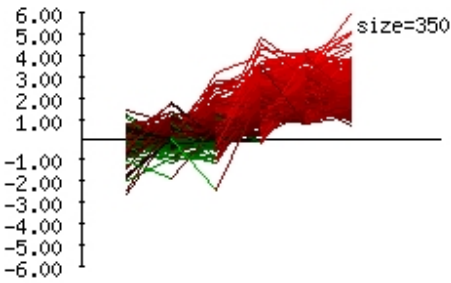
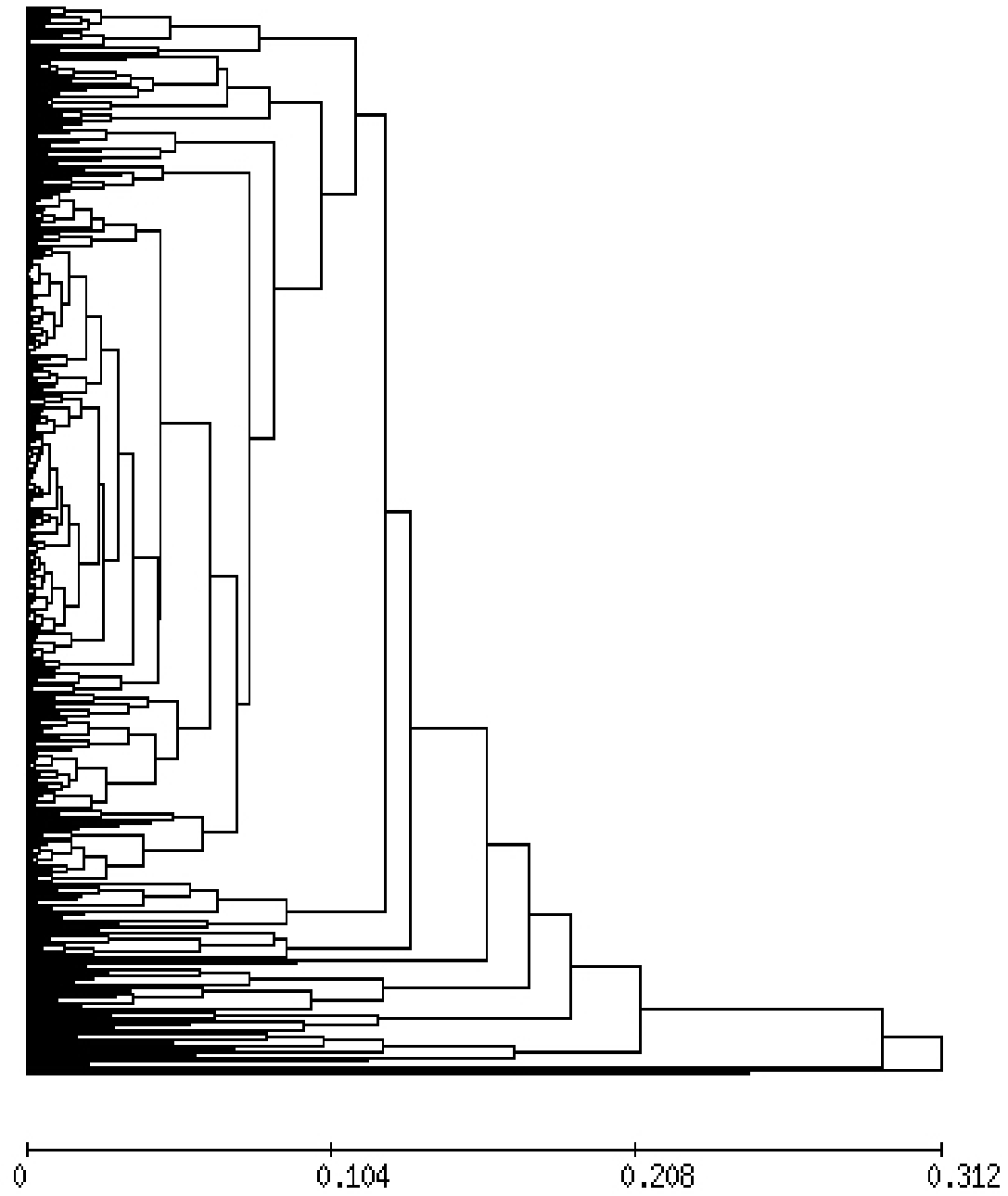
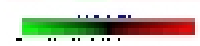
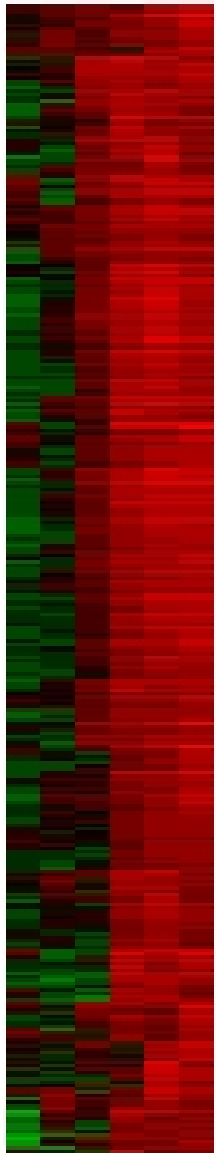


Subtree	Cluster size is 350, joined at the distance 0.311535				1:217			
Spot size:	Width:	Autom.	Height:	Autom.	Tree height:	Automatic	Show titles:	Redraw!
	Autom.							
Colors	Colors	NA color	Number of slots	Discretisation type				



ROX4M.corr.dist.ave.cluster

23 24 25 26 27 28



205-E02 205-E02 Unknown

193-F05 118-G05 gi|2497469|sp|P79703|JUNB_CYPCA TRANSCRIPTION FACTOR JUN-B
>gi|1766028|gb|AAB39939.1| (U81506) junB transcription factor [Cyprinus carpio]

