Description of additional data files

Additional file 1

Title: Supplementary methods

File format: PDF (Adobe Acrobat)

Description: Document listing quantitative RT-PCR probes and oligonucleotides used.

Additional file 2

Title: Supplementary table 2

File format: Tab-delimited spreadsheet (Microsoft Excel spreadsheet)

Description: Spreadsheet containing a list of probe sets regulated by PEDF in A375-pCEP4-PEDF Pool compared to control A375-pCEP4 Pool. For each probe set, linear ratios of GCRMA-normalized expression in PEDF-over-expressing cells compared to control cells in the two hybridizations are shown, as well as Affymetrix probe set ID, gene symbol, Unigene ID Ensemble ID and Gene Ontology (GO) functional categories.

Supplementary Table 2. Orgaz et al Gene expression profile of A375 melanoma cell line overexpressing pigment_epithelium-derived factor unveils molecular aspects of its dual action on angiogenic potential and aggressiveness of human melanoma••••••••••
Supplementary Table 2. Probe sets regulated by PEDF in A375-pCEP4-PEDF cell line compared to control A375-pCEP4 cell line Linear ratios of GCRMA-normalized expression in PEDF-overexpressing cells compared to control cells in the two hybridizations (Hybr. 1 and Hybr. 2) are shown••••••••••

Probe set ID•Descriptions•GCRMA PEDF vs Control Hybr. 1•GCRMA PEDF vs Control Hybr. 2•Title•Gene symbol•Unigene•Ensemble ID•Biological process GO•Cellular component GO•Molecular function GO
202283_at•"gb:NM_002615.1 /DB_XREF=gi:4505708 /GEN=SERPINF1 /FEA=FLmRNA /CNT=211 /TID=Hs.173594.0 /TIER=FL+Stack /STK=146 /UG=Hs.173594 /LL=5176 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived fac"•66.04550743•81.0000421•"serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1"•SERPINF1•Hs.532768•ENSG00000132386•7275 // development // traceable author statement /// 8283 // cell proliferation // traceable author statement /// 16525 // negative regulation of angiogenesis // inferred from direct assay /// 50769 // positive regulation of neurogenesis // inferred from•5576 // extracellular region // inferred from direct assay•4867 // serine-type endopeptidase inhibitor activity // traceable author statement
220217_x_at•"gb:NM_022661.1 /DB_XREF=gi:13435136 /GEN=SPANXC /FEA=FLmRNA /CNT=11 /TID=Hs.178053.0 /TIER=FL /STK=0 /UG=Hs.178053 /LL=64663 /DEF=Homo sapiens SPANX family, member C (SPANXC), mRNA. /PROD=SPANX family, member C /FL=gb:NM_022661.1 gb:BC005382.1"•34.80619013•25.90017443•"SPANX family, member C"•SPANXC•Hs.343879•ENSG00000198573•••
220922_s_at•"gb:NM_013453.1 /DB_XREF=gi:7305516 /GEN=SPANXA1 /FEA=FLmRNA /CNT=3 /TID=Hs.293266.0 /TIER=FL /STK=1 /UG=Hs.293266 /LL=30014 /DEF=Homo sapiens sperm protein associated with the nucleus, X chromosome, family member A1 (SPANXA1), mRNA. /PROD=sperm protein as"•31.8824945•45.30323786•"sperm protein associated with the nucleus, X-linked, family member A1 /// SPANX family, member B1 /// SPANX family, member A2 /// SPANX family, member C /// SPANX family, member B2"•SPANXA1 /// SPANXB1 /// SPANXA2 /// SPANXC /// SPANXB2•Hs.343879•ENSG00000198021 /// ENSG00000198820 /// ENSG00000198573•7283 // spermatogenesis // traceable author statement /// 7286 // spermatid cell development // non-traceable author statement•5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement•
224032_x_at•"gb:AF098306.1 /DB_XREF=gi:6808523 /GEN=SPANX /FEA=FLmRNA /CNT=4 /TID=Hs.293266.1 /TIER=FL /STK=2 /UG=Hs.293266 /LL=30014 /DEF=Homo sapiens nuclear-associated protein SPAN-Xa (SPANX) mRNA, complete cds. /PROD=nuclear-associated protein SPAN-Xa /FL=gb:AF098"•29.67426027•19.37656374•"sperm protein associated with the nucleus, X-linked, family member A1 /// SPANX family, member A2"•SPANXA1 /// SPANXA2•Hs.334464•ENSG00000198021•7283 // spermatogenesis // traceable author statement•5634 // nucleus // traceable author statement /// 5737 // cytoplasm // traceable author statement•
1564491_at•"gb:AK093505.1 /DB_XREF=gi:21752399 /TID=Hs2.376478.1 /CNT=1 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.376478 /UG_TITLE=Homo sapiens cDNA FLJ36186 fis, clone TESTI2027013, weakly similar to FIBRILLARIN. /DEF=Homo sapiens cDNA FLJ36186 fis, clone TESTI2027013, "•18.52708469•26.41751189•"CDNA FLJ36186 fis, clone TESTI2027013, weakly similar to FIBRILLARIN"••Hs.545964••••
219014_at•"gb:NM_016619.1 /DB_XREF=gi:7706157 /GEN=LOC51316 /FEA=FLmRNA /CNT=86 /TID=Hs.107139.0 /TIER=FL /STK=0 /UG=Hs.107139 /LL=51316 /DEF=Homo sapiens hypothetical protein (LOC51316), mRNA. /PROD=hypothetical protein /FL=gb:NM_016619.1 gb:AF208846.1"•15.85369814•35.93977207•placenta-specific 8•PLAC8•Hs.546392•ENSG00000145287•••
218211_s_at•"gb:NM_024101.1 /DB_XREF=gi:13129107 /GEN=MGC2771 /FEA=FLmRNA /CNT=148 /TID=Hs.321130.0 /TIER=FL+Stack /STK=78 /UG=Hs.321130 /LL=79083 /DEF=Homo sapiens hypothetical protein MGC2771 (MGC2771), mRNA. /PROD=hypothetical protein MGC2771 /FL=gb:BC001653.1 gb:N"•15.69713816•28.89682266•melanophilin•MLPH•Hs.102406•ENSG00000115648•6886 // intracellular protein transport // inferred from electronic annotation••5515 // protein binding // inferred from electronic annotation /// 17137 // Rab GTPase binding // inferred from electronic annotation
212012_at•gb:BF342851 /DB_XREF=gi:11289878 /DB_XREF=602015135F1 /CLONE=IMAGE:4150664 /FEA=mRNA /CNT=397 /TID=Hs.118893.0 /TIER=Stack /STK=116 /UG=Hs.118893 /LL=7837 /UG_GENE=D2S448 /UG_TITLE=Melanoma associated gene•15.174786•27.85516329•Melanoma associated gene•D2S448•Hs.332197•ENSG00000130508•6955 // immune response // non-traceable author statement••4601 // peroxidase activity // inferred from electronic annotation /// 5152 // interleukin-1 receptor antagonist activity // non-traceable author statement /// 16491 // oxidoreductase activity // inferred from electronic annotation
212464_s_at•gb:X02761.1 /DB_XREF=gi:31396 /FEA=mRNA /CNT=525 /TID=Hs.287820.1 /TIER=Stack /STK=509 /UG=Hs.287820 /LL=2335 /UG_GENE=FN1 /DEF=Human mRNA for fibronectin (FN precursor). /PROD=fibronectin

```
precursor•14.21826924•16.52472325•fibronectin
1•FN1•Hs.203717•ENSG00000115414•6953 // acute-phase response // inferred from
electronic annotation /// 7155 // cell adhesion // non-traceable author
statement /// 8152 // metabolism // inferred from electronic annotation ///
9611 // response to wounding // non-traceable author statemen•5576 //
extracellular region // inferred from electronic annotation /// 5578 //
extracellular matrix (sensu Metazoa) // non-traceable author statement•5201
// extracellular matrix structural constituent // non-traceable author
statement /// 5518 // collagen binding // non-traceable author statement ///
8201 // heparin binding // non-traceable author statement /// 16491 //
oxidoreductase activity // infe
216442_x_at•"gb:AK026737.1 /DB_XREF=gi:10439658 /FEA=mRNA /CNT=1
/TID=Hs.287820.2 /TIER=ConsEnd /STK=0 /UG=Hs.287820 /LL=2335 /UG_GENE=FN1
/UG_TITLE=fibronectin 1 /DEF=Homo sapiens cDNA: FLJ23084 fis, clone LNG06602,
highly similar to HSFIB1 Human mRNA for
fibronectin"•13.69382814•17.17159443•fibronectin
1•FN1•Hs.203717•ENSG00000115414•6953 // acute-phase response // inferred from
electronic annotation /// 7155 // cell adhesion // non-traceable author
statement /// 8152 // metabolism // inferred from electronic annotation ///
9611 // response to wounding // non-traceable author statemen•5576 //
extracellular region // inferred from electronic annotation /// 5578 //
extracellular matrix (sensu Metazoa) // non-traceable author statement•5201
// extracellular matrix structural constituent // non-traceable author
statement /// 5518 // collagen binding // non-traceable author statement ///
8201 // heparin binding // non-traceable author statement /// 16491 //
oxidoreductase activity // infe
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/DEF=Homo sapiens clone FLC0562 PRO2841 mRNA, complete cds. /PROD=PRO2841
/FL=gb:AF130095.1"•13.45218576•18.24544483•fibronectin
1•FN1•Hs.203717•ENSG00000115414•6953 // acute-phase response // inferred from
electronic annotation /// 7155 // cell adhesion // non-traceable author
statement /// 8152 // metabolism // inferred from electronic annotation ///
9611 // response to wounding // non-traceable author statemen•5576 //
extracellular region // inferred from electronic annotation /// 5578 //
extracellular matrix (sensu Metazoa) // non-traceable author statement•5201
// extracellular matrix structural constituent // non-traceable author
statement /// 5518 // collagen binding // non-traceable author statement ///
8201 // heparin binding // non-traceable author statement /// 16491 //
oxidoreductase activity // infe
212013_at•"gb:D86983.1 /DB_XREF=gi:1504039 /GEN=KIAA0230 /FEA=mRNA /CNT=397
/TID=Hs.118893.0 /TIER=Stack /STK=98 /UG=Hs.118893 /LL=7837
/UG_TITLE=Melanoma associated gene /DEF=Human mRNA for KIAA0230 gene, partial
cds."•12.96386257•21.1040196•Melanoma associated
gene•D2S448•Hs.332197•ENSG00000130508•6955 // immune response //
non-traceable author statement••4601 // peroxidase activity // inferred from
electronic annotation /// 5152 // interleukin-1 receptor antagonist activity
// non-traceable author statement /// 16491 // oxidoreductase activity //
inferred from electronic annotation
234994_at•gb:AA088177 /DB_XREF=gi:1633698 /DB_XREF=zk71a08.s1
/CLONE=IMAGE:488246 /FEA=EST /CNT=35 /TID=Hs.172870.0 /TIER=ConsEnd /STK=1
/UG=Hs.172870
/UG_TITLE=ESTs•12.51511401•7.013363264•KIAA1913•KIAA1913•Hs.172870•ENSG0000016
4484••16021 // integral to membrane // inferred from electronic annotation•
211719_x_at•"gb:BC005858.1 /DB_XREF=gi:13543399 /FEA=FLmRNA /CNT=1
/TID=HsAffx.900722.926 /TIER=FL /STK=0 /DEF=Homo sapiens, clone MGC:3255,
mRNA, complete cds. /PROD=Unknown (protein for MGC:3255)
/FL=gb:BC005858.1"•12.21664886•17.74429307•fibronectin 1 /// fibronectin
1•FN1•Hs.203717•ENSG00000115414•6953 // acute-phase response // inferred from
electronic annotation /// 7155 // cell adhesion // non-traceable author
statement /// 8152 // metabolism // inferred from electronic annotation ///
9611 // response to wounding // non-traceable author statemen•5576 //
extracellular region // inferred from electronic annotation /// 5578 //
extracellular matrix (sensu Metazoa) // non-traceable author statement•5201
// extracellular matrix structural constituent // non-traceable author
statement /// 5518 // collagen binding // non-traceable author statement ///
8201 // heparin binding // non-traceable author statement /// 16491 //
oxidoreductase activity // infe
209598_at•"gb:AB020690.1 /DB_XREF=gi:4240254 /GEN=KIAA0883 /FEA=FLmRNA
/CNT=85 /TID=Hs.7782.0 /TIER=FL+Stack /STK=20 /UG=Hs.7782 /LL=10687 /DEF=Homo
sapiens mRNA for KIAA0883 protein, complete cds. /PROD=KIAA0883 protein
/FL=gb:NM_007257.1 gb:AB020690.1
gb:AF286487."•10.62999254•11.36750894•••••••
205832_at•"gb:NM_016352.1 /DB_XREF=gi:10047105 /GEN=LOC51200 /FEA=FLmRNA
/CNT=38 /TID=Hs.93764.0 /TIER=FL /STK=0 /UG=Hs.93764 /LL=51200 /DEF=Homo
sapiens carboxypeptidase A3 (LOC51200), mRNA. /PROD=carboxypeptidase A3
/FL=gb:NM_016352.1 gb:AF095719.1"•9.840773868•10.96643553•carboxypeptidase
A4•CPA4•Hs.93764•ENSG00000128510•6508 // proteolysis and peptidolysis //
non-traceable author statement /// 16573 // histone acetylation //
non-traceable author statement••4180 // carboxypeptidase activity // inferred
from electronic annotation /// 4182 // carboxypeptidase A activity //
```

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non-traceable author statement /// 8237 // metallopeptidase activity //
inferred from electronic annotation
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/CNT=39 /TID=Hs.75777.0 /TIER=FL /STK=0 /UG=Hs.75777 /LL=6876 /DEF=Homo
sapiens transgelin (TAGLN), mRNA. /PROD=transgelin /FL=gb:NM_003186.2
gb:D17409.1
gb:M95787.1"•9.786239022•8.495929709•transgelin•TAGLN•Hs.503998•ENSG0000014959
1•7517 // muscle development // traceable author statement••3779 // actin
binding // inferred from electronic annotation
1555401_at•"gb:BC025383.1 /DB_XREF=gi:19263486 /TID=Hs2.130546.2 /CNT=1
/FEA=FLmRNA /TIER=FL /STK=1 /LL=54937 /UG_GENE=FLJ20449 /UG=Hs.130546
/DEF=Homo sapiens, clone MGC:26186 IMAGE:4829809, mRNA, complete cds.
/PROD=Unknown (protein for MGC:26186)
/FL=gb:BC025383.1"•9.129536997•4.377122703•hypothetical protein
FLJ20449•FLJ20449•Hs.124519•ENSG00000083622•••
222557_at•gb:AL353715 /DB_XREF=gi:11121028 /FEA=FLmRNA /CNT=140
/TID=Hs.285753.0 /TIER=Stack /STK=66 /UG=Hs.285753 /LL=50861 /UG_GENE=SCLIP
/UG_TITLE=SCG10-like-protein /DEF=Human DNA sequence from clone CTD-3184A7 on
chromosome 20 Contains the 5 end of the GMEB2
(•9.129339648•8.951603164•stathmin-like
3•STMN3•Hs.348326•ENSG00000197457•7242 // intracellular signaling cascade //
inferred from electronic annotation /// 7399 // neurogenesis // traceable
author statement••
201009_s_at•"gb:AI439556 /DB_XREF=gi:4305149 /DB_XREF=tc90c12.x1
/CLONE=IMAGE:2073430 /FEA=FLmRNA /CNT=488 /TID=Hs.179526.0 /TIER=Stack
/STK=91 /UG=Hs.179526 /LL=10628 /UG_GENE=VDUP1 /UG_TITLE=upregulated by
1,25-dihydroxyvitamin D-3 /FL=gb:NM_006472.1
gb:S73591.1"•8.92597045•27.97179704•thioredoxin interacting
protein•TXNIP•Hs.533977•ENSG00000117289•••
201008_s_at•"gb:AA812232 /DB_XREF=gi:2881843 /DB_XREF=ob84h09.s1
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1,25-dihydroxyvitamin D-3 /FL=gb:NM_006472.1
gb:S73591.1"•8.843520316•20.74697562•thioredoxin interacting
protein•TXNIP•Hs.533977•ENSG00000117289•••
237435_at•gb:AI093492 /DB_XREF=gi:3432468 /DB_XREF=qb15c01.x1
/CLONE=IMAGE:1696320 /FEA=EST /CNT=6 /TID=Hs.61596.0 /TIER=ConsEnd /STK=6
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locus••Hs.61596••••
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/CNT=488 /TID=Hs.179526.0 /TIER=FL /STK=0 /UG=Hs.179526 /LL=10628 /DEF=Homo
sapiens upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1), mRNA.
/PROD=upregulated by 1,25-dihydroxyvitamin D-3
/FL=gb:NM_"•8.251454587•18.04908706•thioredoxin interacting
protein•TXNIP•Hs.533977•ENSG00000117289•••
232884_s_at•gb:AL133055.1 /DB_XREF=gi:6453475 /GEN=DKFZp434J1015 /FEA=mRNA
/CNT=4 /TID=Hs.283779.0 /TIER=ConsEnd /STK=0 /UG=Hs.283779 /LL=54753
/DEF=Homo sapiens mRNA; cDNA DKFZp434J1015 (from clone DKFZp434J1015).
/PROD=hypothetical protein•7.626830205•3.670275276•hypothetical protein
DKFZp434J1015•DKFZp434J1015•Hs.381239•ENSG00000175419•••
209035_at•"gb:M69148.1 /DB_XREF=gi:182650 /GEN=hMK-1 /FEA=FLmRNA /CNT=196
/TID=Hs.82045.0 /TIER=FL /STK=1 /UG=Hs.82045 /LL=4192 /DEF=Human midkine
mRNA, complete cds. /PROD=midkine /FL=gb:NM_002391.1
gb:M69148.1"•7.291285814•9.423256966•midkine (neurite growth-promoting factor
2)•MDK•Hs.82045•ENSG00000110492•74 // regulation of cell cycle // inferred
from electronic annotation /// 7165 // signal transduction // non-traceable
author statement /// 7267 // cell-cell signaling // not recorded /// 7399 //
neurogenesis // non-traceable author statement /// 8283 // •5615 //
extracellular space // not recorded•5125 // cytokine activity // not recorded
/// 8083 // growth factor activity // non-traceable author statement /// 8201
// heparin binding // inferred from direct assay
213905_x_at•gb:AA845258 /DB_XREF=gi:2931709 /DB_XREF=ak84a11.s1
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/UG=Hs.821 /LL=633 /UG_GENE=BGN
/UG_TITLE=biglycan•7.041892249•14.21166508•biglycan /// serologically defined
colon cancer antigen 33•BGN /// SDCCAG33•Hs.821•ENSG00000182492 ///
ENSG00000179981•"6355 // regulation of transcription, DNA-dependent //
inferred from electronic annotation"•5578 // extracellular matrix (sensu
Metazoa) // inferred from electronic annotation /// 5578 // extracellular
matrix (sensu Metazoa) // non-traceable author statement /// 5634 // nucleus
// inferred from electronic annotation•5201 // extracellular matrix
structural constituent // non-traceable author statement /// 3700 //
transcription factor activity // inferred from electronic annotation /// 8270
// zinc ion binding // inferred from electronic annotation
205858_at•"gb:NM_002507.1 /DB_XREF=gi:4505392 /GEN=NGFR /FEA=FLmRNA /CNT=33
/TID=Hs.1827.0 /TIER=FL+Stack /STK=16 /UG=Hs.1827 /LL=4804 /DEF=Homo sapiens
nerve growth factor receptor (TNFR superfamily, member 16) (NGFR), mRNA.
/PROD=nerve growth factor receptor precu"•6.674405371•4.560259297•"nerve
growth factor receptor (TNFR superfamily, member
16)"•NGFR•Hs.415768•ENSG00000064300•6915 // apoptosis // inferred from
electronic annotation /// 7165 // signal transduction // inferred from
```

```
electronic annotation /// 7399 // neurogenesis // inferred from electronic
annotation /// 30154 // cell differentiation // inferred from electronic
a•5886 // plasma membrane // traceable author statement /// 5887 // integral
to plasma membrane // traceable author statement•4888 // transmembrane
receptor activity // traceable author statement /// 5515 // protein binding
// inferred from electronic annotation
205229_s_at•gb:AA669336 /DB_XREF=gi:2630835 /DB_XREF=ad47a02.s1
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/UG=Hs.21016 /LL=1690 /UG_GENE=COCH /UG_TITLE=coagulation factor C (Limulus
polyphemus) homology (cochlin) /FL=gb:NM_004086.1
g•6.665126078•5.286138451•"coagulation factor C homolog, cochlin (Limulus
polyphemus)"•COCH•Hs.21016•ENSG00000100473•7605 // perception of sound //
traceable author statement••
226408_at•gb:AA905942 /DB_XREF=gi:3041065 /DB_XREF=oj83b12.s1
/CLONE=IMAGE:1504895 /FEA=EST /CNT=46 /TID=Hs.153053.1 /TIER=Stack /STK=29
/UG=Hs.153053 /LL=951 /UG_GENE=CD37 /UG_TITLE=CD37
antigen•6.4173292•7.32604182•TEA domain family member
2•TEAD2•Hs.515534•ENSG00000074219•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 6355 // regulation of
transcription, DNA-dependent // non-traceable author statement"•5634 //
nucleus // inferred from electronic annotation /// 5634 // nucleus //
non-traceable author statement•3700 // transcription factor activity //
inferred from electronic annotation /// 3700 // transcription factor activity
// non-traceable author statement
212488_at•"gb:N30339 /DB_XREF=gi:1148859 /DB_XREF=yw75f06.s1
/CLONE=IMAGE:258083 /FEA=EST /CNT=164 /TID=Hs.146428.2 /TIER=Stack /STK=53
/UG=Hs.146428 /LL=1289 /UG_GENE=COL5A1 /UG_TITLE=collagen, type V, alpha
1"•6.403080019•14.91145881•"collagen, type V, alpha
1"•COL5A1•Hs.210283•ENSG00000130635•6817 // phosphate transport // inferred
from electronic annotation /// 7155 // cell adhesion // inferred from
electronic annotation•5581 // collagen // inferred from electronic annotation
/// 5588 // collagen type V // traceable author statement /// 5737 //
cytoplasm // inferred from electronic annotation•5201 // extracellular matrix
structural constituent // inferred from electronic annotation /// 8201 //
heparin binding // inferred from electronic annotation
226103_at•gb:AF114264.1 /DB_XREF=gi:4768674 /FEA=mRNA /CNT=107
/TID=Hs.216381.0 /TIER=Stack /STK=15 /UG=Hs.216381 /DEF=Homo sapiens clone
HH409 unknown mRNA. /PROD=unknown•6.281844•6.002869581•nexilin (F actin
binding protein)•NEXN•Hs.22370•ENSG00000162614•••
228716_at•gb:BG494007 /DB_XREF=gi:13455521 /DB_XREF=602542289F1
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/UG=Hs.203213 /UG_TITLE=ESTs•6.222918909•13.21065271•Hypothetical gene
supported by AK096885; AK098084••Hs.551610••••
226701_at•gb:AI692880 /DB_XREF=gi:4970220 /DB_XREF=wd42d02.x1
/CLONE=IMAGE:2330787 /FEA=EST /CNT=66 /TID=Hs.7473.0 /TIER=Stack /STK=27
/UG=Hs.7473 /UG_TITLE=ESTs•6.12832212•5.830934948•"gap junction protein,
alpha 5, 40kDa (connexin 40)"•GJA5•Hs.447968•ENSG00000143140•6810 //
transport // non-traceable author statement /// 6936 // muscle contraction //
traceable author statement /// 7043 // intercellular junction assembly //
traceable author statement /// 7154 // cell communication // inferred from
electronic annotatio•5922 // connexon complex // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from electronic
annotation•15285 // connexon channel activity // traceable author statement
59705_at•"Cluster Incl. AA911739:oi15f09.s1 Homo sapiens cDNA, 3  end
/clone=IMAGE-1476617 /clone_end=3  /gb=AA911739 /gi=3051103 /ug=Hs.21421
/len=1049"•6.042521229•5.84955926•selenocysteine
lyase•SCLY•Hs.512606•ENSG00000132330•6520 // amino acid metabolism //
traceable author statement /// 8152 // metabolism // inferred from electronic
annotation•5829 // cytosol // traceable author statement•8483 // transaminase
activity // inferred from electronic annotation /// 9000 // selenocysteine
lyase activity // traceable author statement /// 16740 // transferase
activity // inferred from electronic annotation /// 16829 // lyase activity
// inferred f
242363_at•gb:BF592008 /DB_XREF=gi:11684332 /DB_XREF=7o35e09.x1
/CLONE=IMAGE:3576280 /FEA=EST /CNT=6 /TID=Hs.87372.1 /TIER=ConsEnd /STK=1
/UG=Hs.87372 /UG_TITLE=ESTs•5.757388088•5.884397428•"Dynein, cytoplasmic,
intermediate polypeptide 2"•DNCI2•Hs.546250•ENSG00000077380•7018 //
microtubule-based movement // non-traceable author statement•5737 //
cytoplasm // non-traceable author statement /// 30286 // dynein complex //
inferred from electronic annotation•3777 // microtubule motor activity //
non-traceable author statement
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mRNA for KIAA1399 protein, partial cds. /PROD=KIAA1399
protein"•5.754819615•10.20200617•membrane-associated ring finger (C3HC4)
4•38780•Hs.170388•ENSG00000144583•16567 // protein ubiquitination // inferred
from electronic annotation•151 // ubiquitin ligase complex // inferred from
electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•4842 // ubiquitin-protein ligase activity // inferred
from electronic annotation /// 8270 // zinc ion binding // inferred from
```

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electronic annotation
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/CLONE=IMAGE:1709688 /FEA=FLmRNA /CNT=102 /TID=Hs.146428.0 /TIER=Stack
/STK=37 /UG=Hs.146428 /LL=1289 /UG_GENE=COL5A1 /UG_TITLE=collagen, type V,
alpha 1 /FL=gb:D90279.1 gb:NM_000093.1
gb:M76729.1"•5.647754005•6.954854734•"collagen, type V, alpha
1"•COL5A1•Hs.210283•ENSG00000130635•6817 // phosphate transport // inferred
from electronic annotation /// 7155 // cell adhesion // inferred from
electronic annotation•5581 // collagen // inferred from electronic annotation
/// 5588 // collagen type V // traceable author statement /// 5737 //
cytoplasm // inferred from electronic annotation•5201 // extracellular matrix
structural constituent // inferred from electronic annotation /// 8201 //
heparin binding // inferred from electronic annotation
230033_at•gb:BF436398 /DB_XREF=gi:11448713 /DB_XREF=7p10d03.x1
/CLONE=IMAGE:3645364 /FEA=EST /CNT=19 /TID=Hs.120036.0 /TIER=Stack /STK=16
/UG=Hs.120036 /UG_TITLE=ESTs•5.428847032•11.65718855•similar to hypothetical
testis protein from macaque•LOC352909•Hs.351582•ENSG00000167646•••
203438_at•gb:AI435828 /DB_XREF=gi:4305913 /DB_XREF=th79e05.x1
/CLONE=IMAGE:2124896 /FEA=FLmRNA /CNT=109 /TID=Hs.155223.0 /TIER=Stack
/STK=18 /UG=Hs.155223 /LL=8614 /UG_GENE=STC2 /UG_TITLE=stanniocalcin 2
/FL=gb:AF098462.1 gb:AF031036.1 gb:NM_003714.1 gb:BC000658.1
•5.403475213•5.783847195•stanniocalcin 2•STC2•Hs.233160•ENSG00000113739•7166
// cell surface receptor linked signal transduction // traceable author
statement /// 7267 // cell-cell signaling // traceable author statement ///
7584 // response to nutrients // traceable author statement•5576 //
extracellular region // inferred from electronic annotation•5179 // hormone
activity // traceable author statement
231921_at•"gb:AK021599.1 /DB_XREF=gi:10432811 /FEA=mRNA /CNT=20
/TID=Hs.278337.0 /TIER=ConsEnd /STK=0 /UG=Hs.278337 /UG_TITLE=Homo sapiens
cDNA FLJ11537 fis, clone HEMBA1002742 /DEF=Homo sapiens cDNA FLJ11537 fis,
clone HEMBA1002742."•5.218415363•6.258205939•hypothetical protein
FLJ13096•FLJ13096•Hs.413518•ENSG00000115827•••
212489_at•"gb:AI983428 /DB_XREF=gi:5810647 /DB_XREF=wt49a04.x1
/CLONE=IMAGE:2510766 /FEA=EST /CNT=164 /TID=Hs.146428.2 /TIER=Stack /STK=33
/UG=Hs.146428 /LL=1289 /UG_GENE=COL5A1 /UG_TITLE=collagen, type V, alpha
1"•4.884225072•9.022496386•"collagen, type V, alpha
1"•COL5A1•Hs.210283•ENSG00000130635•6817 // phosphate transport // inferred
from electronic annotation /// 7155 // cell adhesion // inferred from
electronic annotation•5581 // collagen // inferred from electronic annotation
/// 5588 // collagen type V // traceable author statement /// 5737 //
cytoplasm // inferred from electronic annotation•5201 // extracellular matrix
structural constituent // inferred from electronic annotation /// 8201 //
heparin binding // inferred from electronic annotation
236609_at•gb:BF062287 /DB_XREF=gi:10821185 /DB_XREF=7k76b01.x1
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/UG=Hs.47660 /UG_TITLE=ESTs•4.461115799•2.430322081•PMS1 postmeiotic
segregation increased 1 (S. cerevisiae)•PMS1•Hs.111749•ENSG00000064933•"6298
// mismatch repair // traceable author statement /// 6355 // regulation of
transcription, DNA-dependent // inferred from electronic annotation /// 7049
// cell cycle // inferred from electronic annotation /// 45786 // negative
regulation of cell cycl"•5634 // nucleus // inferred from electronic
annotation /// 5634 // nucleus // traceable author statement /// 19866 //
inner membrane // inferred from electronic annotation•3677 // DNA binding //
traceable author statement /// 5524 // ATP binding // inferred from
electronic annotation
204468_s_at•"gb:NM_005424.1 /DB_XREF=gi:4885630 /GEN=TIE /FEA=FLmRNA /CNT=77
/TID=Hs.78824.0 /TIER=FL+Stack /STK=32 /UG=Hs.78824 /LL=7075 /DEF=Homo
sapiens tyrosine kinase with immunoglobulin and epidermal growth factor
homology domains (TIE), mRNA. /PROD=tyrosine
kin"•4.396206123•17.44242743•tyrosine kinase with immunoglobulin-like and
EGF-like domains 1•TIE1•Hs.78824•ENSG00000066056•6468 // protein amino acid
phosphorylation // inferred from electronic annotation /// 7165 // signal
transduction // traceable author statement /// 7498 // mesoderm development
// traceable author statement•5887 // integral to plasma membrane //
traceable author statement•4714 // transmembrane receptor protein tyrosine
kinase activity // traceable author statement /// 4872 // receptor activity
// inferred from electronic annotation /// 5524 // ATP binding // inferred
from electronic annotation /// 16740 // transferase acti
209318_x_at•gb:BG547855 /DB_XREF=gi:13546520 /DB_XREF=602576153F1
/CLONE=IMAGE:4704108 /FEA=FLmRNA /CNT=143 /TID=Hs.75825.2 /TIER=Stack /STK=24
/UG=Hs.75825 /LL=5325 /UG_GENE=PLAGL1 /UG_TITLE=pleiomorphic adenoma
gene-like 1 /FL=gb:U72621.3•4.347391258•13.8101903•pleiomorphic adenoma
gene-like 1•PLAGL1•Hs.444975•ENSG00000118495•"6350 // transcription //
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6917 // induction of
apoptosis // traceable author statement /// 7050 // cell cycle arrest //
tr"•5634 // nucleus // inferred from electronic annotation•3676 // nucleic
acid binding // inferred from electronic annotation /// 3677 // DNA binding
// inferred from electronic annotation /// 8270 // zinc ion binding //
inferred from electronic annotation
239195_at•gb:BF791698 /DB_XREF=gi:12096752 /DB_XREF=602251863F1
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/CLONE=IMAGE:4344375 /FEA=EST /CNT=7 /TID=Hs.318446.0 /TIER=ConsEnd /STK=1
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207002_s_at•"gb:NM_002656.1 /DB_XREF=gi:4505856 /GEN=PLAGL1 /FEA=FLmRNA
/CNT=7 /TID=Hs.75825.1 /TIER=FL /STK=0 /UG=Hs.75825 /LL=5325 /DEF=Homo
sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 1,
mRNA. /PROD=pleiomorphic adenoma gene-like 1
isoform"•4.208397994•2.004847822•pleiomorphic adenoma gene-like
1•PLAGL1•Hs.444975•ENSG00000118495•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 6917 // induction of apoptosis //
traceable author statement /// 7050 // cell cycle arrest // tr"•5634 //
nucleus // inferred from electronic annotation•3676 // nucleic acid binding
// inferred from electronic annotation /// 3677 // DNA binding // inferred
from electronic annotation /// 8270 // zinc ion binding // inferred from
electronic annotation
229349_at•gb:AL039884 /DB_XREF=gi:5866718 /DB_XREF=DKFZp434F0512_s1
/CLONE=DKFZp434F0512 /FEA=EST /CNT=36 /TID=Hs.23616.0 /TIER=Stack /STK=16
/UG=Hs.23616 /UG_TITLE=ESTs•4.136002004•7.691544971•FLJ16517
protein•FLJ16517•Hs.23616•ENSG00000187772•"6355 // regulation of
transcription, DNA-dependent // inferred from electronic annotation"••3677 //
DNA binding // inferred from electronic annotation
236987_at•gb:AI741514 /DB_XREF=gi:5109802 /DB_XREF=wg21b12.x1
/CLONE=IMAGE:2365727 /FEA=EST /CNT=6 /TID=Hs.24176.0 /TIER=ConsEnd /STK=6
/UG=Hs.24176 /UG_TITLE=ESTs•4.110533671•5.45150907•••••••
1555976_s_at•"gb:BU676221 /DB_XREF=gi:23521013
/DB_XREF=UI-CF-DU1-aao-n-04-0-UI.s1 /CLONE=UI-CF-DU1-aao-n-04-0-UI
/TID=Hs2.311412.1 /CNT=16 /FEA=mRNA /TIER=Stack /STK=9 /UG=Hs.311412
/UG_TITLE=Homo sapiens cDNA FLJ33153 fis, clone
UTERU2000332."•4.110218085•2.568011047•LOC440476••Hs.233936••••
1564166_s_at•"gb:AK098276.1 /DB_XREF=gi:21758257 /TID=Hs2.424660.1 /CNT=1
/FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.424660 /UG_TITLE=Homo sapiens cDNA
FLJ40957 fis, clone UTERU2011574, moderately similar to Human PMS2 related
(hPMSR3) gene. /DEF=Homo sapiens cDNA FLJ40957 "•4.107661964•5.645290257•PRKR
interacting protein 1 (IL11 inducible)•PRKRIP1•Hs.406395•ENSG00000128563•••
208782_at•"gb:BC000055.1 /DB_XREF=gi:12652618 /FEA=FLmRNA /CNT=480
/TID=Hs.296267.1 /TIER=FL+Stack /STK=198 /UG=Hs.296267 /LL=11167
/UG_GENE=FSTL1 /DEF=Homo sapiens, follistatin-like 1, clone MGC:1993, mRNA,
complete cds. /PROD=follistatin-like 1 /FL=gb:U06863.1
gb:"•4.078761079•4.958399037•follistatin-like
1•FSTL1•Hs.269512•ENSG00000163430••5615 // extracellular space // traceable
author statement•5509 // calcium ion binding // inferred from electronic
annotation /// 8201 // heparin binding // traceable author statement
204265_s_at•"gb:NM_022107.1 /DB_XREF=gi:11545816 /GEN=G18.2 /FEA=FLmRNA
/CNT=61 /TID=Hs.288316.0 /TIER=FL+Stack /STK=31 /UG=Hs.288316 /LL=63940
/DEF=Homo sapiens G18.2 protein (G18.2), mRNA. /PROD=G18.2 protein
/FL=gb:NM_022107.1 gb:AF155657.1"•4.011715502•3.681434311•"G-protein
signalling modulator 3 (AGS3-like, C. elegans)"•GPSM3•Hs.520046••6955 //
immune response // non-traceable author statement /// 7165 // signal
transduction // inferred from electronic annotation••5096 // GTPase activator
activity // inferred from electronic annotation
211709_s_at•"gb:BC005810.1 /DB_XREF=gi:13543291 /FEA=FLmRNA /CNT=1
/TID=HsAffx.900692.678 /TIER=FL /STK=0 /DEF=Homo sapiens, stem cell growth
factor; lymphocyte secreted C-type lectin, clone MGC:10378, mRNA, complete
cds. /PROD=stem cell growth factor; lymphocyte
secr"•3.936231097•3.519331679•"C-type lectin domain family 11, member A ///
C-type lectin domain family 11, member
A"•CLEC11A•Hs.512680•ENSG00000105472•8284 // positive regulation of cell
proliferation // inferred from direct assay•5576 // extracellular region //
inferred from direct assay•3676 // nucleic acid binding // inferred from
electronic annotation /// 5529 // sugar binding // non-traceable author
statement /// 8083 // growth factor activity // inferred from direct assay
228850_s_at•gb:AI963304 /DB_XREF=gi:5756017 /DB_XREF=wt61d01.x1
/CLONE=IMAGE:2511937 /FEA=EST /CNT=18 /TID=Hs.110373.0 /TIER=Stack /STK=13
/UG=Hs.110373 /UG_TITLE=ESTs•3.888345286•2.751804597•••••••
204915_s_at•"gb:AB028641.1 /DB_XREF=gi:6527111 /GEN=sox11 /FEA=FLmRNA /CNT=71
/TID=Hs.32964.0 /TIER=FL+Stack /STK=12 /UG=Hs.32964 /LL=6664 /DEF=Homo
sapiens mRNA for SOX11, complete cds. /PROD=SOX11 /FL=gb:AB028641.1
gb:NM_003108.1 gb:U23752.1"•3.850466418•4.098805472•SRY (sex determining
region Y)-box 11•SOX11•Hs.432638•ENSG00000176887•"6350 // transcription //
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 7399 // neurogenesis
// traceable author statement"•5634 // nucleus // inferred from electronic
annotation•3677 // DNA binding // inferred from electronic annotation
1556429_a_at•"gb:BC026969.1 /DB_XREF=gi:20071617 /TID=Hs2.170268.1 /CNT=7
/FEA=mRNA /TIER=ConsEnd /STK=3 /UG=Hs.170268 /UG_TITLE=Homo sapiens, clone
IMAGE:5116073, mRNA, partial cds /DEF=Homo sapiens, clone IMAGE:5116073,
mRNA, partial cds."•3.792604164•3.678367161•unknown MGC21654
product•MGC21654•Hs.492716•ENSG00000156787•••
220007_at•"gb:NM_024770.1 /DB_XREF=gi:13376116 /GEN=FLJ13984 /FEA=FLmRNA
/CNT=12 /TID=Hs.135146.0 /TIER=FL /STK=1 /UG=Hs.135146 /LL=79828 /DEF=Homo
sapiens hypothetical protein FLJ13984 (FLJ13984), mRNA. /PROD=hypothetical
```

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protein FLJ13984 /FL=gb:NM_024770.1"•3.731525461•2.546563772•hypothetical
protein FLJ13984•FLJ13984•Hs.135146•ENSG00000123600•••
221586_s_at•"gb:U15642.1 /DB_XREF=gi:758415 /FEA=FLmRNA /CNT=51
/TID=Hs.2331.0 /TIER=FL /STK=0 /UG=Hs.2331 /LL=1875 /UG_GENE=E2F5 /DEF=Human
transcription factor E2F-5 mRNA, complete cds. /PROD=E2F-5 /FL=gb:U15642.1
gb:NM_001951.2 gb:U31556.1"•3.719645472•3.914098684•"E2F transcription factor
5, p130-binding"•E2F5•Hs.445758•ENSG00000133740•"74 // regulation of cell
cycle // traceable author statement /// 6350 // transcription // inferred
from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation"•5634 // nucleus //
inferred from electronic annotation /// 5667 // transcription factor complex
// inferred from electronic annotation•3700 // transcription factor activity
// non-traceable author statement /// 5515 // protein binding // traceable
author statement
238520_at•gb:BF724270 /DB_XREF=gi:12040179 /DB_XREF=bx02h06.x1 /CLONE=bx02h06
/FEA=EST /CNT=11 /TID=Hs.123364.0 /TIER=ConsEnd /STK=1 /UG=Hs.123364
/UG_TITLE=ESTs•3.682669551•2.65589233•Transcriptional regulating factor
1•TRERF1•Hs.485392•ENSG00000124496•"6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6694 // steroid
biosynthesis // non-traceable author statement /// 6707 // cholesterol
catabolism // non-traceable author statement /// 7275 // development //
no"•5634 // nucleus // inferred from direct assay /// 5634 // nucleus //
inferred from electronic annotation•3677 // DNA binding // inferred from
electronic annotation /// 3700 // transcription factor activity // inferred
from direct assay /// 8134 // transcription factor binding // inferred from
physical interaction /// 8270 // zinc ion binding // inferred from
228158_at•gb:AI623211 /DB_XREF=gi:4648136 /DB_XREF=ts78e11.x1
/CLONE=IMAGE:2237420 /FEA=EST /CNT=24 /TID=Hs.56729.3 /TIER=Stack /STK=17
/UG=Hs.56729 /LL=4046 /UG_GENE=LSP1 /UG_TITLE=lymphocyte-specific protein
1•3.67743156•3.220717838•similar to D(1B) dopamine receptor (D(5) dopamine
receptor) (D1beta dopamine receptor)•LOC440684•Hs.456465••7186 // G-protein
coupled receptor protein signaling pathway // inferred from electronic
annotation•16021 // integral to membrane // inferred from electronic
annotation•1584 // rhodopsin-like receptor activity // inferred from
electronic annotation /// 4872 // receptor activity // inferred from
electronic annotation /// 4952 // dopamine receptor activity // inferred from
electronic annotation
213558_at•"gb:AB011131.1 /DB_XREF=gi:3043641 /GEN=KIAA0559 /FEA=mRNA /CNT=37
/TID=Hs.12376.1 /TIER=Stack /STK=8 /UG=Hs.12376 /LL=27445 /DEF=Homo sapiens
mRNA for KIAA0559 protein, partial cds. /PROD=KIAA0559
protein"•3.604456718•3.339010098•piccolo (presynaptic cytomatrix
protein)•PCLO•Hs.12376••6810 // transport // inferred from electronic
annotation /// 7010 // cytoskeleton organization and biogenesis // inferred
from sequence or structural similarity /// 16080 // synaptic vesicle
targeting // inferred from sequence or structural similarity•5856 //
cytoskeleton // non-traceable author statement /// 8021 // synaptic vesicle
// inferred from electronic annotation /// 16020 // membrane // inferred from
electronic annotation /// 45202 // synapse // inferred from sequence or
structural similarity•5198 // structural molecule activity // inferred from
electronic annotation /// 5215 // transporter activity // inferred from
electronic annotation /// 5509 // calcium ion binding // inferred from
sequence or structural similarity /// 5522 // profilin bin
204913_s_at•gb:AI360875 /DB_XREF=gi:4112496 /DB_XREF=qy01c03.x1
/CLONE=IMAGE:2010724 /FEA=FLmRNA /CNT=71 /TID=Hs.32964.0 /TIER=Stack /STK=12
/UG=Hs.32964 /LL=6664 /UG_GENE=SOX11 /UG_TITLE=SRY (sex determining region
Y)-box 11 /FL=gb:AB028641.1 gb:NM_003108.1
gb:U2375•3.598921652•4.84068802•SRY (sex determining region Y)-box
11•SOX11•Hs.432638•ENSG00000176887•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 7399 // neurogenesis // traceable
author statement"•5634 // nucleus // inferred from electronic annotation•3677
// DNA binding // inferred from electronic annotation
241682_at•"gb:BE873351 /DB_XREF=gi:10322127 /DB_XREF=601450410F1
/CLONE=IMAGE:3854163 /FEA=EST /CNT=8 /TID=Hs.171443.0 /TIER=ConsEnd /STK=0
/UG=Hs.171443 /UG_TITLE=ESTs, Weakly similar to actin binding protein MAYVEN
(H.sapiens)"•3.587757439•3.996615106•hypothetical protein
MGC2610•MGC2610•Hs.470549•ENSG00000144362•••5515 // protein binding //
inferred from electronic annotation
226429_at•gb:BE218238 /DB_XREF=gi:8905556 /DB_XREF=hv36a10.x1
/CLONE=IMAGE:3175482 /FEA=mRNA /CNT=50 /TID=Hs.283709.3 /TIER=Stack /STK=9
/UG=Hs.283709 /LL=55425 /UG_GENE=LSR7 /UG_TITLE=lipopolysaccharide specific
response-7
protein•3.499351417•5.027113126•KIAA1704•KIAA1704•Hs.507922•ENSG00000133114•••
229657_at•gb:BF431989 /DB_XREF=gi:11444103 /DB_XREF=nab84a05.x1
/CLONE=IMAGE:3274280 /FEA=EST /CNT=15 /TID=Hs.203213.1 /TIER=Stack /STK=12
/UG=Hs.203213 /UG_TITLE=ESTs•3.489655869•2.67109826•Hypothetical gene
supported by AK096885; AK098084••Hs.551610••••
204914_s_at•gb:AW157202 /DB_XREF=gi:6228603 /DB_XREF=au92g06.x1
/CLONE=IMAGE:2783770 /FEA=FLmRNA /CNT=71 /TID=Hs.32964.0 /TIER=Stack /STK=8
/UG=Hs.32964 /LL=6664 /UG_GENE=SOX11 /UG_TITLE=SRY (sex determining region
Y)-box 11 /FL=gb:AB028641.1 gb:NM_003108.1
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gb:U23752•3.461887423•4.328038868•SRY (sex determining region Y)-box
11•SOX11•Hs.432638•ENSG00000176887•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 7399 // neurogenesis // traceable
author statement"•5634 // nucleus // inferred from electronic annotation•3677
// DNA binding // inferred from electronic annotation
226982_at•"gb:AI745624 /DB_XREF=gi:5113912 /DB_XREF=wc33h03.x1
/CLONE=IMAGE:2317013 /FEA=EST /CNT=41 /TID=Hs.173334.0 /TIER=Stack /STK=25
/UG=Hs.173334 /LL=22936 /UG_GENE=ELL2 /UG_TITLE=ELL-RELATED RNA POLYMERASE
II, ELONGATION FACTOR"•3.448554128•5.862095008•"Elongation factor, RNA
polymerase II, 2"•ELL2•Hs.192221•ENSG00000118985•"6350 // transcription //
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6368 // RNA
elongation from RNA polymerase II promoter // traceable author
statement"•5634 // nucleus // inferred from electronic annotation /// 8023 //
transcription elongation factor complex // traceable author statement•3702 //
RNA polymerase II transcription factor activity // traceable author
statement
225897_at•"gb:AI709406 /DB_XREF=gi:4999182 /DB_XREF=as37d05.x1
/CLONE=IMAGE:2319369 /FEA=mRNA /CNT=71 /TID=Hs.330716.0 /TIER=Stack /STK=9
/UG=Hs.330716 /UG_TITLE=Homo sapiens mRNA, 3UTR, up-regulated by
BCG-CWS"•3.432744271•3.202863545•Myristoylated alanine-rich protein kinase C
substrate•MARCKS•Hs.519909•ENSG00000155130•6928 // cell motility // not
recorded•5886 // plasma membrane // not recorded /// 15629 // actin
cytoskeleton // traceable author statement•5516 // calmodulin binding //
traceable author statement /// 51015 // actin filament binding // traceable
author statement
226611_s_at•gb:AA722878 /DB_XREF=gi:2740585 /DB_XREF=zg89f10.s1
/CLONE=IMAGE:409771 /FEA=EST /CNT=47 /TID=Hs.326184.0 /TIER=Stack /STK=27
/UG=Hs.326184 /UG_TITLE=ESTs•3.400473388•3.009376866•proline rich
6•PRR6•Hs.433422•ENSG00000166582•8152 // metabolism // inferred from
electronic annotation••16846 // carbon-sulfur lyase activity // inferred from
electronic annotation
237411_at•gb:N71063 /DB_XREF=gi:1227643 /DB_XREF=za86a11.s1
/CLONE=IMAGE:299420 /FEA=EST /CNT=5 /TID=Hs.38173.0 /TIER=ConsEnd /STK=5
/UG=Hs.38173 /UG_TITLE=ESTs•3.390882319•8.659032723•"a disintegrin-like and
metalloprotease (reprolysin type) with thrombospondin type 1 motif,
6"•ADAMTS6•Hs.344757•ENSG00000049192•6508 // proteolysis and peptidolysis //
inferred from electronic annotation•5578 // extracellular matrix (sensu
Metazoa) // inferred from electronic annotation /// 31012 // extracellular
matrix // inferred from electronic annotation•4222 // metalloendopeptidase
activity // inferred from electronic annotation /// 8233 // peptidase
activity // inferred from electronic annotation /// 8270 // zinc ion binding
// inferred from electronic annotation
226610_at•gb:AA722878 /DB_XREF=gi:2740585 /DB_XREF=zg89f10.s1
/CLONE=IMAGE:409771 /FEA=EST /CNT=47 /TID=Hs.326184.0 /TIER=Stack /STK=27
/UG=Hs.326184 /UG_TITLE=ESTs•3.383031406•2.085314982•proline rich
6•PRR6•Hs.433422•ENSG00000166582•8152 // metabolism // inferred from
electronic annotation••16846 // carbon-sulfur lyase activity // inferred from
electronic annotation
227399_at•gb:AI754423 /DB_XREF=gi:5132687 /DB_XREF=cr25b07.x1
/CLONE=HBMSC_cr25b07 /FEA=EST /CNT=67 /TID=Hs.30343.0 /TIER=Stack /STK=23
/UG=Hs.30343 /UG_TITLE=ESTs•3.3225196•6.276333749•vestigial-like
3•VGL-3•Hs.435013••45449 // regulation of transcription // inferred from
electronic annotation•5634 // nucleus // inferred from electronic
annotation•30528 // transcription regulator activity // inferred from
electronic annotation
209604_s_at•"gb:BC003070.1 /DB_XREF=gi:13111765 /FEA=FLmRNA /CNT=105
/TID=Hs.169946.0 /TIER=FL /STK=0 /UG=Hs.169946 /LL=2625 /UG_GENE=GATA3
/DEF=Homo sapiens, GATA-binding protein 3, clone MGC:2346, mRNA, complete
cds. /PROD=GATA-binding protein 3 /FL=gb:NM_002051.1
g"•3.294185372•13.52594972•GATA binding protein
3•GATA3•Hs.524134•ENSG00000107485•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 6366 // transcription from RNA
polymerase II promoter // traceable author statement /// 6952 // "•5634 //
nucleus // inferred from electronic annotation•3700 // transcription factor
activity // traceable author statement
242828_at•gb:BG109695 /DB_XREF=gi:12603201 /DB_XREF=602280828F1
/CLONE=IMAGE:4368415 /FEA=EST /CNT=5 /TID=Hs.170999.0 /TIER=ConsEnd /STK=0
/UG=Hs.170999
/UG_TITLE=ESTs•3.280115561•3.090523309•Fidgetin•FIGN•Hs.170999•ENSG00000182263
•6457 // protein folding // inferred from electronic annotation•5739 //
mitochondrion // inferred from electronic annotation•166 // nucleotide
binding // inferred from electronic annotation /// 5524 // ATP binding //
inferred from electronic annotation /// 17111 // nucleoside-triphosphatase
activity // inferred from electronic annotation /// 51082 // unfolded protein
binding //
227828_s_at•gb:AV700753 /DB_XREF=gi:10302724 /DB_XREF=AV700753
/CLONE=GKCBZE06 /FEA=mRNA /CNT=42 /TID=Hs.75576.1 /TIER=Stack /STK=18
/UG=Hs.75576 /LL=5340 /UG_GENE=PLG
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/UG_TITLE=plasminogen•3.255977507•3.40355209•hypothetical protein
FLJ13391•FLJ13391•Hs.549210•ENSG00000115363•••
208998_at•"gb:U94592.1 /DB_XREF=gi:2052354 /GEN=UCPH /FEA=FLmRNA /CNT=226
/TID=Hs.80658.0 /TIER=FL /STK=1 /UG=Hs.80658 /LL=7351 /DEF=Human uncoupling
protein homolog (UCPH) mRNA, complete cds. /PROD=uncoupling protein homolog
/FL=gb:U76367.1 gb:U82819.1 gb:U94592.1 "•3.239466043•2.950002776•"uncoupling
protein 2 (mitochondrial, proton carrier)"•UCP2•Hs.80658•ENSG00000175567•6810
// transport // non-traceable author statement /// 6839 // mitochondrial
transport // inferred from electronic annotation /// 15992 // proton
transport // traceable author statement•5624 // membrane fraction // not
recorded /// 5739 // mitochondrion // inferred from electronic annotation ///
5743 // mitochondrial inner membrane // non-traceable author statement ///
16021 // integral to membrane // inferred from electronic annotation•5215 //
transporter activity // inferred from electronic annotation /// 5488 //
binding // inferred from electronic annotation
209156_s_at•"gb:AY029208.1 /DB_XREF=gi:13603393 /GEN=COL6A2 /FEA=FLmRNA
/CNT=294 /TID=Hs.159263.1 /TIER=FL+Stack /STK=223 /UG=Hs.159263 /LL=1292
/DEF=Homo sapiens type VI collagen alpha 2 chain precursor (COL6A2) mRNA,
complete cds, alternatively spliced. /PROD=type
V"•3.232952315•7.275632454•"collagen, type VI, alpha
2"•COL6A2•Hs.420269•ENSG00000142173•6817 // phosphate transport // inferred
from electronic annotation /// 16337 // cell-cell adhesion // non-traceable
author statement /// 30198 // extracellular matrix organization and
biogenesis // non-traceable author statement•5581 // collagen // inferred
from electronic annotation /// 5737 // cytoplasm // inferred from electronic
annotation•"5201 // extracellular matrix structural constituent //
non-traceable author statement /// 30674 // protein binding, bridging //
non-traceable author statement"
223791_at•"gb:BC002886.1 /DB_XREF=gi:12804066 /FEA=FLmRNA /CNT=12
/TID=Hs.191817.0 /TIER=FL /STK=7 /UG=Hs.191817 /DEF=Homo sapiens, clone
MGC:11241, mRNA, complete cds. /PROD=Unknown (protein for MGC:11241)
/FL=gb:BC002886.1"•3.198896814•2.418687642•Hypothetical gene supported by
AK131029; BC002886 /// Hypothetical gene supported by AK131029;
BC002886••Hs.455306 /// Hs.455316••••
212057_at•gb:AA206161 /DB_XREF=gi:1801720 /DB_XREF=zq55f01.s1
/CLONE=IMAGE:645529 /FEA=mRNA /CNT=291 /TID=Hs.75909.0 /TIER=Stack /STK=17
/UG=Hs.75909 /LL=23199 /UG_GENE=KIAA0182 /UG_TITLE=KIAA0182
protein•3.189229052•2.927669133•KIAA0182
protein•KIAA0182•Hs.461647•ENSG00000131149•••
201859_at•"gb:NM_002727.1 /DB_XREF=gi:4506044 /GEN=PRG1 /FEA=FLmRNA /CNT=337
/TID=Hs.1908.0 /TIER=FL+Stack /STK=97 /UG=Hs.1908 /LL=5552 /DEF=Homo sapiens
proteoglycan 1, secretory granule (PRG1), mRNA. /PROD=proteoglycan 1,
secretory granule /FL=gb:J03223.1
gb:NM_00"•3.160232569•2.837484849•"proteoglycan 1, secretory
granule"•PRG1•Hs.1908•ENSG00000122862•••
242979_at•gb:AI474666 /DB_XREF=gi:4327711 /DB_XREF=tm35e04.x1
/CLONE=IMAGE:2160126 /FEA=EST /CNT=5 /TID=Hs.257786.0 /TIER=ConsEnd /STK=2
/UG=Hs.257786 /UG_TITLE=ESTs•3.15621762•2.334431177•Transcribed
locus••Hs.257786••••
1555673_at•"gb:BC012486.1 /DB_XREF=gi:15214703 /TID=Hs2Affx.1.428 /CNT=1
/FEA=FLmRNA /TIER=FL /STK=1 /NOTE=sequence(s) not in UniGene /DEF=Homo
sapiens, clone MGC:21715 IMAGE:4472166, mRNA, complete cds. /PROD=Unknown
(protein for MGC:21715) /FL=gb:BC012486.1"•3.137401525•5.312916997•keratin
associated protein 2-1 /// keratin associated protein 2-4•KRTAP2-1 ///
KRTAP2-4•Hs.528921•ENSG00000196103 /// ENSG00000184928••45095 // keratin
filament // inferred from electronic annotation•
209946_at•"gb:U58111.1 /DB_XREF=gi:1373426 /FEA=FLmRNA /CNT=61
/TID=Hs.79141.0 /TIER=FL /STK=2 /UG=Hs.79141 /LL=7424 /UG_GENE=VEGFC
/DEF=Human FLT4 ligand mRNA, complete cds. /PROD=FLT4 ligand DHM
/FL=gb:NM_005429.1 gb:U43142.1 gb:U58111.1"•3.134866502•4.636488185•vascular
endothelial growth factor C•VEGFC•Hs.435215•ENSG00000150630•74 // regulation
of cell cycle // inferred from electronic annotation /// 1525 // angiogenesis
// inferred from electronic annotation /// 6929 // substrate-bound cell
migration // traceable author statement /// 7165 // signal transduction //
traceable aut•16020 // membrane // inferred from electronic annotation•8083
// growth factor activity // inferred from electronic annotation
221730_at•"gb:NM_000393.1 /DB_XREF=gi:4502958 /GEN=COL5A2 /FEA=FLmRNA
/CNT=405 /TID=Hs.82985.0 /TIER=FL+Stack /STK=45 /UG=Hs.82985 /LL=1290
/DEF=Homo sapiens collagen, type V, alpha 2 (COL5A2), mRNA. /PROD=collagen,
type V, alpha 2 /FL=gb:NM_000393.1"•3.130016476•2.819486983•"collagen, type
V, alpha 2"•COL5A2•Hs.445827••6817 // phosphate transport // inferred from
electronic annotation•5581 // collagen // inferred from electronic annotation
/// 5588 // collagen type V // traceable author statement /// 5737 //
cytoplasm // inferred from electronic annotation•5201 // extracellular matrix
structural constituent // not recorded
218880_at•gb:N36408 /DB_XREF=gi:1157550 /DB_XREF=yy33f03.s1
/CLONE=IMAGE:273053 /FEA=FLmRNA /CNT=53 /TID=Hs.325364.0 /TIER=Stack /STK=12
/UG=Hs.325364 /LL=79579 /UG_GENE=FLJ23306 /UG_TITLE=hypothetical protein
FLJ23306 /FL=gb:NM_024530.1•3.122846284•2.50537457•FOS-like antigen
2•FOSL2•Hs.220971•ENSG00000075426•6357 // regulation of transcription from
RNA polymerase II promoter // traceable author statement /// 8219 // cell
```

```
death // traceable author statement•5634 // nucleus // traceable author
statement•3700 // transcription factor activity // traceable author
statement
215933_s_at•gb:Z21533.1 /DB_XREF=gi:32068 /GEN=HEX /FEA=mRNA /CNT=2
/TID=Hs.118651.1 /TIER=ConsEnd /STK=0 /UG=Hs.118651 /LL=3087 /DEF=H.sapiens
HEX gene encoding homeobox related protein. /PROD=homeobox related
protein•3.102967533•4.379330831•hematopoietically expressed
homeobox•HHEX•Hs.118651•ENSG00000152804•"6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 7275 // development
// traceable author statement /// 19735 // antimicrobial humoral response
(sensu Vertebrata) // traceable author statement"•5634 // nucleus // inferred
from electronic annotation /// 5634 // nucleus // not recorded•3700 //
transcription factor activity // inferred from electronic annotation /// 3700
// transcription factor activity // traceable author statement
201792_at•"gb:NM_001129.2 /DB_XREF=gi:4755145 /GEN=AEBP1 /FEA=FLmRNA /CNT=208
/TID=Hs.118397.0 /TIER=FL+Stack /STK=78 /UG=Hs.118397 /LL=165 /DEF=Homo
sapiens AE-binding protein 1 (AEBP1), mRNA. /PROD=adipocyte enhancer binding
protein 1 precursor /FL=gb:AF053944.1 g"•3.091870165•3.305067656•AE binding
protein 1•AEBP1•Hs.439463•ENSG00000106624•1501 // skeletal development //
traceable author statement /// 6508 // proteolysis and peptidolysis //
inferred from electronic annotation /// 7155 // cell adhesion // inferred
from electronic annotation /// 7517 // muscle development // traceable author
•5737 // cytoplasm // not recorded•3700 // transcription factor activity //
traceable author statement /// 4180 // carboxypeptidase activity // traceable
author statement /// 4182 // carboxypeptidase A activity // inferred from
electronic annotation
31845_at•"Cluster Incl. U32645:Human myeloid elf-1 like factor (MEF) mRNA,
complete cds /cds=(382,2373) /gb=U32645 /gi=1761934 /ug=Hs.151139
/len=4167"•3.062837053•3.094320715•E74-like factor 4 (ets domain
transcription factor)•ELF4•Hs.271940•ENSG00000102034•"6355 // regulation of
transcription, DNA-dependent // non-traceable author statement /// 6357 //
regulation of transcription from RNA polymerase II promoter // inferred from
direct assay"•5634 // nucleus // inferred from electronic annotation /// 5634
// nucleus // non-traceable author statement /// 16605 // PML body //
inferred from direct assay•3700 // transcription factor activity // inferred
from electronic annotation /// 3700 // transcription factor activity //
non-traceable author statement /// 3713 // transcription coactivator activity
// traceable author statement /// 16563 // transcriptio
201466_s_at•"gb:NM_002228.2 /DB_XREF=gi:7710122 /GEN=JUN /FEA=FLmRNA /CNT=376
/TID=Hs.78465.0 /TIER=FL+Stack /STK=45 /UG=Hs.78465 /LL=3725 /DEF=Homo
sapiens v-jun avian sarcoma virus 17 oncogene homolog (JUN), mRNA.
/PROD=v-jun avian sarcoma virus 17 oncogene homolog
"•3.062721613•2.259279209•v-jun sarcoma virus 17 oncogene homolog
(avian)•JUN•Hs.525704•ENSG00000177606•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation"•228 // nuclear chromosome //
traceable author statement•3700 // transcription factor activity // traceable
author statement /// 3702 // RNA polymerase II transcription factor activity
// traceable author statement /// 8134 // transcription factor binding //
inferred from physical interaction
205122_at•gb:BF439316 /DB_XREF=gi:11451833 /DB_XREF=nab62g12.x1
/CLONE=IMAGE:3272638 /FEA=FLmRNA /CNT=65 /TID=Hs.78531.0 /TIER=Stack /STK=27
/UG=Hs.78531 /LL=8577 /UG_GENE=TMEFF1 /UG_TITLE=transmembrane protein with
EGF-like and two follistatin-like domains 1
/FL=g•3.01499751•5.539378111•transmembrane protein with EGF-like and two
follistatin-like domains 1•TMEFF1•Hs.336224•ENSG00000066697••16021 //
integral to membrane // inferred from electronic annotation•
219410_at•"gb:NM_018004.1 /DB_XREF=gi:8922242 /GEN=FLJ10134 /FEA=FLmRNA
/CNT=36 /TID=Hs.104800.0 /TIER=FL+Stack /STK=20 /UG=Hs.104800 /LL=55076
/DEF=Homo sapiens hypothetical protein FLJ10134 (FLJ10134), mRNA.
/PROD=hypothetical protein FLJ10134
/FL=gb:NM_018004.1"•2.948642219•3.089077777•transmembrane protein
45A•TMEM45A•Hs.126598•ENSG00000181458••16021 // integral to membrane //
inferred from electronic annotation•
236916_at•gb:AU151944 /DB_XREF=gi:11013465 /DB_XREF=AU151944
/CLONE=NT2RP2006434 /FEA=EST /CNT=6 /TID=Hs.13997.0 /TIER=ConsEnd /STK=5
/UG=Hs.13997 /UG_TITLE=ESTs•2.935480082•2.334211919•Transcribed
locus••Hs.13997••••
229404_at•"gb:AI086614 /DB_XREF=gi:3425037 /DB_XREF=oz76e09.x1
/CLONE=IMAGE:1681288 /FEA=EST /CNT=31 /TID=Hs.32366.0 /TIER=Stack /STK=8
/UG=Hs.32366 /UG_TITLE=ESTs, Highly similar to G01204 twist protein homolog
(H.sapiens)"•2.926777138•4.214082045•twist homolog 2
(Drosophila)•TWIST2•Hs.422585••6350 // transcription // inferred from
electronic annotation /// 30154 // cell differentiation // inferred from
electronic annotation /// 45668 // negative regulation of osteoblast
differentiation // inferred from direct assay /// 45892 // negative
regula•5634 // nucleus // inferred from direct assay /// 5737 // cytoplasm //
inferred from direct assay•3677 // DNA binding // inferred from electronic
annotation /// 16564 // transcriptional repressor activity // inferred from
sequence or structural similarity
212364_at•"gb:BF432550 /DB_XREF=gi:11444700 /DB_XREF=nac56e10.x1
```

```
/CLONE=IMAGE:3406555 /FEA=mRNA /CNT=213 /TID=Hs.121576.0 /TIER=Stack /STK=27
/UG=Hs.121576 /UG_TITLE=Homo sapiens cDNA FLJ20153 fis, clone COL08656,
highly similar to AJ001381 Homo sapiens incomplete
c"•2.92223405•3.096626406•myosin IB•MYO1B•Hs.439620•ENSG00000128641••16459 //
myosin // inferred from electronic annotation•3774 // motor activity //
inferred from electronic annotation /// 3779 // actin binding // inferred
from electronic annotation /// 5516 // calmodulin binding // inferred from
electronic annotation /// 5524 // ATP binding // inferred from electronic
annota
209875_s_at•"gb:M83248.1 /DB_XREF=gi:189150 /GEN=nephropontin /FEA=FLmRNA
/CNT=157 /TID=Hs.313.0 /TIER=FL /STK=0 /UG=Hs.313 /LL=6696 /DEF=Human
nephropontin mRNA, complete cds. /PROD=nephropontin
/FL=gb:M83248.1"•2.910671599•4.289451111•"secreted phosphoprotein 1
(osteopontin, bone sialoprotein I, early T-lymphocyte activation
1)"•SPP1•Hs.313•ENSG00000118785•1503 // ossification // inferred from
electronic annotation /// 1503 // ossification // traceable author statement
/// 6916 // anti-apoptosis // inferred from sequence or structural similarity
/// 7155 // cell adhesion // inferred from electronic annotati•5578 //
extracellular matrix (sensu Metazoa) // traceable author statement•5125 //
cytokine activity // inferred from sequence or structural similarity /// 5178
// integrin binding // non-traceable author statement /// 5515 // protein
binding // inferred from electronic annotation /// 8083 // growth factor
activity // traceable
1552309_a_at•"gb:NM_144573.1 /DB_XREF=gi:21389338 /GEN=nexilin
/TID=Hs2.216381.1 /CNT=24 /FEA=FLmRNA /TIER=FL+Stack /STK=8 /LL=91624
/UG=Hs.216381 /DEF=Homo sapiens likely ortholog of rat F-actin binding
protein nexilin (nexilin), mRNA. /PROD=likely ortholog of rat
F-a"•2.905285743•7.01404278•nexilin (F actin binding
protein)•NEXN•Hs.22370•ENSG00000162614•••
204823_at•"gb:NM_014903.1 /DB_XREF=gi:7662389 /GEN=KIAA0938 /FEA=FLmRNA
/CNT=57 /TID=Hs.174188.0 /TIER=FL+Stack /STK=20 /UG=Hs.174188 /LL=22840
/DEF=Homo sapiens KIAA0938 protein (KIAA0938), mRNA. /PROD=KIAA0938 protein
/FL=gb:AB023155.1 gb:NM_014903.1"•2.891980906•7.250994048•neuron navigator
3•NAV3•Hs.306322•ENSG00000067798••5739 // mitochondrion // inferred from
electronic annotation•166 // nucleotide binding // inferred from electronic
annotation /// 5524 // ATP binding // inferred from electronic annotation ///
17111 // nucleoside-triphosphatase activity // inferred from electronic
annotation
200790_at•gb:NM_002539.1 /DB_XREF=gi:4505488 /GEN=ODC1 /FEA=FLmRNA /CNT=464
/TID=Hs.75212.0 /TIER=FL+Stack /STK=132 /UG=Hs.75212 /LL=4953 /DEF=Homo
sapiens ornithine decarboxylase 1 (ODC1) mRNA. /PROD=ornithine decarboxylase
1 /FL=gb:NM_002539.1 gb:M16650.1•2.885516899•2.806448519•ornithine
decarboxylase 1•ODC1•Hs.467701•ENSG00000115758•6596 // polyamine biosynthesis
// non-traceable author statement••4586 // ornithine decarboxylase activity
// traceable author statement /// 16829 // lyase activity // inferred from
electronic annotation
204689_at•"gb:NM_001529.1 /DB_XREF=gi:10835016 /GEN=HHEX /FEA=FLmRNA /CNT=50
/TID=Hs.118651.0 /TIER=FL+Stack /STK=25 /UG=Hs.118651 /LL=3087 /DEF=Homo
sapiens hematopoietically expressed homeobox (HHEX), mRNA.
/PROD=hematopoietically expressed homeobox
/FL=gb:NM_0015"•2.882766955•3.396837896•hematopoietically expressed
homeobox•HHEX•Hs.118651•ENSG00000152804•"6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 7275 // development
// traceable author statement /// 19735 // antimicrobial humoral response
(sensu Vertebrata) // traceable author statement"•5634 // nucleus // inferred
from electronic annotation /// 5634 // nucleus // not recorded•3700 //
transcription factor activity // inferred from electronic annotation /// 3700
// transcription factor activity // traceable author statement
243514_at•gb:AI475902 /DB_XREF=gi:4328947 /DB_XREF=tc95f02.x1
/CLONE=IMAGE:2073915 /FEA=EST /CNT=5 /TID=Hs.143056.0 /TIER=ConsEnd /STK=1
/UG=Hs.143056 /UG_TITLE=ESTs•2.863185701•5.620230464••••••
204602_at•"gb:NM_012242.1 /DB_XREF=gi:7110718 /GEN=DKK1 /FEA=FLmRNA /CNT=108
/TID=Hs.40499.0 /TIER=FL /STK=0 /UG=Hs.40499 /LL=22943 /DEF=Homo sapiens
dickkopf (Xenopus laevis) homolog 1 (DKK1), mRNA. /PROD=dickkopf (Xenopus
laevis) homolog 1 /FL=gb:AF177394.1 gb:NM_"•2.861384986•2.873163864•dickkopf
homolog 1 (Xenopus laevis)•DKK1•Hs.40499•ENSG00000107984•7275 // development
// inferred from electronic annotation /// 16055 // Wnt receptor signaling
pathway // inferred from electronic annotation /// 30178 // negative
regulation of Wnt receptor signaling pathway // inferred from electronic
annotation•5576 // extracellular region // inferred from electronic
annotation•4871 // signal transducer activity // traceable author statement
/// 8083 // growth factor activity // traceable author statement
225095_at•gb:W81119 /DB_XREF=gi:1391618 /DB_XREF=zh49e09.s1
/CLONE=IMAGE:415432 /FEA=EST /CNT=115 /TID=Hs.315482.0 /TIER=Stack /STK=12
/UG=Hs.315482 /UG_TITLE=ESTs•2.846599813•2.146861753•"Serine
palmitoyltransferase, long chain base subunit
2"•SPTLC2•Hs.435661•ENSG00000100596•9058 // biosynthesis // inferred from
electronic annotation•5783 // endoplasmic reticulum // inferred from
electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•"4758 // serine C-palmitoyltransferase activity //
traceable author statement /// 8415 // acyltransferase activity // inferred
```

