# **GENEMANIA**

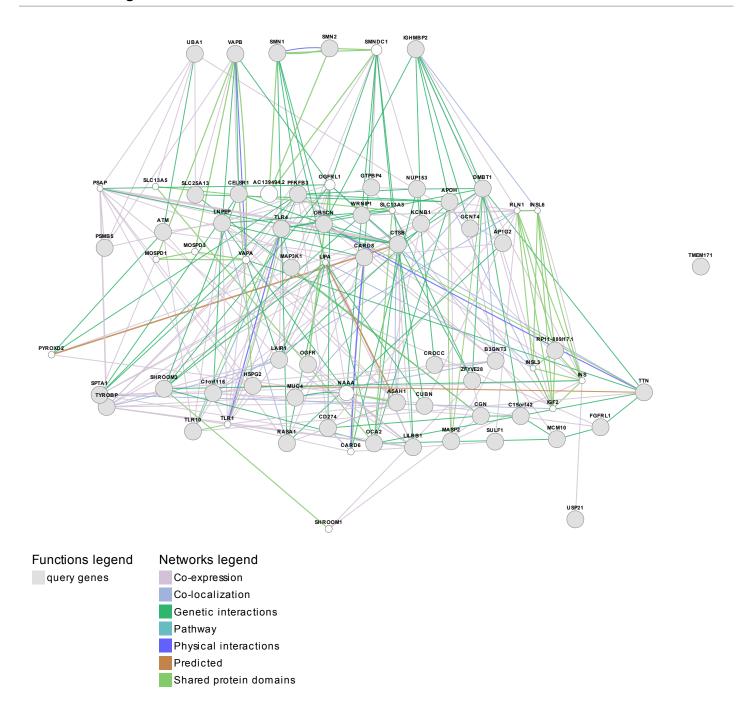
Created on: 14 March 2012 07:30:07

Last database update: 21 December 2011 19:00:00

Application version: 3.0.7

## Report of GeneMANIA search

## Network image



www.genemania.org/print 1/23

### Search parameters

Organism: H. sapiens (human)

Genes: SLC25A13; MASP2; TYROBP; CROCC; OGFR; MCM10; CELSR1; APOH; MAP3K1; PSMB5; OCA2; ASAH1; LILRB1; CARD8; CUBN; GTPBP4; LNPEP; CD274; VAPB; WRNIP1; NUP153; FGFRL1; INS-IGF2; UBA1; IGHMBP2; TLR4; SULF1; SHROOM3; C15orf42; HSPG2; USP21; CGN; MUC4; RASA1; ATM; OBSCN; TTN; TMEM171; KCNB1; ZFYVE28; SPTA1; CTSB; LAIR1; PFKFB3; SMN1; TLR10; GCNT4; B3GNT3; C1orf116; DMBT1; SMN2; AP1G2

#### Networks:

#### Co-expression:

Ariis-Rutaeerts-2009 Berchtold-Cotman-2008 Bild-Nevins-2006 B Burczynski-Dorner-2006 Burington-Shaughnessy-2008 Chen-Brown-2002 Gobble-Singer-2011 Hummel-Siebert-2006 Jones-Libermann-2005 Kang-Willman-2010 Nakayama-Hasegawa-2007 Noble-Diehl-2008 Peng-Katze-2009 Perou-Botstein-1999 Radtke-Downing-2009 Ramaswamy-Golub-2001 Rieger-Chu-2004 Toedter-Baribaud-2011 Wang-Maris-2006 Wu-Garvey-2007

#### Co-localization:

Johnson-Shoemaker-2003 Schadt-Shoemaker-2004

#### Genetic interactions:

BIOGRID-SMALL-SCALE-STUDIES IREF-SMALL-SCALE-STUDIES Lin-Smith-2010

#### Pathway:

PATHWAYCOMMONS-CELL\_MAP PATHWAYCOMMONS-HUMANCYC PATHWAYCOMMONS-IMID PATHWAYCOMMONS-NCI NATURE PATHWAYCOMMONS-REACTOME Wu-Stein-2010