161-B05 156-B03 Unknown

026-E08 113-C05 gi|84880|pir||A28258 actin 5C - fruit fly (Drosophila melanogaster)

152-F05 152-F05 gi|7542476|gb|AAF63471.1|AF231347_1 (AF231347) adenine nucleotide translocase
[Xenopus laevis]

150-B05 150-B05 gi|6678469|ref|NP_033474.1| tubulin alpha 6 [Mus musculus]

>gi|135424|sp|P05216|TBA6_MOUSE TUBULIN ALPHA-6 CHAIN >gi|2119264|pir||I77428 tubulin alpha
chain isotype M-alpha-6 - mouse >gi|202217|gb|AAA40503.1| (M13441) alpha-tubulin isotype M-
alpha-6 [Mus musculus] >gi|304532|gb|AAA37026.1| (M12329) alpha-tubulin III [Cricetulus
griseus] >gi|13435777|gb|AAH04745.1|AAH04745 (BC004745) tubulin alpha 6 [Mus musculus]

027-A09 027-A09 Unknown

099-H04 183-H04 Unknown

209-E05 194-C09 gi|13385280|ref|NP_080090.1| RIKEN cDNA 1200009K13 gene [Mus musculus]

>gi|12836024|dbj|BAB23466.1| (AK004678) putative [Mus musculus]

153-B07 153-B07 Unknown

202-F04 202-F04 Unknown

177-C03 177-C03 "gi|6320303|ref|NP_010383.1| Member of a glutaredoxin subfamily in Sc
together with GRX4 & GRX5. Sign. sequence diff. with the other glutaredoxin subfamily,
formed by the previously described GRX1 & GRX2 glutaredoxins (Luikenhuis MBC 9:1081, 1998);
Grx3p [Saccharomyces cerevisiae] >gi|3025094|sp|Q03835|YD98_YEAST HYPOTHETICAL 32.5 KD
PROTEIN IN MSH6-BMH2 INTERGENIC REGION >gi|1078415|pir||S51247 thioredoxin homolog YDR098c -
yeast (Saccharomyces cerevisiae) >gi|633632|emb|CAA87672.1| (Z47746) probable thioredoxin
[Saccharomyces cerevisiae]"

027-E01 027-E01 "gi|464806|sp|P33731|SR72_CANFA SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN

(SRP72) >gi|423182|pir||A40692 signal recognition particle 72K chain - dog

>gi|297768|emb|CAA48014.1| (X67813) signal recognition particle, 72 kDa subunit [Canis
familiaris]"

024-F02 024-F02 gi|5815467|gb|AAD52686.1| (AF179894) 11-beta-hydroxylase [Oncorhynchus mykiss]

078-E03 078-E03 Unknown

068-F01 145-H05 Unknown

003-E09 003-E09 Unknown

006-B07 006-B07 Unknown

112-C10 112-C10 Unknown

181-B02 102-E07 "gi|1170206|sp|P43091|HEM1_OPSTA 5-AMINOLEVULINIC ACID SYNTHASE, NONSPECIFIC,
MITOCHONDRIAL PRECURSOR (DELTA-AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H)

>gi|532630|gb|AAA49435.1| (L35915) 5-aminolevulinate synthase [Opsanus tau]"

147-C12 147-C12 Unknown

104-A06 052-B06 gi|10242174|gb|AAG15322.1|AF255560_1 (AF255560) alpha tubulin [Notothenia
coriiceps]

061-G09 061-G09 Unknown

097-E11 097-E11 Unknown

038-G04 083-F04 Unknown

146-H09 146-H09 gi|10242286|gb|AAG15366.1|AF263277_1 (AF263277) alpha tubulin [Chionodraco
rastrispinosus]

043-C12 081-D12 Unknown

068-B11 068-B11 Unknown
084-A06 156-H04 gi|3695368|gb|AAC62774.1| (AF093129) zfY1 [Danio rerio]
062-E04 062-E04 Unknown
077-C08 101-D04 gi|5509946|dbj|BAA82513.1| (AB029946) p32 subunit of splicing factor SF2 [Gallus gallus]
142-G10 142-G10 Unknown
156-D07 156-D07 Unknown
206-C05 208-F01 Unknown
202-E01 202-E01 Unknown
014-H05 014-H05 Unknown
146-D01 148-H04 "gi|113288|sp|P10994|ACTS_PLEWA ACTIN, ALPHA SKELETAL MUSCLE
 >gi|85684|pir|A26337 actin, skeletal muscle - Iberian ribbed newt (fragment)
 >gi|64249|emb|CAA28753.1| (X05106) alpha skeletal actin fragment (AA 250-374) [Pleurodeles
 waltl]"
140-H08 058-B04 Unknown
202-E11 202-E11 Unknown
122-H12 172-E07 Unknown
082-E12 165-E09 Unknown
069-H07 134-G03 Unknown
206-E10 206-E10 Unknown
092-G06 049-C07 Unknown
068-E06 076-E09 "gi|6166597|sp|Q00872|MYPS_HUMAN MYOSIN-BINDING PROTEIN C, SLOW-TYPE (SLOW
 MYBP-C) (C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM)"
080-A11 080-A11 Unknown
185-A05 191-H02 Unknown
007-G10 007-G10 gi|14716988|emb|CAC44159.1| (AJ312339) putative ribosomal protein L27A
 protein [Oncorhynchus mykiss]
196-D04 187-G12 Unknown
199-F01 199-F01 Unknown
141-D08 101-A06 Unknown
159-G07 159-G07 Unknown
129-G12 007-C11 Unknown
062-D06 062-D06 Unknown
043-F12 181-F03 Unknown
128-D04 100-C05 Unknown
120-A09 197-A12 gi|15294077|gb|AAK95215.1|AF402841_1 (AF402841) 40S ribosomal protein S30
 [Ictalurus punctatus]
032-F04 032-F04 Unknown
052-G08 052-G08 gi|13162290|ref|NP_060084.2| betaine-homocysteine methyltransferase 2;
 hypothetical protein FLJ20001 [Homo sapiens] >gi|14726316|ref|XP_046045.1| betaine-
 homocysteine methyltransferase 2 [Homo sapiens] >gi|11907831|gb|AAG41356.1|AF257473_1
 (AF257473) betaine-homocysteine methyltransferase 2 [Homo sapiens]
043-C06 156-C10 Unknown
108-B02 116-D08 Unknown
131-E03 131-E03 gi|15293869|gb|AAK95127.1|AF401555_1 (AF401555) ribosomal protein L4
 [Ictalurus punctatus]
030-C06 085-G08 Unknown