```
from electronic annotation /// 16769 // transferase activity, transferring
nitrogenous groups // inferred from electronic annotat"
225262_at•"gb:AI670862 /DB_XREF=gi:4850593 /DB_XREF=wa06b06.x1
/CLONE=IMAGE:2297267 /FEA=EST /CNT=74 /TID=Hs.5890.1 /TIER=Stack /STK=18
/UG=Hs.5890 /UG_TITLE=ESTs, Weakly similar to A49134 Ig kappa chain V-I
region (H.sapiens)"•2.832099821•4.854189153•FOS-like antigen
2•FOSL2•Hs.220971•ENSG00000075426•6357 // regulation of transcription from
RNA polymerase II promoter // traceable author statement /// 8219 // cell
death // traceable author statement•5634 // nucleus // traceable author
statement•3700 // transcription factor activity // traceable author
statement
235976_at•gb:AI680986 /DB_XREF=gi:4891168 /DB_XREF=tx43a12.x1
/CLONE=IMAGE:2272318 /FEA=EST /CNT=6 /TID=Hs.120910.0 /TIER=ConsEnd /STK=5
/UG=Hs.120910 /UG_TITLE=ESTs•2.827163064•2.304388409•"SLIT and NTRK-like
family, member 6"•SLITRK6•Hs.525105•ENSG00000184564••16021 // integral to
membrane // inferred from electronic annotation•
215011_at•"gb:AJ006835.1 /DB_XREF=gi:3236105 /FEA=mRNA /CNT=7
/TID=Hs.196769.0 /TIER=ConsEnd /STK=0 /UG=Hs.196769 /LL=8420 /UG_GENE=RNU17D
/UG_TITLE=RNA, U17D small nucleolar /DEF=Homo sapiens RNA transcript from U17
small nucleolar RNA host gene, variant
U17HG-AB."•2.805041138•3.185930243•"RNA, U17D small nucleolar"•RNU17D•••••
207325_x_at•"gb:NM_004988.1 /DB_XREF=gi:4826821 /GEN=MAGEA1 /FEA=FLmRNA
/CNT=6 /TID=Hs.72879.0 /TIER=FL /STK=1 /UG=Hs.72879 /LL=4100 /DEF=Homo
sapiens melanoma antigen, family A, 1 (directs expression of antigen MZ2-E)
(MAGEA1), mRNA. /PROD=melanoma antigen, family
A,"•2.77615688•2.776163583•"melanoma antigen family A, 1 (directs expression
of antigen MZ2-E)"•MAGEA1•Hs.72879•ENSG00000126977••5886 // plasma membrane
// traceable author statement•
220014_at•"gb:NM_016644.1 /DB_XREF=gi:7706193 /GEN=LOC51334 /FEA=FLmRNA
/CNT=15 /TID=Hs.157461.0 /TIER=FL /STK=3 /UG=Hs.157461 /LL=51334 /DEF=Homo
sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA.
/PROD=mesenchymal stem cell protein DSC54
/FL=gb:NM_01664"•2.769645263•2.439863893•mesenchymal stem cell protein
DSC54•LOC51334•Hs.157461•ENSG00000184838•••
225656_at•gb:AI564473 /DB_XREF=gi:4522930 /DB_XREF=tq57f12.x1
/CLONE=IMAGE:2212943 /FEA=mRNA /CNT=80 /TID=Hs.121073.1 /TIER=Stack /STK=13
/UG=Hs.121073 /LL=55712 /UG_GENE=FLJ10466 /UG_TITLE=hypothetical protein
FLJ10466•2.769614313•2.615217348•EF-hand domain (C-terminal) containing
1•EFHC1•Hs.403171•ENSG00000096093•7517 // muscle development // inferred from
electronic annotation•16459 // myosin // inferred from electronic
annotation•3774 // motor activity // inferred from electronic annotation ///
5509 // calcium ion binding // inferred from electronic annotation
219654_at•"gb:NM_014241.1 /DB_XREF=gi:7657481 /GEN=PTPLA /FEA=FLmRNA /CNT=23
/TID=Hs.114062.0 /TIER=FL+Stack /STK=8 /UG=Hs.114062 /LL=9200 /DEF=Homo
sapiens protein tyrosine phosphatase-like (proline instead of catalytic
arginine), member a (PTPLA), mRNA.
/PROD=prot"•2.769532171•2.304493033•"protein tyrosine phosphatase-like
(proline instead of catalytic arginine), member
a"•PTPLA•Hs.114062•ENSG00000165996•6470 // protein amino acid
dephosphorylation // traceable author statement /// 7165 // signal
transduction // non-traceable author statement /// 7275 // development //
traceable author statement••4725 // protein tyrosine phosphatase activity //
traceable author statement
1552489_s_at•"gb:NM_033066.1 /DB_XREF=gi:14780901 /GEN=MPP4 /TID=Hs2.63085.1
/CNT=16 /FEA=FLmRNA /TIER=FL /STK=3 /LL=58538 /UG=Hs.63085 /DEF=Homo sapiens
membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4) (MPP4),
mRNA. /PROD=membrane protein, palmitoylate"•2.765603076•2.61152846•"membrane
protein, palmitoylated 4 (MAGUK p55 subfamily member
4)"•MPP4•Hs.63085•ENSG00000082126•••5515 // protein binding // inferred from
electronic annotation
210448_s_at•"gb:U49396.1 /DB_XREF=gi:1552523 /FEA=FLmRNA /CNT=8
/TID=Hs.77807.1 /TIER=FL /STK=0 /UG=Hs.77807 /LL=5026 /UG_GENE=P2RX5
/DEF=Human ionotropic ATP receptor P2X5b mRNA, complete cds. /PROD=P2X5b
/FL=gb:U49396.1 gb:AF070573.1"•2.747102148•2.323059214•"purinergic receptor
P2X, ligand-gated ion channel, 5"•P2RX5•Hs.408615•ENSG00000083454•6811 // ion
transport // inferred from electronic annotation•16020 // membrane //
inferred from electronic annotation•4872 // receptor activity // inferred
from electronic annotation /// 5216 // ion channel activity // inferred from
electronic annotation /// 5524 // ATP binding // inferred from electronic
annotation
202075_s_at•"gb:NM_006227.1 /DB_XREF=gi:5453913 /GEN=PLTP /FEA=FLmRNA
/CNT=330 /TID=Hs.283007.0 /TIER=FL+Stack /STK=135 /UG=Hs.283007 /LL=5360
/DEF=Homo sapiens phospholipid transfer protein (PLTP), mRNA.
/PROD=phospholipid transfer protein /FL=gb:NM_006227.1
gb:L2623"•2.728055176•2.708260441•phospholipid transfer
protein•PLTP•Hs.439312•ENSG00000100979•6629 // lipid metabolism // traceable
author statement /// 6869 // lipid transport // inferred from electronic
annotation•5576 // extracellular region // traceable author statement•8289 //
lipid binding // inferred from electronic annotation
229334_at•gb:BF515942 /DB_XREF=gi:11601121 /DB_XREF=UI-H-BW1-aoa-f-07-0-UI.s1
/CLONE=IMAGE:3084061 /FEA=EST /CNT=15 /TID=Hs.35088.1 /TIER=Stack /STK=11
```

```
/UG=Hs.35088 /UG_TITLE=ESTs•2.715674617•2.29486169•Similar to RUN and FYVE
domain-containing 2; Run- and FYVE-domain containing protein••Hs.518801••••
228882_at•"gb:AL042088 /DB_XREF=gi:5935428 /DB_XREF=DKFZp434A1420_s1
/CLONE=DKFZp434A1420 /FEA=mRNA /CNT=25 /TID=Hs.128751.0 /TIER=Stack /STK=11
/UG=Hs.128751 /UG_TITLE=Homo sapiens cDNA FLJ12235 fis, clone
MAMMA1001243"•2.709896911•4.576424897•tubby homolog
(mouse)•TUB•Hs.231850•ENSG00000166402••5634 // nucleus // traceable author
statement /// 5737 // cytoplasm // traceable author statement•
221729_at•"gb:AL575735 /DB_XREF=gi:12937190 /DB_XREF=AL575735
/CLONE=CS0DI070YK23 (3 prime) /FEA=FLmRNA /CNT=405 /TID=Hs.82985.0
/TIER=Stack /STK=18 /UG=Hs.82985 /LL=1290 /UG_GENE=COL5A2 /UG_TITLE=collagen,
type V, alpha 2 /FL=gb:NM_000393.1"•2.65581525•3.405496426•"collagen, type V,
alpha 2"•COL5A2•Hs.445827••6817 // phosphate transport // inferred from
electronic annotation•5581 // collagen // inferred from electronic annotation
/// 5588 // collagen type V // traceable author statement /// 5737 //
cytoplasm // inferred from electronic annotation•5201 // extracellular matrix
structural constituent // not recorded
214110_s_at•gb:BF195104 /DB_XREF=gi:11081627 /DB_XREF=7n15a07.x1
/CLONE=IMAGE:3564565 /FEA=EST /CNT=14 /TID=Hs.56729.2 /TIER=Stack /STK=12
/UG=Hs.56729 /LL=4046 /UG_GENE=LSP1 /UG_TITLE=lymphocyte-specific protein
1•2.649756264•3.264791981•Similar to lymphocyte-specific protein
1••Hs.546673••••
225664_at•"gb:AA788946 /DB_XREF=gi:2849066 /DB_XREF=ag40c06.s1
/CLONE=IMAGE:1119274 /FEA=EST /CNT=118 /TID=Hs.16869.0 /TIER=Stack /STK=91
/UG=Hs.16869 /UG_TITLE=ESTs, Moderately similar to CA1C RAT COLLAGEN ALPHA
1(XII) CHAIN (R.norvegicus)"•2.634888031•8.209536868•"collagen, type XII,
alpha 1"•COL12A1•Hs.101302•ENSG00000111799•1501 // skeletal development //
traceable author statement /// 6817 // phosphate transport // inferred from
electronic annotation /// 7155 // cell adhesion // inferred from electronic
annotation /// 30199 // collagen fibril organization // non-traceable a•5578
// extracellular matrix (sensu Metazoa) // inferred from electronic
annotation /// 5595 // collagen type XII // non-traceable author statement
/// 5595 // collagen type XII // traceable author statement /// 5737 //
cytoplasm // inferred from electron•5198 // structural molecule activity //
inferred from electronic annotation /// 5515 // protein binding // inferred
from electronic annotation /// 30020 // extracellular matrix structural
constituent conferring tensile strength // non-traceable author sta
207686_s_at•"gb:NM_001228.1 /DB_XREF=gi:4502582 /GEN=CASP8 /FEA=FLmRNA /CNT=3
/TID=Hs.19949.0 /TIER=FL /STK=0 /UG=Hs.19949 /LL=841 /DEF=Homo sapiens
caspase 8, apoptosis-related cysteine protease (CASP8), mRNA. /PROD=caspase
8, apoptosis-related cysteine protease /FL="•2.633981682•3.489270188•"caspase
8, apoptosis-related cysteine protease"•CASP8•Hs.369736•ENSG00000064012•6508
// proteolysis and peptidolysis // traceable author statement /// 8632 //
apoptotic program // traceable author statement /// 42981 // regulation of
apoptosis // inferred from electronic annotation /// 43123 // positive
regulation of I-kappaB kinase/•5739 // mitochondrion // traceable author
statement /// 5856 // cytoskeleton // traceable author statement•4871 //
signal transducer activity // inferred from expression pattern /// 5515 //
protein binding // inferred from electronic annotation /// 8234 //
cysteine-type peptidase activity // traceable author statement /// 30693 //
caspase activity // traceable
214717_at•gb:AL137534.1 /DB_XREF=gi:6808209 /GEN=DKFZp434H1419 /FEA=mRNA
/CNT=33 /TID=Hs.56876.0 /TIER=ConsEnd /STK=0 /UG=Hs.56876 /DEF=Homo sapiens
mRNA; cDNA DKFZp434H1419 (from clone DKFZp434H1419); partial cds.
/PROD=hypothetical protein•2.631700344•2.628901578•hypothetical protein
DKFZp434H1419•DKFZp434H1419•Hs.56876••••
228280_at•gb:AI188445 /DB_XREF=gi:3739654 /DB_XREF=qd14b09.x1
/CLONE=IMAGE:1723673 /FEA=EST /CNT=20 /TID=Hs.152618.0 /TIER=Stack /STK=8
/UG=Hs.152618 /UG_TITLE=ESTs•2.623947691•2.286094039•similar to RIKEN cDNA
1200014N16 gene•MGC14289•Hs.512833•ENSG00000146858•••
213201_s_at•"gb:AJ011712 /DB_XREF=gi:4056561 /FEA=mRNA /CNT=448
/TID=Hs.73980.1 /TIER=Stack /STK=29 /UG=Hs.73980 /LL=7138 /UG_GENE=TNNT1
/UG_TITLE=troponin T1, skeletal, slow /DEF=Homo sapiens TNNT1 gene, exons
1-11 (and joined CDS)"•2.619298093•2.395028589•"troponin T1, skeletal,
slow"•TNNT1•Hs.534085•ENSG00000105048•6937 // regulation of muscle
contraction // traceable author statement /// 7517 // muscle development //
inferred from electronic annotation••5523 // tropomyosin binding // traceable
author statement
210220_at•"gb:L37882.1 /DB_XREF=gi:736678 /GEN=frizzled /FEA=FLmRNA /CNT=18
/TID=Hs.81217.0 /TIER=FL /STK=6 /UG=Hs.81217 /LL=2535 /UG_TITLE=frizzled
(Drosophila) homolog 2 /DEF=Human frizzled gene product mRNA, complete cds.
/FL=gb:NM_001466.2 gb:AB017364.1 gb:L3788"•2.604269513•2.37928671•frizzled
homolog 2 (Drosophila)•FZD2•Hs.142912•ENSG00000180340•7164 // establishment
of tissue polarity // traceable author statement /// 7186 // G-protein
coupled receptor protein signaling pathway // inferred from electronic
annotation /// 7275 // development // inferred from electronic annotation ///
16055 // Wnt •5887 // integral to plasma membrane // traceable author
statement /// 16020 // membrane // inferred from electronic annotation•4926
// non-G-protein coupled 7TM receptor activity // inferred from electronic
annotation /// 4930 // G-protein coupled receptor activity // inferred from
electronic annotation
```

```
227726_at•"gb:BF057084 /DB_XREF=gi:10810980 /DB_XREF=7k15f02.x1
/CLONE=IMAGE:3444602 /FEA=EST /CNT=25 /TID=Hs.105280.0 /TIER=Stack /STK=8
/UG=Hs.105280 /UG_TITLE=ESTs, Weakly similar to dJ963K23.2
(H.sapiens)"•2.591620334•2.556374732•ring finger protein
166•RNF166•Hs.513804•ENSG00000158717•16567 // protein ubiquitination //
inferred from electronic annotation•151 // ubiquitin ligase complex //
inferred from electronic annotation /// 5634 // nucleus // inferred from
electronic annotation•3676 // nucleic acid binding // inferred from
electronic annotation /// 4842 // ubiquitin-protein ligase activity //
inferred from electronic annotation /// 8270 // zinc ion binding // inferred
from electronic annotation
205123_s_at•"gb:NM_003692.1 /DB_XREF=gi:4507548 /GEN=TMEFF1 /FEA=FLmRNA
/CNT=65 /TID=Hs.78531.0 /TIER=FL /STK=0 /UG=Hs.78531 /LL=8577 /DEF=Homo
sapiens transmembrane protein with EGF-like and two follistatin-like domains
1 (TMEFF1), mRNA. /PROD=transmembrane protein
w"•2.583638039•2.151563274•transmembrane protein with EGF-like and two
follistatin-like domains 1•TMEFF1•Hs.336224•ENSG00000066697••16021 //
integral to membrane // inferred from electronic annotation•
222258_s_at•"gb:AF015043.1 /DB_XREF=gi:4102710 /FEA=mRNA /CNT=1
/TID=Hs.17667.1 /TIER=ConsEnd /STK=1 /UG=Hs.17667 /LL=23677 /UG_GENE=SH3BP4
/DEF=Homo sapiens EH-binding protein mRNA, partial cds. /PROD=EH-binding
protein"•2.574159877•3.844837956•SH3-domain binding protein
4•SH3BP4•Hs.516777•ENSG00000130147•6897 // endocytosis // traceable author
statement /// 7049 // cell cycle // traceable author statement•5634 //
nucleus // traceable author statement•4871 // signal transducer activity //
traceable author statement
236453_at•gb:AW243154 /DB_XREF=gi:6576958 /DB_XREF=xn29c01.x1
/CLONE=IMAGE:2695104 /FEA=EST /CNT=5 /TID=Hs.121276.0 /TIER=ConsEnd /STK=5
/UG=Hs.121276 /UG_TITLE=ESTs•2.569718714•2.209242242•similar to 60S ribosomal
protein L7a (Surfeit locus protein 3) (PLA-X
polypeptide)•LOC441422•Hs.99081••••
213610_s_at•gb:BE326381 /DB_XREF=gi:9200157 /DB_XREF=hw02e08.x1
/CLONE=IMAGE:3181766 /FEA=EST /CNT=30 /TID=Hs.18724.0 /TIER=Stack /STK=10
/UG=Hs.18724 /UG_TITLE=Homo sapiens mRNA; cDNA DKFZp564F093 (from clone
DKFZp564F093)•2.567573224•2.469808801•hypothetical protein
MGC2610•MGC2610•Hs.470549•ENSG00000144362•••5515 // protein binding //
inferred from electronic annotation
226876_at•gb:AI961778 /DB_XREF=gi:5754491 /DB_XREF=wt67d10.x1
/CLONE=IMAGE:2512531 /FEA=EST /CNT=36 /TID=Hs.124707.0 /TIER=Stack /STK=10
/UG=Hs.124707 /UG_TITLE=ESTs•2.563760898•3.249418478•hypothetical protein
MGC45871•MGC45871•Hs.345588•ENSG00000183688•••
232667_at•"gb:AK023752.1 /DB_XREF=gi:10435780 /FEA=mRNA /CNT=5
/TID=Hs.306657.0 /TIER=ConsEnd /STK=0 /UG=Hs.306657 /UG_TITLE=Homo sapiens
cDNA FLJ13690 fis, clone PLACE2000097 /DEF=Homo sapiens cDNA FLJ13690 fis,
clone PLACE2000097."•2.554002057•3.339829937•"CDNA FLJ13690 fis, clone
PLACE2000097"••Hs.435835••••
203910_at•"gb:NM_004815.1 /DB_XREF=gi:4758881 /GEN=PARG1 /FEA=FLmRNA /CNT=91
/TID=Hs.70983.0 /TIER=FL+Stack /STK=17 /UG=Hs.70983 /LL=9411 /DEF=Homo
sapiens PTPL1-associated RhoGAP 1 (PARG1), mRNA. /PROD=PTPL1-associated
RhoGAP 1 /FL=gb:U90920.1
gb:NM_004815.1"•2.547167006•4.29723847•PTPL1-associated RhoGAP
1•PARG1•Hs.483238•ENSG00000137962•7242 // intracellular signaling cascade //
inferred from electronic annotation /// 7266 // Rho protein signal
transduction // traceable author statement••5100 // Rho GTPase activator
activity // traceable author statement /// 19992 // diacylglycerol binding //
inferred from electronic annotation
1554667_s_at•"gb:BC025250.1 /DB_XREF=gi:19264122 /TID=Hs2.135146.2 /CNT=5
/FEA=FLmRNA /TIER=FL /STK=1 /LL=79828 /UG_GENE=FLJ13984 /UG=Hs.135146
/UG_TITLE=hypothetical protein FLJ13984 /DEF=Homo sapiens, hypothetical
protein FLJ13984, clone MGC:39122 IMAGE:5433692,
mRNA"•2.540769053•3.364315985•hypothetical protein
FLJ13984•FLJ13984•Hs.135146•ENSG00000123600•••
206170_at•"gb:NM_000024.2 /DB_XREF=gi:13162366 /GEN=ADRB2 /FEA=FLmRNA /CNT=35
/TID=Hs.2551.0 /TIER=FL /STK=0 /UG=Hs.2551 /LL=154 /DEF=Homo sapiens
adrenergic, beta-2-, receptor, surface (ADRB2), mRNA. /PROD=adrenergic,
beta-2-, receptor, surface /FL=gb:NM_000024.2
g"•2.526389418•5.277317656•"adrenergic, beta-2-, receptor,
surface"•ADRB2•Hs.2551•ENSG00000169252•187 // activation of MAPK // traceable
author statement /// 6898 // receptor mediated endocytosis // traceable
author statement /// 7171 // transmembrane receptor protein tyrosine kinase
activation (dimerization) // traceable author statement /// 7186 // •5764 //
lysosome // traceable author statement /// 5768 // endosome // traceable
author statement /// 5886 // plasma membrane // traceable author statement
/// 5887 // integral to plasma membrane // traceable author statement•1584 //
rhodopsin-like receptor activity // inferred from electronic annotation ///
4872 // receptor activity // inferred from electronic annotation /// 4941 //
beta2-adrenergic receptor activity // traceable author statement
205659_at•"gb:NM_014707.1 /DB_XREF=gi:7662279 /GEN=HDAC7B-PENDING /FEA=FLmRNA
/CNT=32 /TID=Hs.116753.0 /TIER=FL /STK=6 /UG=Hs.116753 /LL=9734 /DEF=Homo
sapiens histone deacetylase 7B (HDAC7B-PENDING), mRNA. /PROD=histone
deacetylase 7B /FL=gb:AB018287.1
```

```
gb:NM_014707"•2.517783004•3.355270376•histone deacetylase
9•HDAC9•Hs.196054•ENSG00000048052•"74 // regulation of cell cycle //
traceable author statement /// 6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 6954 // inflammatory response
/"•118 // histone deacetylase complex // traceable author statement /// 5634
// nucleus // inferred from electronic annotation /// 5634 // nucleus //
non-traceable author statement /// 5737 // cytoplasm // traceable author
statement•4407 // histone deacetylase activity // non-traceable author
statement /// 8134 // transcription factor binding // traceable author
statement /// 16566 // specific transcriptional repressor activity //
traceable author statement /// 16787 // hydrolase act
203702_s_at•gb:AL043927 /DB_XREF=gi:5935917 /DB_XREF=DKFZp434F1028_s1
/CLONE=DKFZp434F1028 /FEA=FLmRNA /CNT=93 /TID=Hs.169910.0 /TIER=Stack /STK=31
/UG=Hs.169910 /LL=9654 /UG_GENE=KIAA0173 /UG_TITLE=KIAA0173 gene product
/FL=gb:NM_014640.1 gb:D79995.1•2.51326902•2.87824903•"tubulin tyrosine
ligase-like family, member 4"•TTLL4•Hs.471405•ENSG00000135912•6464 // protein
modification // inferred from electronic annotation••4835 // tubulin-tyrosine
ligase activity // inferred from electronic annotation /// 16874 // ligase
activity // inferred from electronic annotation
228987_at•gb:AA156238 /DB_XREF=gi:1727856 /DB_XREF=zl50c10.s1
/CLONE=IMAGE:505362 /FEA=EST /CNT=23 /TID=Hs.32501.0 /TIER=Stack /STK=15
/UG=Hs.32501 /UG_TITLE=ESTs•2.454515722•2.7034823•"Family with sequence
similarity 49, member B"•FAM49B•Hs.492869•ENSG00000153310•••
215767_at•gb:AF052145.1 /DB_XREF=gi:3360454 /FEA=mRNA /CNT=4 /TID=Hs.159528.0
/TIER=ConsEnd /STK=0 /UG=Hs.159528 /UG_TITLE=Homo sapiens clone 24400 mRNA
sequence /DEF=Homo sapiens clone 24400 mRNA
sequence.•2.446333193•4.238097657•chromosome 2 open reading frame
10•C2orf10•Hs.159528•ENSG00000170396••5634 // nucleus // inferred from
electronic annotation•3676 // nucleic acid binding // inferred from
electronic annotation /// 8270 // zinc ion binding // inferred from
electronic annotation
208025_s_at•"gb:NM_003483.2 /DB_XREF=gi:6631086 /GEN=HMGIC /FEA=FLmRNA /CNT=1
/TID=HsAffx.900004.136 /TIER=FL /STK=0 /DEF=Homo sapiens high-mobility group
(nonhistone chromosomal) protein isoform I-C (HMGIC), mRNA.
/PROD=high-mobility group (nonhistone
chromosomal)pro"•2.445292313•3.291838163•high mobility group AT-hook 2 ///
high mobility group AT-hook 2•HMGA2•Hs.505924••"6325 // establishment and/or
maintenance of chromatin architecture // traceable author statement /// 6350
// transcription // inferred from electronic annotation /// 6355 //
regulation of transcription, DNA-dependent // traceable author statement ///
7275"•785 // chromatin // inferred from electronic annotation /// 5634 //
nucleus // inferred from electronic annotation•3680 // AT DNA binding //
traceable author statement
224932_at•"gb:AI814909 /DB_XREF=gi:5426124 /DB_XREF=wk68e04.x1
/CLONE=IMAGE:2420574 /FEA=EST /CNT=174 /TID=Hs.66915.0 /TIER=Stack /STK=113
/UG=Hs.66915 /UG_TITLE=ESTs, Weakly similar to 16.7Kd protein
(H.sapiens)"•2.431785465•2.053811276•chromosome 22 open reading frame
16•C22orf16•Hs.66915•ENSG00000138869•••
219622_at•"gb:NM_017817.1 /DB_XREF=gi:8923400 /GEN=FLJ20429 /FEA=FLmRNA
/CNT=29 /TID=Hs.179791.0 /TIER=FL /STK=0 /UG=Hs.179791 /LL=55647 /DEF=Homo
sapiens hypothetical protein FLJ20429 (FLJ20429), mRNA. /PROD=hypothetical
protein FLJ20429 /FL=gb:NM_017817.1"•2.429696434•2.379064084•"RAB20, member
RAS oncogene family"•RAB20•Hs.508720•ENSG00000139832•7264 // small GTPase
mediated signal transduction // inferred from electronic annotation /// 15031
// protein transport // inferred from electronic annotation••5525 // GTP
binding // inferred from electronic annotation
203286_at•"gb:NM_014901.1 /DB_XREF=gi:7662485 /GEN=KIAA1100 /FEA=FLmRNA
/CNT=120 /TID=Hs.179946.0 /TIER=FL+Stack /STK=53 /UG=Hs.179946 /LL=22838
/DEF=Homo sapiens KIAA1100 protein (KIAA1100), mRNA. /PROD=KIAA1100 protein
/FL=gb:AB029023.1 gb:NM_014901.1"•2.423933754•2.408633846•ring finger protein
44•RNF44•Hs.434888•ENSG00000146083•16567 // protein ubiquitination //
inferred from electronic annotation•151 // ubiquitin ligase complex //
inferred from electronic annotation•4842 // ubiquitin-protein ligase activity
// inferred from electronic annotation /// 8270 // zinc ion binding //
inferred from electronic annotation
242300_at•gb:BF432276 /DB_XREF=gi:11444390 /DB_XREF=nab88e12.x1
/CLONE=IMAGE:3274870 /FEA=EST /CNT=4 /TID=Hs.104580.0 /TIER=ConsEnd /STK=3
/UG=Hs.104580 /UG_TITLE=ESTs•2.420334303•2.220955051••••••
243367_at•gb:AI018561 /DB_XREF=gi:3233080 /DB_XREF=ou30g09.x1
/CLONE=IMAGE:1627840 /FEA=EST /CNT=3 /TID=Hs.122156.0 /TIER=ConsEnd /STK=3
/UG=Hs.122156 /UG_TITLE=ESTs•2.39988025•3.015378058•Similar to D(1B) dopamine
receptor (D(5) dopamine receptor) (D1beta dopamine receptor)••Hs.456465••7186
// G-protein coupled receptor protein signaling pathway // inferred from
electronic annotation•16021 // integral to membrane // inferred from
electronic annotation•1584 // rhodopsin-like receptor activity // inferred
from electronic annotation /// 4872 // receptor activity // inferred from
electronic annotation /// 4952 // dopamine receptor activity // inferred from
electronic annotation
212365_at•"gb:BF215996 /DB_XREF=gi:11109582 /DB_XREF=601881549F1
/CLONE=IMAGE:4093740 /FEA=mRNA /CNT=213 /TID=Hs.121576.0 /TIER=Stack /STK=19
```

```
/UG=Hs.121576 /UG_TITLE=Homo sapiens cDNA FLJ20153 fis, clone COL08656,
highly similar to AJ001381 Homo sapiens incomplete
c"•2.388798857•3.451925589•myosin IB•MYO1B•Hs.439620•ENSG00000128641••16459
// myosin // inferred from electronic annotation•3774 // motor activity //
inferred from electronic annotation /// 3779 // actin binding // inferred
from electronic annotation /// 5516 // calmodulin binding // inferred from
electronic annotation /// 5524 // ATP binding // inferred from electronic
annota
200884_at•"gb:NM_001823.1 /DB_XREF=gi:4502850 /GEN=CKB /FEA=FLmRNA /CNT=452
/TID=Hs.173724.0 /TIER=FL+Stack /STK=171 /UG=Hs.173724 /LL=1152 /DEF=Homo
sapiens creatine kinase, brain (CKB), mRNA. /PROD=creatine kinase, brain
/FL=gb:L47647.1 gb:BC004914.1
gb:NM_001823."•2.383458051•2.248337883•"creatine kinase,
brain"•CKB•Hs.173724•ENSG00000166165••5737 // cytoplasm // not recorded•4111
// creatine kinase activity // traceable author statement
226136_at•gb:N32834 /DB_XREF=gi:1153233 /DB_XREF=yw85h01.s1
/CLONE=IMAGE:259057 /FEA=EST /CNT=61 /TID=Hs.154762.2 /TIER=Stack /STK=16
/UG=Hs.154762 /LL=11103 /UG_GENE=HRB2 /UG_TITLE=HIV-1 rev binding protein
2•2.383362814•5.38889447•••••••
202806_at•"gb:NM_004395.1 /DB_XREF=gi:4758123 /GEN=DBN1 /FEA=FLmRNA /CNT=134
/TID=Hs.89434.0 /TIER=FL+Stack /STK=22 /UG=Hs.89434 /LL=1627 /DEF=Homo
sapiens drebrin 1 (DBN1), mRNA. /PROD=drebrin 1 /FL=gb:D17530.1 gb:BC000283.1
gb:U00802.1 gb:NM_004395.1"•2.379011511•2.241481847•drebrin
1•DBN1•Hs.130316•ENSG00000113758•7015 // actin filament organization //
inferred from sequence or structural similarity /// 7399 // neurogenesis //
inferred from electronic annotation /// 30154 // cell differentiation //
inferred from electronic annotation /// 48168 // regulation of neur•5622 //
intracellular // inferred from electronic annotation /// 5737 // cytoplasm //
non-traceable author statement /// 15629 // actin cytoskeleton // inferred
from sequence or structural similarity /// 30425 // dendrite // non-traceable
author statement•3779 // actin binding // inferred from electronic annotation
/// 3779 // actin binding // non-traceable author statement /// 5522 //
profilin binding // inferred from sequence or structural similarity
225806_at•"gb:AI289311 /DB_XREF=gi:3932575 /DB_XREF=qw28a05.x1
/CLONE=IMAGE:1992368 /FEA=mRNA /CNT=66 /TID=Hs.64552.0 /TIER=Stack /STK=13
/UG=Hs.64552 /UG_TITLE=Homo sapiens cDNA: FLJ21914 fis, clone
HEP03892"•2.378127673•3.612201131•"jub, ajuba homolog (Xenopus
laevis)"•JUB•Hs.508910•ENSG00000129474•••8270 // zinc ion binding // inferred
from electronic annotation
232231_at•gb:AL353944.1 /DB_XREF=gi:7669984 /FEA=mRNA /CNT=13 /TID=Hs.50115.0
/TIER=ConsEnd /STK=7 /UG=Hs.50115 /UG_TITLE=Homo sapiens mRNA; cDNA
DKFZp761J1112 (from clone DKFZp761J1112) /DEF=Homo sapiens mRNA; cDNA
DKFZp761J1112 (from clone
DKFZp761J1112).•2.372693021•2.332245255•Runt-related transcription factor
2•RUNX2•Hs.122116•ENSG00000124813•"1503 // ossification // traceable author
statement /// 6350 // transcription // inferred from electronic annotation
/// 6355 // regulation of transcription, DNA-dependent // inferred from
electronic annotation"•5634 // nucleus // inferred from electronic
annotation•3700 // transcription factor activity // non-traceable author
statement /// 3702 // RNA polymerase II transcription factor activity //
traceable author statement /// 5515 // protein binding // inferred from
physical interaction /// 5524 // ATP binding //
227377_at•"gb:AK022784.1 /DB_XREF=gi:10434388 /FEA=mRNA /CNT=51
/TID=Hs.24739.0 /TIER=Stack /STK=24 /UG=Hs.24739 /UG_TITLE=Homo sapiens cDNA
FLJ12555 fis, clone NT2RM4000764 /DEF=Homo sapiens cDNA FLJ12722 fis, clone
NT2RP1001311."•2.370966449•4.006236137•••••••
206343_s_at•"gb:NM_013959.1 /DB_XREF=gi:7669517 /GEN=NRG1 /FEA=FLmRNA /CNT=25
/TID=Hs.172816.2 /TIER=FL+Stack /STK=12 /UG=Hs.172816 /LL=3084 /DEF=Homo
sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA. /PROD=neuregulin
1 isoform SMDF /FL=gb:L41827.1 gb:NM_013"•2.365782906•2.305997181•neuregulin
1•NRG1•Hs.453951•ENSG00000157168•7399 // neurogenesis // non-traceable author
statement /// 9790 // embryonic development // inferred from electronic
annotation /// 30154 // cell differentiation // non-traceable author
statement•5576 // extracellular region // non-traceable author statement ///
16020 // membrane // non-traceable author statement /// 16021 // integral to
membrane // inferred from electronic annotation•5102 // receptor binding //
inferred from electronic annotation /// 8083 // growth factor activity //
inferred from electronic annotation /// 8083 // growth factor activity //
non-traceable author statement /// 30297 // transmembrane receptor protein
tyro
231192_at•gb:AW274018 /DB_XREF=gi:6661048 /DB_XREF=xv26d05.x1
/CLONE=IMAGE:2814249 /FEA=EST /CNT=8 /TID=Hs.99083.0 /TIER=Stack /STK=8
/UG=Hs.99083 /UG_TITLE=ESTs•2.364837633•2.195193938•"Endothelial
differentiation, lysophosphatidic acid G-protein-coupled receptor,
7"•EDG7•Hs.527909•ENSG00000171517•"7165 // signal transduction // inferred
from electronic annotation /// 7187 // G-protein signaling, coupled to cyclic
nucleotide second messenger // traceable author statement /// 7204 //
positive regulation of cytosolic calcium ion concentration // trace"•5886 //
plasma membrane // traceable author statement /// 5887 // integral to plasma
membrane // traceable author statement•1619 // lysosphingolipid and
lysophosphatidic acid receptor activity // inferred from electronic
```

```
annotation /// 4872 // receptor activity // inferred from electronic
annotation /// 8289 // lipid binding // traceable author statement
227986_at•gb:AW014719 /DB_XREF=gi:5863476 /DB_XREF=UI-H-BI0-aae-a-10-0-UI.s1
/CLONE=IMAGE:2709018 /FEA=EST /CNT=23 /TID=Hs.59317.0 /TIER=Stack /STK=16
/UG=Hs.59317 /UG_TITLE=ESTs•2.342273181•2.471815444•zinc finger protein
343•ZNF343•Hs.516846•ENSG00000088876•"6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation"•5634 // nucleus //
inferred from electronic annotation•3676 // nucleic acid binding // inferred
from electronic annotation /// 3677 // DNA binding // inferred from
electronic annotation /// 8270 // zinc ion binding // inferred from
electronic annotation
212816_s_at•gb:BE613178 /DB_XREF=gi:9894775 /DB_XREF=601452166T1
/CLONE=IMAGE:3855712 /FEA=mRNA /CNT=102 /TID=Hs.84152.2 /TIER=Stack /STK=9
/UG=Hs.84152 /LL=875 /UG_GENE=CBS
/UG_TITLE=cystathionine-beta-synthase•2.327552592•2.910850454•cystathionine-be
ta-synthase•CBS•Hs.533013•ENSG00000160200•6535 // cysteine biosynthesis from
serine // inferred from electronic annotation /// 8152 // metabolism //
inferred from electronic annotation /// 8652 // amino acid biosynthesis //
inferred from electronic annotation /// 19343 // cysteine biosynthesis
vi•5737 // cytoplasm // inferred from electronic annotation•4122 //
cystathionine beta-synthase activity // traceable author statement /// 16829
// lyase activity // inferred from electronic annotation
244359_s_at•gb:H28915 /DB_XREF=gi:899825 /DB_XREF=ym33b09.s1
/CLONE=IMAGE:49766 /FEA=EST /CNT=3 /TID=Hs.117689.0 /TIER=ConsEnd /STK=3
/UG=Hs.117689 /UG_TITLE=ESTs•2.324033912•2.928502274•••••••
206290_s_at•"gb:NM_002924.1 /DB_XREF=gi:11140808 /GEN=RGS7 /FEA=FLmRNA
/CNT=26 /TID=Hs.79348.0 /TIER=FL /STK=4 /UG=Hs.79348 /LL=6000 /DEF=Homo
sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /PROD=regulator of
G-protein signalling 7 /FL=gb:AF090116.1
gb:NM_0"•2.323900791•4.237641817•regulator of G-protein signalling
7•RGS7•Hs.130171•ENSG00000182901•7242 // intracellular signaling cascade //
inferred from electronic annotation /// 8277 // regulation of G-protein
coupled receptor protein signaling pathway // non-traceable author
statement•5834 // heterotrimeric G-protein complex // inferred from
electronic annotation•4871 // signal transducer activity // inferred from
electronic annotation /// 16299 // regulator of G-protein signaling activity
// non-traceable author statement
242346_x_at•gb:BF222929 /DB_XREF=gi:11130106 /DB_XREF=7q25b10.x1
/CLONE=IMAGE:3699402 /FEA=EST /CNT=3 /TID=Hs.290585.0 /TIER=ConsEnd /STK=3
/UG=Hs.290585 /UG_TITLE=ESTs•2.302882486•3.257919735•••••••
210387_at•"gb:BC001131.1 /DB_XREF=gi:12654590 /FEA=FLmRNA /CNT=22
/TID=Hs.247817.1 /TIER=FL /STK=0 /UG=Hs.247817 /LL=8339 /UG_GENE=H2BFA
/DEF=Homo sapiens, H2B histone family, member A, clone MGC:2561, mRNA,
complete cds. /PROD=H2B histone family, member A
/FL=gb:NM"•2.301642011•2.756495359•"histone 1,
H2bg"•HIST1H2BG•Hs.182137•ENSG00000180596 /// ENSG00000197697 ///
ENSG00000197846 /// ENSG00000187990 /// ENSG00000168242•••
201288_at•"gb:NM_001175.1 /DB_XREF=gi:10835001 /GEN=ARHGDIB /FEA=FLmRNA
/CNT=466 /TID=Hs.83656.0 /TIER=FL+Stack /STK=151 /UG=Hs.83656 /LL=397
/DEF=Homo sapiens Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB), mRNA.
/PROD=Rho GDP dissociation inhibitor (GDI) beta"•2.297366627•2.293440087•Rho
GDP dissociation inhibitor (GDI) beta•ARHGDIB•Hs.504877•ENSG00000111348•6955
// immune response // traceable author statement /// 7162 // negative
regulation of cell adhesion // traceable author statement /// 7266 // Rho
protein signal transduction // traceable author statement /// 7275 //
development // traceable author stat•16023 // cytoplasmic vesicle //
traceable author statement•5094 // Rho GDP-dissociation inhibitor activity //
traceable author statement /// 5096 // GTPase activator activity // inferred
from electronic annotation
1553972_a_at•"gb:BC007257.1 /DB_XREF=gi:13938262 /TID=Hs2.84152.2 /CNT=70
/FEA=FLmRNA /TIER=FL+Stack /STK=33 /LL=875 /UG_GENE=CBS /UG=Hs.84152
/DEF=Homo sapiens, cystathionine-beta-synthase, clone MGC:15515
IMAGE:3028099, mRNA, complete cds.
/PROD=cystathionine-beta-sy"•2.290334394•3.733051597•cystathionine-beta-syntha
se•CBS•Hs.533013•ENSG00000160200•6535 // cysteine biosynthesis from serine //
inferred from electronic annotation /// 8152 // metabolism // inferred from
electronic annotation /// 8652 // amino acid biosynthesis // inferred from
electronic annotation /// 19343 // cysteine biosynthesis vi•5737 // cytoplasm
// inferred from electronic annotation•4122 // cystathionine beta-synthase
activity // traceable author statement /// 16829 // lyase activity //
inferred from electronic annotation
230425_at•gb:AI674183 /DB_XREF=gi:4874663 /DB_XREF=wc09c07.x1
/CLONE=IMAGE:2314668 /FEA=EST /CNT=14 /TID=Hs.78436.4 /TIER=Stack /STK=14
/UG=Hs.78436 /LL=2047 /UG_GENE=EPHB1
/UG_TITLE=EphB1•2.288704607•3.45822466•EPH receptor
B1•EPHB1•Hs.116092•ENSG00000154928•6468 // protein amino acid phosphorylation
// inferred from electronic annotation /// 7165 // signal transduction //
traceable author statement /// 7169 // transmembrane receptor protein
tyrosine kinase signaling pathway // inferred from electronic annota•5886 //
plasma membrane // traceable author statement /// 5887 // integral to plasma
membrane // traceable author statement•4872 // receptor activity // inferred
```

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from electronic annotation /// 5003 // ephrin receptor activity // inferred
from electronic annotation /// 5524 // ATP binding // inferred from
electronic annotation /// 16740 // transferase activity // inferred from
230508_at•gb:AL569601 /DB_XREF=gi:12925101 /DB_XREF=AL569601
/CLONE=CS0DE011YL13 (3 prime) /FEA=EST /CNT=14 /TID=Hs.85591.0 /TIER=Stack
/STK=10 /UG=Hs.85591 /UG_TITLE=ESTs•2.283448847•2.848495884•Dickkopf homolog
3 (Xenopus laevis)•DKK3•Hs.292156•ENSG00000050165•6118 // electron transport
// inferred from electronic annotation /// 7275 // development // inferred
from electronic annotation /// 9653 // morphogenesis // traceable author
statement /// 16055 // Wnt receptor signaling pathway // inferred from
electroni•5576 // extracellular region // inferred from electronic annotation
/// 5615 // extracellular space // traceable author statement /// 16020 //
membrane // inferred from electronic annotation /// 45285 //
ubiquinol-cytochrome-c reductase complex // inferre•8121 //
ubiquinol-cytochrome-c reductase activity // inferred from electronic
annotation
213677_s_at•gb:BG434893 /DB_XREF=gi:13341399 /DB_XREF=602507842F1
/CLONE=IMAGE:4604891 /FEA=EST /CNT=30 /TID=Hs.111749.1 /TIER=Stack /STK=19
/UG=Hs.111749 /LL=5378 /UG_GENE=PMS1 /UG_TITLE=postmeiotic segregation
increased (S. cerevisiae) 1•2.283303648•2.571175387•PMS1 postmeiotic
segregation increased 1 (S. cerevisiae)•PMS1•Hs.111749•ENSG00000064933•"6298
// mismatch repair // traceable author statement /// 6355 // regulation of
transcription, DNA-dependent // inferred from electronic annotation /// 7049
// cell cycle // inferred from electronic annotation /// 45786 // negative
regulation of cell cycl"•5634 // nucleus // inferred from electronic
annotation /// 5634 // nucleus // traceable author statement /// 19866 //
inner membrane // inferred from electronic annotation•3677 // DNA binding //
traceable author statement /// 5524 // ATP binding // inferred from
electronic annotation
202976_s_at•"gb:NM_014899.1 /DB_XREF=gi:7662355 /GEN=KIAA0878 /FEA=FLmRNA
/CNT=168 /TID=Hs.188006.0 /TIER=FL+Stack /STK=10 /UG=Hs.188006 /LL=22836
/DEF=Homo sapiens KIAA0878 protein (KIAA0878), mRNA. /PROD=KIAA0878 protein
/FL=gb:NM_014899.1 gb:AB020685.1"•2.276868745•2.445252723•Rho-related BTB
domain containing 3•RHOBTB3•Hs.445030•ENSG00000164292•••3924 // GTPase
activity // non-traceable author statement /// 5515 // protein binding //
inferred from electronic annotation
243366_s_at•gb:AI936034 /DB_XREF=gi:5674904 /DB_XREF=wo47c10.x1
/CLONE=IMAGE:2458482 /FEA=EST /CNT=3 /TID=Hs.43936.0 /TIER=ConsEnd /STK=3
/UG=Hs.43936 /UG_TITLE=ESTs•2.26983377•3.208883825•Transcribed
locus••Hs.541511••••
202936_s_at•"gb:NM_000346.1 /DB_XREF=gi:4557852 /GEN=SOX9 /FEA=FLmRNA
/CNT=136 /TID=Hs.2316.0 /TIER=FL+Stack /STK=39 /UG=Hs.2316 /LL=6662 /DEF=Homo
sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal
sex-reversal) (SOX9), mRNA. /PROD=transcri"•2.268398917•12.33668725•"SRY (sex
determining region Y)-box 9 (campomelic dysplasia, autosomal
sex-reversal)"•SOX9•Hs.2316•ENSG00000125398•1501 // skeletal development //
not recorded /// 1502 // cartilage condensation // not recorded /// 6350 //
transcription // inferred from electronic annotation /// 6357 // regulation
of transcription from RNA polymerase II promoter // traceable author st•5634
// nucleus // traceable author statement•3677 // DNA binding // inferred from
electronic annotation /// 3704 // specific RNA polymerase II transcription
factor activity // traceable author statement
201952_at•gb:AA156721 /DB_XREF=gi:1728335 /DB_XREF=zl18b04.s1
/CLONE=IMAGE:502255 /FEA=FLmRNA /CNT=267 /TID=Hs.10247.0 /TIER=Stack /STK=87
/UG=Hs.10247 /LL=214 /UG_GENE=ALCAM /UG_TITLE=activated leucocyte cell
adhesion molecule /FL=gb:NM_001627.1
gb:L38608.1•2.263320532•2.665619982•••••••
225525_at•"gb:AB051458.1 /DB_XREF=gi:13359214 /GEN=KIAA1671 /FEA=mRNA /CNT=72
/TID=Hs.7890.0 /TIER=Stack /STK=32 /UG=Hs.7890 /DEF=Homo sapiens mRNA for
KIAA1671 protein, partial cds. /PROD=KIAA1671
protein"•2.257437115•4.541134999•KIAA1671 protein•KIAA1671•Hs.419171••••
228188_at•"gb:AI860150 /DB_XREF=gi:5513766 /DB_XREF=wh39g07.x1
/CLONE=IMAGE:2383164 /FEA=EST /CNT=24 /TID=Hs.5890.0 /TIER=Stack /STK=13
/UG=Hs.5890 /UG_TITLE=ESTs, Weakly similar to A49134 Ig kappa chain V-I
region (H.sapiens)"•2.252535997•2.037948208•FOS-like antigen
2•FOSL2•Hs.220971•ENSG00000075426•6357 // regulation of transcription from
RNA polymerase II promoter // traceable author statement /// 8219 // cell
death // traceable author statement•5634 // nucleus // traceable author
statement•3700 // transcription factor activity // traceable author
statement
1560099_at•"gb:BC041488.1 /DB_XREF=gi:27371106 /TID=Hs2.210654.1 /CNT=4
/FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.210654 /UG_TITLE=Homo sapiens cDNA
FLJ32911 fis, clone TESTI2006210. /DEF=Homo sapiens, clone IMAGE:5494257,
mRNA."•2.238788875•3.030885219•Hypothetical gene supported by
BC072410••Hs.441073••••
219002_at•"gb:NM_024622.1 /DB_XREF=gi:13375843 /GEN=FLJ21901 /FEA=FLmRNA
/CNT=45 /TID=Hs.32646.0 /TIER=FL /STK=0 /UG=Hs.32646 /LL=79675 /DEF=Homo
sapiens hypothetical protein FLJ21901 (FLJ21901), mRNA. /PROD=hypothetical
protein FLJ21901 /FL=gb:NM_024622.1"•2.225873997•2.909875544•hypothetical
protein FLJ21901•FLJ21901•Hs.529276•ENSG00000138399•6915 // apoptosis //
inferred from electronic annotation••4672 // protein kinase activity //
```

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inferred from electronic annotation /// 5524 // ATP binding // inferred from
electronic annotation
238035_at•gb:N66313 /DB_XREF=gi:1218438 /DB_XREF=yz38a07.s1
/CLONE=IMAGE:285300 /FEA=EST /CNT=11 /TID=Hs.120770.0 /TIER=ConsEnd /STK=5
/UG=Hs.120770 /UG_TITLE=ESTs•2.224475244•2.944973851•Sp3 transcription
factor•SP3•Hs.531587•ENSG00000172845•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// non-traceable author statement"•5634 // nucleus // non-traceable author
statement•3677 // DNA binding // inferred from electronic annotation /// 8270
// zinc ion binding // inferred from electronic annotation /// 16563 //
transcriptional activator activity // non-traceable author statement ///
16564 // transcriptional repressor activit
228367_at•"gb:BE551416 /DB_XREF=gi:9793119 /DB_XREF=7b64e10.x1
/CLONE=IMAGE:3233034 /FEA=EST /CNT=29 /TID=Hs.55950.0 /TIER=Stack /STK=20
/UG=Hs.55950 /UG_TITLE=ESTs, Weakly similar to KIAA1330 protein
(H.sapiens)"•2.220666363•2.897973295•alpha-kinase
2•ALPK2•Hs.388674•ENSG00000198796•6468 // protein amino acid phosphorylation
// inferred from electronic annotation••4674 // protein serine/threonine
kinase activity // inferred from electronic annotation /// 5524 // ATP
binding // inferred from electronic annotation
230147_at•gb:AI378647 /DB_XREF=gi:4188500 /DB_XREF=tc57a04.x1
/CLONE=IMAGE:2068686 /FEA=EST /CNT=22 /TID=Hs.42502.0 /TIER=Stack /STK=11
/UG=Hs.42502 /UG_TITLE=ESTs•2.217905202•3.083959715•coagulation factor II
(thrombin) receptor-like 2•F2RL2•Hs.42502•ENSG00000164220•7165 // signal
transduction // inferred from electronic annotation /// 7186 // G-protein
coupled receptor protein signaling pathway // inferred from electronic
annotation /// 7596 // blood coagulation // traceable author statement ///
9611 // response to •5886 // plasma membrane // traceable author statement
/// 5887 // integral to plasma membrane // traceable author statement•1584 //
rhodopsin-like receptor activity // inferred from electronic annotation ///
4435 // phosphoinositide phospholipase C activity // traceable author
statement /// 4872 // receptor activity // inferred from electronic
annotation /// 15057 // thrombin
224469_s_at•"gb:BC006173.1 /DB_XREF=gi:13544085 /FEA=FLmRNA /CNT=1
/TID=HsAffx.900892.1010 /TIER=FL /STK=0 /DEF=Homo sapiens, clone MGC:13251,
mRNA, complete cds. /PROD=Unknown (protein for MGC:13251)
/FL=gb:BC006173.1"•2.205421797•2.659248712•chromosome 14 open reading frame
151 /// chromosome 14 open reading frame
151•C14orf151•Hs.317821•ENSG00000130235•16043 // cell organization and
biogenesis // inferred from electronic annotation /// 30036 // actin
cytoskeleton organization and biogenesis // inferred from electronic
annotation••3779 // actin binding // inferred from electronic annotation ///
17048 // Rho GTPase binding // inferred from electronic annotation
223492_s_at•"gb:BC004958.1 /DB_XREF=gi:13436343 /FEA=FLmRNA /CNT=55
/TID=Hs.326740.0 /TIER=FL /STK=0 /UG=Hs.326740 /DEF=Homo sapiens, Similar to
leucine rich repeat (in FLII) interacting protein 1, clone MGC:10947, mRNA,
complete cds. /PROD=Similar to leucine rich
rep"•2.197747823•5.30075484•leucine rich repeat (in FLII) interacting protein
1•LRRFIP1•Hs.471779•ENSG00000124831•6357 // regulation of transcription from
RNA polymerase II promoter // traceable author statement /// 16481 //
negative regulation of transcription // non-traceable author statement•5634
// nucleus // non-traceable author statement /// 5634 // nucleus // traceable
author statement /// 5737 // cytoplasm // traceable author statement /// 5856
// cytoskeleton // traceable author statement•3702 // RNA polymerase II
transcription factor activity // not recorded /// 3725 // double-stranded RNA
binding // traceable author statement /// 16564 // transcriptional repressor
activity // non-traceable author statement
232481_s_at•gb:AL137517.1 /DB_XREF=gi:6808177 /GEN=DKFZp564O1278 /FEA=mRNA
/CNT=7 /TID=Hs.306201.0 /TIER=ConsEnd /STK=0 /UG=Hs.306201 /LL=54773
/DEF=Homo sapiens mRNA; cDNA DKFZp564O1278 (from clone DKFZp564O1278).
/PROD=hypothetical protein•2.19241537•2.234621858•"SLIT and NTRK-like family,
member 6"•SLITRK6•Hs.525105•ENSG00000184564••16021 // integral to membrane //
inferred from electronic annotation•
229572_at•gb:BF037662 /DB_XREF=gi:10745973 /DB_XREF=601462103F1
/CLONE=IMAGE:3865344 /FEA=EST /CNT=17 /TID=Hs.25786.0 /TIER=Stack /STK=13
/UG=Hs.25786 /UG_TITLE=ESTs•2.189866937•3.014588081•"Transcribed locus,
moderately similar to XP_508230.1 zinc finger protein 195 [Pan
troglodytes]"••Hs.25786••••
225703_at•gb:AL583509 /DB_XREF=gi:12952541 /DB_XREF=AL583509
/CLONE=CS0DC009YO13 (5 prime) /FEA=mRNA /CNT=99 /TID=Hs.127270.0 /TIER=Stack
/STK=24 /UG=Hs.127270 /LL=57666 /UG_GENE=KIAA1545 /UG_TITLE=KIAA1545
protein•2.189121178•3.050840991•KIAA1545 protein•KIAA1545•Hs.411138••••
212170_at•gb:BF447705 /DB_XREF=gi:11512843 /DB_XREF=7q94d07.x1
/CLONE=IMAGE:3706021 /FEA=mRNA /CNT=219 /TID=Hs.180895.0 /TIER=Stack /STK=33
/UG=Hs.180895 /LL=10137 /UG_GENE=KIAA0765 /UG_TITLE=putative brain
nuclearly-targeted protein•2.188325051•2.257961539•RNA binding motif protein
12•RBM12•Hs.246413•ENSG00000125976••5634 // nucleus // inferred from
electronic annotation•166 // nucleotide binding // inferred from electronic
annotation /// 3676 // nucleic acid binding // inferred from electronic
annotation /// 3723 // RNA binding // inferred from electronic annotation
218494_s_at•"gb:NM_020062.1 /DB_XREF=gi:13236503 /GEN=GEF /FEA=FLmRNA
```