#### Physical interactions:

Albers-Koegl-2005 Arbuckle-Grant-2010 **BIOGRID-SMALL-SCALE-STUDIES** Bandyopadhyay-Ideker-2010 Behrends-Harper-2010 Barr-Knapp-2009 Barrios-Rodiles-Wrana-2005 Behzadnia-Lührmann-2007 Cannavo-Jiricny-2007 Benzinger-Hermeking-2005 Bouwmeester-Superti-Furga-2004 Camargo-Brandon-2007 Ewing-Figeys-2007 A Ewing-Figeys-2007 B Fenner-Prehn-2010 Colland-Gauthier-2004 Glatter-Gstaiger-2009 Goehler-Wanker-2004 Goudreault-Gingras-2009 Hutchins-Peters-2010 **IREF-BIND IREF-BIND-TRANSLATION** IREF-CORUM **IREF-DIP IREF-GRID IREF-HPRD IREF-INTACT IREF-MINT** IREF-MPPI **IREF-OPHID IREF-SMALL-SCALE-STUDIES** Jeronimo-Coulombe-2007 Jin-Pawson-2004 Lehner-Sanderson-2004 B Jones-MacBeath-2006 Kneissl-Grummt-2003 Lehner-Sanderson-2004 A Meek-Piwnica-Worms-2004 Lim-Zoghbi-2006 Markson-Sanderson-2009 McFarland-Nussbaum-2008 Miyamoto-Sato-Yanagawa-2010 Nakayama-Ohara-2002 Newman-Keating-2003 Ramachandran-LaBaer-2004 Ravasi-Havashizaki-2010 Rual-Vidal-2005 A Rual-Vidal-2005 B Sato-Conaway-2004 Sowa-Harper-2009 A Sowa-Harper-2009 B Stelzl-Wanker-2005 A Stelzl-Wanker-2005 B Svendsen-Harper-2009 Thalappilly-Dusetti-2008 Venkatesan-Vidal-2009 Wang-He-2008 Weinmann-Meister-2009 Wu-Li-2007 de Hoog-Mann-2004 van Wijk-Timmers-2009

#### Predicted:

I2D-BIND-Fly2Human I2D-BIND-Mouse2Human I2D-BIND-Rat2Human I2D-BIND-Worm2Human I2D-BIND-Yeast2Human I2D-BioGRID-Fly2Human I2D-BioGRID-Mouse2Human I2D-BioGRID-Rat2Human I2D-BioGRID-Worm2Human I2D-BioGRID-Yeast2Human I2D-Chen-Pawson-2009-PiwiScreen-Mouse2Human I2D-Formstecher-Daviet-2005-Embryo-Fly2Human I2D-Formstecher-Daviet-2005-Head-Fly2Human I2D-Giot-Rothbert-2003-High-Fly2Human I2D-Giot-Rothbert-2003-Low-Fly2Human I2D-INNATEDB-Mouse2Human I2D-IntAct-Fly2Human I2D-IntAct-Mouse2Human I2D-IntAct-Rat2Human I2D-IntAct-Worm2Human I2D-IntAct-Yeast2Human I2D-Krogan-Greenblatt-2006-Core-Yeast2Human I2D-Krogan-Greenblatt-2006-NonCore-Yeast2Human I2D-Li-Vidal-2004-CE-DATA-Worm2Human I2D-Li-Vidal-2004-CORE-1-Worm2Human I2D-Li-Vidal-2004-CORE-2-Worm2Human I2D-Li-Vidal-2004-interolog-Worm2Human I2D-Li-Vidal-2004-literature-Worm2Human I2D-Li-Vidal-2004-non-core-Worm2Human I2D-MGI-Mouse2Human I2D-MINT-Fly2Human I2D-MINT-Worm2Human I2D-MINT-Mouse2Human I2D-MINT-Rat2Human I2D-MINT-Yeast2Human I2D-MIPS-Yeast2Human I2D-ManualHuman I2D-ManualHuman I2D-Ptacek-Snyder-2005-Yeast2Human I2D-Stanyon-Finley-2004-CellCycle-Fly2Human I2D-Tarassov-PCA-Yeast2Human I2D-Tewari-Vidal-2004-TGFb-Worm2Human I2D-Wang-Orkin-2006-EScmplx-Mouse2Human I2D-Wang-Orkin-2006-EScmplxIP-Mouse2Human I2D-Wang-Orkin-2006-EScmplxlow-Mouse2Human I2D-Yu-Vidal-2008-GoldStd-Yeast2Human I2D-vonMering-Bork-2002-High-Yeast2Human I2D-vonMering-Bork-2002-Low-Yeast2Human I2D-vonMering-Bork-2002-Medium-Yeast2Human Stuart-Kim-2003

#### Shared protein domains:

www.genemania.org/print 2/23

#### INTERPRO PFAM

Network weighting: Automatically selected weighting method (Assigned based on query genes)

Number of gene results: 20

www.genemania.org/print 3/23

#### **Networks**

Co-expression 72.56 %

Arijs-Rutgeerts-2009 15.81 %

Mucosal gene expression of antimicrobial peptides in inflammatory bowel disease before and after first infliximab treatment. Arijs et al. (2009). *PLoS One*.