144-F08 144-F08 Unknown
202-A02 202-A02 gi|3396100|gb|AAC28863.1| (AF080430) ribosomal protein S8 [Apis mellifera]
191-B05 191-B05 Unknown
077-F04 077-F04 Unknown
030-B02 066-A01 gi|14029171|gb|AAK51130.1| (AY032853) CGI-55 [Homo sapiens]
035-D09 035-D09 Unknown
187-A10 187-A10 Unknown
189-F07 162-C10 gi|14734611|ref|XP_040599.1| PAI-1 mRNA-binding protein [Homo sapiens]
>gi|14734616|ref|XP_040595.1| PAI-1 mRNA-binding protein [Homo sapiens]
>gi|12804377|gb|AAH03049.1|AAH03049 (BC003049) Similar to DKFZP564M2423 protein [Homo sapiens]
>gi|14165496|gb|AAH08045.1|AAH08045 (BC008045) Unknown (protein for MGC:16069) [Homo sapiens]
037-G10 135-H05 Unknown
150-D05 150-D05 gi|15294029|gb|AAK95191.1|AF402817_1 (AF402817) 40S ribosomal protein S9 [Ictalurus punctatus]
032-H10 032-H10 Unknown
205-G11 205-G11 gi|12652605|gb|AAH00047.1|AAH00047 (BC000047) Similar to ribosomal protein L8 [Homo sapiens]
141-C02 141-C02 Unknown
070-E06 070-E06 Unknown
203-D12 203-D12 gi|212997|gb|AAC38007.1| (L09744) keratin [Carassius auratus]
154-G02 154-G02 Unknown
066-B08 066-B08 Unknown
002-F09 002-F09 Unknown
169-D04 169-D04 gi|15294063|gb|AAK95208.1|AF402834_1 (AF402834) 40S ribosomal protein S26-1 [Ictalurus punctatus]
087-D11 150-D04 gi|5059077|gb|AAD38906.1|AF128809_1 (AF128809) ZPC domain containing protein 1 [Oryzias latipes]
019-G04 019-G04 Unknown
028-D10 028-D10 gi|12835827|dbj|BAB23379.1| (AK004568) putative [Mus musculus]
132-E11 132-E11 Unknown
029-C02 029-C02 Unknown
055-A01 145-D05 gi|15293877|gb|AAK95131.1| (AF401559) ribosomal protein L7 [Ictalurus punctatus]
131-E09 131-E09 "gi|8979936|gb|AAF82250.1|AC008051_1 (AC008051) Identical to gene XW6 from Arabidopsis thaliana gb|AB008016 and contains a Ribosomal protein S5 PF|00333 domain. ESTs gb|T22200, gb|N38541, gb|T45263 come from this gene. This gene is cut off"
131-F09 131-F09 gi|14750280|ref|XP_032233.1| similar to 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN) (H. sapiens) [Homo sapiens]
186-D07 186-D07 gi|3088335|dbj|BAA25813.1| (AB007147) ribosomal protein S2 [Homo sapiens]
198-E04 027-F05 gi|15293921|gb|AAK95153.1|AF401581_1 (AF401581) ribosomal protein L27 [Ictalurus punctatus]
104-F10 104-F10 Unknown
076-F05 089-H02 Unknown
062-G07 142-H12 gi|212995|gb|AAC38008.1| (L09743) keratin [Carassius auratus]
050-A07 186-B10 gi|15294027|gb|AAK95190.1|AF402816_1 (AF402816) 40S ribosomal protein S8 [Ictalurus punctatus]

002-A10 002-A10 gi|14485765|gb|AAK63073.1|AF385081_1 (AF385081) 60S ribosomal protein L13 [Danio rerio]

131-C09 131-C09 "gi|6912634|ref|NP_036555.1| ribosomal protein L13a; 60S ribosomal protein L13a; 23 kD highly basic protein [Homo sapiens] >gi|14757405|ref|XP_027886.1| ribosomal protein L13a [Homo sapiens] >gi|14757412|ref|XP_027884.1| ribosomal protein L13a [Homo sapiens] >gi|14757414|ref|XP_027885.1| ribosomal protein L13a [Homo sapiens] >gi|730451|sp|P40429|R13A_HUMAN 60S RIBOSOMAL PROTEIN L13A (23 KDA HIGHLY BASIC PROTEIN) >gi|345897|pir||S29539 ribosomal protein L13a, cytosolic - human >gi|23691|emb|CAA40254.1|(X56932) 23 kD highly basic protein [Homo sapiens] >gi|6552365|dbj|BAA88214.1|(AB028893) ribosomal protein L13a [Homo sapiens] >gi|12653485|gb|AAH00514.1|AAH00514 (BC000514) ribosomal protein L13a [Homo sapiens] >gi|12804529|gb|AAH01675.1|AAH01675 (BC001675) ribosomal protein L13a [Homo sapiens] >gi|12804789|gb|AAH01836.1|AAH01836 (BC001836) ribosomal protein L13a [Homo sapiens]"

