative [Ixodes scapularis]
1224	CL4500.Contig1_All	-
1225	CL554.Contig1_All	PREDICTED: similar to n-acetylgalactosaminyltransferase [Tribolium castaneum] >gi|270006291|gb|EFA02739.1| hypothetical protein TcasGA2_TC008465 [Tribolium castaneum]
1226	CL16775.Contig2_All	cysteine proteinase cathepsin L, putative [Ixodes scapularis] >gi|215510564|gb|EEC20017.1| cysteine proteinase cathepsin L, putative [Ixodes scapularis]
1227	CL8386.Contig1_All	PREDICTED: elongation factor Tu-like [Bombus impatiens]
1227	CL8386.Contig2_All	
1228	Unigene55004_All	PREDICTED: UPF0510 protein INM02-like [Apis mellifera]
1229	Unigene63628_All	Serine/threonine-protein phosphatase 4 catalytic subunit [Harpegnathos saltator]
1230	Unigene55610_All	program cell death 5-like [Penaeus monodon]
1231	Unigene25977_All	Transmembrane 9 superfamily member 3 [Cricetulus griseus]
1232	Unigene26347_All	glycylpeptide N-tetRadecanoyltransferase, putative [Pediculus humanus corporis] >gi|212517600|gb|EEB19465.1| glycylpeptide N-tetRadecanoyltransferase, putative [Pediculus humanus corporis]
1233	Unigene57743_All	PREDICTED: hypothetical protein LOC100577823 [Apis mellifera]
1234	Unigene35234_All	PREDICTED: alpha-tocopherol transfer protein-like isoform 1 [Acyrthosiphon pisum] >gi|328708497|ref|XP_003243707.1| PREDICTED: alpha-tocopherol transfer protein-like isoform 2 [Acyrthosiphon pisum]
1235	CL14441.Contig1_All	26S proteasome non-ATPase regulatory subunit 10 [Harpegnathos saltator]
1235	CL14441.Contig2_All	
1236	Unigene69677_All	hCG401289, isoform CRA_b [Homo sapiens]
1237	CL9395.Contig1_All	-
1238	CL7654.Contig2_All	dehydrogenase/reductase (SDR family) member 12 [Callorhinchus milii]
1239	Unigene20359_All	Chain A, Crystal Structure Of The Spop Btb Domain Complexed With The Cul3 N- Terminal Domain >gi|388604346|pdb|4EOZ|C Chain C, Crystal Structure Of The Spop Btb Domain Complexed With The Cul3 N- Terminal Domain

1240	Unigene32627_All	GD24517 [Drosophila simulans] >gi|194203019|gb|EDX16595.1| GD24517 [Drosophila simulans]
1241	Unigene2683_All	PREDICTED: 60S ribosomal protein L30-like [Ornithorhynchus anatinus]
1242	Unigene12472_All	PREDICTED: similar to pre-mRNA-splicing helicase BRR2 [Tribolium castaneum]
1243	CL9337.Contig1_All	hypothetical protein [Locusta migratoria]
1244	Unigene11364_All	PREDICTED: uncharacterized protein LOC100215529 [Hydra magnipapillata]
1245	Unigene57759_All	glucosyl/glucuronosyl transferases [Aedes aegypti] >gi|108873425|gb|EAT37650.1| AAEL010381-PA [Aedes aegypti]
1246	Unigene33824_All	hypothetical protein AND_09925 [Anopheles darlingi]
1247	CL8001.Contig2_All	hypothetical protein SINV_03361 [Solenopsis invicta]
1248	Unigene3088_All	Zeta-crystallin, putative [Pediculus humanus corporis] >gi|212509142|gb|EEB12619.1| Zeta-crystallin, putative [Pediculus humanus corporis]
1249	Unigene72680_All	-
1250	Unigene54875_All	doubleoxidase, partial [Papilio polytes]
1251	Unigene72213_All	NADH:ubiquinone dehydrogenase [Papilio xuthus]
1252	CL15728.Contig5_All	PREDICTED: serine/threonine-protein phosphatase 4 regulatory subunit 1-like, partial [Tursiops truncatus]
1252	CL15728.Contig6_All	
1253	CL8504.Contig1_All	PREDICTED: probable mannose-1-phosphate guanylyltransferase 3-like, partial [Tursiops truncatus]
1254	CL5446.Contig1_All	PREDICTED: venom carboxylesterase-6 isoform 1 [Nasonia vitripennis] >gi|345497206|ref|XP_003427935.1| PREDICTED: venom carboxylesterase-6 isoform 2 [Nasonia vitripennis]
1254	Unigene99465_All	
1255	CL1385.Contig1_All	syntenin [Penaeus monodon]
1256	Unigene17676_All	Uncharacterized protein C14orf119 [Acromyrmex echinatior]
1257	CL11558.Contig2_All	high-affinity copper uptake protein [Culex quinquefasciatus] >gi|167864401|gb|EDS27784.1| high-affinity copper uptake protein [Culex quinquefasciatus]
1258	CL4369.Contig2_All	-
1258	CL8240.Contig2_All	
1259	Unigene35354_All	hypothetical protein AND_01318 [Anopheles darlingi]

1260	Unigene255_All	PREDICTED: similar to ganglioside-induced differentiation-associated-protein 1 [Tribolium castaneum] >gi|270004029|gb|EFA00477.1| hypothetical protein TcasGA2_TC003336 [Tribolium castaneum]
1261	CL11855.Contig1_All	hypothetical protein BRAFLDRAFT_90869 [Branchiostoma floridae] >gi|229270550|gb|EEN41560.1| hypothetical protein BRAFLDRAFT_90869 [Branchiostoma floridae]
1261	CL11855.Contig2_All	
1262	Unigene12813_All	hypothetical protein SINV_13048 [Solenopsis invicta]
1263	CL6164.Contig2_All	PREDICTED: mRNA turnover protein 4 homolog, partial [Takifugu rubripes]
1264	Unigene20341_All	atlastin [Culex quinquefasciatus] >gi|167868202|gb|EDS31585.1| atlastin [Culex quinquefasciatus]
1265	Unigene33006_All	mRNA cap guanine-N7 methyltransferase [Harpegnathos saltator]
1266	CL7071.Contig1_All	NADH kinase, putative [Pediculus humanus corporis] >gi|212507761|gb|EEB11623.1| NADH kinase, putative [Pediculus humanus corporis]
1266	CL7071.Contig3_All	
1266	CL7071.Contig2_All	
1267	CL14970.Contig1_All	hypothetical protein SINV_03875 [Solenopsis invicta]
1267	CL14970.Contig2_All	
1267	CL14970.Contig3_All	
1268	Unigene17583_All	PREDICTED: protein arginine N-methyltransferase 3-like [Strongylocentrotus purpuratus]
1269	Unigene2834_All	dynactin 2, isoform CRA_d [Rattus norvegicus]
1270	Unigene27386_All	beta-glucosidase [Odontotermes formosanus]
1271	Unigene19735_All	unknown [Dendroctonus ponderosae]
1272	Unigene27568_All	dopa decarboxylase, partial [Tegeticula yuccasella]
1273	Unigene27324_All	PREDICTED: uncharacterized protein LOC100868122 [Apis florea]
1274	Unigene64836_All	Anopheles gambiae str. PEST AGAP012705-PA [Anopheles gambiae str. PEST] >gi|118777538|ref|XP_308132.2| AGAP003900-PA [Anopheles gambiae str. PEST] >gi|116132703|gb|EAA03888.3| AGAP003900-PA [Anopheles gambiae str. PEST] >gi|116133122|gb|EAA03125.3| AGAP012705-PA [Anopheles gambiae str. PEST]
1275	CL960.Contig7_All	hypothetical protein SINV_01311 [Solenopsis invicta]
1276	CL5027.Contig4_All	-

1277	Unigene50226_All	Mannose-1-phosphate guanyltransferase alpha [Harpegnathos saltator]
1278	CL16241.Contig1_All	PREDICTED: hypothetical protein LOC100121608 [Nasonia vitripennis]
1278	CL16241.Contig2_All	
1279	CL3913.Contig1_All	PREDICTED: dynamin-like isoform 1 [Bombus impatiens]
1279	CL3913.Contig4_All	
1279	CL3913.Contig3_All	
1279	CL3913.Contig2_All	
1279	CL3913.Contig5_All	
1279	CL3913.Contig6_All	
1280	Unigene62794_All	PREDICTED: hypothetical protein LOC100114196 [Nasonia vitripennis]
1281	Unigene12730_All	hypothetical protein BRAFLDRAFT_67634 [Branchiostoma floridae] >gi|229291728|gb|EEN62397.1| hypothetical protein BRAFLDRAFT_67634 [Branchiostoma floridae]
1282	Unigene141019_All	-
1283	Unigene65229_All	hypothetical protein KGM_12959 [Danaus plexippus]
1284	Unigene27351_All	hypothetical protein Phum_PHUM604570 [Pediculus humanus corporis] >gi|212518423|gb|EEB20176.1| hypothetical protein Phum_PHUM604570 [Pediculus humanus corporis]
1285	Unigene63671_All	PREDICTED: tubulin-folding cofactor B [Tursiops truncatus]
1286	Unigene50233_All	Methionine aminopeptidase 1 [Acromyrmex echinatior]
1287	CL2334.Contig2_All	PREDICTED: decaprenyl-diphosphate synthase subunit 2-like [Megachile rotundata]
1287	Unigene140540_All	
1288	Unigene70933_All	RecName: Full=Endocuticle structural glycoprotein SgAbd-3
1289	CL38.Contig1_All	carboxypeptidase M precursor, putative [Pediculus humanus corporis] >gi|212507220|gb|EEB11212.1| carboxypeptidase M precursor, putative [Pediculus humanus corporis]
1289	CL38.Contig2_All	
1290	Unigene72468_All	PREDICTED: nuclear pore complex protein Nup50 [Apis mellifera]
1291	Unigene3111_All	PREDICTED: synaptic vesicle membrane protein VAT-1 homolog [Taeniopygia guttata]
1292	Unigene12755_All	GD11957 [Drosophila simulans] >gi|194202092|gb|EDX15668.1| GD11957 [Drosophila simulans]
1293	Unigene34847_All	Nucleolysin TIAR [Acromyrmex echinatior]
1294	Unigene47767_All	unnamed protein product [Tetraodon nigroviridis]

1295	CL6995.Contig1_All	E1b-55kD-associated protein, putative [Pediculus humanus corporis] >gi|212508552|gb|EEB12200.1| E1b-55kD-associated protein, putative [Pediculus humanus corporis]
1296	Unigene57554_All	hypothetical protein AND_01042 [Anopheles darlingi]
1297	CL733.Contig1_All	dynactin, putative [Ixodes scapularis] >gi|215501826|gb|EEC11320.1| dynactin, putative [Ixodes scapularis]
1297	CL733.Contig3_All	
1297	CL733.Contig2_All	
1298	Unigene42454_All	PREDICTED: vesicular integral-membrane protein VIP36-like [Megachile rotundata]
1299	CL10575.Contig1_All	hypothetical protein SINV_02820 [Solenopsis invicta]
1300	CL10759.Contig1_All	PREDICTED: nitrilase homolog 1-like [Megachile rotundata]
1301	CL8343.Contig1_All	PREDICTED: methionyl-tRNA synthetase, cytoplasmic-like [Ornithorhynchus anatinus]
1302	Unigene49898_All	unnamed protein product [Macaca fascicularis]
1303	CL3347.Contig3_All	CG33695, isoform C [Drosophila melanogaster] >gi|22946246|gb|AAN10777.1| CG33695, isoform C [Drosophila melanogaster] >gi|60677923|gb|AAX33468.1| RE10350p [Drosophila melanogaster]
1303	CL3347.Contig4_All	
1304	Unigene64678_All	RecName: Full=Ubiquitin-fold modifier 1; Flags: Precursor >gi|108877961|gb|EAT42186.1| AAEL006251-PA [Aedes aegypti]
1305	Unigene25842_All	Luciferin 4-monooxygenase [Harpegnathos saltator]
1306	CL12420.Contig2_All	putative CAAX prenyl protease, partial [Chorthippus parallelus parallelus] >gi|385682805|gb|AFI71083.1| putative CAAX prenyl protease, partial [Chorthippus parallelus parallelus] >gi|385682809|gb|AFI71085.1| putative CAAX prenyl protease, partial [Chorthippus parallelus parallelus] >gi|385682813|gb|AFI71087.1| putative CAAX prenyl protease, partial [Chorthippus parallelus erythropus] >gi|385682815|gb|AFI71088.1| putative CAAX prenyl protease, partial [Chorthippus parallelus erythropus]
1307	Unigene55149_All	C-factor [Caligus clemensi]
1308	Unigene2607_All	PREDICTED: hypothetical protein LOC100088831 [Ornithorhynchus anatinus]
1309	CL17071.Contig1_All	PREDICTED: coiled-coil domain-containing protein 124-like [Hydra magnipapillata]
1310	CL161.Contig1_All	RecName: Full=Innexin inx2; Short=Innexin-2; AltName: Full=G-Inx2 >gi|4761288|gb|AAD29306.1|AF115854_1 innexin-2 [Schistocerca americana]

1310	CL161.Contig2_All	
1311	Unigene32916_All	scavenger receptor class B member 1 [Culex quinquefasciatus] >gi|167865604|gb|EDS28987.1| scavenger receptor class B member 1 [Culex quinquefasciatus]
1312	Unigene35375_All	PREDICTED: hypothetical protein LOC100577578 isoform 2 [Apis mellifera]
1313	CL5906.Contig1_All	carnitine palmitoyltransferase family member cpt-2 [Thermobia domestica]
1313	CL5906.Contig2_All	
1314	CL9065.Contig1_All	hypothetical protein BRAFLDRAFT_203438 [Branchiostoma floridae] >gi|229282534|gb|EEN53283.1| hypothetical protein BRAFLDRAFT_203438 [Branchiostoma floridae]
1315	Unigene57138_All	Replication factor C subunit 1 [Crassostrea gigas]
1316	Unigene72658_All	Cyclin-K, putative [Pediculus humanus corporis] >gi|212513166|gb|EEB15794.1| Cyclin-K, putative [Pediculus humanus corporis]
1317	CL1128.Contig1_All	yellow-d [Heliconius erato lativitta]
1317	CL1128.Contig5_All	
1317	CL1128.Contig3_All	
1318	Unigene42509_All	apoptosis-related protein PNAS-3, partial [Homo sapiens]
1319	CL6339.Contig1_All	PREDICTED: cleavage stimulation factor subunit 1-like [Megachile rotundata]
1320	Unigene18579_All	U3 small nucleolar RNA-associated protein 6 homolog [Salmo salar]
1321	CL1475.Contig1_All	Chain A, Solution Structure Of The Third Kow Motif Of Transcription Elongation Factor Spt5
1321	Unigene7651_All	
1322	Unigene55462_All	PREDICTED: la-related protein 1B-like, partial [Taeniopygia guttata]
1323	Unigene42852_All	GL16561 [Drosophila persimilis] >gi|194117900|gb|EDW39943.1| GL16561 [Drosophila persimilis]
1324	CL5975.Contig1_All	PREDICTED: ras-related protein Rab-6A-like, partial [Ornithorhynchus anatinus]
1324	CL5975.Contig2_All	
1325	Unigene70445_All	rCG46494, isoform CRA_c [Rattus norvegicus]
1326	Unigene48895_All	nuclear progesterone receptor [Penaeus monodon]
1327	Unigene40357_All	UDP-glucose pyrophosphorylase [Locusta migratoria]
1328	Unigene2728_All	similar to CG1969 [Papilio xuthus]
1329	CL15232.Contig1_All	C-type lysozyme [Schistocerca gregaria]
1330	Unigene39884_All	hypothetical protein WUBG_11010, partial [Wuchereria bancrofti]

1331	CL8789.Contig1_All	PREDICTED: synaptic vesicle membrane protein VAT-1 homolog [Oryzias latipes]
1331	CL8789.Contig5_All	
1331	CL8789.Contig4_All	
1332	CL9532.Contig1_All	GM18721 [Drosophila sechellia] >gi|194133882|gb|EDW55398.1| GM18721 [Drosophila sechellia]
1332	CL9532.Contig3_All	
1333	CL6586.Contig1_All	hypothetical protein KGM_06271 [Danaus plexippus]
1333	CL6586.Contig4_All	
1333	CL6586.Contig3_All	
1333	CL6586.Contig2_All	
1334	Unigene64633_All	unknown unsecreted protein, partial [Papilio xuthus]
1335	Unigene57608_All	hypothetical protein KGM_06017 [Danaus plexippus]
1336	CL4964.Contig1_All	17-beta hydroxysteroid dehydrogenase 13 [Camponotus floridanus]
1336	CL4964.Contig3_All	
1337	CL408.Contig1_All	PREDICTED: TIP41-like protein-like [Bombus impatiens]
1338	CL14917.Contig1_All	GK22939 [Drosophila willistoni] >gi|194170920|gb|EDW85821.1| GK22939 [Drosophila willistoni]
1338	CL14917.Contig2_All	
1339	CL12904.Contig1_All	heat shock factor binding protein 1-like [Nasonia vitripennis]
1340	CL9771.Contig1_All	oxysterol-binding protein 1A, putative [Pediculus humanus corporis] >gi|212516092|gb|EEB18143.1| oxysterol-binding protein 1A, putative [Pediculus humanus corporis]
1340	CL9771.Contig2_All	
1341	Unigene42219_All	-
1342	Unigene49906_All	60S ribosomal protein L7 [Harpegnathos saltator]
1343	Unigene17511_All	chitinase [Biston betularia]
1344	CL4994.Contig3_All	cytochrome P450 [Hodotermopsis sjostedti]
1345	Unigene42769_All	GK19947 [Drosophila willistoni] >gi|194160113|gb|EDW75014.1| GK19947 [Drosophila willistoni]
1346	Unigene42367_All	unknown [Dendroctonus ponderosae]
1347	Unigene79500_All	PREDICTED: huntingtin-interacting protein 1-related protein-like [Hydra magnipapillata]
1348	Unigene20425_All	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (predicted), isoform CRA_b [Rattus norvegicus]
1349	Unigene63802_All	alpha-adaptin [Acheta domesticus] >gi|262304801|gb|ACY44993.1| alpha-adaptin [Periplaneta americana]
1350	Unigene12934_All	Thioredoxin, mitochondrial [Acromyrmex echinatior]

1351	Unigene72176_All	PREDICTED: nucleoprotein TPR [Megachile rotundata]
1352	CL10637.Contig1_All	hypothetical protein DAPPUDRAFT_55617 [Daphnia pulex]
1352	CL10637.Contig2_All	
1353	Unigene42858_All	hypothetical protein TcasGA2_TC012992 [Tribolium castaneum]
1354	Unigene55423_All	hypothetical protein [Homo sapiens]
1355	Unigene70460_All	NF-kappa-B-repressing factor [Harpegnathos saltator]
1356	Unigene18758_All	hypothetical protein [Thermobia domestica]
1357	Unigene70113_All	PREDICTED: vacuolar protein sorting-associated protein 26-like [Bombus terrestris] >gi|350404273|ref|XP_003487056.1| PREDICTED: vacuolar protein sorting-associated protein 26-like [Bombus impatiens]
1358	CL4278.Contig3_All	-
1359	CL8546.Contig2_All	hypothetical protein TcasGA2_TC004451 [Tribolium castaneum]
1360	CL12531.Contig1_All	hypothetical protein TcasGA2_TC030773 [Tribolium castaneum]
1361	Unigene41153_All	PREDICTED: farnesyl pyrophosphate synthase-like [Nasonia vitripennis]
1362	Unigene66286_All	PREDICTED: ATP-dependent RNA helicase DDX18 [Taeniopygia guttata]
1363	Unigene49881_All	PREDICTED: tetratricopeptide repeat protein 35-B-like [Apis mellifera]
1364	CL7725.Contig1_All	3-oxoacyl-[acyl-carrier-protein] reductase [Crassostrea gigas]
1365	CL6113.Contig1_All	GF20448 [Drosophila ananassae] >gi|190629194|gb|EDV44611.1| GF20448 [Drosophila ananassae]
1366	Unigene20207_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212508279|gb|EEB12027.1| conserved hypothetical protein [Pediculus humanus corporis]
1367	Unigene12488_All	Prefoldin subunit 2 [Camponotus floridanus]
1368	CL5912.Contig1_All	hypothetical protein AND_12589 [Anopheles darlingi]
1369	Unigene20408_All	Peptidyl-tRNA hydrolase 2, mitochondrial precursor [Salmo salar]
1370	CL5926.Contig2_All	DNA repair and recombination protein RAD54B [Harpegnathos saltator]
1371	CL4280.Contig2_All	PREDICTED: spermidine synthase-like, partial [Ciona intestinalis]
1372	Unigene33862_All	Muscle-specific protein, putative [Pediculus humanus corporis] >gi|212511213|gb|EEB14246.1| Muscle-specific protein, putative [Pediculus humanus corporis]
1373	Unigene32196_All	Guanine deaminase [Camponotus floridanus]