Source: Pearson correlation with 556,213 interactions from GEO

Tags: immune system

Hummel-Siebert-2006 12.26 %

A biologic definition of Burkitt's lymphoma from transcriptional and genomic profiling. Hummel et al. (2006). N Engl J Med.

Source: Pearson correlation with 457,753 interactions from GEO

Tags: cancer

Wu-Garvey-2007 10.78 %

The effect of insulin on expression of genes and biochemical pathways in human skeletal muscle. Wu et al. (2007). Endocrine.

Source: Pearson correlation with 218,210 interactions from GEO

Tags: transcription factors; muscle; cultured cells

#### Burczynski-Dorner-2006

10.54 %

Molecular classification of Crohn's disease and ulcerative colitis patients using transcriptional profiles in peripheral blood mononuclear cells. Burczynski et al. (2006). *J Mol Diagn*.

Source: Pearson correlation with 409,243 interactions from GEO

Rieger-Chu-2004 8.03 %

<u>Toxicity from radiation therapy associated with abnormal transcriptional responses to DNA damage.</u> Rieger et al. (2004). *Proc Natl Acad Sci U S A*.

Source: Pearson correlation with 215,835 interactions from GEO

Tags: cultured cells; cell line

Noble-Diehl-2008 5.49 %

Regional variation in gene expression in the healthy colon is dysregulated in ulcerative colitis. Noble et al. (2008). Gut.

Source: Pearson correlation with 590,459 interactions from GEO

Bild-Nevins-2006 B 4.88 %

Oncogenic pathway signatures in human cancers as a guide to targeted therapies. Bild et al. (2006). Nature.

Note: One of 3 datasets produced from this publication.

Source: Pearson correlation with 248,305 interactions from GEO

Tags: cultured cells; signal transduction; cancer; epithelial cells; cell line; disease; breast; transcription factors; breast cancer

Kang-Willman-2010 2.32 %

Gene expression classifiers for relapse-free survival and minimal residual disease improve risk classification and outcome prediction in pediatric B-precursor acute lymphoblastic leukemia. Kang et al. (2010). *Blood*.

Source: Pearson correlation with 533,406 interactions from GEO

Tags: transcription factors; lymphoma; cancer

#### Nakayama-Hasegawa-2007

1.10 %

Gene expression analysis of soft tissue sarcomas: characterization and reclassification of malignant fibrous

www.genemania.org/print 4/23

histiocytoma. Nakayama et al. (2007). Mod Pathol.

Source: Pearson correlation with 352,017 interactions from GEO

Tags: transcription factors; cancer

Radtke-Downing-2009 1.04 %

Genomic analysis reveals few genetic alterations in pediatric acute myeloid leukemia. Radtke et al. (2009). Proc Natl Acad Sci U S A.

Source: Pearson correlation with 368,256 interactions from GEO

Tags: transcription factors; nervous system; cancer

Gobble-Singer-2011 0.33 %

Expression profiling of liposarcoma yields a multigene predictor of patient outcome and identifies genes that contribute to liposarcomagenesis. Gobble et al. (2011). Cancer Res.

Source: Pearson correlation with 440,127 interactions from GEO

Tags: apoptosis; cell line; cultured cells; cancer; transcription factors

Genetic interactions 11.91 %

Lin-Smith-2010 11.91 %

A genome-wide map of human genetic interactions inferred from radiation hybrid genotypes. Lin et al. (2010). Genome Res.

Source: 4,864,186 interactions from supplementary material

Shared protein domains 6.60 % PFAM 6.60 %

Source: Pearson correlation with 495,299 interactions from Pfam

Co-localization 4.36 %

Johnson-Shoemaker-2003 4.36 %

<u>Genome-wide survey of human alternative pre-mRNA splicing with exon junction microarrays.</u> Johnson et al. (2003). *Science*.

Source: Pearson correlation with 418,515 interactions from GEO

Tags: cultured cells; cell line

Physical interactions 2.18 %

BIOGRID-SMALL-SCALE-STUDIES 2.18 %

Source: <u>Direct interaction</u> with 28,816 interactions from <u>BioGRID</u>

Predicted 2.14 %

Stuart-Kim-2003 2.14 %

A gene-coexpression network for global discovery of conserved genetic modules. Stuart et al. (2003). Science.