193-H06 118-C06 "gi|13569956|ref|NP_112240.1| hypothetical protein similar to actin related protein 2/3 comple [Homo sapiens] >gi|14744212|ref|XP_044794.1| hypothetical protein similar to actin related protein 2/3 comple [Homo sapiens] >gi|12652557|gb|AAH00018.1|AAH00018 (BC000018) Similar to actin related protein 2/3 complex, subunit 5 (16 kD) [Homo sapiens] >gi|12654001|gb|AAH00798.1|AAH00798 (BC000798) Similar to actin related protein 2/3 complex, subunit 5 (16 kD) [Homo sapiens] >gi|12803221|gb|AAH02418.1|AAH02418 (BC002418) Similar to actin related protein 2/3 complex, subunit 5 (16 kD) [Homo sapiens]"

132-B10 132-B10 Unknown

034-A10 034-A10 gi|13904870|ref|NP_001000.2| ribosomal protein S5; 40S ribosomal protein S5 [Homo sapiens] >gi|14755545|ref|XP_034265.1| ribosomal protein S5 [Homo sapiens] >gi|15929961|gb|AAH15405.1|AAH15405 (BC015405) ribosomal protein S5 [Homo sapiens]

023-C10 023-C10 gi|1504020|dbj|BAA13209.1|(D86973) similar to Yeast translation activator GCN1 (P1:A48126) [Homo sapiens]

047-H05 047-H05 gi|13644734|ref|XP_016002.1| similar to 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN) (H. sapiens) [Homo sapiens]

005-B04 005-B04 Unknown

202-E02 202-E02 gi|15228111|ref|NP_181264.1| 40S ribosomal protein S5 [Arabidopsis thaliana] >gi|4056502|gb|AAC98068.1|(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

024-E06 024-E06 Unknown

189-A02 189-A02 Unknown

086-E04 086-E04 gi|15294071|gb|AAK95212.1|AF402838_1 (AF402838) 40S ribosomal protein S27a [Ictalurus punctatus]

168-B03 168-B03 Unknown

063-H10 063-H10 gi|15294047|gb|AAK95200.1|AF402826_1 (AF402826) 40S ribosomal protein S17 [Ictalurus punctatus]

153-A07 074-G11 gi|15294051|gb|AAK95202.1|AF402828_1 (AF402828) 40S ribosomal protein S19 [Ictalurus punctatus]

181-E03 181-E03 gi|15293899|gb|AAK95142.1|AF401570_1 (AF401570) ribosomal protein L15 [Ictalurus punctatus]

197-B03 154-E02 Unknown

185-A08 072-B09 Unknown

068-B04 068-B04 gi|12852098|dbj|BAB29273.1|(AK014324) putative [Mus musculus]

055-A09 027-B05 Unknown

190-E03 190-E03 gi|225901|prf||1403252A ribosomal protein S6 [Rattus norvegicus]

201-A12 201-A12 Unknown

019-D02 181-H05 "gi|3287845|sp|P81399|FAB1_AMBME FATTY ACID-BINDING PROTEIN 1, LIVER (L-FABP)"

199-D07 199-D07 Unknown

197-D05 197-D05 Unknown

002-H06 002-H06 gi|14726331|ref|XP_003920.4| betaine-homocysteine methyltransferase [Homo sapiens] >gi|4530461|gb|AAD22043.1| (AF118378) betaine-homocysteine methyltransferase [Homo sapiens] >gi|15214972|gb|AAH12616.1|AAH12616 (BC012616) Unknown (protein for MGC:13645) [Homo sapiens]

150-E11 150-E11 Unknown

161-E05 049-F01 gi|8096950|gb|AAF61951.2|AF237950_1 (AF237950) arginine:glycine amidinotransferase [Gallus gallus]

193-B12 192-B12 Unknown

053-D08 079-B03 Unknown

058-B09 058-B09 gi|117451|sp|P10044|CRG2_CYPGA GAMMA CRYSTALLIN M2 (GAMMA-M2) >gi|71519|pir|CYCAG2 gamma-crystallin m2 precursor - common carp >gi|62604|emb|CAA31388.1| (X12903) gamma-crystallin gamma-m2 (AA 1 - 173) [Cyprinus carpio]

048-E09 048-E09 Unknown

105-C12 105-C12 Unknown

071-C01 176-C07 Unknown

074-A02 074-A02 gi|11424039|ref|XP_008905.1| ribosomal protein L28 [Homo sapiens] >gi|13904866|ref|NP_000982.2| ribosomal protein L28; 60S ribosomal protein L28 [Homo sapiens] >gi|14757080|ref|XP_035924.1| ribosomal protein L28 [Homo sapiens] >gi|15302227|ref|XP_054333.1| ribosomal protein L28 [Homo sapiens] >gi|12652649|gb|AAH00072.1|AAH00072 (BC000072) ribosomal protein L28 [Homo sapiens] >gi|14603452|gb|AAH10173.1|AAH10173 (BC010173) Unknown (protein for MGC:20081) [Homo sapiens] >gi|15079503|gb|AAH11582.1|AAH11582 (BC011582) Unknown (protein for MGC:20378) [Homo sapiens]

028-A06 028-A06 Unknown

119-D08 007-F10 gi|11693032|gb|AAG38940.1| (AY013297) calcineurin-binding protein calsarcin-2 [Homo sapiens]

106-A12 106-A12 Unknown

209-H11 209-H11 Unknown

060-B11 060-B11 Unknown

038-C06 038-C06 Unknown

196-B12 196-B12 Unknown

019-B12 019-B12 gi|2920833|gb|AAC04625.1| (U92700) ribosomal protein S2 [Rattus norvegicus]