```
/CNT=104 /TID=Hs.170088.0 /TIER=FL /STK=0 /UG=Hs.170088 /LL=56731 /DEF=Homo
sapiens GLUT4 enhancer factor (GEF), mRNA. /PROD=GLUT4 enhancer factor
/FL=gb:AF249267.3 gb:NM_020062.1"•2.187741366•2.204163954•SLC2A4
regulator•SLC2A4RG•Hs.435126•ENSG00000125520•"6350 // transcription //
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // traceable author statement"•5634 // nucleus // non-traceable
author statement•3700 // transcription factor activity // traceable author
statement /// 8270 // zinc ion binding // inferred from electronic
annotation
231806_s_at•gb:AL133630.1 /DB_XREF=gi:6599272 /GEN=DKFZp434N0223 /FEA=FLmRNA
/CNT=3 /TID=Hs.26996.1 /TIER=ConsEnd /STK=0 /UG=Hs.26996 /LL=27148 /DEF=Homo
sapiens mRNA; cDNA DKFZp434N0223 (from clone DKFZp434N0223); partial cds.
/PROD=hypothetical protein
/FL=gb:AF200•2.186252902•6.249008772•"serine/threonine kinase 36 (fused
homolog, Drosophila)"•STK36•Hs.471404•ENSG00000163482•6468 // protein amino
acid phosphorylation // non-traceable author statement /// 7076 // mitotic
chromosome condensation // inferred from electronic annotation••4674 //
protein serine/threonine kinase activity // non-traceable author statement
/// 5488 // binding // inferred from electronic annotation /// 5524 // ATP
binding // non-traceable author statement /// 16740 // transferase activity
// inferred from elec
205930_at•"gb:NM_005513.1 /DB_XREF=gi:5031726 /GEN=GTF2E1 /FEA=FLmRNA /CNT=28
/TID=Hs.145381.0 /TIER=FL+Stack /STK=10 /UG=Hs.145381 /LL=2960 /DEF=Homo
sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD)
(GTF2E1), mRNA. /PROD=general transcr"•2.186176186•2.449048287•"general
transcription factor IIE, polypeptide 1, alpha
56kDa"•GTF2E1•Hs.445272•ENSG00000153767•"6350 // transcription // inferred
from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6367 //
transcription initiation from RNA polymerase II promoter // traceable author
statement"•5634 // nucleus // inferred from electronic annotation /// 5673 //
transcription factor TFIIE complex // not recorded•16251 // general RNA
polymerase II transcription factor activity // not recorded
200988_s_at•"gb:NM_005789.1 /DB_XREF=gi:5031996 /GEN=PSME3 /FEA=FLmRNA
/CNT=330 /TID=Hs.152978.0 /TIER=FL /STK=0 /UG=Hs.152978 /LL=10197 /DEF=Homo
sapiens proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
(PSME3), mRNA. /PROD=proteasome (prosome,
ma"•2.173604313•2.909135876•"proteasome (prosome, macropain) activator
subunit 3 (PA28 gamma; Ki)"•PSME3•Hs.152978•ENSG00000131467••8537 //
proteasome activator complex // inferred from electronic annotation•8538 //
proteasome activator activity // inferred from electronic annotation
227143_s_at•"gb:AA706658 /DB_XREF=gi:2716576 /DB_XREF=ag90h05.r1
/CLONE=IMAGE:1141785 /FEA=EST /CNT=31 /TID=Hs.315689.1 /TIER=Stack /STK=20
/UG=Hs.315689 /UG_TITLE=Homo sapiens cDNA: FLJ22373 fis, clone
HRC06741"•2.17180362•2.275882422•BH3 interacting domain death
agonist•BID•Hs.474150•ENSG00000015475•8625 // induction of apoptosis via
death domain receptors // traceable author statement /// 8637 // apoptotic
mitochondrial changes // traceable author statement /// 43065 // positive
regulation of apoptosis // inferred from electronic annotation•5624 //
membrane fraction // traceable author statement /// 5737 // cytoplasm //
inferred from electronic annotation /// 5739 // mitochondrion // traceable
author statement /// 5829 // cytosol // traceable author statement•5123 //
death receptor binding // traceable author statement
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/UG=Hs.246268 /UG_TITLE=ESTs, Highly similar to RF1M_HUMAN MITOCHONDRIAL
PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR
(H.sapiens)"•2.163604023•2.022705133•mitochondrial translational release
factor 1•MTRF1•Hs.382176•ENSG00000120662•6412 // protein biosynthesis //
inferred from electronic annotation /// 6415 // translational termination //
inferred from electronic annotation /// 6449 // regulation of translational
termination // traceable author statement•5739 // mitochondrion // traceable
author statement•3747 // translation release factor activity // inferred from
electronic annotation /// 3747 // translation release factor activity //
traceable author statement
206377_at•"gb:NM_001452.1 /DB_XREF=gi:4557594 /GEN=FOXF2 /FEA=FLmRNA /CNT=15
/TID=Hs.44481.0 /TIER=FL+Stack /STK=8 /UG=Hs.44481 /LL=2295 /DEF=Homo sapiens
forkhead box F2 (FOXF2), mRNA. /PROD=forkhead box F2 /FL=gb:U13220.1
gb:NM_001452.1"•2.158766665•2.318718032•forkhead box
F2•FOXF2•Hs.484423•ENSG00000137273•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 6366 // transcription from RNA
polymerase II promoter // not recorded"•5634 // nucleus // traceable author
statement /// 5667 // transcription factor complex // traceable author
statement•3700 // transcription factor activity // non-traceable author
statement /// 3702 // RNA polymerase II transcription factor activity // not
recorded /// 3713 // transcription coactivator activity // not recorded
224655_at•gb:AA432267 /DB_XREF=gi:2114655 /DB_XREF=zw78e08.s1
/CLONE=IMAGE:782342 /FEA=FLmRNA /CNT=268 /TID=Hs.43436.1 /TIER=Stack /STK=30
/UG=Hs.43436 /LL=50808 /UG_GENE=AKL3L /UG_TITLE=adenylate kinase 3 alpha like
/FL=gb:NM_016282.1 gb:AB021870.1•2.154872507•2.291640888•adenylate kinase
```

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3•AK3•Hs.493362•ENSG00000147853•"6139 // nucleobase, nucleoside, nucleotide
and nucleic acid metabolism // inferred from electronic annotation /// 8652
// amino acid biosynthesis // inferred from electronic annotation"•5739 //
mitochondrion // inferred from electronic annotation /// 5739 //
mitochondrion // inferred from sequence or structural similarity•4017 //
adenylate kinase activity // inferred from electronic annotation /// 4017 //
adenylate kinase activity // not recorded /// 4765 // shikimate kinase
activity // inferred from electronic annotation /// 5524 // ATP binding //
inferred from electronic
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/CLONE=IMAGE:3699955 /FEA=mRNA /CNT=84 /TID=Hs.22151.1 /TIER=Stack /STK=10
/UG=Hs.22151 /LL=57486 /UG_GENE=KIAA1226 /UG_TITLE=KIAA1226
protein•2.15318262•2.273737937•neurolysin (metallopeptidase M3
family)•NLN•Hs.247460•ENSG00000123213•6508 // proteolysis and peptidolysis //
inferred from electronic annotation•5739 // mitochondrion // inferred from
electronic annotation•4222 // metalloendopeptidase activity // inferred from
electronic annotation /// 8270 // zinc ion binding // inferred from
electronic annotation /// 16787 // hydrolase activity // inferred from
electronic annotation
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/CNT=98 /TID=Hs.152292.0 /TIER=FL+Stack /STK=28 /UG=Hs.152292 /LL=6594
/DEF=Homo sapiens SWISNF related, matrix associated, actin dependent
regulator of chromatin, subfamily a, member 1
(SMARCA1)"•2.145924929•2.398900649•"SWI/SNF related, matrix associated, actin
dependent regulator of chromatin, subfamily a, member
1"•SMARCA1•Hs.152292•ENSG00000102038•"6338 // chromatin remodeling //
traceable author statement /// 6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation"•5634 // nucleus // inferred from
electronic annotation /// 5634 // nucleus // traceable author statement•3677
// DNA binding // inferred from electronic annotation /// 4386 // helicase
activity // inferred from electronic annotation /// 4386 // helicase activity
// traceable author statement /// 5524 // ATP binding // inferred from
electronic annotation ///
211684_s_at•"gb:AF250307.1 /DB_XREF=gi:13649464 /FEA=FLmRNA /CNT=1
/TID=HsAffx.900515.594 /TIER=FL /STK=0 /DEF=Homo sapiens cytoplasmic dynein
intermediate chain 2C mRNA, complete cds. /PROD=cytoplasmic dynein
intermediate chain 2C /FL=gb:AF250307.1"•2.141391738•2.165141845•"dynein,
cytoplasmic, intermediate polypeptide 2 /// dynein, cytoplasmic, intermediate
polypeptide 2"•DNCI2•Hs.546250•ENSG00000077380•7018 // microtubule-based
movement // non-traceable author statement•5737 // cytoplasm // non-traceable
author statement /// 30286 // dynein complex // inferred from electronic
annotation•3777 // microtubule motor activity // non-traceable author
statement
238880_at•gb:AI241331 /DB_XREF=gi:3836728 /DB_XREF=qk17c02.x1
/CLONE=IMAGE:1869218 /FEA=EST /CNT=7 /TID=Hs.131765.0 /TIER=ConsEnd /STK=1
/UG=Hs.131765 /UG_TITLE=ESTs•2.141091724•2.900411142•general transcription
factor IIIA•GTF3A•Hs.445977•ENSG00000122034•"6350 // transcription //
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6383 //
transcription from RNA polymerase III promoter // traceable author statement
/// 9303 //"•5634 // nucleus // inferred from electronic annotation•3677 //
DNA binding // inferred from electronic annotation /// 3709 // RNA polymerase
III transcription factor activity // traceable author statement /// 3723 //
RNA binding // inferred from electronic annotation /// 8270 // zinc ion
binding // inferred f
224995_at•gb:AJ277587.1 /DB_XREF=gi:8920229 /GEN=Spir-1 /FEA=mRNA /CNT=163
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partial mRNA for Spir-1 protein (Spir-1 gene). /PROD=Spir-1
protein•2.134906775•2.153281215•spire homolog 1
(Drosophila)•SPIRE1•Hs.515283•ENSG00000134278••5634 // nucleus // inferred
from electronic annotation•
230130_at•gb:AI692523 /DB_XREF=gi:4969863 /DB_XREF=wd73d06.x1
/CLONE=IMAGE:2337227 /FEA=EST /CNT=13 /TID=Hs.110373.1 /TIER=Stack /STK=10
/UG=Hs.110373 /UG_TITLE=ESTs•2.130605708•3.910086543•Slit homolog 2
(Drosophila)•SLIT2•Hs.29802•ENSG00000145147•1657 // ureteric bud development
// inferred from mutant phenotype /// 6935 // chemotaxis // inferred from
electronic annotation /// 7155 // cell adhesion // inferred from electronic
annotation /// 7186 // G-protein coupled receptor protein signaling path•5615
// extracellular space // not recorded /// 16021 // integral to membrane //
inferred from electronic annotation•4963 // follicle stimulating hormone
receptor activity // inferred from electronic annotation /// 5102 // receptor
binding // traceable author statement /// 5198 // structural molecule
activity // inferred from electronic annotation /// 5509 // calcium io
231766_s_at•gb:U73778.1 /DB_XREF=gi:1846004 /GEN=COL12A1 /FEA=FLmRNA /CNT=26
/TID=Hs.101302.0 /TIER=ConsEnd /STK=0 /UG=Hs.101302 /LL=1303 /DEF=Human
collagen type XII alpha-1 precursor (COL12A1) mRNA. /PROD=collagen type XII
alpha-1 /FL=gb:NM_004370.3•2.12937992•2.719933315•"collagen, type XII, alpha
1"•COL12A1•Hs.101302•ENSG00000111799•1501 // skeletal development //
traceable author statement /// 6817 // phosphate transport // inferred from
electronic annotation /// 7155 // cell adhesion // inferred from electronic
```

```
annotation /// 30199 // collagen fibril organization // non-traceable a•5578
// extracellular matrix (sensu Metazoa) // inferred from electronic
annotation /// 5595 // collagen type XII // non-traceable author statement
/// 5595 // collagen type XII // traceable author statement /// 5737 //
cytoplasm // inferred from electron•5198 // structural molecule activity //
inferred from electronic annotation /// 5515 // protein binding // inferred
from electronic annotation /// 30020 // extracellular matrix structural
constituent conferring tensile strength // non-traceable author sta
210868_s_at•"gb:BC001305.1 /DB_XREF=gi:12654918 /FEA=FLmRNA /CNT=2
/TID=Hs.211556.1 /TIER=FL /STK=0 /UG=Hs.211556 /LL=79071 /UG_GENE=MGC5487
/DEF=Homo sapiens, clone MGC:5487, mRNA, complete cds. /PROD=Unknown (protein
for MGC:5487) /FL=gb:BC001305.1"•2.129329528•2.591424322•"ELOVL family member
6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like,
yeast)"•ELOVL6•Hs.412939•ENSG00000170522••16021 // integral to membrane //
inferred from electronic annotation•
232181_at•"gb:AU157049 /DB_XREF=gi:11018570 /DB_XREF=AU157049
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/UG=Hs.159475 /UG_TITLE=Homo sapiens cDNA FLJ14284 fis, clone
PLACE1005898"•2.127169268•3.531424951•hypothetical protein
LOC153346•LOC153346•••••
202925_s_at•"gb:NM_002657.2 /DB_XREF=gi:6031195 /GEN=PLAGL2 /FEA=FLmRNA
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/DEF=Homo sapiens pleiomorphic adenoma gene-like 2 (PLAGL2), mRNA.
/PROD=pleiomorphic adenoma gene-like 2
/FL=gb:NM_002657.2"•2.124718537•3.492289387•pleiomorphic adenoma gene-like
2•PLAGL2•Hs.154104•ENSG00000126003•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation"•5634 // nucleus // inferred from
electronic annotation•3700 // transcription factor activity // traceable
author statement /// 8270 // zinc ion binding // inferred from electronic
annotation
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/UG=Hs.294018 /UG_TITLE=ESTs•2.120400755•2.488821862•Kruppel-like factor
12•KLF12•Hs.373857•ENSG00000118922•6350 // transcription // inferred from
electronic annotation /// 6357 // regulation of transcription from RNA
polymerase II promoter // traceable author statement•5634 // nucleus //
inferred from electronic annotation•3700 // transcription factor activity //
traceable author statement /// 3714 // transcription corepressor activity //
traceable author statement /// 8270 // zinc ion binding // inferred from
electronic annotation
204540_at•"gb:NM_001958.1 /DB_XREF=gi:4503474 /GEN=EEF1A2 /FEA=FLmRNA
/CNT=112 /TID=Hs.2642.0 /TIER=FL+Stack /STK=16 /UG=Hs.2642 /LL=1917 /DEF=Homo
sapiens eukaryotic translation elongation factor 1 alpha 2 (EEF1A2), mRNA.
/PROD=eukaryotic translation elongation
fac"•2.118715748•2.868424992•eukaryotic translation elongation factor 1 alpha
2•EEF1A2•Hs.433839•ENSG00000101210•6412 // protein biosynthesis // inferred
from electronic annotation /// 6414 // translational elongation // inferred
from electronic annotation•5634 // nucleus // inferred from electronic
annotation /// 5737 // cytoplasm // inferred from electronic annotation•3746
// translation elongation factor activity // inferred from electronic
annotation /// 5525 // GTP binding // inferred from electronic annotation
208995_s_at•"gb:U40763.1 /DB_XREF=gi:1117967 /FEA=FLmRNA /CNT=195
/TID=Hs.77965.0 /TIER=FL /STK=0 /UG=Hs.77965 /LL=9360 /UG_GENE=PPIG
/DEF=Human Clk-associated RS cyclophilin CARS-Cyp mRNA, complete cds.
/PROD=CARS-Cyp /FL=gb:NM_004792.1
gb:U40763.1"•2.117453557•2.027158489•peptidyl-prolyl isomerase G (cyclophilin
G)•PPIG•Hs.470544•ENSG00000138398•6457 // protein folding // inferred from
electronic annotation /// 8380 // RNA splicing // traceable author
statement•5654 // nucleoplasm // traceable author statement•3755 //
peptidyl-prolyl cis-trans isomerase activity // inferred from electronic
annotation /// 16018 // cyclosporin A binding // traceable author statement
/// 16853 // isomerase activity // inferred from electronic annotation
203159_at•"gb:NM_014905.1 /DB_XREF=gi:7662327 /GEN=GLS /FEA=FLmRNA /CNT=140
/TID=Hs.239189.0 /TIER=FL+Stack /STK=52 /UG=Hs.239189 /LL=2744 /DEF=Homo
sapiens glutaminase (GLS), mRNA. /PROD=glutaminase C /FL=gb:AF223943.1
gb:AF327434.1 gb:NM_014905.1 gb:AB020645.1
gb:"•2.109268267•2.020916554•glutaminase•GLS•Hs.116448•ENSG00000115419•6543
// glutamine catabolism // non-traceable author statement•5739 //
mitochondrion // non-traceable author statement•4359 // glutaminase activity
// non-traceable author statement /// 16787 // hydrolase activity // inferred
from electronic annotation
1553764_a_at•"gb:NM_032876.1 /DB_XREF=gi:14249621 /TID=Hs2.64552.1 /CNT=12
/FEA=FLmRNA /TIER=FL /STK=0 /LL=84962 /UG_GENE=JUB /UG=Hs.64552
/UG_TITLE=jub, ajuba homolog (Xenopus laevis) /DEF=Homo sapiens jub, ajuba
homolog (Xenopus laevis) (JUB), mRNA.
/FL=gb:NM_032876."•2.099279274•4.992485733•"jub, ajuba homolog (Xenopus
laevis)"•JUB•Hs.508910•ENSG00000129474•••8270 // zinc ion binding // inferred
from electronic annotation
241687_at•gb:BE886288 /DB_XREF=gi:10340244 /DB_XREF=601509872F1
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locus••Hs.155775••••
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/FEA=EST /CNT=17 /TID=Hs.177788.0 /TIER=ConsEnd /STK=0 /UG=Hs.177788
/UG_TITLE=ESTs•2.093624047•2.654197554•Hypothetical gene supported by
AK096649••Hs.528187••••
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/CLONE=NT2RM4001836 /FEA=mRNA /CNT=64 /TID=Hs.26996.0 /TIER=Stack /STK=31
/UG=Hs.26996 /LL=27148 /UG_GENE=KIAA1278 /UG_TITLE=KIAA1278
protein•2.08641926•2.500748169•"serine/threonine kinase 36 (fused homolog,
Drosophila)"•STK36•Hs.471404•ENSG00000163482•6468 // protein amino acid
phosphorylation // non-traceable author statement /// 7076 // mitotic
chromosome condensation // inferred from electronic annotation••4674 //
protein serine/threonine kinase activity // non-traceable author statement
/// 5488 // binding // inferred from electronic annotation /// 5524 // ATP
binding // non-traceable author statement /// 16740 // transferase activity
// inferred from elec
203875_at•"gb:NM_003069.1 /DB_XREF=gi:4507066 /GEN=SMARCA1 /FEA=FLmRNA
/CNT=98 /TID=Hs.152292.0 /TIER=FL+Stack /STK=28 /UG=Hs.152292 /LL=6594
/DEF=Homo sapiens SWISNF related, matrix associated, actin dependent
regulator of chromatin, subfamily a, member 1
(SMARCA1)"•2.086187632•2.96295447•"SWI/SNF related, matrix associated, actin
dependent regulator of chromatin, subfamily a, member
1"•SMARCA1•Hs.152292•ENSG00000102038•"6338 // chromatin remodeling //
traceable author statement /// 6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation"•5634 // nucleus // inferred from
electronic annotation /// 5634 // nucleus // traceable author statement•3677
// DNA binding // inferred from electronic annotation /// 4386 // helicase
activity // inferred from electronic annotation /// 4386 // helicase activity
// traceable author statement /// 5524 // ATP binding // inferred from
electronic annotation ///
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/UG=Hs.161210 /UG_TITLE=ESTs•2.082787556•2.4543356•Treacher
Collins-Franceschetti syndrome 1•TCOF1•Hs.519672•ENSG00000070814•1501 //
skeletal development // traceable author statement /// 6810 // transport //
inferred from electronic annotation•5634 // nucleus // inferred from
electronic annotation /// 5730 // nucleolus // traceable author
statement•5215 // transporter activity // traceable author statement
219559_at•"gb:NM_022082.1 /DB_XREF=gi:11545794 /GEN=FLJ23412 /FEA=FLmRNA
/CNT=29 /TID=Hs.34487.0 /TIER=FL+Stack /STK=24 /UG=Hs.34487 /LL=63910
/DEF=Homo sapiens hypothetical protein FLJ23412 (FLJ23412), mRNA.
/PROD=hypothetical protein FLJ23412
/FL=gb:NM_022082.1"•2.082337262•2.861953839•chromosome 20 open reading frame
59•C20orf59•Hs.512686•ENSG00000101194•6810 // transport // inferred from
electronic annotation•16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from electronic
annotation•5215 // transporter activity // inferred from electronic
annotation
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/UG=Hs.10432 /UG_TITLE=ESTs•2.068828957•2.118237802•Rho-related BTB domain
containing 3•RHOBTB3•Hs.445030•ENSG00000164292•••3924 // GTPase activity //
non-traceable author statement /// 5515 // protein binding // inferred from
electronic annotation
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(JP1) mRNA, complete cds. /PROD=c-Myc target JP1
/FL=gb:AY029179.1"•2.068601364•2.551220643•cell division cycle associated 7
/// cell division cycle associated 7•CDCA7•Hs.470654•ENSG00000144354•910 //
cytokinesis // inferred from electronic annotation••
224151_s_at•"gb:AF183419.1 /DB_XREF=gi:9963776 /FEA=FLmRNA /CNT=2
/TID=Hs.43436.0 /TIER=FL /STK=0 /UG=Hs.43436 /LL=50808 /UG_GENE=AKL3L
/DEF=Homo sapiens GTP:AMP phosphotransferase mRNA, complete cds; nuclear gene
for mitochondrial product. /PROD=GTP:AMP
phosphotransf"•2.065756364•2.460862268•adenylate kinase
3•AK3•Hs.493362•ENSG00000147853•"6139 // nucleobase, nucleoside, nucleotide
and nucleic acid metabolism // inferred from electronic annotation /// 8652
// amino acid biosynthesis // inferred from electronic annotation"•5739 //
mitochondrion // inferred from electronic annotation /// 5739 //
mitochondrion // inferred from sequence or structural similarity•4017 //
adenylate kinase activity // inferred from electronic annotation /// 4017 //
adenylate kinase activity // not recorded /// 4765 // shikimate kinase
activity // inferred from electronic annotation /// 5524 // ATP binding //
inferred from electronic
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FLJ11689 fis, clone HEMBA1004977. /DEF=Homo sapiens cDNA FLJ11689 fis, clone
HEMBA1004977."•2.058627156•2.383566787•Nucleosome assembly protein 1-like
1•NAP1L1•Hs.524599•ENSG00000187109•6260 // DNA replication // traceable
```

```
author statement /// 6334 // nucleosome assembly // traceable author
statement /// 8284 // positive regulation of cell proliferation // traceable
author statement•5634 // nucleus // inferred from electronic annotation ///
5678 // chromatin assembly complex // traceable author statement•
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/TID=Hs.79334.0 /TIER=FL+Stack /STK=37 /UG=Hs.79334 /LL=4783 /DEF=Homo
sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /PROD=nuclear
factor, interleukin 3 regulated /FL=gb:NM"•2.058042334•3.586866201•"nuclear
factor, interleukin 3 regulated"•NFIL3•Hs.79334•ENSG00000165030•"6355 //
regulation of transcription, DNA-dependent // inferred from electronic
annotation /// 6366 // transcription from RNA polymerase II promoter //
traceable author statement /// 6955 // immune response // traceable author
statement"•5634 // nucleus // traceable author statement•3700 //
transcription factor activity // traceable author statement /// 3714 //
transcription corepressor activity // traceable author statement
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/TID=Hs.8867.1 /TIER=FL /STK=0 /UG=Hs.8867 /LL=3491 /UG_TITLE=cysteine-rich,
angiogenic inducer, 61 /DEF=Homo sapiens CYR61 mRNA, complete cds.
/FL=gb:AF003114.1"•2.057980668•2.547293996•"cysteine-rich, angiogenic
inducer, 61"•CYR61•Hs.8867•ENSG00000142871•1558 // regulation of cell growth
// inferred from electronic annotation /// 6935 // chemotaxis // inferred
from electronic annotation /// 7155 // cell adhesion // inferred from
electronic annotation /// 7600 // sensory perception // inferred from
electro•5576 // extracellular region // inferred from electronic
annotation•5520 // insulin-like growth factor binding // inferred from
electronic annotation /// 8201 // heparin binding // inferred from electronic
annotation
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/UG=Hs.96996 /UG_TITLE=ESTs•2.056405047•2.006488979•Heterogeneous nuclear
ribonucleoprotein A0•HNRPA0•Hs.96996•ENSG00000177733•6397 // mRNA processing
// traceable author statement•30530 // heterogeneous nuclear
ribonucleoprotein complex // traceable author statement•166 // nucleotide
binding // inferred from electronic annotation /// 3723 // RNA binding //
traceable author statement
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/DEF=Homo sapiens neurogenic extracellular slit protein Slit2 mRNA, complete
cds. /PROD=neurogenic extracellular slit protein Slit2
"•2.052969788•3.115307187•slit homolog 2
(Drosophila)•SLIT2•Hs.29802•ENSG00000145147•1657 // ureteric bud development
// inferred from mutant phenotype /// 6935 // chemotaxis // inferred from
electronic annotation /// 7155 // cell adhesion // inferred from electronic
annotation /// 7186 // G-protein coupled receptor protein signaling path•5615
// extracellular space // not recorded /// 16021 // integral to membrane //
inferred from electronic annotation•4963 // follicle stimulating hormone
receptor activity // inferred from electronic annotation /// 5102 // receptor
binding // traceable author statement /// 5198 // structural molecule
activity // inferred from electronic annotation /// 5509 // calcium io
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/UG=Hs.104413 /UG_TITLE=ESTs•2.049595349•3.382698928•"CDNA clone
IMAGE:5295896, partial cds"••Hs.224080••••
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sapiens hypothetical protein FLJ10895 (FLJ10895), mRNA. /PROD=hypothetical
protein FLJ10895 /FL=gb:NM_019084.1"•2.048303242•2.911399121•cyclin
J•CCNJ•Hs.281348•ENSG00000107443•74 // regulation of cell cycle // inferred
from electronic annotation•5634 // nucleus // inferred from electronic
annotation•
214919_s_at•gb:R39094 /DB_XREF=gi:796550 /DB_XREF=yf50c09.s1
/CLONE=IMAGE:25528 /FEA=mRNA /CNT=10 /TID=Hs.301226.2 /TIER=ConsEnd /STK=0
/UG=Hs.301226 /LL=57450 /UG_GENE=KIAA1085 /UG_TITLE=KIAA1085
protein•2.047639336•3.437818512•eukaryotic translation initiation factor 4E
binding protein 3 /// MASK-4E-BP3 alternate reading frame gene•EIF4EBP3 ///
MASK-BP3••ENSG00000131503•6445 // regulation of translation // inferred from
electronic annotation /// 17148 // negative regulation of protein
biosynthesis // inferred from electronic annotation /// 45947 // negative
regulation of translational initiation // non-traceable author s•16281 //
eukaryotic translation initiation factor 4F complex // non-traceable author
statement•8190 // eukaryotic initiation factor 4E binding // inferred from
electronic annotation /// 30371 // translation repressor activity //
non-traceable author statement /// 3676 // nucleic acid binding // inferred
from electronic annotation
242584_at•gb:AI954412 /DB_XREF=gi:5746722 /DB_XREF=wr49a05.x1
/CLONE=IMAGE:2490992 /FEA=EST /CNT=7 /TID=Hs.98427.0 /TIER=ConsEnd /STK=0
/UG=Hs.98427 /UG_TITLE=ESTs•2.045313129•2.349988904•hypothetical protein
FLJ13305•FLJ13305•Hs.440466•ENSG00000170264•••
228308_at•gb:AI452444 /DB_XREF=gi:4285654 /DB_XREF=tj62a09.x1
/CLONE=IMAGE:2146072 /FEA=EST /CNT=19 /TID=Hs.24048.1 /TIER=Stack /STK=9
/UG=Hs.24048 /LL=51303 /UG_GENE=LOC51303 /UG_TITLE=FK506 binding protein
```

```
precursor•2.043707227•2.914934374•"FK506 binding protein 11, 19
kDa"•FKBP11•Hs.438695•ENSG00000134285•6457 // protein folding // inferred
from electronic annotation••3755 // peptidyl-prolyl cis-trans isomerase
activity // inferred from electronic annotation /// 16853 // isomerase
activity // inferred from electronic annotation
233518_at•"gb:AU144449 /DB_XREF=gi:11005970 /DB_XREF=AU144449
/CLONE=HEMBA1001940 /FEA=mRNA /CNT=3 /TID=Hs.324024.0 /TIER=ConsEnd /STK=1
/UG=Hs.324024 /UG_TITLE=Homo sapiens cDNA FLJ11493 fis, clone
HEMBA1001940"•2.042813572•6.830071568•Clone pp9372 unknown
mRNA••Hs.469287••••
221731_x_at•gb:BF218922 /DB_XREF=gi:11112418 /DB_XREF=601885091F1
/CLONE=IMAGE:4103447 /FEA=mRNA /CNT=344 /TID=Hs.81800.4 /TIER=Stack /STK=72
/UG=Hs.81800 /LL=1462 /UG_GENE=CSPG2 /UG_TITLE=chondroitin sulfate
proteoglycan 2 (versican)•2.035585844•2.346026753•chondroitin sulfate
proteoglycan 2 (versican)•CSPG2•Hs.443681•ENSG00000038427•7275 // development
// traceable author statement /// 8037 // cell recognition // traceable
author statement•5578 // extracellular matrix (sensu Metazoa) // traceable
author statement•5509 // calcium ion binding // inferred from electronic
annotation /// 5529 // sugar binding // inferred from electronic annotation
/// 5540 // hyaluronic acid binding // traceable author statement
202786_at•"gb:NM_013233.1 /DB_XREF=gi:7019542 /GEN=SPAK /FEA=FLmRNA /CNT=138
/TID=Hs.199263.0 /TIER=FL+Stack /STK=50 /UG=Hs.199263 /LL=27347 /DEF=Homo
sapiens Ste-20 related kinase (SPAK), mRNA. /PROD=Ste-20 related kinase
/FL=gb:NM_013233.1 gb:AF030403.1 gb:AF09998"•2.033782057•2.577912573•"serine
threonine kinase 39 (STE20/SPS1 homolog,
yeast)"•STK39•Hs.276271•ENSG00000198648•6468 // protein amino acid
phosphorylation // non-traceable author statement /// 6950 // response to
stress // non-traceable author statement•5634 // nucleus // non-traceable
author statement /// 5737 // cytoplasm // non-traceable author statement•4702
// receptor signaling protein serine/threonine kinase activity //
non-traceable author statement /// 4713 // protein-tyrosine kinase activity
// inferred from electronic annotation /// 5524 // ATP binding //
non-traceable author statement /// 16740 /
1555765_a_at•"gb:AF493872.1 /DB_XREF=gi:20147636 /GEN=GNG4 /TID=Hs2.32976.3
/CNT=1 /FEA=FLmRNA /TIER=FL /STK=1 /LL=2786 /UG=Hs.32976 /DEF=Homo sapiens
guanine nucleotide binding protein gamma 4 (GNG4) mRNA, complete cds.
/PROD=guanine nucleotide binding protein gamma
4"•2.020614872•3.023647346•"guanine nucleotide binding protein (G protein),
gamma 4"•GNG4•Hs.159711•ENSG00000168243•7165 // signal transduction //
inferred from electronic annotation /// 8277 // regulation of G-protein
coupled receptor protein signaling pathway // traceable author statement•5834
// heterotrimeric G-protein complex // inferred from electronic annotation
/// 5886 // plasma membrane // traceable author statement•4871 // signal
transducer activity // inferred from electronic annotation
212624_s_at•gb:BF339445 /DB_XREF=gi:11285900 /DB_XREF=602038795F1
/CLONE=IMAGE:4186582 /FEA=mRNA /CNT=135 /TID=Hs.169965.1 /TIER=Stack /STK=42
/UG=Hs.169965 /LL=1123 /UG_GENE=CHN1 /UG_TITLE=chimerin (chimaerin)
1•2.013541258•2.268678916•chimerin (chimaerin)
1•CHN1•Hs.380138•ENSG00000128656•7242 // intracellular signaling cascade //
inferred from electronic annotation••5070 // SH3/SH2 adaptor activity //
traceable author statement /// 5096 // GTPase activator activity // not
recorded /// 19992 // diacylglycerol binding // inferred from electronic
annotation
235573_at•gb:AL536101 /DB_XREF=gi:12799594 /DB_XREF=AL536101
/CLONE=CS0DF022YM06 (3 prime) /FEA=EST /CNT=11 /TID=Hs.201615.0 /TIER=ConsEnd
/STK=0 /UG=Hs.201615 /UG_TITLE=ESTs•2.013374408•4.312608304•Heat shock
105kDa/110kDa protein 1•HSPH1•Hs.36927•ENSG00000120694•6457 // protein
folding // inferred from electronic annotation /// 6986 // response to
unfolded protein // traceable author statement•5737 // cytoplasm // traceable
author statement•5524 // ATP binding // inferred from electronic annotation
204693_at•"gb:NM_007061.1 /DB_XREF=gi:5902007 /GEN=MSE55 /FEA=FLmRNA /CNT=57
/TID=Hs.148101.0 /TIER=FL /STK=0 /UG=Hs.148101 /LL=11135 /DEF=Homo sapiens
serum constituent protein (MSE55), mRNA. /PROD=serum constituent protein
/FL=gb:M88338.1 gb:NM_007061.1"•2.010641162•2.873314705•CDC42 effector
protein (Rho GTPase binding) 1•CDC42EP1•Hs.474797•ENSG00000128283•7275 //
development // traceable author statement•5615 // extracellular space //
traceable author statement•
235392_at•gb:BG403162 /DB_XREF=gi:13296610 /DB_XREF=602418990F1
/CLONE=IMAGE:4525798 /FEA=EST /CNT=14 /TID=Hs.43845.0 /TIER=ConsEnd /STK=0
/UG=Hs.43845 /UG_TITLE=ESTs•2.00716042•2.315951359•Insulin receptor substrate
1•IRS1•Hs.471508•ENSG00000169047•7165 // signal transduction // traceable
author statement•5737 // cytoplasm // traceable author statement•4871 //
signal transducer activity // traceable author statement /// 5069 //
transmembrane receptor protein tyrosine kinase docking protein activity //
traceable author statement /// 5158 // insulin receptor binding // inferred
from electronic annotation
229700_at•gb:BE966267 /DB_XREF=gi:11771500 /DB_XREF=601660507R1
/CLONE=IMAGE:3906240 /FEA=EST /CNT=10 /TID=Hs.158101.0 /TIER=Stack /STK=9
/UG=Hs.158101 /UG_TITLE=ESTs•2.00709271•2.365285405•hypothetical protein
LOC148203•LOC148203•Hs.359535••"6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation"•5622 // intracellular
```

```
// inferred from electronic annotation•3676 // nucleic acid binding //
inferred from electronic annotation
227682_at•"gb:BE645154 /DB_XREF=gi:9969389 /DB_XREF=7e64b02.x1
/CLONE=IMAGE:3287211 /FEA=EST /CNT=33 /TID=Hs.99216.0 /TIER=Stack /STK=22
/UG=Hs.99216 /UG_TITLE=ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY
SX SEQUENCE CONTAMINATION WARNING ENTRY
(H.sapiens)"•0.498765774•0.465094396•Transcribed locus••Hs.99216••••
204359_at•"gb:NM_013231.1 /DB_XREF=gi:7019380 /GEN=FLRT2 /FEA=FLmRNA /CNT=86
/TID=Hs.48998.0 /TIER=FL+Stack /STK=27 /UG=Hs.48998 /LL=23768 /DEF=Homo
sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA.
/PROD=fibronectin leucine rich transmembrane
"•0.497739655•0.247544704•fibronectin leucine rich transmembrane protein
2•FLRT2•Hs.533710•ENSG00000185070•7155 // cell adhesion // inferred from
electronic annotation•5578 // extracellular matrix (sensu Metazoa) //
non-traceable author statement /// 5887 // integral to plasma membrane //
non-traceable author statement•"5057 // receptor signaling protein activity
// non-traceable author statement /// 30674 // protein binding, bridging //
non-traceable author statement"
208936_x_at•"gb:AF074000.1 /DB_XREF=gi:5577965 /FEA=FLmRNA /CNT=266
/TID=Hs.4082.0 /TIER=FL /STK=0 /UG=Hs.4082 /LL=3964 /UG_GENE=LGALS8 /DEF=Homo
sapiens Po66 carbohydrate binding protein mRNA, complete cds. /PROD=Po66
carbohydrate binding protein /FL=gb:AF074000.1
gb"•0.497445045•0.470824799•"lectin, galactoside-binding, soluble, 8
(galectin 8)"•LGALS8•Hs.4082•ENSG00000116977••5615 // extracellular space //
traceable author statement•5529 // sugar binding // inferred from electronic
annotation /// 5529 // sugar binding // traceable author statement
227487_s_at•gb:AI359165 /DB_XREF=gi:4110786 /DB_XREF=qy26d12.x1
/CLONE=IMAGE:2013143 /FEA=EST /CNT=33 /TID=Hs.21858.1 /TIER=Stack /STK=21
/UG=Hs.21858 /LL=10292 /UG_GENE=TNRC3 /UG_TITLE=trinucleotide repeat
containing 3•0.496088147•0.337904897•••••••
204491_at•"gb:R40917 /DB_XREF=gi:823119 /DB_XREF=yf75d09.s1
/CLONE=IMAGE:28220 /FEA=FLmRNA /CNT=58 /TID=Hs.172081.0 /TIER=Stack /STK=8
/UG=Hs.172081 /LL=5144 /UG_GENE=PDE4D /UG_TITLE=phosphodiesterase 4D,
cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase
E"•0.495878127•0.20918572•"Phosphodiesterase 4D, cAMP-specific
(phosphodiesterase E3 dunce homolog,
Drosophila)"•PDE4D•Hs.117545•ENSG00000113448•7165 // signal transduction //
inferred from electronic annotation /// 9187 // cyclic nucleotide metabolism
// inferred from sequence or structural similarity•5625 // soluble fraction
// traceable author statement /// 5626 // insoluble fraction // traceable
author statement•"4114 // 3',5'-cyclic-nucleotide phosphodiesterase activity
// non-traceable author statement /// 4115 // cAMP-specific phosphodiesterase
activity // traceable author statement /// 16787 // hydrolase activity //
inferred from electronic annotation"
209763_at•gb:AL049176 /DB_XREF=gi:4808226 /FEA=FLmRNA /CNT=84 /TID=Hs.82223.0
/TIER=Stack /STK=46 /UG=Hs.82223 /LL=57803 /UG_GENE=LOC57803
/UG_TITLE=chordin-like /DEF=Human DNA sequence from clone 141H5 on chromosome
Xq22.1-23. Contains parts of a novel Chordin
LIK•0.495190031•0.353425976•chordin-like
1•CHRDL1•Hs.496587•ENSG00000101938•7275 // development // inferred from
electronic annotation••
223633_s_at•"gb:BC005081.1 /DB_XREF=gi:13477230 /FEA=FLmRNA /CNT=42
/TID=Hs.158515.0 /TIER=FL /STK=2 /UG=Hs.158515 /DEF=Homo sapiens, clone
MGC:13038, mRNA, complete cds. /PROD=Unknown (protein for MGC:13038)
/FL=gb:BC005081.1"•0.494656489•0.486576549•brevican•BCAN•Hs.516904•ENSG0000013
2692•7155 // cell adhesion // inferred from electronic annotation•16020 //
membrane // inferred from electronic annotation•5529 // sugar binding //
inferred from electronic annotation /// 5540 // hyaluronic acid binding //
inferred from electronic annotation
226748_at•gb:AI674731 /DB_XREF=gi:4875211 /DB_XREF=wd19g07.x1
/CLONE=IMAGE:2328636 /FEA=EST /CNT=44 /TID=Hs.293658.0 /TIER=Stack /STK=21
/UG=Hs.293658 /UG_TITLE=ESTs•0.493731763•0.466308805•hypothetical protein
MGC35274•MGC35274•Hs.134045•ENSG00000140280•16998 // cell wall catabolism //
inferred from electronic annotation••
209102_s_at•"gb:AF019214.1 /DB_XREF=gi:2460168 /FEA=FLmRNA /CNT=179
/TID=Hs.10882.1 /TIER=FL+Stack /STK=98 /UG=Hs.10882 /LL=26959 /UG_GENE=HBP1
/DEF=Homo sapiens HMG box containing protein 1 mRNA, complete cds. /PROD=HMG
box containing protein 1 /FL=gb:AF019214.1"•0.491287807•0.399539028•HMG-box
transcription factor 1•HBP1•Hs.162032•ENSG00000105856•"6355 // regulation of
transcription, DNA-dependent // inferred from electronic annotation"•5634 //
nucleus // inferred from electronic annotation•3677 // DNA binding //
inferred from electronic annotation
219090_at•"gb:NM_020689.2 /DB_XREF=gi:10518346 /GEN=NCKX3 /FEA=FLmRNA /CNT=81
/TID=Hs.12321.0 /TIER=FL+Stack /STK=21 /UG=Hs.12321 /LL=57419 /DEF=Homo
sapiens sodium calcium exchanger (NCKX3), mRNA. /PROD=sodium calcium
exchanger /FL=gb:AF169257.2 gb:NM_020689.2"•0.490291045•0.187346281•"solute
carrier family 24 (sodium/potassium/calcium exchanger), member
3"•SLC24A3•Hs.211252•ENSG00000185052•6811 // ion transport // inferred from
electronic annotation /// 6813 // potassium ion transport // inferred from
electronic annotation /// 6814 // sodium ion transport // inferred from
electronic annotation /// 6816 // calcium ion transport // inferred f•16021
```

```
// integral to membrane // inferred from electronic annotation•15293 //
symporter activity // inferred from electronic annotation /// 15297 //
antiporter activity // inferred from electronic annotation
205364_at•"gb:NM_003500.1 /DB_XREF=gi:4501868 /GEN=ACOX2 /FEA=FLmRNA /CNT=47
/TID=Hs.9795.0 /TIER=FL+Stack /STK=26 /UG=Hs.9795 /LL=8309 /DEF=Homo sapiens
acyl-Coenzyme A oxidase 2, branched chain (ACOX2), mRNA. /PROD=acyl-Coenzyme
A oxidase 2, branched chain /FL=gb:"•0.489066396•0.298773856•"acyl-Coenzyme A
oxidase 2, branched chain"•ACOX2•Hs.444959•ENSG00000168306•6118 // electron
transport // inferred from electronic annotation /// 6629 // lipid metabolism
// inferred from electronic annotation /// 6631 // fatty acid metabolism //
inferred from electronic annotation /// 6635 // fatty acid beta-oxidation //
inferre•5777 // peroxisome // non-traceable author statement•3995 // acyl-CoA
dehydrogenase activity // inferred from electronic annotation /// 3997 //
acyl-CoA oxidase activity // traceable author statement /// 16491 //
oxidoreductase activity // inferred from electronic annotation
206761_at•"gb:NM_005816.1 /DB_XREF=gi:5032140 /GEN=TACTILE /FEA=FLmRNA /CNT=9
/TID=Hs.142023.0 /TIER=FL /STK=1 /UG=Hs.142023 /LL=10225 /DEF=Homo sapiens T
cell activation, increased late expression (TACTILE), mRNA. /PROD=T cell
activation, increased late expression "•0.487977518•0.354348581•CD96
antigen•CD96•Hs.142023•ENSG00000153283•6955 // immune response // traceable
author statement /// 7155 // cell adhesion // traceable author statement•5886
// plasma membrane // traceable author statement /// 5887 // integral to
plasma membrane // traceable author statement•
222269_at•"gb:W87634 /DB_XREF=gi:1401698 /DB_XREF=zh67b09.s1
/CLONE=IMAGE:417113 /FEA=EST /CNT=19 /TID=Hs.17947.0 /TIER=ConsEnd /STK=4
/UG=Hs.17947 /UG_TITLE=ESTs, Weakly similar to K02F3.10
(C.elegans)"•0.487814463•0.386487221•chromosome X open reading frame
33•CXorf33•Hs.512181•ENSG00000155008•••
218706_s_at•gb:AW575493 /DB_XREF=gi:7247032
/DB_XREF=UI-HF-BM0-adp-a-04-0-UI.s1 /CLONE=IMAGE:3062287 /FEA=FLmRNA /CNT=96
/TID=Hs.235445.0 /TIER=Stack /STK=19 /UG=Hs.235445 /LL=65983
/UG_GENE=FLJ21313 /UG_TITLE=hypothetical protein FLJ21313
/FL=gb:NM_023927.1•0.487267562•0.258522569•HCV NS3-transactivated protein
2•NS3TP2•Hs.363558•ENSG00000155324•••
231535_x_at•gb:AI340264 /DB_XREF=gi:4077191 /DB_XREF=qx86d02.x1
/CLONE=IMAGE:2009379 /FEA=EST /CNT=9 /TID=Hs.194093.2 /TIER=Stack /STK=9
/UG=Hs.194093 /LL=54763 /UG_GENE=DKFZp434B1222 /UG_TITLE=AKAP-binding sperm
protein ropporin•0.487173212•0.240528417•"ropporin, rhophilin associated
protein 1"•ROPN1•Hs.458304•ENSG00000065371•7165 // signal transduction //
inferred from electronic annotation•16021 // integral to membrane // inferred
from electronic annotation /// 19867 // outer membrane // inferred from
electronic annotation•8603 // cAMP-dependent protein kinase regulator
activity // inferred from electronic annotation /// 15288 // porin activity
// inferred from electronic annotation
213537_at•gb:AI128225 /DB_XREF=gi:3596739 /DB_XREF=qc33e05.x1
/CLONE=IMAGE:1711424 /FEA=EST /CNT=30 /TID=Hs.914.1 /TIER=Stack /STK=16
/UG=Hs.914 /UG_TITLE=Human mRNA for SB classII histocompatibility antigen
alpha-chain•0.487110537•0.484878743•"major histocompatibility complex, class
II, DP alpha 1"•HLA-DPA1•Hs.347270•ENSG00000168384•"6955 // immune response
// non-traceable author statement /// 19884 // antigen presentation,
exogenous antigen // inferred from electronic annotation /// 19886 // antigen
processing, exogenous antigen via MHC class II // inferred from electronic
annotatio"•5887 // integral to plasma membrane // non-traceable author
statement /// 16020 // membrane // inferred from electronic annotation•45012
// MHC class II receptor activity // non-traceable author statement
201005_at•"gb:NM_001769.1 /DB_XREF=gi:4502692 /GEN=CD9 /FEA=FLmRNA /CNT=342
/TID=Hs.1244.0 /TIER=FL+Stack /STK=126 /UG=Hs.1244 /LL=928 /DEF=Homo sapiens
CD9 antigen (p24) (CD9), mRNA. /PROD=CD9 antigen (p24) /FL=gb:NM_001769.1
gb:L34068.1 gb:M38690.1"•0.485742804•0.473187647•CD9 antigen
(p24)•CD9•Hs.114286•ENSG00000010278•6928 // cell motility // inferred from
direct assay /// 7155 // cell adhesion // inferred from direct assay /// 7342
// fusion of sperm to egg plasma membrane // inferred from direct assay ///
30168 // platelet activation // non-traceable author statement•5886 // plasma
membrane // non-traceable author statement /// 5887 // integral to plasma
membrane // non-traceable author statement•5515 // protein binding //
inferred from physical interaction
222424_s_at•"gb:BC000805.1 /DB_XREF=gi:12654010 /FEA=FLmRNA /CNT=190
/TID=Hs.118064.0 /TIER=FL /STK=0 /UG=Hs.118064 /LL=64710 /UG_GENE=NUCKS
/DEF=Homo sapiens, similar to rat nuclear ubiquitous casein kinase 2, clone
MGC:5494, mRNA, complete cds. /PROD=similar to rat
"•0.484294177•0.371697343•nuclear ubiquitous casein kinase and
cyclin-dependent kinase substrate•NUCKS•Hs.213061•ENSG00000069275••5634 //
nucleus // inferred from electronic annotation•
229232_at•"gb:AW135740 /DB_XREF=gi:6139873 /DB_XREF=UI-H-BI1-acf-a-08-0-UI.s1
/CLONE=IMAGE:2714007 /FEA=EST /CNT=16 /TID=Hs.194071.0 /TIER=Stack /STK=10
/UG=Hs.194071 /UG_TITLE=ESTs, Weakly similar to unnamed protein product
(H.sapiens)"•0.483490329•0.441512199•hypothetical protein
FLJ36812•FLJ36812•Hs.234681•ENSG00000180979•••
216942_s_at•"gb:D28586.1 /DB_XREF=gi:466540 /FEA=mRNA /CNT=1 /TID=Hs.75626.2
/TIER=ConsEnd /STK=0 /UG=Hs.75626 /LL=965 /UG_GENE=CD58 /DEF=Human mRNA for
LFA-3(delta D2), partial cds. /PROD=LFA-3(delta
```

```
D2)"•0.482670273•0.387967681•"CD58 antigen, (lymphocyte function-associated
antigen 3)"•CD58•Hs.34341•ENSG00000116815•16337 // cell-cell adhesion //
non-traceable author statement /// 19735 // antimicrobial humoral response
(sensu Vertebrata) // not recorded•5624 // membrane fraction // not recorded
/// 5887 // integral to plasma membrane // non-traceable author statement ///
16020 // membrane // inferred from electronic annotation•5515 // protein
binding // inferred from physical interaction
232238_at•"gb:AK001380.1 /DB_XREF=gi:7022604 /FEA=mRNA /CNT=10
/TID=Hs.145479.0 /TIER=ConsEnd /STK=3 /UG=Hs.145479 /UG_TITLE=Homo sapiens
cDNA FLJ10518 fis, clone NT2RP2000814 /DEF=Homo sapiens cDNA FLJ10518 fis,
clone NT2RP2000814."•0.480444757•0.439701825•"asp (abnormal spindle)-like,
microcephaly associated (Drosophila)"•ASPM•Hs.121028•ENSG00000066279•910 //
cytokinesis // inferred from electronic annotation /// 7049 // cell cycle //
inferred from electronic annotation /// 7067 // mitosis // inferred from
electronic annotation•5634 // nucleus // inferred from electronic
annotation•5516 // calmodulin binding // inferred from electronic annotation
211990_at•"gb:M27487.1 /DB_XREF=gi:703088 /GEN=HLA-DPA1 /FEA=FLmRNA /CNT=358
/TID=Hs.914.0 /TIER=FL+Stack /STK=139 /UG=Hs.914 /DEF=Homo sapiens MHC class
II DPw3-alpha-1 chain mRNA, complete cds. /PROD=MHC class II DP3-alpha
/FL=gb:M27487.1"•0.480131624•0.401457362•"major histocompatibility complex,
class II, DP alpha 1"•HLA-DPA1•Hs.347270•ENSG00000168384•"6955 // immune
response // non-traceable author statement /// 19884 // antigen presentation,
exogenous antigen // inferred from electronic annotation /// 19886 // antigen
processing, exogenous antigen via MHC class II // inferred from electronic
annotatio"•5887 // integral to plasma membrane // non-traceable author
statement /// 16020 // membrane // inferred from electronic annotation•45012
// MHC class II receptor activity // non-traceable author statement
202191_s_at•gb:BE439987 /DB_XREF=gi:9439470 /DB_XREF=HTM1-745F /FEA=FLmRNA
/CNT=244 /TID=Hs.226133.0 /TIER=Stack /STK=21 /UG=Hs.226133 /LL=8522
/UG_GENE=GAS7 /UG_TITLE=growth arrest-specific 7 /FL=gb:AB007854.1
gb:NM_005890.1•0.478524055•0.472600783•growth arrest-specific
7•GAS7•Hs.462214•ENSG00000007237•7050 // cell cycle arrest // traceable
author statement /// 7399 // neurogenesis // inferred from electronic
annotation /// 30154 // cell differentiation // inferred from electronic
annotation••3700 // transcription factor activity // traceable author
statement
201310_s_at•"gb:NM_004772.1 /DB_XREF=gi:4758865 /GEN=P311 /FEA=FLmRNA
/CNT=470 /TID=Hs.142827.0 /TIER=FL+Stack /STK=195 /UG=Hs.142827 /LL=9315
/DEF=Homo sapiens P311 protein (P311), mRNA. /PROD=P311 protein
/FL=gb:U30521.1 gb:NM_004772.1
gb:U36189.1"•0.478126845•0.344337108•chromosome 5 open reading frame
13•C5orf13•Hs.483067•ENSG00000134986•••
206701_x_at•"gb:NM_003991.1 /DB_XREF=gi:4503466 /GEN=EDNRB /FEA=FLmRNA
/CNT=11 /TID=Hs.82002.1 /TIER=FL /STK=0 /UG=Hs.82002 /LL=1910 /DEF=Homo
sapiens endothelin receptor type B (EDNRB), transcript variant 2, mRNA.
/PROD=endothelin receptor type B isoform 2
/FL=gb:NM_"•0.478053423•0.391106406•endothelin receptor type
B•EDNRB•Hs.82002•ENSG00000136160•"7194 // negative regulation of adenylate
cyclase activity // traceable author statement /// 7200 // G-protein
signaling, coupled to IP3 second messenger (phospholipase C activating) //
traceable author statement /// 7399 // neurogenesis // traceable autho"•5886
// plasma membrane // traceable author statement /// 5887 // integral to
plasma membrane // traceable author statement•1584 // rhodopsin-like receptor
activity // inferred from electronic annotation /// 4872 // receptor activity
// inferred from electronic annotation /// 4962 // endothelin receptor
activity // traceable author statement
206560_s_at•"gb:NM_006533.1 /DB_XREF=gi:5729924 /GEN=MIA /FEA=FLmRNA /CNT=15
/TID=Hs.279651.0 /TIER=FL /STK=5 /UG=Hs.279651 /LL=8190 /DEF=Homo sapiens
melanoma inhibitory activity (MIA), mRNA. /PROD=melanoma inhibitory activity
/FL=gb:NM_006533.1"•0.477749735•0.438956087•melanoma inhibitory
activity•MIA•Hs.279651•ENSG00000187570•8283 // cell proliferation //
traceable author statement•5615 // extracellular space // traceable author
statement•8083 // growth factor activity // inferred from electronic
annotation
211744_s_at•"gb:BC005930.1 /DB_XREF=gi:13543544 /FEA=FLmRNA /CNT=1
/TID=HsAffx.900771.975 /TIER=FL /STK=0 /DEF=Homo sapiens, Similar to CD58
antigen, (lymphocyte function-associated antigen 3), clone MGC:14538, mRNA,
complete cds. /PROD=Similar to CD58 antigen,
(lymph"•0.477654281•0.425737464•"CD58 antigen, (lymphocyte
function-associated antigen 3) /// CD58 antigen, (lymphocyte
function-associated antigen 3)"•CD58•Hs.34341•ENSG00000116815•16337 //
cell-cell adhesion // non-traceable author statement /// 19735 //
antimicrobial humoral response (sensu Vertebrata) // not recorded•5624 //
membrane fraction // not recorded /// 5887 // integral to plasma membrane //
non-traceable author statement /// 16020 // membrane // inferred from
electronic annotation•5515 // protein binding // inferred from physical
interaction
221752_at•gb:AL041728 /DB_XREF=gi:5421076 /DB_XREF=DKFZp434O0717_s1
/CLONE=DKFZp434O0717 /FEA=mRNA /CNT=143 /TID=Hs.60377.0 /TIER=Stack /STK=42
/UG=Hs.60377 /LL=54434 /UG_GENE=KIAA1298 /UG_TITLE=KIAA1298
protein•0.477617619•0.448588433•"Homo sapiens, clone IMAGE:3832417,
```

```
mRNA"••Hs.199763••••
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/TID=Hs.65029.0 /TIER=FL+Stack /STK=22 /UG=Hs.65029 /LL=2619 /DEF=Homo
sapiens growth arrest-specific 1 (GAS1), mRNA. /PROD=growth arrest-specific 1
/FL=gb:NM_002048.1 gb:L13698.1"•0.477348608•0.299755966•growth
arrest-specific 1•GAS1•Hs.65029•ENSG00000180447•7049 // cell cycle //
inferred from electronic annotation /// 7050 // cell cycle arrest //
traceable author statement /// 8285 // negative regulation of cell
proliferation // traceable author statement /// 45749 // negative regulation
of S phase of mitoti•16020 // membrane // inferred from electronic annotation
/// 46658 // anchored to plasma membrane // inferred from sequence or
structural similarity•
215253_s_at•gb:AL049369.1 /DB_XREF=gi:4500160 /FEA=mRNA /CNT=5
/TID=Hs.250724.0 /TIER=ConsEnd /STK=0 /UG=Hs.250724 /UG_TITLE=Homo sapiens
mRNA; cDNA DKFZp586D0518 (from clone DKFZp586D0518) /DEF=Homo sapiens mRNA;
cDNA DKFZp586D0518 (from clone DKFZp586D0518).•0.476932594•0.340893874•Down
syndrome critical region gene 1•DSCR1•Hs.282326•ENSG00000159200•7165 //
signal transduction // traceable author statement /// 7417 // central nervous
system development // traceable author statement /// 8015 // circulation //
traceable author statement /// 19722 // calcium-mediated signaling //
inferred from electroni•5634 // nucleus // traceable author statement•3700 //
transcription factor activity // traceable author statement
221558_s_at•"gb:AF288571.1 /DB_XREF=gi:9858157 /GEN=LEF1 /FEA=FLmRNA /CNT=138
/TID=Hs.44865.1 /TIER=FL /STK=0 /UG=Hs.44865 /LL=51176 /DEF=Homo sapiens
lymphoid enhancer factor-1 (LEF1) mRNA, complete cds. /PROD=lymphoid enhancer
factor-1 /FL=gb:AF288571.1 gb:NM_016269"•0.476700799•0.365278954•lymphoid
enhancer-binding factor 1•LEF1•Hs.125132•ENSG00000138795•"6350 //
transcription // inferred from electronic annotation /// 6355 // regulation
of transcription, DNA-dependent // inferred from electronic annotation ///
16055 // Wnt receptor signaling pathway // inferred from electronic
annotation"•5634 // nucleus // inferred from electronic annotation•3700 //
transcription factor activity // inferred from electronic annotation
224990_at•"gb:BE972723 /DB_XREF=gi:10586059 /DB_XREF=601652143F1
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/UG=Hs.122489 /UG_TITLE=Homo sapiens cDNA FLJ13289 fis, clone
OVARC1001170"•0.476425678•0.388754667•hypothetical protein
LOC201895•LOC201895•Hs.205952•ENSG00000163683•••
230532_at•gb:BF001685 /DB_XREF=gi:10701960 /DB_XREF=7g91g02.x1
/CLONE=IMAGE:3313874 /FEA=EST /CNT=9 /TID=Hs.99736.0 /TIER=Stack /STK=8
/UG=Hs.99736 /UG_TITLE=ESTs•0.47608068•0.466317611•chromosome X open reading
frame 38•CXorf38•Hs.495961•ENSG00000185753•••
225612_s_at•gb:BE672260 /DB_XREF=gi:10032801 /DB_XREF=7d27a05.x1
/CLONE=IMAGE:3248432 /FEA=EST /CNT=63 /TID=Hs.101799.0 /TIER=Stack /STK=22
/UG=Hs.101799 /LL=54532 /UG_GENE=KIAA1350 /UG_TITLE=KIAA1350
protein•0.474927108•0.405075622•"UDP-GlcNAc:betaGal
beta-1,3-N-acetylglucosaminyltransferase
5"•B3GNT5•Hs.208267•ENSG00000176597•6486 // protein amino acid glycosylation
// traceable author statement /// 7417 // central nervous system development
// inferred from direct assay /// 9247 // glycolipid biosynthesis //
traceable author statement•5622 // intracellular // inferred from direct
assay /// 16020 // membrane // inferred from electronic annotation•"8378 //
galactosyltransferase activity // inferred from electronic annotation ///
8457 // beta-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide
beta-1,3-acetylglucosaminyltransferase activity // inferred from direct assay
/// 16757 // transferas"
226034_at•"gb:BE222344 /DB_XREF=gi:8909662 /DB_XREF=hu10g08.x1
/CLONE=IMAGE:3166238 /FEA=EST /CNT=70 /TID=Hs.166975.4 /TIER=Stack /STK=24
/UG=Hs.166975 /LL=6430 /UG_GENE=SFRS5 /UG_TITLE=splicing factor,
arginineserine-rich 5"•0.474647699•0.428456355•"Homo sapiens, clone
IMAGE:3881549, mRNA"••Hs.346735••••
214608_s_at•gb:AJ000098.1 /DB_XREF=gi:3928169 /GEN=EYA1C /FEA=FLmRNA /CNT=16
/TID=Hs.94210.0 /TIER=ConsEnd /STK=7 /UG=Hs.94210 /LL=2138 /UG_TITLE=eyes
absent (Drosophila) homolog 1 /DEF=Homo sapiens mRNA for EYA1C gene.
/FL=gb:NM_000503.1•0.471886076•0.282595378•eyes absent homolog 1
(Drosophila)•EYA1•Hs.491997•ENSG00000104313•"6350 // transcription //
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 7275 // development
// inferred from electronic annotation /// 7605 // perception of sound //
tr"•5634 // nucleus // inferred from electronic annotation•287 // magnesium
ion binding // inferred from electronic annotation /// 4721 // phosphoprotein
phosphatase activity // inferred from electronic annotation /// 4725 //
protein tyrosine phosphatase activity // inferred from electronic annotation
/// 16787 /
212314_at•"gb:AB018289.1 /DB_XREF=gi:3882212 /GEN=KIAA0746 /FEA=mRNA /CNT=199
/TID=Hs.49500.0 /TIER=Stack /STK=73 /UG=Hs.49500 /LL=23231 /DEF=Homo sapiens
mRNA for KIAA0746 protein, partial cds. /PROD=KIAA0746
protein"•0.469871615•0.48806017•KIAA0746
protein•KIAA0746•Hs.479384•ENSG00000091490•••5488 // binding // inferred from
electronic annotation
226353_at•gb:AI674647 /DB_XREF=gi:4875127 /DB_XREF=wd18g05.x1
/CLONE=IMAGE:2328536 /FEA=mRNA /CNT=55 /TID=Hs.28980.0 /TIER=Stack /STK=19
```