Source: 24,115 interactions from supplementary material

Tags: cell proliferation; cultured cells; signal transduction; cancer

Pathway 0.24 %

Wu-Stein-2010 0.24 %

A human functional protein interaction network and its application to cancer data analysis. Wu et al. (2010). Genome Biol.

Source: 76,836 interactions from supplementary material

Tags: transcription factors; cancer

www.genemania.org/print 5/23

#### Genes

SMN2 survival of motor neuron 2, centromeric [Source:HGNC Symbol;Acc:11118]

Synonyms: ENSG00000205571: ENSP00000370117: ENSP00000370118: ENSP00000370119:

ENSP00000424282; ENSP00000424799; SMN2; SMNC;

GO annotations: No significantly enriched annotations

More at Ensembl

RP11-889I17.1 (INS-IGF2) insulin-insulin-like growth factor 2 read-through product [Source:RefSeq peptide;Acc:NP\_001035835]

Synonyms: 723961; ENSG00000129965; ENSP00000348986; ENSP00000380440; INS-IGF2; INSIGF;

NP\_001035835; NR\_003512; RP11-889I17.1;

GO annotations: No significantly enriched annotations

More at Entrez

C15orf42 chromosome 15 open reading frame 42 [Source:HGNC Symbol;Acc:28704]

Synonyms: 90381; C15orf42; ENSG00000140534; ENSP00000268138; FLJ41618; MGC45866; NM 152259;

NP 689472; Q7Z2Z1; TICRR; TICRR HUMAN; Treslin;

GO annotations: | DNA replication | regulation of DNA replication

More at Entrez

SMN1 survival of motor neuron 1, telomeric [Source:HGNC Symbol;Acc:11117]

Synonyms: ENSG00000172062; ENSP00000305857; ENSP00000370083; ENSP00000422679;

ENSP00000423298; ENSP00000424926; ENSP00000428128; ENSP00000430657; SMA; SMA1; SMA2; SMA3;

SMA@; SMN1; SMNT;

GO annotations: No significantly enriched annotations

More at Ensembl

ZFYVE28 zinc finger, FYVE domain containing 28 [Source:HGNC Symbol;Acc:29334]

Synonyms: 57732; ENSG00000159733; ENSP00000290974; ENSP00000422638; ENSP00000423694;

ENSP00000425706; ENSP00000425766; ENSP00000426299; ENSP00000427471; ENSP00000427654;

KIAA1643; LST2 HUMAN; MGC43699; MGC61592; NM 001172656; NM 001172657; NM 001172658;

NM 001172659; NM 001172660; NM 020972; NP 001166127; NP 001166128; NP 001166129; NP 001166130;

NP 001166131; NP 066023; Q9HCC9; ZFYVE28;

GO annotations: No significantly enriched annotations

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**FGFRL1** fibroblast growth factor receptor-like 1 [Source:HGNC Symbol;Acc:3693]

Synonyms: 53834; ENSG00000127418; ENSP00000264748; ENSP00000381498; ENSP00000423091;

ENSP00000424037; ENSP00000425025; ENSP00000426740; ENSP00000438322; FGFR5; FGFRL1;

FGRL1\_HUMAN; FHFR; NM\_001004356; NM\_001004358; NM\_021923; NP\_001004356; NP\_001004358;

NP\_068742; Q8N441;

GO annotations: No significantly enriched annotations

More at Entrez

SHROOM3 shroom family member 3 [Source:HGNC Symbol;Acc:30422]

Synonyms: 57619; APXL3; ENSG00000138771; ENSP00000264907; ENSP00000296043; ENSP00000370111;

KIAA1481; NM\_020859; NP\_065910; Q8TF72; SHRM; SHRM3\_HUMAN; SHROOM3; ShrmL;

GO annotations: No significantly enriched annotations

More at Entrez

CGN cingulin [Source:HGNC Symbol;Acc:17429]

Synonyms: 57530; CGN; CING\_HUMAN; DKFZp779N1112; ENSG00000143375; ENSP00000271636;

www.genemania.org/print 6/23

ENSP00000390686; ENSP00000410836; ENSP00000422299; ENSP00000425532; FLJ39281; KIAA1319; NM 020770; NP 065821; Q9P2M7;

GO annotations: | actin binding | cytoskeletal protein binding

More at Entrez

CD274 CD274 molecule [Source:HGNC Symbol;Acc:17635]