1374	Unigene20000_All	unknown [Dendroctonus ponderosae]
1375	CL14827.Contig1_All	PREDICTED: similar to CG5758 CG5758-PA [Tribolium castaneum] >gi|270007879|gb|EFA04327.1| hypothetical protein TcasGA2_TC014621 [Tribolium castaneum]
1376	Unigene11748_All	-
1377	Unigene238_All	PREDICTED: similar to predicted protein [Tribolium castaneum] >gi|270007823|gb|EFA04271.1| hypothetical protein TcasGA2_TC014561 [Tribolium castaneum]
1378	Unigene49854_All	isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase [Culex quinquefasciatus] >gi|167863496|gb|EDS26879.1| isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase [Culex quinquefasciatus]
1379	Unigene2199_All	-
1380	CL7645.Contig1_All	PREDICTED: ubiquitin-conjugating enzyme E2 G1-like isoform 2 [Bombus terrestris]
1381	CL4994.Contig6_All	cytochrome P450 [Hodotermopsis sjostedti]
1382	Unigene11326_All	RecName: Full=Endocuticle structural glycoprotein SgAbd-2
1383	CL2702.Contig1_All	putative ATP synthase c-subunit [Paralichthys olivaceus]
1384	CL16744.Contig1_All	PREDICTED: hypothetical protein LOC100679457 [Nasonia vitripennis]
1385	Unigene47807_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212516620|gb|EEB18614.1| conserved hypothetical protein [Pediculus humanus corporis]
1386	CL1387.Contig1_All	hypothetical protein SINV_14591 [Solenopsis invicta]
1387	Unigene55129_All	hypothetical protein SINV_12120 [Solenopsis invicta]
1388	Unigene19728_All	hypothetical protein SINV_16344 [Solenopsis invicta]
1389	CL14061.Contig1_All	hypothetical protein TcasGA2_TC009052 [Tribolium castaneum]
1390	CL10944.Contig2_All	PREDICTED: cyclin-dependent kinase 1-like [Megachile rotundata]
1390	Unigene62060_All	
1391	CL4729.Contig2_All	NudC domain-containing protein 1 [Cricetulus griseus]
1391	CL4729.Contig3_All	
1392	CL5782.Contig1_All	AAEL012597-PA [Aedes aegypti]
1392	CL5782.Contig2_All	
1393	Unigene10320_All	PREDICTED: similar to zinc binding dehydrogenase [Tribolium castaneum] >gi|270012629|gb|EFA09077.1| hypothetical protein TcasGA2_TC006794 [Tribolium castaneum]

1394	Unigene19935_All	hypothetical protein SINV_10884 [Solenopsis invicta]
1395	CL1424.Contig1_All	hypothetical protein TcasGA2_TC001001 [Tribolium castaneum]
1396	CL16425.Contig1_All	PREDICTED: protein unzipped-like [Nasonia vitripennis]
1397	Unigene10647_All	Sec61 alpha 1 subunit [Acyrthosiphon pisum] >gi|52630957|gb|AAU84942.1| probable transport protein Sec61 alpha subunit [Toxoptera citricida]
1398	Unigene62309_All	Dephospho-CoA kinase domain-containing protein [Acromyrmex echinatior]
1399	Unigene27668_All	Eukaryotic translation initiation factor 5B [Acromyrmex echinatior]
1400	Unigene34833_All	GL15783 [Drosophila persimilis] >gi|194107973|gb|EDW30016.1| GL15783 [Drosophila persimilis]
1401	Unigene63690_All	CST complex subunit STN1 [Mus musculus] >gi|292495040|sp|Q8K2X3.2|STN1_MOUSE RecName: Full=CST complex subunit STN1; AltName: Full=Alpha-accessory factor of 44 kDa; Short=AAF-44; Short=AAF44; AltName: Full=Oligonucleotide/oligosaccharide-binding fold-containing protein 1; AltName: Full=Suppressor of cdc thirteen homolog >gi|148710089|gb|EDL42035.1| oligonucleotide/oligosaccharide-binding fold containing 1 [Mus musculus]
1402	CL13577.Contig2_All	PREDICTED: heterogeneous nuclear ribonucleoprotein Q-like, partial [Nasonia vitripennis]
1403	CL282.Contig1_All	conserved hypothetical protein [Trypanosoma congolense IL3000]
1404	CL8473.Contig1_All	bile salt sulfotransferase 1 [Culex quinquefasciatus] >gi|167871478|gb|EDS34861.1| bile salt sulfotransferase 1 [Culex quinquefasciatus]
1404	CL8473.Contig2_All	
1405	Unigene25522_All	AAEL012064-PA [Aedes aegypti]
1406	CL9493.Contig1_All	NADP-dependent malic enzyme, putative [Pediculus humanus corporis] >gi|212510851|gb|EEB13942.1| NADP-dependent malic enzyme, putative [Pediculus humanus corporis]
1406	CL9493.Contig4_All	
1407	Unigene36708_All	hypothetical protein CRE_17774 [Caenorhabditis remanei] >gi|308250191|gb|EFO94143.1| hypothetical protein CRE_17774 [Caenorhabditis remanei]
1408	Unigene41350_All	unknown [Dendroctonus ponderosae]
1409	CL4831.Contig1_All	Protein tyrosine phosphatase-like protein ptplad1 [Camponotus floridanus]
1409	CL4831.Contig2_All	

1409	CL4831.Contig3_All	
1410	CL2808.Contig1_All	Ribokinase [Heterocephalus glaber]
1410	CL2808.Contig2_All	
1410	CL2808.Contig4_All	
1410	CL2808.Contig3_All	
1411	Unigene49962_All	PREDICTED: DNA replication licensing factor mcm7-like [Xenopus (Silurana) tropicalis]
1412	CL10200.Contig1_All	trehalose-6-phosphate synthase [Locusta migratoria manilensis]
1412	CL10200.Contig2_All	
1413	Unigene57898_All	PREDICTED: mitochondrial 2-oxoglutarate/malate carrier protein isoform 2 [Otolemur garnettii]
1414	CL2304.Contig4_All	peptidyl-prolyl isomerase F (cyclophilin F) [Clonorchis sinensis]
1415	Unigene19966_All	hypothetical protein SINV_00876 [Solenopsis invicta]
1416	Unigene65039_All	vacuolar ATP synthase subunit S1, putative [Pediculus humanus corporis] >gi|212514993|gb|EEB17209.1| vacuolar ATP synthase subunit S1, putative [Pediculus humanus corporis]
1417	CL7621.Contig3_All	RNA-binding protein Musashi-like protein Rbp6 [Acromyrmex echinatior]
1417	Unigene33527_All	
1418	Unigene61647_All	-
1419	Unigene27777_All	PREDICTED: ADP-ribose pyrophosphatase, mitochondrial-like, partial [Sarcophilus harrisii]
1420	Unigene35223_All	unknown [Dendroctonus ponderosae]
1421	Unigene27977_All	dolichyl-phosphate beta-glucosyltransferase [Ixodes ricinus]
1422	CL7886.Contig1_All	Nuclear pore complex protein Nup93 [Chelonia mydas]
1422	CL7886.Contig2_All	
1423	Unigene3013_All	GJ23589 [Drosophila virilis] >gi|194151059|gb|EDW66493.1| GJ23589 [Drosophila virilis]
1424	Unigene69563_All	PREDICTED: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1-like [Nasonia vitripennis]
1424	Unigene69574_All	
1425	Unigene25072_All	GL10396 [Drosophila persimilis] >gi|194110485|gb|EDW32528.1| GL10396 [Drosophila persimilis]
1426	Unigene64674_All	Actin-related protein 2/3 complex subunit 3 [Harpegnathos saltator]

1427	CL1313.Contig1_All	hypothetical protein TGME49_060870 [Toxoplasma gondii ME49] >gi|211962914|gb|EEA98109.1| hypothetical protein TGME49_060870 [Toxoplasma gondii ME49] >gi|221486899|gb|EEE25145.1| conserved hypothetical protein [Toxoplasma gondii GT1] >gi|221506589|gb|EEE32206.1| conserved hypothetical protein [Toxoplasma gondii VEG]
1427	CL6637.Contig2_All	
1427	CL1313.Contig2_All	
1427	CL6637.Contig1_All	
1428	Unigene55818_All	PREDICTED: ribulose-phosphate 3-epimerase, cytoplasmic isoform-like, partial [Tursiops truncatus]
1429	Unigene57484_All	-
1430	CL14041.Contig1_All	Polyribonucleotide nucleotidyltransferase 1, mitochondrial [Tupaia chinensis]
1430	CL14041.Contig3_All	
1430	CL14041.Contig4_All	
1430	CL14041.Contig2_All	
1431	Unigene18757_All	L-xylulose reductase [Danio rerio] >gi|62202602|gb|AAH93141.1| Dicarbonyl/L-xylulose reductase [Danio rerio]
1432	CL5260.Contig3_All	Gb1-cadherin [Gryllus bimaculatus]
1433	Unigene8429_All	PREDICTED: coatomer subunit epsilon-like [Megachile rotundata]
1434	Unigene141213_All	PREDICTED: DNA-binding protein HU-alpha-like [Bombus impatiens]
1435	Unigene25578_All	PREDICTED: ran GTPase-activating protein 1 [Ornithorhynchus anatinus]
1436	Unigene50274_All	unnamed protein product [Mus musculus]
1437	Unigene71515_All	NADH dehydrogenase [Culex quinquefasciatus] >gi|167880174|gb|EDS43557.1| NADH dehydrogenase [Culex quinquefasciatus]
1438	CL39.Contig1_All	hypothetical protein BRAFLDRAFT_205489 [Branchiostoma floridae] >gi|229285776|gb|EEN56501.1| hypothetical protein BRAFLDRAFT_205489 [Branchiostoma floridae]
1439	CL7947.Contig2_All	unknown unsecreted protein [Papilio polytes]
1440	Unigene484_All	AGAP009973-PA [Anopheles gambiae str. PEST] >gi|157014148|gb|EAA13918.4| AGAP009973-PA [Anopheles gambiae str. PEST]
1441	Unigene72237_All	PREDICTED: ufm1-specific protease 2 [Ciona intestinalis]
1442	CL9264.Contig2_All	PREDICTED: similar to coronin [Tribolium castaneum]
1443	Unigene25148_All	hypothetical protein DAPPUDRAFT_188894 [Daphnia pulex]
1444	Unigene25629_All	serpin peptidase inhibitor 28 [Tribolium castaneum]

1445	CL10133.Contig1_All	AAEL012143-PA, partial [Aedes aegypti]
1445	CL10133.Contig4_All	
1446	CL12965.Contig2_All	PREDICTED: vacuolar protein-sorting-associated protein 25-like [Bombus impatiens]
1447	CL13607.Contig1_All	PREDICTED: sulfatase-modifying factor 1-like, partial [Ornithorhynchus anatinus]
1448	CL4165.Contig1_All	endonuclease-reverse transcriptase [Danaus plexippus]
1449	CL421.Contig1_All	Isocitrate lyase, putative [Perkinsus marinus ATCC 50983] >gi|239876778|gb|EER04351.1| Isocitrate lyase, putative [Perkinsus marinus ATCC 50983]
1450	Unigene12477_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167875700|gb|EDS39083.1| conserved hypothetical protein [Culex quinquefasciatus]
1451	Unigene68536_All	PREDICTED: 30S ribosomal protein S2-like [Bombus impatiens]
1452	CL15868.Contig2_All	PREDICTED: E3 UFM1-protein ligase 1-like [Strongylocentrotus purpuratus]
1453	CL17766.Contig3_All	hypothetical protein AND_15412 [Anopheles darlingi]
1453	CL17766.Contig5_All	
1453	CL17766.Contig6_All	
1453	CL17766.Contig4_All	
1454	Unigene33483_All	unknown [Schistosoma japonicum]
1455	CL2359.Contig1_All	GF18622 [Drosophila ananassae] >gi|190628179|gb|EDV43703.1| GF18622 [Drosophila ananassae]
1456	Unigene57324_All	low density lipid receptor-related protein, putative [Ixodes scapularis] >gi|215496981|gb|EEC06621.1| low density lipid receptor-related protein, putative [Ixodes scapularis]
1457	Unigene18120_All	hypothetical protein AND_00838 [Anopheles darlingi]
1458	Unigene42397_All	unnamed protein product [Tetraodon nigroviridis]
1459	CL10396.Contig1_All	Aggrecan core protein [Acromyrmex echinatior]
1459	CL10396.Contig2_All	
1460	Unigene65159_All	Ubiquitin thioesterase otubain-like [Camponotus floridanus]
1461	CL12785.Contig1_All	receptor accessory protein 5, isoform CRA_b [Mus musculus]
1462	Unigene52858_All	-
1463	CL7956.Contig1_All	PREDICTED: hypothetical protein LOC100747200 [Bombus impatiens]
1463	CL7956.Contig3_All	
1464	Unigene40473_All	PREDICTED: DNA polymerase alpha catalytic subunit [Loxodonta africana]

1465	CL11602.Contig1_All	hypothetical protein BRAFLDRAFT_241504 [Branchiostoma floridae] >gi|229272019|gb|EEN42901.1| hypothetical protein BRAFLDRAFT_241504 [Branchiostoma floridae]
1465	CL11602.Contig2_All	
1466	Unigene55163_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212506638|gb|EEB10786.1| conserved hypothetical protein [Pediculus humanus corporis]
1467	CL5377.Contig1_All	PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 2-like, partial [Meleagris gallopavo]
1467	CL5377.Contig3_All	
1468	CL9849.Contig1_All	predicted protein [Pediculus humanus corporis] >gi|212510885|gb|EEB13976.1| predicted protein [Pediculus humanus corporis]
1469	Unigene33314_All	Protein Y41E3.7, isoform c [Caenorhabditis elegans] >gi|87251914|emb|CAJ76976.1| Protein Y41E3.7, isoform c [Caenorhabditis elegans]
1470	CL11081.Contig1_All	Endonuclease III-like protein 1 [Chelonia mydas]
1471	Unigene17240_All	hypothetical protein IscW_ISCW000519 [Ixodes scapularis] >gi|215492847|gb|EEC02488.1| hypothetical protein IscW_ISCW000519 [Ixodes scapularis]
1471	CL17911.Contig4_All	
1472	Unigene35403_All	PREDICTED: probable deoxyhypusine synthase-like [Bombus impatiens]
1473	Unigene17725_All	Ras association family member [Gryllus bimaculatus]
1474	CL3930.Contig1_All	ribosomal protein S11 [Chrysomela tremula]
1475	CL12815.Contig2_All	tRNA (cytosine-5-)-methyltransferase CG6133 [Camponotus floridanus]
1476	Unigene50359_All	glutamate--cysteine ligase regulatory subunit, putative [Pediculus humanus corporis] >gi|212518106|gb|EEB19898.1| glutamate--cysteine ligase regulatory subunit, putative [Pediculus humanus corporis]
1477	Unigene27074_All	SJCHGC07135 protein [Schistosoma japonicum]
1478	CL6152.Contig1_All	hypothetical protein SINV_05410 [Solenopsis invicta]
1479	CL1302.Contig5_All	S-adenosylmethionine synthetase [Acromyrmex echinatior]
1480	Unigene41106_All	hypothetical protein DAPPUDRAFT_331045 [Daphnia pulex]
1481	Unigene26319_All	GDP mannose-4,6-dehydratase, putative [Pediculus humanus corporis] >gi|212515472|gb|EEB17610.1| GDP mannose-4,6-dehydratase, putative [Pediculus humanus corporis]

1482	Unigene72291_All	PREDICTED: similar to ribosomal protein L14 [Tribolium castaneum] >gi|270004603|gb|EFA01051.1| hypothetical protein TcasGA2_TC003967 [Tribolium castaneum]
1483	Unigene27466_All	Polb protein [Mus musculus]
1484	CL3414.Contig3_All	ceramidase, putative [Pediculus humanus corporis] >gi|212518958|gb|EEB20546.1| ceramidase, putative [Pediculus humanus corporis]
1485	CL11577.Contig1_All	hypothetical protein EAI_15782 [Harpegnathos saltator]
1486	Unigene2873_All	PREDICTED: MOSC domain-containing protein 1, mitochondrial-like [Apis mellifera]
1487	CL9300.Contig1_All	TPA_inf: glutamate transporter EAAC1-interacting protein GTRAP3-18 [Amblyomma variegatum]
1487	Unigene70481_All	
1487	CL9300.Contig2_All	
1488	CL15114.Contig1_All	hypothetical protein TcasGA2_TC008876 [Tribolium castaneum]
1489	Unigene2931_All	transcription elongation factor B polypeptide 1 isoform b [Homo sapiens] >gi|325652048|ref|NP_001191793.1| transcription elongation factor B polypeptide 1 isoform b [Homo sapiens] >gi|21730759|pdb|1LM8|C Chain C, Structure Of A Hif-1a-Pvhl-Elonginb-Elonginc Complex >gi|21730826|pdb|1LQB|B Chain B, Crystal Structure Of A Hydroxylated Hif-1 Alpha Peptide Bound To The PvhlELONGIN-CELONGIN-B Complex >gi|93279655|pdb|2FNJ|C Chain C, Crystal Structure Of A B30.2SPRY DOMAIN-Containing Protein Gustavus In Complex With Elongin B And Elongin C >gi|206581662|pdb|2JZ3|C Chain C, Socs Box Elonginbc Ternary Complex >gi|444302115|pdb|3ZKJ|B Chain B, Crystal Structure Of Ankyrin Repeat And Socs Box-containing Protein 9 (asb9) In Complex With Elonginb And Elonginc >gi|444302118|pdb|3ZKJ|E Chain E, Crystal Structure Of Ankyrin Repeat And Socs Box-containing Protein 9 (asb9) In Complex With Elonginb And Elonginc >gi|432097001|gb|ELK27500.1| Transcription elongation factor B polypeptide 1 [Myotis davidii] >gi|444732688|gb|ELW72964.1| Transcription elongation factor B polypeptide 1 [Tupaia chinensis]
1490	CL12213.Contig1_All	C-type lysozyme [Schistocerca gregaria]
1491	CL275.Contig1_All	PREDICTED: phenylalanyl-tRNA synthetase beta chain-like [Sus scrofa]
1492	Unigene32601_All	PREDICTED: E3 ubiquitin-protein ligase synoviolin A-like, partial [Gallus gallus]
1493	CL13636.Contig1_All	unnamed protein product [Tetraodon nigroviridis]