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/UG=Hs.28980 /UG_TITLE=Homo sapiens clone
HQ0270•0.46968837•0.419141996•signal peptide peptidase-like
2A•SPPL2A•Hs.401537•ENSG00000138600•6508 // proteolysis and peptidolysis //
inferred from electronic annotation•16021 // integral to membrane // inferred
from electronic annotation•8233 // peptidase activity // inferred from
electronic annotation /// 8717 // D-alanyl-D-alanine endopeptidase activity
// inferred from electronic annotation
222631_at•gb:AI862887 /DB_XREF=gi:5526994 /DB_XREF=tz91e02.x1
/CLONE=IMAGE:2295962 /FEA=FLmRNA /CNT=97 /TID=Hs.23920.0 /TIER=Stack /STK=30
/UG=Hs.23920 /LL=55300 /UG_GENE=FLJ11105 /UG_TITLE=hypothetical protein
FLJ11105 /FL=gb:NM_018323.1•0.468403462•0.49443516•phosphatidylinositol
4-kinase type-II beta•PI4K2B•Hs.443733•ENSG00000038210•••"16301 // kinase
activity // inferred from electronic annotation /// 16773 //
phosphotransferase activity, alcohol group as acceptor // inferred from
electronic annotation"
225847_at•"gb:AB037784.1 /DB_XREF=gi:7243106 /GEN=KIAA1363 /FEA=mRNA /CNT=76
/TID=Hs.22941.0 /TIER=Stack /STK=14 /UG=Hs.22941 /LL=57552 /DEF=Homo sapiens
mRNA for KIAA1363 protein, partial cds. /PROD=KIAA1363
protein"•0.467970058•0.354005654•arylacetamide deacetylase-like
1•AADACL1•Hs.444099•ENSG00000144959•••3824 // catalytic activity // inferred
from electronic annotation
221487_s_at•"gb:AF157510.1 /DB_XREF=gi:8886010 /FEA=FLmRNA /CNT=217
/TID=Hs.111680.1 /TIER=FL /STK=6 /UG=Hs.111680 /LL=2029 /UG_GENE=ENSA
/DEF=Homo sapiens beta endosulfine mRNA, complete cds. /PROD=beta endosulfine
/FL=gb:AF067170.1 gb:AF157510.1"•0.467728248•0.186751804•endosulfine
alpha•ENSA•Hs.510087•ENSG00000143420•6810 // transport // traceable author
statement /// 7584 // response to nutrients // traceable author
statement••5102 // receptor binding // traceable author statement /// 8200 //
ion channel inhibitor activity // traceable author statement
228840_at•gb:AW451115 /DB_XREF=gi:6991891 /DB_XREF=UI-H-BI3-alg-g-01-0-UI.s1
/CLONE=IMAGE:2736936 /FEA=EST /CNT=18 /TID=Hs.101550.0 /TIER=Stack /STK=16
/UG=Hs.101550 /UG_TITLE=ESTs•0.46762636•0.360925221•angiomotin like
1•AMOTL1•Hs.503594•ENSG00000166025•••
229735_s_at•gb:W15435 /DB_XREF=gi:1289816 /DB_XREF=zc19a07.s1
/CLONE=IMAGE:322740 /FEA=EST /CNT=14 /TID=Hs.13804.0 /TIER=Stack /STK=10
/UG=Hs.13804 /LL=57185 /UG_GENE=DJ462O23.2 /UG_TITLE=hypothetical protein
dJ462O23.2•0.467190984•0.218331319•Hypothetical protein
dJ462O23.2•DJ462O23.2•Hs.523442•ENSG00000001461•••
223125_s_at•gb:AL563236 /DB_XREF=gi:12912430 /DB_XREF=AL563236
/CLONE=CS0DD001YG18 (3 prime) /FEA=FLmRNA /CNT=166 /TID=Hs.12532.0
/TIER=Stack /STK=33 /UG=Hs.12532 /LL=81563 /UG_GENE=C1ORF21
/UG_TITLE=chromosome 1 open reading frame 21
/FL=gb:AF312864.1•0.467049905•0.409739697•chromosome 1 open reading frame
21•C1orf21•Hs.132369•ENSG00000116667•••
210367_s_at•"gb:AF010316.1 /DB_XREF=gi:2415307 /GEN=PIG12 /FEA=FLmRNA /CNT=21
/TID=Hs.146688.1 /TIER=FL /STK=0 /UG=Hs.146688 /LL=9536 /DEF=Homo sapiens
Pig12 (PIG12) mRNA, complete cds. /PROD=Pig12
/FL=gb:AF010316.1"•0.466587336•0.152820105•prostaglandin E
synthase•PTGES•Hs.146688•ENSG00000148344•6693 // prostaglandin metabolism //
traceable author statement /// 7165 // signal transduction // non-traceable
author statement /// 19735 // antimicrobial humoral response (sensu
Vertebrata) // not recorded•5624 // membrane fraction // traceable author
statement /// 16021 // integral to membrane // inferred from electronic
annotation•16853 // isomerase activity // inferred from electronic annotation
/// 50220 // prostaglandin-E synthase activity // inferred from electronic
annotation
218618_s_at•"gb:NM_022763.1 /DB_XREF=gi:12232434 /GEN=FLJ23399 /FEA=FLmRNA
/CNT=82 /TID=Hs.299883.0 /TIER=FL /STK=2 /UG=Hs.299883 /LL=64778 /DEF=Homo
sapiens hypothetical protein FLJ23399 (FLJ23399), mRNA. /PROD=hypothetical
protein FLJ23399 /FL=gb:NM_022763.1"•0.463063905•0.450217962•fibronectin type
III domain containing 3B•FNDC3B•Hs.159430•ENSG00000075420•••
224965_at•"gb:AU118419 /DB_XREF=gi:10933467 /DB_XREF=AU118419
/CLONE=HEMBA1003560 /FEA=mRNA /CNT=125 /TID=Hs.289026.1 /TIER=Stack /STK=8
/UG=Hs.289026 /LL=54331 /UG_GENE=GNG2 /UG_TITLE=guanine nucleotide binding
protein (G protein), gamma 2"•0.46107951•0.290642789•"guanine nucleotide
binding protein (G protein), gamma 2"•GNG2•Hs.187772•ENSG00000186469•7165 //
signal transduction // inferred from electronic annotation /// 7186 //
G-protein coupled receptor protein signaling pathway // inferred from
electronic annotation•5834 // heterotrimeric G-protein complex // inferred
from electronic annotation•4871 // signal transducer activity // inferred
from electronic annotation
202859_x_at•"gb:NM_000584.1 /DB_XREF=gi:10834977 /GEN=IL8 /FEA=FLmRNA
/CNT=368 /TID=Hs.624.0 /TIER=FL+Stack /STK=80 /UG=Hs.624 /LL=3576 /DEF=Homo
sapiens interleukin 8 (IL8), mRNA. /PROD=interleukin 8 /FL=gb:M17017.1
gb:M26383.1 gb:NM_000584.1"•0.460623895•0.46690573•interleukin
8•IL8•Hs.624•ENSG00000169429•1525 // angiogenesis // traceable author
statement /// 6928 // cell motility // traceable author statement /// 6935 //
chemotaxis // traceable author statement /// 7050 // cell cycle arrest //
inferred from direct assay /// 7186 // G-protein coupled recep•5615 //
extracellular space // traceable author statement /// 5625 // soluble
fraction // traceable author statement•5153 // interleukin-8 receptor binding
```

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// inferred from physical interaction /// 5515 // protein binding // inferred
from physical interaction /// 8009 // chemokine activity // traceable author
statement
224212_s_at•"gb:AF169689.1 /DB_XREF=gi:9587673 /GEN=PCDH-alpha10 /FEA=FLmRNA
/CNT=1 /TID=Hs.247735.1 /TIER=FL /STK=0 /UG=Hs.247735 /LL=56139 /DEF=Homo
sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA,
complete cds. /PROD=protocadherin alpha 10
alte"•0.460514063•0.484640652•"protocadherin alpha 9 /// protocadherin alpha
subfamily C, 2 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha
13 /// protocadherin alpha 12 /// protocadherin alpha 11 /// protocadherin
alpha 10 /// protocadherin alpha 8 /// protocadherin alp"•PCDHA9 /// PCDHAC2
/// PCDHAC1 /// PCDHA13 /// PCDHA12 /// PCDHA11 /// PCDHA10 /// PCDHA8 ///
PCDHA7 /// PCDHA6 /// PCDHA5 /// PCDHA4 /// PCDHA3 /// PCDHA2 ///
PCDHA1•Hs.199343•ENSG00000081842•7155 // cell adhesion // inferred from
electronic annotation /// 7156 // homophilic cell adhesion // inferred from
electronic annotation /// 7155 // cell adhesion // traceable author statement
/// 7399 // neurogenesis // traceable author statement•16020 // membrane //
inferred from electronic annotation /// 16021 // integral to membrane //
inferred from electronic annotation /// 5887 // integral to plasma membrane
// traceable author statement•5509 // calcium ion binding // inferred from
electronic annotation /// 5515 // protein binding // inferred from electronic
annotation
227176_at•gb:AL565362 /DB_XREF=gi:12916662 /DB_XREF=AL565362
/CLONE=CS0DF003YB20 (3 prime) /FEA=EST /CNT=32 /TID=Hs.90431.0 /TIER=Stack
/STK=13 /UG=Hs.90431 /UG_TITLE=ESTs•0.458383734•0.375322936•"Solute carrier
family 2 (facilitated glucose transporter), member
13"•SLC2A13•Hs.524341•ENSG00000151229•8643 // carbohydrate transport //
inferred from electronic annotation•16020 // membrane // inferred from
electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•5215 // transporter activity // inferred from
electronic annotation /// 5351 // sugar porter activity // inferred from
electronic annotation
228164_at•gb:BE964704 /DB_XREF=gi:11768297 /DB_XREF=601658243R1
/CLONE=IMAGE:3885682 /FEA=EST /CNT=24 /TID=Hs.36250.0 /TIER=Stack /STK=14
/UG=Hs.36250 /UG_TITLE=ESTs•0.457695909•0.392633932•Transcribed
locus••Hs.552817••••
233907_s_at•gb:R81445 /DB_XREF=gi:858048 /DB_XREF=yj02d01.r1
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/UG=Hs.21068 /LL=56256 /UG_GENE=DJ667H12.2 /UG_TITLE=hypothetical
protein•0.4571934•0.276744273•••••••
209539_at•"gb:D25304.1 /DB_XREF=gi:435445 /GEN=KIAA0006 /FEA=FLmRNA /CNT=81
/TID=Hs.79307.0 /TIER=Stack /STK=21 /UG=Hs.79307 /LL=9459 /UG_TITLE=RacCdc42
guanine exchange factor (GEF) 6 /DEF=Human mRNA for KIAA0006 gene, partial
cds. /FL=gb:D13631.1"•0.457093037•0.231673061•Rac/Cdc42 guanine nucleotide
exchange factor (GEF) 6•ARHGEF6•Hs.522795•ENSG00000129675•6915 // apoptosis
// non-traceable author statement /// 7254 // JNK cascade // non-traceable
author statement•5622 // intracellular // Unknown•5089 // Rho
guanyl-nucleotide exchange factor activity // non-traceable author statement
/// 5096 // GTPase activator activity // non-traceable author statement
227230_s_at•gb:BE855799 /DB_XREF=gi:10368049 /DB_XREF=7g07a07.x1
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/UG=Hs.205293 /LL=57482 /UG_GENE=KIAA1211 /UG_TITLE=KIAA1211
protein•0.456626231•0.462494764•KIAA1211
protein•KIAA1211•Hs.479783•ENSG00000109265•••
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/TID=Hs.75268.0 /TIER=FL+Stack /STK=36 /UG=Hs.75268 /LL=6484 /DEF=Homo
sapiens sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)
(SIAT4C), mRNA. /PROD=sialyltransferase "•0.455676391•0.451294355•"ST3
beta-galactoside alpha-2,3-sialyltransferase
4"•ST3GAL4•Hs.504251•ENSG00000110080•6486 // protein amino acid glycosylation
// inferred from electronic annotation•5794 // Golgi apparatus // inferred
from electronic annotation /// 16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from electronic
annotation•"3836 // beta-galactoside alpha-2,3-sialyltransferase activity //
traceable author statement /// 16757 // transferase activity, transferring
glycosyl groups // inferred from electronic annotation"
214895_s_at•gb:AU135154 /DB_XREF=gi:10995693 /DB_XREF=AU135154
/CLONE=PLACE1001348 /FEA=mRNA /CNT=11 /TID=Hs.172028.1 /TIER=ConsEnd /STK=0
/UG=Hs.172028 /LL=102 /UG_GENE=ADAM10 /UG_TITLE=a disintegrin and
metalloproteinase domain 10•0.455292361•0.459375035•a disintegrin and
metalloproteinase domain 10•ADAM10•Hs.172028•ENSG00000137845•1701 //
embryonic development (sensu Mammalia) // inferred from sequence or
structural similarity /// 6468 // protein amino acid phosphorylation //
inferred from sequence or structural similarity /// 6913 // nucleocytoplasmic
transport // inferred from se•5634 // nucleus // inferred from sequence or
structural similarity /// 5798 // Golgi vesicle // inferred from direct assay
/// 5887 // integral to plasma membrane // traceable author statement ///
9986 // cell surface // inferred from direct assay•4222 //
metalloendopeptidase activity // non-traceable author statement /// 5178 //
integrin binding // non-traceable author statement /// 5515 // protein
binding // inferred from sequence or structural similarity /// 8270 // zinc
```

```
ion binding // inferred
212230_at•"gb:AV725664 /DB_XREF=gi:10831279 /DB_XREF=AV725664 /CLONE=HTCAOD07
/FEA=EST /CNT=335 /TID=Hs.173717.0 /TIER=Stack /STK=123 /UG=Hs.173717
/UG_TITLE=Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B),
mRNA"•0.45458197•0.388316083•phosphatidic acid phosphatase type
2B•PPAP2B•Hs.405156•ENSG00000162407•6629 // lipid metabolism // non-traceable
author statement /// 8354 // germ cell migration // traceable author
statement•16020 // membrane // traceable author statement /// 16021 //
integral to membrane // inferred from electronic annotation•4721 //
phosphoprotein phosphatase activity // traceable author statement /// 8195 //
phosphatidate phosphatase activity // inferred from electronic annotation ///
16787 // hydrolase activity // inferred from electronic annotation
1568633_a_at•"gb:BC009735.1 /DB_XREF=gi:22800375 /TID=Hs2.126790.1 /CNT=7
/FEA=mRNA /TIER=ConsEnd /STK=5 /UG=Hs.126790 /UG_TITLE=Homo sapiens, clone
IMAGE:3878708, mRNA /DEF=Homo sapiens, clone IMAGE:3878708,
mRNA."•0.45413377•0.168746911•"CDNA clone IMAGE:3878708, partial
cds"••Hs.259498••••
222111_at•"gb:AU145293 /DB_XREF=gi:11006814 /DB_XREF=AU145293
/CLONE=HEMBA1004405 /FEA=mRNA /CNT=40 /TID=Hs.61773.0 /TIER=ConsEnd /STK=2
/UG=Hs.61773 /UG_TITLE=Homo sapiens cDNA FLJ11648 fis, clone
HEMBA1004405"•0.453782866•0.456399574•Hypothetical protein
KIAA1164•KIAA1164•Hs.368548••••
207086_x_at•"gb:NM_001474.1 /DB_XREF=gi:4503882 /GEN=GAGE4 /FEA=FLmRNA /CNT=6
/TID=Hs.183199.0 /TIER=FL /STK=1 /UG=Hs.183199 /LL=2576 /DEF=Homo sapiens G
antigen 4 (GAGE4), mRNA. /PROD=G antigen 4 /FL=gb:U19145.1
gb:NM_001474.1"•0.452435101•0.382594788•G antigen 2 /// G antigen 4 /// G
antigen 5 /// G antigen 6 /// G antigen 7 /// G antigen 7B /// G antigen
8•GAGE2 /// GAGE4 /// GAGE5 /// GAGE6 /// GAGE7 /// GAGE7B ///
GAGE8•Hs.278606•ENSG00000068990 /// ENSG00000189064 /// ENSG00000198716•6968
// cellular defense response // traceable author statement••
204015_s_at•"gb:BC002671.1 /DB_XREF=gi:12803670 /FEA=FLmRNA /CNT=105
/TID=Hs.2359.0 /TIER=FL+Stack /STK=9 /UG=Hs.2359 /LL=1846 /UG_GENE=DUSP4
/DEF=Homo sapiens, dual specificity phosphatase 4, clone MGC:3713, mRNA,
complete cds. /PROD=dual specificity phosphatase 4
/F"•0.450339761•0.480137266•dual specificity phosphatase
4•DUSP4•Hs.417962•ENSG00000120875•74 // regulation of cell cycle //
non-traceable author statement /// 165 // MAPKKK cascade // traceable author
statement /// 6470 // protein amino acid dephosphorylation // inferred from
electronic annotation /// 6470 // protein amino acid dephosphorylati•5634 //
nucleus // traceable author statement•4725 // protein tyrosine phosphatase
activity // inferred from electronic annotation /// 8330 // protein
tyrosine/threonine phosphatase activity // traceable author statement ///
16787 // hydrolase activity // inferred from electronic annotation /// 17017
203854_at•"gb:NM_000204.1 /DB_XREF=gi:4504578 /GEN=IF /FEA=FLmRNA /CNT=232
/TID=Hs.36602.0 /TIER=FL+Stack /STK=47 /UG=Hs.36602 /LL=3426 /DEF=Homo
sapiens I factor (complement) (IF), mRNA. /PROD=I factor (complement)
/FL=gb:NM_000204.1 gb:J02770.1"•0.449805411•0.263205608•I factor
(complement)•IF•Hs.312485••"6508 // proteolysis and peptidolysis // inferred
from electronic annotation /// 6955 // immune response // inferred from
electronic annotation /// 6958 // complement activation, classical pathway //
inferred from electronic annotation"•5576 // extracellular region // not
recorded /// 16020 // membrane // inferred from electronic annotation•3818 //
complement factor I activity // traceable author statement /// 4263 //
chymotrypsin activity // inferred from electronic annotation /// 4295 //
trypsin activity // inferred from electronic annotation /// 5044 // scavenger
receptor activity // infe
227578_at•gb:H28597 /DB_XREF=gi:898950 /DB_XREF=yl64e11.s1
/CLONE=IMAGE:163052 /FEA=EST /CNT=32 /TID=Hs.11355.3 /TIER=Stack /STK=10
/UG=Hs.11355 /LL=7112 /UG_GENE=TMPO
/UG_TITLE=thymopoietin•0.449701374•0.390670884•Thymopoietin•TMPO•Hs.11355•ENSG
00000120802••5635 // nuclear membrane // traceable author statement /// 5694
// chromosome // inferred from electronic annotation /// 16021 // integral to
membrane // inferred from electronic annotation•3677 // DNA binding //
inferred from electronic annotation /// 5521 // lamin binding // traceable
author statement
209184_s_at•gb:BF700086 /DB_XREF=gi:11985494 /DB_XREF=602127569F1
/CLONE=IMAGE:4284401 /FEA=FLmRNA /CNT=165 /TID=Hs.143648.0 /TIER=Stack
/STK=12 /UG=Hs.143648 /LL=8660 /UG_GENE=IRS2 /UG_TITLE=insulin receptor
substrate 2 /FL=gb:NM_003749.1 gb:AF073310.1•0.44941711•0.400164799•insulin
receptor substrate 2•IRS2•Hs.442344•ENSG00000185950•6006 // glucose
metabolism // traceable author statement /// 7165 // signal transduction //
traceable author statement /// 8284 // positive regulation of cell
proliferation // not recorded••4871 // signal transducer activity //
traceable author statement /// 5158 // insulin receptor binding // inferred
from electronic annotation
225397_at•"gb:AW575737 /DB_XREF=gi:7247276
/DB_XREF=UI-HF-BM0-adv-e-01-0-UI.s1 /CLONE=IMAGE:3062881 /FEA=mRNA /CNT=88
/TID=Hs.324127.0 /TIER=Stack /STK=50 /UG=Hs.324127 /UG_TITLE=Homo sapiens,
clone IMAGE:2823236, mRNA, partial cds"•0.449361867•0.483677388•hypothetical
protein MGC20481•MGC20481•Hs.146520•ENSG00000128891•••
221911_at•gb:BE881590 /DB_XREF=gi:10330366 /DB_XREF=601490008F1
```

```
/CLONE=IMAGE:3892465 /FEA=mRNA /CNT=59 /TID=Hs.10684.0 /TIER=Stack /STK=19
/UG=Hs.10684 /UG_TITLE=Homo sapiens clone 24421 mRNA
sequence•0.447962681•0.445952887•ets variant gene 1 /// hypothetical protein
LOC221810•ETV1 /// LOC221810•Hs.22634•ENSG00000006468•"6350 // transcription
// inferred from electronic annotation /// 6355 // regulation of
transcription, DNA-dependent // inferred from electronic annotation /// 6366
// transcription from RNA polymerase II promoter // traceable author
statement"•5634 // nucleus // inferred from electronic annotation•3700 //
transcription factor activity // traceable author statement
203071_at•"gb:NM_004636.1 /DB_XREF=gi:4759091 /GEN=SEMA3B /FEA=FLmRNA
/CNT=141 /TID=Hs.82222.0 /TIER=FL+Stack /STK=35 /UG=Hs.82222 /LL=7869
/DEF=Homo sapiens sema domain, immunoglobulin domain (Ig), short basic
domain, secreted, (semaphorin) 3B (SEMA3B), mRNA.
/PROD"•0.446794639•0.24784767•"sema domain, immunoglobulin domain (Ig), short
basic domain, secreted, (semaphorin) 3B"•SEMA3B•Hs.82222•ENSG00000012171•7267
// cell-cell signaling // traceable author statement /// 7275 // development
// inferred from electronic annotation /// 7411 // axon guidance // traceable
author statement•5783 // endoplasmic reticulum // traceable author statement
/// 16020 // membrane // inferred from electronic annotation /// 16021 //
integral to membrane // inferred from electronic annotation•4872 // receptor
activity // inferred from electronic annotation
236798_at•gb:AW268719 /DB_XREF=gi:6655749 /DB_XREF=xv35c04.x1
/CLONE=IMAGE:2815110 /FEA=EST /CNT=5 /TID=Hs.122113.0 /TIER=ConsEnd /STK=5
/UG=Hs.122113 /UG_TITLE=ESTs•0.445731252•0.272020108•"CDNA FLJ32438 fis,
clone SKMUS2001402"••Hs.552759••••
212202_s_at•gb:BG493972 /DB_XREF=gi:13455486 /DB_XREF=602542252F1
/CLONE=IMAGE:4673316 /FEA=mRNA /CNT=222 /TID=Hs.16492.0 /TIER=Stack /STK=38
/UG=Hs.16492 /LL=25963 /UG_GENE=DKFZP564G2022 /UG_TITLE=DKFZP564G2022
protein•0.445496874•0.427154583•DKFZP564G2022
protein•DKFZP564G2022•Hs.511138•ENSG00000103978••16021 // integral to
membrane // inferred from electronic annotation•
217904_s_at•"gb:NM_012104.1 /DB_XREF=gi:6912265 /GEN=BACE /FEA=FLmRNA
/CNT=280 /TID=Hs.49349.0 /TIER=FL /STK=1 /UG=Hs.49349 /LL=23621 /DEF=Homo
sapiens beta-site APP-cleaving enzyme (BACE), mRNA. /PROD=beta-site
APP-cleaving enzyme /FL=gb:AF200343.1 gb:AF204943.1
gb:A"•0.445463166•0.284151707•beta-site APP-cleaving enzyme
1•BACE1•Hs.504003•ENSG00000186318•6508 // proteolysis and peptidolysis //
inferred from electronic annotation /// 6509 // membrane protein ectodomain
proteolysis // inferred from sequence or structural similarity /// 6509 //
membrane protein ectodomain proteolysis // traceable author stat•5768 //
endosome // inferred from direct assay /// 5768 // endosome // inferred from
sequence or structural similarity /// 5794 // Golgi apparatus // inferred
from direct assay /// 5794 // Golgi apparatus // inferred from sequence or
structural similarity•4194 // pepsin A activity // inferred from electronic
annotation /// 8233 // peptidase activity // inferred from electronic
annotation /// 8798 // beta-aspartyl-peptidase activity // traceable author
statement /// 9049 // aspartic-type signal peptidase ac
204806_x_at•"gb:NM_018950.1 /DB_XREF=gi:9665231 /GEN=HLA-F /FEA=FLmRNA
/CNT=39 /TID=Hs.110309.0 /TIER=FL /STK=0 /UG=Hs.110309 /LL=3134 /DEF=Homo
sapiens major histocompatibility complex, class I, F (HLA-F), mRNA.
/PROD=major histocompatibility complex, class I, F
/FL="•0.445240623•0.400234262•"major histocompatibility complex, class I,
F"•HLA-F•Hs.519972•ENSG00000137403•"19883 // antigen presentation, endogenous
antigen // inferred from electronic annotation /// 19885 // antigen
processing, endogenous antigen via MHC class I // inferred from electronic
annotation"•16021 // integral to membrane // inferred from electronic
annotation /// 42612 // MHC class I protein complex // inferred from
electronic annotation•30106 // MHC class I receptor activity // traceable
author statement
200706_s_at•"gb:NM_004862.1 /DB_XREF=gi:4758913 /GEN=PIG7 /FEA=FLmRNA
/CNT=435 /TID=Hs.76507.0 /TIER=FL+Stack /STK=72 /UG=Hs.76507 /LL=9516
/DEF=Homo sapiens LPS-induced TNF-alpha factor (PIG7), mRNA.
/PROD=LPS-induced TNF-alpha factor /FL=gb:AF010312.1 gb:U77396.1
gb"•0.443656488•0.454063954•lipopolysaccharide-induced TNF
factor•LITAF•Hs.459940••6350 // transcription // inferred from electronic
annotation /// 6357 // regulation of transcription from RNA polymerase II
promoter // traceable author statement /// 43123 // positive regulation of
I-kappaB kinase/NF-kappaB cascade // inferred from mutan•5634 // nucleus //
inferred from electronic annotation•3702 // RNA polymerase II transcription
factor activity // traceable author statement /// 4871 // signal transducer
activity // inferred from mutant phenotype
213029_at•gb:BG478428 /DB_XREF=gi:13410807 /DB_XREF=602523839F1
/CLONE=IMAGE:4642353 /FEA=mRNA /CNT=97 /TID=Hs.326416.0 /TIER=Stack /STK=53
/UG=Hs.326416 /UG_TITLE=Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone
DKFZp564H1916)•0.442939501•0.335978234•Nuclear factor
I/B•NFIB•Hs.370359•ENSG00000147862•"6260 // DNA replication // inferred from
electronic annotation /// 6350 // transcription // inferred from electronic
annotation /// 6355 // regulation of transcription, DNA-dependent // inferred
from electronic annotation"•5634 // nucleus // inferred from electronic
annotation /// 5634 // nucleus // traceable author statement•3700 //
transcription factor activity // inferred from electronic annotation /// 3700
```

```
// transcription factor activity // traceable author statement
201826_s_at•"gb:NM_016002.1 /DB_XREF=gi:7705766 /GEN=LOC51097 /FEA=FLmRNA
/CNT=244 /TID=Hs.238126.0 /TIER=FL+Stack /STK=10 /UG=Hs.238126 /LL=51097
/DEF=Homo sapiens CGI-49 protein (LOC51097), mRNA. /PROD=CGI-49 protein
/FL=gb:NM_016002.1 gb:AF151807.1"•0.442750904•0.371922564•CGI-49
protein•CGI-49•Hs.498397•ENSG00000143653•••
223384_s_at•"gb:BE501464 /DB_XREF=gi:9703872 /DB_XREF=hw32d01.x1
/CLONE=IMAGE:3184609 /FEA=FLmRNA /CNT=51 /TID=Hs.65736.0 /TIER=Stack /STK=8
/UG=Hs.65736 /UG_TITLE=Homo sapiens tripartite motif protein TRIM4 isoform
beta (TRIM4) mRNA, complete cds; alternatively
splic"•0.442118801•0.394898608•tripartite motif-containing
4•TRIM4•Hs.50749•ENSG00000146833•16567 // protein ubiquitination // inferred
from electronic annotation•151 // ubiquitin ligase complex // inferred from
electronic annotation•4842 // ubiquitin-protein ligase activity // inferred
from electronic annotation /// 8270 // zinc ion binding // inferred from
electronic annotation
235199_at•gb:AI969697 /DB_XREF=gi:5766515 /DB_XREF=wz70e09.x1
/CLONE=IMAGE:2563432 /FEA=EST /CNT=15 /TID=Hs.276860.0 /TIER=ConsEnd /STK=0
/UG=Hs.276860 /UG_TITLE=ESTs•0.440427072•0.377102724•"Transcribed locus,
weakly similar to XP_513408.1 similar to origin recognition complex, subunit
1; origin recognition complex, subunit 1, S. cerevisiae, homolog-like; origin
recognition complex 1; replication control protein 1; origin recognition
complex,"••Hs.276860••••
221486_at•"gb:AF067170.1 /DB_XREF=gi:4894373 /FEA=FLmRNA /CNT=217
/TID=Hs.111680.1 /TIER=FL+Stack /STK=50 /UG=Hs.111680 /LL=2029 /UG_GENE=ENSA
/DEF=Homo sapiens alpha endosulfine mRNA, complete cds. /PROD=alpha
endosulfine /FL=gb:AF067170.1
gb:AF157510.1"•0.439724451•0.45448301•endosulfine
alpha•ENSA•Hs.510087•ENSG00000143420•6810 // transport // traceable author
statement /// 7584 // response to nutrients // traceable author
statement••5102 // receptor binding // traceable author statement /// 8200 //
ion channel inhibitor activity // traceable author statement
239719_at•gb:BF978262 /DB_XREF=gi:12345477 /DB_XREF=602148220F1
/CLONE=IMAGE:4306996 /FEA=EST /CNT=7 /TID=Hs.134182.0 /TIER=ConsEnd /STK=3
/UG=Hs.134182 /UG_TITLE=ESTs•0.438485968•0.463478221•CD109 antigen (Gov
platelet alloantigens)•CD109•Hs.399891•ENSG00000156535•••4867 // serine-type
endopeptidase inhibitor activity // inferred from electronic annotation ///
17114 // wide-spectrum protease inhibitor activity // inferred from
electronic annotation
204279_at•"gb:NM_002800.1 /DB_XREF=gi:4506204 /GEN=PSMB9 /FEA=FLmRNA /CNT=70
/TID=Hs.9280.0 /TIER=FL /STK=1 /UG=Hs.9280 /LL=5698 /DEF=Homo sapiens
proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional
protease 2) (PSMB9), mRNA.
/PROD=proteasom"•0.437673706•0.194677748•"proteasome (prosome, macropain)
subunit, beta type, 9 (large multifunctional protease
2)"•PSMB9•Hs.381081•ENSG00000112082•6508 // proteolysis and peptidolysis //
not recorded /// 6511 // ubiquitin-dependent protein catabolism // inferred
from electronic annotation /// 6955 // immune response // inferred from
electronic annotation•5839 // proteasome core complex (sensu Eukaryota) //
inferred from electronic annotation•4298 // threonine endopeptidase activity
// inferred from electronic annotation
228478_at•"gb:AA889954 /DB_XREF=gi:3016833 /DB_XREF=aj95e11.s1
/CLONE=IMAGE:1404236 /FEA=EST /CNT=22 /TID=Hs.167619.0 /TIER=Stack /STK=16
/UG=Hs.167619 /UG_TITLE=ESTs, Moderately similar to ALUC_HUMAN !!!! ALU CLASS
C WARNING ENTRY !!! (H.sapiens)"•0.435053104•0.381280343•Full length insert
cDNA YH99G08••Hs.167619••••
213455_at•gb:W87466 /DB_XREF=gi:1401521 /DB_XREF=zh67c05.s1
/CLONE=IMAGE:417128 /FEA=EST /CNT=52 /TID=Hs.246885.1 /TIER=Stack /STK=38
/UG=Hs.246885 /LL=55041 /UG_GENE=FLJ20783 /UG_TITLE=hypothetical protein
FLJ20783•0.432537215•0.250840931•Hypothetical protein
BC001096•LOC92689•Hs.476517•ENSG00000197712•••
209032_s_at•"gb:AF132811.1 /DB_XREF=gi:7767238 /GEN=NECL2 /FEA=FLmRNA
/CNT=252 /TID=Hs.70337.0 /TIER=FL+Stack /STK=25 /UG=Hs.70337 /LL=23705
/DEF=Homo sapiens nectin-like protein 2 (NECL2) mRNA, complete cds.
/PROD=nectin-like protein 2 /FL=gb:NM_014333.1
gb:AF132811."•0.431220131•0.429637615•"immunoglobulin superfamily, member
4"•IGSF4•Hs.370510•ENSG00000182985•••
1553672_at•"gb:NM_145240.1 /DB_XREF=gi:21687113 /TID=Hs2.32399.1 /CNT=33
/FEA=FLmRNA /TIER=FL /STK=0 /LL=113521 /UG_GENE=LOC113521 /UG=Hs.32399
/UG_TITLE=similar to avenaII /DEF=Homo sapiens similar to avenaII
(LOC113521), mRNA. /FL=gb:NM_145240.1
gb:BC010414.1"•0.430976756•0.342682395•enabled homolog
(Drosophila)•ENAH•Hs.497893•ENSG00000154380•7399 // neurogenesis // inferred
from electronic annotation /// 30154 // cell differentiation // inferred from
electronic annotation••
225524_at•gb:AU152178 /DB_XREF=gi:11013699 /DB_XREF=AU152178
/CLONE=NT2RP3000356 /FEA=mRNA /CNT=116 /TID=Hs.5897.0 /TIER=Stack /STK=67
/UG=Hs.5897 /UG_TITLE=Homo sapiens mRNA; cDNA DKFZp586P1622 (from clone
DKFZp586P1622)•0.427750705•0.30863352•anthrax toxin receptor
2•ANTXR2•Hs.162963•ENSG00000163297••16021 // integral to membrane // inferred
from electronic annotation•4872 // receptor activity // inferred from
```

```
electronic annotation
229674_at•gb:AL035414 /DB_XREF=gi:6822166 /FEA=FLmRNA /CNT=23 /TID=Hs.21068.0
/TIER=Stack /STK=8 /UG=Hs.21068 /LL=56256 /UG_GENE=DJ667H12.2
/UG_TITLE=hypothetical protein /DEF=Human DNA sequence from clone RP4-667H12
on chromosome 1q32.1-41. Contains up to two
nove•0.423759123•0.379446071•SERTA domain containing
4•SERTAD4•Hs.445835•ENSG00000082497•••
209290_s_at•"gb:BC001283.1 /DB_XREF=gi:12654878 /FEA=FLmRNA /CNT=149
/TID=Hs.33287.1 /TIER=FL+Stack /STK=18 /UG=Hs.33287 /LL=4781 /UG_GENE=NFIB
/DEF=Homo sapiens, Similar to nuclear factor IB, clone MGC:5146, mRNA,
complete cds. /PROD=Similar to nuclear factor IB
/FL="•0.423547584•0.488681451•nuclear factor
I/B•NFIB•Hs.370359•ENSG00000147862•"6260 // DNA replication // inferred from
electronic annotation /// 6350 // transcription // inferred from electronic
annotation /// 6355 // regulation of transcription, DNA-dependent // inferred
from electronic annotation"•5634 // nucleus // inferred from electronic
annotation /// 5634 // nucleus // traceable author statement•3700 //
transcription factor activity // inferred from electronic annotation /// 3700
// transcription factor activity // traceable author statement
204472_at•"gb:NM_005261.1 /DB_XREF=gi:4885262 /GEN=GEM /FEA=FLmRNA /CNT=81
/TID=Hs.79022.0 /TIER=FL+Stack /STK=35 /UG=Hs.79022 /LL=2669 /DEF=Homo
sapiens GTP-binding protein overexpressed in skeletal muscle (GEM), mRNA.
/PROD=GTP-binding protein overexpressed in ske"•0.422467351•0.495277457•GTP
binding protein overexpressed in skeletal
muscle•GEM•Hs.345139•ENSG00000164949•6955 // immune response // traceable
author statement /// 7166 // cell surface receptor linked signal transduction
// traceable author statement /// 7264 // small GTPase mediated signal
transduction // inferred from electronic annotation•16020 // membrane //
inferred from electronic annotation•5516 // calmodulin binding // inferred
from electronic annotation /// 5525 // GTP binding // traceable author
statement
211991_s_at•"gb:M27487.1 /DB_XREF=gi:703088 /GEN=HLA-DPA1 /FEA=FLmRNA
/CNT=358 /TID=Hs.914.0 /TIER=FL+Stack /STK=139 /UG=Hs.914 /DEF=Homo sapiens
MHC class II DPw3-alpha-1 chain mRNA, complete cds. /PROD=MHC class II
DP3-alpha /FL=gb:M27487.1"•0.422275942•0.291777219•"major histocompatibility
complex, class II, DP alpha 1"•HLA-DPA1•Hs.347270•ENSG00000168384•"6955 //
immune response // non-traceable author statement /// 19884 // antigen
presentation, exogenous antigen // inferred from electronic annotation ///
19886 // antigen processing, exogenous antigen via MHC class II // inferred
from electronic annotatio"•5887 // integral to plasma membrane //
non-traceable author statement /// 16020 // membrane // inferred from
electronic annotation•45012 // MHC class II receptor activity //
non-traceable author statement
200897_s_at•"gb:NM_016081.1 /DB_XREF=gi:7706354 /GEN=KIAA0992 /FEA=FLmRNA
/CNT=425 /TID=Hs.194431.0 /TIER=FL+Stack /STK=152 /UG=Hs.194431 /LL=23022
/DEF=Homo sapiens palladin (KIAA0992), mRNA. /PROD=palladin /FL=gb:AF151909.1
gb:AF077041.1
gb:NM_016081.1"•0.418080218•0.180618883•palladin•KIAA0992•Hs.151220•ENSG000001
29116•6468 // protein amino acid phosphorylation // inferred from electronic
annotation••5021 // vascular endothelial growth factor receptor activity //
inferred from electronic annotation /// 5524 // ATP binding // inferred from
electronic annotation
200920_s_at•"gb:AL535380 /DB_XREF=gi:12798873 /DB_XREF=AL535380
/CLONE=CS0DF009YN13 (5 prime) /FEA=FLmRNA /CNT=488 /TID=Hs.77054.0
/TIER=Stack /STK=181 /UG=Hs.77054 /LL=694 /UG_GENE=BTG1 /UG_TITLE=B-cell
translocation gene 1, anti-proliferative
/FL=gb:NM_001731.1"•0.416782751•0.452403802•"B-cell translocation gene 1,
anti-proliferative"•BTG1•Hs.255935•ENSG00000133639•7286 // spermatid cell
development // inferred from sequence or structural similarity /// 8285 //
negative regulation of cell proliferation // inferred from direct assay ///
16477 // cell migration // non-traceable author statement /// 30308 //
negative r•5634 // nucleus // inferred from expression pattern /// 5634 //
nucleus // inferred from mutant phenotype /// 5737 // cytoplasm // inferred
from mutant phenotype•3712 // transcription cofactor activity //
non-traceable author statement /// 19900 // kinase binding // non-traceable
author statement
212226_s_at•"gb:AA628586 /DB_XREF=gi:2540973 /DB_XREF=af39f12.s1
/CLONE=IMAGE:1034063 /FEA=EST /CNT=335 /TID=Hs.173717.0 /TIER=Stack /STK=14
/UG=Hs.173717 /UG_TITLE=Homo sapiens phosphatidic acid phosphatase type 2B
(PPAP2B), mRNA"•0.416682244•0.272031761•phosphatidic acid phosphatase type
2B•PPAP2B•Hs.405156•ENSG00000162407•6629 // lipid metabolism // non-traceable
author statement /// 8354 // germ cell migration // traceable author
statement•16020 // membrane // traceable author statement /// 16021 //
integral to membrane // inferred from electronic annotation•4721 //
phosphoprotein phosphatase activity // traceable author statement /// 8195 //
phosphatidate phosphatase activity // inferred from electronic annotation ///
16787 // hydrolase activity // inferred from electronic annotation
224443_at•"gb:BC005997.1 /DB_XREF=gi:13543694 /FEA=FLmRNA /CNT=1
/TID=HsAffx.900821.625 /TIER=FL /STK=0 /DEF=Homo sapiens, clone MGC:14801,
mRNA, complete cds. /PROD=Unknown (protein for MGC:14801)
/FL=gb:BC005997.1"•0.416577394•0.388279839•hypothetical protein MGC14801 ///
```

```
hypothetical protein MGC14801•MGC14801•Hs.523932•ENSG00000153363•••
212848_s_at•gb:BG036668 /DB_XREF=gi:12432092 /DB_XREF=602326882F1
/CLONE=IMAGE:4428237 /FEA=EST /CNT=91 /TID=Hs.18075.0 /TIER=Stack /STK=61
/UG=Hs.18075 /LL=23733 /UG_GENE=C9ORF3 /UG_TITLE=chromosome 9 open reading
frame 3•0.414757456•0.130419511•chromosome 9 open reading frame
3•C9orf3•Hs.434253•ENSG00000148120•6508 // proteolysis and peptidolysis //
inferred from direct assay••4177 // aminopeptidase activity // inferred from
direct assay /// 4179 // membrane alanyl aminopeptidase activity // inferred
from electronic annotation /// 8237 // metallopeptidase activity // inferred
from direct assay
1568592_at•"gb:BM976092 /DB_XREF=gi:19593683
/DB_XREF=UI-CF-EN1-acy-e-14-0-UI.s1 /CLONE=UI-CF-EN1-acy-e-14-0-UI
/TID=Hs2.374986.1 /CNT=104 /FEA=mRNA /TIER=Stack /STK=14 /UG=Hs.374986
/UG_TITLE=Homo sapiens, clone IMAGE:5277162,
mRNA"•0.414577198•0.43358534•hypothetical gene supported by
BC031266•LOC400368•Hs.489254••••
201506_at•"gb:NM_000358.1 /DB_XREF=gi:4507466 /GEN=TGFBI /FEA=FLmRNA /CNT=491
/TID=Hs.118787.0 /TIER=FL+Stack /STK=253 /UG=Hs.118787 /LL=7045 /DEF=Homo
sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA.
/PROD=transforming growth factor,
beta-induc"•0.414357905•0.432139104•"transforming growth factor,
beta-induced, 68kDa"•TGFBI•Hs.369397•ENSG00000120708•7155 // cell adhesion //
inferred from electronic annotation /// 7162 // negative regulation of cell
adhesion // traceable author statement /// 7600 // sensory perception //
inferred from electronic annotation /// 7601 // visual perception //
traceable au•5578 // extracellular matrix (sensu Metazoa) // inferred from
electronic annotation /// 5615 // extracellular space // traceable author
statement•5178 // integrin binding // traceable author statement /// 5515 //
protein binding // inferred from electronic annotation
229900_at•"gb:AL576908 /DB_XREF=gi:12939516 /DB_XREF=AL576908
/CLONE=CS0DI081YB18 (3 prime) /FEA=EST /CNT=24 /TID=Hs.55964.0 /TIER=Stack
/STK=17 /UG=Hs.55964 /UG_TITLE=ESTs, Weakly similar to C4HU complement C4A
precursor (H.sapiens)"•0.413998325•0.283778354•CD109 antigen (Gov platelet
alloantigens)•CD109•Hs.399891•ENSG00000156535•••4867 // serine-type
endopeptidase inhibitor activity // inferred from electronic annotation ///
17114 // wide-spectrum protease inhibitor activity // inferred from
electronic annotation
231307_at•"gb:AW002915 /DB_XREF=gi:5849831 /DB_XREF=wr02h09.x1
/CLONE=IMAGE:2480417 /FEA=EST /CNT=16 /TID=Hs.293317.0 /TIER=Stack /STK=16
/UG=Hs.293317 /UG_TITLE=ESTs, Weakly similar to JM27
(H.sapiens)"•0.413900522•0.347153308•Hypothetical
LOC389860•LOC389860•Hs.293317•ENSG00000187761•••
226343_at•gb:W74486 /DB_XREF=gi:1384960 /DB_XREF=zd56b07.s1
/CLONE=IMAGE:344629 /FEA=EST /CNT=69 /TID=Hs.6119.0 /TIER=Stack /STK=40
/UG=Hs.6119 /UG_TITLE=ESTs•0.413106104•0.463482496•Dipeptidylpeptidase
8•DPP8•Hs.458609•ENSG00000074603•6508 // proteolysis and peptidolysis //
inferred from electronic annotation /// 6508 // proteolysis and peptidolysis
// non-traceable author statement /// 6508 // proteolysis and peptidolysis //
traceable author statement /// 6955 // immune response // tr•5737 //
cytoplasm // non-traceable author statement /// 5737 // cytoplasm //
traceable author statement /// 16020 // membrane // inferred from electronic
annotation•3824 // catalytic activity // inferred from electronic annotation
/// 4274 // dipeptidyl-peptidase IV activity // inferred from electronic
annotation
227174_at•gb:Z98443 /DB_XREF=gi:2326591 /DB_XREF=HSZ98443
/CLONE=DKFZphthm1_1e10 /FEA=EST /CNT=39 /TID=Hs.86366.0 /TIER=Stack /STK=20
/UG=Hs.86366 /UG_TITLE=ESTs•0.412077545•0.344206873•hypothetical protein
FLJ38736•FLJ38736•Hs.208067•ENSG00000166415•••
201850_at•"gb:NM_001747.1 /DB_XREF=gi:4502560 /GEN=CAPG /FEA=FLmRNA /CNT=265
/TID=Hs.82422.0 /TIER=FL+Stack /STK=106 /UG=Hs.82422 /LL=822 /DEF=Homo
sapiens capping protein (actin filament), gelsolin-like (CAPG), mRNA.
/PROD=capping protein (actin filament),
gelsolin"•0.412010411•0.441914366•"capping protein (actin filament),
gelsolin-like"•CAPG•Hs.516155•ENSG00000042493•"6461 // protein complex
assembly // non-traceable author statement /// 9613 // response to pest,
pathogen or parasite // traceable author statement /// 51016 // barbed-end
actin filament capping // traceable author statement"•5634 // nucleus //
inferred from electronic annotation /// 8290 // F-actin capping protein
complex // traceable author statement•3779 // actin binding // inferred from
electronic annotation
225116_at•"gb:AW300045 /DB_XREF=gi:6709722 /DB_XREF=xs45a11.x1
/CLONE=IMAGE:2772572 /FEA=EST /CNT=104 /TID=Hs.75354.1 /TIER=Stack /STK=8
/UG=Hs.75354 /LL=10985 /UG_GENE=GCN1L1 /UG_TITLE=GCN1 (general control of
amino-acid synthesis 1, yeast)-like 1"•0.411892932•0.411740456•Homeodomain
interacting protein kinase 2•HIPK2•Hs.397465•ENSG00000064393•"74 //
regulation of cell cycle // non-traceable author statement /// 6350 //
transcription // inferred from electronic annotation /// 6355 // regulation
of transcription, DNA-dependent // inferred from electronic annotation ///
6468 // protein amino acid "•5634 // nucleus // inferred from direct assay
/// 5737 // cytoplasm // inferred from sequence or structural similarity ///
16604 // nuclear body // traceable author statement•3714 // transcription
```

```
corepressor activity // traceable author statement /// 4674 // protein
serine/threonine kinase activity // inferred from electronic annotation ///
5515 // protein binding // inferred from physical interaction /// 5524 // ATP
binding
224952_at•gb:BF115054 /DB_XREF=gi:10984530 /DB_XREF=hr73f11.x1
/CLONE=IMAGE:3134157 /FEA=mRNA /CNT=107 /TID=Hs.4996.1 /TIER=Stack /STK=28
/UG=Hs.4996 /LL=26115 /UG_GENE=DKFZP564D166 /UG_TITLE=putative ankyrin-repeat
containing protein•0.411477271•0.455240951•putative ankyrin-repeat containing
protein•DKFZP564D166•Hs.410889•ENSG00000170921•••5488 // binding // inferred
from electronic annotation
202201_at•"gb:NM_000713.1 /DB_XREF=gi:4502418 /GEN=BLVRB /FEA=FLmRNA /CNT=192
/TID=Hs.76289.0 /TIER=FL+Stack /STK=82 /UG=Hs.76289 /LL=645 /DEF=Homo sapiens
biliverdin reductase B (flavin reductase (NADPH)) (BLVRB), mRNA.
/PROD=biliverdin reductase B (flavin
reductas"•0.410997386•0.231592297•biliverdin reductase B (flavin reductase
(NADPH))•BLVRB•Hs.515785•ENSG00000090013•9225 // nucleotide-sugar metabolism
// inferred from electronic annotation••4074 // biliverdin reductase activity
// traceable author statement /// 16491 // oxidoreductase activity //
inferred from electronic annotation /// 42602 // flavin reductase activity //
inferred from electronic annotation
204034_at•"gb:NM_014297.1 /DB_XREF=gi:7657686 /GEN=YF13H12 /FEA=FLmRNA
/CNT=100 /TID=Hs.7486.0 /TIER=FL+Stack /STK=83 /UG=Hs.7486 /LL=23474
/DEF=Homo sapiens protein expressed in thyroid (YF13H12), mRNA. /PROD=protein
expressed in thyroid /FL=gb:NM_014297.1"•0.410168094•0.443419337•ethylmalonic
encephalopathy 1•ETHE1•Hs.7486•ENSG00000105755•••16787 // hydrolase activity
// inferred from electronic annotation
206172_at•"gb:NM_000640.1 /DB_XREF=gi:10834991 /GEN=IL13RA2 /FEA=FLmRNA
/CNT=23 /TID=Hs.25954.0 /TIER=FL /STK=0 /UG=Hs.25954 /LL=3598 /DEF=Homo
sapiens interleukin 13 receptor, alpha 2 (IL13RA2), mRNA. /PROD=interleukin
13 receptor, alpha 2 /FL=gb:U70981.1
gb:NM_000"•0.409209733•0.444132952•"interleukin 13 receptor, alpha
2"•IL13RA2•Hs.336046•ENSG00000123496••5615 // extracellular space //
traceable author statement /// 5625 // soluble fraction // traceable author
statement /// 16020 // membrane // inferred from electronic annotation ///
16021 // integral to membrane // inferred from electronic annotation•4872 //
receptor activity // inferred from electronic annotation /// 4907 //
interleukin receptor activity // traceable author statement
203719_at•"gb:NM_001983.1 /DB_XREF=gi:4503598 /GEN=ERCC1 /FEA=FLmRNA /CNT=117
/TID=Hs.59544.0 /TIER=FL+Stack /STK=27 /UG=Hs.59544 /LL=2067 /DEF=Homo
sapiens excision repair cross-complementing rodent repair deficiency,
complementation group 1 (includes overlapping
a"•0.408765851•0.418580394•"excision repair cross-complementing rodent repair
deficiency, complementation group 1 (includes overlapping antisense
sequence)"•ERCC1•Hs.435981•ENSG00000012061•6281 // DNA repair // inferred
from electronic annotation /// 6289 // nucleotide-excision repair // not
recorded /// 9653 // morphogenesis // traceable author statement•5634 //
nucleus // inferred from electronic annotation /// 5634 // nucleus //
traceable author statement•3684 // damaged DNA binding // inferred from
electronic annotation /// 4519 // endonuclease activity // inferred from
electronic annotation /// 4520 // endodeoxyribonuclease activity // not
recorded /// 16787 // hydrolase activity // inferred from electro
221875_x_at•"gb:AW514210 /DB_XREF=gi:7152378 /DB_XREF=hd75b05.x1
/CLONE=IMAGE:2915313 /FEA=EST /CNT=43 /TID=Hs.110309.1 /TIER=Stack /STK=30
/UG=Hs.110309 /LL=3134 /UG_GENE=HLA-F /UG_TITLE=major histocompatibility
complex, class I, F"•0.408629326•0.418756127•"major histocompatibility
complex, class I, F"•HLA-F•Hs.519972•ENSG00000137403•"19883 // antigen
presentation, endogenous antigen // inferred from electronic annotation ///
19885 // antigen processing, endogenous antigen via MHC class I // inferred
from electronic annotation"•16021 // integral to membrane // inferred from
electronic annotation /// 42612 // MHC class I protein complex // inferred
from electronic annotation•30106 // MHC class I receptor activity //
traceable author statement
203313_s_at•"gb:NM_003244.1 /DB_XREF=gi:4507472 /GEN=TGIF /FEA=FLmRNA
/CNT=128 /TID=Hs.90077.0 /TIER=FL+Stack /STK=32 /UG=Hs.90077 /LL=7050
/DEF=Homo sapiens TG-interacting factor (TALE family homeobox) (TGIF), mRNA.
/PROD=TG-interacting factor (TALE family homeobox)
"•0.408265837•0.460226533•TGFB-induced factor (TALE family
homeobox)•TGIF•Hs.373550•ENSG00000177426•"122 // negative regulation of
transcription from RNA polymerase II promoter // traceable author statement
/// 6350 // transcription // inferred from electronic annotation /// 6355 //
regulation of transcription, DNA-dependent // inferred from electronic
a"•5634 // nucleus // inferred from electronic annotation /// 5634 // nucleus
// not recorded•3700 // transcription factor activity // inferred from
electronic annotation /// 3700 // transcription factor activity // traceable
author statement /// 3714 // transcription corepressor activity // traceable
author statement
203988_s_at•"gb:NM_004480.1 /DB_XREF=gi:4758407 /GEN=FUT8 /FEA=FLmRNA /CNT=78
/TID=Hs.118722.0 /TIER=FL /STK=0 /UG=Hs.118722 /LL=2530 /DEF=Homo sapiens
fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA.
/PROD=fucosyltransferase 8 (alpha
(1,6)fucosyltr"•0.408163022•0.388781721•"fucosyltransferase 8 (alpha (1,6)
```

```
fucosyltransferase)"•FUT8•Hs.118722•ENSG00000033170•1701 // embryonic
development (sensu Mammalia) // non-traceable author statement /// 6491 //
N-glycan processing // traceable author statement /// 9312 // oligosaccharide
biosynthesis // traceable author statement /// 42355 // L-fucose catabolism
// non-t•5794 // Golgi apparatus // non-traceable author statement /// 16021
// integral to membrane // inferred from electronic annotation•"8424 //
glycoprotein 6-alpha-L-fucosyltransferase activity // traceable author
statement /// 16757 // transferase activity, transferring glycosyl groups //
inferred from electronic annotation"
228038_at•gb:AI669815 /DB_XREF=gi:4834589 /DB_XREF=tu31f07.x1
/CLONE=IMAGE:2252677 /FEA=EST /CNT=31 /TID=Hs.129911.0 /TIER=Stack /STK=25
/UG=Hs.129911 /UG_TITLE=ESTs•0.406076844•0.461003072•SRY (sex determining
region Y)-box 2•SOX2•Hs.518438•ENSG00000181449•"6325 // establishment and/or
maintenance of chromatin architecture // non-traceable author statement ///
6350 // transcription // inferred from electronic annotation /// 6355 //
regulation of transcription, DNA-dependent // non-traceable author
statement"•5634 // nucleus // non-traceable author statement•3700 //
transcription factor activity // non-traceable author statement
228293_at•gb:AJ245600.1 /DB_XREF=gi:5763726 /GEN=TR2D15 /FEA=mRNA /CNT=32
/TID=Hs.180545.0 /TIER=Stack /STK=18 /UG=Hs.180545 /DEF=Homo sapiens mRNA for
hypothetical protein (TR2D15 gene). /PROD=hypothetical
protein•0.405949363•0.300162246•novel 58.3 KDA
protein•LOC91614•Hs.280990•ENSG00000121690•7242 // intracellular signaling
cascade // inferred from electronic annotation•5634 // nucleus // inferred
from electronic annotation•3677 // DNA binding // inferred from electronic
annotation
222487_s_at•"gb:BC003667.1 /DB_XREF=gi:13277527 /FEA=FLmRNA /CNT=230
/TID=Hs.108957.0 /TIER=ConsEnd /STK=0 /UG=Hs.108957 /LL=51065
/UG_GENE=LOC51065 /DEF=Homo sapiens, Similar to 40S ribosomal protein S27
isoform, clone MGC:12175, mRNA, complete cds. /PROD=Similar to
"•0.402423364•0.357800605•ribosomal protein
S27-like•RPS27L•Hs.108957•ENSG00000185088•6412 // protein biosynthesis //
inferred from electronic annotation•5840 // ribosome // inferred from
electronic annotation•3735 // structural constituent of ribosome // inferred
from electronic annotation
217080_s_at•"gb:Y19026.1 /DB_XREF=gi:6996435 /GEN=Homer-2 /FEA=mRNA /CNT=1
/TID=Hs.93564.3 /TIER=ConsEnd /STK=0 /UG=Hs.93564 /LL=9455 /DEF=Homo sapiens
mRNA for Homer-2 protein, Homer-2B splicing form. /PROD=Homer-2 protein,
Homer-2B splicing form"•0.401726718•0.419772495•homer homolog 2
(Drosophila)•HOMER2•Hs.93564•ENSG00000103942•7216 // metabotropic glutamate
receptor signaling pathway // traceable author statement••
238877_at•gb:BE674583 /DB_XREF=gi:10035124 /DB_XREF=7e02h07.x1
/CLONE=IMAGE:3281341 /FEA=EST /CNT=7 /TID=Hs.102408.0 /TIER=ConsEnd /STK=4
/UG=Hs.102408 /UG_TITLE=ESTs•0.401046982•0.378191097•Eyes absent homolog 4
(Drosophila)•EYA4•Hs.549032•ENSG00000112319•"6350 // transcription //
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 7275 // development
// inferred from electronic annotation /// 7601 // visual perception //
trac"•5634 // nucleus // inferred from electronic annotation•287 // magnesium
ion binding // inferred from electronic annotation /// 3824 // catalytic
activity // inferred from electronic annotation /// 4725 // protein tyrosine
phosphatase activity // inferred from electronic annotation /// 16787 //
hydrolase activ
223614_at•gb:AL136588.1 /DB_XREF=gi:13276678 /GEN=DKFZp761D112 /FEA=FLmRNA
/CNT=28 /TID=Hs.103849.0 /TIER=FL+Stack /STK=20 /UG=Hs.103849 /DEF=Homo
sapiens mRNA; cDNA DKFZp761D112 (from clone DKFZp761D112); complete cds.
/PROD=hypothetical protein
/FL=gb:AL136588.1•0.399716625•0.479980677•hypothetical protein
DKFZp761D112•DKFZp761D112•Hs.492187••••
222877_at•"gb:AK024680.1 /DB_XREF=gi:10437021 /FEA=FLmRNA /CNT=61
/TID=Hs.63382.0 /TIER=Stack /STK=32 /UG=Hs.63382 /LL=55403 /UG_GENE=PRO2714
/UG_TITLE=hypothetical protein PRO2714 /DEF=Homo sapiens cDNA: FLJ21027 fis,
clone CAE07110. /FL=gb:NM_018534.1"•0.398508487•0.412770677•Neuropilin
2•NRP2•Hs.471200•ENSG00000118257•1525 // angiogenesis // non-traceable author
statement /// 6118 // electron transport // inferred from electronic
annotation /// 7155 // cell adhesion // inferred from electronic annotation
/// 7155 // cell adhesion // non-traceable author statement /// 7•5624 //
membrane fraction // traceable author statement /// 16020 // membrane //
inferred from electronic annotation /// 16021 // integral to membrane //
inferred from electronic annotation /// 16021 // integral to membrane //
non-traceable author stateme•4872 // receptor activity // traceable author
statement /// 5021 // vascular endothelial growth factor receptor activity //
non-traceable author statement /// 5021 // vascular endothelial growth factor
receptor activity // traceable author statement /// 5
208894_at•"gb:M60334.1 /DB_XREF=gi:188255 /GEN=HLA-DRA /FEA=FLmRNA /CNT=470
/TID=Hs.76807.0 /TIER=FL /STK=0 /UG=Hs.76807 /LL=3122 /DEF=Human MHC class II
HLA-DR-alpha mRNA, complete cds. /PROD=cell surface glycoprotein
/FL=gb:M60334.1 gb:NM_019111.1"•0.397295711•0.273340003•"major
histocompatibility complex, class II, DR alpha /// major histocompatibility
complex, class II, DR alpha"•HLA-DRA•Hs.520048•ENSG00000168423 ///
ENSG00000198334•"6955 // immune response // inferred from electronic
```

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annotation /// 6955 // immune response // non-traceable author statement ///
19884 // antigen presentation, exogenous antigen // inferred from electronic
annotation /// 19886 // antigen processing, exoge"•5887 // integral to plasma
membrane // non-traceable author statement /// 16020 // membrane // inferred
from electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•45012 // MHC class II receptor activity //
non-traceable author statement
203060_s_at•"gb:AF074331.1 /DB_XREF=gi:5052074 /GEN=PAPSS2 /FEA=FLmRNA
/CNT=156 /TID=Hs.274230.0 /TIER=FL+Stack /STK=29 /UG=Hs.274230 /LL=9060
/DEF=Homo sapiens PAPS synthetase-2 (PAPSS2) mRNA, complete cds. /PROD=PAPS
synthetase-2 /FL=gb:AF313907.1 gb:AF173365.1
gb:A"•0.397190655•0.420607315•3'-phosphoadenosine 5'-phosphosulfate synthase
2•PAPSS2•Hs.524491•ENSG00000198682•"103 // sulfate assimilation // inferred
from electronic annotation /// 1501 // skeletal development // inferred from
sequence or structural similarity /// 6139 // nucleobase, nucleoside,
nucleotide and nucleic acid metabolism // not recorded"•5622 // intracellular
// inferred from sequence or structural similarity•4020 // adenylyl-sulfate
kinase activity // inferred from electronic annotation /// 4781 // sulfate
adenylyltransferase (ATP) activity // inferred from sequence or structural
similarity /// 5524 // ATP binding // inferred from sequence or structural
simil
205567_at•"gb:NM_003654.1 /DB_XREF=gi:4502840 /GEN=CHST1 /FEA=FLmRNA /CNT=52
/TID=Hs.104576.0 /TIER=FL+Stack /STK=29 /UG=Hs.104576 /LL=8534 /DEF=Homo
sapiens carbohydrate (chondroitin 6keratan) sulfotransferase 1 (CHST1), mRNA.
/PROD=carbohydrate (chondroitin 6kerat"•0.396331704•0.400611059•carbohydrate
(keratan sulfate Gal-6) sulfotransferase
1•CHST1•Hs.104576•ENSG00000175264•5976 // polysaccharide metabolism //
traceable author statement /// 6012 // galactose metabolism // inferred from
direct assay /// 6954 // inflammatory response // inferred from electronic
annotation /// 42339 // keratan sulfate metabolism // inferred fro•5794 //
Golgi apparatus // inferred from electronic annotation /// 16021 // integral
to membrane // non-traceable author statement /// 31228 // intrinsic to Golgi
membrane // inferred from sequence or structural similarity•16740 //
transferase activity // inferred from electronic annotation /// 45130 //
keratan sulfotransferase activity // inferred from direct assay
218162_at•"gb:NM_020190.1 /DB_XREF=gi:9910269 /GEN=HNOEL-iso /FEA=FLmRNA
/CNT=185 /TID=Hs.9315.0 /TIER=FL /STK=0 /UG=Hs.9315 /LL=56944 /DEF=Homo
sapiens HNOEL-iso protein (HNOEL-iso), mRNA. /PROD=HNOEL-iso protein
/FL=gb:NM_020190.1 gb:AF201945.1"•0.395020558•0.286809714•olfactomedin-like
3•OLFML3•Hs.9315•ENSG00000116774•••
224455_s_at•"gb:BC006112.1 /DB_XREF=gi:13543939 /FEA=FLmRNA /CNT=1
/TID=HsAffx.900856.463 /TIER=FL /STK=0 /DEF=Homo sapiens, Similar to RIKEN
cDNA 2610017G09 gene, clone MGC:12975, mRNA, complete cds. /PROD=Similar to
RIKEN cDNA 2610017G09 gene
/FL=gb:BC006112.1"•0.394881929•0.384062406•ADP-dependent glucokinase ///
ADP-dependent glucokinase•ADPGK•Hs.513013•ENSG00000159322•5975 //
carbohydrate metabolism // inferred from electronic annotation••"16773 //
phosphotransferase activity, alcohol group as acceptor // inferred from
electronic annotation"
219641_at•"gb:NM_017996.1 /DB_XREF=gi:8922230 /GEN=FLJ10103 /FEA=FLmRNA
/CNT=27 /TID=Hs.42140.0 /TIER=FL+Stack /STK=12 /UG=Hs.42140 /LL=55070
/DEF=Homo sapiens hypothetical protein FLJ10103 (FLJ10103), mRNA.
/PROD=hypothetical protein FLJ10103 /FL=gb:BC001242.1
gb:N"•0.393239993•0.247291887•de-etiolated homolog 1
(Arabidopsis)•DET1•Hs.42140•ENSG00000140543•6512 // ubiquitin cycle //
inferred from electronic annotation•5634 // nucleus // inferred from
electronic annotation•
201860_s_at•"gb:NM_000930.1 /DB_XREF=gi:4505860 /GEN=PLAT /FEA=FLmRNA
/CNT=265 /TID=Hs.274404.0 /TIER=FL+Stack /STK=118 /UG=Hs.274404 /LL=5327
/DEF=Homo sapiens plasminogen activator, tissue (PLAT), mRNA.
/PROD=plasminogen activator, tissue /FL=gb:NM_000930.1
gb:NM_00"•0.392603088•0.397742182•"plasminogen activator,
tissue"•PLAT•Hs.491582•ENSG00000104368•6464 // protein modification //
traceable author statement /// 6508 // proteolysis and peptidolysis //
inferred from electronic annotation /// 6508 // proteolysis and peptidolysis
// traceable author statement /// 7596 // blood coagulation // traceable
au•5576 // extracellular region // inferred from electronic annotation•4263
// chymotrypsin activity // inferred from electronic annotation /// 4295 //
trypsin activity // inferred from electronic annotation /// 8233 // peptidase
activity // inferred from electronic annotation /// 8243 // plasminogen
activator activity // in
217478_s_at•"gb:X76775 /DB_XREF=gi:512468 /FEA=DNA_1 /CNT=1 /TID=Hs.77522.1
/TIER=ConsEnd /STK=0 /UG=Hs.77522 /LL=3108 /UG_GENE=HLA-DMA /UG_TITLE=major
histocompatibility complex, class II, DM alpha /DEF=H.sapiens HLA-DMA
gene"•0.392526553•0.176028156•"major histocompatibility complex, class II, DM
alpha"•HLA-DMA•Hs.351279•ENSG00000124546•"6955 // immune response // inferred
from electronic annotation /// 9596 // detection of pest, pathogen or
parasite // traceable author statement /// 19884 // antigen presentation,
exogenous antigen // inferred from electronic annotation /// 19886 //
antig"•16020 // membrane // inferred from electronic annotation /// 16021 //
integral to membrane // inferred from electronic annotation•5515 // protein
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binding // traceable author statement /// 45012 // MHC class II receptor
activity // inferred from electronic annotation /// 45012 // MHC class II
receptor activity // non-traceable author statement
206256_at•"gb:NM_001308.1 /DB_XREF=gi:4503010 /GEN=CPN1 /FEA=FLmRNA /CNT=22
/TID=Hs.2246.0 /TIER=FL+Stack /STK=14 /UG=Hs.2246 /LL=1369 /DEF=Homo sapiens
carboxypeptidase N, polypeptide 1, 50kD (CPN1), mRNA. /PROD=carboxypeptidase
N, polypeptide 1, 50kDprecursor
/FL="•0.392081707•0.247931577•"carboxypeptidase N, polypeptide 1,
50kD"•CPN1•Hs.2246•ENSG00000120054•6508 // proteolysis and peptidolysis //
inferred from electronic annotation•5615 // extracellular space // traceable
author statement•4182 // carboxypeptidase A activity // inferred from
electronic annotation /// 4184 // lysine carboxypeptidase activity //
inferred from electronic annotation /// 8237 // metallopeptidase activity //
inferred from electronic annotation
202032_s_at•"gb:NM_006122.1 /DB_XREF=gi:5540099 /GEN=MAN2A2 /FEA=FLmRNA
/CNT=161 /TID=Hs.295605.0 /TIER=FL+Stack /STK=54 /UG=Hs.295605 /LL=4122
/DEF=Homo sapiens mannosidase, alpha, class 2A, member 2 (MAN2A2), mRNA.
/PROD=mannosidase, alpha, class 2A, member 2
/FL=gb"•0.391527667•0.389772804•"mannosidase, alpha, class 2A, member
2"•MAN2A2•Hs.116459••5975 // carbohydrate metabolism // non-traceable author
statement /// 6013 // mannose metabolism // inferred from electronic
annotation•139 // Golgi membrane // non-traceable author statement /// 16021
// integral to membrane // inferred from electronic annotation•"4559 //
alpha-mannosidase activity // inferred from electronic annotation /// 4572 //
mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity // non-traceable
author statement /// 16798 // hydrolase activity, acting on glycosyl bonds //
inferred from "
201998_at•"gb:AI743792 /DB_XREF=gi:5112080 /DB_XREF=wg53h11.x1
/CLONE=IMAGE:2368869 /FEA=FLmRNA /CNT=240 /TID=Hs.2554.0 /TIER=Stack /STK=107
/UG=Hs.2554 /LL=6480 /UG_GENE=SIAT1 /UG_TITLE=sialyltransferase 1
(beta-galactoside alpha-2,6-sialytransferase)
/FL=gb:NM_003"•0.391063229•0.331896825•"ST6 beta-galactosamide
alpha-2,6-sialyltranferase 1"•ST6GAL1•Hs.207459•ENSG00000073849•6486 //
protein amino acid glycosylation // inferred from electronic annotation ///
6959 // humoral immune response // traceable author statement /// 9311 //
oligosaccharide metabolism // inferred from sequence or structural similarity
/// 40007 // growth•5794 // Golgi apparatus // inferred from electronic
annotation /// 16020 // membrane // inferred from electronic annotation ///
16021 // integral to membrane // inferred from sequence or structural
similarity•"3835 // beta-galactoside alpha-2,6-sialyltransferase activity //
inferred from sequence or structural similarity"
230493_at•gb:AW664964 /DB_XREF=gi:7457508 /DB_XREF=hi98e03.x1
/CLONE=IMAGE:2980348 /FEA=EST /CNT=13 /TID=Hs.128899.0 /TIER=Stack /STK=10
/UG=Hs.128899 /UG_TITLE=ESTs•0.390452473•0.461336168•transmembrane protein
46•TMEM46•Hs.433791•ENSG00000180730••16021 // integral to membrane //
inferred from electronic annotation•
204014_at•"gb:NM_001394.2 /DB_XREF=gi:12707552 /GEN=DUSP4 /FEA=FLmRNA
/CNT=105 /TID=Hs.2359.0 /TIER=FL /STK=4 /UG=Hs.2359 /LL=1846 /DEF=Homo
sapiens dual specificity phosphatase 4 (DUSP4), mRNA. /PROD=dual specificity
phosphatase 4 /FL=gb:NM_001394.2 gb:BC002671.1
g"•0.388623967•0.323797205•dual specificity phosphatase
4•DUSP4•Hs.417962•ENSG00000120875•74 // regulation of cell cycle //
non-traceable author statement /// 165 // MAPKKK cascade // traceable author
statement /// 6470 // protein amino acid dephosphorylation // inferred from
electronic annotation /// 6470 // protein amino acid dephosphorylati•5634 //
nucleus // traceable author statement•4725 // protein tyrosine phosphatase
activity // inferred from electronic annotation /// 8330 // protein
tyrosine/threonine phosphatase activity // traceable author statement ///
16787 // hydrolase activity // inferred from electronic annotation /// 17017
218007_s_at•"gb:NM_015920.1 /DB_XREF=gi:7705705 /GEN=LOC51065 /FEA=FLmRNA
/CNT=230 /TID=Hs.108957.0 /TIER=FL+Stack /STK=142 /UG=Hs.108957 /LL=51065
/DEF=Homo sapiens 40S ribosomal protein S27 isoform (LOC51065), mRNA.
/PROD=40S ribosomal protein S27 isoform
/FL=gb:NM_"•0.388044463•0.488953891•ribosomal protein
S27-like•RPS27L•Hs.108957•ENSG00000185088•6412 // protein biosynthesis //
inferred from electronic annotation•5840 // ribosome // inferred from
electronic annotation•3735 // structural constituent of ribosome // inferred
from electronic annotation
204137_at•"gb:NM_003272.1 /DB_XREF=gi:4507544 /GEN=TM7SF1 /FEA=FLmRNA /CNT=93
/TID=Hs.15791.0 /TIER=FL+Stack /STK=43 /UG=Hs.15791 /LL=7107 /DEF=Homo
sapiens transmembrane 7 superfamily member 1 (upregulated in kidney)
(TM7SF1), mRNA. /PROD=transmembrane 7
superfamil"•0.386683752•0.279466874•transmembrane 7 superfamily member 1
(upregulated in kidney)•TM7SF1•Hs.498160•ENSG00000077585••5624 // membrane
fraction // traceable author statement /// 5887 // integral to plasma
membrane // traceable author statement•
202447_at•"gb:NM_001359.1 /DB_XREF=gi:4503300 /GEN=DECR1 /FEA=FLmRNA /CNT=168
/TID=Hs.81548.0 /TIER=FL+Stack /STK=60 /UG=Hs.81548 /LL=1666 /DEF=Homo
sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), nuclear gene
encoding mitochondrial protein, mRNA.
/PROD="•0.38616285•0.431639712•"2,4-dienoyl CoA reductase 1,
```

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mitochondrial"•DECR1•Hs.492212•ENSG00000104325•8152 // metabolism // inferred
from electronic annotation•5739 // mitochondrion // traceable author
statement•"8670 // 2,4-dienoyl-CoA reductase (NADPH) activity // traceable
author statement /// 16491 // oxidoreductase activity // inferred from
electronic annotation"
203058_s_at•gb:AW299958 /DB_XREF=gi:6709635 /DB_XREF=xs44g05.x1
/CLONE=IMAGE:2772536 /FEA=FLmRNA /CNT=156 /TID=Hs.274230.0 /TIER=Stack
/STK=31 /UG=Hs.274230 /LL=9060 /UG_GENE=PAPSS2 /UG_TITLE=3-phosphoadenosine
5-phosphosulfate synthase 2 /FL=gb:AF313907.1
gb:AF17336•0.385586063•0.419968482•3'-phosphoadenosine 5'-phosphosulfate
synthase 2•PAPSS2•Hs.524491•ENSG00000198682•"103 // sulfate assimilation //
inferred from electronic annotation /// 1501 // skeletal development //
inferred from sequence or structural similarity /// 6139 // nucleobase,
nucleoside, nucleotide and nucleic acid metabolism // not recorded"•5622 //
intracellular // inferred from sequence or structural similarity•4020 //
adenylyl-sulfate kinase activity // inferred from electronic annotation ///
4781 // sulfate adenylyltransferase (ATP) activity // inferred from sequence
or structural similarity /// 5524 // ATP binding // inferred from sequence or
structural simil
202187_s_at•"gb:NM_006243.1 /DB_XREF=gi:5453949 /GEN=PPP2R5A /FEA=FLmRNA
/CNT=214 /TID=Hs.155079.0 /TIER=FL+Stack /STK=87 /UG=Hs.155079 /LL=5525
/DEF=Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha
isoform (PPP2R5A), mRNA. /PROD=protein
phosphata"•0.385210751•0.356344664•"protein phosphatase 2, regulatory subunit
B (B56), alpha isoform"•PPP2R5A•Hs.497684•ENSG00000066027•7165 // signal
transduction // inferred from electronic annotation•159 // protein
phosphatase type 2A complex // inferred from electronic annotation /// 5737
// cytoplasm // traceable author statement•4721 // phosphoprotein phosphatase
activity // inferred from electronic annotation /// 5515 // protein binding
// inferred from physical interaction /// 8601 // protein phosphatase type 2A
regulator activity // traceable author statement /// 16787 // hydr
202598_at•"gb:NM_005979.1 /DB_XREF=gi:5174658 /GEN=S100A13 /FEA=FLmRNA
/CNT=149 /TID=Hs.14331.0 /TIER=FL+Stack /STK=81 /UG=Hs.14331 /LL=6284
/DEF=Homo sapiens S100 calcium-binding protein A13 (S100A13), mRNA.
/PROD=S100 calcium-binding protein A13 /FL=gb:BC000632.1
"•0.384911001•0.329287525•S100 calcium binding protein
A13•S100A13•Hs.516505•ENSG00000189171•30154 // cell differentiation //
non-traceable author statement••5509 // calcium ion binding // traceable
author statement
224959_at•"gb:AI718385 /DB_XREF=gi:5035641 /DB_XREF=as59f10.x1
/CLONE=IMAGE:2333035 /FEA=mRNA /CNT=144 /TID=Hs.302738.0 /TIER=Stack /STK=34
/UG=Hs.302738 /UG_TITLE=Homo sapiens cDNA: FLJ21425 fis, clone
COL04162"•0.384136788•0.3751153•"solute carrier family 26 (sulfate
transporter), member 2"•SLC26A2•Hs.302738•ENSG00000155850•6810 // transport
// inferred from electronic annotation /// 8272 // sulfate transport //
traceable author statement•5624 // membrane fraction // traceable author
statement /// 5887 // integral to plasma membrane // traceable author
statement /// 16020 // membrane // inferred from electronic annotation•8271
// sulfate porter activity // inferred from electronic annotation
235337_at•gb:AI276403 /DB_XREF=gi:3898677 /DB_XREF=qw06b03.x1
/CLONE=IMAGE:1990253 /FEA=EST /CNT=14 /TID=Hs.88143.0 /TIER=ConsEnd /STK=2
/UG=Hs.88143 /UG_TITLE=ESTs•0.380236771•0.333425224•SERTA domain containing
4•SERTAD4•Hs.445835•ENSG00000082497•••
225102_at•gb:BG168471 /DB_XREF=gi:12675184 /DB_XREF=602339623F1
/CLONE=IMAGE:4447685 /FEA=mRNA /CNT=101 /TID=Hs.3964.0 /TIER=Stack /STK=31
/UG=Hs.3964 /UG_TITLE=Homo sapiens clone 24877 mRNA
sequence•0.37982234•0.360708155•monoglyceride
lipase•MGLL•Hs.277035•ENSG00000074416•6629 // lipid metabolism // traceable
author statement /// 6725 // aromatic compound metabolism // inferred from
electronic annotation /// 6954 // inflammatory response // traceable author
statement••4622 // lysophospholipase activity // traceable author statement
/// 4759 // serine esterase activity // inferred from electronic annotation
/// 16787 // hydrolase activity // inferred from electronic annotation ///
47372 // acylglycerol lipase activity /
228060_at•gb:AI809083 /DB_XREF=gi:5395649 /DB_XREF=wf68b10.x1
/CLONE=IMAGE:2360731 /FEA=EST /CNT=30 /TID=Hs.20976.0 /TIER=Stack /STK=12
/UG=Hs.20976 /UG_TITLE=ESTs•0.379195861•0.423854532•"solute carrier family
35, member F1"•SLC35F1•Hs.549284•ENSG00000196376•••
203408_s_at•"gb:NM_002971.1 /DB_XREF=gi:4506790 /GEN=SATB1 /FEA=FLmRNA
/CNT=196 /TID=Hs.74592.0 /TIER=FL+Stack /STK=31 /UG=Hs.74592 /LL=6304
/DEF=Homo sapiens special AT-rich sequence binding protein 1 (binds to
nuclear matrixscaffold-associating DNAs) (SATB1), mRNA.
"•0.378378075•0.232377319•special AT-rich sequence binding protein 1 (binds
to nuclear matrix/scaffold-associating
DNA's)•SATB1•Hs.517717•ENSG00000182568•"6325 // establishment and/or
maintenance of chromatin architecture // traceable author statement /// 6355
// regulation of transcription, DNA-dependent // inferred from electronic
annotation"•5634 // nucleus // traceable author statement•3690 //
double-stranded DNA binding // traceable author statement /// 3700 //
transcription factor activity // inferred from electronic annotation
211000_s_at•"gb:AB015706.1 /DB_XREF=gi:4972293 /GEN=gp130 /FEA=FLmRNA /CNT=2
```

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/TID=Hs.82065.1 /TIER=FL /STK=0 /UG=Hs.82065 /LL=3572 /DEF=Homo sapiens mRNA
for gp130 of the rheumatoid arthritis antigenic peptide-bearing soluble form
(gp130-RAPS), complete cds. /PROD=gp1"•0.375248776•0.381619715•"interleukin 6
signal transducer (gp130, oncostatin M
receptor)"•IL6ST•Hs.532082•ENSG00000134352•6955 // immune response //
traceable author statement /// 7166 // cell surface receptor linked signal
transduction // traceable author statement•5886 // plasma membrane //
traceable author statement /// 5887 // integral to plasma membrane //
traceable author statement•4872 // receptor activity // traceable author
statement /// 4915 // interleukin-6 receptor activity // traceable author
statement /// 4924 // oncostatin-M receptor activity // traceable author
statement
232270_at•gb:AL137535.1 /DB_XREF=gi:6808211 /FEA=mRNA /CNT=11 /TID=Hs.15806.0
/TIER=ConsEnd /STK=0 /UG=Hs.15806 /UG_TITLE=Homo sapiens mRNA; cDNA
DKFZp434H2019 (from clone DKFZp434H2019) /DEF=Homo sapiens mRNA; cDNA
DKFZp434H2019 (from clone DKFZp434H2019).•0.374375004•0.418956372•Chromosome
9 open reading frame 3•C9orf3•Hs.434253•ENSG00000148120•6508 // proteolysis
and peptidolysis // inferred from direct assay••4177 // aminopeptidase
activity // inferred from direct assay /// 4179 // membrane alanyl
aminopeptidase activity // inferred from electronic annotation /// 8237 //
metallopeptidase activity // inferred from direct assay
225685_at•gb:AI801777 /DB_XREF=gi:5367249 /DB_XREF=to95d04.x1
/CLONE=IMAGE:2186023 /FEA=EST /CNT=92 /TID=Hs.6774.0 /TIER=Stack /STK=38
/UG=Hs.6774 /UG_TITLE=ESTs•0.373518748•0.432762819•CDC42 effector protein
(Rho GTPase binding) 3•CDC42EP3•Hs.369574•ENSG00000163171•7165 // signal
transduction // traceable author statement••5519 // cytoskeletal regulatory
protein binding // traceable author statement
203932_at•"gb:NM_002118.1 /DB_XREF=gi:4504398 /GEN=HLA-DMB /FEA=FLmRNA
/CNT=91 /TID=Hs.1162.0 /TIER=FL+Stack /STK=49 /UG=Hs.1162 /LL=3109 /DEF=Homo
sapiens major histocompatibility complex, class II, DM beta (HLA-DMB), mRNA.
/PROD=major histocompatibility complex, c"•0.37343969•0.301885343•"major
histocompatibility complex, class II, DM beta /// major histocompatibility
complex, class II, DM beta"•HLA-DMB•Hs.1162•ENSG00000112091•"6955 // immune
response // inferred from electronic annotation /// 9596 // detection of
pest, pathogen or parasite // traceable author statement /// 19884 // antigen
presentation, exogenous antigen // inferred from electronic annotation ///
19886 // antig"•16020 // membrane // inferred from electronic annotation ///
16021 // integral to membrane // inferred from electronic annotation•45012 //
MHC class II receptor activity // inferred from electronic annotation
203845_at•gb:AV727449 /DB_XREF=gi:10836870 /DB_XREF=AV727449 /CLONE=HTCAYG01
/FEA=FLmRNA /CNT=86 /TID=Hs.199061.0 /TIER=Stack /STK=25 /UG=Hs.199061
/LL=8850 /UG_GENE=PCAF /UG_TITLE=p300CBP-associated factor /FL=gb:NM_003884.2
gb:U57317.2•0.372691509•0.293167749•p300/CBP-associated
factor•PCAF•Hs.533055•ENSG00000114166•"6338 // chromatin remodeling //
non-traceable author statement /// 6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 6473 // protein amino acid
ac"•5634 // nucleus // traceable author statement•3712 // transcription
cofactor activity // inferred from physical interaction /// 4402 // histone
acetyltransferase activity // inferred from electronic annotation /// 8080 //
N-acetyltransferase activity // inferred from electronic annotation /// 16740
/
218039_at•"gb:NM_016359.1 /DB_XREF=gi:7705950 /GEN=LOC51203 /FEA=FLmRNA
/CNT=141 /TID=Hs.279905.0 /TIER=FL+Stack /STK=29 /UG=Hs.279905 /LL=51203
/DEF=Homo sapiens clone HQ0310 PRO0310p1 (LOC51203), mRNA. /PROD=clone HQ0310
PRO0310p1 /FL=gb:NM_016359.1 gb:AF305711.1
"•0.372505532•0.451181342•nucleolar and spindle associated protein
1•NUSAP1•Hs.511093•ENSG00000137804••5634 // nucleus // inferred from
electronic annotation•
217787_s_at•gb:AL525086 /DB_XREF=gi:12788579 /DB_XREF=AL525086
/CLONE=CS0DC005YC04 (3 prime) /FEA=FLmRNA /CNT=282 /TID=Hs.130181.0
/TIER=Stack /STK=18 /UG=Hs.130181 /LL=2590 /UG_GENE=GALNT2
/UG_TITLE=UDP-N-acetyl-alpha-D-galactosamine:polypeptide
N-acetylgalactosamin•0.370598092•0.232286231•UDP-N-acetyl-alpha-D-galactosamin
e:polypeptide N-acetylgalactosaminyltransferase 2
(GalNAc-T2)•GALNT2•Hs.300834•ENSG00000143641•6493 // O-linked glycosylation
// traceable author statement•5794 // Golgi apparatus // inferred from
electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•"4653 // polypeptide N-acetylgalactosaminyltransferase
activity // traceable author statement /// 5529 // sugar binding // inferred
from electronic annotation /// 16757 // transferase activity, transferring
glycosyl groups // inferred from electronic annot"
209822_s_at•"gb:L22431.1 /DB_XREF=gi:437386 /FEA=FLmRNA /CNT=57
/TID=Hs.73729.1 /TIER=FL+Stack /STK=23 /UG=Hs.73729 /LL=7436 /UG_GENE=VLDLR
/DEF=Human very low density lipoprotein receptor, complete cds. /PROD=very
low density lipoprotein receptor /FL=gb:D16493.1
gb:N"•0.370071816•0.327683806•very low density lipoprotein
receptor•VLDLR•Hs.370422•ENSG00000147852•6629 // lipid metabolism // inferred
from electronic annotation /// 6869 // lipid transport // inferred from
electronic annotation /// 6897 // endocytosis // inferred from electronic
annotation /// 7165 // signal transduction // traceable author statement•5905
```

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// coated pit // inferred from electronic annotation /// 16020 // membrane //
inferred from electronic annotation /// 16021 // integral to membrane //
inferred from electronic annotation•4872 // receptor activity // inferred
from electronic annotation /// 5041 // low-density lipoprotein receptor
activity // traceable author statement /// 5319 // lipid transporter activity
// inferred from electronic annotation /// 5509 // calcium ion bind
209289_at•gb:AI700518 /DB_XREF=gi:4988418 /DB_XREF=we37d09.x1
/CLONE=IMAGE:2343281 /FEA=FLmRNA /CNT=149 /TID=Hs.33287.1 /TIER=Stack /STK=42
/UG=Hs.33287 /LL=4781 /UG_GENE=NFIB /UG_TITLE=nuclear factor IB
/FL=gb:BC001283.1 gb:NM_005596.1 gb:U85193.1•0.369999233•0.403082808•Nuclear
factor I/B•NFIB•Hs.370359•ENSG00000147862•"6260 // DNA replication //
inferred from electronic annotation /// 6350 // transcription // inferred
from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation"•5634 // nucleus //
inferred from electronic annotation /// 5634 // nucleus // traceable author
statement•3700 // transcription factor activity // inferred from electronic
annotation /// 3700 // transcription factor activity // traceable author
statement
204451_at•"gb:NM_003505.1 /DB_XREF=gi:4503824 /GEN=FZD1 /FEA=FLmRNA /CNT=64
/TID=Hs.94234.0 /TIER=FL /STK=0 /UG=Hs.94234 /LL=8321 /DEF=Homo sapiens
frizzled (Drosophila) homolog 1 (FZD1), mRNA. /PROD=frizzled 1
/FL=gb:AB017363.1 gb:NM_003505.1
gb:AF072872.1"•0.369881163•0.419885961•frizzled homolog 1
(Drosophila)•FZD1•Hs.94234•ENSG00000157240•7186 // G-protein coupled receptor
protein signaling pathway // inferred from electronic annotation /// 7275 //
development // inferred from electronic annotation /// 16055 // Wnt receptor
signaling pathway // inferred from electronic annotation•16020 // membrane //
inferred from electronic annotation /// 16021 // integral to membrane //
inferred from electronic annotation•4926 // non-G-protein coupled 7TM
receptor activity // inferred from electronic annotation /// 4930 //
G-protein coupled receptor activity // inferred from electronic annotation
203627_at•gb:AI830698 /DB_XREF=gi:5451454 /DB_XREF=wj52f06.x1
/CLONE=IMAGE:2406467 /FEA=FLmRNA /CNT=95 /TID=Hs.239176.0 /TIER=Stack /STK=11
/UG=Hs.239176 /LL=3480 /UG_GENE=IGF1R /UG_TITLE=insulin-like growth factor 1
receptor /FL=gb:NM_000875.2•0.366260543•0.332987729•Insulin-like growth
factor 1 receptor•IGF1R•Hs.20573•ENSG00000140443•74 // regulation of cell
cycle // traceable author statement /// 6468 // protein amino acid
phosphorylation // inferred from electronic annotation /// 6916 //
anti-apoptosis // traceable author statement /// 7165 // signal transduction
// traceable author•16020 // membrane // inferred from electronic annotation
/// 16021 // integral to membrane // inferred from electronic annotation•4872
// receptor activity // inferred from electronic annotation /// 5006 //
epidermal growth factor receptor activity // inferred from electronic
annotation /// 5010 // insulin-like growth factor receptor activity //
traceable author statement /// 5515 /
210982_s_at•"gb:M60333.1 /DB_XREF=gi:188268 /GEN=HLA-DRA /FEA=FLmRNA /CNT=2
/TID=Hs.76807.1 /TIER=FL /STK=0 /UG=Hs.76807 /LL=3122 /DEF=Human MHC class II
HLA-DRA mRNA, complete cds. /PROD=MHC cell surface glycoprotein
/FL=gb:M60333.1"•0.366195799•0.272812144•"major histocompatibility complex,
class II, DR alpha"•HLA-DRA•Hs.520048•ENSG00000168423 ///
ENSG00000198334•"6955 // immune response // inferred from electronic
annotation /// 6955 // immune response // non-traceable author statement ///
19884 // antigen presentation, exogenous antigen // inferred from electronic
annotation /// 19886 // antigen processing, exoge"•5887 // integral to plasma
membrane // non-traceable author statement /// 16020 // membrane // inferred
from electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•45012 // MHC class II receptor activity //
non-traceable author statement
210951_x_at•"gb:AF125393.1 /DB_XREF=gi:5410356 /FEA=FLmRNA /CNT=2
/TID=Hs.50477.2 /TIER=FL /STK=0 /UG=Hs.50477 /LL=5873 /UG_GENE=RAB27A
/DEF=Homo sapiens Rab27 isoform mRNA, complete cds. /PROD=Rab27 isoform
/FL=gb:AF125393.1"•0.365996259•0.336271768•"RAB27A, member RAS oncogene
family"•RAB27A•Hs.298651•ENSG00000069974•7264 // small GTPase mediated signal
transduction // inferred from electronic annotation••3924 // GTPase activity
// traceable author statement /// 5525 // GTP binding // inferred from
electronic annotation
212906_at•gb:BE044440 /DB_XREF=gi:8361493 /DB_XREF=ho45e07.x1
/CLONE=IMAGE:3040356 /FEA=mRNA /CNT=91 /TID=Hs.251278.0 /TIER=Stack /STK=29
/UG=Hs.251278 /LL=57476 /UG_GENE=KIAA1201 /UG_TITLE=KIAA1201
protein•0.36571003•0.175366957•KIAA1201
protein•KIAA1201•Hs.144725•ENSG00000023171•••
209355_s_at•"gb:AB000889.1 /DB_XREF=gi:2467299 /FEA=FLmRNA /CNT=126
/TID=Hs.331371.1 /TIER=FL+Stack /STK=8 /UG=Hs.331371 /LL=8613 /UG_GENE=PPAP2B
/DEF=Homo sapiens mRNA for phosphatidic acid phosphatase 2b, complete cds.
/PROD=phosphatidic acid phosphatase 2b
/FL=gb:A"•0.365618269•0.200966532•phosphatidic acid phosphatase type
2B•PPAP2B•Hs.405156•ENSG00000162407•6629 // lipid metabolism // non-traceable
author statement /// 8354 // germ cell migration // traceable author
statement•16020 // membrane // traceable author statement /// 16021 //
integral to membrane // inferred from electronic annotation•4721 //
phosphoprotein phosphatase activity // traceable author statement /// 8195 //
```

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phosphatidate phosphatase activity // inferred from electronic annotation ///
16787 // hydrolase activity // inferred from electronic annotation
221916_at•gb:BF055311 /DB_XREF=gi:10809207 /DB_XREF=7j78a07.x1
/CLONE=IMAGE:3392532 /FEA=EST /CNT=58 /TID=Hs.302689.1 /TIER=Stack /STK=36
/UG=Hs.302689 /LL=29951 /UG_GENE=DKFZp434B0417 /UG_TITLE=hypothetical
protein•0.364237476•0.330228323•"Neurofilament, light polypeptide
68kDa"•NEFL•Hs.521461•ENSG00000104725••5882 // intermediate filament //
inferred from electronic annotation /// 5883 // neurofilament // traceable
author statement /// 30424 // axon // inferred from direct assay•5198 //
structural molecule activity // inferred from electronic annotation /// 5200
// structural constituent of cytoskeleton // traceable author statement ///
5515 // protein binding // inferred from physical interaction
210538_s_at•"gb:U37546.1 /DB_XREF=gi:1145290 /GEN=MIHC /FEA=FLmRNA /CNT=5
/TID=Hs.127799.2 /TIER=FL /STK=0 /UG=Hs.127799 /LL=330 /DEF=Human IAP homolog
C (MIHC) mRNA, complete cds. /PROD=MIHC
/FL=gb:U37546.1"•0.364204914•0.185080104•baculoviral IAP repeat-containing
3•BIRC3•Hs.127799•ENSG00000023445•6916 // anti-apoptosis // traceable author
statement /// 7166 // cell surface receptor linked signal transduction //
traceable author statement /// 16567 // protein ubiquitination // inferred
from electronic annotation /// 42981 // regulation of apoptosis•151 //
ubiquitin ligase complex // inferred from electronic annotation•4842 //
ubiquitin-protein ligase activity // inferred from electronic annotation ///
5515 // protein binding // inferred from electronic annotation /// 5515 //
protein binding // non-traceable author statement /// 8270 // zinc ion
binding // inferred from
204151_x_at•"gb:NM_001353.2 /DB_XREF=gi:5453542 /GEN=AKR1C1 /FEA=FLmRNA
/CNT=107 /TID=Hs.306098.0 /TIER=FL+Stack /STK=25 /UG=Hs.306098 /LL=1645
/DEF=Homo sapiens aldo-keto reductase family 1, member C1 (dihydrodiol
dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid
de"•0.362659638•0.250531157•"aldo-keto reductase family 1, member C1
(dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid
dehydrogenase)"•AKR1C1•Hs.460260•ENSG00000187134•6805 // xenobiotic
metabolism // traceable author statement•5737 // cytoplasm // not
recorded•4033 // aldo-keto reductase activity // traceable author statement
/// 5488 // binding // traceable author statement /// 5489 // electron
transporter activity // not recorded /// 15125 // bile acid transporter
activity // traceable author statement /// 47
225056_at•"gb:AB037810.1 /DB_XREF=gi:7243158 /GEN=KIAA1389 /FEA=mRNA /CNT=143
/TID=Hs.18760.0 /TIER=Stack /STK=40 /UG=Hs.18760 /LL=57568 /DEF=Homo sapiens
mRNA for KIAA1389 protein, partial cds. /PROD=KIAA1389
protein"•0.361641438•0.104449867•signal-induced proliferation-associated 1
like 2•SIPA1L2•Hs.268774•ENSG00000116991•••5096 // GTPase activator activity
// inferred from electronic annotation /// 5515 // protein binding //
inferred from electronic annotation
203303_at•"gb:NM_006520.1 /DB_XREF=gi:5730086 /GEN=TCTE1L /FEA=FLmRNA
/CNT=110 /TID=Hs.75307.0 /TIER=FL+Stack /STK=29 /UG=Hs.75307 /LL=6990
/DEF=Homo sapiens t-complex-associated-testis-expressed 1-like (TCTE1L),
mRNA. /PROD=t-complex-associated-testis-expressed
1-l"•0.36151872•0.312690591•t-complex-associated-testis-expressed
1-like•TCTE1L•Hs.446392•ENSG00000165169•••
219634_at•"gb:NM_018413.1 /DB_XREF=gi:8923757 /GEN=C4ST /FEA=FLmRNA /CNT=28
/TID=Hs.287402.0 /TIER=FL /STK=0 /UG=Hs.287402 /LL=50515 /DEF=Homo sapiens
chondroitin 4-sulfotransferase (C4ST), mRNA. /PROD=chondroitin
4-sulfotransferase /FL=gb:AB042326.1 gb:NM_018413.1
"•0.360620317•0.18772636•carbohydrate (chondroitin 4) sulfotransferase
11•CHST11•Hs.546386•ENSG00000171310•5975 // carbohydrate metabolism //
inferred from electronic annotation /// 30206 // chondroitin sulfate
biosynthesis // inferred from direct assay•5794 // Golgi apparatus //
inferred from electronic annotation /// 16021 // integral to membrane //
non-traceable author statement•1537 // N-acetylgalactosamine
4-O-sulfotransferase activity // inferred from direct assay /// 16740 //
transferase activity // inferred from electronic annotation /// 47756 //
chondroitin 4-sulfotransferase activity // inferred from direct assay
211506_s_at•"gb:AF043337.1 /DB_XREF=gi:12641914 /GEN=IL8 /FEA=FLmRNA /CNT=1
/TID=Hs.624.1 /TIER=FL /STK=0 /UG=Hs.624 /LL=3576 /DEF=Homo sapiens
interleukin 8 C-terminal variant (IL8) mRNA, complete cds. /PROD=interleukin
8 C-terminal variant /FL=gb:AF043337.1"•0.3600904•0.357918713•interleukin
8•IL8•Hs.624•ENSG00000169429•1525 // angiogenesis // traceable author
statement /// 6928 // cell motility // traceable author statement /// 6935 //
chemotaxis // traceable author statement /// 7050 // cell cycle arrest //
inferred from direct assay /// 7186 // G-protein coupled recep•5615 //
extracellular space // traceable author statement /// 5625 // soluble
fraction // traceable author statement•5153 // interleukin-8 receptor binding
// inferred from physical interaction /// 5515 // protein binding // inferred
from physical interaction /// 8009 // chemokine activity // traceable author
statement
228523_at•gb:AW970089 /DB_XREF=gi:8159934 /DB_XREF=EST382170 /FEA=EST /CNT=36
/TID=Hs.284136.6 /TIER=ConsEnd /STK=0 /UG=Hs.284136 /LL=29029
/UG_GENE=PRO2047 /UG_TITLE=PRO2047 protein•0.359505681•0.324154224•nanos
homolog 1 (Drosophila)•NANOS1•Hs.351851•ENSG00000188613•6445 // regulation of
translation // inferred from electronic annotation••3723 // RNA binding //
```