Synonyms: 29126; B7-H; B7H1; CD274; ENSG00000120217; ENSP00000370985; ENSP00000370989; MGC142294; MGC142296; NM\_014143; NP\_054862; PD-L1; PD1L1\_HUMAN; PDCD1L1; PDCD1LG1; PDL1; Q9NZQ7:

GO annotations: No significantly enriched annotations

More at Entrez

CROCC ciliary rootlet coiled-coil, rootletin [Source:HGNC Symbol;Acc:21299]

Synonyms: 9696; CROCC; CROCC\_HUMAN; ENSG00000058453; ENSP00000364691; ENSP00000402626; KIAA0445; NM\_014675; NP\_055490; Q5TZA2; ROLT; rootletin;

GO annotations: | cytoskeletal protein binding

More at Entrez

TLR10 toll-like receptor 10 [Source:HGNC Symbol;Acc:15634]

Synonyms: 81793; CD290; ENSG00000174123; ENSP00000308925; ENSP00000354459; ENSP00000421483; ENSP00000424923; ENSP00000427606; MGC104967; MGC126398; MGC126399; NM\_001017388; NM\_001195106; NM\_001195107; NM\_001195108; NM\_030956; NP\_001017388; NP\_001182035;

NP 001182036; NP 001182037; NP 112218; Q9BXR5; TLR10; TLR10 HUMAN;

GO annotations: No significantly enriched annotations

More at Entrez

OBSCN obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF [Source:HGNC Symbol;Acc:15719]

Synonyms: 84033; ARHGEF30; DKFZp666E245; ENSG00000154358; ENSP00000284548; ENSP00000352613; ENSP00000355665; ENSP00000355667; ENSP00000355668; ENSP00000355670; ENSP00000388554; ENSP00000409493; FLJ14124; KIAA1556; KIAA1639; MGC120409; MGC120410; MGC120411; MGC120412; MGC138590; NM\_001098623; NM\_052843; NP\_001092093; NP\_443075; OBSCN; OBSCN\_HUMAN; Q5VST9; UNC89;

GO annotations: | cytoskeletal protein binding

More at Entrez

MASP2 mannan-binding lectin serine peptidase 2 [Source:HGNC Symbol;Acc:6902]

Synonyms: 10747; ENSG00000009724; ENSP00000383690; ENSP00000383691; MAP19; MASP-2; MASP1P1; MASP2; MASP2 HUMAN; NM 006610; NM 139208; NP 006601; NP 631947; O00187;

GO annotations: No significantly enriched annotations

More at Entrez

WRNIP1 Werner helicase interacting protein 1 [Source:HGNC Symbol;Acc:20876]

Synonyms: 56897; ENSG00000124535; ENSP00000370141; ENSP00000370146; ENSP00000370148; ENSP00000370150; ENSP00000412661; FLJ22526; NM\_020135; NM\_130395; NP\_064520; NP\_569079; Q96S55; RP11-420G6.2; WHIP; WRIP1 HUMAN; WRNIP1; bA420G6.2;

GO annotations: | DNA replication | regulation of DNA replication

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C1orf116 chromosome 1 open reading frame 116 [Source:HGNC Symbol;Acc:28667]

Synonyms: 79098; C1orf116; DKFZp666H2010; ENSG00000182795; ENSP00000352447; ENSP00000436862; FLJ36507; MGC2742; MGC4309; NM\_001083924; NM\_023938; NP\_001077393; NP\_076427; Q9BW04; SARG; SARG\_HUMAN;

GO annotations: No significantly enriched annotations

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www.genemania.org/print 7/23

#### MUC4 mucin 4, cell surface associated [Source:HGNC Symbol;Acc:7514]

Synonyms: 4585; ENSG00000145113; ENSP00000304207; ENSP00000310528; ENSP00000338109; ENSP00000345378; ENSP00000376208; ENSP00000376209; ENSP00000389780; ENSP00000407750; ENSP00000417397; ENSP00000417498; ENSP00000417657; ENSP00000417722; ENSP00000417757; ENSP00000418306; ENSP00000419798; ENSP00000419989; ENSP00000420243; ENSP00000420439; HSA276359; MUC4; MUC4\_HUMAN; NM\_004532; NM\_018406; NM\_138297; NP\_004523; NP\_060876; NP\_612154; Q99102;