1494	CL14110.Contig1_All	hypothetical protein SINV_08746 [Solenopsis invicta]
1494	CL14110.Contig3_All	
1494	CL14110.Contig2_All	
1495	Unigene55855_All	hypothetical protein KGM_20175 [Danaus plexippus]
1496	Unigene57351_All	PREDICTED: trypsin-1-like [Acyrthosiphon pisum]
1497	CL16424.Contig1_All	PREDICTED: alpha-tocopherol transfer protein-like [Bombus impatiens]
1498	Unigene11299_All	PREDICTED: protein TSSC1-like [Strongylocentrotus purpuratus]
1499	Unigene35070_All	60S ribosomal protein L27a [Camponotus floridanus]
1500	Unigene34853_All	heat shock protein 70-14 [Bombyx mori]
1501	Unigene35036_All	PREDICTED: similar to CG14407 CG14407-PA [Tribolium castaneum] >gi|270006202|gb|EFA02650.1| hypothetical protein TcasGA2_TC008371 [Tribolium castaneum]
1502	CL4983.Contig1_All	transcription elongation regulator 1 [Culex quinquefasciatus] >gi|167873217|gb|EDS36600.1| transcription elongation regulator 1 [Culex quinquefasciatus]
1502	CL4983.Contig5_All	
1502	CL4983.Contig2_All	
1503	Unigene56609_All	unnamed protein product [Mus musculus]
1504	Unigene72222_All	Nuclear transcription factor Y subunit gamma [Tupaia chinensis]
1505	Unigene72709_All	Ras-related protein Rac1 [Camponotus floridanus] >gi|307199440|gb|EFN80053.1| Ras-related protein Rac1 [Harpegnathos saltator] >gi|332026886|gb|EGI66987.1| Ras-related protein Rac1 [Acromyrmex echinatior]
1506	CL17081.Contig1_All	nuclear autoantigenic sperm protein [Penaeus monodon]
1506	CL17081.Contig2_All	
1507	CL5332.Contig1_All	PREDICTED: testin [Ciona intestinalis]
1507	CL5332.Contig2_All	
1507	CL5332.Contig5_All	
1508	CL7637.Contig2_All	HLA-B associated transcript 3 [Sus scrofa]
1509	Unigene42333_All	hypothetical protein CAPTEDRAFT_106804, partial [Capitella teleta]
1510	Unigene10445_All	condensin [Culex quinquefasciatus] >gi|167863698|gb|EDS27081.1| condensin [Culex quinquefasciatus]
1511	CL10427.Contig1_All	hypothetical protein AND_00723 [Anopheles darlingi]
1511	CL10427.Contig2_All	
1512	Unigene27483_All	ATPase family, AAA domain containing 3A, isoform CRA_a [Homo sapiens]

1513	Unigene72503_All	PREDICTED: probable Bax inhibitor 1-like [Acyrthosiphon pisum]
1514	CL3488.Contig10_All	vitellogenin receptor [Periplaneta americana]
1514	CL3488.Contig6_All	
1514	CL3488.Contig7_All	
1514	CL3488.Contig8_All	
1515	Unigene18157_All	Sparc [Schistocerca gregaria]
1516	CL7230.Contig1_All	Inositol polyphosphate 1-phosphatase, partial [Columba livia]
1517	CL16875.Contig1_All	ribosomal protein S23, partial [Cydia pomonella]
1517	CL16875.Contig3_All	
1518	CL15812.Contig2_All	-
1519	CL13450.Contig1_All	PREDICTED: proteasomal ubiquitin receptor ADRM1 homolog [Acyrthosiphon pisum]
1519	CL13450.Contig2_All	
1520	CL7074.Contig1_All	pumilio RBD [Schistocerca americana]
1520	CL7074.Contig5_All	
1520	CL7074.Contig8_All	
1520	CL7074.Contig6_All	
1520	CL7074.Contig9_All	
1520	CL7074.Contig2_All	
1521	CL13927.Contig1_All	PREDICTED: DNA-directed RNA polymerases I and III subunit RPAC1-like [Bombus terrestris]
1521	CL13927.Contig2_All	
1522	CL13172.Contig2_All	20-hydroxysteroid dehydrogenase, putative [Ixodes scapularis] >gi|215510361|gb|EEC19814.1| 20-hydroxysteroid dehydrogenase, putative [Ixodes scapularis]
1523	Unigene19070_All	vacuolar protein sorting-associated protein VTA1 homolog [Bombyx mori] >gi|95102786|gb|ABF51334.1| 1110059p08rik-like protein [Bombyx mori] >gi|411100660|gb|AFW03815.1| Vta1 [Bombyx mori]
1524	Unigene2372_All	hypothetical protein CRE_18364 [Caenorhabditis remanei] >gi|308248115|gb|EFO92067.1| hypothetical protein CRE_18364 [Caenorhabditis remanei]
1525	CL16947.Contig2_All	hypothetical protein KGM_11925 [Danaus plexippus]
1525	CL16947.Contig3_All	
1526	Unigene20412_All	hypothetical protein DAPPUDRAFT_93031 [Daphnia pulex]
1527	CL7591.Contig1_All	Kinesin light chain [Camponotus floridanus]
1527	CL7591.Contig2_All	
1527	CL7591.Contig3_All	
1528	Unigene33931_All	CCR4-NOT transcription complex subunit 6-like-B [Harpegnathos saltator]
1529	CL8585.Contig1_All	GBE1 [Equus caballus]

1530	Unigene32542_All	GH18429 [Drosophila grimshawi] >gi|193894282|gb|EDV93148.1| GH18429 [Drosophila grimshawi]
1531	Unigene49921_All	short chain dehydrogenase [Nilaparvata lugens]
1532	Unigene33387_All	GI11727 [Drosophila mojavensis] >gi|193913201|gb|EDW12068.1| GI11727 [Drosophila mojavensis]
1533	CL16880.Contig2_All	similar to CG12162 [Papilio xuthus]
1534	CL14323.Contig1_All	acetyltransferase [Acheta domesticus]
1535	CL4537.Contig2_All	atonal-like protein 8 [Bombyx mori]
1536	Unigene69929_All	PREDICTED: probable cation-transporting ATPase 13A1-like [Strongylocentrotus purpuratus]
1537	CL12207.Contig2_All	PREDICTED: enhancer of mRNA-decapping protein 4, partial [Ornithorhynchus anatinus]
1537	CL12207.Contig3_All	
1538	Unigene12498_All	predicted protein [Nematostella vectensis] >gi|156217808|gb|EDO38717.1| predicted protein [Nematostella vectensis]
1539	CL8270.Contig1_All	FACT complex subunit Ssrp1 [Harpegnathos saltator]
1540	CL13298.Contig2_All	leukocyte elastase inhibitor [Bos taurus] >gi|148887190|sp|Q1JPB0.2|ILEU_BOVIN RecName: Full=Leukocyte elastase inhibitor; Short=LEI; AltName: Full=Serpin B1
1540	CL13298.Contig4_All	
1541	Unigene55839_All	GJ20377 [Drosophila virilis] >gi|194149144|gb|EDW64842.1| GJ20377 [Drosophila virilis]
1542	CL4094.Contig1_All	PREDICTED: cytochrome P450 6k1-like [Bombus terrestris]
1543	Unigene127323_All	PREDICTED: 60 kDa chaperonin-like [Bombus impatiens]
1544	Unigene124296_All	-
1545	Unigene11756_All	PREDICTED: WD40 repeat-containing protein SMU1-like isoform 1 [Apis mellifera] >gi|380024792|ref|XP_003696175.1| PREDICTED: WD40 repeat-containing protein SMU1-like [Apis florea]
1546	Unigene42384_All	ribosomal protein L32 [Chortoicetes terminifera]
1547	Unigene70911_All	p70 S6 kinase, partial [Carcinus maenas]
1548	CL1141.Contig2_All	male accessory gland protein [Drosophila simulans]
1549	Unigene7356_All	unknown unsecreted protein, partial [Papilio xuthus]
1550	Unigene55390_All	PREDICTED: spectrin beta chain, brain 4-like [Bombus impatiens]
1551	Unigene119753_All	hexamerin-like protein 1 [Locusta migratoria]
1552	Unigene58_All	PREDICTED: putative helicase MOV-10 [Papio anubis]
1552	CL4109.Contig3_All	

1553	CL13495.Contig1_All	phosphoglucomutase [Locusta migratoria]
1553	CL13495.Contig2_All	
1554	CL6415.Contig3_All	PREDICTED: splicing factor 1-like [Acyrthosiphon pisum]
1554	CL6415.Contig5_All	
1555	CL10486.Contig2_All	hypothetical protein AND_20651 [Anopheles darlingi]
1556	CL5312.Contig1_All	PREDICTED: similar to endophilin B CG9834-PA [Tribolium castaneum]
1556	CL5312.Contig4_All	
1556	CL5312.Contig3_All	
1556	CL5312.Contig5_All	
1557	CL5852.Contig1_All	Cysteine protease ATG4B [Acromyrmex echinatior]
1557	CL5852.Contig2_All	
1558	CL14709.Contig2_All	AGAP009826-PA [Anopheles gambiae str. PEST] >gi|157014046|gb|EAA13949.5| AGAP009826-PA [Anopheles gambiae str. PEST]
1559	Unigene57671_All	unknown [Dendroctonus ponderosae]
1560	CL1962.Contig1_All	hypothetical protein TcasGA2_TC007632 [Tribolium castaneum]
1560	CL1962.Contig2_All	
1561	CL6531.Contig1_All	variable lymphocyte receptor A [Eptatretus stoutii]
1562	Unigene30569_All	PREDICTED: hypothetical protein LOC412607 [Apis mellifera]
1562	Unigene74007_All	
1563	CL8330.Contig1_All	hypothetical protein BEWA_029520 [Babesia equi]
1564	CL15616.Contig2_All	PREDICTED: hypothetical protein LOC100563307, partial [Anolis carolinensis]
1565	Unigene12629_All	PREDICTED: thioredoxin domain-containing protein 12-like, partial [Ornithorhynchus anatinus]
1566	CL9001.Contig1_All	GM10595 [Drosophila sechellia] >gi|194133492|gb|EDW55008.1| GM10595 [Drosophila sechellia]
1567	CL15923.Contig1_All	PREDICTED: gephyrin-like [Strongylocentrotus purpuratus]
1568	CL3010.Contig1_All	vitellogenin receptor [Periplaneta americana]
1568	CL3010.Contig2_All	
1568	CL3010.Contig3_All	
1569	CL7530.Contig1_All	peroxiredoxin, partial [Schistocerca gregaria]
1569	CL7530.Contig3_All	
1569	CL7530.Contig2_All	
1570	Unigene2989_All	Replication factor C subunit 3 [Myotis davidii]
1571	CL1575.Contig1_All	PREDICTED: similar to CG3077 CG3077-PA [Tribolium castaneum] >gi|270007065|gb|EFA03513.1| hypothetical protein TcasGA2_TC013515 [Tribolium castaneum]

1572	Unigene33681_All	ubiquinol-cytochrome c reductase [Locusta migratoria manilensis]
1573	Unigene2986_All	-
1574	Unigene32268_All	hypothetical protein EAI_09840 [Harpegnathos saltator]
1575	Unigene10852_All	Alpha-tocopherol transfer protein-like [Harpegnathos saltator]
1576	Unigene47478_All	Multidrug resistance-associated protein 1 [Camponotus floridanus]
1577	Unigene72242_All	PREDICTED: CG12171-like [Saccoglossus kowalevskii]
1578	Unigene72274_All	Dipeptidyl peptidase 4, putative [Pediculus humanus corporis] >gi|212506747|gb|EEB10861.1| Dipeptidyl peptidase 4, putative [Pediculus humanus corporis]
1579	CL1647.Contig1_All	hypothetical protein DAPPUDRAFT_223322 [Daphnia pulex]
1580	CL11967.Contig1_All	hypothetical protein TcasGA2_TC000101 [Tribolium castaneum]
1580	CL11967.Contig2_All	
1581	CL17851.Contig1_All	GD19387 [Drosophila simulans] >gi|194198580|gb|EDX12156.1| GD19387 [Drosophila simulans]
1582	Unigene27670_All	PREDICTED: signal peptidase complex subunit 3-like [Megachile rotundata]
1583	CL7348.Contig1_All	PREDICTED: similar to glutathione-s-transferase theta, gst [Tribolium castaneum] >gi|270001660|gb|EEZ98107.1| hypothetical protein TcasGA2_TC000522 [Tribolium castaneum]
1583	CL7348.Contig3_All	
1584	CL786.Contig2_All	PREDICTED: 3-hydroxyisobutyrate dehydrogenase, mitochondrial-like [Cavia porcellus]
1584	CL786.Contig3_All	
1585	Unigene3064_All	Vacuolar protein sorting-associated protein 29 [Camponotus floridanus]
1586	Unigene42827_All	PREDICTED: uncharacterized protein LOC100877733 [Megachile rotundata]
1587	Unigene1382_All	-
1588	CL3832.Contig1_All	-
1588	CL3832.Contig2_All	
1589	Unigene3010_All	unknown [Dendroctonus ponderosae]
1590	Unigene55650_All	Adenylosuccinate lyase [Harpegnathos saltator]
1591	CL13890.Contig1_All	PREDICTED: similar to DAZAP2-like protein [Tribolium castaneum]
1591	CL13890.Contig2_All	
1592	CL11068.Contig1_All	PREDICTED: Golgi to ER traffic protein 4 homolog [Saimiri boliviensis boliviensis]

1593	Unigene12985_All	hypothetical protein SINV_02639 [Solenopsis invicta]
1594	CL3171.Contig1_All	Huntingtin-interacting protein K [Camponotus floridanus]
1595	Unigene40810_All	hypothetical protein AND_10886 [Anopheles darlingi]
1596	CL15874.Contig1_All	Chain A, Solution Structure Of The Cap-Binding Domain Of Parn Complexed With The Cap Analog
1596	CL15874.Contig3_All	
1597	CL11229.Contig1_All	PREDICTED: uncharacterized protein LOC100879171 [Megachile rotundata]
1597	CL11229.Contig2_All	
1598	CL10054.Contig1_All	PREDICTED: clavesin-2-like [Nasonia vitripennis]
1599	CL15882.Contig1_All	PREDICTED: syntaxin-12-like [Megachile rotundata]
1599	CL15882.Contig2_All	
1600	CL3174.Contig1_All	PREDICTED: uncharacterized protein LOC100870716 [Apis florea]
1601	Unigene40881_All	PREDICTED: 60S ribosomal protein L4-like [Nasonia vitripennis]
1602	CL15585.Contig1_All	PREDICTED: vacuolar protein-sorting-associated protein 36-like [Macaca mulatta]
1603	CL15744.Contig1_All	AAEL002924-PB [Aedes aegypti]
1604	Unigene50080_All	Neutral and basic amino acid transport protein rBAT, putative [Pediculus humanus corporis] >gi|212511639|gb|EEB14560.1| Neutral and basic amino acid transport protein rBAT, putative [Pediculus humanus corporis]
1605	CL14857.Contig1_All	hypothetical protein SINV_03501 [Solenopsis invicta]
1605	CL14857.Contig2_All	
1606	CL2660.Contig1_All	aldo-keto reductase, partial [Schistocerca gregaria]
1607	Unigene39898_All	Neurocalcin-like protein [Camponotus floridanus] >gi|307196596|gb|EFN78102.1| Neurocalcin-like protein [Harpegnathos saltator] >gi|332025022|gb|EGI65209.1| Neurocalcin-like protein [Acromyrmex echinatior]
1608	CL10470.Contig2_All	Neurexin-4 [Camponotus floridanus]
1608	CL10470.Contig4_All	
1609	CL6054.Contig1_All	GM11058 [Drosophila sechellia] >gi|194123281|gb|EDW45324.1| GM11058 [Drosophila sechellia]
1609	CL6054.Contig2_All	
1610	Unigene20159_All	ribosomal protein S27 [Xenopsylla cheopis]
1611	Unigene49104_All	hypothetical protein SINV_05935 [Solenopsis invicta]
1612	CL1568.Contig2_All	hypothetical protein Smp_150450 [Schistosoma mansoni]

<table>
<tr><td>1613</td><td>Unigene19862_All</td><td>FNTA protein [Bos taurus]</td></tr>
<tr><td>1614</td><td>Unigene27524_All</td><td>-</td></tr>
<tr><td>1615</td><td>Unigene64904_All</td><td>mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268403|gb|ACZ65743.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268405|gb|ACZ65744.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268407|gb|ACZ65745.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268409|gb|ACZ65746.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268411|gb|ACZ65747.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268413|gb|ACZ65748.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268415|gb|ACZ65749.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268417|gb|ACZ65750.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268419|gb|ACZ65751.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268421|gb|ACZ65752.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268423|gb|ACZ65753.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268425|gb|ACZ65754.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268427|gb|ACZ65755.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268429|gb|ACZ65756.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268431|gb|ACZ65757.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268433|gb|ACZ65758.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268435|gb|ACZ65759.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia vitripennis] >gi|270268437|gb|ACZ65760.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268439|gb|ACZ65761.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268441|gb|ACZ65762.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268443|gb|ACZ65763.1| mitochondrial processing peptidase</td></tr>
</table>

		alpha subunit-like protein [Nasonia longicornis] >gi|270268445|gb|ACZ65764.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268447|gb|ACZ65765.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268449|gb|ACZ65766.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268451|gb|ACZ65767.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268453|gb|ACZ65768.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268455|gb|ACZ65769.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268457|gb|ACZ65770.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268459|gb|ACZ65771.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268461|gb|ACZ65772.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268463|gb|ACZ65773.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268465|gb|ACZ65774.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268467|gb|ACZ65775.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268469|gb|ACZ65776.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia longicornis] >gi|270268471|gb|ACZ65777.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268473|gb|ACZ65778.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268475|gb|ACZ65779.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268477|gb|ACZ65780.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268481|gb|ACZ65782.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268483|gb|ACZ65783.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268485|gb|ACZ65784.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268487|gb|ACZ65785.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268489|gb|ACZ65786.1| mitochondrial processing peptidase

		alpha subunit-like protein [Nasonia giraulti] >gi|270268491|gb|ACZ65787.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268493|gb|ACZ65788.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268495|gb|ACZ65789.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti] >gi|270268497|gb|ACZ65790.1| mitochondrial processing peptidase alpha subunit-like protein [Nasonia giraulti]
1616	CL11377.Contig1_All	PREDICTED: protein phosphatase PP2A 55 kDa regulatory subunit-like isoform 4 [Nasonia vitripennis]
1616	CL11377.Contig2_All	
1617	CL8321.Contig1_All	mannosyltransferase [Aedes aegypti] >gi|108881857|gb|EAT46082.1| AAEL002701-PA [Aedes aegypti]
1617	CL8321.Contig2_All	
1618	CL1413.Contig3_All	Plectin-1 [Harpegnathos saltator]
1618	Unigene32351_All	
1619	Unigene35233_All	mitochondrial NADH dehydrogenase ubiquinone flavoprotein 2 [Aedes aegypti]
1620	CL2231.Contig1_All	Type 2A phosphatase-associated protein, putative [Pediculus humanus corporis] >gi|212514087|gb|EEB16460.1| Type 2A phosphatase-associated protein, putative [Pediculus humanus corporis]
1621	Unigene27970_All	Nuclear protein Hcc-1, putative [Pediculus humanus corporis] >gi|212517137|gb|EEB19067.1| Nuclear protein Hcc-1, putative [Pediculus humanus corporis]
1622	CL7636.Contig3_All	doubletime [Schistocerca gregaria]
1622	Unigene65092_All	
1623	CL13444.Contig1_All	PREDICTED: ubiquitin conjugation factor E4 B-like [Sus scrofa]