051-F12 051-F12 "gi|4506671|ref|NP_000995.1| ribosomal protein, large P2 [Homo sapiens] >gi|133061|sp|P05387|RLA2_HUMAN 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi|71152|pir|R6HUP2 acidic ribosomal protein P2, cytosolic [validated] - human >gi|190236|gb|AAA36472.1| (M17887) acidic ribosomal phosphoprotein (P2) [Homo sapiens] >gi|13529170|gb|AAH05354.1|AAH05354 (BC005354) ribosomal protein, large P2 [Homo sapiens] >gi|13543524|gb|AAH05920.1|AAH05920 (BC005920) ribosomal protein, large P2 [Homo sapiens] >gi|14043171|gb|AAH07573.1|AAH07573 (BC007573) ribosomal protein, large P2 [Homo sapiens]"

031-H01 031-H01 gi|15294065|gb|AAK95209.1|AF402835_1 (AF402835) 40S ribosomal protein S26-2 [Ictalurus punctatus]

124-G07 037-D08 Unknown

031-A08 031-A08 Unknown

048-E06 108-G11 Unknown
213-F02 164-C06 Unknown
086-E05 108-C04 gi|5880681|gb|AAD54776.1|AF134852_1 (AF134852) acidic ribosomal phosphoprotein P0 [Danio rerio]
105-H11 148-D05 Unknown
090-H02 027-C10 Unknown
170-F02 170-F02 Unknown
184-A02 050-F02 gi|15294019|gb|AAK95186.1|AF402812_1 (AF402812) 40S ribosomal protein S4 [Ictalurus punctatus]
193-A08 192-C12 Unknown
018-A09 004-D09 Unknown
064-H07 064-H07 Unknown
194-H01 194-H01 Unknown
005-A05 081-G03 Unknown
061-G08 167-G10 gi|15293923|gb|AAK95154.1|AF401582_1 (AF401582) ribosomal protein L27a [Ictalurus punctatus]
204-F06 204-F06 gi|14721839|ref|XP_036934.1| similar to 40S RIBOSOMAL PROTEIN SA (P40) (34/67 KDA LAMININ RECEPTOR) (COLON CARCINOMA LAMININ-BINDING PROTEIN) (NEM/1CHD4) (H. sapiens) [Homo sapiens]
051-D08 051-D08 Unknown
044-C08 058-B08 gi|15804744|ref|NP_290785.1| beta-lactamase; penicillin resistance protein [Escherichia coli 0157:H7 EDL933] >gi|15834385|ref|NP_313158.1| beta-lactamase [Escherichia coli 0157:H7] >gi|12519134|gb|AAG59351.1|AE005648_13 (AE005648) beta-lactamase; penicillin resistance protein [Escherichia coli 0157:H7 EDL933] >gi|13364608|dbj|BAB38554.1| (AP002568) beta-lactamase [Escherichia coli 0157:H7]
196-A01 196-A01 Unknown
069-D07 102-B05 Unknown
196-G12 196-G12 Unknown
193-D03 168-B09 Unknown
178-A01 178-A01 Unknown
112-F09 112-F09 Unknown
027-B03 027-B03 "gi|139875|sp|P29126|XYNA_RUMFL BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR >gi|97772|pir|S20907 endo-1,4-beta-xylanase (EC 3.2.1.8) precursor, bifunctional - Ruminococcus flavefaciens >gi|581505|emb|CAA77476.1| (Z11127) XYLA of Ruminococcus flavefaciens"
120-B02 062-C04 gi|12845526|dbj|BAB26785.1| (AK010234) putative [Mus musculus]
132-F05 174-B06 gi|15293895|gb|AAK95140.1| (AF401568) ribosomal protein L13a [Ictalurus punctatus]
170-F08 170-F08 Unknown
150-E03 118-A07 gi|15294011|gb|AAK95182.1|AF402808_1 (AF402808) 40S ribosomal protein Sa [Ictalurus punctatus]
172-G04 161-A10 gi|15803966|ref|NP_290002.1| high-affinity branched-chain amino acid transport [Escherichia coli 0157:H7 EDL933] >gi|15833557|ref|NP_312330.1| high-affinity branched-chain amino acid transport protein [Escherichia coli 0157:H7] >gi|12518110|gb|AAG58563.1|AE005569_3 (AE005569) high-affinity branched-chain amino acid transport [Escherichia coli 0157:H7 EDL933] >gi|13363777|dbj|BAB37726.1| (AP002565) high-affinity branched-chain amino acid transport protein [Escherichia coli 0157:H7]