```
inferred from electronic annotation /// 8270 // zinc ion binding // inferred
from electronic annotation
217744_s_at•"gb:NM_022121.1 /DB_XREF=gi:11545842 /GEN=PIGPC1 /FEA=FLmRNA
/CNT=376 /TID=Hs.303125.0 /TIER=FL /STK=6 /UG=Hs.303125 /LL=64065 /DEF=Homo
sapiens p53-induced protein PIGPC1 (PIGPC1), mRNA. /PROD=p53-induced protein
PIGPC1 /FL=gb:AF317550.1 gb:NM_022121.1"•0.359079846•0.450540062•"PERP, TP53
apoptosis effector"•PERP•Hs.520421•ENSG00000112378••16021 // integral to
membrane // inferred from electronic annotation•
220230_s_at•"gb:NM_016229.1 /DB_XREF=gi:7706442 /GEN=LOC51700 /FEA=FLmRNA
/CNT=9 /TID=Hs.22142.0 /TIER=FL /STK=5 /UG=Hs.22142 /LL=51700 /DEF=Homo
sapiens cytochrome b5 reductase b5R.2 (LOC51700), mRNA. /PROD=cytochrome b5
reductase b5R.2 /FL=gb:AF169802.1
gb:NM_016229"•0.358765735•0.380932092•cytochrome b5 reductase
b5R.2•CYB5R2•Hs.414362•ENSG00000166394•6118 // electron transport // inferred
from direct assay /// 6118 // electron transport // inferred from electronic
annotation /// 6695 // cholesterol biosynthesis // inferred from electronic
annotation•5625 // soluble fraction // non-traceable author statement ///
5783 // endoplasmic reticulum // inferred from electronic annotation ///
16020 // membrane // inferred from direct assay•4128 // cytochrome-b5
reductase activity // inferred from direct assay /// 16491 // oxidoreductase
activity // inferred from electronic annotation
220425_x_at•"gb:NM_017578.1 /DB_XREF=gi:13487901 /GEN=DKFZp434B1222
/FEA=FLmRNA /CNT=6 /TID=Hs.194093.0 /TIER=FL /STK=2 /UG=Hs.194093 /LL=54763
/DEF=Homo sapiens AKAP-binding sperm protein ropporin (DKFZp434B1222), mRNA.
/PROD=AKAP-binding sperm protein ropporin
/FL=g"•0.355847735•0.147364415•"ropporin, rhophilin associated protein
1B"•ROPN1B•Hs.528203•ENSG00000114547•910 // cytokinesis // non-traceable
author statement /// 7165 // signal transduction // inferred from electronic
annotation /// 7266 // Rho protein signal transduction // traceable author
statement /// 7283 // spermatogenesis // non-traceable author state•5737 //
cytoplasm // inferred from direct assay /// 16021 // integral to membrane //
inferred from electronic annotation /// 19861 // flagellum // inferred from
direct assay /// 19867 // outer membrane // inferred from electronic
annotation•8603 // cAMP-dependent protein kinase regulator activity //
inferred from electronic annotation /// 15288 // porin activity // inferred
from electronic annotation /// 30159 // receptor signaling complex scaffold
activity // non-traceable author statement
205190_at•"gb:NM_002670.1 /DB_XREF=gi:4505896 /GEN=PLS1 /FEA=FLmRNA /CNT=45
/TID=Hs.430.0 /TIER=FL+Stack /STK=14 /UG=Hs.430 /LL=5357 /DEF=Homo sapiens
plastin 1 (I isoform) (PLS1), mRNA. /PROD=plastin 1 /FL=gb:NM_002670.1
gb:L20826.1"•0.355773112•0.457937763•plastin 1 (I
isoform)•PLS1•Hs.203637•ENSG00000120756••5903 // brush border // not recorded
/// 15629 // actin cytoskeleton // not recorded•5200 // structural
constituent of cytoskeleton // traceable author statement /// 5509 // calcium
ion binding // inferred from electronic annotation /// 51015 // actin
filament binding // traceable author statement
219073_s_at•"gb:NM_017784.1 /DB_XREF=gi:8923336 /GEN=FLJ20363 /FEA=FLmRNA
/CNT=56 /TID=Hs.321622.0 /TIER=FL+Stack /STK=12 /UG=Hs.321622 /LL=54907
/DEF=Homo sapiens hypothetical protein FLJ20363 (FLJ20363), mRNA.
/PROD=hypothetical protein FLJ20363 /FL=gb:NM_017784.1
g"•0.355458045•0.331875791•oxysterol binding protein-like
10•OSBPL10•Hs.150122•ENSG00000144645•6869 // lipid transport // inferred from
electronic annotation /// 8202 // steroid metabolism // inferred from
electronic annotation••
231808_at•gb:AY007106.1 /DB_XREF=gi:9955998 /FEA=mRNA /CNT=64 /TID=Hs.16773.2
/TIER=ConsEnd /STK=0 /UG=Hs.16773 /UG_TITLE=Homo sapiens clone TCCCIA00427
mRNA sequence /DEF=Homo sapiens clone TCCCIA00427 mRNA
sequence.•0.355034279•0.301639408•keratin associated protein
4-7•KRTAP4-7•Hs.380164•••45095 // keratin filament // inferred from
electronic annotation•
201309_x_at•"gb:U36189.1 /DB_XREF=gi:1244509 /GEN=hP311 /FEA=FLmRNA /CNT=470
/TID=Hs.142827.0 /TIER=FL /STK=0 /UG=Hs.142827 /LL=9315 /DEF=Human p311
protein (hP311) mRNA, complete cds. /PROD=p311 protein /FL=gb:U30521.1
gb:NM_004772.1 gb:U36189.1"•0.354112437•0.256627831•chromosome 5 open reading
frame 13•C5orf13•Hs.483067•ENSG00000134986•••
219521_at•"gb:NM_018644.1 /DB_XREF=gi:12408651 /GEN=B3GAT1 /FEA=FLmRNA
/CNT=55 /TID=Hs.3353.0 /TIER=FL+Stack /STK=15 /UG=Hs.3353 /LL=27087 /DEF=Homo
sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)
(B3GAT1), mRNA.
/PROD=beta-1,3-glucuronyltransfe"•0.352706643•0.290207334•"beta-1,3-glucuronyl
transferase 1 (glucuronosyltransferase
P)"•B3GAT1•Hs.381050•ENSG00000109956•5975 // carbohydrate metabolism //
traceable author statement /// 6486 // protein amino acid glycosylation //
not recorded•5794 // Golgi apparatus // inferred from electronic annotation
/// 16020 // membrane // inferred from electronic annotation /// 16021 //
integral to membrane // traceable author statement•15018 //
galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase activity //
inferred from electronic annotation /// 16740 // transferase activity //
inferred from electronic annotation /// 30145 // manganese ion binding //
inferred from electro
209493_at•"gb:AF338650.1 /DB_XREF=gi:12751451 /GEN=AIPC /FEA=FLmRNA /CNT=154
```

```
/TID=Hs.173035.0 /TIER=FL+Stack /STK=56 /UG=Hs.173035 /LL=23037 /DEF=Homo
sapiens PDZ domain-containing protein AIPC (AIPC) mRNA, complete cds.
/PROD=PDZ domain-containing protein AIPC /FL="•0.351692658•0.498600114•PDZ
domain containing 3•PDZK3•Hs.481819•ENSG00000133401•7155 // cell adhesion //
inferred from electronic annotation•5576 // extracellular region // inferred
from sequence or structural similarity /// 5634 // nucleus // inferred from
sequence or structural similarity /// 5783 // endoplasmic reticulum //
inferred from sequence or structural similarity /// 5911 // interce•5198 //
structural molecule activity // inferred from electronic annotation /// 5515
// protein binding // inferred from sequence or structural similarity
216874_at•gb:U80770.1 /DB_XREF=gi:2921608 /FEA=mRNA /CNT=1 /TID=Hs.42192.1
/TIER=ConsEnd /STK=0 /UG=Hs.42192 /UG_TITLE=Human EST clone 251800 mariner
transposon Hsmar1 sequence /DEF=Human EST clone 251800 mariner transposon
Hsmar1 sequence.•0.350547892•0.347848143•"Homo sapiens, clone IMAGE:5538654,
mRNA"••Hs.546989••••
1554014_at•"gb:BC007347.1 /DB_XREF=gi:13938415 /TID=Hs2.36787.2 /CNT=14
/FEA=FLmRNA /TIER=FL /STK=7 /LL=1106 /UG_GENE=CHD2 /UG=Hs.36787 /DEF=Homo
sapiens, clone MGC:1566 IMAGE:3050321, mRNA, complete cds. /PROD=Unknown
(protein for MGC:1566) /FL=gb:BC007347.1
gb:BC02"•0.350414011•0.477254353•chromodomain helicase DNA binding protein
2•CHD2•Hs.546244•ENSG00000173575•6333 // chromatin assembly or disassembly //
inferred from electronic annotation /// 6357 // regulation of transcription
from RNA polymerase II promoter // traceable author statement /// 7001 //
chromosome organization and biogenesis (sensu Eukaryota) // •785 // chromatin
// inferred from electronic annotation /// 5634 // nucleus // inferred from
electronic annotation•3682 // chromatin binding // inferred from electronic
annotation /// 4003 // ATP-dependent DNA helicase activity // traceable
author statement /// 4386 // helicase activity // inferred from electronic
annotation /// 5524 // ATP binding // inferred from el
204955_at•"gb:NM_006307.1 /DB_XREF=gi:5454085 /GEN=SRPX /FEA=FLmRNA /CNT=73
/TID=Hs.15154.0 /TIER=FL+Stack /STK=37 /UG=Hs.15154 /LL=8406 /DEF=Homo
sapiens sushi-repeat-containing protein, X chromosome (SRPX), mRNA.
/PROD=sushi-repeat-containing protein, X
chromosome"•0.349602813•0.412023628•"sushi-repeat-containing protein,
X-linked"•SRPX•Hs.15154•ENSG00000101955•7155 // cell adhesion // inferred
from electronic annotation•16020 // membrane // traceable author
statement•5515 // protein binding // inferred from electronic annotation
209288_s_at•gb:AL136842.1 /DB_XREF=gi:6807668 /GEN=DKFZp434A0530 /FEA=FLmRNA
/CNT=172 /TID=Hs.260024.0 /TIER=FL /STK=0 /UG=Hs.260024 /LL=10602 /DEF=Homo
sapiens mRNA; cDNA DKFZp434A0530 (from clone DKFZp434A0530); complete cds.
/PROD=hypothetical protein /FL=gb:AF164•0.348909769•0.326303541•CDC42
effector protein (Rho GTPase binding)
3•CDC42EP3•Hs.369574•ENSG00000163171•7165 // signal transduction // traceable
author statement••5519 // cytoskeletal regulatory protein binding //
traceable author statement
207739_s_at•"gb:NM_001472.1 /DB_XREF=gi:4503878 /GEN=GAGE2 /FEA=FLmRNA /CNT=3
/TID=Hs.278444.0 /TIER=FL /STK=0 /UG=Hs.278444 /LL=2574 /DEF=Homo sapiens G
antigen 2 (GAGE2), mRNA. /PROD=G antigen 2 /FL=gb:U19143.1
gb:NM_001472.1"•0.348051267•0.457391181•G antigen 1 /// G antigen 2 /// G
antigen 3 /// G antigen 4 /// G antigen 5 /// G antigen 6 /// G antigen 7 ///
G antigen 7B /// G antigen 8•GAGE1 /// GAGE2 /// GAGE3 /// GAGE4 /// GAGE5
/// GAGE6 /// GAGE7 /// GAGE7B /// GAGE8•Hs.278606•ENSG00000068990 ///
ENSG00000189064 /// ENSG00000198716•6968 // cellular defense response //
traceable author statement /// 6968 // cellular defense response // traceable
author statement••
205860_x_at•"gb:NM_004476.1 /DB_XREF=gi:4758397 /GEN=FOLH1 /FEA=FLmRNA
/CNT=34 /TID=Hs.1915.0 /TIER=FL+Stack /STK=16 /UG=Hs.1915 /LL=2346 /DEF=Homo
sapiens folate hydrolase (prostate-specific membrane antigen) 1 (FOLH1),
mRNA. /PROD=folate hydrolase
(prostate-specific"•0.347668243•0.294365976•folate hydrolase
(prostate-specific membrane antigen) 1•FOLH1•Hs.380325•ENSG00000086205•6508
// proteolysis and peptidolysis // non-traceable author statement•5624 //
membrane fraction // traceable author statement /// 5887 // integral to
plasma membrane // traceable author statement /// 16020 // membrane //
non-traceable author statement•4180 // carboxypeptidase activity // inferred
from electronic annotation /// 8237 // metallopeptidase activity // inferred
from electronic annotation /// 16805 // dipeptidase activity // inferred from
electronic annotation /// 43275 // glutamate carboxype
227059_at•gb:AI651255 /DB_XREF=gi:4735234 /DB_XREF=wa98e07.x1
/CLONE=IMAGE:2304228 /FEA=EST /CNT=45 /TID=Hs.75113.2 /TIER=Stack /STK=37
/UG=Hs.75113 /LL=2971 /UG_GENE=GTF3A /UG_TITLE=general transcription factor
IIIA•0.347276172•0.478393655•Glypican 6•GPC6•Hs.444329•ENSG00000183098••5578
// extracellular matrix (sensu Metazoa) // inferred from electronic
annotation /// 5887 // integral to plasma membrane // traceable author
statement /// 16020 // membrane // inferred from electronic annotation•
235911_at•gb:AI885815 /DB_XREF=gi:5590979 /DB_XREF=wl61h04.x1
/CLONE=IMAGE:2429431 /FEA=EST /CNT=8 /TID=Hs.184727.0 /TIER=ConsEnd /STK=7
/UG=Hs.184727 /UG_TITLE=ESTs•0.346341717•0.316212713•Hypothetical gene
supported by BC034933; BC068085••Hs.552645••••
204698_at•"gb:NM_002201.2 /DB_XREF=gi:6857799 /GEN=ISG20 /FEA=FLmRNA /CNT=51
/TID=Hs.183487.0 /TIER=FL+Stack /STK=21 /UG=Hs.183487 /LL=3669 /DEF=Homo
```

```
sapiens interferon stimulated gene (20kD) (ISG20), mRNA. /PROD=interferon
stimulated gene (20kD) /FL=gb:U88964.1
gb:"•0.346247733•0.324685004•interferon stimulated gene
20kDa•ISG20•Hs.459265•ENSG00000172183•"738 // DNA catabolism, exonucleolytic
// inferred from direct assay /// 6401 // RNA catabolism // inferred from
direct assay /// 8283 // cell proliferation // traceable author statement ///
9615 // response to virus // inferred from direct assay"•5654 // nucleoplasm
// traceable author statement /// 16605 // PML body // inferred from direct
assay•175 // 3'-5'-exoribonuclease activity // inferred from direct assay ///
3723 // RNA binding // inferred from electronic annotation /// 4527 //
exonuclease activity // inferred from electronic annotation /// 8310 //
single-stranded DNA specific 3'-5' exode
218804_at•"gb:NM_018043.1 /DB_XREF=gi:8922319 /GEN=FLJ10261 /FEA=FLmRNA
/CNT=83 /TID=Hs.26176.0 /TIER=FL /STK=5 /UG=Hs.26176 /LL=55107 /DEF=Homo
sapiens hypothetical protein FLJ10261 (FLJ10261), mRNA. /PROD=hypothetical
protein FLJ10261 /FL=gb:NM_018043.1"•0.345593338•0.432629408•transmembrane
protein 16A•TMEM16A•Hs.503074•ENSG00000131620•••
201162_at•"gb:NM_001553.1 /DB_XREF=gi:4504618 /GEN=IGFBP7 /FEA=FLmRNA
/CNT=409 /TID=Hs.119206.0 /TIER=FL+Stack /STK=157 /UG=Hs.119206 /LL=3490
/DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7),
mRNA. /PROD=insulin-like growth factor binding
pro"•0.342326531•0.499391894•insulin-like growth factor binding protein
7•IGFBP7•Hs.479808•ENSG00000163453•1558 // regulation of cell growth //
inferred from electronic annotation /// 8285 // negative regulation of cell
proliferation // traceable author statement•5576 // extracellular region //
inferred from electronic annotation•5520 // insulin-like growth factor
binding // inferred from electronic annotation
207275_s_at•"gb:NM_001995.1 /DB_XREF=gi:4503650 /GEN=FACL1 /FEA=FLmRNA /CNT=5
/TID=Hs.278333.0 /TIER=FL /STK=0 /UG=Hs.278333 /LL=2179 /DEF=Homo sapiens
fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1), nuclear gene encoding
mitochondrial protein, mRNA. /PROD=long-ch"•0.34226572•0.390259071•acyl-CoA
synthetase long-chain family member 1•ACSL1•Hs.406678•ENSG00000151726•6629 //
lipid metabolism // inferred from electronic annotation /// 6631 // fatty
acid metabolism // not recorded /// 7586 // digestion // traceable author
statement /// 8152 // metabolism // inferred from electronic annotation•16021
// integral to membrane // inferred from electronic annotation•287 //
magnesium ion binding // inferred from electronic annotation /// 4467 //
long-chain-fatty-acid-CoA ligase activity // traceable author statement ///
16874 // ligase activity // inferred from electronic annotation
228863_at•gb:N69091 /DB_XREF=gi:1225252 /DB_XREF=yz60e11.s1
/CLONE=IMAGE:287468 /FEA=EST /CNT=15 /TID=Hs.12268.0 /TIER=Stack /STK=12
/UG=Hs.12268 /UG_TITLE=ESTs•0.341732229•0.272482417•Hypothetical protein
LOC144997•PCDH17•Hs.106511•ENSG00000118946•7155 // cell adhesion // inferred
from electronic annotation /// 7156 // homophilic cell adhesion // inferred
from electronic annotation•16020 // membrane // inferred from electronic
annotation•5509 // calcium ion binding // inferred from electronic annotation
/// 5515 // protein binding // inferred from electronic annotation
206026_s_at•"gb:NM_007115.1 /DB_XREF=gi:6005905 /GEN=TNFAIP6 /FEA=FLmRNA
/CNT=25 /TID=Hs.29352.0 /TIER=FL /STK=0 /UG=Hs.29352 /LL=7130 /DEF=Homo
sapiens tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA.
/PROD=tumor necrosis factor, alpha-induced protein
"•0.34111468•0.323464224•"tumor necrosis factor, alpha-induced protein
6"•TNFAIP6•Hs.437322•ENSG00000123610•6954 // inflammatory response //
traceable author statement /// 7155 // cell adhesion // inferred from
electronic annotation /// 7165 // signal transduction // traceable author
statement /// 7267 // cell-cell signaling // traceable author statement•5576
// extracellular region // not recorded•5515 // protein binding // inferred
from electronic annotation /// 5540 // hyaluronic acid binding // traceable
author statement
202644_s_at•"gb:NM_006290.1 /DB_XREF=gi:5454131 /GEN=TNFAIP3 /FEA=FLmRNA
/CNT=151 /TID=Hs.211600.0 /TIER=FL+Stack /STK=55 /UG=Hs.211600 /LL=7128
/DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3),
mRNA. /PROD=tumor necrosis factor,
alpha-induce"•0.341055608•0.212819576•"tumor necrosis factor, alpha-induced
protein 3"•TNFAIP3•Hs.211600•ENSG00000118503•6512 // ubiquitin cycle //
inferred from electronic annotation /// 6915 // apoptosis // non-traceable
author statement /// 6916 // anti-apoptosis // non-traceable author statement
/// 16481 // negative regulation of transcription // non-traceable author
s•5634 // nucleus // non-traceable author statement•3677 // DNA binding //
inferred from electronic annotation /// 5515 // protein binding //
non-traceable author statement /// 8234 // cysteine-type peptidase activity
// inferred from electronic annotation /// 8270 // zinc ion binding //
inferred from elec
218113_at•"gb:NM_013390.1 /DB_XREF=gi:7019554 /GEN=TMEM2 /FEA=FLmRNA /CNT=123
/TID=Hs.160417.0 /TIER=FL+Stack /STK=11 /UG=Hs.160417 /LL=23670 /DEF=Homo
sapiens transmembrane protein 2 (TMEM2), mRNA. /PROD=transmembrane protein 2
/FL=gb:AF137030.1 gb:NM_013390.1"•0.340755884•0.303198801•transmembrane
protein 2•TMEM2•Hs.494146•ENSG00000135048••16021 // integral to membrane //
traceable author statement•
213032_at•gb:AI186739 /DB_XREF=gi:3737377 /DB_XREF=qe79c01.x1
/CLONE=IMAGE:1745184 /FEA=mRNA /CNT=97 /TID=Hs.326416.0 /TIER=Stack /STK=16
```

```
/UG=Hs.326416 /UG_TITLE=Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone
DKFZp564H1916)•0.338828605•0.306483063•Nuclear factor
I/B•NFIB•Hs.370359•ENSG00000147862•"6260 // DNA replication // inferred from
electronic annotation /// 6350 // transcription // inferred from electronic
annotation /// 6355 // regulation of transcription, DNA-dependent // inferred
from electronic annotation"•5634 // nucleus // inferred from electronic
annotation /// 5634 // nucleus // traceable author statement•3700 //
transcription factor activity // inferred from electronic annotation /// 3700
// transcription factor activity // traceable author statement
231738_at•"gb:NM_018940.1 /DB_XREF=gi:11036655 /GEN=PCDHB7 /FEA=FLmRNA /CNT=7
/TID=Hs.203830.0 /TIER=FL /STK=3 /UG=Hs.203830 /LL=56129 /DEF=Homo sapiens
protocadherin beta 7 (PCDHB7), mRNA. /PROD=protocadherin beta 7
/FL=gb:NM_018940.1 gb:AF152500.1"•0.338366396•0.342126918•protocadherin beta
7•PCDHB7•Hs.203830•ENSG00000113212•7155 // cell adhesion // inferred from
electronic annotation /// 7156 // homophilic cell adhesion // inferred from
electronic annotation /// 16339 // calcium-dependent cell-cell adhesion //
non-traceable author statement•16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // Unknown•5509 // calcium ion
binding // Unknown /// 5515 // protein binding // inferred from electronic
annotation
212956_at•gb:AI348094 /DB_XREF=gi:4085300 /DB_XREF=qp61g12.x1
/CLONE=IMAGE:1927558 /FEA=mRNA /CNT=71 /TID=Hs.90419.0 /TIER=Stack /STK=21
/UG=Hs.90419 /LL=23158 /UG_GENE=KIAA0882 /UG_TITLE=KIAA0882
protein•0.33777808•0.469652941•KIAA0882
protein•KIAA0882•Hs.480819•ENSG00000109436•••5509 // calcium ion binding //
inferred from electronic annotation
235775_at•gb:AI765006 /DB_XREF=gi:5231515 /DB_XREF=wh56a08.x1
/CLONE=IMAGE:2384726 /FEA=EST /CNT=9 /TID=Hs.145014.0 /TIER=ConsEnd /STK=5
/UG=Hs.145014 /UG_TITLE=ESTs•0.337510372•0.347833519•hypothetical protein
DKFZp762A217•DKFZp762A217•Hs.444240•ENSG00000179104•••5488 // binding //
inferred from electronic annotation
203607_at•"gb:NM_014937.1 /DB_XREF=gi:7662413 /GEN=KIAA0966 /FEA=FLmRNA
/CNT=103 /TID=Hs.52463.0 /TIER=FL+Stack /STK=37 /UG=Hs.52463 /LL=22876
/DEF=Homo sapiens KIAA0966 protein (KIAA0966), mRNA. /PROD=KIAA0966 protein
/FL=gb:AB023183.1 gb:NM_014937.1
gb:AF113227.1"•0.335320835•0.350032006•inositol polyphosphate-5-phosphatase
F•INPP5F•Hs.369755•ENSG00000198825•••
33304_at•"Cluster Incl. U88964:Human HEM45 mRNA, complete cds /cds=(37,582)
/gb=U88964 /gi=2062679 /ug=Hs.183487
/len=701"•0.335312814•0.35206473•interferon stimulated gene
20kDa•ISG20•Hs.459265•ENSG00000172183•"738 // DNA catabolism, exonucleolytic
// inferred from direct assay /// 6401 // RNA catabolism // inferred from
direct assay /// 8283 // cell proliferation // traceable author statement ///
9615 // response to virus // inferred from direct assay"•5654 // nucleoplasm
// traceable author statement /// 16605 // PML body // inferred from direct
assay•175 // 3'-5'-exoribonuclease activity // inferred from direct assay ///
3723 // RNA binding // inferred from electronic annotation /// 4527 //
exonuclease activity // inferred from electronic annotation /// 8310 //
single-stranded DNA specific 3'-5' exode
201666_at•"gb:NM_003254.1 /DB_XREF=gi:4507508 /GEN=TIMP1 /FEA=FLmRNA /CNT=282
/TID=Hs.5831.0 /TIER=FL+Stack /STK=220 /UG=Hs.5831 /LL=7076 /DEF=Homo sapiens
tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity,
collagenase inhibitor) (TIMP1), mRNA"•0.332816101•0.318693098•"tissue
inhibitor of metalloproteinase 1 (erythroid potentiating activity,
collagenase inhibitor)"•TIMP1•Hs.522632•ENSG00000102265•7275 // development
// not recorded /// 8284 // positive regulation of cell proliferation //
traceable author statement /// 51045 // negative regulation of membrane
protein ectodomain proteolysis // inferred from direct assay•5578 //
extracellular matrix (sensu Metazoa) // inferred from electronic
annotation•4857 // enzyme inhibitor activity // inferred from electronic
annotation /// 8191 // metalloendopeptidase inhibitor activity // inferred
from direct assay
208812_x_at•"gb:BC004489.1 /DB_XREF=gi:13325360 /FEA=FLmRNA /CNT=490
/TID=Hs.277477.0 /TIER=FL+Stack /STK=335 /UG=Hs.277477 /LL=3107
/UG_GENE=HLA-C /DEF=Homo sapiens, major histocompatibility complex, class I,
C, clone MGC:11039, mRNA, complete cds. /PROD=major
histoc"•0.331251899•0.320048567•"major histocompatibility complex, class I,
C"•HLA-C•Hs.534125•ENSG00000198479•"19882 // antigen presentation // inferred
from electronic annotation /// 19883 // antigen presentation, endogenous
antigen // inferred from electronic annotation /// 19885 // antigen
processing, endogenous antigen via MHC class I // inferred from
electron"•5887 // integral to plasma membrane // non-traceable author
statement /// 16020 // membrane // non-traceable author statement /// 16021
// integral to membrane // inferred from electronic annotation /// 42612 //
MHC class I protein complex // inferred fro•30106 // MHC class I receptor
activity // inferred from electronic annotation /// 30106 // MHC class I
receptor activity // non-traceable author statement /// 45012 // MHC class II
receptor activity // non-traceable author statement
207281_x_at•"gb:NM_016378.1 /DB_XREF=gi:7706758 /GEN=VCX-2r /FEA=FLmRNA
/CNT=13 /TID=Hs.279737.0 /TIER=FL+Stack /STK=10 /UG=Hs.279737 /LL=51480
/DEF=Homo sapiens variable charge protein on X with two repeats (VCX-2r),
```

```
mRNA. /PROD=variable charge protein on X with two
"•0.330924745•0.184259314•"variable charge, X-linked /// variable charge,
X-linked 2 /// variable charge, X-linked 3A /// variably charged X-C"•VCX ///
VCX2 /// VCX3A /// VCX-C•Hs.278906•ENSG00000182583 /// ENSG00000177504 ///
ENSG00000169059•6325 // establishment and/or maintenance of chromatin
architecture // traceable author statement /// 7283 // spermatogenesis //
inferred from expression pattern /// 42255 // ribosome assembly //
non-traceable author statement /// 6325 // establishment and•5730 //
nucleolus // inferred from expression pattern /// 5730 // nucleolus //
inferred from sequence or structural similarity•3682 // chromatin binding //
traceable author statement /// 5515 // protein binding // non-traceable
author statement /// 3682 // chromatin binding // inferred from sequence or
structural similarity /// 5515 // protein binding // inferred from sequence
or
204749_at•"gb:NM_004538.1 /DB_XREF=gi:4758757 /GEN=NAP1L3 /FEA=FLmRNA /CNT=71
/TID=Hs.21365.0 /TIER=FL+Stack /STK=32 /UG=Hs.21365 /LL=4675 /DEF=Homo
sapiens nucleosome assembly protein 1-like 3 (NAP1L3), mRNA. /PROD=nucleosome
assembly protein 1-like 3 /FL=gb:NM_004"•0.330293751•0.350791122•nucleosome
assembly protein 1-like 3•NAP1L3•Hs.21365•ENSG00000186310•6334 // nucleosome
assembly // traceable author statement•5634 // nucleus // inferred from
electronic annotation /// 5678 // chromatin assembly complex // traceable
author statement•
229893_at•gb:BF589413 /DB_XREF=gi:11681737 /DB_XREF=nab26b11.x1
/CLONE=IMAGE:3267020 /FEA=EST /CNT=22 /TID=Hs.55501.0 /TIER=Stack /STK=17
/UG=Hs.55501 /UG_TITLE=ESTs•0.330275529•0.273880769•FERM domain containing
3•FRMD3•Hs.127535•ENSG00000172159•8152 // metabolism // inferred from
electronic annotation•5737 // cytoplasm // inferred from electronic
annotation /// 5856 // cytoskeleton // inferred from electronic annotation
/// 16020 // membrane // inferred from electronic annotation•287 // magnesium
ion binding // inferred from electronic annotation /// 5488 // binding //
inferred from electronic annotation /// 8092 // cytoskeletal protein binding
// inferred from electronic annotation /// 16462 // pyrophosphatase activity
// inferre
206508_at•"gb:NM_001252.1 /DB_XREF=gi:4507604 /GEN=TNFSF7 /FEA=FLmRNA /CNT=19
/TID=Hs.99899.0 /TIER=FL /STK=1 /UG=Hs.99899 /LL=970 /DEF=Homo sapiens tumor
necrosis factor (ligand) superfamily, member 7 (TNFSF7), mRNA. /PROD=CD70
antigen (CD27 ligand) /FL=gb:NM_00125"•0.329885903•0.347688001•"tumor
necrosis factor (ligand) superfamily, member
7"•TNFSF7•Hs.501497•ENSG00000125726•6915 // apoptosis // not recorded ///
6955 // immune response // inferred from electronic annotation /// 7165 //
signal transduction // traceable author statement /// 7267 // cell-cell
signaling // traceable author statement /// 8283 // cell proliferation•5887
// integral to plasma membrane // traceable author statement /// 16020 //
membrane // inferred from electronic annotation•5164 // tumor necrosis factor
receptor binding // inferred from electronic annotation
205334_at•"gb:NM_006271.1 /DB_XREF=gi:5454031 /GEN=S100A1 /FEA=FLmRNA /CNT=73
/TID=Hs.292707.0 /TIER=FL+Stack /STK=14 /UG=Hs.292707 /LL=6271 /DEF=Homo
sapiens S100 calcium-binding protein A1 (S100A1), mRNA. /PROD=S100
calcium-binding protein A1 /FL=gb:NM_006271.1"•0.329447163•0.126082802•S100
calcium binding protein A1•S100A1•Hs.515715•ENSG00000160678•7154 // cell
communication // not recorded /// 7242 // intracellular signaling cascade //
not recorded /// 7399 // neurogenesis // not recorded••5509 // calcium ion
binding // non-traceable author statement /// 5515 // protein binding //
inferred from physical interaction /// 8270 // zinc ion binding //
non-traceable author statement
226189_at•"gb:BF513121 /DB_XREF=gi:11598300
/DB_XREF=UI-H-BW1-amn-g-04-0-UI.s1 /CLONE=IMAGE:3070639 /FEA=EST /CNT=70
/TID=Hs.52620.3 /TIER=Stack /STK=24 /UG=Hs.52620 /LL=3696 /UG_GENE=ITGB8
/UG_TITLE=integrin, beta 8"•0.329361311•0.42903489•"Homo sapiens, clone
IMAGE:4794726, mRNA"••Hs.367688••••
221805_at•"gb:AL537457 /DB_XREF=gi:12800950 /DB_XREF=AL537457
/CLONE=CS0DF025YH07 (3 prime) /FEA=FLmRNA /CNT=134 /TID=Hs.211584.0
/TIER=Stack /STK=35 /UG=Hs.211584 /LL=4747 /UG_GENE=NEFL
/UG_TITLE=neurofilament, light polypeptide (68kD)
/FL=gb:NM_006158.1"•0.329140318•0.250857103•"neurofilament, light polypeptide
68kDa"•NEFL•Hs.521461•ENSG00000104725••5882 // intermediate filament //
inferred from electronic annotation /// 5883 // neurofilament // traceable
author statement /// 30424 // axon // inferred from direct assay•5198 //
structural molecule activity // inferred from electronic annotation /// 5200
// structural constituent of cytoskeleton // traceable author statement ///
5515 // protein binding // inferred from physical interaction
238009_at•gb:AI446064 /DB_XREF=gi:4292592 /DB_XREF=tj33c10.x1
/CLONE=IMAGE:2143314 /FEA=EST /CNT=20 /TID=Hs.28107.0 /TIER=ConsEnd /STK=5
/UG=Hs.28107 /UG_TITLE=ESTs•0.328349811•0.266495752•SRY (sex determining
region Y)-box 5•SOX5•Hs.505007•ENSG00000134532•"6350 // transcription //
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6366 //
transcription from RNA polymerase II promoter // traceable author
statement"•5634 // nucleus // inferred from electronic annotation•3700 //
transcription factor activity // traceable author statement
223279_s_at•"gb:AF322916.1 /DB_XREF=gi:12240160 /FEA=FLmRNA /CNT=78
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/TID=Hs.49753.0 /TIER=FL+Stack /STK=8 /UG=Hs.49753 /LL=55075
/UG_GENE=FLJ10128 /DEF=Homo sapiens uveal autoantigen mRNA, complete cds.
/PROD=uveal autoantigen /FL=gb:AF322916.1"•0.328077579•0.456112333•uveal
autoantigen with coiled-coil domains and ankyrin
repeats•UACA•Hs.108049•ENSG00000137831•16032 // viral life cycle // inferred
from electronic annotation•5576 // extracellular region // non-traceable
author statement•
219221_at•"gb:NM_024724.1 /DB_XREF=gi:13376033 /GEN=FLJ22332 /FEA=FLmRNA
/CNT=45 /TID=Hs.111092.0 /TIER=FL+Stack /STK=18 /UG=Hs.111092 /LL=79779
/DEF=Homo sapiens hypothetical protein FLJ22332 (FLJ22332), mRNA.
/PROD=hypothetical protein FLJ22332
/FL=gb:NM_024724.1"•0.325495212•0.475734725•zinc finger and BTB domain
containing 38•ZBTB38•Hs.518301•••5634 // nucleus // inferred from electronic
annotation•3676 // nucleic acid binding // inferred from electronic
annotation /// 8270 // zinc ion binding // inferred from electronic
annotation
229839_at•gb:AI799784 /DB_XREF=gi:5365256 /DB_XREF=wc43b08.x1
/CLONE=IMAGE:2321367 /FEA=EST /CNT=10 /TID=Hs.49696.0 /TIER=Stack /STK=9
/UG=Hs.49696 /UG_TITLE=ESTs•0.325481945•0.201093114•Hypothetical protein
MGC45780•MGC45780•Hs.146246•ENSG00000168079•6817 // phosphate transport //
inferred from electronic annotation•5737 // cytoplasm // inferred from
electronic annotation /// 16020 // membrane // inferred from electronic
annotation•4872 // receptor activity // inferred from electronic annotation
/// 5044 // scavenger receptor activity // inferred from electronic
annotation
213203_at•"gb:AI633709 /DB_XREF=gi:4685039 /DB_XREF=th71f03.x1
/CLONE=IMAGE:2124125 /FEA=mRNA /CNT=59 /TID=Hs.30174.0 /TIER=Stack /STK=35
/UG=Hs.30174 /LL=10302 /UG_GENE=SNAPC5 /UG_TITLE=small nuclear RNA activating
complex, polypeptide 5, 19kD"•0.322856093•0.296966444•"Small nuclear RNA
activating complex, polypeptide 5,
19kDa"•SNAPC5•Hs.30174•ENSG00000174446•"6350 // transcription // inferred
from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6366 //
transcription from RNA polymerase II promoter // traceable author statement
/// 6384 // "•5634 // nucleus // traceable author statement•3700 //
transcription factor activity // traceable author statement
201163_s_at•"gb:NM_001553.1 /DB_XREF=gi:4504618 /GEN=IGFBP7 /FEA=FLmRNA
/CNT=409 /TID=Hs.119206.0 /TIER=FL+Stack /STK=157 /UG=Hs.119206 /LL=3490
/DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7),
mRNA. /PROD=insulin-like growth factor binding
pro"•0.322828653•0.452974194•insulin-like growth factor binding protein
7•IGFBP7•Hs.479808•ENSG00000163453•1558 // regulation of cell growth //
inferred from electronic annotation /// 8285 // negative regulation of cell
proliferation // traceable author statement•5576 // extracellular region //
inferred from electronic annotation•5520 // insulin-like growth factor
binding // inferred from electronic annotation
225876_at•gb:T84558 /DB_XREF=gi:712910 /DB_XREF=yd53d09.r1
/CLONE=IMAGE:111953 /FEA=mRNA /CNT=68 /TID=Hs.13804.1 /TIER=Stack /STK=11
/UG=Hs.13804 /LL=57185 /UG_GENE=DJ462O23.2 /UG_TITLE=hypothetical protein
dJ462O23.2•0.321922938•0.327428899•hypothetical protein
dJ462O23.2•DJ462O23.2•Hs.523442•ENSG00000001461•••
221601_s_at•gb:AI084226 /DB_XREF=gi:3422649 /DB_XREF=oy72g09.x1
/CLONE=IMAGE:1671424 /FEA=FLmRNA /CNT=75 /TID=Hs.58831.0 /TIER=Stack /STK=27
/UG=Hs.58831 /LL=9214 /UG_GENE=TOSO /UG_TITLE=regulator of Fas-induced
apoptosis /FL=gb:NM_005449.1 gb:AF057557.1•0.321435111•0.301615731•Fas
apoptotic inhibitory molecule /// Fas apoptotic inhibitory
molecule•FAIM3•Hs.58831•ENSG00000162894•6916 // anti-apoptosis // traceable
author statement /// 6968 // cellular defense response // traceable author
statement••
235122_at•gb:AI800713 /DB_XREF=gi:5366107 /DB_XREF=tc13c06.x1
/CLONE=IMAGE:2063722 /FEA=EST /CNT=30 /TID=Hs.16365.0 /TIER=ConsEnd /STK=3
/UG=Hs.16365 /UG_TITLE=ESTs•0.321186607•0.312179861•CDNA clone
IMAGE:6254031••Hs.403972••••
209287_s_at•"gb:AF104857.1 /DB_XREF=gi:4324453 /FEA=FLmRNA /CNT=172
/TID=Hs.260024.0 /TIER=FL /STK=0 /UG=Hs.260024 /LL=10602 /UG_GENE=CEP3
/DEF=Homo sapiens Cdc42 effector protein 3 mRNA, complete cds. /PROD=Cdc42
effector protein 3 /FL=gb:AF164118.1 gb:NM_006449.1
gb"•0.320948255•0.476620103•CDC42 effector protein (Rho GTPase binding)
3•CDC42EP3•Hs.369574•ENSG00000163171•7165 // signal transduction // traceable
author statement••5519 // cytoskeletal regulatory protein binding //
traceable author statement
224950_at•gb:BF476250 /DB_XREF=gi:11547077 /DB_XREF=naa19c02.x1
/CLONE=IMAGE:3255170 /FEA=mRNA /CNT=164 /TID=Hs.300591.0 /TIER=Stack /STK=30
/UG=Hs.300591 /LL=57174 /UG_GENE=KIAA1436 /UG_TITLE=KIAA1436
protein•0.320869397•0.245895375•prostaglandin F2 receptor negative
regulator•PTGFRN•Hs.418093•ENSG00000134247•17148 // negative regulation of
protein biosynthesis // inferred from sequence or structural similarity•16021
// integral to membrane // inferred from electronic annotation•5515 //
protein binding // inferred from sequence or structural similarity
227193_at•gb:AI955713 /DB_XREF=gi:5748023 /DB_XREF=wt37f01.x1
/CLONE=IMAGE:2509657 /FEA=EST /CNT=40 /TID=Hs.23023.0 /TIER=Stack /STK=15
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BRCOC2015944"••Hs.375762••••
1553177_at•"gb:BC022407.1 /DB_XREF=gi:18490408 /TID=Hs2.350581.1 /CNT=11
/FEA=FLmRNA /TIER=FL /STK=1 /LL=117157 /UG_GENE=EAT2 /UG=Hs.350581 /DEF=Homo
sapiens, SH2 domain-containing molecule EAT2, clone MGC:24157 IMAGE:4717041,
mRNA, complete cds. /PROD=SH2 domain-con"•0.319992164•0.140769287•SH2
domain-containing molecule EAT2•EAT2•Hs.350581•ENSG00000198574•7242 //
intracellular signaling cascade // inferred from electronic annotation••
214459_x_at•"gb:M12679.1 /DB_XREF=gi:187911 /GEN=HLA-C /FEA=FLmRNA /CNT=13
/TID=Hs.274485.0 /TIER=FL /STK=1 /UG=Hs.274485 /LL=51353 /UG_TITLE=Cw1
antigen /DEF=Human Cw1 antigen mRNA, complete cds.
/FL=gb:M12679.1"•0.319863005•0.275255734•"major histocompatibility complex,
class I, C"•HLA-C•Hs.534125•ENSG00000198479•"19882 // antigen presentation //
inferred from electronic annotation /// 19883 // antigen presentation,
endogenous antigen // inferred from electronic annotation /// 19885 //
antigen processing, endogenous antigen via MHC class I // inferred from
electron"•5887 // integral to plasma membrane // non-traceable author
statement /// 16020 // membrane // non-traceable author statement /// 16021
// integral to membrane // inferred from electronic annotation /// 42612 //
MHC class I protein complex // inferred fro•30106 // MHC class I receptor
activity // inferred from electronic annotation /// 30106 // MHC class I
receptor activity // non-traceable author statement /// 45012 // MHC class II
receptor activity // non-traceable author statement
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/CLONE=DKFZp434D186 /FEA=mRNA /CNT=18 /TID=Hs.188228.0 /TIER=ConsEnd /STK=2
/UG=Hs.188228 /UG_TITLE=Homo sapiens cDNA FLJ11003 fis, clone
PLACE1002851"•0.318758994•0.09761486•ERO1-like beta (S.
cerevisiae)•ERO1LB•Hs.424926•ENSG00000086619•6118 // electron transport //
inferred from electronic annotation /// 6457 // protein folding // traceable
author statement /// 6810 // transport // inferred from electronic
annotation•5783 // endoplasmic reticulum // traceable author statement ///
16020 // membrane // inferred from electronic annotation•16491 //
oxidoreductase activity // non-traceable author statement /// 51082 //
unfolded protein binding // non-traceable author statement
224458_at•"gb:BC006115.1 /DB_XREF=gi:13543948 /FEA=FLmRNA /CNT=1
/TID=HsAffx.900859.640 /TIER=FL /STK=0 /DEF=Homo sapiens, Similar to RIKEN
cDNA 2810432L12 gene, clone MGC:12992, mRNA, complete cds. /PROD=Similar to
RIKEN cDNA 2810432L12 gene
/FL=gb:BC006115.1"•0.318357825•0.332268609•chromosome 9 open reading frame
125 /// chromosome 9 open reading frame
125•C9orf125•Hs.254609•ENSG00000165152•••
230831_at•gb:AW294986 /DB_XREF=gi:6701622 /DB_XREF=UI-H-BI2-ahs-c-05-0-UI.s1
/CLONE=IMAGE:2727920 /FEA=EST /CNT=10 /TID=Hs.21439.0 /TIER=Stack /STK=10
/UG=Hs.21439 /UG_TITLE=ESTs•0.318320445•0.234532512•Hypothetical protein
MGC14161•MGC14161•Hs.368399•ENSG00000171877••5737 // cytoplasm // inferred
from electronic annotation /// 5856 // cytoskeleton // inferred from
electronic annotation /// 16020 // membrane // inferred from electronic
annotation•5488 // binding // inferred from electronic annotation /// 8092 //
cytoskeletal protein binding // inferred from electronic annotation
216526_x_at•"gb:AK024836.1 /DB_XREF=gi:10437242 /FEA=mRNA /CNT=1
/TID=Hs.277477.2 /TIER=ConsEnd /STK=0 /UG=Hs.277477 /LL=3107 /UG_GENE=HLA-C
/UG_TITLE=major histocompatibility complex, class I, C /DEF=Homo sapiens
cDNA: FLJ21183 fis, clone CAS11634, highly similar to
"•0.317720115•0.327962158•"major histocompatibility complex, class I,
C"•HLA-C•Hs.534125•ENSG00000198479•"19882 // antigen presentation // inferred
from electronic annotation /// 19883 // antigen presentation, endogenous
antigen // inferred from electronic annotation /// 19885 // antigen
processing, endogenous antigen via MHC class I // inferred from
electron"•5887 // integral to plasma membrane // non-traceable author
statement /// 16020 // membrane // non-traceable author statement /// 16021
// integral to membrane // inferred from electronic annotation /// 42612 //
MHC class I protein complex // inferred fro•30106 // MHC class I receptor
activity // inferred from electronic annotation /// 30106 // MHC class I
receptor activity // non-traceable author statement /// 45012 // MHC class II
receptor activity // non-traceable author statement
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/CLONE=IMAGE:594502 /FEA=FLmRNA /CNT=60 /TID=Hs.82359.0 /TIER=Stack /STK=13
/UG=Hs.82359 /LL=355 /UG_GENE=TNFRSF6 /UG_TITLE=tumor necrosis factor
receptor superfamily, member 6 /FL=gb:NM_000043.1
gb:M674"•0.317225659•0.300139465•"Fas (TNF receptor superfamily, member
6)"•FAS•Hs.244139•ENSG00000026103•6461 // protein complex assembly //
traceable author statement /// 6915 // apoptosis // inferred from electronic
annotation /// 6916 // anti-apoptosis // traceable author statement /// 6917
// induction of apoptosis // traceable author statement /// 6955 •5625 //
soluble fraction // traceable author statement /// 5829 // cytosol //
non-traceable author statement /// 16020 // membrane // inferred from
electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•4888 // transmembrane receptor activity // inferred
from electronic annotation /// 5515 // protein binding // inferred from
electronic annotation
1555471_a_at•"gb:BC014364.1 /DB_XREF=gi:15680077 /TID=Hs2.24889.2 /CNT=1
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sapiens, clone MGC:24252 IMAGE:3932604, mRNA, complete cds. /PROD=Unknown
(protein for MGC:24252) /FL=gb:BC014364.1"•0.31518639•0.178515726•formin
2•FMN2•Hs.24889••7242 // intracellular signaling cascade // inferred from
electronic annotation /// 7275 // development // inferred from electronic
annotation /// 7275 // development // non-traceable author statement ///
16043 // cell organization and biogenesis // inferr•5634 // nucleus //
inferred from electronic annotation•3779 // actin binding // inferred from
electronic annotation
202481_at•"gb:NM_004753.1 /DB_XREF=gi:4759083 /GEN=SDR1 /FEA=FLmRNA /CNT=134
/TID=Hs.17144.0 /TIER=FL+Stack /STK=62 /UG=Hs.17144 /LL=9249 /DEF=Homo
sapiens short-chain dehydrogenasereductase 1 (SDR1), mRNA. /PROD=short-chain
dehydrogenasereductase 1
/FL=gb:BC002730."•0.314932119•0.241452785•dehydrogenase/reductase (SDR
family) member 3•DHRS3•Hs.289347•ENSG00000162496•6631 // fatty acid
metabolism // traceable author statement /// 7601 // visual perception //
traceable author statement /// 8152 // metabolism // inferred from electronic
annotation•16021 // integral to membrane // inferred from electronic
annotation•166 // nucleotide binding // traceable author statement /// 4022
// alcohol dehydrogenase activity // inferred from electronic annotation ///
5489 // electron transporter activity // traceable author statement /// 16491
// oxidoreductase activity // infer
238513_at•gb:BF905445 /DB_XREF=gi:12296904 /DB_XREF=MR3-MT0329-261200-002-a08
/FEA=EST /CNT=13 /TID=Hs.25978.0 /TIER=ConsEnd /STK=0 /UG=Hs.25978
/UG_TITLE=ESTs•0.313951821•0.441616491•Proline rich Gla (G-carboxyglutamic
acid) 4 (transmembrane)•PRRG4•Hs.471695•ENSG00000135378••5576 //
extracellular region // inferred from electronic annotation /// 16021 //
integral to membrane // non-traceable author statement•5509 // calcium ion
binding // inferred from electronic annotation
226051_at•gb:BF973568 /DB_XREF=gi:12340783 /DB_XREF=602242731F1
/CLONE=IMAGE:4331335 /FEA=EST /CNT=65 /TID=Hs.55940.0 /TIER=Stack /STK=31
/UG=Hs.55940 /UG_TITLE=ESTs•0.313462008•0.473771578•selenoprotein
M•SELM•Hs.55940••••
209286_at•gb:AI754416 /DB_XREF=gi:5132680 /DB_XREF=cr25a08.x1
/CLONE=HBMSC_cr25a08 /FEA=FLmRNA /CNT=172 /TID=Hs.260024.0 /TIER=Stack
/STK=26 /UG=Hs.260024 /LL=10602 /UG_GENE=CEP3 /UG_TITLE=Cdc42 effector
protein 3 /FL=gb:AF164118.1 gb:NM_006449.1 gb:AF094521.1
gb:A•0.313215413•0.364798852•CDC42 effector protein (Rho GTPase binding)
3•CDC42EP3•Hs.369574•ENSG00000163171•7165 // signal transduction // traceable
author statement••5519 // cytoskeletal regulatory protein binding //
traceable author statement
242997_at•gb:AW664311 /DB_XREF=gi:7456852 /DB_XREF=hi09f06.x1
/CLONE=IMAGE:2971811 /FEA=EST /CNT=5 /TID=Hs.259498.0 /TIER=ConsEnd /STK=3
/UG=Hs.259498 /UG_TITLE=ESTs•0.313035013•0.280343179•"CDNA clone
IMAGE:3878708, partial cds"••Hs.259498••••
204627_s_at•"gb:M35999.1 /DB_XREF=gi:183532 /FEA=FLmRNA /CNT=66
/TID=Hs.87149.0 /TIER=FL /STK=0 /UG=Hs.87149 /LL=3690 /UG_GENE=ITGB3
/UG_TITLE=integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
/DEF=Human platelet glycoprotein IIIa (GPIIIa) mRNA, complete
cds"•0.311760513•0.308651659•"integrin, beta 3 (platelet glycoprotein IIIa,
antigen CD61)"•ITGB3•Hs.218040•ENSG00000056345•7160 // cell-matrix adhesion
// inferred from electronic annotation /// 7229 // integrin-mediated
signaling pathway // inferred from electronic annotation /// 7596 // blood
coagulation // traceable author statement•8305 // integrin complex //
traceable author statement•4872 // receptor activity // inferred from
electronic annotation /// 5515 // protein binding // inferred from electronic
annotation
221215_s_at•"gb:NM_020639.1 /DB_XREF=gi:10190675 /GEN=ANKRD3 /FEA=FLmRNA
/CNT=2 /TID=Hs.55565.0 /TIER=FL /STK=1 /UG=Hs.55565 /LL=54101 /DEF=Homo
sapiens ankyrin repeat domain 3 (ANKRD3), mRNA. /PROD=ankyrin repeat domain 3
/FL=gb:NM_020639.1"•0.31105269•0.327297024•receptor-interacting
serine-threonine kinase 4•RIPK4•Hs.517310•ENSG00000183421•6468 // protein
amino acid phosphorylation // inferred from direct assay /// 6468 // protein
amino acid phosphorylation // inferred from electronic annotation••4674 //
protein serine/threonine kinase activity // inferred from direct assay ///
4674 // protein serine/threonine kinase activity // inferred from electronic
annotation /// 5515 // protein binding // inferred from physical interaction
/// 5524 // ATP bi
218035_s_at•"gb:NM_019027.1 /DB_XREF=gi:9506670 /GEN=FLJ20273 /FEA=FLmRNA
/CNT=177 /TID=Hs.95549.0 /TIER=FL+Stack /STK=22 /UG=Hs.95549 /LL=54502
/DEF=Homo sapiens hypothetical protein (FLJ20273), mRNA. /PROD=hypothetical
protein /FL=gb:NM_019027.1"•0.310521165•0.283122316•RNA-binding
protein•FLJ20273•Hs.518727•ENSG00000163694•••166 // nucleotide binding //
inferred from electronic annotation /// 3676 // nucleic acid binding //
inferred from electronic annotation
217362_x_at•"gb:AF005487.1 /DB_XREF=gi:5915893 /FEA=mRNA /CNT=2
/TID=Hs.167385.0 /TIER=ConsEnd /STK=0 /UG=Hs.167385 /UG_TITLE=Homo sapiens
MHC class II antigen HLA-DRB6 mRNA, partial cds /DEF=Homo sapiens MHC class
II antigen (DRB6) mRNA, HLA-DRB6*0201 allele,
sequenc"•0.310278639•0.248200861•"major histocompatibility complex, class II,
DR beta 6 (pseudogene)"•HLA-DRB6•Hs.545653••••
```

```
1554093_a_at•"gb:BC014315.1 /DB_XREF=gi:15680008 /TID=Hs2.30174.2 /CNT=12
/FEA=FLmRNA /TIER=FL /STK=4 /LL=10302 /UG_GENE=SNAPC5 /UG=Hs.30174 /DEF=Homo
sapiens, Similar to small nuclear RNA activating complex, polypeptide 5,
19kD, clone MGC:22700 IMAGE:3997264, mRNA, co"•0.309358042•0.371366591•"small
nuclear RNA activating complex, polypeptide 5,
19kDa"•SNAPC5•Hs.30174•ENSG00000174446•"6350 // transcription // inferred
from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6366 //
transcription from RNA polymerase II promoter // traceable author statement
/// 6384 // "•5634 // nucleus // traceable author statement•3700 //
transcription factor activity // traceable author statement
214838_at•gb:AL035297.1 /DB_XREF=gi:4200248 /FEA=mRNA /CNT=12
/TID=Hs.119254.0 /TIER=ConsEnd /STK=0 /UG=Hs.119254 /DEF=H.sapiens gene from
PAC 747L4. /PROD=hypothetical protein•0.308202256•0.303020022•hypothetical
protein LOC375035•LOC375035•Hs.546557•ENSG00000184197•••
209514_s_at•"gb:BE502030 /DB_XREF=gi:9704438 /DB_XREF=hy11d05.x1
/CLONE=IMAGE:3197001 /FEA=FLmRNA /CNT=83 /TID=Hs.50477.1 /TIER=Stack /STK=12
/UG=Hs.50477 /LL=5873 /UG_GENE=RAB27A /UG_TITLE=RAB27A, member RAS oncogene
family /FL=gb:U38654.3"•0.308099948•0.223938749•"RAB27A, member RAS oncogene
family"•RAB27A•Hs.298651•ENSG00000069974•7264 // small GTPase mediated signal
transduction // inferred from electronic annotation••3924 // GTPase activity
// traceable author statement /// 5525 // GTP binding // inferred from
electronic annotation
1554049_s_at•"gb:BC013107.1 /DB_XREF=gi:15341858 /TID=Hs2.110707.2 /CNT=29
/FEA=FLmRNA /TIER=FL /STK=5 /LL=50717 /UG_GENE=H326 /UG=Hs.110707 /DEF=Homo
sapiens, clone MGC:9478 IMAGE:3918647, mRNA, complete cds. /PROD=Unknown
(protein for MGC:9478) /FL=gb:BC013107.1"•0.306339094•0.333325774•WD repeat
domain 42A•WDR42A•Hs.492236•ENSG00000132716•••
213599_at•gb:BE045993 /DB_XREF=gi:8363046 /DB_XREF=hd91c08.x4
/CLONE=IMAGE:2916878 /FEA=mRNA /CNT=31 /TID=Hs.116206.0 /TIER=Stack /STK=12
/UG=Hs.116206 /LL=11339 /UG_GENE=OIP5 /UG_TITLE=Opa-interacting protein
5•0.304903478•0.266589565•Opa interacting protein
5•OIP5•Hs.511092•ENSG00000104147•7154 // cell communication // non-traceable
author statement••5515 // protein binding // traceable author statement
201825_s_at•gb:AL572542 /DB_XREF=gi:12930912 /DB_XREF=AL572542
/CLONE=CS0DI008YC09 (3 prime) /FEA=FLmRNA /CNT=244 /TID=Hs.238126.0
/TIER=Stack /STK=69 /UG=Hs.238126 /LL=51097 /UG_GENE=LOC51097
/UG_TITLE=CGI-49 protein /FL=gb:NM_016002.1
gb:AF151807.1•0.304714068•0.322588409•CGI-49
protein•CGI-49•Hs.498397•ENSG00000143653•••
201925_s_at•"gb:NM_000574.1 /DB_XREF=gi:10835142 /GEN=DAF /FEA=FLmRNA
/CNT=314 /TID=Hs.1369.0 /TIER=FL+Stack /STK=84 /UG=Hs.1369 /LL=1604 /DEF=Homo
sapiens decay accelerating factor for complement (CD55, Cromer blood group
system) (DAF), mRNA. /PROD=decay accelerating"•0.303353317•0.210470539•"decay
accelerating factor for complement (CD55, Cromer blood group
system)"•DAF•Hs.527653•ENSG00000196352•"6955 // immune response // inferred
from electronic annotation /// 6958 // complement activation, classical
pathway // inferred from electronic annotation"•5625 // soluble fraction //
traceable author statement /// 5887 // integral to plasma membrane //
traceable author statement /// 16020 // membrane // inferred from electronic
annotation•
204268_at•"gb:NM_005978.2 /DB_XREF=gi:9845513 /GEN=S100A2 /FEA=FLmRNA /CNT=73
/TID=Hs.38991.0 /TIER=FL+Stack /STK=32 /UG=Hs.38991 /LL=6273 /DEF=Homo
sapiens S100 calcium-binding protein A2 (S100A2), mRNA. /PROD=S100
calcium-binding protein A2 /FL=gb:NM_005978.2
gb:B"•0.302570694•0.273671908•S100 calcium binding protein
A2•S100A2•Hs.516484•ENSG00000196754•••5509 // calcium ion binding //
non-traceable author statement
203921_at•"gb:NM_004267.1 /DB_XREF=gi:4757983 /GEN=CHST2 /FEA=FLmRNA /CNT=82
/TID=Hs.8786.0 /TIER=FL+Stack /STK=43 /UG=Hs.8786 /LL=9435 /DEF=Homo sapiens
carbohydrate (chondroitin 6keratan) sulfotransferase 2 (CHST2), mRNA.
/PROD=carbohydrate (chondroitin
6keratan)s"•0.300448341•0.306711863•carbohydrate (N-acetylglucosamine-6-O)
sulfotransferase 2•CHST2•Hs.8786•ENSG00000175040•5975 // carbohydrate
metabolism // inferred from electronic annotation /// 6044 //
N-acetylglucosamine metabolism // inferred from direct assay /// 6790 //
sulfur metabolism // inferred from direct assay /// 6954 // inflammatory
response // inferred from •5802 // Golgi trans face // inferred from direct
assay /// 16021 // integral to membrane // inferred from electronic
annotation /// 31228 // intrinsic to Golgi membrane // non-traceable author
statement•1517 // N-acetylglucosamine 6-O-sulfotransferase activity //
inferred from direct assay /// 16740 // transferase activity // inferred from
electronic annotation
226991_at•"gb:AA489681 /DB_XREF=gi:2219283 /DB_XREF=aa50c04.s1
/CLONE=IMAGE:824358 /FEA=mRNA /CNT=51 /TID=Hs.102248.0 /TIER=Stack /STK=30
/UG=Hs.102248 /UG_TITLE=Homo sapiens cDNA: FLJ22105 fis, clone
HEP17660"•0.300143304•0.180361942•"Nuclear factor of activated T-cells,
cytoplasmic, calcineurin-dependent 2"•NFATC2•Hs.356321•ENSG00000101096•"6355
// regulation of transcription, DNA-dependent // inferred from electronic
annotation /// 6355 // regulation of transcription, DNA-dependent //
traceable author statement"•5634 // nucleus // inferred from electronic
```