1624	Unigene21567_All	GK15672 [Drosophila willistoni] >gi|194159968|gb|EDW74869.1| GK15672 [Drosophila willistoni]
1625	CL2481.Contig1_All	GK20569 [Drosophila willistoni] >gi|194161966|gb|EDW76867.1| GK20569 [Drosophila willistoni]
1626	CL5704.Contig1_All	hypothetical protein CAPTEDRAFT_220900 [Capitella teleta]
1626	CL5704.Contig2_All	
1627	Unigene42404_All	PREDICTED: cytochrome b5-like isoform 2 [Nasonia vitripennis]
1628	CL7858.Contig1_All	PREDICTED: mitochondrial import receptor subunit TOM70, partial [Tursiops truncatus]
1628	CL7858.Contig2_All	
1629	Unigene48477_All	PREDICTED: set1/Ash2 histone methyltransferase complex subunit ASH2-like [Megachile rotundata]
1630	Unigene50178_All	hypothetical protein AND_12515 [Anopheles darlingi]
1631	Unigene57699_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167882486|gb|EDS45869.1| conserved hypothetical protein [Culex quinquefasciatus]
1632	Unigene63217_All	AAEL015302-PA [Aedes aegypti]
1633	CL2473.Contig1_All	GK13598 [Drosophila willistoni] >gi|194162030|gb|EDW76931.1| GK13598 [Drosophila willistoni]
1633	CL2473.Contig2_All	
1634	Unigene72127_All	Chain B, Nmr Solution Structure Of The Human Spliceosomal Protein Complex P14-Sf3b155
1635	Unigene39905_All	PREDICTED: ras-related GTP-binding protein D-like [Bombus impatiens]
1636	Unigene48170_All	PREDICTED: kinesin family member 14 [Rattus norvegicus]
1637	CL1952.Contig3_All	bile salt sulfotransferase 1 [Culex quinquefasciatus] >gi|167871478|gb|EDS34861.1| bile salt sulfotransferase 1 [Culex quinquefasciatus]
1637	CL5792.Contig2_All	
1638	CL6373.Contig1_All	PREDICTED: CLIP-associating protein 2-like isoform 1 [Cricetulus griseus]
1638	CL6373.Contig5_All	
1639	Unigene19516_All	predicted protein [Nematostella vectensis] >gi|156220315|gb|EDO41185.1| predicted protein [Nematostella vectensis]
1640	Unigene10968_All	hypothetical protein [Macaca fascicularis]
1640	Unigene87241_All	
1641	Unigene42451_All	aldose-1-epimerase [Danaus plexippus]

1642	Unigene62398_All	AGAP007478-PA [Anopheles gambiae str. PEST] >gi|157020074|gb|EAA04622.5| AGAP007478-PA [Anopheles gambiae str. PEST]
1643	Unigene2889_All	Chain A, Solution Structure Of Rsgi Ruh-042, A Uba Domain From Human Mitochondrial Elongation Factor Ts
1644	Unigene2457_All	I-type lysozyme [Coptotermes formosanus]
1645	CL6751.Contig1_All	hexokinase [Locusta migratoria]
1646	CL4493.Contig6_All	PREDICTED: putative cystatin-like [Saccoglossus kowalevskii]
1647	Unigene63302_All	ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969081|gb|ACZ54770.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969083|gb|ACZ54771.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969085|gb|ACZ54772.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969087|gb|ACZ54773.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969089|gb|ACZ54774.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969091|gb|ACZ54775.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969093|gb|ACZ54776.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969095|gb|ACZ54777.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969097|gb|ACZ54778.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969099|gb|ACZ54779.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969101|gb|ACZ54780.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969103|gb|ACZ54781.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969105|gb|ACZ54782.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969109|gb|ACZ54784.1| ENSANGP00000031746-like protein [Nasonia longicornis] >gi|269969111|gb|ACZ54785.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969113|gb|ACZ54786.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969115|gb|ACZ54787.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969117|gb|ACZ54788.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969119|gb|ACZ54789.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969121|gb|ACZ54790.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969123|gb|ACZ54791.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969125|gb|ACZ54792.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969127|gb|ACZ54793.1| ENSANGP00000031746-like protein

		[Nasonia giraulti] >gi|269969129|gb|ACZ54794.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969131|gb|ACZ54795.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969133|gb|ACZ54796.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969135|gb|ACZ54797.1| ENSANGP00000031746-like protein [Nasonia giraulti] >gi|269969137|gb|ACZ54798.1| ENSANGP00000031746-like protein [Nasonia giraulti]
1648	Unigene55579_All	partner of Y14 and mago isoform 4 [Mus musculus]
1649	CL6691.Contig1_All	hypothetical protein SINV_01162 [Solenopsis invicta]
1649	CL6691.Contig2_All	
1650	CL12482.Contig1_All	actin [Spodoptera exigua]
1650	CL12482.Contig2_All	
1651	CL12300.Contig1_All	GD19750 [Drosophila simulans] >gi|194198077|gb|EDX11653.1| GD19750 [Drosophila simulans]
1652	Unigene17559_All	AAEL009946-PA [Aedes aegypti]
1653	CL7012.Contig1_All	60 kDa SS-A/Ro ribonucleoprotein, putative [Pediculus humanus corporis] >gi|212508898|gb|EEB12452.1| 60 kDa SS-A/Ro ribonucleoprotein, putative [Pediculus humanus corporis]
1654	Unigene55405_All	PREDICTED: probable leucine--tRNA ligase, mitochondrial-like [Metaseiulus occidentalis]
1655	CL7137.Contig2_All	sphingomyelin phosphodiesterase, putative [Pediculus humanus corporis] >gi|212514220|gb|EEB16579.1| sphingomyelin phosphodiesterase, putative [Pediculus humanus corporis]
1655	CL7137.Contig3_All	

1656	CL16955.Contig1_All	Nucleobindin-2 [Acromyrmex echinatior]
1656	CL16955.Contig2_All	
1657	CL10633.Contig1_All	cystathionine beta-synthase [Ictalurus punctatus]
1658	CL9322.Contig1_All	hypothetical protein KGM_01607 [Danaus plexippus]
1658	CL9322.Contig5_All	
1659	Unigene35273_All	Spo0B-associated GTP-binding protein [Culex quinquefasciatus] >gi|167863509|gb|EDS26892.1| Spo0B-associated GTP-binding protein [Culex quinquefasciatus]
1660	CL8204.Contig1_All	hypothetical protein AND_15202 [Anopheles darlingi]
1661	Unigene39820_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167862356|gb|EDS25739.1| conserved hypothetical protein [Culex quinquefasciatus]
1662	Unigene9922_All	PIH1 domain-containing protein 1 [Crassostrea gigas]
1662	Unigene9924_All	
1663	Unigene48859_All	Chain A, Crystal Structure Of The Cyclophiln_ring Domain Of Human Peptidylprolyl Isomerase (Cyclophilin)-Like 2 Isoform B >gi|75765773|pdb|1ZKC|B Chain B, Crystal Structure Of The Cyclophiln_ring Domain Of Human Peptidylprolyl Isomerase (Cyclophilin)-Like 2 Isoform B
1663	Unigene90549_All	
1664	Unigene10073_All	Putative regulator of nonsense transcripts 1 [Acromyrmex echinatior]
1665	Unigene57583_All	innexin 3 [Schistocerca gregaria]
1666	Unigene33934_All	Ribosome biogenesis protein NSA2-like protein [Heterocephalus glaber]
1667	Unigene747_All	putative ARP-like protein [Danaus plexippus]
1668	Unigene32671_All	PREDICTED: dystroglycan-like [Apis mellifera]
1669	CL2906.Contig1_All	hypothetical protein NEMVEDRAFT_v1g224534 [Nematostella vectensis] >gi|156201520|gb|EDO26981.1| predicted protein [Nematostella vectensis]
1669	CL2906.Contig6_All	
1670	CL865.Contig1_All	PREDICTED: ubiquitin carboxyl-terminal hydrolase 64E-like [Hydra magnipapillata]
1671	CL3622.Contig2_All	protein-L-isoaspartate O-methyltransferase, putative [Pediculus humanus corporis] >gi|212512322|gb|EEB15115.1| protein-L-isoaspartate O-methyltransferase, putative [Pediculus humanus corporis]
1672	Unigene62716_All	hypothetical protein SINV_12675 [Solenopsis invicta]
1673	CL7965.Contig1_All	-

1674	CL11864.Contig4_All	Wdr5 protein, partial [Mus musculus]
1675	CL13963.Contig1_All	PREDICTED: septin-4-like [Bombus terrestris] >gi|350423255|ref|XP_003493421.1| PREDICTED: septin-4-like isoform 1 [Bombus impatiens]
1676	CL14565.Contig3_All	elongation factor Tu C-terminal domain containing protein [Entamoeba histolytica HM-1:IMSS-B]
1677	Unigene12963_All	heat shock protein 20.7 [Schistocerca gregaria]
1678	Unigene56604_All	golgin IMH1, putative [Pediculus humanus corporis] >gi|212505871|gb|EEB10217.1| golgin IMH1, putative [Pediculus humanus corporis]
1679	Unigene716_All	calcium-regulated heat stable protein, putative [Pediculus humanus corporis] >gi|212517238|gb|EEB19159.1| calcium-regulated heat stable protein, putative [Pediculus humanus corporis]
1680	Unigene27877_All	Charged multivesicular body protein 1b [Camponotus floridanus]
1681	Unigene42738_All	Anopheles gambiae str. PEST AGAP012896-PA [Anopheles gambiae str. PEST] >gi|157021154|gb|EAL42444.3| AGAP012896-PA [Anopheles gambiae str. PEST]
1682	CL10882.Contig1_All	PREDICTED: phospholipase A-2-activating protein-like, partial [Hydra magnipapillata]
1682	CL10882.Contig2_All	
1683	Unigene11233_All	ribosomal protein L27e [Georissus sp. APV-2005]
1684	CL9718.Contig1_All	-
1685	CL3900.Contig1_All	hypothetical protein SINV_10565 [Solenopsis invicta]
1685	CL3900.Contig2_All	

1686	Unigene47427_All	stat, partial [Daphnia arenata] >gi|385048268|gb|AFI39895.1| stat, partial [Daphnia pulex] >gi|385048270|gb|AFI39896.1| stat, partial [Daphnia pulex] >gi|385048272|gb|AFI39897.1| stat, partial [Daphnia pulex] >gi|385048274|gb|AFI39898.1| stat, partial [Daphnia pulex] >gi|385048276|gb|AFI39899.1| stat, partial [Daphnia pulex] >gi|385048278|gb|AFI39900.1| stat, partial [Daphnia pulex] >gi|385048280|gb|AFI39901.1| stat, partial [Daphnia pulex] >gi|385048282|gb|AFI39902.1| stat, partial [Daphnia pulex] >gi|385048284|gb|AFI39903.1| stat, partial [Daphnia pulex] >gi|385048286|gb|AFI39904.1| stat, partial [Daphnia pulex] >gi|385048288|gb|AFI39905.1| stat, partial [Daphnia parvula] >gi|385048290|gb|AFI39906.1| stat, partial [Daphnia pulex] >gi|385048292|gb|AFI39907.1| stat, partial [Daphnia parvula] >gi|385048294|gb|AFI39908.1| stat, partial [Daphnia parvula]
1687	CL14610.Contig1_All	hypothetical protein BRAFLDRAFT_208841 [Branchiostoma floridae] >gi|229279695|gb|EEN50472.1| hypothetical protein BRAFLDRAFT_208841 [Branchiostoma floridae]
1687	CL14610.Contig2_All	
1688	Unigene33315_All	Patj-like protein [Harpegnathos saltator]
1688	Unigene97198_All	
1689	Unigene92448_All	hypothetical protein CAPTEDRAFT_136770 [Capitella teleta]
1690	Unigene55344_All	Glutathione peroxidase 3 [Crassostrea gigas]
1691	Unigene12646_All	import inner membrane translocase subunit TIM50-C, putative [Pediculus humanus corporis] >gi|212513414|gb|EEB15991.1| import inner membrane translocase subunit TIM50-C, putative [Pediculus humanus corporis]
1692	Unigene27407_All	PREDICTED: leucine-rich repeat-containing protein 15 [Taeniopygia guttata]
1693	Unigene56268_All	PREDICTED: mitogen-activated protein kinase 14B-like isoform 1 [Bombus impatiens]
1694	CL13576.Contig1_All	hypothetical protein TcasGA2_TC002424 [Tribolium castaneum]
1694	CL13576.Contig2_All	
1695	Unigene20202_All	3'(2'),5'-bisphosphate nucleotidase 1 [Camponotus floridanus]
1696	CL1745.Contig1_All	ACYPI004051 [Acyrthosiphon pisum]
1696	CL1745.Contig2_All	
1697	Unigene42530_All	PREDICTED: acyl-CoA dehydrogenase family member 9, mitochondrial-like, partial [Ornithorhynchus anatinus]

1698	Unigene71973_All	putative ATP-dependent RNA helicase DDX46-like protein, partial [Apis mellifera] >gi|351634475|gb|AEQ55058.1| putative ATP-dependent RNA helicase DDX46-like protein, partial [Apis mellifera] >gi|351634477|gb|AEQ55059.1| putative ATP-dependent RNA helicase DDX46-like protein, partial [Apis mellifera] >gi|351634479|gb|AEQ55060.1| putative ATP-dependent RNA helicase DDX46-like protein, partial [Apis mellifera] >gi|351634521|gb|AEQ55081.1| putative ATP-dependent RNA helicase DDX46-like protein, partial [Apis mellifera] >gi|351634523|gb|AEQ55082.1| putative ATP-dependent RNA helicase DDX46-like protein, partial [Apis mellifera]
1699	Unigene62919_All	Ankyrin repeat domain-containing protein 13B [Camponotus floridanus]
1700	CL9935.Contig1_All	hypothetical protein SINV_15265 [Solenopsis invicta]
1701	Unigene49826_All	macrophage migration inhibitory factor-like protein [Maconellicoccus hirsutus]
1702	CL3415.Contig2_All	hypothetical protein TcasGA2_TC010492 [Tribolium castaneum]
1703	Unigene40559_All	PREDICTED: hypothetical protein LOC100646562 [Bombus terrestris]
1704	CL312.Contig1_All	PREDICTED: nuclear factor NF-kappa-B p100 subunit-like [Bombus impatiens]
1704	CL312.Contig3_All	
1705	Unigene148858_All	unnamed protein product [Trypanosoma congolense IL3000]
1706	Unigene70060_All	PREDICTED: fatty-acid amide hydrolase 2-like [Papio anubis]
1707	Unigene17913_All	nuclear transcription factor Tfp1 [Locusta migratoria]
1708	CL6538.Contig1_All	2-hydroxyacyl-CoA lyase 1 [Acromyrmex echinatior]
1708	CL6538.Contig3_All	
1709	Unigene2826_All	Transmembrane emp24 domain-containing protein [Camponotus floridanus]
1710	Unigene10437_All	unnamed protein product [Mus musculus]
1711	Unigene20154_All	PREDICTED: protein canopy-1-like [Apis mellifera]
1712	Unigene50086_All	hypothetical protein TcasGA2_TC030690, partial [Tribolium castaneum]
1713	CL3210.Contig1_All	map/microtubule affinity-regulating kinase 2,4 [Culex quinquefasciatus] >gi|167870591|gb|EDS33974.1| map/microtubule affinity-regulating kinase 2,4 [Culex quinquefasciatus]
1713	CL3210.Contig2_All	

1713	Unigene69619_All	
1713	CL3210.Contig3_All	
1713	Unigene69620_All	
1713	CL3210.Contig6_All	
1713	CL3210.Contig7_All	
1713	CL3210.Contig5_All	
1714	Unigene1625_All	-
1715	CL449.Contig1_All	hypothetical protein SINV_12569 [Solenopsis invicta]
1716	Unigene57571_All	simila to CG7484 [Papilio polytes]
1717	CL6683.Contig1_All	heterochromatin protein 1-1, partial [Schmidtea mediterranea]
1717	CL6683.Contig2_All	
1718	CL14315.Contig1_All	forkhead box K2 (predicted), isoform CRA_b [Rattus norvegicus]
1718	CL14315.Contig2_All	
1719	CL4684.Contig2_All	hypothetical protein KGM_04184 [Danaus plexippus]
1719	CL4684.Contig3_All	
1720	CL14593.Contig3_All	AAEL003272-PA [Aedes aegypti]
1721	Unigene64785_All	NADH-ubiquinone oxidoreductase 42 kDa subunit [Drosophila melanogaster]
1722	CL4552.Contig1_All	PREDICTED: hypothetical protein LOC100644542 [Bombus terrestris]
1723	CL7565.Contig1_All	RNA-binding protein 1 [Harpegnathos saltator]
1724	CL1961.Contig1_All	hypothetical protein KGM_18710 [Danaus plexippus]
1725	Unigene27369_All	PREDICTED: ankyrin repeat and MYND domain-containing protein 2-like [Nasonia vitripennis]
1726	Unigene70261_All	PREDICTED: protein LSM12 homolog [Nasonia vitripennis]
1727	CL10152.Contig1_All	hypothetical protein AND_16831 [Anopheles darlingi]
1728	CL310.Contig10_All	semaphorin 2a [Gryllus bimaculatus]
1728	Unigene54767_All	
1728	CL310.Contig2_All	
1728	Unigene54768_All	
1728	CL310.Contig7_All	
1728	CL310.Contig4_All	
1728	CL310.Contig5_All	
1728	CL310.Contig3_All	
1728	CL310.Contig1_All	
1728	CL310.Contig6_All	
1728	Unigene25628_All	
1729	Unigene63123_All	LOC432204 protein, partial [Xenopus laevis]
1730	Unigene42353_All	Poly(A) polymerase gamma [Acromyrmex echinatior]

1731	CL11536.Contig2_All	DNA methyltransferase 1, partial [Schistocerca gregaria]
1732	Unigene56086_All	Sps2 protein, partial [Mus musculus]
1733	CL1433.Contig1_All	hypothetical protein IscW_ISCW011816 [Ixodes scapularis] >gi|215505465|gb|EEC14959.1| hypothetical protein IscW_ISCW011816 [Ixodes scapularis]
1734	Unigene10168_All	GH18488 [Drosophila grimshawi] >gi|193894190|gb|EDV93056.1| GH18488 [Drosophila grimshawi]
1734	CL14328.Contig2_All	
1734	CL14328.Contig1_All	
1735	Unigene12862_All	PREDICTED: exportin-2-like [Apis florea]
1736	Unigene3125_All	PREDICTED: flap endonuclease 1-like [Nasonia vitripennis]
1737	Unigene63071_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212511198|gb|EEB14231.1| conserved hypothetical protein [Pediculus humanus corporis]
1738	CL2464.Contig2_All	40S ribosomal protein S21, putative [Pediculus humanus corporis] >gi|212505360|gb|EEB09832.1| 40S ribosomal protein S21, putative [Pediculus humanus corporis]
1739	Unigene16851_All	glyceraldehyde-3-phosphate dehydrogenase [Brachionus plicatilis]
1740	Unigene1526_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212516163|gb|EEB18205.1| conserved hypothetical protein [Pediculus humanus corporis]
1741	CL6259.Contig1_All	PREDICTED: single-stranded DNA-binding protein, mitochondrial-like [Apis florea]
1741	Unigene46934_All	
1742	Unigene57833_All	hypothetical protein SINV_03726 [Solenopsis invicta]
1743	CL4818.Contig1_All	PREDICTED: methionine--tRNA ligase, mitochondrial-like [Strongylocentrotus purpuratus]
1743	CL4818.Contig3_All	
1744	CL2669.Contig1_All	tRNA pseudouridine synthase A [Culex quinquefasciatus] >gi|167868280|gb|EDS31663.1| tRNA pseudouridine synthase A [Culex quinquefasciatus]
1745	CL2203.Contig2_All	PREDICTED: similar to serine/threonine-protein kinase 38 (ndr2 protein kinase) [Tribolium castaneum] >gi|270003267|gb|EEZ99714.1| hypothetical protein TcasGA2_TC002475 [Tribolium castaneum]
1745	CL2203.Contig3_All	
1746	Unigene25245_All	syntaxin interacting protein 1 [Triatoma infestans]