008-C03 008-C03 Unknown
094-E05 149-D01 Unknown
077-A05 077-A05 Unknown
202-F11 202-F11 Unknown
028-G06 028-G06 gi|227229|prf||1617101C ribosomal protein S4 [Rattus norvegicus]
002-A02 002-A02 "gi|6325176|ref|NP_015244.1| Homology to rat S9 and E.coli S4; Rps9ap
[Saccharomyces cerevisiae] >gi|6094198|sp|013516|RS9A_YEAST 40S RIBOSOMAL PROTEIN S9-A (S13)
(YS11) (RP21) (YP28) >gi|101575|pir||S16822 ribosomal protein S9.e.A, cytosolic - yeast
(Saccharomyces cerevisiae) >gi|218515|dbj|BAA00626.1| (D00724) YS11 [Saccharomyces
cerevisiae] >gi|2347168|gb|AAB68268.1| (U41849) Ypl081wp [Saccharomyces cerevisiae]"
193-F04 028-E08 gi|15678710|ref|NP_275826.1| ribonuclease PH [Methanothermobacter
thermautotrophicus] >gi|7435295|pir||A69191 tRNA nucleotidyltransferase (EC 2.7.7.56) -
Methanobacterium thermoautotrophicum (strain Delta H) >gi|2621768|gb|AAB85188.1| (AE000848)
ribonuclease PH [Methanothermobacter thermautotrophicus]
003-B03 003-B03 gi|15293933|gb|AAK95159.1|AF401587_1 (AF401587) ribosomal protein L32
[Ictalurus punctatus]
070-C04 070-C04 Unknown
028-A07 028-A07 Unknown
185-G08 176-D10 Unknown
191-B09 191-B09 Unknown
053-F10 053-F10 gi|14762991|ref|XP_018300.2| hypothetical protein MGC2628 [Homo sapiens]
>gi|14042913|dbj|BAB55443.1| (AK027901) unnamed protein product [Homo sapiens]
042-F08 042-F08 gi|13124861|gb|AAK11731.1| (AY027434) ribosomal protein S16 [Heteropneustes
fossilis]
002-C03 002-C03 gi|15294013|gb|AAK95183.1|AF402809_1 (AF402809) 40S ribosomal protein S2
[Ictalurus punctatus]
089-F11 197-C01 gi|15294057|gb|AAK95205.1|AF402831_1 (AF402831) 40S ribosomal protein S23
[Ictalurus punctatus]
064-C05 182-E05 gi|11415026|ref|NP_000971.1| ribosomal protein L18a; 60S ribosomal protein
L18a [Homo sapiens] >gi|14766238|ref|XP_038593.1| ribosomal protein L18a [Homo sapiens]
>gi|730538|sp|Q02543|RL1X_HUMAN 60S RIBOSOMAL PROTEIN L18A >gi|401845|gb|AAC18781.1| (L05093)
ribosomal protein L18a [Homo sapiens] >gi|3702270|gb|AAC62828.1| (AC005796) ribosomal
protein L18a [Homo sapiens] >gi|13960144|gb|AAH07512.1|AAH07512 (BC007512) ribosomal protein
L18a [Homo sapiens]
128-C12 188-G11 Unknown
213-B10 213-B10 Unknown
111-A02 207-G08 Unknown
019-E06 019-E06 gi|15294041|gb|AAK95197.1|AF402823_1 (AF402823) 40S ribosomal protein S15
[Ictalurus punctatus]
037-G11 037-G11 gi|15294061|gb|AAK95207.1|AF402833_1 (AF402833) 40S ribosomal protein S25
[Ictalurus punctatus]
053-B07 053-B07 Unknown
024-E02 024-E02 Unknown
114-B05 114-B05 Unknown
128-F02 056-E04 Unknown
032-B05 173-D01 gi|15294037|gb|AAK95195.1|AF402821_1 (AF402821) 40S ribosomal protein S13
[Ictalurus punctatus]

141-H09 141-H09 Unknown

111-A08 111-A08 Unknown

062-C06 062-C06 "gi|1172982|sp|P11249|RL1X_RAT 60S RIBOSOMAL PROTEIN L18A

>gi|1363321|pir||JC4231 ribosomal protein L18a - rat >gi|11383876|pir||R5RT18 ribosomal protein L18a, cytosolic [validated] - rat >gi|416554|emb|CAA32385.1| (X14181) ribosomal protein L18a (AA 1-175) [Rattus rattus] >gi|12846793|dbj|BAB27304.1| (AK010983) putative [Mus musculus]"

146-F12 146-F12 Unknown

195-A09 195-A09 Unknown

191-B10 191-B10 Unknown

183-G06 102-G06 gi|6633991|dbj|BAA88568.1| (AB036060) ubiquitin [Oncorhynchus mykiss]

008-E04 058-H08 Unknown

193-H08 169-B10 gi|6681273|ref|NP_031932.1| eukaryotic translation elongation factor 1 alpha 2 [Mus musculus] >gi|1711567|sp|P27706|EF12_MOUSE ELONGATION FACTOR 1-ALPHA 2 (EF-1-ALPHA-2) (ELONGATION FACTOR 1 A-2) (EEF1A-2) (STATIN S1) >gi|112321|pir||A40389 translation elongation factor eEF-1 alpha chain (clone pS1) - rat >gi|1083500|pir||JC2445 translation elongation factor eEF-1 alpha-like protein S1 - mouse >gi|206438|gb|AAA41966.1| (M62751) statin-related protein [Rattus norvegicus] >gi|1220410|gb|AAA91870.1| (L26479) elongation factor-1 alpha [Mus musculus] >gi|14330029|emb|CAC40737.1| (AL450341) bM401L17.4 (eukaryotic translation elongation factor 1 alpha 2) [Mus musculus]

161-F04 161-F04 Unknown

213-C03 213-C03 Unknown

023-C07 023-C07 gi|4758790|ref|NP_004543.1| NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) [Homo sapiens] >gi|14745227|ref|XP_044981.1| NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) [Homo sapiens] >gi|3914138|sp|043920|NIPM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 15 KDA SUBUNIT (COMPLEX I-15 KDA) (CI-15 KDA) >gi|2655055|gb|AAB87866.1| (AF020352) NADH:ubiquinone oxidoreductase 15 kDa IP subunit [Homo sapiens] >gi|2911482|gb|AAC39878.1| (AF047434) NADH-ubiquinone oxidoreductase 15kDa subunit; CI-15 protein [Homo sapiens] >gi|12804873|gb|AAH01884.1|AAH01884 (BC001884) NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) [Homo sapiens]

197-B01 173-F09 Unknown

174-C03 171-D05 Unknown

147-B06 147-B06 Unknown

070-D04 070-D04 Unknown

191-C08 191-C08 gi|13325445|gb|AAH04520.1|AAH04520 (BC004520) Unknown (protein for IMAGE:3938975) [Homo sapiens]

188-H06 162-D11 Unknown

209-H12 209-H12 Unknown

050-C04 050-C04 gi|1710775|sp|P50894|RS7_FUGRU 40S RIBOSOMAL PROTEIN S7

>gi|1160445|emb|CAA64412.1| (X94942) ribosomal protein S7 [Takifugu rubripes]

104-B12 104-B12 gi|6180205|gb|AAF05846.1|AF197880_1 (AF197880) type I cytokeratin [Danio rerio]

135-F11 007-D01 gi|13938404|gb|AAH07340.1|AAH07340 (BC007340) Unknown (protein for MGC:1526) [Homo sapiens]