```
annotation /// 5634 // nucleus // traceable author statement /// 5737 //
cytoplasm // traceable author statement•3700 // transcription factor activity
// inferred from electronic annotation /// 3700 // transcription factor
activity // traceable author statement
227827_at•gb:AW138143 /DB_XREF=gi:6142543 /DB_XREF=UI-H-BI1-acy-b-09-0-UI.s1
/CLONE=IMAGE:2715976 /FEA=EST /CNT=32 /TID=Hs.71721.0 /TIER=Stack /STK=16
/UG=Hs.71721 /UG_TITLE=ESTs•0.299211701•0.283903787•Arg/Abl-interacting
protein ArgBP2•ARGBP2•Hs.481342•ENSG00000154556••5634 // nucleus // inferred
from electronic annotation /// 5634 // nucleus // non-traceable author
statement /// 5634 // nucleus // traceable author statement /// 5856 //
cytoskeleton // inferred from electronic annotation /// 15629 // actin
cytoskeleton •3676 // nucleic acid binding // inferred from electronic
annotation /// 5200 // structural constituent of cytoskeleton // traceable
author statement /// 5515 // protein binding // non-traceable author
statement /// 8093 // cytoskeletal adaptor activity //
202488_s_at•"gb:NM_005971.2 /DB_XREF=gi:11612675 /GEN=FXYD3 /FEA=FLmRNA
/CNT=217 /TID=Hs.301350.0 /TIER=FL+Stack /STK=18 /UG=Hs.301350 /LL=5349
/DEF=Homo sapiens FXYD domain-containing ion transport regulator 3 (FXYD3),
transcript variant 1, mRNA. /PROD=MAT-8
protein,"•0.298821164•0.078494809•FXYD domain containing ion transport
regulator 3•FXYD3•Hs.301350•ENSG00000089356•6811 // ion transport // inferred
from electronic annotation /// 6821 // chloride transport // traceable author
statement•5887 // integral to plasma membrane // traceable author statement
/// 16020 // membrane // inferred from electronic annotation•5216 // ion
channel activity // inferred from electronic annotation /// 5254 // chloride
channel activity // traceable author statement
204628_s_at•"gb:NM_000212.1 /DB_XREF=gi:4557676 /GEN=ITGB3 /FEA=FLmRNA
/CNT=66 /TID=Hs.87149.0 /TIER=FL /STK=0 /UG=Hs.87149 /LL=3690 /DEF=Homo
sapiens integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) (ITGB3),
mRNA. /PROD=integrin beta chain, beta 3
precurso"•0.298712975•0.260757517•"integrin, beta 3 (platelet glycoprotein
IIIa, antigen CD61)"•ITGB3•Hs.218040•ENSG00000056345•7160 // cell-matrix
adhesion // inferred from electronic annotation /// 7229 // integrin-mediated
signaling pathway // inferred from electronic annotation /// 7596 // blood
coagulation // traceable author statement•8305 // integrin complex //
traceable author statement•4872 // receptor activity // inferred from
electronic annotation /// 5515 // protein binding // inferred from electronic
annotation
205097_at•"gb:AI025519 /DB_XREF=gi:3241132 /DB_XREF=ov75c04.x1
/CLONE=IMAGE:1643142 /FEA=FLmRNA /CNT=44 /TID=Hs.29981.0 /TIER=Stack /STK=19
/UG=Hs.29981 /LL=1836 /UG_GENE=SLC26A2 /UG_TITLE=solute carrier family 26
(sulfate transporter), member 2 /FL=gb:U14528.1
gb:N"•0.29748411•0.303042601•"solute carrier family 26 (sulfate transporter),
member 2"•SLC26A2•Hs.302738•ENSG00000155850•6810 // transport // inferred
from electronic annotation /// 8272 // sulfate transport // traceable author
statement•5624 // membrane fraction // traceable author statement /// 5887 //
integral to plasma membrane // traceable author statement /// 16020 //
membrane // inferred from electronic annotation•8271 // sulfate porter
activity // inferred from electronic annotation
205101_at•"gb:NM_000246.1 /DB_XREF=gi:4557748 /GEN=MHC2TA /FEA=FLmRNA /CNT=54
/TID=Hs.3076.0 /TIER=FL /STK=0 /UG=Hs.3076 /LL=4261 /DEF=Homo sapiens MHC
class II transactivator (MHC2TA), mRNA. /PROD=MHC class II transactivator
/FL=gb:U18259.1 gb:NM_000246.1"•0.295373757•0.428976164•MHC class II
transactivator•MHC2TA•Hs.126714•ENSG00000179583•"6355 // regulation of
transcription, DNA-dependent // inferred from electronic annotation /// 6955
// immune response // traceable author statement /// 9596 // detection of
pest, pathogen or parasite // traceable author statement /// 42829 // defense
resp"•5634 // nucleus // inferred from electronic annotation•3677 // DNA
binding // traceable author statement /// 3702 // RNA polymerase II
transcription factor activity // traceable author statement /// 3713 //
transcription coactivator activity // traceable author statement /// 5524 //
ATP binding // inferred fr
203973_s_at•"gb:NM_005195.1 /DB_XREF=gi:4885130 /GEN=CEBPD /FEA=FLmRNA
/CNT=116 /TID=Hs.76722.0 /TIER=FL+Stack /STK=69 /UG=Hs.76722 /LL=1052
/DEF=Homo sapiens CCAATenhancer binding protein (CEBP), delta (CEBPD), mRNA.
/PROD=CCAATenhancer binding protein (CEBP), delta
"•0.294973117•0.255817514•"CCAAT/enhancer binding protein (C/EBP),
delta"•CEBPD•Hs.440829•ENSG00000180733•"6350 // transcription // inferred
from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6366 //
transcription from RNA polymerase II promoter // traceable author
statement"•5634 // nucleus // inferred from electronic annotation•3677 // DNA
binding // inferred from electronic annotation
218404_at•"gb:NM_013322.1 /DB_XREF=gi:7019536 /GEN=SNX10 /FEA=FLmRNA /CNT=110
/TID=Hs.106260.0 /TIER=FL+Stack /STK=23 /UG=Hs.106260 /LL=29887 /DEF=Homo
sapiens sorting nexin 10 (SNX10), mRNA. /PROD=sorting nexin 10
/FL=gb:AF121860.1 gb:NM_013322.1"•0.294837401•0.282136589•sorting nexin
10•SNX10•Hs.520714•ENSG00000086300•7242 // intracellular signaling cascade //
inferred from electronic annotation /// 15031 // protein transport //
inferred from electronic annotation••
230645_at•"gb:BF110588 /DB_XREF=gi:10940278 /DB_XREF=7n39e12.x1
```

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/CLONE=IMAGE:3567071 /FEA=EST /CNT=10 /TID=Hs.150478.0 /TIER=Stack /STK=9
/UG=Hs.150478 /UG_TITLE=ESTs, Weakly similar to KIAA0987 protein
(H.sapiens)"•0.294088466•0.227629134•FERM domain containing
3•FRMD3•Hs.127535•ENSG00000172159•8152 // metabolism // inferred from
electronic annotation•5737 // cytoplasm // inferred from electronic
annotation /// 5856 // cytoskeleton // inferred from electronic annotation
/// 16020 // membrane // inferred from electronic annotation•287 // magnesium
ion binding // inferred from electronic annotation /// 5488 // binding //
inferred from electronic annotation /// 8092 // cytoskeletal protein binding
// inferred from electronic annotation /// 16462 // pyrophosphatase activity
// inferre
219377_at•"gb:NM_022751.1 /DB_XREF=gi:12232414 /GEN=FLJ21610 /FEA=FLmRNA
/CNT=44 /TID=Hs.12727.0 /TIER=FL /STK=2 /UG=Hs.12727 /LL=64762 /DEF=Homo
sapiens hypothetical protein FLJ21610 (FLJ21610), mRNA. /PROD=hypothetical
protein FLJ21610 /FL=gb:NM_022751.1"•0.294063071•0.465847214•"family with
sequence similarity 59, member A"•FAM59A•Hs.444314•ENSG00000141441•••5529 //
sugar binding // inferred from electronic annotation
235944_at•gb:BF446673 /DB_XREF=gi:11511811 /DB_XREF=7q90e09.x1
/CLONE=IMAGE:3705689 /FEA=EST /CNT=10 /TID=Hs.150042.0 /TIER=ConsEnd /STK=1
/UG=Hs.150042
/UG_TITLE=ESTs•0.293530078•0.34247325•hemicentin•FIBL-6•Hs.58877•ENSG000001433
41•6468 // protein amino acid phosphorylation // inferred from electronic
annotation /// 7155 // cell adhesion // inferred from electronic annotation
/// 7156 // homophilic cell adhesion // inferred from electronic annotation
/// 7596 // blood coagulation //•16020 // membrane // inferred from
electronic annotation•4888 // transmembrane receptor activity // inferred
from electronic annotation /// 5021 // vascular endothelial growth factor
receptor activity // inferred from electronic annotation /// 5509 // calcium
ion binding // inferred from electronic annotation /
209728_at•"gb:BC005312.1 /DB_XREF=gi:13529055 /FEA=FLmRNA /CNT=84
/TID=Hs.318720.0 /TIER=FL+Stack /STK=31 /UG=Hs.318720 /DEF=Homo sapiens,
clone MGC:12387, mRNA, complete cds. /PROD=Unknown (protein for MGC:12387)
/FL=gb:M16942.1 gb:BC005312.1"•0.293224614•0.180698512•"major
histocompatibility complex, class II, DR beta 4 /// major histocompatibility
complex, class II, DR beta 4"•HLA-DRB4•Hs.534321•ENSG00000196915•"6955 //
immune response // inferred from electronic annotation /// 7165 // signal
transduction // non-traceable author statement /// 9405 // pathogenesis //
traceable author statement /// 19884 // antigen presentation, exogenous
antigen // inferred from e"•5887 // integral to plasma membrane // not
recorded /// 16020 // membrane // inferred from electronic annotation ///
16021 // integral to membrane // inferred from electronic annotation•45012 //
MHC class II receptor activity // inferred from electronic annotation ///
45012 // MHC class II receptor activity // traceable author statement
203561_at•"gb:NM_021642.1 /DB_XREF=gi:11056051 /GEN=FCGR2A /FEA=FLmRNA
/CNT=142 /TID=Hs.78864.0 /TIER=FL+Stack /STK=8 /UG=Hs.78864 /LL=2212
/DEF=Homo sapiens Fc fragment of IgG, low affinity IIa, receptor for (CD32)
(FCGR2A), mRNA. /PROD=Fc fragment of IgG, low
affi"•0.291275903•0.243931508•"Fc fragment of IgG, low affinity IIa, receptor
(CD32)"•FCGR2A•Hs.352642•ENSG00000143226•6955 // immune response // not
recorded•5886 // plasma membrane // non-traceable author statement /// 16021
// integral to membrane // inferred from electronic annotation•4872 //
receptor activity // inferred from electronic annotation /// 5057 // receptor
signaling protein activity // not recorded /// 19864 // IgG binding //
inferred from electronic annotation
223991_s_at•"gb:AF130059.1 /DB_XREF=gi:11493424 /FEA=FLmRNA /CNT=3
/TID=Hs.99858.1 /TIER=FL /STK=0 /UG=Hs.99858 /LL=6130 /UG_GENE=RPL7A
/DEF=Homo sapiens clone FLB5634 PRO1477 mRNA, complete cds. /PROD=PRO1477
/FL=gb:AF130059.1"•0.291120475•0.219294329•UDP-N-acetyl-alpha-D-galactosamine:
polypeptide N-acetylgalactosaminyltransferase 2
(GalNAc-T2)•GALNT2•Hs.300834•ENSG00000143641•6493 // O-linked glycosylation
// traceable author statement•5794 // Golgi apparatus // inferred from
electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•"4653 // polypeptide N-acetylgalactosaminyltransferase
activity // traceable author statement /// 5529 // sugar binding // inferred
from electronic annotation /// 16757 // transferase activity, transferring
glycosyl groups // inferred from electronic annot"
227998_at•gb:AA045184 /DB_XREF=gi:1523386 /DB_XREF=zk66c01.s1
/CLONE=IMAGE:487776 /FEA=EST /CNT=23 /TID=Hs.738.3 /TIER=Stack /STK=16
/UG=Hs.738 /LL=9045 /UG_GENE=RPL14 /UG_TITLE=ribosomal protein
L14•0.290239401•0.355984084•S100 calcium binding protein
A16•S100A16•Hs.515714•ENSG00000188643•••5509 // calcium ion binding //
inferred from electronic annotation
225681_at•"gb:AA584310 /DB_XREF=gi:2368919 /DB_XREF=nn79g01.s1
/CLONE=IMAGE:1090128 /FEA=EST /CNT=87 /TID=Hs.283713.0 /TIER=Stack /STK=54
/UG=Hs.283713 /UG_TITLE=ESTs, Weakly similar to ORF YGL050w
(S.cerevisiae)"•0.288349646•0.23214703•collagen triple helix repeat
containing 1•CTHRC1•Hs.405614•ENSG00000164932•6817 // phosphate transport //
inferred from electronic annotation /// 7155 // cell adhesion // inferred
from electronic annotation•5737 // cytoplasm // inferred from electronic
annotation•5198 // structural molecule activity // inferred from electronic
annotation /// 5515 // protein binding // inferred from electronic
```

```
annotation
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/TID=Hs.170157.0 /TIER=FL /STK=7 /UG=Hs.170157 /LL=4644 /DEF=Homo sapiens
myosin VA (heavy polypeptide 12, myoxin) (MYO5A), mRNA. /PROD=myosin VA
(heavy polypeptide 12, myoxin) /FL=gb:U909"•0.288078303•0.357998865•"myosin
VA (heavy polypeptide 12, myoxin)"•MYO5A•Hs.21213•ENSG00000197535•6810 //
transport // non-traceable author statement /// 30048 // actin filament-based
movement // non-traceable author statement•16459 // myosin // inferred from
electronic annotation /// 30426 // growth cone // non-traceable author
statement /// 43005 // neuronal cell projection // non-traceable author
statement•146 // microfilament motor activity // non-traceable author
statement /// 3779 // actin binding // inferred from electronic annotation
/// 5516 // calmodulin binding // inferred from electronic annotation ///
5524 // ATP binding // inferred from electroni
203263_s_at•gb:AI625739 /DB_XREF=gi:4650670 /DB_XREF=ty65g05.x1
/CLONE=IMAGE:2283992 /FEA=FLmRNA /CNT=119 /TID=Hs.54697.0 /TIER=Stack /STK=12
/UG=Hs.54697 /LL=23229 /UG_GENE=ARHGEF9 /UG_TITLE=Cdc42 guanine exchange
factor (GEF) 9 /FL=gb:NM_015185.1•0.287807239•0.222283704•Cdc42 guanine
nucleotide exchange factor (GEF) 9•ARHGEF9•Hs.54697•ENSG00000131089•••
229285_at•gb:AI669749 /DB_XREF=gi:4834523 /DB_XREF=tu12f11.x1
/CLONE=IMAGE:2250861 /FEA=EST /CNT=12 /TID=Hs.56156.0 /TIER=Stack /STK=11
/UG=Hs.56156 /UG_TITLE=ESTs•0.287376276•0.254177171•"ribonuclease L
(2',5'-oligoisoadenylate
synthetase-dependent)"•RNASEL•Hs.518545•ENSG00000135828•6397 // mRNA
processing // inferred from electronic annotation /// 6468 // protein amino
acid phosphorylation // non-traceable author statement••3723 // RNA binding
// inferred from direct assay /// 4672 // protein kinase activity // inferred
from electronic annotation /// 5524 // ATP binding // inferred from
electronic annotation /// 16787 // hydrolase activity // inferred from
electronic annotat
227067_x_at•gb:AW024960 /DB_XREF=gi:5878490 /DB_XREF=wu70c08.x1
/CLONE=IMAGE:2525390 /FEA=EST /CNT=32 /TID=Hs.8121.2 /TIER=Stack /STK=26
/UG=Hs.8121 /LL=4853 /UG_GENE=NOTCH2 /UG_TITLE=Notch (Drosophila) homolog
2•0.287266534•0.259946741•Notch homolog 2 (Drosophila) N-terminal
like•NOTCH2NL•Hs.502564•ENSG00000163386•••5509 // calcium ion binding //
inferred from electronic annotation
228442_at•gb:AI770171 /DB_XREF=gi:5236626 /DB_XREF=wi79b10.x1
/CLONE=IMAGE:2399515 /FEA=EST /CNT=23 /TID=Hs.112157.0 /TIER=Stack /STK=23
/UG=Hs.112157 /UG_TITLE=ESTs•0.286310597•0.224929837•"Nuclear factor of
activated T-cells, cytoplasmic, calcineurin-dependent
2"•NFATC2•Hs.356321•ENSG00000101096•"6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6355 // regulation
of transcription, DNA-dependent // traceable author statement"•5634 //
nucleus // inferred from electronic annotation /// 5634 // nucleus //
traceable author statement /// 5737 // cytoplasm // traceable author
statement•3700 // transcription factor activity // inferred from electronic
annotation /// 3700 // transcription factor activity // traceable author
statement
1561691_at•"gb:BC039371.1 /DB_XREF=gi:24659793 /TID=Hs2.407549.1 /CNT=1
/FEA=mRNA /TIER=ConsEnd /STK=1 /LL=285735 /UG_GENE=LOC285735 /UG=Hs.407549
/UG_TITLE=hypothetical protein LOC285735 /DEF=Homo sapiens, clone
IMAGE:5271214, mRNA."•0.285653768•0.206420453•hypothetical protein
LOC285735•LOC285735•Hs.407549••••
203455_s_at•"gb:NM_002970.1 /DB_XREF=gi:4506788 /GEN=SAT /FEA=FLmRNA /CNT=192
/TID=Hs.28491.0 /TIER=FL+Stack /STK=183 /UG=Hs.28491 /LL=6303 /DEF=Homo
sapiens spermidinespermine N1-acetyltransferase (SAT), mRNA.
/PROD=spermidinespermine N1-acetyltransferase
/FL=gb:M776"•0.285561654•0.275182508•spermidine/spermine
N1-acetyltransferase•SAT•Hs.28491•ENSG00000130066•••4145 // diamine
N-acetyltransferase activity // traceable author statement /// 8415 //
acyltransferase activity // inferred from electronic annotation /// 16740 //
transferase activity // inferred from electronic annotation
228247_at•"gb:H43637 /DB_XREF=gi:919689 /DB_XREF=yp24b06.s1
/CLONE=IMAGE:188339 /FEA=EST /CNT=28 /TID=Hs.10726.0 /TIER=Stack /STK=11
/UG=Hs.10726 /UG_TITLE=ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J
SEQUENCE CONTAMINATION WARNING ENTRY
(H.sapiens)"•0.285303228•0.254259418•Similar to FRG1 protein (FSHD region
gene 1 protein)•MGC72104•Hs.529357•ENSG00000149531•••
229327_s_at•gb:BE674528 /DB_XREF=gi:10035069 /DB_XREF=7e02b02.x1
/CLONE=IMAGE:3281259 /FEA=EST /CNT=33 /TID=Hs.30250.2 /TIER=Stack /STK=13
/UG=Hs.30250 /LL=4094 /UG_GENE=MAF /UG_TITLE=v-maf musculoaponeurotic
fibrosarcoma (avian) oncogene homolog•0.284643464•0.16928561•V-maf
musculoaponeurotic fibrosarcoma oncogene homolog
(avian)•MAF•Hs.134859•ENSG00000178573•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 6366 // transcription from RNA
polymerase II promoter // traceable author statement"•785 // chromatin //
traceable author statement /// 5634 // nucleus // inferred from electronic
annotation•3677 // DNA binding // inferred from electronic annotation ///
3702 // RNA polymerase II transcription factor activity // traceable author
statement
```

```
219049_at•"gb:NM_018371.1 /DB_XREF=gi:8922959 /GEN=FLJ11264 /FEA=FLmRNA
/CNT=52 /TID=Hs.11260.0 /TIER=FL /STK=1 /UG=Hs.11260 /LL=55790 /DEF=Homo
sapiens hypothetical protein FLJ11264 (FLJ11264), mRNA. /PROD=hypothetical
protein FLJ11264 /FL=gb:NM_018371.1"•0.284049643•0.175014499•"chondroitin
beta1,4
N-acetylgalactosaminyltransferase"•ChGn•Hs.387794•ENSG00000147408•7399 //
neurogenesis // non-traceable author statement /// 8037 // cell recognition
// non-traceable author statement /// 8283 // cell proliferation //
non-traceable author statement /// 9653 // morphogenesis // non-traceable
author statement /// 15014 //•5622 // intracellular // inferred from sequence
or structural similarity /// 5625 // soluble fraction // inferred from direct
assay /// 5794 // Golgi apparatus // inferred from electronic annotation ///
16021 // integral to membrane // inferred from elect•5515 // protein binding
// inferred from sequence or structural similarity /// 8955 // peptidoglycan
glycosyltransferase activity // inferred from direct assay /// 15020 //
glucuronosyltransferase activity // inferred from direct assay /// 16740 //
transf
207012_at•gb:U79292.1 /DB_XREF=gi:1710273 /FEA=FLmRNA /CNT=23 /TID=Hs.90800.1
/TIER=Stack /STK=8 /UG=Hs.90800 /LL=4325 /UG_GENE=MMP16 /UG_TITLE=matrix
metalloproteinase 16 (membrane-inserted) /DEF=Human clone 23734 mRNA
sequence. /FL=gb:AB009303.1 gb:D83646.1 gb:D8•0.283333623•0.332531645••••••
223704_s_at•"gb:AF284225.1 /DB_XREF=gi:9247124 /GEN=DMRT2 /FEA=FLmRNA /CNT=16
/TID=Hs.59506.0 /TIER=FL+Stack /STK=12 /UG=Hs.59506 /LL=10655 /DEF=Homo
sapiens DMRT2terra-like protein (DMRT2) mRNA, complete cds, alternatively
spliced. /PROD=DMRT2terra-like protein
/FL=g"•0.283042143•0.245295245•doublesex and mab-3 related transcription
factor 2•DMRT2•Hs.59506•ENSG00000173253•"6350 // transcription // inferred
from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 7530 // sex
determination // traceable author statement /// 7548 // sex differentiation
// infer"•5634 // nucleus // inferred from electronic annotation•3700 //
transcription factor activity // inferred from electronic annotation /// 3700
// transcription factor activity // traceable author statement
229310_at•"gb:BE465475 /DB_XREF=gi:9511250 /DB_XREF=hw20g02.x1
/CLONE=IMAGE:3183506 /FEA=EST /CNT=20 /TID=Hs.272572.1 /TIER=Stack /STK=13
/UG=Hs.272572 /LL=3040 /UG_GENE=HBA2 /UG_TITLE=hemoglobin, alpha
2"•0.282951148•0.19812354•kelch repeat and BTB (POZ) domain containing
9•KBTBD9•Hs.130593•ENSG00000119771••5634 // nucleus // inferred from
electronic annotation•5515 // protein binding // inferred from electronic
annotation
203140_at•"gb:NM_001706.1 /DB_XREF=gi:4502382 /GEN=BCL6 /FEA=FLmRNA /CNT=123
/TID=Hs.155024.0 /TIER=FL+Stack /STK=54 /UG=Hs.155024 /LL=604 /DEF=Homo
sapiens B-cell CLLlymphoma 6 (zinc finger protein 51) (BCL6), mRNA.
/PROD=B-cell CLLlymphoma 6 (zinc finger protein
5"•0.282179286•0.351701201•B-cell CLL/lymphoma 6 (zinc finger protein 51) ///
B-cell CLL/lymphoma 6 (zinc finger protein
51)•BCL6•Hs.478588•ENSG00000113916•"122 // negative regulation of
transcription from RNA polymerase II promoter // not recorded /// 6350 //
transcription // inferred from electronic annotation /// 6355 // regulation
of transcription, DNA-dependent // traceable author statement /// 6954 //
i"•119 // mediator complex // not recorded /// 5634 // nucleus // inferred
from direct assay•3700 // transcription factor activity // non-traceable
author statement /// 5515 // protein binding // inferred from physical
interaction /// 8270 // zinc ion binding // inferred from electronic
annotation
204612_at•"gb:NM_006823.1 /DB_XREF=gi:5803126 /GEN=PKIA /FEA=FLmRNA /CNT=91
/TID=Hs.75209.0 /TIER=FL+Stack /STK=22 /UG=Hs.75209 /LL=5569 /DEF=Homo
sapiens protein kinase (cAMP-dependent, catalytic) inhibitor alpha (PKIA),
mRNA. /PROD=protein kinase, cAMP-dependent,
"•0.282028802•0.313447206•"protein kinase (cAMP-dependent, catalytic)
inhibitor alpha"•PKIA•Hs.433700•ENSG00000171033•6469 // negative regulation
of protein kinase activity // inferred from electronic annotation••4862 //
cAMP-dependent protein kinase inhibitor activity // inferred from electronic
annotation
238432_at•gb:AI275162 /DB_XREF=gi:3897436 /DB_XREF=qw08b10.x1
/CLONE=IMAGE:1990459 /FEA=EST /CNT=14 /TID=Hs.93714.0 /TIER=ConsEnd /STK=0
/UG=Hs.93714 /UG_TITLE=ESTs•0.281777012•0.293101967•"CDNA FLJ35776 fis, clone
TESTI2005326"••Hs.19872••••
239492_at•gb:R12499 /DB_XREF=gi:765575 /DB_XREF=yf29g05.s1
/CLONE=IMAGE:128312 /FEA=EST /CNT=7 /TID=Hs.20468.0 /TIER=ConsEnd /STK=4
/UG=Hs.20468 /UG_TITLE=ESTs•0.280897327•0.244814895•SEC14-like 4 (S.
cerevisiae)•SEC14L4•Hs.517541•ENSG00000133488•6810 // transport // inferred
from electronic annotation /// 6886 // intracellular protein transport //
inferred from electronic annotation•5622 // intracellular // inferred from
electronic annotation /// 16020 // membrane // inferred from electronic
annotation•5215 // transporter activity // inferred from electronic
annotation /// 8289 // lipid binding // inferred from electronic annotation
/// 8320 // protein carrier activity // inferred from electronic annotation
228245_s_at•"gb:AW594320 /DB_XREF=gi:7281578 /DB_XREF=hg59d01.x1
/CLONE=IMAGE:2949889 /FEA=EST /CNT=39 /TID=Hs.110080.0 /TIER=Stack /STK=25
/UG=Hs.110080 /UG_TITLE=ESTs, Weakly similar to S13495 pregnancy zone protein
```

```
(H.sapiens)"•0.280756135•0.281887755•ovostatin
2•OVOS2•Hs.524331•ENSG00000177359•••4866 // endopeptidase inhibitor activity
// inferred from electronic annotation
225337_at•gb:AI346910 /DB_XREF=gi:4084116 /DB_XREF=qp59b12.x1
/CLONE=IMAGE:1927295 /FEA=EST /CNT=101 /TID=Hs.9006.1 /TIER=Stack /STK=52
/UG=Hs.9006 /LL=9218 /UG_GENE=VAPA /UG_TITLE=VAMP (vesicle-associated
membrane protein)-associated protein A
(33kD)•0.280271993•0.248267708•Abhydrolase domain containing
2•ABHD2•Hs.122337•ENSG00000140526••16021 // integral to membrane //
non-traceable author statement•3824 // catalytic activity // inferred from
electronic annotation
215501_s_at•"gb:AK022513.1 /DB_XREF=gi:10433943 /FEA=mRNA /CNT=3
/TID=Hs.177534.1 /TIER=ConsEnd /STK=0 /UG=Hs.177534 /LL=11221 /UG_GENE=DUSP10
/UG_TITLE=dual specificity phosphatase 10 /DEF=Homo sapiens cDNA FLJ12451
fis, clone NT2RM1000377, highly similar to Homo
sap"•0.279882432•0.290143771•dual specificity phosphatase
10•DUSP10•Hs.497822•ENSG00000143507•6470 // protein amino acid
dephosphorylation // inferred from electronic annotation /// 6470 // protein
amino acid dephosphorylation // traceable author statement /// 6950 //
response to stress // traceable author statement /// 7254 // JNK cascade //
trac•5634 // nucleus // traceable author statement /// 5737 // cytoplasm //
traceable author statement•16787 // hydrolase activity // inferred from
electronic annotation /// 17017 // MAP kinase phosphatase activity //
inferred from electronic annotation
228653_at•gb:AI700341 /DB_XREF=gi:4988241 /DB_XREF=wd06e10.x1
/CLONE=IMAGE:2327370 /FEA=EST /CNT=23 /TID=Hs.110406.0 /TIER=Stack /STK=14
/UG=Hs.110406 /UG_TITLE=ESTs•0.279784309•0.146477606•Similar to RIKEN cDNA
E130306M17 gene••Hs.269122••••
227055_at•"gb:AI827972 /DB_XREF=gi:5448730 /DB_XREF=wk31c11.x1
/CLONE=IMAGE:2413940 /FEA=EST /CNT=33 /TID=Hs.51483.0 /TIER=Stack /STK=18
/UG=Hs.51483 /UG_TITLE=ESTs, Weakly similar to hypothetical protein
(H.sapiens)"•0.279646268•0.395524054•hypothetical protein
MGC17301•MGC17301•Hs.51483•ENSG00000170439•••8757 //
S-adenosylmethionine-dependent methyltransferase activity // inferred from
electronic annotation /// 16740 // transferase activity // inferred from
electronic annotation
209312_x_at•"gb:U65585.1 /DB_XREF=gi:5478215 /GEN=HLA-DRB1 /FEA=FLmRNA
/CNT=126 /TID=Hs.180255.0 /TIER=FL /STK=0 /UG=Hs.180255 /LL=3123 /DEF=Homo
sapiens MHC class II antigen (HLA-DRB1) mRNA, HLA-DRB1*PBL allele, complete
cds. /PROD=MHC class II antigen
/FL=gb:NM_0021"•0.279297569•0.198766104•"major histocompatibility complex,
class II, DR beta 1 /// major histocompatibility complex, class II, DR beta
1"•HLA-DRB1•Hs.520049•ENSG00000196126•"6955 // immune response // inferred
from electronic annotation /// 19884 // antigen presentation, exogenous
antigen // inferred from electronic annotation /// 19886 // antigen
processing, exogenous antigen via MHC class II // inferred from electronic
anno"•16020 // membrane // inferred from electronic annotation /// 16021 //
integral to membrane // inferred from electronic annotation•45012 // MHC
class II receptor activity // inferred from electronic annotation
214770_at•gb:AI299239 /DB_XREF=gi:3958893 /DB_XREF=qn33g02.x1
/CLONE=IMAGE:1900082 /FEA=mRNA /CNT=18 /TID=Hs.49.2 /TIER=ConsEnd /STK=1
/UG=Hs.49 /LL=4481 /UG_GENE=MSR1 /UG_TITLE=macrophage scavenger receptor
1•0.278856486•0.282990929•macrophage scavenger receptor
1•MSR1•Hs.446291•ENSG00000038945•6817 // phosphate transport // inferred from
electronic annotation /// 6898 // receptor mediated endocytosis // inferred
from electronic annotation /// 6898 // receptor mediated endocytosis //
traceable author statement•5737 // cytoplasm // inferred from electronic
annotation /// 5887 // integral to plasma membrane // traceable author
statement /// 16020 // membrane // inferred from electronic annotation•4872
// receptor activity // inferred from electronic annotation /// 5044 //
scavenger receptor activity // inferred from electronic annotation /// 5044
// scavenger receptor activity // traceable author statement /// 5319 //
lipid transporter activity //
205266_at•"gb:NM_002309.2 /DB_XREF=gi:6006018 /GEN=LIF /FEA=FLmRNA /CNT=44
/TID=Hs.2250.0 /TIER=FL+Stack /STK=14 /UG=Hs.2250 /LL=3976 /DEF=Homo sapiens
leukemia inhibitory factor (cholinergic differentiation factor) (LIF), mRNA.
/PROD=leukemia inhibitory factor (cho"•0.278067299•0.278755455•leukemia
inhibitory factor (cholinergic differentiation
factor)•LIF•Hs.2250•ENSG00000128342•6955 // immune response // inferred from
electronic annotation /// 7166 // cell surface receptor linked signal
transduction // not recorded /// 7267 // cell-cell signaling // not recorded
/// 7275 // development // traceable author statement /// 8284 // p•5615 //
extracellular space // not recorded•5125 // cytokine activity // inferred
from electronic annotation /// 5146 // leukemia inhibitory factor receptor
binding // not recorded /// 5147 // oncostatin-M receptor binding // not
recorded /// 8083 // growth factor activity // inferred from electron
231727_s_at•"gb:NM_020679.1 /DB_XREF=gi:10190723 /GEN=AD023 /FEA=FLmRNA
/CNT=9 /TID=Hs.325631.1 /TIER=FL /STK=1 /UG=Hs.325631 /LL=57409 /DEF=Homo
sapiens AD023 protein (AD023), mRNA. /PROD=AD023 protein
/FL=gb:NM_020679.1"•0.277366017•0.26942769•AD023
protein•AD023•Hs.325631•ENSG00000125457•••3723 // RNA binding // inferred
```

```
from electronic annotation
244825_at•gb:AI005420 /DB_XREF=gi:3214930 /DB_XREF=ou08b08.x1
/CLONE=IMAGE:1625655 /FEA=EST /CNT=4 /TID=Hs.130650.0 /TIER=ConsEnd /STK=3
/UG=Hs.130650 /UG_TITLE=ESTs•0.275643018•0.191345388•KIAA1202
protein•KIAA1202•Hs.420541•ENSG00000158352•••5515 // protein binding //
inferred from electronic annotation
226777_at•gb:AA147933 /DB_XREF=gi:1717306 /DB_XREF=zl50d02.s1
/CLONE=IMAGE:505347 /FEA=EST /CNT=76 /TID=Hs.8895.0 /TIER=Stack /STK=28
/UG=Hs.8895 /UG_TITLE=ESTs•0.27472012•0.471959434•A disintegrin and
metalloproteinase domain 12 (meltrin
alpha)•ADAM12•Hs.386283•ENSG00000148848•6508 // proteolysis and peptidolysis
// inferred from electronic annotation /// 7155 // cell adhesion // inferred
from electronic annotation /// 7520 // myoblast fusion // traceable author
statement•5886 // plasma membrane // traceable author statement /// 16021 //
integral to membrane // inferred from electronic annotation•4222 //
metalloendopeptidase activity // inferred from electronic annotation /// 5515
// protein binding // inferred from electronic annotation /// 8270 // zinc
ion binding // inferred from electronic annotation
214596_at•"gb:T15991 /DB_XREF=gi:518153 /DB_XREF=IB2413 /FEA=FLmRNA /CNT=18
/TID=Hs.7138.0 /TIER=ConsEnd /STK=1 /UG=Hs.7138 /LL=1131 /UG_GENE=CHRM3
/UG_TITLE=cholinergic receptor, muscarinic 3
/FL=gb:NM_000740.1"•0.273789427•0.396855444•"cholinergic receptor, muscarinic
3"•CHRM3•Hs.7138•ENSG00000133019•6464 // protein modification // traceable
author statement /// 7165 // signal transduction // traceable author
statement /// 7186 // G-protein coupled receptor protein signaling pathway //
traceable author statement /// 7268 // synaptic transmission // in•5886 //
plasma membrane // traceable author statement /// 5887 // integral to plasma
membrane // traceable author statement•1584 // rhodopsin-like receptor
activity // inferred from electronic annotation /// 4435 // phosphoinositide
phospholipase C activity // traceable author statement /// 4872 // receptor
activity // traceable author statement /// 4981 // muscarinic acetylch
213988_s_at•gb:BE971383 /DB_XREF=gi:10584719 /DB_XREF=601651561F1
/CLONE=IMAGE:3934935 /FEA=EST /CNT=19 /TID=Hs.28491.3 /TIER=Stack /STK=17
/UG=Hs.28491 /LL=6303 /UG_GENE=SAT /UG_TITLE=spermidinespermine
N1-acetyltransferase•0.273626687•0.39933789•spermidine/spermine
N1-acetyltransferase•SAT•Hs.28491•ENSG00000130066•••4145 // diamine
N-acetyltransferase activity // traceable author statement /// 8415 //
acyltransferase activity // inferred from electronic annotation /// 16740 //
transferase activity // inferred from electronic annotation
214787_at•gb:BE268538 /DB_XREF=gi:9142145 /DB_XREF=601125471F1
/CLONE=IMAGE:3345232 /FEA=mRNA /CNT=18 /TID=Hs.135202.0 /TIER=ConsEnd /STK=0
/UG=Hs.135202 /LL=10260 /UG_GENE=IRLB /UG_TITLE=c-myc promoter-binding
protein•0.273286293•0.349535021•c-myc promoter binding
protein•MYCPBP•Hs.513817•ENSG00000174485•"6355 // regulation of
transcription, DNA-dependent // non-traceable author statement"•5634 //
nucleus // non-traceable author statement•3677 // DNA binding //
non-traceable author statement
204781_s_at•"gb:NM_000043.1 /DB_XREF=gi:4507582 /GEN=TNFRSF6 /FEA=FLmRNA
/CNT=60 /TID=Hs.82359.0 /TIER=FL+Stack /STK=15 /UG=Hs.82359 /LL=355 /DEF=Homo
sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), mRNA.
/PROD=apoptosis (APO-1) antigen 1 /FL=g"•0.272839486•0.290458845•"Fas (TNF
receptor superfamily, member 6)"•FAS•Hs.244139•ENSG00000026103•6461 //
protein complex assembly // traceable author statement /// 6915 // apoptosis
// inferred from electronic annotation /// 6916 // anti-apoptosis //
traceable author statement /// 6917 // induction of apoptosis // traceable
author statement /// 6955 •5625 // soluble fraction // traceable author
statement /// 5829 // cytosol // non-traceable author statement /// 16020 //
membrane // inferred from electronic annotation /// 16021 // integral to
membrane // inferred from electronic annotation•4888 // transmembrane
receptor activity // inferred from electronic annotation /// 5515 // protein
binding // inferred from electronic annotation
213142_x_at•gb:AV700415 /DB_XREF=gi:10302386 /DB_XREF=AV700415
/CLONE=GKCDGA04 /FEA=mRNA /CNT=62 /TID=Hs.12969.0 /TIER=Stack /STK=37
/UG=Hs.12969 /LL=54103 /UG_GENE=LOC54103 /UG_TITLE=hypothetical
protein•0.272736215•0.232942401•hypothetical protein
LOC54103•LOC54103•Hs.186649•ENSG00000135174•••
204364_s_at•gb:BE535746 /DB_XREF=gi:9764391 /DB_XREF=601060419F1
/CLONE=IMAGE:3446788 /FEA=FLmRNA /CNT=132 /TID=Hs.7358.0 /TIER=Stack /STK=31
/UG=Hs.7358 /LL=65055 /UG_GENE=FLJ13110 /UG_TITLE=hypothetical protein
FLJ13110 /FL=gb:NM_022912.1•0.272308449•0.17901772•chromosome 2 open reading
frame 23•C2orf23•Hs.368884•ENSG00000068615•••4872 // receptor activity //
inferred from electronic annotation
204670_x_at•"gb:NM_002125.1 /DB_XREF=gi:4504412 /GEN=HLA-DRB5 /FEA=FLmRNA
/CNT=62 /TID=Hs.308026.0 /TIER=FL /STK=1 /UG=Hs.308026 /LL=3127 /DEF=Homo
sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5),
mRNA. /PROD=major histocompatibility complex,
"•0.271462746•0.167047497•"major histocompatibility complex, class II, DR
beta 1"•HLA-DRB1•Hs.520049•ENSG00000196126•"6955 // immune response //
inferred from electronic annotation /// 19884 // antigen presentation,
exogenous antigen // inferred from electronic annotation /// 19886 // antigen
processing, exogenous antigen via MHC class II // inferred from electronic
```

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anno"•16020 // membrane // inferred from electronic annotation /// 16021 //
integral to membrane // inferred from electronic annotation•45012 // MHC
class II receptor activity // inferred from electronic annotation
221815_at•"gb:BE671816 /DB_XREF=gi:10032446 /DB_XREF=7a47d01.x1
/CLONE=IMAGE:3221857 /FEA=EST /CNT=71 /TID=Hs.21921.0 /TIER=Stack /STK=26
/UG=Hs.21921 /UG_TITLE=ESTs, Moderately similar to AF119917 63 PRO2831
(H.sapiens)"•0.271109117•0.300796333•abhydrolase domain containing
2•ABHD2•Hs.122337•ENSG00000140526••16021 // integral to membrane //
non-traceable author statement•3824 // catalytic activity // inferred from
electronic annotation
205743_at•"gb:NM_003149.1 /DB_XREF=gi:4507246 /GEN=STAC /FEA=FLmRNA /CNT=30
/TID=Hs.56045.0 /TIER=FL+Stack /STK=12 /UG=Hs.56045 /LL=6769 /DEF=Homo
sapiens src homology three (SH3) and cysteine rich domain (STAC), mRNA.
/PROD=src homology three (SH3) and cysteine ric"•0.270141137•0.270483148•SH3
and cysteine rich domain•STAC•Hs.56045•ENSG00000144681•7242 // intracellular
signaling cascade // inferred from electronic annotation•5625 // soluble
fraction // traceable author statement•19992 // diacylglycerol binding //
inferred from electronic annotation
230363_s_at•gb:BE858808 /DB_XREF=gi:10374225 /DB_XREF=7f95h05.x1
/CLONE=IMAGE:3304761 /FEA=EST /CNT=15 /TID=Hs.52463.1 /TIER=Stack /STK=14
/UG=Hs.52463 /LL=22876 /UG_GENE=KIAA0966 /UG_TITLE=KIAA0966
protein•0.269685135•0.254600018•inositol polyphosphate-5-phosphatase
F•INPP5F•Hs.369755•ENSG00000198825•••
201744_s_at•"gb:NM_002345.1 /DB_XREF=gi:4505046 /GEN=LUM /FEA=FLmRNA /CNT=472
/TID=Hs.79914.0 /TIER=FL+Stack /STK=235 /UG=Hs.79914 /LL=4060 /DEF=Homo
sapiens lumican (LUM), mRNA. /PROD=lumican /FL=gb:NM_002345.1 gb:U18728.1
gb:U21128.1"•0.268363516•0.169181764•lumican•LUM•Hs.406475•ENSG00000139329•760
1 // visual perception // traceable author statement /// 30199 // collagen
fibril organization // non-traceable author statement•5578 // extracellular
matrix (sensu Metazoa) // traceable author statement /// 5583 // fibrillar
collagen // inferred from direct assay•5201 // extracellular matrix
structural constituent // non-traceable author statement /// 5518 // collagen
binding // inferred from direct assay
221802_s_at•gb:AU157109 /DB_XREF=gi:11018630 /DB_XREF=AU157109
/CLONE=PLACE1006159 /FEA=mRNA /CNT=94 /TID=Hs.23740.1 /TIER=Stack /STK=26
/UG=Hs.23740 /LL=57698 /UG_GENE=KIAA1598 /UG_TITLE=KIAA1598
protein•0.267646189•0.253759738•KIAA1598•KIAA1598•Hs.501140•ENSG00000187164•••
211959_at•gb:AW007532 /DB_XREF=gi:5856310 /DB_XREF=ws52h07.x1
/CLONE=IMAGE:2500861 /FEA=mRNA /CNT=430 /TID=Hs.103391.0 /TIER=Stack /STK=15
/UG=Hs.103391 /UG_TITLE=Human insulin-like growth factor binding protein 5
(IGFBP5) mRNA•0.267225029•0.269734046•insulin-like growth factor binding
protein 5•IGFBP5•Hs.369982•ENSG00000115461•1558 // regulation of cell growth
// inferred from electronic annotation /// 7165 // signal transduction //
non-traceable author statement•5576 // extracellular region // non-traceable
author statement•5520 // insulin-like growth factor binding // inferred from
electronic annotation
205234_at•"gb:NM_004696.1 /DB_XREF=gi:4759113 /GEN=SLC16A4 /FEA=FLmRNA
/CNT=60 /TID=Hs.23590.0 /TIER=FL /STK=4 /UG=Hs.23590 /LL=9122 /DEF=Homo
sapiens solute carrier family 16 (monocarboxylic acid transporters), member 4
(SLC16A4), mRNA. /PROD=solute carrier family
"•0.266339873•0.353127336•"solute carrier family 16 (monocarboxylic acid
transporters), member 4"•SLC16A4•Hs.351306•ENSG00000168679•6810 // transport
// inferred from electronic annotation /// 15718 // monocarboxylic acid
transport // traceable author statement•5624 // membrane fraction //
traceable author statement /// 5887 // integral to plasma membrane //
traceable author statement /// 16021 // integral to membrane // inferred from
electronic annotation•5215 // transporter activity // inferred from
electronic annotation /// 8028 // monocarboxylic acid transporter activity //
traceable author statement /// 15293 // symporter activity // inferred from
electronic annotation
208306_x_at•"gb:NM_021983.2 /DB_XREF=gi:11875206 /GEN=HLA-DRB4 /FEA=FLmRNA
/CNT=2 /TID=Hs.293934.0 /TIER=FL /STK=0 /UG=Hs.293934 /LL=3126 /DEF=Homo
sapiens major histocompatibility complex, class II, DR beta 4 (HLA-DRB4),
mRNA. /PROD=major histocompatibility complex,
"•0.266282328•0.171698177•"Major histocompatibility complex, class II, DR
beta 4"•HLA-DRB1•Hs.520049•ENSG00000196126•"6955 // immune response //
inferred from electronic annotation /// 19884 // antigen presentation,
exogenous antigen // inferred from electronic annotation /// 19886 // antigen
processing, exogenous antigen via MHC class II // inferred from electronic
anno"•16020 // membrane // inferred from electronic annotation /// 16021 //
integral to membrane // inferred from electronic annotation•45012 // MHC
class II receptor activity // inferred from electronic annotation
230333_at•gb:BE326919 /DB_XREF=gi:9200695 /DB_XREF=hr67f02.x1
/CLONE=IMAGE:3133563 /FEA=EST /CNT=14 /TID=Hs.28491.4 /TIER=Stack /STK=14
/UG=Hs.28491 /LL=6303 /UG_GENE=SAT /UG_TITLE=spermidinespermine
N1-acetyltransferase•0.265287619•0.407840509•Spermidine/spermine
N1-acetyltransferase•SAT•Hs.28491•ENSG00000130066•••4145 // diamine
N-acetyltransferase activity // traceable author statement /// 8415 //
acyltransferase activity // inferred from electronic annotation /// 16740 //
transferase activity // inferred from electronic annotation
219922_s_at•"gb:NM_021070.1 /DB_XREF=gi:10835104 /GEN=LTBP3 /FEA=FLmRNA
```

```
/CNT=18 /TID=Hs.289019.0 /TIER=FL /STK=0 /UG=Hs.289019 /LL=4054 /DEF=Homo
sapiens latent transforming growth factor beta binding protein 3 (LTBP3),
mRNA. /PROD=latent transforming growth factor
be"•0.265152268•0.38770538•latent transforming growth factor beta binding
protein 3•LTBP3•Hs.289019•ENSG00000168056•••5509 // calcium ion binding //
inferred from electronic annotation /// 19838 // growth factor binding //
inferred from electronic annotation
204836_at•"gb:NM_000170.1 /DB_XREF=gi:4504012 /GEN=GLDC /FEA=FLmRNA /CNT=59
/TID=Hs.27.0 /TIER=FL+Stack /STK=26 /UG=Hs.27 /LL=2731 /DEF=Homo sapiens
glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine
cleavage system protein P) (GLDC), mRNA.
/PROD"•0.264783188•0.230959896•"glycine dehydrogenase (decarboxylating;
glycine decarboxylase, glycine cleavage system protein
P)"•GLDC•Hs.149156••6546 // glycine catabolism // traceable author
statement•5739 // mitochondrion // inferred from electronic annotation ///
5961 // glycine dehydrogenase complex (decarboxylating) // inferred from
electronic annotation•4375 // glycine dehydrogenase (decarboxylating)
activity // traceable author statement /// 5489 // electron transporter
activity // traceable author statement /// 16491 // oxidoreductase activity
// inferred from electronic annotation
208729_x_at•"gb:D83043.1 /DB_XREF=gi:1871135 /GEN=HLA-B /FEA=FLmRNA /CNT=488
/TID=Hs.77961.1 /TIER=FL /STK=0 /UG=Hs.77961 /LL=3106 /UG_TITLE=major
histocompatibility complex, class I, B /DEF=Human HLA-B mRNA, allele A*2711,
complete cds. /FL=gb:U50710.1 gb:U01848.1 gb"•0.263802283•0.241195431•"major
histocompatibility complex, class I, B"•HLA-B•Hs.77961•ENSG00000198638•"19883
// antigen presentation, endogenous antigen // inferred from electronic
annotation /// 19885 // antigen processing, endogenous antigen via MHC class
I // inferred from electronic annotation"•5887 // integral to plasma membrane
// non-traceable author statement /// 16021 // integral to membrane //
inferred from electronic annotation /// 42612 // MHC class I protein complex
// inferred from electronic annotation•30106 // MHC class I receptor activity
// inferred from electronic annotation /// 30106 // MHC class I receptor
activity // non-traceable author statement
230538_at•gb:AI027957 /DB_XREF=gi:3245266 /DB_XREF=ov84c05.x1
/CLONE=IMAGE:1644008 /FEA=EST /CNT=16 /TID=Hs.121005.0 /TIER=Stack /STK=12
/UG=Hs.121005 /UG_TITLE=ESTs•0.261721578•0.3877819•rai-like
protein•RaLP•Hs.552630•ENSG00000185634•7242 // intracellular signaling
cascade // inferred from electronic annotation••
226925_at•gb:AW069729 /DB_XREF=gi:6024727 /DB_XREF=cr51d05.x1
/CLONE=HBMSC_cr51d05 /FEA=mRNA /CNT=35 /TID=Hs.37443.0 /TIER=Stack /STK=17
/UG=Hs.37443 /UG_TITLE=Homo sapiens mRNA; cDNA DKFZp434B2119 (from clone
DKFZp434B2119); partial cds•0.261433584•0.241512563•acid phosphatase-like
2•ACPL2•Hs.255491•ENSG00000155893•••3993 // acid phosphatase activity //
inferred from electronic annotation
202340_x_at•"gb:NM_002135.1 /DB_XREF=gi:4504440 /GEN=NR4A1 /FEA=FLmRNA
/CNT=145 /TID=Hs.1119.0 /TIER=FL+Stack /STK=57 /UG=Hs.1119 /LL=3164 /DEF=Homo
sapiens nuclear receptor subfamily 4, group A, member 1 (NR4A1), mRNA.
/PROD=nuclear receptor subfamily 4, group A,
mem"•0.260119832•0.237116468•"nuclear receptor subfamily 4, group A, member
1"•NR4A1•Hs.524430•ENSG00000123358•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 7165 // signal transduction //
traceable author statement"•5634 // nucleus // inferred from electronic
annotation•3700 // transcription factor activity // inferred from electronic
annotation /// 3707 // steroid hormone receptor activity // inferred from
electronic annotation /// 4879 // ligand-dependent nuclear receptor activity
// inferred from electronic annotation
225327_at•"gb:AB037791.1 /DB_XREF=gi:7243120 /GEN=KIAA1370 /FEA=mRNA /CNT=93
/TID=Hs.29716.0 /TIER=Stack /STK=15 /UG=Hs.29716 /LL=56204 /DEF=Homo sapiens
mRNA for KIAA1370 protein, partial cds. /PROD=KIAA1370
protein"•0.259214141•0.407698922•hypothetical protein
FLJ10980•FLJ10980•Hs.152385•ENSG00000047346•••
215193_x_at•"gb:AJ297586.1 /DB_XREF=gi:10185079 /GEN=HLA-DRB1 /FEA=mRNA
/CNT=7 /TID=Hs.279930.1 /TIER=ConsEnd /STK=0 /UG=Hs.279930 /LL=3125 /DEF=Homo
sapiens mRNA for MHC class II antigen (HLA-DRB1 gene), DRB1*0402 allele.
/PROD=MHC class II antigen"•0.257766347•0.170593997•"major histocompatibility
complex, class II, DR beta 1"•HLA-DRB1•Hs.520049•ENSG00000196126•"6955 //
immune response // inferred from electronic annotation /// 19884 // antigen
presentation, exogenous antigen // inferred from electronic annotation ///
19886 // antigen processing, exogenous antigen via MHC class II // inferred
from electronic anno"•16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from electronic
annotation•45012 // MHC class II receptor activity // inferred from
electronic annotation
238935_at•"gb:AW958475 /DB_XREF=gi:8148159 /DB_XREF=EST370545 /FEA=EST /CNT=7
/TID=Hs.293947.0 /TIER=ConsEnd /STK=0 /UG=Hs.293947 /UG_TITLE=ESTs, Weakly
similar to I38022 hypothetical protein
(H.sapiens)"•0.257176254•0.286609611•Ribosomal protein
S27-like•RPS27L•Hs.108957•ENSG00000185088•6412 // protein biosynthesis //
inferred from electronic annotation•5840 // ribosome // inferred from
electronic annotation•3735 // structural constituent of ribosome // inferred
```

```
from electronic annotation
1563498_s_at•gb:AK090434.1 /DB_XREF=gi:21748555 /TID=Hs2.407102.1 /CNT=1
/FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.407102 /UG_TITLE=Homo sapiens mRNA for
FLJ00351 protein. /DEF=Homo sapiens mRNA for FLJ00351
protein.•0.253759538•0.438626825•hypothetical protein
LOC283130•LOC283130•Hs.435510•ENSG00000162241•6810 // transport // inferred
from electronic annotation•5743 // mitochondrial inner membrane // inferred
from electronic annotation /// 16020 // membrane // inferred from electronic
annotation•5215 // transporter activity // inferred from electronic
annotation /// 5488 // binding // inferred from electronic annotation
203628_at•gb:H05812 /DB_XREF=gi:869364 /DB_XREF=yl77f04.s1 /CLONE=IMAGE:44149
/FEA=FLmRNA /CNT=95 /TID=Hs.239176.0 /TIER=Stack /STK=24 /UG=Hs.239176
/LL=3480 /UG_GENE=IGF1R /UG_TITLE=insulin-like growth factor 1 receptor
/FL=gb:NM_000875.2•0.25302582•0.247385627•insulin-like growth factor 1
receptor•IGF1R•Hs.20573•ENSG00000140443•74 // regulation of cell cycle //
traceable author statement /// 6468 // protein amino acid phosphorylation //
inferred from electronic annotation /// 6916 // anti-apoptosis // traceable
author statement /// 7165 // signal transduction // traceable author•16020 //
membrane // inferred from electronic annotation /// 16021 // integral to
membrane // inferred from electronic annotation•4872 // receptor activity //
inferred from electronic annotation /// 5006 // epidermal growth factor
receptor activity // inferred from electronic annotation /// 5010 //
insulin-like growth factor receptor activity // traceable author statement
/// 5515 /
205428_s_at•"gb:NM_001740.2 /DB_XREF=gi:6031158 /GEN=CALB2 /FEA=FLmRNA
/CNT=36 /TID=Hs.106857.0 /TIER=FL+Stack /STK=15 /UG=Hs.106857 /LL=794
/DEF=Homo sapiens calbindin 2, (29kD, calretinin) (CALB2), transcript variant
CALB2, mRNA. /PROD=calbindin 2, full length
prote"•0.250640444•0.245213116•"calbindin 2, 29kDa
(calretinin)"•CALB2•Hs.106857•ENSG00000172137•••5509 // calcium ion binding
// inferred from electronic annotation /// 5509 // calcium ion binding // not
recorded
226731_at•gb:AA156873 /DB_XREF=gi:1728488 /DB_XREF=zl20h08.s1
/CLONE=IMAGE:502527 /FEA=EST /CNT=65 /TID=Hs.184411.5 /TIER=Stack /STK=43
/UG=Hs.184411 /LL=213 /UG_GENE=ALB
/UG_TITLE=albumin•0.250567439•0.307572375•"Integrin, alpha
1"•PELO•Hs.519304•ENSG00000152684•6412 // protein biosynthesis // inferred
from electronic annotation•5634 // nucleus // inferred from electronic
annotation•
211799_x_at•"gb:U62824.1 /DB_XREF=gi:1575443 /GEN=HLA-Cw*1701 /FEA=FLmRNA
/CNT=5 /TID=Hs.287811.0 /TIER=FL /STK=0 /UG=Hs.287811 /DEF=Homo sapiens HLA
class I heavy chain (HLA-Cw*1701) mRNA, complete cds. /PROD=HLA class I heavy
chain /FL=gb:U62824.1"•0.249968844•0.338861617•"Major histocompatibility
complex, class I, C"•HLA-C•Hs.534125•ENSG00000198479•"19882 // antigen
presentation // inferred from electronic annotation /// 19883 // antigen
presentation, endogenous antigen // inferred from electronic annotation ///
19885 // antigen processing, endogenous antigen via MHC class I // inferred
from electron"•5887 // integral to plasma membrane // non-traceable author
statement /// 16020 // membrane // non-traceable author statement /// 16021
// integral to membrane // inferred from electronic annotation /// 42612 //
MHC class I protein complex // inferred fro•30106 // MHC class I receptor
activity // inferred from electronic annotation /// 30106 // MHC class I
receptor activity // non-traceable author statement /// 45012 // MHC class II
receptor activity // non-traceable author statement
201926_s_at•"gb:BC001288.1 /DB_XREF=gi:12654888 /FEA=FLmRNA /CNT=314
/TID=Hs.1369.0 /TIER=FL /STK=0 /UG=Hs.1369 /LL=1604 /UG_GENE=DAF /DEF=Homo
sapiens, Similar to decay accelerating factor for complement (CD55, Cromer
blood group system), clone MGC:5192, mRNA,
comple"•0.249576464•0.15250219•"decay accelerating factor for complement
(CD55, Cromer blood group system)"•DAF•Hs.527653•ENSG00000196352•"6955 //
immune response // inferred from electronic annotation /// 6958 // complement
activation, classical pathway // inferred from electronic annotation"•5625 //
soluble fraction // traceable author statement /// 5887 // integral to plasma
membrane // traceable author statement /// 16020 // membrane // inferred from
electronic annotation•
1554352_s_at•"gb:BC041706.1 /DB_XREF=gi:27469518 /TID=Hs2.145631.1 /CNT=3
/FEA=FLmRNA /TIER=FL /STK=2 /LL=10260 /UG_GENE=IRLB /UG=Hs.145631 /DEF=Homo
sapiens, Similar to KIAA0476 gene product, clone MGC:48955 IMAGE:5530033,
mRNA, complete cds. /PROD=Similar to KIAA0476"•0.249388797•0.304021065•c-myc
promoter binding protein•MYCPBP•Hs.513817•ENSG00000174485•"6355 // regulation
of transcription, DNA-dependent // non-traceable author statement"•5634 //
nucleus // non-traceable author statement•3677 // DNA binding //
non-traceable author statement
212158_at•"gb:AL577322 /DB_XREF=gi:12940338 /DB_XREF=AL577322
/CLONE=CS0DI085YI06 (3 prime) /FEA=mRNA /CNT=306 /TID=Hs.1501.0 /TIER=Stack
/STK=61 /UG=Hs.1501 /LL=6383 /UG_GENE=SDC2 /UG_TITLE=syndecan 2 (heparan
sulfate proteoglycan 1, cell surface-associated,
fibrog"•0.249284714•0.158688429•"syndecan 2 (heparan sulfate proteoglycan 1,
cell surface-associated, fibroglycan)"•SDC2•Hs.1501•ENSG00000169439••5887 //
integral to plasma membrane // non-traceable author statement /// 16020 //
membrane // inferred from electronic annotation•8092 // cytoskeletal protein
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binding // inferred from electronic annotation
1561757_a_at•"gb:BC035922.1 /DB_XREF=gi:23273119 /TID=Hs2.123542.1 /CNT=1
/FEA=mRNA /TIER=ConsEnd /STK=1 /UG=Hs.123542 /UG_TITLE=Homo sapiens, clone
IMAGE:4639114, mRNA /DEF=Homo sapiens, clone IMAGE:5398658,
mRNA."•0.2492339•0.345535048•hypothetical protein
LOC283352•LOC283352•Hs.507268••••
219978_s_at•"gb:NM_018454.1 /DB_XREF=gi:8922094 /GEN=BM037 /FEA=FLmRNA
/CNT=12 /TID=Hs.283649.0 /TIER=FL /STK=1 /UG=Hs.283649 /LL=55838 /DEF=Homo
sapiens uncharacterized bone marrow protein BM037 (BM037), mRNA.
/PROD=uncharacterized bone marrow protein BM037
/FL=gb:AF"•0.248857912•0.214940836•nucleolar and spindle associated protein
1•NUSAP1•Hs.511093•ENSG00000137804••5634 // nucleus // inferred from
electronic annotation•
203072_at•"gb:NM_004998.1 /DB_XREF=gi:4826843 /GEN=MYO1C /FEA=FLmRNA /CNT=121
/TID=Hs.82251.0 /TIER=FL /STK=2 /UG=Hs.82251 /LL=4641 /DEF=Homo sapiens
myosin IC (MYO1C), mRNA. /PROD=myosin IC /FL=gb:U14391.1
gb:NM_004998.1"•0.2481883•0.300960432•myosin
IE•MYO1E•Hs.370392•ENSG00000157483•30048 // actin filament-based movement //
traceable author statement•16459 // myosin // inferred from electronic
annotation•146 // microfilament motor activity // traceable author statement
/// 3779 // actin binding // inferred from electronic annotation /// 5516 //
calmodulin binding // inferred from electronic annotation /// 5524 // ATP
binding // inferred from electronic an
223524_s_at•"gb:BC000568.1 /DB_XREF=gi:12653584 /FEA=FLmRNA /CNT=57
/TID=Hs.280740.0 /TIER=FL /STK=0 /UG=Hs.280740 /LL=66000 /UG_GENE=MGC3040
/DEF=Homo sapiens, clone MGC:3040, mRNA, complete cds. /PROD=Unknown (protein
for MGC:3040) /FL=gb:BC000568.1"•0.247286627•0.129843044•hypothetical protein
MGC3040•MGC3040•Hs.191616•ENSG00000144868•••
216252_x_at•gb:Z70519.1 /DB_XREF=gi:1418817 /FEA=mRNA /CNT=3 /TID=Hs.82359.1
/TIER=ConsEnd /STK=0 /UG=Hs.82359 /LL=355 /UG_GENE=TNFRSF6 /DEF=H.sapiens
FASApo 1 mRNA for FAS soluble protein (clone FAS Exo4Del). /PROD=FAS soluble
protein•0.246726829•0.184439289•"Fas (TNF receptor superfamily, member
6)"•FAS•Hs.244139•ENSG00000026103•6461 // protein complex assembly //
traceable author statement /// 6915 // apoptosis // inferred from electronic
annotation /// 6916 // anti-apoptosis // traceable author statement /// 6917
// induction of apoptosis // traceable author statement /// 6955 •5625 //
soluble fraction // traceable author statement /// 5829 // cytosol //
non-traceable author statement /// 16020 // membrane // inferred from
electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•4888 // transmembrane receptor activity // inferred
from electronic annotation /// 5515 // protein binding // inferred from
electronic annotation
230362_at•gb:BE858808 /DB_XREF=gi:10374225 /DB_XREF=7f95h05.x1
/CLONE=IMAGE:3304761 /FEA=EST /CNT=15 /TID=Hs.52463.1 /TIER=Stack /STK=14
/UG=Hs.52463 /LL=22876 /UG_GENE=KIAA0966 /UG_TITLE=KIAA0966
protein•0.246346175•0.072948165•inositol polyphosphate-5-phosphatase
F•INPP5F•Hs.369755•ENSG00000198825•••
224963_at•"gb:AK025078.1 /DB_XREF=gi:10437520 /FEA=mRNA /CNT=144
/TID=Hs.302738.0 /TIER=Stack /STK=39 /UG=Hs.302738 /UG_TITLE=Homo sapiens
cDNA: FLJ21425 fis, clone COL04162 /DEF=Homo sapiens cDNA: FLJ21425 fis,
clone COL04162."•0.246098241•0.257535484•"solute carrier family 26 (sulfate
transporter), member 2"•SLC26A2•Hs.302738•ENSG00000155850•6810 // transport
// inferred from electronic annotation /// 8272 // sulfate transport //
traceable author statement•5624 // membrane fraction // traceable author
statement /// 5887 // integral to plasma membrane // traceable author
statement /// 16020 // membrane // inferred from electronic annotation•8271
// sulfate porter activity // inferred from electronic annotation
235275_at•gb:AA610122 /DB_XREF=gi:2458550 /DB_XREF=af19h06.s1
/CLONE=IMAGE:1032155 /FEA=EST /CNT=13 /TID=Hs.112819.0 /TIER=ConsEnd /STK=6
/UG=Hs.112819 /UG_TITLE=ESTs•0.244472238•0.183719027•Bone morphogenetic
protein 8b (osteogenic protein 2)•BMP8B•Hs.409964•ENSG00000116985•1501 //
skeletal development // traceable author statement /// 30154 // cell
differentiation // inferred from electronic annotation /// 40007 // growth //
inferred from electronic annotation•5576 // extracellular region // inferred
from electronic annotation•5125 // cytokine activity // inferred from
electronic annotation /// 8083 // growth factor activity // inferred from
electronic annotation
40560_at•"Cluster Incl. U28049:Human TBX2 (TXB2) mRNA, complete cds
/cds=(47,2155) /gb=U28049 /gi=924927 /ug=Hs.168357
/len=2279"•0.24444769•0.190152728•T-box
2•TBX2•Hs.531085•ENSG00000121068•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 7275 // development // inferred
from electronic annotation"•5634 // nucleus // inferred from electronic
annotation•3700 // transcription factor activity // inferred from electronic
annotation
209417_s_at•"gb:BC001356.1 /DB_XREF=gi:12655016 /FEA=FLmRNA /CNT=99
/TID=Hs.50842.0 /TIER=FL+Stack /STK=52 /UG=Hs.50842 /LL=3430 /UG_GENE=IFI35
/DEF=Homo sapiens, Similar to interferon-induced protein 35, clone MGC:2935,
mRNA, complete cds. /PROD=Similar to
interferon"•0.243990589•0.123884812•interferon-induced protein
```

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35•IFI35•Hs.50842•ENSG00000068079•6955 // immune response // non-traceable
author statement /// 9615 // response to virus // non-traceable author
statement•5634 // nucleus // inferred from direct assay•5515 // protein
binding // inferred from physical interaction
211026_s_at•"gb:BC006230.1 /DB_XREF=gi:13623260 /FEA=FLmRNA /CNT=1
/TID=HsAffx.900931.246 /TIER=FL /STK=0 /DEF=Homo sapiens,
lysophospholipase-like, clone MGC:10338, mRNA, complete cds.
/PROD=lysophospholipase-like
/FL=gb:BC006230.1"•0.243837876•0.435641148•monoglyceride lipase ///
monoglyceride lipase•MGLL•Hs.277035•ENSG00000074416•6629 // lipid metabolism
// traceable author statement /// 6725 // aromatic compound metabolism //
inferred from electronic annotation /// 6954 // inflammatory response //
traceable author statement••4622 // lysophospholipase activity // traceable
author statement /// 4759 // serine esterase activity // inferred from
electronic annotation /// 16787 // hydrolase activity // inferred from
electronic annotation /// 47372 // acylglycerol lipase activity /
64942_at•"Cluster Incl. AI937160:wp73h02.x1 Homo sapiens cDNA, 3  end
/clone=IMAGE-2467443 /clone_end=3  /gb=AI937160 /gi=5676030 /ug=Hs.7967
/len=552"•0.242757074•0.210976831•G protein-coupled receptor
153•GPR153•Hs.531581•ENSG00000158292•7186 // G-protein coupled receptor
protein signaling pathway // inferred from electronic annotation•16021 //
integral to membrane // inferred from electronic annotation•1584 //
rhodopsin-like receptor activity // inferred from electronic annotation ///
4872 // receptor activity // inferred from electronic annotation
211911_x_at•"gb:L07950.1 /DB_XREF=gi:307236 /GEN=HLA-B /FEA=FLmRNA /CNT=1
/TID=HsAffx.900418.1142 /TIER=FL /STK=0 /DEF=Homo sapiens MHC class I HLA B71
mRNA, complete cds. /PROD=MHC HLA B71
/FL=gb:L07950.1"•0.242419029•0.237105221•"major histocompatibility complex,
class I, B /// major histocompatibility complex, class I,
B"•HLA-B•Hs.77961•ENSG00000198638•"19883 // antigen presentation, endogenous
antigen // inferred from electronic annotation /// 19885 // antigen
processing, endogenous antigen via MHC class I // inferred from electronic
annotation"•5887 // integral to plasma membrane // non-traceable author
statement /// 16021 // integral to membrane // inferred from electronic
annotation /// 42612 // MHC class I protein complex // inferred from
electronic annotation•30106 // MHC class I receptor activity // inferred from
electronic annotation /// 30106 // MHC class I receptor activity //
non-traceable author statement
210145_at•"gb:M68874.1 /DB_XREF=gi:190003 /GEN=cPLA2 /FEA=FLmRNA /CNT=23
/TID=Hs.211587.0 /TIER=FL+Stack /STK=10 /UG=Hs.211587 /LL=5321 /DEF=Homo
sapiens phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, complete cds.
/PROD=phosphatidylcholine 2-acylhydrolase
/FL=gb"•0.241909878•0.382865424•"phospholipase A2, group IVA (cytosolic,
calcium-dependent)"•PLA2G4A•Hs.497200•ENSG00000116711•6663 // platelet
activating factor biosynthesis // non-traceable author statement /// 6690 //
icosanoid metabolism // non-traceable author statement /// 9395 //
phospholipid catabolism // inferred from electronic annotation /// 16042 //
lipid catabolism /•5829 // cytosol // non-traceable author statement ///
16021 // integral to membrane // non-traceable author statement•4622 //
lysophospholipase activity // inferred from electronic annotation /// 4623 //
phospholipase A2 activity // non-traceable author statement /// 16787 //
hydrolase activity // inferred from electronic annotation
202489_s_at•"gb:BC005238.1 /DB_XREF=gi:13528881 /FEA=FLmRNA /CNT=217
/TID=Hs.301350.0 /TIER=FL+Stack /STK=76 /UG=Hs.301350 /LL=5349 /UG_GENE=FXYD3
/DEF=Homo sapiens, FXYD domain-containing ion transport regulator 3, clone
MGC:12265, mRNA, complete cds. /PROD=FXYD doma"•0.240405886•0.140433152•FXYD
domain containing ion transport regulator
3•FXYD3•Hs.301350•ENSG00000089356•6811 // ion transport // inferred from
electronic annotation /// 6821 // chloride transport // traceable author
statement•5887 // integral to plasma membrane // traceable author statement
/// 16020 // membrane // inferred from electronic annotation•5216 // ion
channel activity // inferred from electronic annotation /// 5254 // chloride
channel activity // traceable author statement
202718_at•"gb:NM_000597.1 /DB_XREF=gi:10835156 /GEN=IGFBP2 /FEA=FLmRNA
/CNT=257 /TID=Hs.162.0 /TIER=FL+Stack /STK=153 /UG=Hs.162 /LL=3485 /DEF=Homo
sapiens insulin-like growth factor binding protein 2 (36kD) (IGFBP2), mRNA.
/PROD=insulin-like growth factor binding
p"•0.23997716•0.144312147•"insulin-like growth factor binding protein 2,
36kDa"•IGFBP2•Hs.438102•ENSG00000115457•1558 // regulation of cell growth //
inferred from electronic annotation•5615 // extracellular space // not
recorded•5520 // insulin-like growth factor binding // inferred from
electronic annotation
222150_s_at•"gb:AK026747.1 /DB_XREF=gi:10439670 /FEA=mRNA /CNT=9
/TID=Hs.12969.1 /TIER=ConsEnd /STK=0 /UG=Hs.12969 /LL=54103 /UG_GENE=LOC54103
/UG_TITLE=hypothetical protein /DEF=Homo sapiens cDNA: FLJ23094 fis, clone
LNG07379, highly similar to HST000007 Homo
sapiens"•0.239901361•0.183441665•hypothetical protein
LOC54103•LOC54103•Hs.186649•ENSG00000135174•••
63825_at•"Cluster Incl. AI557319:PT2.1_16_F08.r Homo sapiens cDNA, 3  end
/clone_end=3  /gb=AI557319 /gi=4489682 /ug=Hs.21921
/len=876"•0.239812714•0.375049527•abhydrolase domain containing
```

```
2•ABHD2•Hs.122337•ENSG00000140526••16021 // integral to membrane //
non-traceable author statement•3824 // catalytic activity // inferred from
electronic annotation
226939_at•gb:AI202327 /DB_XREF=gi:3754933 /DB_XREF=qs66a07.x1
/CLONE=IMAGE:1943028 /FEA=EST /CNT=33 /TID=Hs.44833.0 /TIER=Stack /STK=12
/UG=Hs.44833 /UG_TITLE=ESTs•0.237638829•0.162475906•cytoplasmic
polyadenylation element binding protein
2•CPEB2•Hs.374216•ENSG00000137449•••166 // nucleotide binding // inferred
from electronic annotation /// 3676 // nucleic acid binding // inferred from
electronic annotation
235534_at•"gb:AI624156 /DB_XREF=gi:4649087 /DB_XREF=ts26f03.x1
/CLONE=IMAGE:2229725 /FEA=EST /CNT=10 /TID=Hs.153944.0 /TIER=ConsEnd /STK=1
/UG=Hs.153944 /UG_TITLE=ESTs, Weakly similar to ALUA_HUMAN !!!! ALU CLASS A
WARNING ENTRY !!! (H.sapiens)"•0.237428661•0.243041341•"Transcribed locus,
weakly similar to NP_872301.1 hypothetical protein FLJ25224 [Homo
sapiens]"••Hs.153944••••
208235_x_at•"gb:NM_021123.1 /DB_XREF=gi:11024640 /GEN=GAGE7 /FEA=FLmRNA
/CNT=2 /TID=Hs.278606.0 /TIER=FL /STK=0 /UG=Hs.278606 /LL=2579 /DEF=Homo
sapiens G antigen 7 (GAGE7), mRNA. /PROD=G antigen 7 /FL=gb:NM_021123.1
gb:AF058988.1"•0.236529938•0.305737003•G antigen 5 /// G antigen 7 /// G
antigen 7B•GAGE5 /// GAGE7 /// GAGE7B•Hs.278606•ENSG00000189064 ///
ENSG00000198716•••
232504_at•gb:AL389942.1 /DB_XREF=gi:9367848 /FEA=mRNA /CNT=6 /TID=Hs.157752.0
/TIER=ConsEnd /STK=3 /UG=Hs.157752 /UG_TITLE=Homo sapiens mRNA full length
insert cDNA clone EUROIMAGE 2005635 /DEF=Homo sapiens mRNA full length insert
cDNA clone EUROIMAGE 2005635.•0.235807027•0.197553642•hypothetical protein
LOC285628•LOC285628•Hs.406790••••
212154_at•"gb:AI380298 /DB_XREF=gi:4190151 /DB_XREF=tf99h06.x1
/CLONE=IMAGE:2107451 /FEA=mRNA /CNT=306 /TID=Hs.1501.0 /TIER=Stack /STK=12
/UG=Hs.1501 /LL=6383 /UG_GENE=SDC2 /UG_TITLE=syndecan 2 (heparan sulfate
proteoglycan 1, cell surface-associated,
fibroglycan)"•0.23434024•0.162969885•"syndecan 2 (heparan sulfate
proteoglycan 1, cell surface-associated,
fibroglycan)"•SDC2•Hs.1501•ENSG00000169439••5887 // integral to plasma
membrane // non-traceable author statement /// 16020 // membrane // inferred
from electronic annotation•8092 // cytoskeletal protein binding // inferred
from electronic annotation
210592_s_at•"gb:M55580.1 /DB_XREF=gi:338335 /GEN=spermidinespermine
N1-acetyltransferase /FEA=FLmRNA /CNT=8 /TID=Hs.28491.1 /TIER=FL /STK=0
/UG=Hs.28491 /LL=6303 /DEF=Human spermidinespermine N1-acetyltransferase
mRNA, complete cds. /PROD=spermidinespermine
N1-acetylt"•0.233929075•0.214789363•spermidine/spermine
N1-acetyltransferase•SAT•Hs.28491•ENSG00000130066•••4145 // diamine
N-acetyltransferase activity // traceable author statement /// 8415 //
acyltransferase activity // inferred from electronic annotation /// 16740 //
transferase activity // inferred from electronic annotation
213164_at•"gb:AI867198 /DB_XREF=gi:5540214 /DB_XREF=wa01c11.x1
/CLONE=IMAGE:2296820 /FEA=FLmRNA /CNT=70 /TID=Hs.324787.0 /TIER=Stack /STK=17
/UG=Hs.324787 /LL=6526 /UG_GENE=SLC5A3 /UG_TITLE=solute carrier family 5
(inositol transporters), member 3
/FL=gb:NM_006933.1"•0.233398586•0.271867791•"solute carrier family 5
(inositol transporters), member 3"•SLC5A3•Hs.534348••6811 // ion transport //
inferred from electronic annotation /// 6814 // sodium ion transport //
inferred from electronic annotation•5887 // integral to plasma membrane //
traceable author statement /// 16020 // membrane // inferred from electronic
annotation•5215 // transporter activity // inferred from electronic
annotation /// 5367 // myo-inositol:sodium symporter activity // traceable
author statement /// 15293 // symporter activity // inferred from electronic
annotation
228006_at•gb:BG403361 /DB_XREF=gi:13296809 /DB_XREF=602419035F1
/CLONE=IMAGE:4526192 /FEA=EST /CNT=24 /TID=Hs.98267.0 /TIER=Stack /STK=9
/UG=Hs.98267 /UG_TITLE=ESTs•0.232152538•0.285909512•Phosphatase and tensin
homolog (mutated in multiple advanced cancers
1)•PTEN•Hs.500466•ENSG00000171862•6470 // protein amino acid
dephosphorylation // inferred from electronic annotation /// 7049 // cell
cycle // inferred from electronic annotation /// 45786 // negative regulation
of cell cycle // inferred from electronic annotation••"4725 // protein
tyrosine phosphatase activity // inferred from electronic annotation /// 8138
// protein tyrosine/serine/threonine phosphatase activity // inferred from
electronic annotation /// 16314 // phosphatidylinositol-3,4,5-trisphosphate
3-phosphat"
225875_s_at•gb:T84558 /DB_XREF=gi:712910 /DB_XREF=yd53d09.r1
/CLONE=IMAGE:111953 /FEA=mRNA /CNT=68 /TID=Hs.13804.1 /TIER=Stack /STK=11
/UG=Hs.13804 /LL=57185 /UG_GENE=DJ462O23.2 /UG_TITLE=hypothetical protein
dJ462O23.2•0.228721902•0.197495354•hypothetical protein
dJ462O23.2•DJ462O23.2•Hs.523442•ENSG00000001461•••
208949_s_at•"gb:BC001120.1 /DB_XREF=gi:12654570 /FEA=FLmRNA /CNT=324
/TID=Hs.621.0 /TIER=FL+Stack /STK=37 /UG=Hs.621 /LL=3958 /UG_GENE=LGALS3
/DEF=Homo sapiens, lectin, galactoside-binding, soluble, 3 (galectin 3),
clone MGC:2058, mRNA, complete cds. /PROD=lectin,
gal"•0.228116479•0.20884008•"lectin, galactoside-binding, soluble, 3
```

```
(galectin 3) /// galectin-3 internal gene"•LGALS3 ///
GALIG•Hs.531081•ENSG00000131981••5576 // extracellular region // not recorded
/// 5634 // nucleus // inferred from electronic annotation /// 5886 // plasma
membrane // traceable author statement•5529 // sugar binding // traceable
author statement /// 19863 // IgE binding // inferred from electronic
annotation
229865_at•gb:AW058617 /DB_XREF=gi:5934256 /DB_XREF=wy59b06.x1
/CLONE=IMAGE:2552819 /FEA=EST /CNT=13 /TID=Hs.58217.0 /TIER=Stack /STK=11
/UG=Hs.58217 /UG_TITLE=ESTs•0.225935406•0.275568133•fibronectin type III
domain containing 3B•FNDC3B•Hs.159430•ENSG00000075420•••
212944_at•"gb:AK024896.1 /DB_XREF=gi:10437310 /FEA=mRNA /CNT=106
/TID=Hs.268016.0 /TIER=Stack /STK=54 /UG=Hs.268016 /UG_TITLE=Homo sapiens
cDNA: FLJ21243 fis, clone COL01164 /DEF=Homo sapiens cDNA: FLJ21243 fis,
clone COL01164."•0.224349691•0.273541852•Mitochondrial ribosomal protein
S6•MRPS6•Hs.302742•ENSG00000198743•6412 // protein biosynthesis //
non-traceable author statement•5739 // mitochondrion // inferred from
electronic annotation /// 15935 // small ribosomal subunit // non-traceable
author statement•3735 // structural constituent of ribosome // non-traceable
author statement
212730_at•"gb:AK026420.1 /DB_XREF=gi:10439281 /FEA=mRNA /CNT=111
/TID=Hs.10587.0 /TIER=Stack /STK=26 /UG=Hs.10587 /LL=23336 /UG_GENE=KIAA0353
/UG_TITLE=KIAA0353 protein /DEF=Homo sapiens cDNA: FLJ22767 fis, clone
KAIA1191."•0.223472847•0.155521574•desmuslin•DMN•Hs.207106•ENSG00000182253••58
82 // intermediate filament // non-traceable author statement•5515 // protein
binding // inferred from physical interaction /// 8307 // structural
constituent of muscle // non-traceable author statement
214297_at•gb:BE857703 /DB_XREF=gi:10371993 /DB_XREF=7g46a02.x1
/CLONE=IMAGE:3309482 /FEA=EST /CNT=11 /TID=Hs.9004.1 /TIER=Stack /STK=10
/UG=Hs.9004 /LL=1464 /UG_GENE=CSPG4 /UG_TITLE=chondroitin sulfate
proteoglycan 4 (melanoma-associated)•0.222993715•0.14912628•Chondroitin
sulfate proteoglycan 4
(melanoma-associated)•CSPG4•Hs.513044•ENSG00000173546•6928 // cell motility
// not recorded /// 7155 // cell adhesion // inferred from electronic
annotation•5887 // integral to plasma membrane // traceable author
statement•5198 // structural molecule activity // inferred from electronic
annotation
1555950_a_at•"gb:CA448665 /DB_XREF=gi:24813085
/DB_XREF=UI-H-EI0-ayo-p-15-0-UI.s1 /CLONE=UI-H-EI0-ayo-p-15-0-UI
/TID=Hs2.1369.3 /CNT=31 /FEA=mRNA /TIER=Stack /STK=9 /LL=1604 /UG_GENE=DAF
/UG=Hs.1369 /UG_TITLE=decay accelerating factor for complement (CD55, Cromer
blood"•0.22238023•0.20763166•"decay accelerating factor for complement (CD55,
Cromer blood group system)"•DAF•Hs.527653•ENSG00000196352•"6955 // immune
response // inferred from electronic annotation /// 6958 // complement
activation, classical pathway // inferred from electronic annotation"•5625 //
soluble fraction // traceable author statement /// 5887 // integral to plasma
membrane // traceable author statement /// 16020 // membrane // inferred from
electronic annotation•
203543_s_at•"gb:NM_001206.1 /DB_XREF=gi:4557374 /GEN=BTEB1 /FEA=FLmRNA
/CNT=168 /TID=Hs.150557.0 /TIER=FL /STK=0 /UG=Hs.150557 /LL=687 /DEF=Homo
sapiens basic transcription element binding protein 1 (BTEB1), mRNA.
/PROD=basic transcription element binding protein 1
/F"•0.222260429•0.164241615•Kruppel-like factor
9•KLF9•Hs.150557•ENSG00000119138•6350 // transcription // inferred from
electronic annotation /// 6357 // regulation of transcription from RNA
polymerase II promoter // traceable author statement•5634 // nucleus //
inferred from electronic annotation•3700 // transcription factor activity //
traceable author statement /// 8270 // zinc ion binding // inferred from
electronic annotation
221563_at•gb:N36770 /DB_XREF=gi:1157912 /DB_XREF=yy34c02.s1
/CLONE=IMAGE:273122 /FEA=FLmRNA /CNT=68 /TID=Hs.177534.0 /TIER=Stack /STK=12
/UG=Hs.177534 /LL=11221 /UG_GENE=DUSP10 /UG_TITLE=dual specificity
phosphatase 10 /FL=gb:AB026436.1 gb:NM_007207.2
gb:AF179212.1•0.222082631•0.187312882•dual specificity phosphatase
10•DUSP10•Hs.497822•ENSG00000143507•6470 // protein amino acid
dephosphorylation // inferred from electronic annotation /// 6470 // protein
amino acid dephosphorylation // traceable author statement /// 6950 //
response to stress // traceable author statement /// 7254 // JNK cascade //
trac•5634 // nucleus // traceable author statement /// 5737 // cytoplasm //
traceable author statement•16787 // hydrolase activity // inferred from
electronic annotation /// 17017 // MAP kinase phosphatase activity //
inferred from electronic annotation
203304_at•"gb:NM_012342.1 /DB_XREF=gi:6912533 /GEN=NMA /FEA=FLmRNA /CNT=150
/TID=Hs.78776.0 /TIER=FL+Stack /STK=41 /UG=Hs.78776 /LL=25805 /DEF=Homo
sapiens putative transmembrane protein (NMA), mRNA. /PROD=putative
transmembrane protein /FL=gb:NM_012342.1
gb:U23070."•0.221866345•0.149735718•BMP and activin membrane-bound
inhibitor•BAMBI•Hs.533336•ENSG00000095739••16021 // integral to membrane //
traceable author statement•
230204_at•gb:AU144114 /DB_XREF=gi:11005635 /DB_XREF=AU144114
/CLONE=HEMBA1000915 /FEA=EST /CNT=17 /TID=Hs.2799.1 /TIER=Stack /STK=8
/UG=Hs.2799 /LL=1404 /UG_GENE=CRTL1 /UG_TITLE=cartilage linking protein
```

```
1•0.220595103•0.166744438•Hyaluronan and proteoglycan link protein
1•HAPLN1•Hs.2799•ENSG00000145681•7155 // cell adhesion // inferred from
electronic annotation•5578 // extracellular matrix (sensu Metazoa) //
traceable author statement•5540 // hyaluronic acid binding // inferred from
electronic annotation
213107_at•gb:R59093 /DB_XREF=gi:829788 /DB_XREF=yh03e12.s1 /CLONE=IMAGE:41943
/FEA=FLmRNA /CNT=70 /TID=Hs.170204.0 /TIER=ConsEnd /STK=4 /UG=Hs.170204
/LL=23043 /UG_GENE=KIAA0551 /UG_TITLE=KIAA0551 protein
/FL=gb:AF172264.1•0.220275857•0.173028337•TRAF2 and NCK interacting
kinase•TNIK•Hs.34024•ENSG00000154310•6445 // regulation of translation //
inferred from direct assay /// 6468 // protein amino acid phosphorylation //
non-traceable author statement /// 6950 // response to stress // inferred
from direct assay /// 7243 // protein kinase cascade // inferred fr••4674 //
protein serine/threonine kinase activity // inferred from direct assay ///
4674 // protein serine/threonine kinase activity // non-traceable author
statement /// 5083 // small GTPase regulator activity // inferred from
electronic annotation /// 55
230090_at•gb:AW296078 /DB_XREF=gi:6702714 /DB_XREF=UI-H-BW0-aiu-h-11-0-UI.s1
/CLONE=IMAGE:2730860 /FEA=EST /CNT=14 /TID=Hs.29590.0 /TIER=Stack /STK=9
/UG=Hs.29590 /UG_TITLE=ESTs•0.215320298•0.186208596•"Homo sapiens, clone
IMAGE:4179986, mRNA, partial cds"••Hs.271721••••
204679_at•"gb:NM_002245.1 /DB_XREF=gi:4504846 /GEN=KCNK1 /FEA=FLmRNA /CNT=59
/TID=Hs.79351.0 /TIER=FL+Stack /STK=9 /UG=Hs.79351 /LL=3775 /DEF=Homo sapiens
potassium channel, subfamily K, member 1 (TWIK-1) (KCNK1), mRNA.
/PROD=potassium channel, subfamily K, member
1"•0.214530602•0.21539831•"potassium channel, subfamily K, member
1"•KCNK1•Hs.208544•ENSG00000135750•6811 // ion transport // inferred from
electronic annotation /// 6813 // potassium ion transport // traceable author
statement•5624 // membrane fraction // not recorded /// 8076 // voltage-gated
potassium channel complex // traceable author statement /// 16020 // membrane
// inferred from electronic annotation /// 16021 // integral to membrane //
inferred from electronic annotati•5242 // inward rectifier potassium channel
activity // traceable author statement /// 5244 // voltage-gated ion channel
activity // inferred from electronic annotation /// 5267 // potassium channel
activity // inferred from electronic annotation
205603_s_at•"gb:NM_007309.1 /DB_XREF=gi:6382070 /GEN=DIAPH2 /FEA=FLmRNA
/CNT=40 /TID=Hs.226483.1 /TIER=FL+Stack /STK=27 /UG=Hs.226483 /LL=1730
/DEF=Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript
variant 12C, mRNA. /PROD=diaphanous 2 isoform 12C
/"•0.212036263•0.256900237•diaphanous homolog 2
(Drosophila)•DIAPH2•Hs.226483•ENSG00000147202•910 // cytokinesis // traceable
author statement /// 7292 // female gamete generation // traceable author
statement /// 16043 // cell organization and biogenesis // inferred from
electronic annotation /// 30036 // actin cytoskeleton organization and
bioge•16020 // membrane // inferred from electronic annotation•3779 // actin
binding // inferred from electronic annotation /// 5102 // receptor binding
// traceable author statement /// 17048 // Rho GTPase binding // inferred
from electronic annotation
210233_at•"gb:AF167343.1 /DB_XREF=gi:8050486 /GEN=IL1RAP /FEA=FLmRNA /CNT=16
/TID=Hs.173880.1 /TIER=FL /STK=0 /UG=Hs.173880 /LL=3556 /DEF=Homo sapiens
soluble interleukin-1 receptor accessory protein (IL1RAP) mRNA, complete cds.
/PROD=soluble interleukin-1 receptor "•0.211395454•0.238383796•interleukin 1
receptor accessory protein•IL1RAP•Hs.478673•ENSG00000196083•6461 // protein
complex assembly // traceable author statement /// 6954 // inflammatory
response // traceable author statement•5887 // integral to plasma membrane //
traceable author statement /// 16020 // membrane // inferred from electronic
annotation•4888 // transmembrane receptor activity // inferred from
electronic annotation /// 4908 // interleukin-1 receptor activity // inferred
from electronic annotation
205968_at•"gb:NM_002252.1 /DB_XREF=gi:4504862 /GEN=KCNS3 /FEA=FLmRNA /CNT=38
/TID=Hs.47584.0 /TIER=FL+Stack /STK=11 /UG=Hs.47584 /LL=3790 /DEF=Homo
sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S,
member 3 (KCNS3), mRNA. /PROD=potassium
volta"•0.211030769•0.123167263•"potassium voltage-gated channel,
delayed-rectifier, subfamily S, member
3"•KCNS3•Hs.414489•ENSG00000170745•6812 // cation transport // inferred from
electronic annotation /// 6813 // potassium ion transport // traceable author
statement•5624 // membrane fraction // not recorded /// 8076 // voltage-gated
potassium channel complex // inferred from electronic annotation /// 16020 //
membrane // inferred from electronic annotation•5251 // delayed rectifier
potassium channel activity // traceable author statement /// 5515 // protein
binding // inferred from electronic annotation /// 15459 // potassium channel
regulator activity // traceable author statement
202284_s_at•"gb:NM_000389.1 /DB_XREF=gi:11386202 /GEN=CDKN1A /FEA=FLmRNA
/CNT=215 /TID=Hs.179665.0 /TIER=FL+Stack /STK=131 /UG=Hs.179665 /LL=1026
/DEF=Homo sapiens cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A),
mRNA. /PROD=cyclin-dependent kinase
inhibitor"•0.208915608•0.37047057•"cyclin-dependent kinase inhibitor 1A (p21,
Cip1)"•CDKN1A•Hs.370771•ENSG00000124762•79 // regulation of cyclin dependent
protein kinase activity // traceable author statement /// 7050 // cell cycle
arrest // inferred from electronic annotation /// 7050 // cell cycle arrest
```