1747	Unigene57809_All	Nuclear pore complex protein Nup93, putative [Pediculus humanus corporis] >gi|212517883|gb|EEB19712.1| Nuclear pore complex protein Nup93, putative [Pediculus humanus corporis]
1748	CL7999.Contig1_All	PREDICTED: hypothetical protein LOC100164379 [Acyrthosiphon pisum]
1748	Unigene110048_All	
1749	CL11632.Contig1_All	Regenectin [Periplaneta americana]
1749	CL11632.Contig2_All	
1750	CL7325.Contig1_All	hypothetical protein SINV_14274 [Solenopsis invicta]
1750	CL7325.Contig4_All	
1750	CL7325.Contig3_All	
1750	CL7325.Contig2_All	
1751	CL14714.Contig1_All	Protein peanut [Acromyrmex echinatior]
1751	CL14714.Contig2_All	
1752	CL5123.Contig3_All	hypothetical protein WUBG_16084, partial [Wuchereria bancrofti]
1753	CL6052.Contig1_All	PREDICTED: microtubule-associated protein Jupiter-like isoform 2 [Bombus impatiens]
1753	CL6052.Contig5_All	
1753	CL6052.Contig2_All	
1753	CL6052.Contig3_All	
1753	CL6052.Contig4_All	
1753	CL6052.Contig6_All	
1754	CL14390.Contig1_All	hypothetical protein CAPTEDRAFT_223725 [Capitella teleta]
1754	CL14390.Contig2_All	
1755	Unigene56790_All	Ubiquitin carboxyl-terminal hydrolase 7 [Harpegnathos saltator]
1756	Unigene72643_All	PREDICTED: NIF3-like protein 1-like [Nasonia vitripennis]
1757	CL16091.Contig1_All	PREDICTED: phosphoribosylformylglycinamidine synthase-like [Strongylocentrotus purpuratus]
1757	CL16091.Contig3_All	
1758	Unigene55174_All	ADP-ribosylation factor, arf, putative [Pediculus humanus corporis] >gi|212508721|gb|EEB12318.1| ADP-ribosylation factor, arf, putative [Pediculus humanus corporis]
1759	Unigene26367_All	PREDICTED: 28S ribosomal protein S35, mitochondrial [Pongo abelii]
1760	Unigene1539_All	PREDICTED: mRNA export factor-like [Nasonia vitripennis]
1761	CL11294.Contig1_All	PREDICTED: similar to bridging integrator [Tribolium castaneum]

1761	CL11294.Contig2_All	
1762	Unigene27848_All	PREDICTED: podocalyxin-like protein 2-like [Macaca mulatta]
1763	Unigene70243_All	PREDICTED: TATA-binding protein-associated factor 172, partial [Ornithorhynchus anatinus]
1764	CL14672.Contig1_All	hypothetical protein AND_23205 [Anopheles darlingi]
1765	Unigene64802_All	Replication protein A 32 kDa subunit [Pteropus alecto]
1766	Unigene72635_All	PREDICTED: similar to NADH-ubiquinone oxidoreductase 39 kda subunit [Tribolium castaneum] >gi|270006426|gb|EFA02874.1| hypothetical protein TcasGA2_TC007967 [Tribolium castaneum]
1767	CL3068.Contig1_All	unknown [Dendroctonus ponderosae]
1768	Unigene62303_All	AGAP002713-PA [Anopheles gambiae str. PEST] >gi|333468013|gb|EAA08128.5| AGAP002713-PA [Anopheles gambiae str. PEST]
1769	Unigene69873_All	AT05180p [Drosophila melanogaster]
1769	Unigene89903_All	
1770	CL890.Contig1_All	chitin deacetylase 5 [Nilaparvata lugens]
1770	CL890.Contig2_All	
1771	CL14754.Contig2_All	PREDICTED: uncharacterized protein LOC100871753, partial [Apis florea]
1772	Unigene50252_All	ribosomal protein L18A [Blattella germanica]
1773	Unigene32440_All	pelle, partial [Daphnia parvula]
1774	Unigene70021_All	unnamed protein product [Tetraodon nigroviridis]
1775	CL6566.Contig2_All	alpha-mannosidase, putative [Pediculus humanus corporis] >gi|212505880|gb|EEB10226.1| alpha-mannosidase, putative [Pediculus humanus corporis]
1776	Unigene88766_All	PREDICTED: peroxisomal acyl-coenzyme A oxidase 1 [Ovis aries]
1777	Unigene65152_All	GJ17423 [Drosophila virilis] >gi|194148652|gb|EDW64350.1| GJ17423 [Drosophila virilis]
1778	CL9578.Contig1_All	PREDICTED: target of rapamycin complex subunit lst8-like [Bombus impatiens]
1778	CL9578.Contig3_All	
1779	CL6386.Contig1_All	putative 4-nitrophenylphosphatase [Danaus plexippus]
1779	CL6386.Contig2_All	
1779	CL6386.Contig3_All	
1780	CL14785.Contig1_All	hypothetical protein AND_06095 [Anopheles darlingi]
1781	CL11779.Contig2_All	Papilin [Acromyrmex echinatior]
1782	CL6343.Contig1_All	Metaxin-1 [Acromyrmex echinatior]
1782	CL6343.Contig3_All	
1783	Unigene12302_All	PREDICTED: parafibromin-like, partial [Oryzias latipes]

1784	CL17579.Contig3_All	splicing factor 3A subunit 2 [Scylla paramamosain]
1785	CL559.Contig2_All	Leucine-rich repeat protein SHOC-2 [Harpegnathos saltator]
1785	Unigene77250_All	
1786	Unigene107663_All	-
1787	Unigene57869_All	AGAP003567-PA [Anopheles gambiae str. PEST] >gi|55241030|gb|EAA08876.2| AGAP003567-PA [Anopheles gambiae str. PEST]
1788	Unigene10194_All	hypothetical protein SINV_08651 [Solenopsis invicta]
1789	CL3530.Contig1_All	PREDICTED: putative helicase MOV-10-like [Xenopus (Silurana) tropicalis]
1790	CL15323.Contig1_All	GK13544 [Drosophila willistoni] >gi|194168789|gb|EDW83690.1| GK13544 [Drosophila willistoni]
1791	CL15436.Contig1_All	PREDICTED: aggrecan core protein-like [Xenopus (Silurana) tropicalis]
1792	Unigene63159_All	PREDICTED: putative ATP-dependent RNA helicase DDX11-like protein 8-like isoform 2 [Orcinus orca]
1793	CL10737.Contig1_All	GF19747 [Drosophila ananassae] >gi|190618581|gb|EDV34105.1| GF19747 [Drosophila ananassae]
1793	CL10737.Contig3_All	
1794	CL13458.Contig1_All	PREDICTED: RNA-binding protein 27-like isoform 2 [Nasonia vitripennis]
1794	CL13458.Contig2_All	
1795	CL1867.Contig1_All	hypothetical protein BRAFLDRAFT_90729 [Branchiostoma floridae] >gi|229295250|gb|EEN65898.1| hypothetical protein BRAFLDRAFT_90729 [Branchiostoma floridae]
1795	CL1867.Contig2_All	
1795	CL1867.Contig3_All	
1796	CL946.Contig1_All	hypothetical protein TcasGA2_TC009594 [Tribolium castaneum]
1797	CL14339.Contig4_All	PREDICTED: regucalcin-like isoform 1 [Acyrthosiphon pisum] >gi|328721294|ref|XP_003247264.1| PREDICTED: regucalcin-like isoform 2 [Acyrthosiphon pisum]
1798	Unigene42560_All	dyskerin [Thermobia domestica]
1799	CL6456.Contig1_All	hypothetical protein SINV_01649 [Solenopsis invicta]
1799	CL6456.Contig2_All	
1800	Unigene2783_All	chitin binding peritrophin-A, putative [Pediculus humanus corporis] >gi|212514415|gb|EEB16743.1| chitin binding peritrophin-A, putative [Pediculus humanus corporis]
1801	CL803.Contig2_All	-

1801	CL803.Contig3_All	
1802	Unigene42837_All	PREDICTED: similar to leucine rich repeat containing 59 [Tribolium castaneum] >gi|270003717|gb|EFA00165.1| hypothetical protein TcasGA2_TC002987 [Tribolium castaneum]
1803	Unigene51331_All	ribosomal protein L14 - pea aphid symbiont bacterium
1804	CL7007.Contig1_All	-
1805	Unigene40330_All	-
1806	Unigene12636_All	RWD domain-containing protein 4A [Camponotus floridanus]
1807	Unigene61553_All	Putative cytochrome P450 6a20 [Acromyrmex echinatior]
1807	Unigene62330_All	
1808	CL3022.Contig2_All	hypothetical protein DAPPUDRAFT_299978 [Daphnia pulex]
1809	CL14052.Contig1_All	hypothetical protein TcasGA2_TC006121 [Tribolium castaneum]
1810	CL16342.Contig1_All	PREDICTED: protein bicaudal D-like, partial [Apis florea]
1810	CL16342.Contig2_All	
1811	CL3325.Contig1_All	mCG1036761 [Mus musculus]
1812	CL13670.Contig1_All	hypothetical protein DAPPUDRAFT_302577 [Daphnia pulex]
1812	CL13670.Contig2_All	
1813	Unigene64690_All	Methylosome protein, putative [Pediculus humanus corporis] >gi|212505786|gb|EEB10166.1| Methylosome protein, putative [Pediculus humanus corporis]
1814	Unigene62951_All	laminin beta chain [Schistocerca gregaria]
1815	CL795.Contig1_All	glutathione S-transferase theta 1 [Locusta migratoria]
1815	CL5093.Contig3_All	
1815	CL795.Contig4_All	
1816	Unigene25193_All	GI10980 [Drosophila mojavensis] >gi|193906768|gb|EDW05635.1| GI10980 [Drosophila mojavensis]
1817	CL10975.Contig1_All	PREDICTED: uncharacterized protein LOC100893485 [Strongylocentrotus purpuratus]
1818	Unigene49871_All	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa, isoform CRA_d [Homo sapiens]
1819	CL12285.Contig1_All	BAG domain-containing protein Samui [Acromyrmex echinatior]
1819	CL12285.Contig2_All	
1820	Unigene34389_All	PREDICTED: signal recognition particle receptor subunit alpha homolog [Apis florea]

1821	CL15818.Contig4_All	hypothetical protein CAPTEDRAFT_187673 [Capitella teleta]
1822	Unigene69666_All	AGAP007802-PA [Anopheles gambiae str. PEST] >gi|157015214|gb|EAA12443.4| AGAP007802-PA [Anopheles gambiae str. PEST]
1823	CL4970.Contig1_All	mCG15924, isoform CRA_f [Mus musculus]
1824	Unigene18730_All	ELG protein, isoform CRA_b [Homo sapiens]
1825	Unigene12598_All	RE33648p [Drosophila melanogaster]
1826	CL12581.Contig1_All	PREDICTED: protein sly1 homolog [Nasonia vitripennis]
1827	CL9664.Contig1_All	hypothetical protein SINV_04663 [Solenopsis invicta]
1828	CL7173.Contig2_All	hypothetical protein SINV_01197 [Solenopsis invicta]
1829	Unigene90110_All	NAD-specific glutamate dehydrogenase [Capsaspora owczarzaki ATCC 30864] >gi|320170749|gb|EFW47648.1| NAD-specific glutamate dehydrogenase [Capsaspora owczarzaki ATCC 30864]
1830	CL379.Contig10_All	GJ14169 [Drosophila virilis] >gi|194142258|gb|EDW58666.1| GJ14169 [Drosophila virilis]
1830	CL379.Contig32_All	
1830	CL379.Contig34_All	
1830	CL379.Contig25_All	
1830	CL379.Contig21_All	
1830	CL379.Contig27_All	
1830	CL379.Contig28_All	
1830	CL379.Contig8_All	
1830	CL379.Contig9_All	
1830	CL379.Contig20_All	
1830	CL379.Contig33_All	
1830	CL379.Contig30_All	
1830	CL379.Contig24_All	
1830	CL379.Contig7_All	
1830	CL379.Contig40_All	
1830	CL379.Contig41_All	
1830	CL379.Contig13_All	
1830	CL379.Contig36_All	
1830	CL379.Contig15_All	
1830	CL379.Contig37_All	
1830	CL379.Contig2_All	
1830	CL379.Contig17_All	
1830	CL379.Contig23_All	
1830	CL379.Contig14_All	
1830	CL379.Contig6_All	

1830	CL379.Contig5_All	
1830	CL379.Contig31_All	
1830	CL379.Contig39_All	
1830	CL379.Contig18_All	
1830	CL379.Contig16_All	
1830	CL379.Contig12_All	
1831	Unigene70835_All	GD10948 [Drosophila simulans] >gi|194193309|gb|EDX06885.1| GD10948 [Drosophila simulans]
1832	Unigene12505_All	PREDICTED: nuclear pore complex protein Nup88-like [Apis florea]
1833	CL10725.Contig1_All	PREDICTED: hypothetical protein LOC100625123 [Sus scrofa]
1834	Unigene1882_All	PREDICTED: scaffold attachment factor B2-like [Oryctolagus cuniculus]
1835	CL9819.Contig1_All	hypothetical protein [Monosiga brevicollis MX1] >gi|163778460|gb|EDQ92075.1| predicted protein [Monosiga brevicollis MX1]
1835	CL9819.Contig2_All	
1836	Unigene57823_All	guanine nucleotide-binding protein subunit beta-like [Microplitis mediator]
1837	CL3035.Contig3_All	E3 ubiquitin-protein ligase HUWE1 [Chelonia mydas]
1838	Unigene6439_All	-
1839	Unigene140354_All	-
1840	CL989.Contig3_All	cAMP-dependent protein kinase C1 [Danaus plexippus]
1840	Unigene40375_All	
1841	CL12302.Contig1_All	Chain A, Crystal Structure Of Beta-Glucosidase From Termite Neotermes Koshunensis In Complex With Para-Nitrophenyl-Beta-D-Glucopyranoside >gi|393715259|pdb|3VIM|A Chain A, Crystal Structure Of Beta-Glucosidase From Termite Neotermes Koshunensis In Complex With A New Glucopyranosidic Product >gi|393715260|pdb|3VIN|A Chain A, Crystal Structure Of Beta-Glucosidase From Termite Neotermes Koshunensis In Complex With A New Glucopyranosidic Product >gi|393715261|pdb|3VIO|A Chain A, Crystal Structure Of Beta-Glucosidase From Termite Neotermes Koshunensis In Complex With A New Glucopyranosidic Product >gi|393715262|pdb|3VIP|A Chain A, Crystal Structure Of Beta-Glucosidase From Termite Neotermes Koshunensis In Complex With A New Glucopyranosidic Product
1841	CL12302.Contig2_All	
1842	Unigene10309_All	hypothetical protein TcasGA2_TC004857 [Tribolium castaneum]

1843	CL1632.Contig1_All	GE22195 [Drosophila yakuba] >gi|194181197|gb|EDW94808.1| GE22195 [Drosophila yakuba]
1844	Unigene17968_All	vacuolar protein sorting 52 [Salmo salar] >gi|260182162|gb|ACX35591.1| vacuolar protein sorting 52 [Salmo salar]
1845	CL9926.Contig4_All	PREDICTED: uncharacterized protein LOC100878635 [Megachile rotundata]
1846	Unigene47530_All	PREDICTED: nucleoporin p54 [Trichechus manatus latirostris]
1847	CL1548.Contig2_All	Protein phosphatase 2, regulatory subunit B', gamma isoform [Homo sapiens]
1848	Unigene104059_All	-
1849	CL12947.Contig1_All	RRP6 protein, partial [Chironomus tentans]
1850	Unigene41181_All	Probable splicing factor 3B subunit 5 [Harpegnathos saltator]
1851	Unigene64722_All	ribosomal protein L13 [Chrysomela tremula]
1852	CL3812.Contig1_All	Serine/threonine-protein kinase TAO1 [Acromyrmex echinatior]
1852	CL3812.Contig2_All	
1852	CL3812.Contig3_All	
1853	Unigene42570_All	WD-repeat protein, putative [Ixodes scapularis] >gi|215490837|gb|EEC00478.1| WD-repeat protein, putative [Ixodes scapularis]
1854	Unigene102332_All	-
1855	Unigene54820_All	hypothetical protein WUBG_17438 [Wuchereria bancrofti]
1856	Unigene89662_All	unnamed protein product [Mus musculus]
1857	CL10554.Contig2_All	-
1858	CL4862.Contig1_All	unknown [Dendroctonus ponderosae]
1859	Unigene12780_All	Maspardin [Camponotus floridanus]
1860	Unigene62738_All	CG2082, isoform D [Drosophila melanogaster] >gi|23175929|gb|AAN14320.1| CG2082, isoform D [Drosophila melanogaster]
1861	CL8295.Contig1_All	Tyrosine-protein phosphatase non-receptor type 1 [Harpegnathos saltator]
1861	CL8295.Contig2_All	
1862	Unigene72049_All	putative endonuclease/reverse transcriptase [Lymantria dispar]
1863	Unigene27955_All	hypothetical protein AND_07275 [Anopheles darlingi]
1864	Unigene126085_All	-
1865	CL4994.Contig5_All	cytochrome P450 [Hodotermopsis sjostedti]
1865	Unigene62079_All	

1866	CL1426.Contig1_All	PREDICTED: 15-hydroxyprostaglandin dehydrogenase [NAD+]-like isoform 1 [Nasonia vitripennis] >gi|345479364|ref|XP_003423936.1| PREDICTED: 15-hydroxyprostaglandin dehydrogenase [NAD+]-like isoform 2 [Nasonia vitripennis]
1866	CL1426.Contig2_All	
1867	CL9351.Contig2_All	PREDICTED: protein disulfide-isomerase A4-like [Apis mellifera]
1868	CL10548.Contig1_All	PREDICTED: 5'-3' exoribonuclease 1-like [Cavia porcellus]
1869	CL6836.Contig1_All	-
1870	CL12073.Contig2_All	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B, putative [Pediculus humanus corporis] >gi|212515092|gb|EEB17292.1| Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B, putative [Pediculus humanus corporis]
1870	CL12073.Contig3_All	
1871	CL5093.Contig1_All	glutathione S-transferase theta 1 [Locusta migratoria]
1871	CL5093.Contig2_All	
1872	CL7729.Contig1_All	PREDICTED: similar to Rpb8 CG11246-PA [Tribolium castaneum] >gi|270009448|gb|EFA05896.1| hypothetical protein TcasGA2_TC008708 [Tribolium castaneum]
1872	CL7729.Contig3_All	
1872	CL7729.Contig2_All	
1872	CL7729.Contig4_All	
1873	Unigene47898_All	PREDICTED: 60S ribosomal protein L28-like isoform 1 [Bombus terrestris] >gi|340728567|ref|XP_003402592.1| PREDICTED: 60S ribosomal protein L28-like isoform 2 [Bombus terrestris] >gi|340728569|ref|XP_003402593.1| PREDICTED: 60S ribosomal protein L28-like isoform 3 [Bombus terrestris] >gi|350408755|ref|XP_003488502.1| PREDICTED: 60S ribosomal protein L28-like [Bombus impatiens]
1874	Unigene2934_All	chitinase [Bactrocera dorsalis]
1875	Unigene42526_All	ATP-dependent RNA helicase Ddx1 [Acromyrmex echinatior]
1876	CL536.Contig12_All	Focal adhesion kinase 1 [Acromyrmex echinatior]
1876	CL536.Contig4_All	
1876	CL536.Contig9_All	
1876	CL536.Contig3_All	
1876	CL536.Contig6_All	
1876	CL536.Contig14_All	
1876	CL536.Contig8_All	