141-G02 141-G02 Unknown

143-B06 145-H08 Unknown

213-G02 213-G02 Unknown
039-C10 039-C10 gi|1522685|gb|AAC48632.1| (U53421) betaine-homocysteine methyltransferase [Sus scrofa]
052-H04 052-H04 Unknown
210-C06 210-C06 Unknown
051-H02 051-H02 Unknown
060-H11 060-H11 Unknown
043-E12 081-E10 Unknown
063-G11 174-A12 Unknown
049-E06 098-D03 Unknown
130-G11 130-G11 Unknown
096-F03 096-F03 Unknown
165-A01 165-A01 gi|3913050|sp|042363|APA1_BRARE APOLIPOPROTEIN A-I PRECURSOR (APO-AI) >gi|2440055|emb|CAA74004.1| (Y13653) apolipoprotein A-I precursor protein [Danio rerio]
040-A02 058-E03 Unknown
201-D12 201-D12 gi|13938595|gb|AAH07449.1|AAH07449 (BC007449) Similar to CG7818 gene product [Homo sapiens]
206-D03 206-D03 Unknown
207-D07 207-D07 Unknown
015-A12 015-A12 Unknown
155-F01 155-F01 Unknown
158-B12 158-B12 Unknown
095-D06 095-D06 Unknown
015-F10 063-H05 Unknown
131-E08 131-E08 Unknown
027-F06 156-A10 gi|10441411|gb|AAG17026.1|AF186844_1 (AF186844) transcription factor Sox4 [Xenopus laevis]
052-F12 052-F12 Unknown
135-G09 135-G09 Unknown
122-A08 122-A08 Unknown
105-B11 065-C02 gi|15293931|gb|AAK95158.1|AF401586_1 (AF401586) ribosomal protein L31 [Ictalurus punctatus]
187-D07 028-H01 gi|7595804|gb|AAF64457.1| (AF240374) ribosomal protein L18 [Oreochromis niloticus] >gi|7595806|gb|AAF64458.1|AF240375_1 (AF240375) ribosomal protein L18 [Oreochromis niloticus] >gi|7595809|gb|AAF64459.1|AF240376_1 (AF240376) ribosomal protein L18 [Oreochromis mossambicus]
084-C08 081-B06 Unknown
192-E03 192-E03 Unknown
078-C04 078-C04 gi|9294786|gb|AAF86670.1|AF178449_1 (AF178449) beta-galactosidase alpha peptide [Integration vector pCD11PKS] >gi|9294795|gb|AAF86676.1|AF178452_1 (AF178452) beta-galactosidase alpha peptide [Integration vector pCD13PKS]
201-A03 201-A03 Unknown
067-D03 067-D03 Unknown
207-E07 207-E07 Unknown
086-E03 065-B07 Unknown
170-F05 154-B03 gi|15294049|gb|AAK95201.1|AF402827_1 (AF402827) 40S ribosomal protein S18 [Ictalurus punctatus]

084-D10 174-F07 gi|12834891|dbj|BAB23079.1| (AK003930) putative [Mus musculus]
 >gi|15029834|gb|AAH11140.1|AAH11140 (BC011140) RIKEN cDNA 1190005M04 gene [Mus musculus]
158-C05 163-E04 gi|7949088|ref|NP_058029.1| myosin binding protein H [Mus musculus]
 >gi|6093458|sp|P70402|MYPH_MOUSE MYOSIN-BINDING PROTEIN H (MYBP-H) (H-PROTEIN)
 >gi|1546813|gb|AAB08426.1| (U68267) myosin binding protein H [Mus musculus]
208-A03 208-A03 Unknown
150-E07 160-H01 Unknown
166-G01 166-G01 Unknown
008-A11 054-C11 "gi|14785305|ref|XP_030712.1| one cut domain, family member 1 [Homo sapiens]
 >gi|13627184|sp|Q9UBC0|HNF6_HUMAN HEPATOCYTE NUCLEAR FACTOR 6 (HNF-6) (ONE CUT DOMAIN FAMILY
 MEMBER 1) >gi|4100316|gb|AAD00826.1| (U96173) hepatocyte nuclear factor-6 alpha [Homo
 sapiens] >gi|4104419|gb|AAD02033.1| (AF035581) hepatocyte nuclear factor 6 [Homo sapiens]"
133-D11 133-D11 Unknown
126-B07 170-B02 Unknown
192-C09 192-C09 Unknown
181-H08 181-H08 Unknown
143-A09 143-A09 Unknown
213-G11 213-G11 Unknown
163-D09 163-D09 Unknown
086-B05 086-B05 Unknown
150-A04 150-A04 Unknown
134-C05 147-F04 Unknown
042-E12 177-F06 gi|1943496|pdb|10EN| Phosphoenolpyruvate Carboxykinase
075-F03 088-C06 gi|127099|sp|P03817|MIOC_ECOLI PROTEIN MIOC >gi|7429210|pir||QQEC16 mioC
 protein - Escherichia coli >gi|290591|gb|AAA62094.1| (L10328) involved in modulation of
 initiation at oriC [Escherichia coli] >gi|455178|gb|AAA24251.1| (K00826) 16K protein
 [Escherichia coli] >gi|1790181|gb|AAC76765.1| (AE000451) initiation of chromosome
 replication [Escherichia coli K12] >gi|223847|prf||1002215A protein 16kD [Escherichia coli]
036-A08 166-B02 Unknown
086-A12 086-A12 Unknown
052-B10 144-D12 gi|14734140|ref|XP_034711.1| ribosomal protein L34 [Homo sapiens]
 >gi|14734145|ref|XP_034712.1| ribosomal protein L34 [Homo sapiens]
 >gi|12804693|gb|AAH01773.1|AAH01773 (BC001773) Similar to ribosomal protein L34 [Homo
 sapiens]
162-E05 166-A07 Unknown
028-A12 028-A12 Unknown
189-D05 189-D05 gi|13569612|gb|AAK31162.1| (AF348700) ubiquitin A-52 residue ribosomal
 protein fusion product 1 [Homo sapiens]
018-A01 154-E05 gi|15294039|gb|AAK95196.1|AF402822_1 (AF402822) 40S ribosomal protein S14
 [Ictalurus punctatus]
087-A08 087-A08 Unknown
018-A05 164-D09 Unknown
167-G03 172-H04 Unknown
082-F02 082-F02 gi|7709990|ref|NP_057877.1| betaine-homocysteine methyltransferase [Mus
 musculus] >gi|5915784|sp|O35490|BHMT_MOUSE BETAIN--HOMOCYSTEINE S-METHYLTRANSFERASE
 >gi|2645804|gb|AAB87501.1| (AF033381) betaine homocysteine methyl transferase [Mus musculus]
 >gi|9230663|gb|AAF85944.1| (AF227432) betaine-homocysteine S-methyltransferase [Mus musculus]