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// traceable author statement /// 8285 // negative regulation of •5634 //
nucleus // inferred from electronic annotation /// 5634 // nucleus //
traceable author statement•4672 // protein kinase activity // not recorded
/// 4861 // cyclin-dependent protein kinase inhibitor activity // inferred
from electronic annotation /// 4861 // cyclin-dependent protein kinase
inhibitor activity // traceable author statement /// 16301 //
230251_at•gb:AA041523 /DB_XREF=gi:1517776 /DB_XREF=zk44d03.s1
/CLONE=IMAGE:485669 /FEA=EST /CNT=16 /TID=Hs.31917.0 /TIER=Stack /STK=8
/UG=Hs.31917 /UG_TITLE=ESTs•0.206369719•0.052321588•Chromosome 6 open reading
frame 176•C6orf176•Hs.31917••••
227410_at•gb:AW264102 /DB_XREF=gi:6640918 /DB_XREF=xq83g09.x1
/CLONE=IMAGE:2757280 /FEA=EST /CNT=31 /TID=Hs.39168.0 /TIER=Stack /STK=11
/UG=Hs.39168 /UG_TITLE=ESTs•0.204776315•0.283266368•"family with sequence
similarity 43, member A"•FAM43A•Hs.435080••••
223618_at•"gb:AF225426.1 /DB_XREF=gi:9963854 /FEA=FLmRNA /CNT=28
/TID=Hs.24889.0 /TIER=FL+Stack /STK=17 /UG=Hs.24889 /LL=56776 /UG_GENE=FMN2
/DEF=Homo sapiens HT016 mRNA, complete cds. /PROD=HT016
/FL=gb:AF225426.1"•0.204002973•0.271179281•formin 2•FMN2•Hs.24889••7242 //
intracellular signaling cascade // inferred from electronic annotation ///
7275 // development // inferred from electronic annotation /// 7275 //
development // non-traceable author statement /// 16043 // cell organization
and biogenesis // inferr•5634 // nucleus // inferred from electronic
annotation•3779 // actin binding // inferred from electronic annotation
203562_at•"gb:NM_005103.2 /DB_XREF=gi:12025681 /GEN=FEZ1 /FEA=FLmRNA /CNT=101
/TID=Hs.79226.1 /TIER=FL+Stack /STK=49 /UG=Hs.79226 /LL=9638 /DEF=Homo
sapiens fasciculation and elongation protein zeta 1 (zygin I) (FEZ1),
transcript variant 1, mRNA. /PROD=zygin 1,
isof"•0.203986334•0.221956099•fasciculation and elongation protein zeta 1
(zygin I)•FEZ1•Hs.224008•ENSG00000149557•7155 // cell adhesion // traceable
author statement /// 7399 // neurogenesis // traceable author statement ///
7411 // axon guidance // traceable author statement••
212573_at•gb:AF131747.1 /DB_XREF=gi:4406562 /FEA=mRNA /CNT=133
/TID=Hs.167115.0 /TIER=Stack /STK=59 /UG=Hs.167115 /LL=23052
/UG_GENE=KIAA0830 /UG_TITLE=KIAA0830 protein /DEF=Homo sapiens clone 24951
mRNA sequence.•0.202250552•0.088891883•KIAA0830
protein•KIAA0830•Hs.167115•ENSG00000149218•••3676 // nucleic acid binding //
inferred from electronic annotation /// 4519 // endonuclease activity //
inferred from electronic annotation /// 16787 // hydrolase activity //
inferred from electronic annotation
242093_at•gb:AW263497 /DB_XREF=gi:6640313 /DB_XREF=xn80a06.x1
/CLONE=IMAGE:2700754 /FEA=EST /CNT=6 /TID=Hs.97774.0 /TIER=ConsEnd /STK=3
/UG=Hs.97774 /UG_TITLE=ESTs•0.20152607•0.221353997••••••
207336_at•"gb:NM_006940.1 /DB_XREF=gi:5902113 /GEN=SOX5 /FEA=FLmRNA /CNT=6
/TID=Hs.87224.0 /TIER=FL /STK=3 /UG=Hs.87224 /LL=6660 /DEF=Homo sapiens SRY
(sex determining region Y)-box 5 (SOX5), mRNA. /PROD=SRY (sex determining
region Y)-box 5 /FL=gb:NM_006940.1"•0.201156907•0.079515232•SRY (sex
determining region Y)-box 5•SOX5•Hs.505007•ENSG00000134532•"6350 //
transcription // inferred from electronic annotation /// 6355 // regulation
of transcription, DNA-dependent // inferred from electronic annotation ///
6366 // transcription from RNA polymerase II promoter // traceable author
statement"•5634 // nucleus // inferred from electronic annotation•3700 //
transcription factor activity // traceable author statement
39248_at•"Cluster Incl. N74607:za55a01.s1 Homo sapiens cDNA, 3  end
/clone=IMAGE-296424 /clone_end=3  /gb=N74607 /gi=1231892 /ug=Hs.234642
/len=487"•0.200713145•0.141677221•aquaporin
3•AQP3•Hs.234642•ENSG00000165272•6810 // transport // non-traceable author
statement /// 7588 // excretion // traceable author statement•5624 //
membrane fraction // not recorded /// 5887 // integral to plasma membrane //
not recorded /// 16020 // membrane // inferred from electronic
annotation•5215 // transporter activity // non-traceable author statement
229649_at•gb:AI129949 /DB_XREF=gi:3598463 /DB_XREF=qc45g07.x1
/CLONE=IMAGE:1712604 /FEA=EST /CNT=27 /TID=Hs.22269.1 /TIER=Stack /STK=9
/UG=Hs.22269 /LL=9369 /UG_GENE=NRXN3 /UG_TITLE=neurexin
3•0.200644278•0.236405695•neurexin 3•NRXN3•Hs.368307•ENSG00000021645•7155 //
cell adhesion // inferred from electronic annotation /// 7411 // axon
guidance // traceable author statement•5887 // integral to plasma membrane //
traceable author statement /// 16021 // integral to membrane // inferred from
electronic annotation•4872 // receptor activity // traceable author statement
/// 5198 // structural molecule activity // inferred from electronic
annotation /// 5515 // protein binding // inferred from electronic
annotation
200907_s_at•gb:AU157932 /DB_XREF=gi:11019453 /DB_XREF=AU157932
/CLONE=PLACE1010217 /FEA=FLmRNA /CNT=425 /TID=Hs.194431.0 /TIER=Stack /STK=12
/UG=Hs.194431 /LL=23022 /UG_GENE=KIAA0992 /UG_TITLE=palladin
/FL=gb:AF151909.1 gb:AF077041.1
gb:NM_016081.1•0.200102893•0.174446508•palladin•KIAA0992•Hs.151220•ENSG0000012
9116•6468 // protein amino acid phosphorylation // inferred from electronic
annotation••5021 // vascular endothelial growth factor receptor activity //
inferred from electronic annotation /// 5524 // ATP binding // inferred from
electronic annotation
201694_s_at•"gb:NM_001964.1 /DB_XREF=gi:4503492 /GEN=EGR1 /FEA=FLmRNA
```

```
/CNT=235 /TID=Hs.326035.0 /TIER=FL+Stack /STK=42 /UG=Hs.326035 /LL=1958
/DEF=Homo sapiens early growth response 1 (EGR1), mRNA. /PROD=early growth
response 1 /FL=gb:M62829.1 gb:NM_001964.1"•0.199904901•0.149387589•early
growth response 1•EGR1•Hs.326035•ENSG00000120738•"6350 // transcription //
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation"•5634 // nucleus //
inferred from electronic annotation•3700 // transcription factor activity //
traceable author statement /// 8270 // zinc ion binding // inferred from
electronic annotation
203144_s_at•"gb:NM_014656.1 /DB_XREF=gi:7657258 /GEN=KIAA0040 /FEA=FLmRNA
/CNT=111 /TID=Hs.158282.0 /TIER=FL+Stack /STK=8 /UG=Hs.158282 /LL=9674
/DEF=Homo sapiens KIAA0040 gene product (KIAA0040), mRNA. /PROD=KIAA0040 gene
product /FL=gb:D25539.1
gb:NM_014656.1"•0.198851606•0.202438626•KIAA0040•KIAA0040•Hs.518138•ENSG000001
62666•••
209140_x_at•"gb:L42024.1 /DB_XREF=gi:804748 /GEN=HLA-B39 /FEA=FLmRNA /CNT=515
/TID=Hs.77961.0 /TIER=FL /STK=0 /UG=Hs.77961 /LL=3106 /DEF=Homo sapiens MHC
HLA-B39 mRNA, complete cds. /PROD=major histocompatibility complex
/FL=gb:L24373.1 gb:AF189017.1 gb:D85761.1 gb:D8"•0.198673767•0.1858554•"major
histocompatibility complex, class I, B"•HLA-B•Hs.77961•ENSG00000198638•"19883
// antigen presentation, endogenous antigen // inferred from electronic
annotation /// 19885 // antigen processing, endogenous antigen via MHC class
I // inferred from electronic annotation"•5887 // integral to plasma membrane
// non-traceable author statement /// 16021 // integral to membrane //
inferred from electronic annotation /// 42612 // MHC class I protein complex
// inferred from electronic annotation•30106 // MHC class I receptor activity
// inferred from electronic annotation /// 30106 // MHC class I receptor
activity // non-traceable author statement
236489_at•gb:AI282097 /DB_XREF=gi:3920330 /DB_XREF=qn31g05.x1
/CLONE=IMAGE:1899896 /FEA=EST /CNT=6 /TID=Hs.72307.0 /TIER=ConsEnd /STK=6
/UG=Hs.72307 /UG_TITLE=ESTs•0.197353179•0.218441159•Transcribed
locus••Hs.72307••••
209426_s_at•"gb:AF047020.1 /DB_XREF=gi:4204096 /FEA=FLmRNA /CNT=163
/TID=Hs.128749.0 /TIER=FL+Stack /STK=24 /UG=Hs.128749 /LL=23600
/UG_GENE=AMACR /DEF=Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete
cds. /PROD=alpha-methylacyl-CoA racemase
/FL=gb:NM_014324."•0.196933806•0.083040601•alpha-methylacyl-CoA
racemase•AMACR•Hs.508343•ENSG00000082196•8152 // metabolism // inferred from
electronic annotation•5739 // mitochondrion // traceable author statement ///
5777 // peroxisome // traceable author statement•3824 // catalytic activity
// inferred from electronic annotation /// 8111 // alpha-methylacyl-CoA
racemase activity // inferred from electronic annotation /// 16853 //
isomerase activity // inferred from electronic annotation
209099_x_at•"gb:U73936.1 /DB_XREF=gi:1695273 /GEN=HJ1 /FEA=FLmRNA /CNT=199
/TID=Hs.91143.0 /TIER=FL+Stack /STK=38 /UG=Hs.91143 /LL=182 /DEF=Homo sapiens
Jagged 1 (HJ1) mRNA, complete cds. /PROD=Jagged 1 /FL=gb:AF003837.1
gb:U61276.1 gb:NM_000214.1 gb:U73936.1
gb:AF028"•0.196365367•0.167077966•jagged 1 (Alagille
syndrome)•JAG1•Hs.224012•ENSG00000101384•1525 // angiogenesis //
non-traceable author statement /// 1709 // cell fate determination //
non-traceable author statement /// 7154 // cell communication // inferred
from electronic annotation /// 7219 // Notch signaling pathway //
non-traceable author •5576 // extracellular region // non-traceable author
statement /// 5887 // integral to plasma membrane // non-traceable author
statement /// 16020 // membrane // traceable author statement•5112 // Notch
binding // non-traceable author statement /// 5198 // structural molecule
activity // non-traceable author statement /// 5509 // calcium ion binding //
inferred from electronic annotation /// 5509 // calcium ion binding //
non-traceable auth
235238_at•"gb:BF676462 /DB_XREF=gi:11950357 /DB_XREF=602086260F1
/CLONE=IMAGE:4250534 /FEA=EST /CNT=17 /TID=Hs.219907.0 /TIER=ConsEnd /STK=2
/UG=Hs.219907 /UG_TITLE=ESTs, Moderately similar to Transforming Protein
(H.sapiens)"•0.195821749•0.483434045•rai-like
protein•RaLP•Hs.552630•ENSG00000185634•7242 // intracellular signaling
cascade // inferred from electronic annotation••
219229_at•"gb:NM_013272.2 /DB_XREF=gi:7706713 /GEN=SLC21A11 /FEA=FLmRNA
/CNT=46 /TID=Hs.14805.0 /TIER=FL+Stack /STK=16 /UG=Hs.14805 /LL=28232
/DEF=Homo sapiens solute carrier family 21 (organic anion transporter),
member 11 (SLC21A11), mRNA. /PROD=solute carrier
fam"•0.195761347•0.140814779•"solute carrier organic anion transporter
family, member 3A1"•SLCO3A1•Hs.311187•ENSG00000176463•6811 // ion transport
// inferred from electronic annotation•16020 // membrane // inferred from
electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•5215 // transporter activity // inferred from
electronic annotation
201170_s_at•"gb:NM_003670.1 /DB_XREF=gi:4503298 /GEN=BHLHB2 /FEA=FLmRNA
/CNT=243 /TID=Hs.171825.0 /TIER=FL+Stack /STK=55 /UG=Hs.171825 /LL=8553
/DEF=Homo sapiens basic helix-loop-helix domain containing, class B, 2
(BHLHB2), mRNA. /PROD=differentiated embryo
chondrocy"•0.193337306•0.287603531•"basic helix-loop-helix domain containing,
class B, 2"•BHLHB2•Hs.171825•ENSG00000134107•"6350 // transcription //
```

```
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // non-traceable author statement"•5634 // nucleus //
non-traceable author statement•3700 // transcription factor activity //
non-traceable author statement
204736_s_at•"gb:NM_001897.1 /DB_XREF=gi:4503098 /GEN=CSPG4 /FEA=FLmRNA
/CNT=51 /TID=Hs.9004.0 /TIER=FL /STK=1 /UG=Hs.9004 /LL=1464 /DEF=Homo sapiens
chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA.
/PROD=melanoma-associated chondroitin
sulfatepr"•0.19312958•0.244159942•chondroitin sulfate proteoglycan 4
(melanoma-associated)•CSPG4•Hs.513044•ENSG00000173546•6928 // cell motility
// not recorded /// 7155 // cell adhesion // inferred from electronic
annotation•5887 // integral to plasma membrane // traceable author
statement•5198 // structural molecule activity // inferred from electronic
annotation
227140_at•"gb:AI343467 /DB_XREF=gi:4080673 /DB_XREF=tb97a02.x1
/CLONE=IMAGE:2062250 /FEA=mRNA /CNT=47 /TID=Hs.28792.0 /TIER=Stack /STK=17
/UG=Hs.28792 /UG_TITLE=Homo sapiens cDNA FLJ11041 fis, clone
PLACE1004405"•0.192529138•0.283206274•"Inhibin, beta A (activin A, activin AB
alpha polypeptide)"•INHBA•Hs.28792•ENSG00000122641•1501 // skeletal
development // traceable author statement /// 1541 // ovarian follicle
development // non-traceable author statement /// 6917 // induction of
apoptosis // inferred from direct assay /// 6952 // defense response //
traceable author stateme•5576 // extracellular region // traceable author
statement•5125 // cytokine activity // traceable author statement /// 5160 //
transforming growth factor beta receptor binding // not recorded /// 5179 //
hormone activity // traceable author statement /// 5515 // protein binding //
inferred from physical interacti
203476_at•"gb:NM_006670.1 /DB_XREF=gi:5729717 /GEN=5T4 /FEA=FLmRNA /CNT=119
/TID=Hs.82128.0 /TIER=FL /STK=5 /UG=Hs.82128 /LL=10860 /DEF=Homo sapiens 5T4
oncofetal trophoblast glycoprotein (5T4), mRNA. /PROD=5T4 oncofetal
trophoblast glycoprotein
/FL=gb:NM_006670.1"•0.192481902•0.384555701•trophoblast
glycoprotein•TPBG•Hs.82128•ENSG00000146242•6928 // cell motility // not
recorded /// 7155 // cell adhesion // non-traceable author statement•5578 //
extracellular matrix (sensu Metazoa) // inferred from electronic annotation
/// 5887 // integral to plasma membrane // traceable author statement•
219806_s_at•"gb:NM_020179.1 /DB_XREF=gi:9910225 /GEN=FN5 /FEA=FLmRNA /CNT=16
/TID=Hs.259737.0 /TIER=FL /STK=0 /UG=Hs.259737 /LL=56935 /DEF=Homo sapiens
FN5 protein (FN5), mRNA. /PROD=FN5 protein /FL=gb:NM_020179.1
gb:AF197137.1"•0.192178648•0.254224076•FN5
protein•FN5•Hs.438064•ENSG00000166002•••
241355_at•gb:BF528433 /DB_XREF=gi:11615796 /DB_XREF=602043786F1
/CLONE=IMAGE:4181517 /FEA=EST /CNT=7 /TID=Hs.165565.0 /TIER=ConsEnd /STK=0
/UG=Hs.165565 /UG_TITLE=ESTs•0.191982014•0.126237877•hairless homolog
(mouse)•HR•Hs.272367•ENSG00000168453•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// non-traceable author statement"•5634 // nucleus // non-traceable author
statement•3700 // transcription factor activity // non-traceable author
statement
212135_s_at•"gb:AW517686 /DB_XREF=gi:7155768 /DB_XREF=xs86d05.x1
/CLONE=IMAGE:2776521 /FEA=EST /CNT=223 /TID=Hs.305923.2 /TIER=Stack /STK=12
/UG=Hs.305923 /LL=493 /UG_GENE=ATP2B4 /UG_TITLE=ATPase, Ca++ transporting,
plasma membrane 4"•0.19057487•0.146824421•"ATPase, Ca++ transporting, plasma
membrane 4"•ATP2B4•Hs.343522•ENSG00000058668•6812 // cation transport //
inferred from electronic annotation /// 6816 // calcium ion transport //
inferred from electronic annotation /// 8152 // metabolism // inferred from
electronic annotation•5886 // plasma membrane // traceable author statement
/// 5887 // integral to plasma membrane // traceable author statement•287 //
magnesium ion binding // inferred from electronic annotation /// 5388 //
calcium-transporting ATPase activity // traceable author statement /// 5509
// calcium ion binding // inferred from electronic annotation /// 5516 //
calmodulin binding // inf
209277_at•gb:AL574096 /DB_XREF=gi:12933969 /DB_XREF=AL574096
/CLONE=CS0DI040YI17 (3 prime) /FEA=FLmRNA /CNT=478 /TID=Hs.295944.0
/TIER=Stack /STK=16 /UG=Hs.295944 /LL=7980 /UG_GENE=TFPI2 /UG_TITLE=tissue
factor pathway inhibitor 2 /FL=gb:D29992.1 gb:L27624.1
gb:NM_•0.189184296•0.141693333•Tissue factor pathway inhibitor
2•TFPI2•Hs.438231•ENSG00000105825•7596 // blood coagulation // inferred from
electronic annotation•5578 // extracellular matrix (sensu Metazoa) //
traceable author statement•4867 // serine-type endopeptidase inhibitor
activity // not recorded /// 5201 // extracellular matrix structural
constituent // traceable author statement
215719_x_at•"gb:X83493.1 /DB_XREF=gi:971457 /FEA=mRNA /CNT=4 /TID=Hs.82359.2
/TIER=ConsEnd /STK=0 /UG=Hs.82359 /LL=355 /UG_GENE=TNFRSF6 /UG_TITLE=tumor
necrosis factor receptor superfamily, member 6 /DEF=H.sapiens mRNA for
FasApo-1 (clone pCRTM11-FasdeltaTM)."•0.186964957•0.189284893•"Fas (TNF
receptor superfamily, member 6)"•FAS•Hs.244139•ENSG00000026103•6461 //
protein complex assembly // traceable author statement /// 6915 // apoptosis
// inferred from electronic annotation /// 6916 // anti-apoptosis //
traceable author statement /// 6917 // induction of apoptosis // traceable
author statement /// 6955 •5625 // soluble fraction // traceable author
```

```
statement /// 5829 // cytosol // non-traceable author statement /// 16020 //
membrane // inferred from electronic annotation /// 16021 // integral to
membrane // inferred from electronic annotation•4888 // transmembrane
receptor activity // inferred from electronic annotation /// 5515 // protein
binding // inferred from electronic annotation
1560448_at•"gb:BC041422.1 /DB_XREF=gi:27371084 /TID=Hs2.434427.1 /CNT=3
/FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.434427 /UG_TITLE=Homo sapiens, clone
IMAGE:3878345, mRNA /DEF=Homo sapiens, clone IMAGE:3878345,
mRNA."•0.185715214•0.193108595•hypothetical protein LOC340037•LOC340037•••••
241456_at•gb:AI147384 /DB_XREF=gi:3675066 /DB_XREF=qg64d06.s1
/CLONE=IMAGE:1839947 /FEA=EST /CNT=5 /TID=Hs.133029.0 /TIER=ConsEnd /STK=4
/UG=Hs.133029 /UG_TITLE=ESTs•0.182855241•0.200712044•"CDNA FLJ30785 fis,
clone FEBRA2000901"••Hs.133029••••
209278_s_at•"gb:L27624.1 /DB_XREF=gi:441149 /FEA=FLmRNA /CNT=478
/TID=Hs.295944.0 /TIER=FL+Stack /STK=17 /UG=Hs.295944 /LL=7980 /UG_GENE=TFPI2
/DEF=Homo sapiens tissue factor pathway inhibitor-2 mRNA, complete cds.
/PROD=tissue factor pathway inhibitor-2
/FL=gb:D29992"•0.181924103•0.177328684•tissue factor pathway inhibitor
2•TFPI2•Hs.438231•ENSG00000105825•7596 // blood coagulation // inferred from
electronic annotation•5578 // extracellular matrix (sensu Metazoa) //
traceable author statement•4867 // serine-type endopeptidase inhibitor
activity // not recorded /// 5201 // extracellular matrix structural
constituent // traceable author statement
225436_at•gb:AI339710 /DB_XREF=gi:4076637 /DB_XREF=qk68d02.x1
/CLONE=IMAGE:1874115 /FEA=mRNA /CNT=111 /TID=Hs.26765.0 /TIER=Stack /STK=8
/UG=Hs.26765 /LL=58489 /UG_GENE=LOC58489 /UG_TITLE=hypothetical protein from
EUROIMAGE 588495•0.179320865•0.191219193•hypothetical protein from EUROIMAGE
588495•LOC58489•Hs.459072•ENSG00000136379•••3824 // catalytic activity //
inferred from electronic annotation
218980_at•"gb:NM_025135.1 /DB_XREF=gi:13399325 /GEN=KIAA1695 /FEA=FLmRNA
/CNT=64 /TID=Hs.288841.0 /TIER=FL+Stack /STK=31 /UG=Hs.288841 /LL=80206
/DEF=Homo sapiens hypothetical protein FLJ22297 (KIAA1695), mRNA.
/PROD=hypothetical protein KIAA1695
/FL=gb:NM_025135.1"•0.178325954•0.176536193•formin homology 2 domain
containing 3•FHOD3•Hs.436636••16043 // cell organization and biogenesis //
inferred from electronic annotation••3779 // actin binding // inferred from
electronic annotation
226497_s_at•"gb:AA149648 /DB_XREF=gi:1720449 /DB_XREF=zl39e08.s1
/CLONE=IMAGE:504326 /FEA=mRNA /CNT=78 /TID=Hs.22968.0 /TIER=Stack /STK=25
/UG=Hs.22968 /UG_TITLE=Homo sapiens clone IMAGE:451939, mRNA
sequence"•0.177557363•0.168380946•Fms-related tyrosine kinase 1 (vascular
endothelial growth factor/vascular permeability factor
receptor)•FLT1•Hs.507621•ENSG00000102755•1525 // angiogenesis // inferred
from electronic annotation /// 6468 // protein amino acid phosphorylation //
inferred from electronic annotation /// 7169 // transmembrane receptor
protein tyrosine kinase signaling pathway // traceable author statement
//•5615 // extracellular space // traceable author statement /// 5887 //
integral to plasma membrane // traceable author statement /// 16020 //
membrane // inferred from electronic annotation•4872 // receptor activity //
traceable author statement /// 5021 // vascular endothelial growth factor
receptor activity // traceable author statement /// 5524 // ATP binding //
inferred from electronic annotation /// 16740 // transferase activity //
infe
210511_s_at•"gb:M13436.1 /DB_XREF=gi:186414 /GEN=INHBA /FEA=FLmRNA /CNT=5
/TID=Hs.727.1 /TIER=FL /STK=0 /UG=Hs.727 /LL=3624 /UG_TITLE=inhibin, beta A
(activin A, activin AB alpha polypeptide) /DEF=Human ovarian beta-A inhibin
mRNA, complete cds. /FL=gb:M13436.1"•0.176481031•0.242267706•"inhibin, beta A
(activin A, activin AB alpha
polypeptide)"•INHBA•Hs.28792•ENSG00000122641•1501 // skeletal development //
traceable author statement /// 1541 // ovarian follicle development //
non-traceable author statement /// 6917 // induction of apoptosis // inferred
from direct assay /// 6952 // defense response // traceable author
stateme•5576 // extracellular region // traceable author statement•5125 //
cytokine activity // traceable author statement /// 5160 // transforming
growth factor beta receptor binding // not recorded /// 5179 // hormone
activity // traceable author statement /// 5515 // protein binding //
inferred from physical interacti
202202_s_at•"gb:NM_002290.2 /DB_XREF=gi:9845494 /GEN=LAMA4 /FEA=FLmRNA
/CNT=195 /TID=Hs.78672.0 /TIER=FL /STK=3 /UG=Hs.78672 /LL=3910 /DEF=Homo
sapiens laminin, alpha 4 (LAMA4), mRNA. /PROD=laminin, alpha 4 precursor
/FL=gb:NM_002290.2"•0.176115214•0.197296847•"laminin, alpha
4"•LAMA4•Hs.213861•ENSG00000112769•30155 // regulation of cell adhesion //
inferred from electronic annotation /// 30334 // regulation of cell migration
// inferred from electronic annotation /// 45995 // regulation of embryonic
development // inferred from electronic annotation•5605 // basal lamina //
traceable author statement /// 5606 // laminin-1 // inferred from electronic
annotation•5102 // receptor binding // inferred from electronic annotation
/// 5201 // extracellular matrix structural constituent // traceable author
statement /// 5515 // protein binding // inferred from electronic annotation
209351_at•"gb:BC002690.1 /DB_XREF=gi:12803708 /FEA=FLmRNA /CNT=212
/TID=Hs.117729.0 /TIER=FL+Stack /STK=53 /UG=Hs.117729 /LL=3861 /UG_GENE=KRT14
```

```
/DEF=Homo sapiens, keratin 14 (epidermolysis bullosa simplex, Dowling-Meara,
Koebner), clone MGC:3944, mRNA, complete
cds"•0.174257423•0.159066152•"keratin 14 (epidermolysis bullosa simplex,
Dowling-Meara, Koebner)"•KRT14•Hs.355214•ENSG00000186847•8544 // epidermis
development // traceable author statement•5882 // intermediate filament //
not recorded•5200 // structural constituent of cytoskeleton // traceable
author statement
222496_s_at•gb:AW241742 /DB_XREF=gi:6575496 /DB_XREF=xn74e04.x1
/CLONE=IMAGE:2700222 /FEA=FLmRNA /CNT=177 /TID=Hs.95549.0 /TIER=Stack /STK=13
/UG=Hs.95549 /LL=54502 /UG_GENE=FLJ20273 /UG_TITLE=hypothetical protein
/FL=gb:NM_019027.1•0.172735708•0.402146781•RNA-binding
protein•FLJ20273•Hs.518727•ENSG00000163694•••166 // nucleotide binding //
inferred from electronic annotation /// 3676 // nucleic acid binding //
inferred from electronic annotation
1569470_a_at•"gb:BC020191.1 /DB_XREF=gi:22507482 /TID=Hs2.161134.3 /CNT=5
/FEA=mRNA /TIER=ConsEnd /STK=0 /LL=84978 /UG_GENE=MGC14161 /UG=Hs.161134
/UG_TITLE=hypothetical protein MGC14161 /DEF=Homo sapiens, Similar to
hypothetical protein MGC14161, clone IMAGE:4844595,
"•0.172114079•0.17525004•hypothetical protein
MGC14161•MGC14161•Hs.368399•ENSG00000171877••5737 // cytoplasm // inferred
from electronic annotation /// 5856 // cytoskeleton // inferred from
electronic annotation /// 16020 // membrane // inferred from electronic
annotation•5488 // binding // inferred from electronic annotation /// 8092 //
cytoskeletal protein binding // inferred from electronic annotation
202295_s_at•"gb:NM_004390.1 /DB_XREF=gi:4758095 /GEN=CTSH /FEA=FLmRNA
/CNT=216 /TID=Hs.288181.0 /TIER=FL+Stack /STK=108 /UG=Hs.288181 /LL=1512
/DEF=Homo sapiens cathepsin H (CTSH), mRNA. /PROD=cathepsin H
/FL=gb:BC002479.1 gb:NM_004390.1"•0.170765162•0.296606172•cathepsin
H•CTSH•Hs.148641•ENSG00000103811•6508 // proteolysis and peptidolysis //
inferred from electronic annotation /// 6508 // proteolysis and peptidolysis
// traceable author statement•5764 // lysosome // not recorded•4197 //
cysteine-type endopeptidase activity // inferred from electronic annotation
/// 4215 // cathepsin H activity // traceable author statement
221766_s_at•gb:AW246673 /DB_XREF=gi:6589666 /DB_XREF=2821951.3prime
/CLONE=IMAGE:2821951 /FEA=DNA /CNT=155 /TID=Hs.10784.3 /TIER=Stack /STK=12
/UG=Hs.10784 /LL=55603 /UG_GENE=FLJ20037 /UG_TITLE=hypothetical protein
FLJ20037•0.169340918•0.076494733•"family with sequence similarity 46, member
A"•FAM46A•Hs.10784•ENSG00000112773•••
203917_at•"gb:NM_001338.1 /DB_XREF=gi:4503172 /GEN=CXADR /FEA=FLmRNA /CNT=84
/TID=Hs.79187.0 /TIER=FL+Stack /STK=40 /UG=Hs.79187 /LL=1525 /DEF=Homo
sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA.
/PROD=coxsackie virus and adenovirus receptor
/FL=gb:U9"•0.167831428•0.191532504•coxsackie virus and adenovirus
receptor•CXADR•Hs.473417•ENSG00000154639••5886 // plasma membrane //
non-traceable author statement /// 5887 // integral to plasma membrane //
traceable author statement•4872 // receptor activity // inferred from
electronic annotation /// 4872 // receptor activity // traceable author
statement
210086_at•"gb:AF039196.2 /DB_XREF=gi:5042382 /GEN=hairless /FEA=FLmRNA
/CNT=27 /TID=Hs.284126.0 /TIER=FL+Stack /STK=13 /UG=Hs.284126 /LL=3264
/DEF=Homo sapiens putative single zinc finger transcription factor protein
(hairless) mRNA, complete cds. /PROD=putative
sin"•0.167110596•0.272093836•hairless homolog
(mouse)•HR•Hs.272367•ENSG00000168453•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// non-traceable author statement"•5634 // nucleus // non-traceable author
statement•3700 // transcription factor activity // non-traceable author
statement
205227_at•"gb:NM_002182.1 /DB_XREF=gi:4504660 /GEN=IL1RAP /FEA=FLmRNA /CNT=48
/TID=Hs.173880.0 /TIER=FL+Stack /STK=8 /UG=Hs.173880 /LL=3556 /DEF=Homo
sapiens interleukin 1 receptor accessory protein (IL1RAP), mRNA.
/PROD=interleukin 1 receptor accessory protein
/FL="•0.166793019•0.143264878•interleukin 1 receptor accessory
protein•IL1RAP•Hs.478673•ENSG00000196083•6461 // protein complex assembly //
traceable author statement /// 6954 // inflammatory response // traceable
author statement•5887 // integral to plasma membrane // traceable author
statement /// 16020 // membrane // inferred from electronic annotation•4888
// transmembrane receptor activity // inferred from electronic annotation ///
4908 // interleukin-1 receptor activity // inferred from electronic
annotation
242447_at•gb:AI656180 /DB_XREF=gi:4740159 /DB_XREF=tt38e08.x1
/CLONE=IMAGE:2243078 /FEA=EST /CNT=5 /TID=Hs.196284.0 /TIER=ConsEnd /STK=0
/UG=Hs.196284 /UG_TITLE=ESTs•0.165824249•0.090425015•Transcribed
locus••Hs.551039••••
231656_x_at•gb:AW593467 /DB_XREF=gi:7280725 /DB_XREF=hg16f07.x1
/CLONE=IMAGE:2945797 /FEA=EST /CNT=8 /TID=Hs.321622.1 /TIER=Stack /STK=8
/UG=Hs.321622 /LL=54907 /UG_GENE=FLJ20363 /UG_TITLE=hypothetical protein
FLJ20363•0.164525098•0.384486555••••••
203542_s_at•gb:AI690205 /DB_XREF=gi:4901499 /DB_XREF=tx33d02.x1
/CLONE=IMAGE:2271363 /FEA=FLmRNA /CNT=168 /TID=Hs.150557.0 /TIER=Stack
/STK=33 /UG=Hs.150557 /LL=687 /UG_GENE=BTEB1 /UG_TITLE=basic transcription
```

```
element binding protein 1 /FL=gb:D31716.1
gb:NM_001206.1•0.16397893•0.098308083•Kruppel-like factor
9•KLF9•Hs.150557•ENSG00000119138•6350 // transcription // inferred from
electronic annotation /// 6357 // regulation of transcription from RNA
polymerase II promoter // traceable author statement•5634 // nucleus //
inferred from electronic annotation•3700 // transcription factor activity //
traceable author statement /// 8270 // zinc ion binding // inferred from
electronic annotation
205893_at•"gb:NM_014932.1 /DB_XREF=gi:7662469 /GEN=NLGN1 /FEA=FLmRNA /CNT=23
/TID=Hs.71132.0 /TIER=FL /STK=0 /UG=Hs.71132 /LL=22871 /DEF=Homo sapiens
neuroligin 1 (NLGN1), mRNA. /PROD=neuroligin 1 /FL=gb:AB028993.1
gb:NM_014932.1"•0.163365335•0.134433846•neuroligin
1•NLGN1•Hs.549114•ENSG00000169760•6605 // protein targeting // inferred from
sequence or structural similarity /// 7155 // cell adhesion // inferred from
electronic annotation /// 7416 // synaptogenesis // inferred from sequence or
structural similarity /// 16080 // synaptic vesicle targe•5887 // integral to
plasma membrane // inferred from sequence or structural similarity /// 16020
// membrane // inferred from electronic annotation /// 45202 // synapse //
inferred from sequence or structural similarity•3824 // catalytic activity //
inferred from electronic annotation /// 16789 // carboxylic ester hydrolase
activity // inferred from sequence or structural similarity /// 42043 //
neurexin binding // inferred from sequence or structural similarity
210089_s_at•"gb:BC004241.1 /DB_XREF=gi:13278992 /FEA=FLmRNA /CNT=34
/TID=Hs.327703.0 /TIER=FL+Stack /STK=27 /UG=Hs.327703 /DEF=Homo sapiens,
Similar to laminin, alpha 4, clone MGC:10389, mRNA, complete cds.
/PROD=Similar to laminin, alpha 4
/FL=gb:BC004241.1"•0.161854899•0.331978575•"laminin, alpha
4"•LAMA4•Hs.213861•ENSG00000112769•30155 // regulation of cell adhesion //
inferred from electronic annotation /// 30334 // regulation of cell migration
// inferred from electronic annotation /// 45995 // regulation of embryonic
development // inferred from electronic annotation•5605 // basal lamina //
traceable author statement /// 5606 // laminin-1 // inferred from electronic
annotation•5102 // receptor binding // inferred from electronic annotation
/// 5201 // extracellular matrix structural constituent // traceable author
statement /// 5515 // protein binding // inferred from electronic annotation
210118_s_at•"gb:M15329.1 /DB_XREF=gi:186277 /GEN=IL1A /FEA=FLmRNA /CNT=29
/TID=Hs.1722.1 /TIER=FL /STK=0 /UG=Hs.1722 /LL=3552 /DEF=Human interleukin
1-alpha (IL1A) mRNA, complete cds. /PROD=interleukin 1-alpha
/FL=gb:M15329.1"•0.157934634•0.105944702•"interleukin 1,
alpha"•IL1A•Hs.1722•ENSG00000115008•74 // regulation of cell cycle //
inferred from electronic annotation /// 6915 // apoptosis // traceable author
statement /// 6916 // anti-apoptosis // traceable author statement /// 6935
// chemotaxis // not recorded /// 6954 // inflammatory response // •5615 //
extracellular space // traceable author statement /// 5737 // cytoplasm //
not recorded•4871 // signal transducer activity // traceable author statement
/// 5149 // interleukin-1 receptor binding // inferred from electronic
annotation /// 5515 // protein binding // inferred from physical interaction
205130_at•"gb:NM_014226.1 /DB_XREF=gi:7657497 /GEN=RAGE /FEA=FLmRNA /CNT=52
/TID=Hs.104119.0 /TIER=FL+Stack /STK=38 /UG=Hs.104119 /LL=5891 /DEF=Homo
sapiens renal tumor antigen (RAGE), mRNA. /PROD=renal tumor antigen
/FL=gb:NM_014226.1 gb:AB022694.1"•0.157224305•0.14094359•renal tumor
antigen•RAGE•Hs.104119•ENSG00000080823•6468 // protein amino acid
phosphorylation // traceable author statement /// 7165 // signal transduction
// traceable author statement•5737 // cytoplasm // traceable author
statement•4674 // protein serine/threonine kinase activity // traceable
author statement /// 5524 // ATP binding // inferred from electronic
annotation /// 16740 // transferase activity // inferred from electronic
annotation
226829_at•gb:AW138743 /DB_XREF=gi:6143061 /DB_XREF=UI-H-BI1-add-g-07-0-UI.s1
/CLONE=IMAGE:2716597 /FEA=EST /CNT=41 /TID=Hs.23972.0 /TIER=Stack /STK=12
/UG=Hs.23972
/UG_TITLE=ESTs•0.156814729•0.203148975•KIAA1914•KIAA1914•Hs.501106•ENSG0000016
9129•••
212136_at•"gb:AW517686 /DB_XREF=gi:7155768 /DB_XREF=xs86d05.x1
/CLONE=IMAGE:2776521 /FEA=EST /CNT=223 /TID=Hs.305923.2 /TIER=Stack /STK=12
/UG=Hs.305923 /LL=493 /UG_GENE=ATP2B4 /UG_TITLE=ATPase, Ca++ transporting,
plasma membrane 4"•0.156768888•0.192823064•"ATPase, Ca++ transporting, plasma
membrane 4"•ATP2B4•Hs.343522•ENSG00000058668•6812 // cation transport //
inferred from electronic annotation /// 6816 // calcium ion transport //
inferred from electronic annotation /// 8152 // metabolism // inferred from
electronic annotation•5886 // plasma membrane // traceable author statement
/// 5887 // integral to plasma membrane // traceable author statement•287 //
magnesium ion binding // inferred from electronic annotation /// 5388 //
calcium-transporting ATPase activity // traceable author statement /// 5509
// calcium ion binding // inferred from electronic annotation /// 5516 //
calmodulin binding // inf
205016_at•"gb:NM_003236.1 /DB_XREF=gi:4507460 /GEN=TGFA /FEA=FLmRNA /CNT=49
/TID=Hs.170009.0 /TIER=FL /STK=0 /UG=Hs.170009 /LL=7039 /DEF=Homo sapiens
transforming growth factor, alpha (TGFA), mRNA. /PROD=transforming growth
factor, alpha /FL=gb:NM_003236.1
gb:K03222"•0.155673887•0.129539894•"transforming growth factor,
```

```
alpha"•TGFA•Hs.170009•ENSG00000163235•74 // regulation of cell cycle //
inferred from electronic annotation /// 7267 // cell-cell signaling // not
recorded /// 8283 // cell proliferation // traceable author statement•5615 //
extracellular space // not recorded /// 5625 // soluble fraction // not
recorded /// 5886 // plasma membrane // non-traceable author statement ///
5887 // integral to plasma membrane // not recorded•4713 // protein-tyrosine
kinase activity // traceable author statement /// 4871 // signal transducer
activity // traceable author statement /// 5155 // epidermal growth factor
receptor activating ligand activity // not recorded /// 5515 // protein
binding
209424_s_at•gb:AI796120 /DB_XREF=gi:5361583 /DB_XREF=wh42f03.x1
/CLONE=IMAGE:2383421 /FEA=FLmRNA /CNT=163 /TID=Hs.128749.0 /TIER=Stack /STK=9
/UG=Hs.128749 /LL=23600 /UG_GENE=AMACR /UG_TITLE=alpha-methylacyl-CoA
racemase /FL=gb:NM_014324.1 gb:AF047020.1
gb:AF158378.1•0.152725718•0.123105673•alpha-methylacyl-CoA
racemase•AMACR•Hs.508343•ENSG00000082196•8152 // metabolism // inferred from
electronic annotation•5739 // mitochondrion // traceable author statement ///
5777 // peroxisome // traceable author statement•3824 // catalytic activity
// inferred from electronic annotation /// 8111 // alpha-methylacyl-CoA
racemase activity // inferred from electronic annotation /// 16853 //
isomerase activity // inferred from electronic annotation
206027_at•"gb:NM_002960.1 /DB_XREF=gi:4506762 /GEN=S100A3 /FEA=FLmRNA /CNT=26
/TID=Hs.2961.0 /TIER=FL+Stack /STK=11 /UG=Hs.2961 /LL=6274 /DEF=Homo sapiens
S100 calcium-binding protein A3 (S100A3), mRNA. /PROD=S100 calcium-binding
protein A3 /FL=gb:NM_002960.1"•0.152032253•0.123073833•S100 calcium binding
protein A3•S100A3•Hs.433168•ENSG00000188015•••5509 // calcium ion binding //
not recorded
203143_s_at•gb:T79953 /DB_XREF=gi:698462 /DB_XREF=yd85c11.s1
/CLONE=IMAGE:115028 /FEA=FLmRNA /CNT=111 /TID=Hs.158282.0 /TIER=Stack /STK=32
/UG=Hs.158282 /LL=9674 /UG_GENE=KIAA0040 /UG_TITLE=KIAA0040 gene product
/FL=gb:D25539.1
gb:NM_014656.1•0.151362667•0.130342222•KIAA0040•KIAA0040•Hs.518138•ENSG0000016
2666•••
226424_at•gb:AI683754 /DB_XREF=gi:4893936 /DB_XREF=tw53f02.x1
/CLONE=IMAGE:2263419 /FEA=EST /CNT=66 /TID=Hs.26685.0 /TIER=Stack /STK=26
/UG=Hs.26685 /LL=828 /UG_GENE=CAPS
/UG_TITLE=calcyphosine•0.149313947•0.178546824•calcyphosine•CAPS•Hs.549024•ENS
G00000105519•7242 // intracellular signaling cascade // traceable author
statement••5509 // calcium ion binding // inferred from electronic annotation
/// 5509 // calcium ion binding // traceable author statement
206070_s_at•"gb:AF213459.1 /DB_XREF=gi:12003434 /GEN=EPHA3 /FEA=FLmRNA
/CNT=20 /TID=Hs.123642.0 /TIER=FL /STK=0 /UG=Hs.123642 /LL=2042 /DEF=Homo
sapiens ephrin receptor EPHA3 complete form (EPHA3) mRNA, complete cds.
/PROD=ephrin receptor EPHA3 complete form
/FL=gb:NM"•0.148807676•0.09370497•EPH receptor
A3•EPHA3•Hs.123642•ENSG00000044524•6468 // protein amino acid phosphorylation
// inferred from electronic annotation /// 7165 // signal transduction //
traceable author statement /// 7169 // transmembrane receptor protein
tyrosine kinase signaling pathway // inferred from electronic annota•5887 //
integral to plasma membrane // traceable author statement /// 16020 //
membrane // inferred from electronic annotation•4674 // protein
serine/threonine kinase activity // inferred from electronic annotation ///
4713 // protein-tyrosine kinase activity // inferred from electronic
annotation /// 4872 // receptor activity // inferred from electronic
annotation /// 5003 // ep
227404_s_at•gb:AI459194 /DB_XREF=gi:4311773 /DB_XREF=tj54g06.x1
/CLONE=IMAGE:2145370 /FEA=EST /CNT=42 /TID=Hs.326035.1 /TIER=Stack /STK=26
/UG=Hs.326035 /LL=1958 /UG_GENE=EGR1 /UG_TITLE=early growth response
1•0.147997489•0.272497284•Early growth response
1•EGR1•Hs.326035•ENSG00000120738•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation"•5634 // nucleus // inferred from
electronic annotation•3700 // transcription factor activity // traceable
author statement /// 8270 // zinc ion binding // inferred from electronic
annotation
224973_at•gb:AL078599 /DB_XREF=gi:5804908 /FEA=DNA /CNT=155 /TID=Hs.10784.3
/TIER=Stack /STK=60 /UG=Hs.10784 /LL=55603 /UG_GENE=FLJ20037
/UG_TITLE=hypothetical protein FLJ20037 /DEF=Human DNA sequence from clone
RP5-991C6 on chromosome 6q14.1-15. Contains the gene
•0.147743838•0.260987778•"family with sequence similarity 46, member
A"•FAM46A•Hs.10784•ENSG00000112773•••
233329_s_at•"gb:AK025986.1 /DB_XREF=gi:10438677 /FEA=mRNA /CNT=3
/TID=Hs.5721.1 /TIER=ConsEnd /STK=0 /UG=Hs.5721 /LL=51315 /UG_GENE=LOC51315
/UG_TITLE=hypothetical protein /DEF=Homo sapiens cDNA: FLJ22333 fis, clone
HRC05801, highly similar to AF217520 Homo sapiens
un"•0.147674822•0.170536723•hypothetical protein
LOC51315•LOC51315•Hs.469254•ENSG00000172086•••
218303_x_at•"gb:NM_016618.1 /DB_XREF=gi:7706155 /GEN=LOC51315 /FEA=FLmRNA
/CNT=127 /TID=Hs.5721.0 /TIER=FL+Stack /STK=35 /UG=Hs.5721 /LL=51315
/DEF=Homo sapiens hypothetical protein (LOC51315), mRNA. /PROD=hypothetical
protein /FL=gb:AF217520.1 gb:NM_016618.1
```

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gb:AF208"•0.146342337•0.066109514•hypothetical protein
LOC51315•LOC51315•Hs.469254•ENSG00000172086•••
210095_s_at•gb:M31159.1 /DB_XREF=gi:183115 /GEN=IGFBP1 /FEA=FLmRNA /CNT=41
/TID=Hs.77326.0 /TIER=FL /STK=0 /UG=Hs.77326 /LL=3486 /UG_TITLE=insulin-like
growth factor binding protein 3 /DEF=Human growth hormone-dependent
insulin-like growth factor-binding protein
mRNA•0.145254545•0.245586144•insulin-like growth factor binding protein
3•IGFBP3•Hs.450230•ENSG00000146674•1558 // regulation of cell growth //
inferred from electronic annotation /// 9968 // negative regulation of signal
transduction // non-traceable author statement /// 43065 // positive
regulation of apoptosis // inferred from mutant phenotype /// 45663 // •5576
// extracellular region // inferred from electronic annotation /// 5576 //
extracellular region // non-traceable author statement•5520 // insulin-like
growth factor binding // inferred from electronic annotation /// 5520 //
insulin-like growth factor binding // non-traceable author statement /// 8160
// protein tyrosine phosphatase activator activity // inferred from direct
assay //
216268_s_at•"gb:U77914.1 /DB_XREF=gi:1684889 /FEA=mRNA /CNT=2 /TID=Hs.91143.3
/TIER=ConsEnd /STK=0 /UG=Hs.91143 /LL=182 /UG_GENE=JAG1 /DEF=Human soluble
protein Jagged mRNA, partial cds. /PROD=soluble protein
Jagged"•0.141987241•0.125527815•jagged 1 (Alagille
syndrome)•JAG1•Hs.224012•ENSG00000101384•1525 // angiogenesis //
non-traceable author statement /// 1709 // cell fate determination //
non-traceable author statement /// 7154 // cell communication // inferred
from electronic annotation /// 7219 // Notch signaling pathway //
non-traceable author •5576 // extracellular region // non-traceable author
statement /// 5887 // integral to plasma membrane // non-traceable author
statement /// 16020 // membrane // traceable author statement•5112 // Notch
binding // non-traceable author statement /// 5198 // structural molecule
activity // non-traceable author statement /// 5509 // calcium ion binding //
inferred from electronic annotation /// 5509 // calcium ion binding //
non-traceable auth
235372_at•"gb:AW575245 /DB_XREF=gi:7246784
/DB_XREF=UI-HF-BK0-aaw-h-09-0-UI.s1 /CLONE=IMAGE:3055360 /FEA=EST /CNT=12
/TID=Hs.266331.1 /TIER=ConsEnd /STK=7 /UG=Hs.266331 /UG_TITLE=ESTs, Weakly
similar to A39878 Fc gamma (H.sapiens)"•0.141671217•0.079722431•Fc receptor
homolog expressed in B cells•FREB•Hs.266331•ENSG00000132185•••4872 //
receptor activity // inferred from electronic annotation
205110_s_at•"gb:NM_004114.1 /DB_XREF=gi:4758365 /GEN=FGF13 /FEA=FLmRNA
/CNT=55 /TID=Hs.6540.0 /TIER=FL+Stack /STK=30 /UG=Hs.6540 /LL=2258 /DEF=Homo
sapiens fibroblast growth factor 13 (FGF13), mRNA. /PROD=fibroblast growth
factor 13 /FL=gb:AF100143.1 gb:NM_004114.1
gb"•0.140677277•0.08270913•fibroblast growth factor
13•FGF13•Hs.6540•ENSG00000129682•7165 // signal transduction // traceable
author statement /// 7267 // cell-cell signaling // traceable author
statement /// 7399 // neurogenesis // traceable author statement•5615 //
extracellular space // not recorded•8083 // growth factor activity //
traceable author statement
209348_s_at•"gb:AF055376.1 /DB_XREF=gi:3335147 /GEN=c-maf /FEA=FLmRNA
/CNT=175 /TID=Hs.30250.1 /TIER=FL+Stack /STK=20 /UG=Hs.30250 /LL=4094
/DEF=Homo sapiens short form transcription factor C-MAF (c-maf) mRNA,
complete cds. /PROD=short form transcription factor C-MAF
"•0.136001137•0.195376072•v-maf musculoaponeurotic fibrosarcoma oncogene
homolog (avian)•MAF•Hs.134859•ENSG00000178573•"6350 // transcription //
inferred from electronic annotation /// 6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 6366 //
transcription from RNA polymerase II promoter // traceable author
statement"•785 // chromatin // traceable author statement /// 5634 // nucleus
// inferred from electronic annotation•3677 // DNA binding // inferred from
electronic annotation /// 3702 // RNA polymerase II transcription factor
activity // traceable author statement
204916_at•"gb:NM_005855.1 /DB_XREF=gi:5032018 /GEN=RAMP1 /FEA=FLmRNA /CNT=71
/TID=Hs.32989.0 /TIER=FL+Stack /STK=27 /UG=Hs.32989 /LL=10267 /DEF=Homo
sapiens receptor (calcitonin) activity modifying protein 1 (RAMP1), mRNA.
/PROD=receptor (calcitonin) activity modify"•0.13566716•0.17045588•receptor
(calcitonin) activity modifying protein
1•RAMP1•Hs.471783•ENSG00000132329•6810 // transport // inferred from
electronic annotation /// 6886 // intracellular protein transport // inferred
from electronic annotation /// 8277 // regulation of G-protein coupled
receptor protein signaling pathway // traceable author statement•5886 //
plasma membrane // traceable author statement /// 5887 // integral to plasma
membrane // traceable author statement•4872 // receptor activity // inferred
from electronic annotation /// 8565 // protein transporter activity //
traceable author statement
204743_at•"gb:NM_013259.1 /DB_XREF=gi:10047091 /GEN=NP25 /FEA=FLmRNA /CNT=59
/TID=Hs.169330.0 /TIER=FL+Stack /STK=28 /UG=Hs.169330 /LL=29114 /DEF=Homo
sapiens neuronal protein (NP25), mRNA. /PROD=neuronal protein
/FL=gb:NM_013259.1 gb:AF112201.1"•0.134255511•0.093989165•transgelin
3•TAGLN3•Hs.169330•ENSG00000144834•7417 // central nervous system development
// traceable author statement /// 7517 // muscle development // inferred from
electronic annotation••
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228490_at•"gb:AW292816 /DB_XREF=gi:6699452 /DB_XREF=UI-H-BW0-aij-h-04-0-UI.s1
/CLONE=IMAGE:2729695 /FEA=EST /CNT=25 /TID=Hs.18948.0 /TIER=Stack /STK=18
/UG=Hs.18948 /UG_TITLE=ESTs, Highly similar to A31026 probable membrane
receptor protein (H.sapiens)"•0.132610356•0.387854506•abhydrolase domain
containing 2•ABHD2•Hs.122337•ENSG00000140526••16021 // integral to membrane
// non-traceable author statement•3824 // catalytic activity // inferred from
electronic annotation
221042_s_at•"gb:NM_024734.1 /DB_XREF=gi:13376053 /GEN=FLJ12383 /FEA=FLmRNA
/CNT=2 /TID=Hs.118164.0 /TIER=FL /STK=0 /UG=Hs.118164 /LL=79789 /DEF=Homo
sapiens hypothetical protein FLJ12383 (FLJ12383), mRNA. /PROD=hypothetical
protein FLJ12383 /FL=gb:NM_024734.1"•0.128960122•0.347822935•"calmin
(calponin-like, transmembrane)"•CLMN•Hs.301478•ENSG00000165959••16021 //
integral to membrane // inferred from electronic annotation•3779 // actin
binding // inferred from electronic annotation
227826_s_at•gb:AW138143 /DB_XREF=gi:6142543
/DB_XREF=UI-H-BI1-acy-b-09-0-UI.s1 /CLONE=IMAGE:2715976 /FEA=EST /CNT=32
/TID=Hs.71721.0 /TIER=Stack /STK=16 /UG=Hs.71721
/UG_TITLE=ESTs•0.128402204•0.141862433•Arg/Abl-interacting protein
ArgBP2•ARGBP2•Hs.481342•ENSG00000154556••5634 // nucleus // inferred from
electronic annotation /// 5634 // nucleus // non-traceable author statement
/// 5634 // nucleus // traceable author statement /// 5856 // cytoskeleton //
inferred from electronic annotation /// 15629 // actin cytoskeleton •3676 //
nucleic acid binding // inferred from electronic annotation /// 5200 //
structural constituent of cytoskeleton // traceable author statement /// 5515
// protein binding // non-traceable author statement /// 8093 // cytoskeletal
adaptor activity //
236277_at•gb:H23551 /DB_XREF=gi:892246 /DB_XREF=ym53e01.s1 /CLONE=IMAGE:51798
/FEA=EST /CNT=10 /TID=Hs.30974.0 /TIER=ConsEnd /STK=7 /UG=Hs.30974
/UG_TITLE=ESTs•0.126201227•0.349790115•P21 (CDKN1A)-activated kinase
3•PAK3•Hs.390616•ENSG00000077264•6468 // protein amino acid phosphorylation
// not recorded••4674 // protein serine/threonine kinase activity // not
recorded /// 4713 // protein-tyrosine kinase activity // inferred from
electronic annotation /// 5524 // ATP binding // inferred from electronic
annotation /// 16740 // transferase activity // inferr
205523_at•"gb:U43328.1 /DB_XREF=gi:1151008 /FEA=FLmRNA /CNT=44 /TID=Hs.2799.0
/TIER=FL+Stack /STK=19 /UG=Hs.2799 /LL=1404 /UG_GENE=CRTL1 /DEF=Human link
protein mRNA, complete cds. /PROD=link protein /FL=gb:NM_001884.1
gb:U43328.1"•0.125689477•0.138332887•hyaluronan and proteoglycan link protein
1•HAPLN1•Hs.2799•ENSG00000145681•7155 // cell adhesion // inferred from
electronic annotation•5578 // extracellular matrix (sensu Metazoa) //
traceable author statement•5540 // hyaluronic acid binding // inferred from
electronic annotation
209686_at•"gb:BC001766.1 /DB_XREF=gi:12804680 /FEA=FLmRNA /CNT=139
/TID=Hs.83384.0 /TIER=FL+Stack /STK=47 /UG=Hs.83384 /LL=6285 /UG_GENE=S100B
/DEF=Homo sapiens, S100 calcium-binding protein, beta (neural), clone
MGC:1323, mRNA, complete cds. /PROD=S100
calcium-bind"•0.125238465•0.099309785•"S100 calcium binding protein, beta
(neural)"•S100B•Hs.422181•ENSG00000160307•6112 // energy reserve metabolism
// inferred from sequence or structural similarity /// 6874 // calcium ion
homeostasis // inferred from sequence or structural similarity /// 6917 //
induction of apoptosis // inferred from sequence or structural similari•5576
// extracellular region // inferred from sequence or structural similarity
/// 5634 // nucleus // inferred from electronic annotation /// 5737 //
cytoplasm // inferred from sequence or structural similarity•5509 // calcium
ion binding // inferred from sequence or structural similarity /// 5509 //
calcium ion binding // non-traceable author statement /// 8270 // zinc ion
binding // inferred from sequence or structural similarity /// 19210 //
kinase inhibitor
206513_at•"gb:NM_004833.1 /DB_XREF=gi:4757733 /GEN=AIM2 /FEA=FLmRNA /CNT=15
/TID=Hs.105115.0 /TIER=FL /STK=7 /UG=Hs.105115 /LL=9447 /DEF=Homo sapiens
absent in melanoma 2 (AIM2), mRNA. /PROD=absent in melanoma 2
/FL=gb:AF024714.1 gb:NM_004833.1"•0.124209322•0.078612815•absent in melanoma
2•AIM2•Hs.281898•ENSG00000163568•6955 // immune response // traceable author
statement••
230895_at•gb:AI760252 /DB_XREF=gi:5175919 /DB_XREF=wg59b07.x1
/CLONE=IMAGE:2369365 /FEA=EST /CNT=10 /TID=Hs.43227.0 /TIER=Stack /STK=8
/UG=Hs.43227 /UG_TITLE=ESTs•0.123969626•0.073142275•Hyaluronan and
proteoglycan link protein 1•HAPLN1•Hs.2799•ENSG00000145681•7155 // cell
adhesion // inferred from electronic annotation•5578 // extracellular matrix
(sensu Metazoa) // traceable author statement•5540 // hyaluronic acid binding
// inferred from electronic annotation
242488_at•gb:R55784 /DB_XREF=gi:825859 /DB_XREF=yg89g05.s1 /CLONE=IMAGE:40842
/FEA=EST /CNT=5 /TID=Hs.140942.0 /TIER=ConsEnd /STK=2 /UG=Hs.140942
/UG_TITLE=ESTs•0.123399634•0.168928224•"CDNA FLJ38396 fis, clone
FEBRA2007957"••Hs.155736••••
205524_s_at•"gb:NM_001884.1 /DB_XREF=gi:4503052 /GEN=CRTL1 /FEA=FLmRNA
/CNT=44 /TID=Hs.2799.0 /TIER=FL /STK=1 /UG=Hs.2799 /LL=1404 /DEF=Homo sapiens
cartilage linking protein 1 (CRTL1), mRNA. /PROD=cartilage linking protein 1
/FL=gb:NM_001884.1 gb:U43328.1"•0.122111364•0.086582551•hyaluronan and
proteoglycan link protein 1•HAPLN1•Hs.2799•ENSG00000145681•7155 // cell
adhesion // inferred from electronic annotation•5578 // extracellular matrix
```