1876	CL536.Contig2_All	
1876	CL536.Contig5_All	
1876	CL536.Contig1_All	
1877	Unigene73982_All	serine protease inhibitor 10 [Danaus plexippus]
1878	CL7148.Contig1_All	arf gtpase-activating protein [Aedes aegypti] >gi|108883414|gb|EAT47639.1| AAEL001277-PA [Aedes aegypti]
1878	CL7148.Contig2_All	
1879	CL11577.Contig2_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212510309|gb|EEB13508.1| conserved hypothetical protein [Pediculus humanus corporis]
1880	Unigene10139_All	PREDICTED: superkiller viralicidic activity 2-like 2-like, partial [Tursiops truncatus]
1881	Unigene64854_All	carboxylesterase [Athalia rosae]
1882	CL8574.Contig1_All	GF10842 [Drosophila ananassae] >gi|190625563|gb|EDV41087.1| GF10842 [Drosophila ananassae]
1882	CL8574.Contig2_All	
1883	CL12338.Contig1_All	hypothetical protein PANDA_011417 [Ailuropoda melanoleuca]
1884	Unigene35129_All	gp150 protein [Culex quinquefasciatus] >gi|167882236|gb|EDS45619.1| gp150 protein [Culex quinquefasciatus]
1885	CL4118.Contig1_All	eukaryotic porin [Capsaspora owczarzaki ATCC 30864] >gi|320165844|gb|EFW42743.1| eukaryotic porin [Capsaspora owczarzaki ATCC 30864]
1885	Unigene52525_All	
1886	Unigene10906_All	glutathione-S-transferase theta, GST, putative [Pediculus humanus corporis] >gi|212510153|gb|EEB13368.1| glutathione-S-transferase theta, GST, putative [Pediculus humanus corporis]
1887	Unigene12384_All	PREDICTED: vacuolar protein sorting-associated protein VTA1 homolog [Bombus impatiens]
1888	Unigene19797_All	survival motor neuron protein 1 [Ictalurus furcatus]
1889	Unigene64707_All	Beta-galactosidase [Camponotus floridanus]
1890	Unigene11269_All	signal peptide protease, partial [Papilio xuthus]
1891	Unigene20064_All	unnamed protein product [Tetraodon nigroviridis]
1892	Unigene72253_All	phosphatidylethanolamine-binding protein 2 [Culex quinquefasciatus] >gi|167870076|gb|EDS33459.1| phosphatidylethanolamine-binding protein 2 [Culex quinquefasciatus]
1893	Unigene62554_All	vitellogenin receptor [Periplaneta americana]
1893	Unigene74992_All	
1893	Unigene97055_All	

1893	Unigene97052_All	
1894	CL9735.Contig1_All	PREDICTED: 50S ribosomal protein L5-like [Bombus impatiens]
1895	Unigene27889_All	chloride intracellular channel isoform 1 [Scylla paramamosain]
1896	CL9856.Contig1_All	Serine protease gd [Camponotus floridanus]
1896	CL9856.Contig2_All	
1897	Unigene87149_All	hypothetical protein NEMVEDRAFT_v1g146786 [Nematostella vectensis] >gi|156206297|gb|EDO28780.1| predicted protein [Nematostella vectensis]
1898	CL13452.Contig1_All	protein kinase [Acheta domesticus]
1898	CL13452.Contig2_All	
1899	Unigene132526_All	hypothetical protein CAPTEDRAFT_122393, partial [Capitella teleta]
1900	Unigene24983_All	Piwi-like protein 2 [Crassostrea gigas]
1901	CL7165.Contig3_All	GL24600 [Drosophila persimilis] >gi|194111153|gb|EDW33196.1| GL24600 [Drosophila persimilis]
1902	CL4362.Contig1_All	Putative tRNA pseudouridine synthase Pus10 [Acromyrmex echinatior]
1902	CL4362.Contig2_All	
1902	CL4362.Contig4_All	
1902	CL4362.Contig3_All	
1903	CL11865.Contig1_All	PREDICTED: eukaryotic translation initiation factor 4 gamma, 2-like [Saccoglossus kowalevskii]
1904	CL8432.Contig1_All	PREDICTED: anoctamin-1-like [Megachile rotundata]
1904	CL8432.Contig2_All	
1904	CL8432.Contig3_All	
1905	CL13002.Contig1_All	TPA_exp: transcription factor NFAT subunit NF90 [Amblyomma variegatum]
1905	CL13002.Contig2_All	
1906	Unigene72200_All	hypothetical protein BRAFLDRAFT_110162 [Branchiostoma floridae] >gi|229271110|gb|EEN42038.1| hypothetical protein BRAFLDRAFT_110162 [Branchiostoma floridae]
1907	Unigene9895_All	PREDICTED: threonine aspartase 1-like, partial [Sus scrofa]
1908	Unigene26391_All	nuclear transcription factor Tfp1 [Locusta migratoria]
1909	CL3631.Contig2_All	predicted protein [Nematostella vectensis] >gi|156212125|gb|EDO33198.1| predicted protein [Nematostella vectensis]
1910	Unigene32883_All	hypothetical protein SINV_14142 [Solenopsis invicta]

1911	CL9441.Contig1_All	AGAP011162-PA [Anopheles gambiae str. PEST] >gi|157019660|gb|EAA05144.4| AGAP011162-PA [Anopheles gambiae str. PEST]
1912	CL2992.Contig6_All	hypothetical protein SINV_06859 [Solenopsis invicta]
1912	CL2992.Contig9_All	
1913	CL14659.Contig1_All	sensory neuron membrane protein 2 [Chilo suppressalis]
1913	CL14659.Contig2_All	
1914	CL17220.Contig1_All	GH10662 [Drosophila grimshawi] >gi|193905914|gb|EDW04781.1| GH10662 [Drosophila grimshawi]
1915	Unigene1506_All	Contactin [Camponotus floridanus]
1916	CL943.Contig1_All	hypothetical protein [Schistosoma mansoni] >gi|353228642|emb|CCD74813.1| hypothetical protein Smp_003340 [Schistosoma mansoni]
1916	CL943.Contig2_All	
1917	CL9313.Contig2_All	hypothetical protein KGM_09491 [Danaus plexippus]
1918	Unigene69294_All	lactoylglutathione lyase [Danaus plexippus]
1919	Unigene135670_All	-
1920	Unigene27335_All	putative ATP-dependent transporter [Danaus plexippus]
1921	Unigene2743_All	primo-1 [Papilio xuthus]
1922	CL7678.Contig1_All	juvenile hormone epoxide hydrolase 2, partial [Papilio xuthus]
1922	CL7678.Contig3_All	
1923	Unigene49984_All	PREDICTED: thymidylate synthase, partial [Nomascus leucogenys]
1924	Unigene50482_All	hypothetical protein KGM_06199 [Danaus plexippus]
1925	Unigene69888_All	PREDICTED: similar to Juvenile hormone-inducible protein, putative [Tribolium castaneum] >gi|270005969|gb|EFA02417.1| hypothetical protein TcasGA2_TC008102 [Tribolium castaneum]
1926	Unigene85758_All	-
1927	Unigene1082_All	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1 [Myotis davidii]
1928	CL12888.Contig1_All	hypothetical protein NEMVEDRAFT_v1g5663 [Nematostella vectensis] >gi|156203128|gb|EDO27507.1| predicted protein [Nematostella vectensis]
1929	CL9279.Contig1_All	PREDICTED: uncharacterized protein LOC100879167 [Megachile rotundata]
1929	CL9279.Contig2_All	
1930	CL5908.Contig1_All	PREDICTED: WD repeat domain phosphoinositide-interacting protein 2-like [Megachile rotundata]
1930	CL5908.Contig3_All	

1930	CL5908.Contig5_All	
1931	Unigene56099_All	PREDICTED: poly(ADP-ribose) glycohydrolase-like, partial [Pan paniscus]
1932	CL8463.Contig5_All	unnamed protein product [Tetraodon nigroviridis]
1932	Unigene62342_All	
1933	CL8906.Contig1_All	PREDICTED: probable nuclear transport factor 2-like isoform 2 [Apis mellifera]
1934	Unigene42524_All	PREDICTED: similar to ribosomal protein L13a [Tribolium castaneum] >gi|270007030|gb|EFA03478.1| hypothetical protein TcasGA2_TC013477 [Tribolium castaneum]
1935	Unigene19958_All	mitochondrial ribosomal protein, L23 [Culex quinquefasciatus] >gi|170053999|ref|XP_001862929.1| mitochondrial ribosomal protein, L23 [Culex quinquefasciatus] >gi|167874398|gb|EDS37781.1| mitochondrial ribosomal protein, L23 [Culex quinquefasciatus] >gi|167874399|gb|EDS37782.1| mitochondrial ribosomal protein, L23 [Culex quinquefasciatus]
1936	CL9240.Contig1_All	-
1936	CL9240.Contig2_All	
1936	CL9240.Contig6_All	
1936	CL9240.Contig5_All	
1936	CL9240.Contig3_All	
1936	CL9240.Contig7_All	
1936	CL9240.Contig8_All	
1936	CL9240.Contig4_All	
1937	Unigene10659_All	hypothetical protein TcasGA2_TC008789 [Tribolium castaneum]
1938	Unigene96775_All	-
1939	CL15840.Contig2_All	Protein phosphatase 1 regulatory subunit 7 [Camponotus floridanus]
1940	CL3462.Contig1_All	hypothetical protein SINV_80496 [Solenopsis invicta]
1940	CL3462.Contig4_All	
1940	CL3462.Contig3_All	
1940	CL3462.Contig2_All	
1941	Unigene57325_All	heat shock protein 40 [Locusta migratoria]
1942	Unigene1034_All	PREDICTED: serine-protein kinase ATM-like [Bombus terrestris]
1943	CL222.Contig10_All	PREDICTED: LOW QUALITY PROTEIN: PDZ and LIM domain protein Zasp-like [Apis florea]
1943	CL222.Contig16_All	
1943	CL222.Contig2_All	
1943	CL222.Contig6_All	
1943	CL222.Contig18_All	

1943	CL222.Contig8_All	
1943	CL222.Contig17_All	
1943	CL222.Contig11_All	
1943	CL222.Contig13_All	
1943	Unigene69513_All	
1943	CL222.Contig12_All	
1943	CL222.Contig4_All	
1943	CL222.Contig14_All	
1943	Unigene69512_All	
1943	CL222.Contig1_All	
1944	Unigene129840_All	-
1945	Unigene17747_All	-
1946	Unigene3103_All	PREDICTED: similar to AGAP012249-PA [Tribolium castaneum] >gi|270002367|gb|EEZ98814.1| hypothetical protein TcasGA2_TC004420 [Tribolium castaneum]
1947	Unigene35314_All	PREDICTED: cleavage and polyadenylation specificity factor subunit 2-like, partial [Ailuropoda melanoleuca]
1948	Unigene18264_All	Pyrroline-5-carboxylate reductase, putative [Pediculus humanus corporis] >gi|212514649|gb|EEB16926.1| Pyrroline-5-carboxylate reductase, putative [Pediculus humanus corporis]
1949	CL13663.Contig1_All	GTP-binding protein 128up, putative [Pediculus humanus corporis] >gi|212517682|gb|EEB19535.1| GTP-binding protein 128up, putative [Pediculus humanus corporis]
1950	CL4879.Contig1_All	hypothetical protein SINV_10498 [Solenopsis invicta]
1950	CL4879.Contig4_All	
1950	CL4879.Contig3_All	
1950	CL4879.Contig5_All	
1951	Unigene12388_All	eukaryotic initiation factor 4A-III [Danaus plexippus]
1952	Unigene12373_All	PREDICTED: inosine triphosphate pyrophosphatase-like [Megachile rotundata]
1953	CL90.Contig3_All	hypothetical protein SINV_06266 [Solenopsis invicta]
1953	CL17269.Contig7_All	
1953	CL17269.Contig3_All	
1953	CL90.Contig4_All	
1953	CL17269.Contig2_All	
1953	CL17269.Contig4_All	
1953	CL17269.Contig1_All	
1954	Unigene12984_All	-

1955	CL16976.Contig1_All	pyruvate carboxylase [Acanthamoeba castellanii str. Neff] >gi|440795354|gb|ELR16480.1| pyruvate carboxylase [Acanthamoeba castellanii str. Neff]
1955	CL16976.Contig2_All	
1956	Unigene35389_All	PREDICTED: similar to eukaryotic peptide chain release factor GTP-binding subunit [Tribolium castaneum] >gi|270004497|gb|EFA00945.1| hypothetical protein TcasGA2_TC003854 [Tribolium castaneum]
1957	Unigene48348_All	hypothetical protein TcasGA2_TC006564 [Tribolium castaneum]
1958	CL11227.Contig2_All	hypothetical protein AND_12652 [Anopheles darlingi]
1959	CL14897.Contig1_All	PREDICTED: polyadenylate-binding protein-interacting protein 1-like [Megachile rotundata]
1960	Unigene19269_All	Nipped-B-like protein [Camponotus floridanus]
1961	Unigene36892_All	PREDICTED: 50S ribosomal protein L11-like [Bombus impatiens]
1962	CL130.Contig1_All	carboxylesterase-like protein [Locusta migratoria manilensis]
1962	Unigene34739_All	
1962	CL130.Contig3_All	
1962	CL130.Contig4_All	
1962	CL245.Contig2_All	
1963	Unigene68481_All	hypothetical protein Phum_PHUM536400 [Pediculus humanus corporis] >gi|212516868|gb|EEB18827.1| hypothetical protein Phum_PHUM536400 [Pediculus humanus corporis]
1964	Unigene47485_All	glucosamine (N-acetyl)-6-sulfatase b precursor [Danio rerio] >gi|28277517|gb|AAH45323.1| Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID), b [Danio rerio] >gi|182891244|gb|AAI64157.1| Gnsb protein [Danio rerio]
1965	CL1096.Contig2_All	-
1966	CL2424.Contig1_All	similar to Drosophila melanogaster CG4666, partial [Drosophila yakuba]
1967	Unigene58407_All	-
1968	Unigene35120_All	Chain A, Solution Structure Of The Rna Binding Domain Of Squamous Cell Carcinoma Antigen Recognized By T Cells 3
1969	Unigene2987_All	unknown [Dendroctonus ponderosae]
1970	CL13754.Contig1_All	conserved hypothetical protein [Culex quinquefasciatus] >gi|167879743|gb|EDS43126.1| conserved hypothetical protein [Culex quinquefasciatus]
1970	CL13754.Contig2_All	
1971	Unigene740_All	hypothetical protein AND_00902 [Anopheles darlingi]

1971	CL10794.Contig1_All	
1972	CL4262.Contig1_All	-
1972	CL4262.Contig2_All	
1973	Unigene25934_All	peptidyl-prolyl cis-trans isomerase h, ppih [Papilio xuthus]
1974	Unigene27752_All	hypothetical protein DAPPUDRAFT_221117 [Daphnia pulex]
1975	Unigene6797_All	reverse transcriptase [Shijimiaeoides divina]
1976	Unigene128435_All	DNA gyrase subunit B, putative [Ixodes scapularis] >gi|215492575|gb|EEC02216.1| DNA gyrase subunit B, putative [Ixodes scapularis]
1977	Unigene57781_All	truncated histone macroH2A1 [Gallus gallus]
1978	CL7847.Contig3_All	PREDICTED: spermine synthase-like [Bombus terrestris]
1978	CL7847.Contig1_All	
1979	CL11360.Contig1_All	AAEL002831-PA [Aedes aegypti]
1979	Unigene57374_All	
1979	Unigene12905_All	
1980	CL4731.Contig1_All	40S ribosomal protein S15 [Aplysia californica]
1980	Unigene11287_All	
1980	CL4731.Contig2_All	
1980	Unigene77361_All	
1981	Unigene71835_All	PREDICTED: similar to mitochondrial ribosomal protein, L40, putative [Tribolium castaneum] >gi|270010911|gb|EFA07359.1| hypothetical protein TcasGA2_TC015959 [Tribolium castaneum]
1982	Unigene12361_All	hypothetical protein SINV_14383 [Solenopsis invicta]
1983	Unigene72428_All	4E-binding protein thor, putative [Pediculus humanus corporis] >gi|212510899|gb|EEB13990.1| 4E-binding protein thor, putative [Pediculus humanus corporis]
1984	CL8180.Contig1_All	hypothetical protein TcasGA2_TC012433 [Tribolium castaneum]
1985	CL11885.Contig2_All	-
1986	Unigene26553_All	PREDICTED: DNA ligase 1-like [Bombus terrestris]
1987	Unigene153295_All	-
1988	Unigene98464_All	-
1989	Unigene3048_All	PREDICTED: chromatin assembly factor 1 subunit B-like [Strongylocentrotus purpuratus]
1990	CL6278.Contig1_All	PREDICTED: ATP-dependent RNA helicase abstrakt-like [Bombus impatiens]
1991	CL17190.Contig1_All	Endoplasmic reticulum metallopeptidase 1 [Tupaia chinensis]
1991	CL17190.Contig2_All	

1992	Unigene50024_All	PREDICTED: t-complex protein 11-like protein 1-like isoform 2 [Apis mellifera]
1993	Unigene50188_All	PREDICTED: hypothetical protein LOC100645089 [Bombus terrestris]
1994	Unigene12156_All	ribosomal protein L39 [Bombyx mori] >gi|209571492|ref|NP_001129377.1| ribosomal protein L39 [Apis mellifera] >gi|209571494|ref|NP_001129378.1| ribosomal protein L39 [Tribolium castaneum] >gi|209862827|ref|NP_001129486.1| ribosomal protein L39 [Nasonia vitripennis] >gi|54036254|sp|Q6F482.1|RL39_PLUXY RecName: Full=60S ribosomal protein L39 >gi|54036316|sp|Q962S4.1|RL39_SPOFR RecName: Full=60S ribosomal protein L39 >gi|15213798|gb|AAK92174.1|AF400202_1 ribosomal protein L39 [Spodoptera frugiperda] >gi|49532834|dbj|BAD26652.1| Ribosomal protein L39 [Plutella xylostella] >gi|54609275|gb|AAV34853.1| ribosomal protein L39 [Bombyx mori] >gi|70909903|emb|CAJ17438.1| ribosomal protein L39e [Biphyllus lunatus] >gi|70909905|emb|CAJ17439.1| ribosomal protein L39e [Cicindela litorea] >gi|264667447|gb|ACY71309.1| ribosomal protein L39 [Chrysomela tremula] >gi|268306482|gb|ACY95362.1| ribosomal protein L39 [Manduca sexta] >gi|315115461|gb|ADT80703.1| ribosomal protein L39 [Euphydryas aurinia] >gi|332019965|gb|EGI60425.1| 60S ribosomal protein L39 [Acromyrmex echinatior] >gi|342356449|gb|AEL28883.1| ribosomal protein L39 [Heliconius melpomene cythera] >gi|389608661|dbj|BAM17940.1| ribosomal protein L39 [Papilio xuthus] >gi|389611453|dbj|BAM19338.1| ribosomal protein L39 [Papilio polytes]
1995	Unigene32803_All	PREDICTED: U6 snRNA-associated Sm-like protein LSm2-like [Tursiops truncatus]
1996	Unigene72437_All	GF12628 [Drosophila ananassae] >gi|190620230|gb|EDV35754.1| GF12628 [Drosophila ananassae]
1997	CL10606.Contig3_All	-
1998	Unigene143619_All	-
1999	Unigene67526_All	chemosensory protein 2 precursor [Bombyx mori] >gi|112032057|gb|ABH88195.1| chemosensory protein 2 [Bombyx mori]
1999	Unigene140715_All	
1999	Unigene101037_All	
2000	Unigene47698_All	hypothetical protein SINV_07362 [Solenopsis invicta]
2001	CL2114.Contig1_All	PREDICTED: catenin delta-2 isoform 2 [Nasonia vitripennis]
2001	CL2114.Contig3_All	