088-E08 088-E08 Unknown
 002-B08 002-B08 Unknown
 199-G07 199-G07 Unknown
 003-A03 003-A03 Unknown
 144-C08 144-C08 Unknown
 103-D06 103-D06 Unknown
 140-D08 140-D08 gi|14716982|emb|CAC44156.1| (AJ312336) putative 40S ribosomal protein 20S protein [Oncorhynchus mykiss]
 189-E03 078-H08 gi|14735047|ref|XP_030760.1| similar to hypothetical protein (H. sapiens) [Homo sapiens]
 061-B02 061-B02 Unknown
 029-H11 029-H11 Unknown
 060-G06 060-G06 Unknown
 204-E11 204-E11 Unknown
 198-G05 198-G05 Unknown
 027-H12 027-H12 Unknown
 193-D07 192-D07 Unknown
 123-H07 123-H07 Unknown
 187-B01 187-B01 Unknown
 200-G10 200-G10 Unknown
 016-C12 180-D01 Unknown
 026-C06 117-C04 Unknown
 192-G02 192-G02 Unknown
 208-G05 208-G05 Unknown
 208-G02 208-G02 Unknown
 065-A07 101-G09 gi|5921705|sp|057312|CKKN_PAROL PROCHOLECYSTOKININ PRECURSOR (CCK) >gi|2662289|dbj|BAA23734.1| (AB009281) cholecystokinin [Paralichthys olivaceus]
 200-A12 200-A12 Unknown
 188-F12 158-D09 Unknown
 075-C11 151-F06 Unknown
 126-F07 018-F04 Unknown
 207-E10 207-E10 Unknown
 160-G07 160-G07 Unknown
 164-E12 013-F09 gi|8698677|gb|AAF78472.1|AF180889_1 (AF180889) fast skeletal muscle troponin T [Danio rerio]
 139-F06 176-D08 Unknown
 039-B08 039-B08 "gi|122004|sp|P02264|H2A_ONCMY HISTONE H2A, GONADAL >gi|64325|emb|CAA25528.1| (X01064) histone H2A [Oncorhynchus mykiss]"
 002-B12 002-B12 Unknown
 147-C04 160-A08 gi|3421386|gb|AAC32193.1| (AF081462) myosin light chain 2 [Danio rerio]
 177-H02 207-H10 gi|4588532|gb|AAD26140.1|AF109780_1 (AF109780) basic domain leucine zipper protein [Danio rerio]
 074-H08 074-H08 Unknown
 206-F11 206-F11 Unknown
 068-F11 053-G03 Unknown
 037-B02 001-F03 gi|1216293|gb|AAA91763.1| (L35239) cardiac tropomyosin [Xenopus laevis]

032-G04 032-G04 "gi|14783427|ref|XP_045643.1| phosphorylase, glycogen; muscle (McArdle syndrome, glycogen storage disease type V) [Homo sapiens]"
001-G05 001-G05 Unknown
193-H12 165-D08 Unknown
001-F09 026-B02 Unknown
177-F02 177-F02 gi|14009437|dbj|BAB47389.1| (AB042437) mitochondrial ATP synthase alpha-subunit [Cyprinus carpio]
196-G04 118-B05 gi|2134201|pir||I51172 transcription factor RcC/EBP-2 - bullfrog
 >gi|478891|gb|AAA52224.1| (U08605) transcription factor RcC/EBP-2 [Rana catesbeiana]
073-B09 044-D05 gi|1703696|gb|AAB37708.1| (S82440) cyclophilin [Hemicentrotus pulcherrimus]
073-G09 156-F06 Unknown
005-E08 135-G06 gi|6665780|gb|AAF23012.1|AF211852_1 (AF211852) GAP-associated phosphoprotein p62 [Danio rerio]
206-B05 206-B05 Unknown
108-A05 108-H04 Unknown
092-A09 092-A09 Unknown
063-A11 063-A11 Unknown
153-B08 153-B08 Unknown
010-D11 072-A06 gi|12845734|dbj|BAB26874.1| (AK010354) putative [Mus musculus]
 >gi|12856575|dbj|BAB30712.1| (AK017371) putative [Mus musculus]
062-D03 062-D03 Unknown
131-D12 131-D12 Unknown
155-D09 068-B05 Unknown
038-H08 024-H12 Unknown
103-D04 155-D01 gi|13399318|ref|NP_080580.1| RIKEN cDNA 0610007P06 gene [Mus musculus]
 >gi|12832191|dbj|BAB22001.1| (AK002306) putative [Mus musculus]
 >gi|13278142|gb|AAH03916.1|AAH03916 (BC003916) RIKEN cDNA 0610007P06 gene [Mus musculus]
047-D05 047-D05 Unknown
188-G04 062-F03 gi|4063849|gb|AAC98491.1| (AF069994) vimentin [Danio rerio]
143-C01 143-C01 Unknown