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(sensu Metazoa) // traceable author statement•5540 // hyaluronic acid binding
// inferred from electronic annotation
214660_at•"gb:X68742.1 /DB_XREF=gi:33949 /FEA=mRNA /CNT=96 /TID=Hs.116774.0
/TIER=ConsEnd /STK=0 /UG=Hs.116774 /LL=3672 /UG_GENE=ITGA1
/UG_TITLE=integrin, alpha 1 /DEF=H.sapiens mRNA for integrin, alpha
subunit."•0.121832295•0.147977257•"Integrin, alpha
1"•PELO•Hs.519304•ENSG00000152684•6412 // protein biosynthesis // inferred
from electronic annotation•5634 // nucleus // inferred from electronic
annotation•
1554332_a_at•"gb:BC025345.1 /DB_XREF=gi:19263726 /TID=Hs2.211250.1 /CNT=4
/FEA=FLmRNA /TIER=FL /STK=2 /UG=Hs.211250 /DEF=Homo sapiens, Similar to
LOC149651, clone MGC:39393 IMAGE:4862156, mRNA, complete cds. /PROD=Similar
to LOC149651 /FL=gb:BC025345.1"•0.120354021•0.083533171•"Solute carrier
organic anion transporter family, member
4A1"•SLCO4A1•Hs.235782•ENSG00000101187•6811 // ion transport // inferred from
electronic annotation•16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from electronic
annotation•5215 // transporter activity // inferred from electronic
annotation
209425_at•gb:AA888589 /DB_XREF=gi:3004264 /DB_XREF=oe68e10.s1
/CLONE=IMAGE:1416810 /FEA=FLmRNA /CNT=163 /TID=Hs.128749.0 /TIER=ConsEnd
/STK=5 /UG=Hs.128749 /LL=23600 /UG_GENE=AMACR /UG_TITLE=alpha-methylacyl-CoA
racemase /FL=gb:NM_014324.1 gb:AF047020.1
gb:AF158378•0.120167777•0.100646725•••••••
217875_s_at•"gb:NM_020182.1 /DB_XREF=gi:9910497 /GEN=TMEPAI /FEA=FLmRNA
/CNT=273 /TID=Hs.83883.0 /TIER=FL /STK=0 /UG=Hs.83883 /LL=56937 /DEF=Homo
sapiens transmembrane, prostate androgen induced RNA (TMEPAI), mRNA.
/PROD=transmembrane, prostate androgen induced RNA
/F"•0.119388873•0.131898635•"transmembrane, prostate androgen induced
RNA"•TMEPAI•Hs.517155•ENSG00000124225•30521 // androgen receptor signaling
pathway // non-traceable author statement•16021 // integral to membrane //
non-traceable author statement•
209610_s_at•"gb:BF340083 /DB_XREF=gi:11286545 /DB_XREF=602037236F1
/CLONE=IMAGE:4185248 /FEA=FLmRNA /CNT=59 /TID=Hs.323878.0 /TIER=ConsEnd
/STK=0 /UG=Hs.323878 /LL=6509 /UG_GENE=SLC1A4 /UG_TITLE=solute carrier family
1 (glutamateneutral amino acid transporter),
member"•0.117962009•0.131483292•"solute carrier family 1 (glutamate/neutral
amino acid transporter), member 4"•SLC1A4•Hs.323878•ENSG00000115902•6810 //
transport // inferred from electronic annotation /// 6835 // dicarboxylic
acid transport // inferred from electronic annotation /// 15804 // neutral
amino acid transport // traceable author statement•5624 // membrane fraction
// traceable author statement /// 5887 // integral to plasma membrane //
traceable author statement /// 16020 // membrane // inferred from electronic
annotation•15175 // neutral amino acid transporter activity // traceable
author statement /// 15293 // symporter activity // inferred from electronic
annotation /// 17153 // sodium:dicarboxylate symporter activity // inferred
from electronic annotation
1569469_a_at•"gb:BC040321.1 /DB_XREF=gi:26007890 /TID=Hs2.403934.1 /CNT=5
/FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.403934 /UG_TITLE=Homo sapiens, Similar
to LIM homeobox protein 8, clone IMAGE:4797854, mRNA /DEF=Homo sapiens,
Similar to LIM homeobox protein 8, clone IMAGE"•0.116936614•0.433121038•LIM
homeobox 8•LHX8•Hs.403934•ENSG00000162624•"6355 // regulation of
transcription, DNA-dependent // inferred from electronic annotation"•5634 //
nucleus // inferred from electronic annotation•3700 // transcription factor
activity // inferred from electronic annotation /// 8270 // zinc ion binding
// inferred from electronic annotation
231935_at•gb:AL133109.1 /DB_XREF=gi:6453595 /GEN=DKFZp566N1047 /FEA=mRNA
/CNT=24 /TID=Hs.21333.0 /TIER=ConsEnd /STK=0 /UG=Hs.21333 /DEF=Homo sapiens
mRNA; cDNA DKFZp566N1047 (from clone DKFZp566N1047); partial cds.
/PROD=hypothetical protein•0.116889062•0.074991137•"cyclic AMP-regulated
phosphoprotein, 21 kD"•ARPP-21•Hs.475902•ENSG00000172995•••3676 // nucleic
acid binding // inferred from electronic annotation
213338_at•gb:BF062629 /DB_XREF=gi:10821539 /DB_XREF=7h62h07.x1
/CLONE=IMAGE:3320605 /FEA=mRNA /CNT=52 /TID=Hs.35861.0 /TIER=Stack /STK=26
/UG=Hs.35861 /LL=25907 /UG_GENE=DKFZP586E1621 /UG_TITLE=DKFZP586E1621
protein•0.116878858•0.132585705•Ras-induced senescence 1•RIS1•Hs.35861••••
215363_x_at•"gb:AW168915 /DB_XREF=gi:6400440 /DB_XREF=xj15b10.x1
/CLONE=IMAGE:2657275 /FEA=mRNA /CNT=4 /TID=Hs.283946.0 /TIER=ConsEnd /STK=3
/UG=Hs.283946 /UG_TITLE=Homo sapiens prostate-specific membrane antigen PSM
mRNA, exon 18 alternative splice variant, partial
c"•0.116240554•0.066948898•folate hydrolase (prostate-specific membrane
antigen) 1•FOLH1•Hs.380325•ENSG00000086205•6508 // proteolysis and
peptidolysis // non-traceable author statement•5624 // membrane fraction //
traceable author statement /// 5887 // integral to plasma membrane //
traceable author statement /// 16020 // membrane // non-traceable author
statement•4180 // carboxypeptidase activity // inferred from electronic
annotation /// 8237 // metallopeptidase activity // inferred from electronic
annotation /// 16805 // dipeptidase activity // inferred from electronic
annotation /// 43275 // glutamate carboxype
206640_x_at•"gb:NM_001477.1 /DB_XREF=gi:4503888 /GEN=GAGE7B /FEA=FLmRNA
/CNT=12 /TID=Hs.251677.0 /TIER=FL /STK=0 /UG=Hs.251677 /LL=26748 /DEF=Homo
```

```
sapiens G antigen 7B (GAGE7B), mRNA. /PROD=G antigen 7B /FL=gb:AF055474.1
gb:NM_001477.1"•0.114989139•0.101191341•G antigen 2 /// G antigen 4 /// G
antigen 5 /// G antigen 6 /// G antigen 7 /// G antigen 7B•GAGE2 /// GAGE4
/// GAGE5 /// GAGE6 /// GAGE7 /// GAGE7B•Hs.278606•ENSG00000068990 ///
ENSG00000189064 /// ENSG00000198716•••
223730_at•"gb:AF111178.1 /DB_XREF=gi:4877642 /GEN=GPC6 /FEA=FLmRNA /CNT=27
/TID=Hs.118407.0 /TIER=FL+Stack /STK=15 /UG=Hs.118407 /LL=10082 /DEF=Homo
sapiens glypican-6 (GPC6) mRNA, complete cds. /PROD=glypican-6
/FL=gb:AF105267.1 gb:NM_005708.2
gb:AF111178.1"•0.114421512•0.244049106•glypican
6•GPC6•Hs.444329•ENSG00000183098••5578 // extracellular matrix (sensu
Metazoa) // inferred from electronic annotation /// 5887 // integral to
plasma membrane // traceable author statement /// 16020 // membrane //
inferred from electronic annotation•
212810_s_at•gb:W72527 /DB_XREF=gi:1382184 /DB_XREF=zd63a09.s1
/CLONE=IMAGE:345304 /FEA=EST /CNT=108 /TID=Hs.286049.2 /TIER=Stack /STK=29
/UG=Hs.286049 /LL=29968 /UG_GENE=PSA /UG_TITLE=phosphoserine
aminotransferase•0.111827078•0.042080476•"solute carrier family 1
(glutamate/neutral amino acid transporter), member
4"•SLC1A4•Hs.323878•ENSG00000115902•6810 // transport // inferred from
electronic annotation /// 6835 // dicarboxylic acid transport // inferred
from electronic annotation /// 15804 // neutral amino acid transport //
traceable author statement•5624 // membrane fraction // traceable author
statement /// 5887 // integral to plasma membrane // traceable author
statement /// 16020 // membrane // inferred from electronic annotation•15175
// neutral amino acid transporter activity // traceable author statement ///
15293 // symporter activity // inferred from electronic annotation /// 17153
// sodium:dicarboxylate symporter activity // inferred from electronic
annotation
213249_at•gb:AU145127 /DB_XREF=gi:11006648 /DB_XREF=AU145127
/CLONE=HEMBA1003978 /FEA=FLmRNA /CNT=70 /TID=Hs.76798.0 /TIER=Stack /STK=34
/UG=Hs.76798 /LL=23194 /UG_GENE=FBXL7 /UG_TITLE=f-box and leucine-rich repeat
protein 7 /FL=gb:NM_012304.1 gb:AF199356.1•0.111600507•0.183428585•F-box and
leucine-rich repeat protein 7•FBXL7•Hs.433057•ENSG00000183580•6511 //
ubiquitin-dependent protein catabolism // non-traceable author statement ///
6512 // ubiquitin cycle // inferred from electronic annotation•151 //
ubiquitin ligase complex // non-traceable author statement•4842 //
ubiquitin-protein ligase activity // non-traceable author statement
207601_at•"gb:NM_014465.1 /DB_XREF=gi:7657620 /GEN=ST1B2 /FEA=FLmRNA /CNT=4
/TID=Hs.129742.0 /TIER=FL /STK=0 /UG=Hs.129742 /LL=27284 /DEF=Homo sapiens
thyroid hormone slfotransferase (ST1B2), mRNA. /PROD=thyroid hormone
slfotransferase /FL=gb:D89479.1
gb:NM_014465.1"•0.111374175•0.073612685•"sulfotransferase family, cytosolic,
1B, member 1"•SULT1B1•Hs.129742•ENSG00000173597•6629 // lipid metabolism //
inferred from electronic annotation /// 8202 // steroid metabolism //
inferred from electronic annotation /// 18958 // phenol metabolism //
inferred from direct assay /// 42403 // thyroid hormone metabolism //
inferred from dir•5829 // cytosol // non-traceable author statement•8146 //
sulfotransferase activity // inferred from direct assay /// 16740 //
transferase activity // inferred from electronic annotation
1569454_a_at•"gb:BG475827 /DB_XREF=gi:13408095 /DB_XREF=602520843F1
/CLONE=IMAGE:4639114 /TID=Hs2.123542.3 /CNT=4 /FEA=mRNA /TIER=ConsEnd /STK=0
/UG=Hs.123542 /UG_TITLE=Homo sapiens, clone IMAGE:4639114,
mRNA"•0.111020905•0.151150519•hypothetical protein
LOC283352•LOC283352•Hs.507268••••
211656_x_at•"gb:M32577.1 /DB_XREF=gi:188194 /GEN=HLA-DQB1 /FEA=FLmRNA /CNT=1
/TID=HsAffx.900420.361 /TIER=FL /STK=0 /DEF=Human MHC HLA-DQ beta mRNA,
complete cds. /FL=gb:M32577.1"•0.110940149•0.052585694•"major
histocompatibility complex, class II, DQ beta 1 /// major histocompatibility
complex, class II, DQ beta 1"•HLA-DQB1•Hs.409934••"6955 // immune response //
inferred from electronic annotation /// 6955 // immune response //
non-traceable author statement /// 19884 // antigen presentation, exogenous
antigen // inferred from electronic annotation /// 19886 // antigen
processing, exoge"•16020 // membrane // inferred from electronic annotation
/// 16020 // membrane // non-traceable author statement /// 16021 // integral
to membrane // inferred from electronic annotation•45012 // MHC class II
receptor activity // inferred from electronic annotation /// 45012 // MHC
class II receptor activity // non-traceable author statement
220012_at•"gb:NM_019891.1 /DB_XREF=gi:9845248 /GEN=ERO1-L(BETA) /FEA=FLmRNA
/CNT=19 /TID=Hs.150763.0 /TIER=FL /STK=0 /UG=Hs.150763 /LL=56605 /DEF=Homo
sapiens endoplasmic reticulum oxidoreductin 1-Lbeta (ERO1-L(BETA)), mRNA.
/PROD=endoplasmic reticulum oxidoreductin"•0.110018004•0.150562053•ERO1-like
beta (S. cerevisiae)•ERO1LB•Hs.424926•ENSG00000086619•6118 // electron
transport // inferred from electronic annotation /// 6457 // protein folding
// traceable author statement /// 6810 // transport // inferred from
electronic annotation•5783 // endoplasmic reticulum // traceable author
statement /// 16020 // membrane // inferred from electronic annotation•16491
// oxidoreductase activity // non-traceable author statement /// 51082 //
unfolded protein binding // non-traceable author statement
212143_s_at•gb:BF340228 /DB_XREF=gi:11286690 /DB_XREF=602036816F1
/CLONE=IMAGE:4185050 /FEA=FLmRNA /CNT=452 /TID=Hs.77326.1 /TIER=Stack /STK=9
```

```
/UG=Hs.77326 /LL=3486 /UG_GENE=IGFBP3 /UG_TITLE=insulin-like growth factor
binding protein 3 /FL=gb:NM_000598.1•0.109697262•0.221369249•insulin-like
growth factor binding protein 3•IGFBP3•Hs.450230•ENSG00000146674•1558 //
regulation of cell growth // inferred from electronic annotation /// 9968 //
negative regulation of signal transduction // non-traceable author statement
/// 43065 // positive regulation of apoptosis // inferred from mutant
phenotype /// 45663 // •5576 // extracellular region // inferred from
electronic annotation /// 5576 // extracellular region // non-traceable
author statement•5520 // insulin-like growth factor binding // inferred from
electronic annotation /// 5520 // insulin-like growth factor binding //
non-traceable author statement /// 8160 // protein tyrosine phosphatase
activator activity // inferred from direct assay //
238689_at•"gb:BG426455 /DB_XREF=gi:13332961 /DB_XREF=602492853F1
/CLONE=IMAGE:4606932 /FEA=EST /CNT=9 /TID=Hs.256897.0 /TIER=ConsEnd /STK=0
/UG=Hs.256897 /UG_TITLE=ESTs, Weakly similar to dJ365O12.1
(H.sapiens)"•0.108025082•0.393579478•G protein-coupled receptor
110•GPR110•Hs.256897•ENSG00000153292•7165 // signal transduction // inferred
from electronic annotation /// 7218 // neuropeptide signaling pathway //
inferred from electronic annotation•16020 // membrane // inferred from
electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation•4872 // receptor activity // inferred from electronic
annotation /// 4930 // G-protein coupled receptor activity // inferred from
electronic annotation
231040_at•gb:AW512988 /DB_XREF=gi:7151066 /DB_XREF=xt76b02.x1
/CLONE=IMAGE:2792331 /FEA=EST /CNT=9 /TID=Hs.184780.0 /TIER=Stack /STK=9
/UG=Hs.184780 /UG_TITLE=ESTs•0.107947505•0.2027467•"CDNA FLJ43172 fis, clone
FCBBF3007242"••Hs.446660••••
205816_at•"gb:NM_002214.1 /DB_XREF=gi:4504778 /GEN=ITGB8 /FEA=FLmRNA /CNT=26
/TID=Hs.52620.0 /TIER=FL /STK=0 /UG=Hs.52620 /LL=3696 /DEF=Homo sapiens
integrin, beta 8 (ITGB8), mRNA. /PROD=integrin, beta 8 /FL=gb:NM_002214.1
gb:M73780.1"•0.107837992•0.187497338•"integrin, beta
8"•ITGB8•Hs.285724•ENSG00000105855•7160 // cell-matrix adhesion // inferred
from electronic annotation /// 7229 // integrin-mediated signaling pathway //
inferred from electronic annotation•8305 // integrin complex // traceable
author statement /// 16021 // integral to membrane // inferred from
electronic annotation•4872 // receptor activity // inferred from electronic
annotation /// 5515 // protein binding // inferred from electronic
annotation
229831_at•gb:BE221817 /DB_XREF=gi:8909135 /DB_XREF=hr59h08.x1
/CLONE=IMAGE:3132831 /FEA=mRNA /CNT=17 /TID=Hs.35089.0 /TIER=Stack /STK=8
/UG=Hs.35089 /LL=5067 /UG_GENE=CNTN3 /UG_TITLE=contactin 3 (plasmacytoma
associated)•0.107103389•0.079832617•contactin 3 (plasmacytoma
associated)•CNTN3•Hs.12723•ENSG00000113805•7155 // cell adhesion // inferred
from electronic annotation•16020 // membrane // inferred from electronic
annotation•5515 // protein binding // inferred from electronic annotation
1553033_at•"gb:NM_138780.1 /DB_XREF=gi:20270304 /GEN=SYTL5 /TID=Hs2.367758.1
/CNT=2 /FEA=FLmRNA /TIER=FL /STK=2 /LL=94122 /UG=Hs.367758 /DEF=Homo sapiens
synaptotagmin-like 5 (SYTL5), mRNA. /PROD=synaptotagmin-like 5
/FL=gb:NM_138780.1 gb:AB080222.1"•0.106382071•0.228294406•synaptotagmin-like
5•SYTL5•Hs.97774•ENSG00000147041•6886 // intracellular protein transport //
inferred from electronic annotation••5515 // protein binding // inferred from
electronic annotation /// 17137 // Rab GTPase binding // inferred from
electronic annotation
209459_s_at•"gb:AF237813.1 /DB_XREF=gi:9963907 /FEA=FLmRNA /CNT=144
/TID=Hs.283675.0 /TIER=FL+Stack /STK=50 /UG=Hs.283675 /LL=57416
/UG_GENE=NPD009 /DEF=Homo sapiens NPD009 mRNA, complete cds. /PROD=NPD009
/FL=gb:NM_020686.1 gb:AF237813.1"•0.105606686•0.35370866•4-aminobutyrate
aminotransferase•ABAT•Hs.336768•ENSG00000183044•7268 // synaptic transmission
// non-traceable author statement /// 9448 // gamma-aminobutyric acid
metabolism // inferred from electronic annotation /// 42135 //
neurotransmitter catabolism // inferred from electronic annotation•5759 //
mitochondrial matrix // non-traceable author statement•3867 //
4-aminobutyrate transaminase activity // non-traceable author statement ///
16740 // transferase activity // inferred from electronic annotation ///
30170 // pyridoxal phosphate binding // inferred from electronic annotation
/// 47298 // (S)-3-ami
231729_s_at•"gb:NM_004058.1 /DB_XREF=gi:4757907 /GEN=CAPS /FEA=FLmRNA /CNT=10
/TID=Hs.26685.1 /TIER=FL /STK=0 /UG=Hs.26685 /LL=828 /DEF=Homo sapiens
calcyphosine (CAPS), mRNA. /PROD=calcyphosine
/FL=gb:NM_004058.1"•0.105054705•0.121922884•calcyphosine•CAPS•Hs.549024•ENSG00
000105519•7242 // intracellular signaling cascade // traceable author
statement••5509 // calcium ion binding // inferred from electronic annotation
/// 5509 // calcium ion binding // traceable author statement
206214_at•"gb:NM_005084.1 /DB_XREF=gi:4826883 /GEN=PLA2G7 /FEA=FLmRNA /CNT=21
/TID=Hs.93304.0 /TIER=FL+Stack /STK=8 /UG=Hs.93304 /LL=7941 /DEF=Homo sapiens
phospholipase A2, group VII (platelet-activating factor acetylhydrolase,
plasma) (PLA2G7), mRNA. /PROD=phospho"•0.103817825•0.293810062•"phospholipase
A2, group VII (platelet-activating factor acetylhydrolase, plasma) ///
phospholipase A2, group VII (platelet-activating factor acetylhydrolase,
plasma)"•PLA2G7•Hs.93304•ENSG00000146070•6954 // inflammatory response //
traceable author statement /// 16042 // lipid catabolism // inferred from
```

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electronic annotation•5576 // extracellular region // traceable author
statement /// 8247 // 2-acetyl-1-alkylglycerophosphocholine esterase complex
// inferred from electronic annotation•3847 //
1-alkyl-2-acetylglycerophosphocholine esterase activity // inferred from
electronic annotation /// 5543 // phospholipid binding // traceable author
statement /// 16787 // hydrolase activity // inferred from electronic
annotation
212811_x_at•gb:AI889380 /DB_XREF=gi:5594544 /DB_XREF=wm98e02.x1
/CLONE=IMAGE:2443994 /FEA=EST /CNT=108 /TID=Hs.286049.2 /TIER=Stack /STK=22
/UG=Hs.286049 /LL=29968 /UG_GENE=PSA /UG_TITLE=phosphoserine
aminotransferase•0.103652418•0.105139694•"solute carrier family 1
(glutamate/neutral amino acid transporter), member
4"•SLC1A4•Hs.323878•ENSG00000115902•6810 // transport // inferred from
electronic annotation /// 6835 // dicarboxylic acid transport // inferred
from electronic annotation /// 15804 // neutral amino acid transport //
traceable author statement•5624 // membrane fraction // traceable author
statement /// 5887 // integral to plasma membrane // traceable author
statement /// 16020 // membrane // inferred from electronic annotation•15175
// neutral amino acid transporter activity // traceable author statement ///
15293 // symporter activity // inferred from electronic annotation /// 17153
// sodium:dicarboxylate symporter activity // inferred from electronic
annotation
228635_at•gb:AI640307 /DB_XREF=gi:4703416 /DB_XREF=wa16f11.x1
/CLONE=IMAGE:2298285 /FEA=mRNA /CNT=26 /TID=Hs.146858.0 /TIER=Stack /STK=8
/UG=Hs.146858 /LL=57575 /UG_GENE=PCDH10 /UG_TITLE=protocadherin
10•0.101703829•0.124060607•protocadherin
10•PCDH10•Hs.192859•ENSG00000138650•7155 // cell adhesion // inferred from
electronic annotation /// 7156 // homophilic cell adhesion // inferred from
electronic annotation•16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from electronic
annotation•5509 // calcium ion binding // inferred from electronic annotation
/// 5515 // protein binding // inferred from electronic annotation
205899_at•"gb:NM_003914.1 /DB_XREF=gi:4502610 /GEN=CCNA1 /FEA=FLmRNA /CNT=39
/TID=Hs.79378.0 /TIER=FL+Stack /STK=23 /UG=Hs.79378 /LL=8900 /DEF=Homo
sapiens cyclin A1 (CCNA1), mRNA. /PROD=cyclin A1 /FL=gb:NM_003914.1
gb:U66838.1"•0.100625716•0.079106949•cyclin
A1•CCNA1•Hs.417050•ENSG00000133101•79 // regulation of cyclin dependent
protein kinase activity // not recorded /// 910 // cytokinesis // inferred
from electronic annotation /// 7067 // mitosis // inferred from electronic
annotation /// 7126 // meiosis // inferred from electronic annotatio•5634 //
nucleus // inferred from electronic annotation /// 5829 // cytosol //
traceable author statement•
235401_s_at•"gb:AL560266 /DB_XREF=gi:12906564 /DB_XREF=AL560266
/CLONE=CS0DG007YG20 (5 prime) /FEA=EST /CNT=29 /TID=Hs.266331.0 /TIER=ConsEnd
/STK=0 /UG=Hs.266331 /UG_TITLE=ESTs, Weakly similar to A39878 Fc gamma
(H.sapiens)"•0.100208492•0.167202032•Fc receptor homolog expressed in B
cells•FREB•Hs.266331•ENSG00000132185•••4872 // receptor activity // inferred
from electronic annotation
203186_s_at•"gb:NM_002961.2 /DB_XREF=gi:9845514 /GEN=S100A4 /FEA=FLmRNA
/CNT=158 /TID=Hs.81256.0 /TIER=FL+Stack /STK=85 /UG=Hs.81256 /LL=6275
/DEF=Homo sapiens S100 calcium-binding protein A4 (calcium protein,
calvasculin, metastasin, murine placental homolog)
(S100A4"•0.10002544•0.091204395•"S100 calcium binding protein A4 (calcium
protein, calvasculin, metastasin, murine placental
homolog)"•S100A4•Hs.81256•ENSG00000196154•••5509 // calcium ion binding //
traceable author statement
205566_at•"gb:NM_007011.1 /DB_XREF=gi:5901977 /GEN=HS1-2 /FEA=FLmRNA /CNT=30
/TID=Hs.99364.0 /TIER=FL+Stack /STK=16 /UG=Hs.99364 /LL=11057 /DEF=Homo
sapiens putative transmembrane protein (HS1-2), mRNA. /PROD=putative
transmembrane protein /FL=gb:NM_007011.1"•0.097176989•0.391731358•abhydrolase
domain containing 2•ABHD2•Hs.122337•ENSG00000140526••16021 // integral to
membrane // non-traceable author statement•3824 // catalytic activity //
inferred from electronic annotation
231728_at•"gb:NM_004058.1 /DB_XREF=gi:4757907 /GEN=CAPS /FEA=FLmRNA /CNT=10
/TID=Hs.26685.1 /TIER=FL /STK=0 /UG=Hs.26685 /LL=828 /DEF=Homo sapiens
calcyphosine (CAPS), mRNA. /PROD=calcyphosine
/FL=gb:NM_004058.1"•0.094848677•0.203588093•calcyphosine•CAPS•Hs.549024•ENSG00
000105519•7242 // intracellular signaling cascade // traceable author
statement••5509 // calcium ion binding // inferred from electronic annotation
/// 5509 // calcium ion binding // traceable author statement
202986_at•"gb:NM_014862.1 /DB_XREF=gi:7662049 /GEN=KIAA0307 /FEA=FLmRNA
/CNT=136 /TID=Hs.6111.0 /TIER=FL+Stack /STK=60 /UG=Hs.6111 /LL=9915 /DEF=Homo
sapiens KIAA0307 gene product (KIAA0307), mRNA. /PROD=KIAA0307 gene product
/FL=gb:AB002305.1 gb:NM_014862.1"•0.094604796•0.068925702•aryl-hydrocarbon
receptor nuclear translocator 2•ARNT2•Hs.459070•ENSG00000172379•1666 //
response to hypoxia // inferred from direct assay /// 1701 // embryonic
development (sensu Mammalia) // inferred from sequence or structural
similarity /// 6350 // transcription // inferred from electronic annotation
/// 6355 // regulation of tran•5634 // nucleus // inferred from direct assay
/// 5634 // nucleus // inferred from electronic annotation•3700 //
transcription factor activity // inferred from electronic annotation /// 3700
```

```
// transcription factor activity // inferred from sequence or structural
similarity /// 4871 // signal transducer activity // inferred from electronic
annotation /// 506
226695_at•gb:AA775472 /DB_XREF=gi:2834806 /DB_XREF=zf29b06.s1
/CLONE=IMAGE:378323 /FEA=EST /CNT=60 /TID=Hs.9071.2 /TIER=Stack /STK=47
/UG=Hs.9071 /LL=10424 /UG_GENE=PMBP /UG_TITLE=progesterone membrane binding
protein•0.094502012•0.100223241•paired related homeobox
1•PRRX1•Hs.283416•ENSG00000116132•"6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 7275 // development
// inferred from electronic annotation"•5634 // nucleus // inferred from
electronic annotation•3700 // transcription factor activity // inferred from
electronic annotation /// 3713 // transcription coactivator activity //
traceable author statement
206363_at•"gb:NM_005360.2 /DB_XREF=gi:5453735 /GEN=MAF /FEA=FLmRNA /CNT=15
/TID=Hs.30250.0 /TIER=FL /STK=5 /UG=Hs.30250 /LL=4094 /DEF=Homo sapiens v-maf
musculoaponeurotic fibrosarcoma (avian) oncogene homolog (MAF), mRNA.
/PROD=v-maf musculoaponeurotic fibrosarcoma"•0.091295455•0.101234751•v-maf
musculoaponeurotic fibrosarcoma oncogene homolog
(avian)•MAF•Hs.134859•ENSG00000178573•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 6366 // transcription from RNA
polymerase II promoter // traceable author statement"•785 // chromatin //
traceable author statement /// 5634 // nucleus // inferred from electronic
annotation•3677 // DNA binding // inferred from electronic annotation ///
3702 // RNA polymerase II transcription factor activity // traceable author
statement
222450_at•"gb:AL035541 /DB_XREF=gi:11546043 /FEA=FLmRNA /CNT=273
/TID=Hs.83883.0 /TIER=Stack /STK=85 /UG=Hs.83883 /LL=56937 /UG_GENE=TMEPAI
/UG_TITLE=transmembrane, prostate androgen induced RNA /DEF=Human DNA
sequence from clone RP4-718J7 on chromosome
20q13.31-13."•0.09036371•0.119402112•"transmembrane, prostate androgen
induced RNA"•TMEPAI•Hs.517155•ENSG00000124225•30521 // androgen receptor
signaling pathway // non-traceable author statement•16021 // integral to
membrane // non-traceable author statement•
1556200_a_at•"gb:BC021140.1 /DB_XREF=gi:18088969 /TID=Hs2.129481.1 /CNT=11
/FEA=mRNA /TIER=ConsEnd /STK=4 /LL=118611 /UG_GENE=FLJ32938 /UG=Hs.129481
/UG_TITLE=hypothetical protein FLJ32938 /DEF=Homo sapiens, Similar to RIKEN
cDNA 4933400E14 gene, clone IMAGE:4871932,
m"•0.089976297•0.122790807•chromosome 10 open reading frame
90•C10orf90•Hs.44939•ENSG00000154493•••
222449_at•"gb:AL035541 /DB_XREF=gi:10198628 /FEA=FLmRNA /CNT=273
/TID=Hs.83883.0 /TIER=Stack /STK=21 /UG=Hs.83883 /LL=56937 /UG_GENE=TMEPAI
/UG_TITLE=transmembrane, prostate androgen induced RNA /DEF=Human DNA
sequence from clone 718J7 on chromosome 20q13.31-13.33.
"•0.0842706•0.124374955•"transmembrane, prostate androgen induced
RNA"•TMEPAI•Hs.517155•ENSG00000124225•30521 // androgen receptor signaling
pathway // non-traceable author statement•16021 // integral to membrane //
non-traceable author statement•
206046_at•"gb:NM_003812.1 /DB_XREF=gi:4501912 /GEN=ADAM23 /FEA=FLmRNA /CNT=26
/TID=Hs.7164.0 /TIER=FL+Stack /STK=11 /UG=Hs.7164 /LL=8745 /DEF=Homo sapiens
a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /PROD=a
disintegrin and metalloproteinase domain "•0.084204157•0.102485831•a
disintegrin and metalloproteinase domain
23•ADAM23•Hs.370287•ENSG00000114948•6508 // proteolysis and peptidolysis //
inferred from electronic annotation /// 7155 // cell adhesion // inferred
from electronic annotation /// 7417 // central nervous system development //
traceable author statement•5887 // integral to plasma membrane // traceable
author statement•4222 // metalloendopeptidase activity // inferred from
electronic annotation /// 5178 // integrin binding // traceable author
statement /// 5515 // protein binding // inferred from electronic annotation
215001_s_at•gb:AL161952.1 /DB_XREF=gi:7328002 /GEN=DKFZp434M0813 /FEA=mRNA
/CNT=10 /TID=Hs.170171.1 /TIER=ConsEnd /STK=0 /UG=Hs.170171 /LL=2752
/DEF=Homo sapiens mRNA; cDNA DKFZp434M0813 (from clone DKFZp434M0813);
partial cds. /PROD=hypothetical
protein•0.082418868•0.462450308•glutamate-ammonia ligase (glutamine
synthase)•GLUL•Hs.518525•ENSG00000135821•1505 // regulation of
neurotransmitter levels // not recorded /// 6542 // glutamine biosynthesis //
inferred from electronic annotation /// 6542 // glutamine biosynthesis // not
recorded /// 6807 // nitrogen compound metabolism // inferred from
electronic••4356 // glutamate-ammonia ligase activity // inferred from
electronic annotation /// 16874 // ligase activity // inferred from
electronic annotation
228827_at•gb:AI217416 /DB_XREF=gi:3797231 /DB_XREF=qh22h01.x1
/CLONE=IMAGE:1845457 /FEA=mRNA /CNT=28 /TID=Hs.90858.0 /TIER=Stack /STK=12
/UG=Hs.90858 /UG_TITLE=Homo sapiens clone 25023 mRNA
sequence•0.079814977•0.09407927•"Runt-related transcription factor 1;
translocated to, 1 (cyclin
D-related)"•RUNX1T1•Hs.368431•ENSG00000079102•"6091 // generation of
precursor metabolites and energy // traceable author statement /// 6350 //
transcription // inferred from electronic annotation /// 6355 // regulation
of transcription, DNA-dependent // inferred from electronic annotation"•5634
```

```
// nucleus // inferred from electronic annotation•3700 // transcription
factor activity // inferred from electronic annotation /// 3700 //
transcription factor activity // traceable author statement
212942_s_at•"gb:AB033025.1 /DB_XREF=gi:6330400 /GEN=KIAA1199 /FEA=mRNA
/CNT=110 /TID=Hs.50081.1 /TIER=Stack /STK=30 /UG=Hs.50081 /LL=57214 /DEF=Homo
sapiens mRNA for KIAA1199 protein, partial cds. /PROD=KIAA1199
protein"•0.078064868•0.056895906•KIAA1199•KIAA1199•Hs.459088•ENSG00000103888•7
605 // perception of sound // inferred from electronic annotation••
218872_at•"gb:NM_017899.1 /DB_XREF=gi:8923562 /GEN=FLJ20607 /FEA=FLmRNA
/CNT=78 /TID=Hs.18791.0 /TIER=FL /STK=0 /UG=Hs.18791 /LL=54997 /DEF=Homo
sapiens hypothetical protein FLJ20607 (FLJ20607), mRNA. /PROD=hypothetical
protein FLJ20607 /FL=gb:NM_017899.1"•0.076566756•0.118094084•hypothetical
protein FLJ20607•TSC•Hs.525709•ENSG00000088992•••5509 // calcium ion binding
// inferred from electronic annotation
202016_at•"gb:NM_002402.1 /DB_XREF=gi:4505154 /GEN=MEST /FEA=FLmRNA /CNT=338
/TID=Hs.79284.0 /TIER=FL+Stack /STK=133 /UG=Hs.79284 /LL=4232 /DEF=Homo
sapiens mesoderm specific transcript (mouse) homolog (MEST), mRNA.
/PROD=mesoderm specific transcript (mouse)
homolog"•0.076289883•0.424846248•mesoderm specific transcript homolog
(mouse)•MEST•Hs.270978•ENSG00000106484•6805 // xenobiotic metabolism //
inferred from electronic annotation /// 7498 // mesoderm development //
traceable author statement /// 9636 // response to toxin // inferred from
electronic annotation••3824 // catalytic activity // inferred from electronic
annotation /// 16787 // hydrolase activity // inferred from electronic
annotation
202450_s_at•"gb:NM_000396.1 /DB_XREF=gi:4503150 /GEN=CTSK /FEA=FLmRNA
/CNT=288 /TID=Hs.83942.0 /TIER=FL+Stack /STK=163 /UG=Hs.83942 /LL=1513
/DEF=Homo sapiens cathepsin K (pycnodysostosis) (CTSK), mRNA. /PROD=cathepsin
K (pycnodysostosis) /FL=gb:NM_000396.1
gb:U13665."•0.075433961•0.099812796•cathepsin K
(pycnodysostosis)•CTSK•Hs.523594•ENSG00000143387•6508 // proteolysis and
peptidolysis // traceable author statement•5764 // lysosome // not
recorded•4216 // cathepsin K activity // traceable author statement
209823_x_at•"gb:M17955.1 /DB_XREF=gi:188178 /FEA=FLmRNA /CNT=88
/TID=Hs.73931.2 /TIER=FL /STK=0 /UG=Hs.73931 /LL=3119 /UG_GENE=HLA-DQB1
/UG_TITLE=major histocompatibility complex, class II, DQ beta 1 /DEF=Human
MHC class II HLA-DQ-beta mRNA, complete cds.
/FL=gb:M3390"•0.074002214•0.053890145•"major histocompatibility complex,
class II, DQ beta 1"•HLA-DQB1•Hs.409934••"6955 // immune response // inferred
from electronic annotation /// 6955 // immune response // non-traceable
author statement /// 19884 // antigen presentation, exogenous antigen //
inferred from electronic annotation /// 19886 // antigen processing,
exoge"•16020 // membrane // inferred from electronic annotation /// 16020 //
membrane // non-traceable author statement /// 16021 // integral to membrane
// inferred from electronic annotation•45012 // MHC class II receptor
activity // inferred from electronic annotation /// 45012 // MHC class II
receptor activity // non-traceable author statement
238852_at•gb:AA424567 /DB_XREF=gi:2103537 /DB_XREF=zv91f03.s1
/CLONE=IMAGE:767165 /FEA=EST /CNT=7 /TID=Hs.283549.0 /TIER=ConsEnd /STK=3
/UG=Hs.283549 /UG_TITLE=ESTs•0.07382592•0.062747688•Paired related homeobox
1•PRRX1•Hs.283416•ENSG00000116132•"6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 7275 // development
// inferred from electronic annotation"•5634 // nucleus // inferred from
electronic annotation•3700 // transcription factor activity // inferred from
electronic annotation /// 3713 // transcription coactivator activity //
traceable author statement
236044_at•gb:BF130943 /DB_XREF=gi:10969983 /DB_XREF=601819760F1
/CLONE=IMAGE:4051623 /FEA=EST /CNT=9 /TID=Hs.40479.0 /TIER=ConsEnd /STK=0
/UG=Hs.40479 /UG_TITLE=ESTs•0.073438667•0.065126078•phosphatidic acid
phosphatase type 2 domain containing 1•PPAPDC1•Hs.40479••••
209550_at•"gb:U35139.1 /DB_XREF=gi:1754970 /FEA=FLmRNA /CNT=122
/TID=Hs.50130.0 /TIER=FL+Stack /STK=51 /UG=Hs.50130 /LL=4692 /UG_GENE=NDN
/DEF=Human NECDIN related protein mRNA, complete cds. /PROD=NECDIN related
protein /FL=gb:U35139.1 gb:NM_002487.2"•0.073287067•0.087249588•necdin
homolog (mouse)•NDN•Hs.50130•ENSG00000182636•"74 // regulation of cell cycle
// non-traceable author statement /// 1558 // regulation of cell growth //
inferred from electronic annotation /// 6350 // transcription // inferred
from electronic annotation /// 6355 // regulation of transcription,
DNA-dep"•5634 // nucleus // inferred from electronic annotation•3677 // DNA
binding // inferred from electronic annotation
225996_at•gb:AV709727 /DB_XREF=gi:10727657 /DB_XREF=AV709727 /CLONE=ADCAZA04
/FEA=mRNA /CNT=62 /TID=Hs.21380.0 /TIER=Stack /STK=19 /UG=Hs.21380
/UG_TITLE=Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone
DKFZp586P1124)•0.072656787•0.180565831•"CDNA FLJ36725 fis, clone
UTERU2012230"••Hs.21380••••
204513_s_at•"gb:NM_014800.1 /DB_XREF=gi:7662037 /GEN=KIAA0281 /FEA=FLmRNA
/CNT=73 /TID=Hs.31463.0 /TIER=FL+Stack /STK=27 /UG=Hs.31463 /LL=9844
/DEF=Homo sapiens KIAA0281 gene product (KIAA0281), mRNA. /PROD=KIAA0281 gene
product /FL=gb:BC003051.1 gb:NM_014800.1
gb:D87"•0.071908125•0.117363161•"engulfment and cell motility 1 (ced-12
homolog, C. elegans)"•ELMO1•Hs.304578•ENSG00000155849•"6911 // phagocytosis,
```

```
engulfment // inferred from genetic interaction /// 6915 // apoptosis //
non-traceable author statement /// 6928 // cell motility // inferred from
genetic interaction /// 16601 // Rac protein signal transduction // inferred
from gene"•5737 // cytoplasm // inferred from direct assay /// 5856 //
cytoskeleton // inferred from electronic annotation /// 5886 // plasma
membrane // inferred from direct assay•17124 // SH3 domain binding //
inferred from physical interaction
201185_at•"gb:NM_002775.1 /DB_XREF=gi:4506140 /GEN=PRSS11 /FEA=FLmRNA
/CNT=347 /TID=Hs.75111.0 /TIER=FL+Stack /STK=154 /UG=Hs.75111 /LL=5654
/DEF=Homo sapiens protease, serine, 11 (IGF binding) (PRSS11), mRNA.
/PROD=protease, serine, 11 (IGF binding)
/FL=gb:D87258.1"•0.071838285•0.039448213•"protease, serine, 11 (IGF
binding)"•PRSS11•Hs.501280•ENSG00000166033•1558 // regulation of cell growth
// inferred from electronic annotation /// 6508 // proteolysis and
peptidolysis // inferred from electronic annotation•5615 // extracellular
space // traceable author statement•4295 // trypsin activity // inferred from
electronic annotation /// 5520 // insulin-like growth factor binding //
inferred from electronic annotation /// 8233 // peptidase activity //
inferred from electronic annotation
211258_s_at•"gb:AF149096.1 /DB_XREF=gi:6175597 /FEA=FLmRNA /CNT=2
/TID=Hs.170009.1 /TIER=FL /STK=0 /UG=Hs.170009 /LL=7039 /UG_GENE=TGFA
/DEF=Homo sapiens transforming growth factor-alpha variant I mRNA,
alternatively spliced product, complete cds. /PROD=transforming
g"•0.070410046•0.345628682•"transforming growth factor,
alpha"•TGFA•Hs.170009•ENSG00000163235•74 // regulation of cell cycle //
inferred from electronic annotation /// 7267 // cell-cell signaling // not
recorded /// 8283 // cell proliferation // traceable author statement•5615 //
extracellular space // not recorded /// 5625 // soluble fraction // not
recorded /// 5886 // plasma membrane // non-traceable author statement ///
5887 // integral to plasma membrane // not recorded•4713 // protein-tyrosine
kinase activity // traceable author statement /// 4871 // signal transducer
activity // traceable author statement /// 5155 // epidermal growth factor
receptor activating ligand activity // not recorded /// 5515 // protein
binding
205576_at•"gb:NM_000185.2 /DB_XREF=gi:7262380 /GEN=SERPIND1 /FEA=FLmRNA
/CNT=83 /TID=Hs.1478.0 /TIER=FL+Stack /STK=30 /UG=Hs.1478 /LL=3053 /DEF=Homo
sapiens serine (or cysteine) proteinase inhibitor, clade D (heparin
cofactor), member 1 (SERPIND1), mRNA.
/PROD=hepar"•0.06902562•0.071191392•"serine (or cysteine) proteinase
inhibitor, clade D (heparin cofactor), member
1"•SERPIND1•Hs.474270•ENSG00000099937•6935 // chemotaxis // inferred from
electronic annotation /// 7596 // blood coagulation // inferred from
electronic annotation /// 7600 // sensory perception // inferred from
electronic annotation•5576 // extracellular region // non-traceable author
statement•4867 // serine-type endopeptidase inhibitor activity // inferred
from electronic annotation /// 8201 // heparin binding // inferred from
electronic annotation
205991_s_at•"gb:NM_006902.2 /DB_XREF=gi:12707578 /GEN=PMX1 /FEA=FLmRNA
/CNT=27 /TID=Hs.155606.0 /TIER=FL /STK=0 /UG=Hs.155606 /LL=5396 /DEF=Homo
sapiens paired mesoderm homeo box 1 (PMX1), transcript variant pmx-1a, mRNA.
/PROD=paired mesoderm homeobox 1, isoform
pmx-"•0.068980332•0.041073178•paired related homeobox
1•PRRX1•Hs.283416•ENSG00000116132•"6355 // regulation of transcription,
DNA-dependent // inferred from electronic annotation /// 7275 // development
// inferred from electronic annotation"•5634 // nucleus // inferred from
electronic annotation•3700 // transcription factor activity // inferred from
electronic annotation /// 3713 // transcription coactivator activity //
traceable author statement
206115_at•"gb:NM_004430.1 /DB_XREF=gi:4758251 /GEN=EGR3 /FEA=FLmRNA /CNT=33
/TID=Hs.74088.0 /TIER=FL+Stack /STK=20 /UG=Hs.74088 /LL=1960 /DEF=Homo
sapiens early growth response 3 (EGR3), mRNA. /PROD=early growth response 3
/FL=gb:NM_004430.1"•0.06857129•0.115488468•early growth response
3•EGR3•Hs.534313•ENSG00000179388•"6350 // transcription // inferred from
electronic annotation /// 6355 // regulation of transcription, DNA-dependent
// inferred from electronic annotation /// 7517 // muscle development //
traceable author statement /// 7623 // circadian rhythm // traceab"•5634 //
nucleus // inferred from electronic annotation•3700 // transcription factor
activity // traceable author statement /// 8270 // zinc ion binding //
inferred from electronic annotation
225619_at•gb:AV730849 /DB_XREF=gi:10840270 /DB_XREF=AV730849 /CLONE=HTFAHH11
/FEA=EST /CNT=70 /TID=Hs.173438.2 /TIER=Stack /STK=9 /UG=Hs.173438 /LL=55179
/UG_GENE=FLJ10582 /UG_TITLE=hypothetical protein
FLJ10582•0.068549648•0.082131058•hypothetical protein
FLJ30046•FLJ30046•Hs.349955•ENSG00000139737•••
230746_s_at•gb:AW003173 /DB_XREF=gi:5850089 /DB_XREF=wq63e07.x1
/CLONE=IMAGE:2475972 /FEA=EST /CNT=17 /TID=Hs.25590.1 /TIER=Stack /STK=17
/UG=Hs.25590 /LL=6781 /UG_GENE=STC1 /UG_TITLE=stanniocalcin
1•0.06450052•0.228403612•Stanniocalcin 1•STC1•Hs.25590•ENSG00000159167•6874
// calcium ion homeostasis // traceable author statement /// 7166 // cell
surface receptor linked signal transduction // traceable author statement ///
7267 // cell-cell signaling // traceable author statement /// 7584 //
```

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response to nutrients // tra•5576 // extracellular region // inferred from
electronic annotation•5179 // hormone activity // traceable author statement
226415_at•gb:AA156723 /DB_XREF=gi:1728337 /DB_XREF=zl18c02.s1
/CLONE=IMAGE:502274 /FEA=mRNA /CNT=54 /TID=Hs.22975.0 /TIER=Stack /STK=19
/UG=Hs.22975 /LL=57687 /UG_GENE=KIAA1576 /UG_TITLE=KIAA1576
protein•0.062264316•0.07620782•KIAA1576
protein•KIAA1576•Hs.461405•ENSG00000171724•••8270 // zinc ion binding //
inferred from electronic annotation /// 16491 // oxidoreductase activity //
inferred from electronic annotation
206569_at•"gb:NM_006850.1 /DB_XREF=gi:5803085 /GEN=ST16 /FEA=FLmRNA /CNT=12
/TID=Hs.315463.0 /TIER=FL /STK=2 /UG=Hs.315463 /LL=11009 /DEF=Homo sapiens
suppression of tumorigenicity 16 (melanoma differentiation) (ST16), mRNA.
/PROD=suppression of tumorigenicity 16 (m"•0.059773452•0.06970569•interleukin
24•IL24•Hs.411311•ENSG00000162892•6915 // apoptosis // traceable author
statement /// 6955 // immune response // inferred from electronic
annotation•5576 // extracellular region // inferred from electronic
annotation•5125 // cytokine activity // inferred from electronic annotation
209765_at•gb:Y13786.2 /DB_XREF=gi:12053590 /FEA=FLmRNA /CNT=58
/TID=Hs.278679.1 /TIER=Stack /STK=24 /UG=Hs.278679 /LL=8728 /UG_GENE=ADAM19
/DEF=Homo sapiens mRNA for meltrin-betaADAM 19 homologue.
/PROD=meltrin-betaADAM 19 homologue
/FL=gb:AF311317.1•0.056639445•0.094997402•a disintegrin and metalloproteinase
domain 19 (meltrin beta)•ADAM19•Hs.483944•ENSG00000135074•6508 // proteolysis
and peptidolysis // inferred from electronic annotation•16021 // integral to
membrane // inferred from electronic annotation•4222 // metalloendopeptidase
activity // inferred from electronic annotation /// 8270 // zinc ion binding
// inferred from electronic annotation
214451_at•"gb:NM_003221.1 /DB_XREF=gi:4507442 /GEN=TFAP2B /FEA=FLmRNA /CNT=25
/TID=Hs.33102.0 /TIER=FL /STK=0 /UG=Hs.33102 /LL=7021 /DEF=Homo sapiens
transcription factor AP-2 beta (activating enhancer-binding protein 2 beta)
(TFAP2B), mRNA. /PROD=transcription
fact"•0.055867128•0.06089434•transcription factor AP-2 beta (activating
enhancer binding protein 2 beta)•TFAP2B•Hs.33102•ENSG00000008196•6350 //
transcription // inferred from electronic annotation /// 6357 // regulation
of transcription from RNA polymerase II promoter // traceable author
statement /// 7399 // neurogenesis // traceable author statement•5634 //
nucleus // inferred from electronic annotation•3700 // transcription factor
activity // non-traceable author statement /// 3713 // transcription
coactivator activity // traceable author statement
241399_at•gb:AI142028 /DB_XREF=gi:3649485 /DB_XREF=oo21g02.x1
/CLONE=IMAGE:1566866 /FEA=EST /CNT=7 /TID=Hs.143399.0 /TIER=ConsEnd /STK=4
/UG=Hs.143399 /UG_TITLE=ESTs•0.054322261•0.093902186•"family with sequence
similarity 19 (chemokine (C-C motif)-like), member
A2"•FAM19A2•Hs.269745•ENSG00000198673•••
206163_at•"gb:NM_005584.1 /DB_XREF=gi:5031896 /GEN=MAB21L1 /FEA=FLmRNA
/CNT=27 /TID=Hs.239506.0 /TIER=FL /STK=0 /UG=Hs.239506 /LL=4081 /DEF=Homo
sapiens mab-21 (C. elegans)-like 1 (MAB21L1), mRNA. /PROD=mab-21 (C.
elegans)-like 1 /FL=gb:U38810.1
gb:NM_005584.1"•0.054052943•0.071607292•mab-21-like 1 (C.
elegans)•MAB21L1•Hs.532575•ENSG00000180660•9653 // morphogenesis // traceable
author statement••
204288_s_at•"gb:NM_021069.1 /DB_XREF=gi:10947117 /GEN=ARGBP2 /FEA=FLmRNA
/CNT=71 /TID=Hs.278626.0 /TIER=FL+Stack /STK=33 /UG=Hs.278626 /LL=8470
/DEF=Homo sapiens ArgAbl-interacting protein ArgBP2 (ARGBP2), transcript
variant 2, mRNA. /PROD=ArgAbl-interacting protein
2"•0.053929572•0.098492168•Arg/Abl-interacting protein
ArgBP2•ARGBP2•Hs.481342•ENSG00000154556••5634 // nucleus // inferred from
electronic annotation /// 5634 // nucleus // non-traceable author statement
/// 5634 // nucleus // traceable author statement /// 5856 // cytoskeleton //
inferred from electronic annotation /// 15629 // actin cytoskeleton •3676 //
nucleic acid binding // inferred from electronic annotation /// 5200 //
structural constituent of cytoskeleton // traceable author statement /// 5515
// protein binding // non-traceable author statement /// 8093 // cytoskeletal
adaptor activity //
223975_at•"gb:BC005014.1 /DB_XREF=gi:13477118 /FEA=FLmRNA /CNT=3
/TID=Hs.326734.0 /TIER=FL /STK=0 /UG=Hs.326734 /DEF=Homo sapiens, Similar to
ring finger protein 18, clone MGC:10977, mRNA, complete cds. /PROD=Similar to
ring finger protein 18 /FL=gb:BC005014.1"•0.053363868•0.049276935•tripartite
motif-containing 51•TRIM51•Hs.326734•ENSG00000124900•••
219895_at•"gb:NM_017938.1 /DB_XREF=gi:8923642 /GEN=FLJ20716 /FEA=FLmRNA
/CNT=17 /TID=Hs.144517.0 /TIER=FL+Stack /STK=9 /UG=Hs.144517 /LL=55026
/DEF=Homo sapiens hypothetical protein FLJ20716 (FLJ20716), mRNA.
/PROD=hypothetical protein FLJ20716
/FL=gb:NM_017938.1"•0.052413734•0.183582594•hypothetical protein
FLJ20716•FLJ20716•Hs.437563•ENSG00000125355•••
212998_x_at•"gb:AI583173 /DB_XREF=gi:4569070 /DB_XREF=tq64e04.x1
/CLONE=IMAGE:2213598 /FEA=EST /CNT=76 /TID=Hs.73931.3 /TIER=Stack /STK=32
/UG=Hs.73931 /LL=3119 /UG_GENE=HLA-DQB1 /UG_TITLE=major histocompatibility
complex, class II, DQ beta 1"•0.051703705•0.054883427•"major
histocompatibility complex, class II, DQ beta 1 /// major histocompatibility
complex, class II, DQ beta 1"•HLA-DQB1•Hs.409934••"6955 // immune response //
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inferred from electronic annotation /// 6955 // immune response //
non-traceable author statement /// 19884 // antigen presentation, exogenous
antigen // inferred from electronic annotation /// 19886 // antigen
processing, exoge"•16020 // membrane // inferred from electronic annotation
/// 16020 // membrane // non-traceable author statement /// 16021 // integral
to membrane // inferred from electronic annotation•45012 // MHC class II
receptor activity // inferred from electronic annotation /// 45012 // MHC
class II receptor activity // non-traceable author statement
235400_at•"gb:AL560266 /DB_XREF=gi:12906564 /DB_XREF=AL560266
/CLONE=CS0DG007YG20 (5 prime) /FEA=EST /CNT=29 /TID=Hs.266331.0 /TIER=ConsEnd
/STK=0 /UG=Hs.266331 /UG_TITLE=ESTs, Weakly similar to A39878 Fc gamma
(H.sapiens)"•0.051478987•0.063396799•Fc receptor homolog expressed in B
cells•FREB•Hs.266331•ENSG00000132185•••4872 // receptor activity // inferred
from electronic annotation
226498_at•"gb:AA149648 /DB_XREF=gi:1720449 /DB_XREF=zl39e08.s1
/CLONE=IMAGE:504326 /FEA=mRNA /CNT=78 /TID=Hs.22968.0 /TIER=Stack /STK=25
/UG=Hs.22968 /UG_TITLE=Homo sapiens clone IMAGE:451939, mRNA
sequence"•0.050457437•0.073344291•Fms-related tyrosine kinase 1 (vascular
endothelial growth factor/vascular permeability factor
receptor)•FLT1•Hs.507621•ENSG00000102755•1525 // angiogenesis // inferred
from electronic annotation /// 6468 // protein amino acid phosphorylation //
inferred from electronic annotation /// 7169 // transmembrane receptor
protein tyrosine kinase signaling pathway // traceable author statement
//•5615 // extracellular space // traceable author statement /// 5887 //
integral to plasma membrane // traceable author statement /// 16020 //
membrane // inferred from electronic annotation•4872 // receptor activity //
traceable author statement /// 5021 // vascular endothelial growth factor
receptor activity // traceable author statement /// 5524 // ATP binding //
inferred from electronic annotation /// 16740 // transferase activity //
infe
216598_s_at•"gb:S69738.1 /DB_XREF=gi:545464 /GEN=MCP-1 /FEA=mRNA /CNT=1
/TID=Hs.303649.1 /TIER=ConsEnd /STK=0 /UG=Hs.303649 /LL=6347
/DEF=MCP-1=monocyte chemotactic protein (human, aortic endothelial cells,
mRNA, 661 nt). /PROD=MCP-1"•0.050357144•0.010537452•chemokine (C-C motif)
ligand 2•CCL2•Hs.303649•ENSG00000108691•6468 // protein amino acid
phosphorylation // traceable author statement /// 6874 // calcium ion
homeostasis // traceable author statement /// 6916 // anti-apoptosis //
inferred from direct assay /// 6935 // chemotaxis // traceable author
statement /// 69•5615 // extracellular space // traceable author statement
/// 16020 // membrane // inferred from electronic annotation•4672 // protein
kinase activity // traceable author statement /// 8009 // chemokine activity
// traceable author statement
206897_at•"gb:NM_003785.2 /DB_XREF=gi:9558760 /GEN=GAGEB1 /FEA=FLmRNA /CNT=11
/TID=Hs.128231.0 /TIER=FL /STK=0 /UG=Hs.128231 /LL=8712 /DEF=Homo sapiens G
antigen, family B, 1 (prostate associated) (GAGEB1), mRNA. /PROD=G antigen B1
/FL=gb:BC004861.1 gb:NM_003785.2 g"•0.050148587•0.052580123•"P antigen
family, member 1 (prostate associated)"•PAGE1•Hs.128231•ENSG00000068985•6968
// cellular defense response // traceable author statement••
202376_at•"gb:NM_001085.2 /DB_XREF=gi:9665246 /GEN=SERPINA3 /FEA=FLmRNA
/CNT=230 /TID=Hs.234726.0 /TIER=FL+Stack /STK=128 /UG=Hs.234726 /LL=12
/DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1
antiproteinase, antitrypsin), member 3
(SERPI"•0.047946601•0.038105515•"serine (or cysteine) proteinase inhibitor,
clade A (alpha-1 antiproteinase, antitrypsin), member
3"•SERPINA3•Hs.534293•ENSG00000196136•6953 // acute-phase response //
inferred from electronic annotation /// 6954 // inflammatory response //
non-traceable author statement /// 19216 // regulation of lipid metabolism //
non-traceable author statement•5576 // extracellular region // non-traceable
author statement /// 5622 // intracellular // non-traceable author
statement•3677 // DNA binding // Unknown /// 4867 // serine-type
endopeptidase inhibitor activity // inferred from electronic annotation ///
5515 // protein binding // inferred from physical interaction /// 30569 //
chymotrypsin inhibitor activity // non-traceable
206953_s_at•"gb:NM_012302.1 /DB_XREF=gi:6912463 /GEN=KIAA0786 /FEA=FLmRNA
/CNT=8 /TID=Hs.24212.0 /TIER=FL /STK=0 /UG=Hs.24212 /LL=23266 /DEF=Homo
sapiens latrophilin (KIAA0786), mRNA. /PROD=latrophilin /FL=gb:NM_012302.1
gb:AF104939.1"•0.047748569•0.142770243•latrophilin
2•LPHN2•Hs.24212•ENSG00000117114•7165 // signal transduction // inferred from
electronic annotation /// 7218 // neuropeptide signaling pathway // inferred
from electronic annotation•16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from electronic
annotation /// 16021 // integral to membrane // non-traceable author
statement•4872 // receptor activity // inferred from electronic annotation
/// 4930 // G-protein coupled receptor activity // inferred from electronic
annotation /// 5529 // sugar binding // inferred from electronic annotation
/// 16524 // latrotoxin receptor activ
1559258_a_at•"gb:AK026566.1 /DB_XREF=gi:10439448 /TID=Hs2.97892.1 /CNT=6
/FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.97892 /UG_TITLE=Homo sapiens cDNA:
FLJ22913 fis, clone KAT06142. /DEF=Homo sapiens cDNA: FLJ22913 fis, clone
KAT06142."•0.040963869•0.035241604•Hypothetical
LOC203413•LOC203413•Hs.97892••••
```

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227145_at•"gb:AW190565 /DB_XREF=gi:6465045 /DB_XREF=xl40b02.x1
/CLONE=IMAGE:2677131 /FEA=mRNA /CNT=39 /TID=Hs.306814.0 /TIER=Stack /STK=15
/UG=Hs.306814 /UG_TITLE=Homo sapiens cDNA: FLJ21889 fis, clone
HEP03178"•0.036785313•0.07990465•lysyl oxidase-like
4•LOXL4•Hs.306814•ENSG00000138131••16020 // membrane // inferred from
electronic annotation•4720 // protein-lysine 6-oxidase activity // inferred
from electronic annotation /// 5044 // scavenger receptor activity //
inferred from electronic annotation /// 5507 // copper ion binding //
inferred from electronic annotation /// 16491 // oxidoreducta
205681_at•"gb:NM_004049.1 /DB_XREF=gi:4757839 /GEN=BCL2A1 /FEA=FLmRNA /CNT=32
/TID=Hs.227817.0 /TIER=FL+Stack /STK=11 /UG=Hs.227817 /LL=597 /DEF=Homo
sapiens BCL2-related protein A1 (BCL2A1), mRNA. /PROD=BCL2-related protein A1
/FL=gb:U27467.1 gb:U29680.1 gb:NM_0040"•0.036706698•0.04872355•BCL2-related
protein A1•BCL2A1•Hs.227817•ENSG00000140379•6916 // anti-apoptosis //
traceable author statement /// 42981 // regulation of apoptosis // inferred
from electronic annotation•5622 // intracellular // non-traceable author
statement•
225728_at•gb:AI659533 /DB_XREF=gi:4763103 /DB_XREF=tu12a12.x1
/CLONE=IMAGE:2250814 /FEA=EST /CNT=103 /TID=Hs.278626.2 /TIER=Stack /STK=28
/UG=Hs.278626 /LL=8470 /UG_GENE=ARGBP2 /UG_TITLE=ArgAbl-interacting protein
ArgBP2•0.036157846•0.043453452•importin 9•IPO9•Hs.497384•ENSG00000198700•"59
// protein-nucleus import, docking // inferred from electronic annotation ///
15031 // protein transport // inferred from electronic annotation"•5634 //
nucleus // inferred from electronic annotation /// 5643 // nuclear pore //
inferred from electronic annotation /// 5737 // cytoplasm // inferred from
electronic annotation•5488 // binding // inferred from electronic annotation
/// 8565 // protein transporter activity // inferred from electronic
annotation
231265_at•"gb:AI126453 /DB_XREF=gi:3594967 /DB_XREF=qd78d05.x1
/CLONE=IMAGE:1735593 /FEA=EST /CNT=22 /TID=Hs.98701.0 /TIER=Stack /STK=19
/UG=Hs.98701 /UG_TITLE=ESTs, Weakly similar to OSHU7B cytochrome-c oxidase
(H.sapiens)"•0.034417965•0.105513294•cytochrome c oxidase subunit
VIIb2•COX7B2•Hs.479656•ENSG00000170516•6118 // electron transport // inferred
from electronic annotation•5739 // mitochondrion // inferred from electronic
annotation /// 5746 // mitochondrial electron transport chain // inferred
from electronic annotation /// 16021 // integral to membrane // inferred from
electronic annotation /// 19866 // inner membrane // •4129 // cytochrome-c
oxidase activity // inferred from electronic annotation /// 16491 //
oxidoreductase activity // inferred from electronic annotation
205015_s_at•"gb:M31172.1 /DB_XREF=gi:339537 /GEN=TGFA /FEA=FLmRNA /CNT=49
/TID=Hs.170009.0 /TIER=FL /STK=0 /UG=Hs.170009 /LL=7039
/UG_TITLE=transforming growth factor, alpha /DEF=Human transforming growth
factor-alpha mRNA, complete cds. /FL=gb:NM_003236.1
gb:K03222.1"•0.034267853•0.038435149•"transforming growth factor,
alpha"•TGFA•Hs.170009•ENSG00000163235•74 // regulation of cell cycle //
inferred from electronic annotation /// 7267 // cell-cell signaling // not
recorded /// 8283 // cell proliferation // traceable author statement•5615 //
extracellular space // not recorded /// 5625 // soluble fraction // not
recorded /// 5886 // plasma membrane // non-traceable author statement ///
5887 // integral to plasma membrane // not recorded•4713 // protein-tyrosine
kinase activity // traceable author statement /// 4871 // signal transducer
activity // traceable author statement /// 5155 // epidermal growth factor
receptor activating ligand activity // not recorded /// 5515 // protein
binding
212671_s_at•"gb:BG397856 /DB_XREF=gi:13291304 /DB_XREF=602438950F1
/CLONE=IMAGE:4564956 /FEA=mRNA /CNT=167 /TID=Hs.198253.2 /TIER=Stack /STK=59
/UG=Hs.198253 /LL=3117 /UG_GENE=HLA-DQA1 /UG_TITLE=major histocompatibility
complex, class II, DQ alpha 1"•0.031542141•0.006992358•"major
histocompatibility complex, class II, DQ alpha 1 /// major histocompatibility
complex, class II, DQ alpha 2"•HLA-DQA1 ///
HLA-DQA2•Hs.550475•ENSG00000196735 /// ENSG00000166623•"6955 // immune
response // inferred from electronic annotation /// 19884 // antigen
presentation, exogenous antigen // inferred from electronic annotation ///
19886 // antigen processing, exogenous antigen via MHC class II // inferred
from electronic anno"•16020 // membrane // inferred from electronic
annotation /// 16021 // integral to membrane // inferred from electronic
annotation /// 5887 // integral to plasma membrane // non-traceable author
statement•45012 // MHC class II receptor activity // inferred from electronic
annotation /// 45012 // MHC class II receptor activity // traceable author
statement /// 45012 // MHC class II receptor activity // non-traceable author
statement
219263_at•"gb:NM_024539.1 /DB_XREF=gi:13375696 /GEN=FLJ23516 /FEA=FLmRNA
/CNT=88 /TID=Hs.9238.0 /TIER=FL /STK=0 /UG=Hs.9238 /LL=79589 /DEF=Homo
sapiens hypothetical protein FLJ23516 (FLJ23516), mRNA. /PROD=hypothetical
protein FLJ23516 /FL=gb:NM_024539.1"•0.02590177•0.027373242•ring finger
protein 128•RNF128•Hs.496542•ENSG00000133135•6508 // proteolysis and
peptidolysis // inferred from electronic annotation /// 6915 // apoptosis //
inferred from electronic annotation /// 16567 // protein ubiquitination //
inferred from electronic annotation•151 // ubiquitin ligase complex //
inferred from electronic annotation /// 16021 // integral to membrane //
inferred from electronic annotation•4842 // ubiquitin-protein ligase activity
```

```
// inferred from electronic annotation /// 8233 // peptidase activity //
inferred from electronic annotation /// 8270 // zinc ion binding // inferred
from electronic annotation
229352_at•gb:AA885360 /DB_XREF=gi:2994437 /DB_XREF=al45h12.s1
/CLONE=IMAGE:1460327 /FEA=EST /CNT=31 /TID=Hs.236676.0 /TIER=Stack /STK=21
/UG=Hs.236676 /UG_TITLE=ESTs•0.025546236•0.037112446•sperm equatorial segment
protein 1•SPESP1••ENSG00000175374•••
203708_at•"gb:NM_002600.1 /DB_XREF=gi:4505662 /GEN=PDE4B /FEA=FLmRNA /CNT=100
/TID=Hs.188.0 /TIER=FL /STK=2 /UG=Hs.188 /LL=5142 /DEF=Homo sapiens
phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog
phosphodiesterase E4) (PDE4B), mRNA.
/PROD=phosphodieste"•0.024942238•0.059199279•"phosphodiesterase 4B,
cAMP-specific (phosphodiesterase E4 dunce homolog,
Drosophila)"•PDE4B•Hs.198072•ENSG00000184588•7165 // signal transduction //
inferred from electronic annotation•5625 // soluble fraction // traceable
author statement /// 5626 // insoluble fraction // traceable author
statement•4115 // cAMP-specific phosphodiesterase activity // traceable
author statement /// 16787 // hydrolase activity // inferred from electronic
annotation
206552_s_at•"gb:NM_003182.1 /DB_XREF=gi:4507340 /GEN=TAC1 /FEA=FLmRNA /CNT=13
/TID=Hs.2563.2 /TIER=FL /STK=6 /UG=Hs.2563 /LL=6863 /DEF=Homo sapiens
tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin
2, neuromedin L, neurokinin alpha,
neuropept"•0.022413749•0.014922364•"tachykinin, precursor 1 (substance K,
substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha,
neuropeptide K, neuropeptide gamma)"•TAC1•Hs.2563•ENSG00000006128•7217 //
tachykinin signaling pathway // inferred from electronic annotation /// 7218
// neuropeptide signaling pathway // inferred from electronic annotation ///
7267 // cell-cell signaling // traceable author statement /// 7268 //
synaptic transmission /•5615 // extracellular space // traceable author
statement•5102 // receptor binding // traceable author statement /// 5184 //
neuropeptide hormone activity // not recorded
```

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Supplementary Methods

Quantitative RT-PCR probes and oligonucleotides

TaqMan® probes (Applied Biosystems) were used to detect mRNA levels of *PEDF* (Hs00171467_m1), *IL8* (Hs00174103_m1) and *GAPDH* (Hs99999905_m1).

Universal Probe Library (UPL) (Roche, Basel, Switzerland) probes and oligonucleotides used to detect mRNA levels of *COL4A2*, *FGF13*, *FN1*, *GAPDH*, *IL8*, *JAG1*, *LGALS3*, *MIA*, *MLPH*, *RAB27A*, *S100B* and *TGFA* are listed in Supplementary Table 1.

Supplementary Table 1. List of probes and oligonucleotides for quantitative RT-PCR

Gene	UPL probe	Forward oligonucleotide 5’-3’	Reverse oligonucleotide 5’-3’
COL4A2	#81	gggatatttggcctgaaagg	caggaagagcagcagaacct
FGF13	#56	ccattgatggcaccaaagat	ccacagggatgaggttaaaca
FN1	#15	ctttggtgcagcacaacttc	cctcctcgagtctgaaccaa
GAPDH	#60	agccacatcgctcagacac	gcccaatacgaccaaatcc
IGFBP3	#4	agaagggattttataagaaaaagcagt	cttatccacacaccagcagaag
IL8	#72	agacagcagagcacacaagc	cacagtgagatggttccttcc
JAG1	#42	gaatggcaacaaaacttgcat	agccttgtcggcaaatagc
LGALS3	#59	cttctggacagccaagtgc	aaaggcaggttataaggcacaa
MIA	#16	gggccaagtggtgtatgtct	cagatctccatagtaatctccctga
MLPH	#67	cacagttgtgcctcccttg	ggcctcctcctctacatcg
RAB27A	#51	aggccagagaatccacctg	cgctgtcgttaagctacgaa
S100B	#78	ggaaggggtgagacaagga	ggtggaaaacgtcgatgag
TGFA	#63	tgctgccactcagaaacagt	atctgccacagtccacctg