2001	CL2114.Contig2_All	
2002	Unigene39980_All	matrix metalloproteinase, putative [Ixodes scapularis] >gi|215507296|gb|EEC16790.1| matrix metalloproteinase, putative [Ixodes scapularis]
2003	CL15.Contig1_All	hypothetical protein IscW_ISCW006465 [Ixodes scapularis] >gi|215498251|gb|EEC07745.1| hypothetical protein IscW_ISCW006465 [Ixodes scapularis]
2003	CL15.Contig3_All	
2003	CL15.Contig2_All	
2004	CL11635.Contig1_All	PREDICTED: pleckstrin homology domain-containing family D member 1 [Orcinus orca]
2004	CL11635.Contig2_All	
2005	Unigene40039_All	-
2006	Unigene3066_All	acylamino-acid-releasing enzyme, putative [Pediculus humanus corporis] >gi|212505641|gb|EEB10045.1| acylamino-acid-releasing enzyme, putative [Pediculus humanus corporis]
2007	Unigene131412_All	-
2008	Unigene115052_All	PREDICTED: hypothetical protein LOC100537186 [Danio rerio]
2009	Unigene71238_All	ACYPI000583 [Acyrthosiphon pisum]
2010	Unigene41530_All	Cullin-3, putative [Pediculus humanus corporis] >gi|212517918|gb|EEB19747.1| Cullin-3, putative [Pediculus humanus corporis]
2011	Unigene9947_All	PREDICTED: fatty acid synthase-like [Acyrthosiphon pisum]
2012	Unigene12872_All	PREDICTED: transcription initiation factor IIB-like [Megachile rotundata]
2013	Unigene79617_All	-
2014	Unigene136540_All	ornithine carbamoyltransferase [Xenopus (Silurana) tropicalis] >gi|49522349|gb|AAH75343.1| ornithine carbamoyltransferase [Xenopus (Silurana) tropicalis]
2015	Unigene2735_All	THO complex subunit 1 [Harpegnathos saltator]
2016	Unigene70385_All	NEDD8-conjugating enzyme Ubc12, putative [Pediculus humanus corporis] >gi|212517798|gb|EEB19637.1| NEDD8-conjugating enzyme Ubc12, putative [Pediculus humanus corporis]
2017	Unigene133850_All	PREDICTED: chaperone protein DnaK-like [Bombus impatiens]
2018	Unigene42880_All	PREDICTED: eukaryotic translation initiation factor 3 subunit M-like, partial [Apis florea]
2019	Unigene134060_All	-
2020	CL2796.Contig1_All	hypothetical protein SINV_80725 [Solenopsis invicta]

2021	CL10074.Contig4_All	hypothetical protein SINV_00899 [Solenopsis invicta]
2022	CL2453.Contig5_All	agonaute 2, partial [Sogatella furcifera]
2023	Unigene650_All	GH11754 [Drosophila grimshawi] >gi|193906122|gb|EDW04989.1| GH11754 [Drosophila grimshawi]
2024	CL16521.Contig1_All	Transmembrane 9 superfamily member 4 [Acromyrmex echinatior]
2025	Unigene80528_All	-
2026	Unigene10781_All	chaperone protein ClpB, putative [Entamoeba histolytica KU27]
2027	Unigene235_All	hypothetical protein PANDA_015249 [Ailuropoda melanoleuca]
2028	Unigene57361_All	PREDICTED: similar to smad nuclear-interacting protein 1 [Tribolium castaneum] >gi|270002268|gb|EEZ98715.1| hypothetical protein TcasGA2_TC001256 [Tribolium castaneum]
2029	Unigene142590_All	-
2030	CL197.Contig3_All	-
2031	CL4067.Contig1_All	Actin-binding protein anillin [Crassostrea gigas]
2032	Unigene11190_All	-
2033	Unigene86217_All	phenylalanyl-tRNA synthetase beta subunit, putative [Ixodes scapularis] >gi|215499449|gb|EEC08943.1| phenylalanyl-tRNA synthetase beta subunit, putative [Ixodes scapularis]
2034	CL4844.Contig1_All	PREDICTED: similar to AGAP004824-PA [Tribolium castaneum] >gi|270005394|gb|EFA01842.1| hypothetical protein TcasGA2_TC007444 [Tribolium castaneum]
2035	CL11751.Contig1_All	PREDICTED: mitogen-activated protein kinase ERK-A-like, partial [Nasonia vitripennis]
2036	CL14866.Contig2_All	unnamed protein product [Tetraodon nigroviridis]
2037	CL6503.Contig1_All	PREDICTED: uncharacterized protein LOC101241719 [Hydra magnipapillata]
2038	CL7925.Contig1_All	pol-like protein [Takifugu rubripes]
2039	Unigene66035_All	PREDICTED: 30S ribosomal protein S11-like [Bombus impatiens]
2040	CL15006.Contig1_All	-
2041	CL12311.Contig2_All	GE25236 [Drosophila yakuba] >gi|194175353|gb|EDW88964.1| GE25236 [Drosophila yakuba]
2042	CL15312.Contig1_All	putative alpha-N-acetylgalactosaminidase [Chorthippus parallelus]
2043	CL7556.Contig1_All	PREDICTED: ero1-like protein-like [Megachile rotundata]
2043	CL7556.Contig3_All	
2044	Unigene76952_All	proton pump 58 kDa subunit [Homo sapiens]
2045	Unigene5135_All	-

2046	CL12608.Contig1_All	-
2047	CL4140.Contig1_All	spaghetti, partial [Papilio polytes]
2047	CL4140.Contig2_All	
2048	CL15108.Contig1_All	PREDICTED: calpain-B-like [Nasonia vitripennis]
2048	CL15108.Contig2_All	
2048	CL15108.Contig5_All	
2048	CL15108.Contig3_All	
2048	CL15108.Contig4_All	
2049	Unigene40504_All	PREDICTED: uncharacterized protein LOC101233993 [Taeniopygia guttata]
2050	Unigene49929_All	PREDICTED: protein CLP1 homolog [Bombus impatiens]
2051	Unigene40925_All	PREDICTED: hypothetical protein LOC100643575 [Bombus terrestris]
2052	Unigene19926_All	GJ18263 [Drosophila virilis] >gi|194141330|gb|EDW57749.1| GJ18263 [Drosophila virilis]
2053	CL1228.Contig2_All	clathrin coat assembly protein [Acheta domesticus]
2054	Unigene90674_All	unnamed protein product [Mus musculus]
2055	Unigene42596_All	ubiquitin-activating enzyme, putative [Ixodes scapularis] >gi|215510935|gb|EEC20388.1| ubiquitin-activating enzyme, putative [Ixodes scapularis]
2056	Unigene10452_All	PREDICTED: MGC83996 protein-like [Saccoglossus kowalevskii]
2057	Unigene26195_All	-
2058	CL1997.Contig1_All	hypothetical protein BRAFLDRAFT_125548 [Branchiostoma floridae] >gi|229275860|gb|EEN46675.1| hypothetical protein BRAFLDRAFT_125548 [Branchiostoma floridae]
2058	CL1997.Contig2_All	
2059	CL4663.Contig1_All	60S ribosomal protein L31 [Salmo salar] >gi|223672287|gb|ACN12325.1| 60S ribosomal protein L31 [Salmo salar]
2060	Unigene38187_All	-
2061	Unigene75063_All	-
2062	Unigene88513_All	-
2063	Unigene6405_All	hypothetical protein CAPTEDRAFT_136770 [Capitella teleta]
2064	Unigene82857_All	-
2065	CL16507.Contig3_All	conserved hypothetical protein [Trichinella spiralis] >gi|316966792|gb|EFV51330.1| conserved hypothetical protein [Trichinella spiralis]
2066	CL16121.Contig3_All	PREDICTED: hypothetical protein LOC100563775 [Anolis carolinensis]
2067	Unigene85656_All	DKFZP459H041 protein [Pongo abelii]

2068	CL3582.Contig1_All	GF15779 [Drosophila ananassae] >gi|190616809|gb|EDV32333.1| GF15779 [Drosophila ananassae]
2068	CL3582.Contig3_All	
2068	Unigene47526_All	
2068	Unigene24768_All	
2068	CL3582.Contig2_All	
2068	Unigene123786_All	
2069	Unigene93507_All	-
2070	Unigene104601_All	-
2071	Unigene64413_All	PREDICTED: cleavage stimulation factor subunit 3-like, partial [Xenopus (Silurana) tropicalis]
2072	Unigene32528_All	hairy gene
2073	Unigene50176_All	Atrial natriuretic peptide receptor A [Acromyrmex echinatior]
2074	CL5160.Contig1_All	Ena/VASP protein [Gryllus bimaculatus]
2074	CL5160.Contig4_All	
2074	CL5160.Contig2_All	
2074	CL5160.Contig5_All	
2074	CL5160.Contig3_All	
2075	Unigene98703_All	-
2076	Unigene19437_All	Golgi apparatus protein 1 [Harpegnathos saltator]
2077	CL5005.Contig1_All	conserved hypothetical protein [Pediculus humanus corporis] >gi|212516745|gb|EEB18719.1| conserved hypothetical protein [Pediculus humanus corporis]
2078	Unigene143919_All	PREDICTED: hypothetical protein LOC100162931 [Acyrthosiphon pisum]
2079	Unigene17883_All	hypothetical protein KGM_08305 [Danaus plexippus]
2080	CL11958.Contig1_All	PREDICTED: aspartate aminotransferase, cytoplasmic-like, partial [Mus musculus]
2080	CL11958.Contig2_All	
2081	Unigene18244_All	-
2082	CL4630.Contig1_All	hypothetical protein KGM_09135 [Danaus plexippus]
2082	CL4630.Contig2_All	
2083	CL2799.Contig2_All	hypothetical protein TcasGA2_TC012981 [Tribolium castaneum]
2084	CL5316.Contig2_All	hypothetical protein DDB_G0292060 [Dictyostelium discoideum AX4] >gi|60463193|gb|EAL61386.1| hypothetical protein DDB_G0292060 [Dictyostelium discoideum AX4]

Appendix F Differentially the sametrend correlation and oppositetrend correlation between mRNAs and proteins.

N2 vs D2 same trend

Protein	log2(D2/N2)	GeneID	log2(D2/N2)

Unigene72701_All	0.658097205	Unigene72701_All	1.02512971
Unigene54651_All	0.796597754	Unigene54651_All	1.63976963
CL12531.Contig1_All	-4.79585928	CL12531.Contig1_All	-1.1002014
Unigene88766_All	-2.08926734	Unigene88766_All	-11.183325
Unigene80801_All	-3.69899774	Unigene80801_All	-11.415742
Unigene50237_All	1.183962835	Unigene50237_All	1.03495486
Unigene78266_All	-2.2243173	Unigene78266_All	-10.361176
CL6511.Contig1_All	-0.41119543	CL6511.Contig1_All	-1.4619006
Unigene65135_All	2.150234709	Unigene65135_All	1.73073963
CL14985.Contig1_All	-0.30935942	CL14985.Contig1_All	-1.6242829
CL8936.Contig3_All	-0.48196851	CL8936.Contig3_All	-1.4249139
Unigene63746_All	1.421694581	Unigene63746_All	2.66679572
CL5314.Contig2_All	-0.94341647	CL5314.Contig2_All	-1.0445477
CL7809.Contig1_All	-3.85725983	CL7809.Contig1_All	-1.5732648
Unigene18896_All	-1.32553935	Unigene18896_All	-5.0484161
CL8176.Contig1_All	-1.51870106	CL8176.Contig1_All	-1.1346495
CL10396.Contig1_All	-0.50430484	CL10396.Contig1_All	-1.9163137
CL769.Contig3_All	-1.03209363	CL769.Contig3_All	-7.699315
Unigene61379_All	-1.86249648	Unigene61379_All	-10.799363
Unigene34952_All	-0.50225991	Unigene34952_All	-3.1234996
Unigene36708_All	-2.71785677	Unigene36708_All	-11.45897
CL12410.Contig2_All	-0.43635373	CL12410.Contig2_All	-1.1905361
CL1128.Contig1_All	0.295135249	CL1128.Contig1_All	4.17986591
CL9339.Contig1_All	-0.9770996	CL9339.Contig1_All	-2.0259217
Unigene20248_All	0.525066592	Unigene20248_All	1.39979706
CL2123.Contig1_All	-0.55215636	CL2123.Contig1_All	-3.6440842
Unigene10852_All	1.243059706	Unigene10852_All	1.36257773
Unigene55918_All	1.038436182	Unigene55918_All	1.46531526
Unigene25909_All	0.480265122	Unigene25909_All	1.13813316
Unigene12632_All	0.321928095	Unigene12632_All	1.18315807
CL15839.Contig1_All	0.438292852	CL15839.Contig1_All	2.50198078
CL10609.Contig1_All	0.439357178	CL10609.Contig1_All	1.35472853
CL7193.Contig1_All	2.367930141	CL7193.Contig1_All	1.42185829
Unigene82_All	1.518031493	Unigene82_All	1.38437128
CL14565.Contig1_All	-4.50635267	CL14565.Contig1_All	-7.2918351
Unigene56242_All	0.649845352	Unigene56242_All	1.55301541
Unigene63488_All	-3.89969509	Unigene63488_All	-4.0530253
N3 vs D3 same trend			
Protein	log2(D3/N3)	GeneID	log2(D3/N3)
Unigene63260_All	0.386259141	Unigene63260_All	1.25286698
CL14565.Contig3_All	1.201006466	CL14565.Contig3_All	10.5185548
Unigene56689_All	-0.34190279	Unigene56689_All	-1.6885138
Unigene54651_All	2.514501036	Unigene54651_All	2.82674682

Unigene32747_All	-1.11716134	Unigene32747_All	-1.4929501
Unigene25700_All	-0.4639471	Unigene25700_All	-3.6149171
Unigene70717_All	1.243669081	Unigene70717_All	3.46203251
Unigene25498_All	-0.26534457	Unigene25498_All	-1.1728893
Unigene72738_All	-0.2968993	Unigene72738_All	-1.2498359
CL14656.Contig1_All	0.606915942	CL14656.Contig1_All	1.58806211
Unigene49823_All	0.565597176	Unigene49823_All	2.97980461
CL14473.Contig1_All	-0.74903843	CL14473.Contig1_All	-1.254334
CL13867.Contig1_All	-0.28454587	CL13867.Contig1_All	-1.1775329
Unigene57357_All	-0.26881676	Unigene57357_All	-1.2261112
Unigene72257_All	-0.61043319	Unigene72257_All	-2.2613863
Unigene18790_All	-0.78587519	Unigene18790_All	-1.6544327
Unigene72416_All	1.469885976	Unigene72416_All	2.84036714
Unigene63746_All	1.003602237	Unigene63746_All	1.00893253
Unigene33315_All	-0.27055599	Unigene33315_All	-1.5829114
Unigene3081_All	0.431890348	Unigene3081_All	2.41930353
Unigene100401_All	-1.15521265	Unigene100401_All	-3.8691195
CL12266.Contig1_All	0.32308179	CL12266.Contig1_All	1.22394287
CL8546.Contig2_All	-0.3075728	CL8546.Contig2_All	-1.3410587
CL212.Contig2_All	0.688851744	CL212.Contig2_All	1.16884623
CL5314.Contig2_All	-0.61263746	CL5314.Contig2_All	-1.042791
CL13593.Contig1_All	-0.35845397	CL13593.Contig1_All	-2.4052838
CL15952.Contig2_All	0.93960272	CL15952.Contig2_All	1.28252686
Unigene48297_All	-0.28630419	Unigene48297_All	-1.0471094
CL7809.Contig1_All	-1.01741705	CL7809.Contig1_All	-3.3827486
Unigene26210_All	0.96051171	Unigene26210_All	1.69767913
Unigene50143_All	1.01649632	Unigene50143_All	1.9008316
Unigene50433_All	-0.5542733	Unigene50433_All	-1.1849068
Unigene50248_All	-0.32192809	Unigene50248_All	-1.3121797
Unigene34952_All	-0.71548587	Unigene34952_All	-1.036694
CL9337.Contig1_All	3.006118461	CL9337.Contig1_All	1.60929935
CL392.Contig5_All	-0.41888982	CL392.Contig5_All	-1.3446852
Unigene9341_All	1.282143229	Unigene9341_All	1.19052124
CL1128.Contig1_All	0.328836464	CL1128.Contig1_All	1.60795244
Unigene26479_All	1.707082992	Unigene26479_All	1.4910863
Unigene72331_All	0.979659552	Unigene72331_All	3.20094452
Unigene104059_All	-1.32192809	Unigene104059_All	-5.1723907
CL419.Contig1_All	-0.33097323	CL419.Contig1_All	-1.2620458
Unigene41170_All	-0.59727782	Unigene41170_All	-1.7850866
Unigene71219_All	1.081339627	Unigene71219_All	1.87200934
CL14635.Contig1_All	0.566571641	CL14635.Contig1_All	1.52969194
Unigene57763_All	-0.26534457	Unigene57763_All	-1.9455124
Unigene34530_All	1.745452483	Unigene34530_All	1.20938912

CL2563.Contig2_All	-0.40927823	CL2563.Contig2_All	-1.0631215
CL2123.Contig1_All	-0.63486741	CL2123.Contig1_All	-3.5885017
Unigene12482_All	-0.37145968	Unigene12482_All	-1.3410205
CL15969.Contig1_All	-0.34923544	CL15969.Contig1_All	-2.4139587
Unigene55918_All	0.810648748	Unigene55918_All	2.1960604
CL6510.Contig1_All	1.295723025	CL6510.Contig1_All	1.27753398
Unigene12632_All	0.365132593	Unigene12632_All	1.64228075
Unigene40395_All	2.663572335	Unigene40395_All	1.15781358
Unigene19928_All	1.392866916	Unigene19928_All	1.57497497
CL2935.Contig1_All	0.305678743	CL2935.Contig1_All	1.12752431
Unigene33112_All	-0.85725983	Unigene33112_All	-2.697065
CL5934.Contig1_All	1.155749233	CL5934.Contig1_All	1.75949262
Unigene25563_All	-0.58207999	Unigene25563_All	-3.6913828
Unigene42315_All	-0.89164282	Unigene42315_All	-1.5558713
Unigene42359_All	0.367371066	Unigene42359_All	1.7247994
CL9332.Contig1_All	0.977463111	CL9332.Contig1_All	3.25581219
CL9227.Contig2_All	-0.36215794	CL9227.Contig2_All	-1.6961566
Unigene19872_All	0.929033479	Unigene19872_All	1.0542381
CL5172.Contig1_All	2.002882509	CL5172.Contig1_All	2.23817983
CL13366.Contig1_All	-0.37519723	CL13366.Contig1_All	-1.2785719
Unigene9768_All	-0.73216461	Unigene9768_All	-1.2616446
Unigene27386_All	0.408168371	Unigene27386_All	1.57159669
Unigene41326_All	-0.38082178	Unigene41326_All	-1.4305939
CL6511.Contig6_All	-0.68269593	CL6511.Contig6_All	-2.9128556
Unigene63726_All	1.899948986	Unigene63726_All	2.68880842
CL39.Contig1_All	1.10634832	CL39.Contig1_All	1.05169078
Unigene17725_All	-1.25842515	Unigene17725_All	-1.3536141
Unigene35277_All	1.187767747	Unigene35277_All	2.16333826
N2 vs N3 same trend			
Protein	log2(N3/N2)	GeneID	log2(N3/N2)
Unigene56689_All	-0.57992188	Unigene56689_All	-3.1487616
Unigene32747_All	-0.32192809	Unigene32747_All	-1.8978673
Unigene50075_All	0.524063676	Unigene50075_All	5.21358106
Unigene80801_All	-1.69899774	Unigene80801_All	-11.415742
Unigene41443_All	-0.65290133	Unigene41443_All	-2.4451991
Unigene78266_All	-2.3075728	Unigene78266_All	-4.2443124
CL6511.Contig1_All	-0.38835546	CL6511.Contig1_All	-3.2247427
Unigene27713_All	-0.34923544	Unigene27713_All	-1.1215433
Unigene72608_All	-1.18442457	Unigene72608_All	-1.237539
Unigene72257_All	-0.39024504	Unigene72257_All	-1.0388755
Unigene18790_All	-0.57132159	Unigene18790_All	-1.5685414
CL9852.Contig3_All	0.334568276	CL9852.Contig3_All	1.19654804
Unigene42500_All	-0.40927823	Unigene42500_All	-1.095224

CL8936.Contig3_All	-0.59074485	CL8936.Contig3_All	-1.404357
Unigene34645_All	-0.72977009	Unigene34645_All	-3.0399985
Unigene41153_All	0.292781749	Unigene41153_All	1.26375921
Unigene11787_All	-0.40927823	Unigene11787_All	-1.2922814
Unigene57871_All	-0.33278909	Unigene57871_All	-1.4784562
Unigene12058_All	-0.59074485	Unigene12058_All	-1.1203412
Unigene10898_All	0.399444565	Unigene10898_All	1.0485316
Unigene1034_All	-1.36959453	Unigene1034_All	-1.1749008
CL5772.Contig1_All	-0.42468767	CL5772.Contig1_All	-3.1136917
Unigene18896_All	-0.82623293	Unigene18896_All	-1.1512804
CL4897.Contig1_All	0.731183242	CL4897.Contig1_All	1.3371929
Unigene40566_All	-0.98279071	Unigene40566_All	-1.4492935
CL7470.Contig2_All	-0.68038207	CL7470.Contig2_All	-1.3167751
Unigene50216_All	-1.31114826	Unigene50216_All	-1.5771196
Unigene27346_All	0.780730036	Unigene27346_All	1.68959978
Unigene34952_All	-0.68501351	Unigene34952_All	-3.1381504
CL11771.Contig1_All	-0.35660555	CL11771.Contig1_All	-1.5617197
Unigene48022_All	-0.4150375	Unigene48022_All	-6.0959441
CL15578.Contig1_All	-0.32192809	CL15578.Contig1_All	-4.8746566
Unigene42370_All	-0.85725983	Unigene42370_All	-3.3425954
Unigene20248_All	0.462575888	Unigene20248_All	2.51593338
CL5742.Contig2_All	0.714575239	CL5742.Contig2_All	1.12657696
Unigene64634_All	-0.42662547	Unigene64634_All	-1.2197016
CL1081.Contig6_All	0.506906555	CL1081.Contig6_All	1.59577136
CL461.Contig14_All	0.941857519	CL461.Contig14_All	7.25605915
CL12583.Contig1_All	-0.45798964	CL12583.Contig1_All	-1.0750338
Unigene63363_All	-0.55639335	Unigene63363_All	-1.0513174
Unigene27624_All	0.526068812	Unigene27624_All	1.8927263
CL550.Contig1_All	-0.75389599	CL550.Contig1_All	-1.7122211
Unigene12349_All	-0.35475949	Unigene12349_All	-2.3985323
CL3222.Contig2_All	0.444667067	CL3222.Contig2_All	1.05137844
Unigene19137_All	-0.3075728	Unigene19137_All	-1.0425397
CL15839.Contig1_All	0.429749851	CL15839.Contig1_All	1.62600989
Unigene40395_All	1.185232254	Unigene40395_All	2.62792468
Unigene35414_All	-0.55639335	Unigene35414_All	-2.3947208
Unigene72549_All	-0.85464861	Unigene72549_All	-2.1787839
CL16904.Contig3_All	-0.70134168	CL16904.Contig3_All	-2.258871
Unigene82_All	1.464145457	Unigene82_All	7.91307055
CL7470.Contig1_All	0.569491092	CL7470.Contig1_All	1.61308585
CL17826.Contig1_All	0.284514133	CL17826.Contig1_All	1.44917713
Unigene77688_All	-1.84684321	Unigene77688_All	-3.9762451
CL5172.Contig1_All	0.5360529	CL5172.Contig1_All	3.11594523
Unigene32439_All	0.497740089	Unigene32439_All	1.24353097

CL14554.Contig1_All	-0.30935942	CL14554.Contig1_All	-2.8326293
Unigene3020_All	-1.04097178	Unigene3020_All	-2.5692448
CL13581.Contig2_All	-0.26534457	CL13581.Contig2_All	-2.3586022
Unigene17156_All	-0.60603472	Unigene17156_All	-2.5576801
Unigene12848_All	-0.33097323	Unigene12848_All	-1.4553139
Unigene56242_All	0.706641057	Unigene56242_All	5.93923022
CL2876.Contig1_All	-0.68038207	CL2876.Contig1_All	-2.5852983
Unigene27974_All	0.87892148	Unigene27974_All	1.08115394
N2 vs N3 same trend			
Protein	log2(D3/D2)	GeneID	log2(D3/D2)
CL14565.Contig3_All	4.098032083	CL14565.Contig3_All	3.39961374
CL12137.Contig1_All	2.713035895	CL12137.Contig1_All	4.37064552
CL14806.Contig2_All	-0.66886808	CL14806.Contig2_All	-1.6942163
Unigene9264_All	-1.44222233	Unigene9264_All	-1.250461
Unigene65168_All	0.951587795	Unigene65168_All	1.3385714
Unigene32747_All	-1.15521265	Unigene32747_All	-1.9353167
CL12441.Contig1_All	-0.44026348	CL12441.Contig1_All	-1.0855363
CL7791.Contig1_All	-0.56277226	CL7791.Contig1_All	-5.1122954
Unigene25498_All	-0.63486741	Unigene25498_All	-1.2993357
CL13112.Contig4_All	-0.65744525	CL13112.Contig4_All	-1.02416
Unigene41621_All	-0.99136969	Unigene41621_All	-1.0219819
Unigene48541_All	-0.60384051	Unigene48541_All	-1.1869018
Unigene65135_All	-0.40163479	Unigene65135_All	-1.4256168
CL14473.Contig1_All	-0.65744525	CL14473.Contig1_All	-1.4641345
Unigene27781_All	1.783247097	Unigene27781_All	1.74519395
CL13867.Contig1_All	-0.72737955	CL13867.Contig1_All	-1.1269009
Unigene9947_All	4.14135104	Unigene9947_All	5.54631426
Unigene42234_All	-0.28630419	Unigene42234_All	-1.2474744
Unigene63746_All	-0.3921371	Unigene63746_All	-4.5237334
CL568.Contig1_All	-0.30222618	CL568.Contig1_All	-1.1705863
Unigene126085_All	2.503603156	Unigene126085_All	10.7142455
Unigene12666_All	-0.36587144	Unigene12666_All	-1.5795017
Unigene48297_All	-0.62593428	Unigene48297_All	-2.1426475
Unigene18896_All	0.295135249	Unigene18896_All	5.14170928
Unigene70653_All	-0.27055599	Unigene70653_All	-1.3861624
CL5446.Contig1_All	1.727267011	CL5446.Contig1_All	1.53970652
CL2390.Contig2_All	-0.65063472	CL2390.Contig2_All	-2.4548554
Unigene61379_All	1.171206827	Unigene61379_All	11.7293233
CL2528.Contig4_All	-0.69899774	CL2528.Contig4_All	-1.2178296
Unigene20306_All	-1.00868224	Unigene20306_All	-1.0220442
Unigene32673_All	-0.87302714	Unigene32673_All	-1.5495935
Unigene48130_All	-0.45205669	Unigene48130_All	-1.0048618
Unigene34913_All	1.062812492	Unigene34913_All	4.2800659

Unigene36708_All	2.410069692	Unigene36708_All	9.76304634
CL4177.Contig3_All	-0.6597226	CL4177.Contig3_All	-1.2676697
CL2563.Contig2_All	-1.35475949	CL2563.Contig2_All	-1.2021289
Unigene10852_All	-0.72737955	Unigene10852_All	-1.2192305
CL1987.Contig2_All	-0.46195855	CL1987.Contig2_All	-2.0275931
CL960.Contig7_All	-0.76366046	CL960.Contig7_All	-1.5640928
CL15969.Contig1_All	-0.84166297	CL15969.Contig1_All	-2.6784373
CL7594.Contig1_All	-0.40163479	CL7594.Contig1_All	-1.01084
Unigene62019_All	3.818543833	Unigene62019_All	2.61072041
Unigene35325_All	-1.70839644	Unigene35325_All	-2.3489988
CL550.Contig1_All	-0.57561533	CL550.Contig1_All	-1.1665379
Unigene141213_All	0.771463058	Unigene141213_All	13.0860699
Unigene40395_All	1.614003045	Unigene40395_All	1.33122045
Unigene142717_All	2.351628329	Unigene142717_All	10.8777442
CL16928.Contig1_All	-0.41696238	CL16928.Contig1_All	-1.4561512
Unigene2398_All	-0.85725983	Unigene2398_All	-2.6766617
CL11671.Contig1_All	-1.25842515	CL11671.Contig1_All	-1.4975213
Unigene42315_All	-1.45403163	Unigene42315_All	-1.6516361
Unigene18160_All	-0.75389599	Unigene18160_All	-1.5304116
CL7193.Contig1_All	-1.20423305	CL7193.Contig1_All	-3.1982967
CL15987.Contig1_All	-0.50225991	CL15987.Contig1_All	-1.0985257
CL559.Contig1_All	-0.47593632	CL559.Contig1_All	-4.0567226
CL2407.Contig1_All	-0.78090894	CL2407.Contig1_All	-1.5910052
CL5172.Contig1_All	2.594787387	CL5172.Contig1_All	3.39298806
CL2867.Contig3_All	-0.59727782	CL2867.Contig3_All	-1.7977438
CL14565.Contig1_All	4.648753033	CL14565.Contig1_All	7.48538082
Unigene17537_All	-0.74419716	Unigene17537_All	-3.880365
Unigene41326_All	-0.77349147	Unigene41326_All	-1.699661
Unigene70933_All	5.602735976	Unigene70933_All	7.27598146
CL5027.Contig4_All	-0.39973025	CL5027.Contig4_All	-1.0940756
Unigene132526_All	2.537296067	Unigene132526_All	10.9749881
CL5707.Contig1_All	-1.80087736	CL5707.Contig1_All	-1.6968418
Unigene63488_All	3.861062085	Unigene63488_All	6.47211775
CL16830.Contig1_All	-0.63039393	CL16830.Contig1_All	-1.0574689
N2 vsD2 opposite trend			
Protein	log2(D2/N2)	GeneID	log2(D2/N2)
Unigene1085_All	-1.26534457	Unigene1085_All	1.16013045
Unigene34768_All	-1.1109159	Unigene34768_All	1.14801812
Unigene70717_All	-5.05889369	Unigene70717_All	1.17999852
Unigene9947_All	-2.14560532	Unigene9947_All	1.36699018
Unigene72416_All	-5.26534457	Unigene72416_All	1.71343974
CL10780.Contig1_All	0.720716243	CL10780.Contig1_All	-1.0974228
CL2238.Contig1_All	-0.28982725	CL2238.Contig1_All	2.32575795

Unigene32302_All	0.746742716	Unigene32302_All	-1.5862352
CL2542.Contig2_All	0.678973308	CL2542.Contig2_All	-1.135877
CL8001.Contig2_All	-1.9268653	CL8001.Contig2_All	2.10194021
Unigene57759_All	0.299830762	Unigene57759_All	-2.2896703
CL5172.Contig1_All	-0.35845397	CL5172.Contig1_All	1.961137
Unigene27689_All	0.453122447	Unigene27689_All	-1.488097
Unigene70460_All	-1.53533173	Unigene70460_All	1.28529201
N3vsD3 oppositetrend			
Protein	log2(D3/N3)	GeneID	log2(D3/N3)
CL155.Contig1_All	1.570462931	CL155.Contig1_All	-5.1086697
Unigene762_All	-1.15842936	Unigene762_All	1.72471925
Unigene72016_All	0.739848103	Unigene72016_All	-9.3691611
Unigene24757_All	0.595503661	Unigene24757_All	-2.1464396
Unigene50299_All	-0.94064472	Unigene50299_All	1.01609081
Unigene126085_All	-0.78587519	Unigene126085_All	10.7142455
CL2132.Contig15_All	0.495695163	CL2132.Contig15_All	-2.3948978
Unigene47794_All	0.424384672	Unigene47794_All	-1.2130765
CL2218.Contig1_All	0.438292852	CL2218.Contig1_All	-1.0363503
Unigene61379_All	-0.63710936	Unigene61379_All	2.70031225
Unigene42795_All	-0.30578839	Unigene42795_All	1.0194576
CL2438.Contig2_All	-0.26707962	CL2438.Contig2_All	2.98227335
Unigene55183_All	0.348232419	Unigene55183_All	-1.0849084
Unigene42370_All	-0.68269593	Unigene42370_All	2.29899374
CL9339.Contig1_All	-0.87038726	CL9339.Contig1_All	1.4988898
CL5742.Contig2_All	0.44148348	CL5742.Contig2_All	-1.2283554
Unigene62019_All	3.23526753	Unigene62019_All	-3.3485727
CL198.Contig5_All	3.385845149	CL198.Contig5_All	-3.6850471
CL9375.Contig1_All	0.481298942	CL9375.Contig1_All	-1.420689
CL15203.Contig1_All	0.311503115	CL15203.Contig1_All	-2.2303249
Unigene27367_All	0.511973982	Unigene27367_All	-2.8990936
Unigene82_All	1.246712101	Unigene82_All	-3.3351813
CL889.Contig6_All	-0.49005085	CL889.Contig6_All	1.50545585
CL9820.Contig1_All	-0.35845397	CL9820.Contig1_All	1.14187504
CL2876.Contig1_All	-0.40354186	CL2876.Contig1_All	1.02976379
CL9587.Contig3_All	1.0614306	CL9587.Contig3_All	-3.0060138
CL2953.Contig1_All	-1.16812276	CL2953.Contig1_All	1.06395142
N2 vs N3 opposite trend			
Protein	log2(N3/N2)	GeneID	log2(N3/N2)
Unigene54651_All	0.967168608	Unigene54651_All	-2.8210543
CL4067.Contig1_All	1.872631791	CL4067.Contig1_All	-2.6770556
CL12137.Contig1_All	-1.00288828	CL12137.Contig1_All	5.05106284
CL14806.Contig2_All	0.648925559	CL14806.Contig2_All	-2.1529441
CL7791.Contig1_All	0.3068455	CL7791.Contig1_All	-2.3865644

Unigene27900_All	-0.33460723	Unigene27900_All	1.11302962
Unigene25498_All	0.377401431	Unigene25498_All	-1.1188634
CL4414.Contig2_All	0.808179084	CL4414.Contig2_All	-2.3410621
CL14656.Contig1_All	0.527070336	CL14656.Contig1_All	-2.0858293
CL6119.Contig1_All	0.3068455	CL6119.Contig1_All	-1.1259588
CL9358.Contig1_All	0.337996464	CL9358.Contig1_All	-1.9753817
CL3844.Contig3_All	0.566571641	CL3844.Contig3_All	-1.4822359
CL1974.Contig12_All	-0.55639335	CL1974.Contig12_All	1.82210949
Unigene63746_All	1.470927257	Unigene63746_All	-2.8658702
Unigene12370_All	0.3950628	Unigene12370_All	-3.4094382
CL2667.Contig1_All	0.334568276	CL2667.Contig1_All	-1.2191318
CL212.Contig2_All	0.868686765	CL212.Contig2_All	-3.3298281
Unigene32301_All	0.996388746	Unigene32301_All	-2.752286
CL15952.Contig2_All	0.39835037	CL15952.Contig2_All	-1.7706108
CL10780.Contig1_All	0.602171791	CL10780.Contig1_All	-1.4213639
CL12451.Contig1_All	0.3068455	CL12451.Contig1_All	-2.9654592
Unigene26210_All	0.462575888	Unigene26210_All	-2.5587819
CL5446.Contig1_All	-3.33642766	CL5446.Contig1_All	1.21892287
CL5260.Contig3_All	1.726395292	CL5260.Contig3_All	-1.1854884
CL9379.Contig1_All	-1.06491748	CL9379.Contig1_All	2.47084267
CL3079.Contig1_All	1.045442971	CL3079.Contig1_All	-2.8879112
Unigene40827_All	0.557777671	Unigene40827_All	-1.3462882
Unigene32302_All	0.588804567	Unigene32302_All	-4.6311743
Unigene56240_All	0.890641244	Unigene56240_All	-2.3575296
Unigene32673_All	0.515005916	Unigene32673_All	-1.7136302
CL3079.Contig3_All	0.610700062	CL3079.Contig3_All	-3.7815771
CL5159.Contig3_All	0.742437445	CL5159.Contig3_All	-3.2096304
Unigene9341_All	1.046840254	Unigene9341_All	-2.8088743
CL2542.Contig2_All	0.2880632	CL2542.Contig2_All	-2.8237033
CL17546.Contig1_All	0.885183866	CL17546.Contig1_All	-1.2594874
CL419.Contig1_All	-0.78836475	CL419.Contig1_All	1.49676375
CL6113.Contig1_All	-1.07400058	CL6113.Contig1_All	1.27765816
CL3079.Contig4_All	0.764685853	CL3079.Contig4_All	-3.8009186
CL14635.Contig1_All	0.305678743	CL14635.Contig1_All	-2.5861678
Unigene87758_All	0.771463058	Unigene87758_All	-2.8530372
Unigene34530_All	1.031395196	Unigene34530_All	-2.9205593
CL16040.Contig1_All	0.510961919	CL16040.Contig1_All	-2.968674
Unigene25522_All	-0.76856759	Unigene25522_All	1.54475272
Unigene104155_All	-0.84944032	Unigene104155_All	5.75772497
Unigene55918_All	0.742437445	Unigene55918_All	-2.4562302
CL16775.Contig2_All	0.535057595	CL16775.Contig2_All	-7.9260419
Unigene62019_All	-0.69198869	Unigene62019_All	4.99250087
Unigene14590_All	0.485426827	Unigene14590_All	-1.9694911

Unigene54875_All	0.527070336	Unigene54875_All	-2.1346745
Unigene19928_All	0.670840336	Unigene19928_All	-1.2166848
Unigene2398_All	0.38294387	Unigene2398_All	-2.7251754
CL11671.Contig1_All	0.573374526	CL11671.Contig1_All	-1.4080997
CL5934.Contig1_All	0.680774425	CL5934.Contig1_All	-2.5159018
Unigene25563_All	-0.69432126	Unigene25563_All	2.80066415
CL4203.Contig2_All	1.272023189	CL4203.Contig2_All	-2.2908598
CL7193.Contig1_All	1.810237431	CL7193.Contig1_All	-2.6153424
Unigene32911_All	0.337996464	Unigene32911_All	-1.1936817
CL559.Contig1_All	0.749319725	CL559.Contig1_All	-10.176921
CL6511.Contig6_All	-0.54371952	CL6511.Contig6_All	1.48998042
Unigene63726_All	1.24610401	Unigene63726_All	-4.8381407
Unigene42351_All	0.541019153	Unigene42351_All	-2.3839002
Unigene35277_All	1.096261853	Unigene35277_All	-2.3001756
D2 vs D3 opposite trend			
Protein	log2(D3/D2)	GeneID	log2(D3/D2)
Unigene1085_All	0.564622052	Unigene1085_All	-1.0737375
CL4278.Contig1_All	0.617298483	CL4278.Contig1_All	-1.244891
CL12041.Contig2_All	0.301002256	CL12041.Contig2_All	-1.0030284
CL4500.Contig5_All	-0.54371952	CL4500.Contig5_All	1.26268555
Unigene72416_All	7.006735614	Unigene72416_All	-4.6451921
Unigene17559_All	0.40599236	Unigene17559_All	-1.0149885
CL7809.Contig1_All	2.767231037	CL7809.Contig1_All	-1.5682706
Unigene26210_All	0.767231037	Unigene26210_All	-1.8580886
CL9379.Contig1_All	-1.77595973	CL9379.Contig1_All	2.87819378
Unigene50143_All	2.329697689	Unigene50143_All	-2.1680562
Unigene40827_All	0.562669826	Unigene40827_All	-1.2968947
Unigene20220_All	1.038436182	Unigene20220_All	-1.895348
CL9337.Contig1_All	9.608731637	CL9337.Contig1_All	-2.6645873
Unigene10802_All	-1.00288828	Unigene10802_All	3.96644914
CL15578.Contig1_All	1.338567037	CL15578.Contig1_All	-3.265918
CL11694.Contig2_All	0.351628329	CL11694.Contig2_All	-1.2087579
Unigene19269_All	-1.77595973	Unigene19269_All	1.1736266
CL14635.Contig1_All	0.381837084	CL14635.Contig1_All	-1.7442354
CL13333.Contig1_All	-0.3789445	CL13333.Contig1_All	1.47343759
CL9640.Contig1_All	1.03562391	CL9640.Contig1_All	-3.1111702
CL6510.Contig1_All	0.833497337	CL6510.Contig1_All	-1.4612725
Unigene14590_All	2.451013243	Unigene14590_All	-3.3253205
CL5934.Contig1_All	0.804879608	CL5934.Contig1_All	-1.7089491
Unigene72527_All	0.975263322	Unigene72527_All	-1.9197356
Unigene27386_All	0.719840555	Unigene27386_All	-1.7698292
Unigene56242_All	-0.59509688	Unigene56242_All	2.97771219