GO annotations: No significantly enriched annotations

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#### VAPB VAMP (vesicle-associated membrane protein)-associated protein B and C [Source:HGNC Symbol;Acc:12649]

Synonyms: 9217; ALS8; ENSG00000124164; ENSP00000379147; ENSP00000417175; ENSP00000430426; NM\_001195677; NM\_004738; NP\_001182606; NP\_004729; NR\_036633; O95292; VAMP-B; VAP-B; VAP-B; VAPB\_HUMAN;

GO annotations: | cytoskeletal protein binding | membrane lipid metabolic process | sphingolipid metabolic process | More at Entrez

CELSR1 cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) [Source:HGNC Symbol;Acc:1850]

Synonyms: 9620; CDHF9; CELR1\_HUMAN; CELSR1; DKFZp434P0729; ENSG00000075275; ENSP00000262738; ENSP00000379293; ENSP00000414689; FMI2; HFMI2; NM 014246; NP 055061; Q9NYQ6;

GO annotations: No significantly enriched annotations

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#### USP21 ubiquitin specific peptidase 21 [Source: HGNC Symbol; Acc: 12620]

Synonyms: 27005; ENSG00000143258; ENSP00000289865; ENSP00000356980; ENSP00000356981; MGC3394; NM 001014443; NM 012475; NP 001014443; NP 036607; Q9UK80; UBP21 HUMAN; USP21; USP23;

GO annotations: No significantly enriched annotations

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#### MCM10 minichromosome maintenance complex component 10 [Source:HGNC Symbol;Acc:18043]

Synonyms: 55388; CNA43; DNA43; ENSG00000065328; ENSP00000354945; ENSP00000367966; ENSP00000367986; ENSP00000417094; ENSP00000418268; MCM10; MCM10\_HUMAN; MGC126776; NM\_018518; NM\_182751; NP\_060988; NP\_877428; PRO2249; Q7L590;

GO annotations: | DNA replication

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#### **HSPG2** heparan sulfate proteoglycan 2 [Source:HGNC Symbol;Acc:5273]

Synonyms: 3339; ENSG00000142798; ENSP00000363805; ENSP00000363808; ENSP00000363827; ENSP00000392022; ENSP00000395884; ENSP00000396310; ENSP00000397573; ENSP00000405412; ENSP00000416385; ENSP00000436271; HSPG2; NM\_005529; NP\_005520; P98160; PGBM\_HUMAN; PLC; PRCAN; SJA; SJS; SJS1; perlecan;

GO annotations: No significantly enriched annotations

More at Entrez

#### **ASAH1** N-acylsphingosine amidohydrolase (acid ceramidase) 1 [Source:HGNC Symbol;Acc:735]

Synonyms: 427; AC; ACDase; ASAH; ASAH1; ASAH1\_HUMAN; ENSG00000104763; ENSP00000262097; ENSP00000326970; ENSP00000371152; ENSP00000394125; ENSP00000427751; FLJ21558; FLJ22079; NM\_001127505; NM\_004315; NM\_177924; NP\_001120977; NP\_004306; NP\_808592; PHP32; Q13510;

GO annotations: | membrane lipid metabolic process | sphingolipid metabolic process

More at Entrez

#### SULF1 sulfatase 1 [Source:HGNC Symbol;Acc:20391]

Synonyms: 23213; ENSG00000137573; ENSP00000260128; ENSP00000385704; ENSP00000390315; ENSP00000403040; ENSP00000431308; ENSP00000431753; ENSP00000432178; ENSP00000434128;

www.genemania.org/print 8/23

ENSP00000436608; ENSP00000436949; FLJ30905; FLJ38022; FLJ41750; HSULF-1; KIAA1077; NM\_001128204; NM\_001128205; NM\_001128206; NM\_015170; NP\_001121676; NP\_001121677; NP\_001121678; NP\_055985; Q8IWU6; SULF-1; SULF1; SULF1\_HUMAN;

GO annotations: No significantly enriched annotations

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SLC25A13 solute carrier family 25, member 13 (citrin) [Source:HGNC Symbol;Acc:10983]

Synonyms: 10165; ARALAR2; CITRIN; CMC2\_HUMAN; CTLN2; ENSG00000004864; ENSP00000265631; ENSP00000400101; ENSP00000440484; NM\_001160210; NM\_014251; NP\_001153682; NP\_055066; NR\_027662; Q9UJS0; SLC25A13;

GO annotations: No significantly enriched annotations

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CARD8 caspase recruitment domain family, member 8 [Source:HGNC Symbol;Acc:17057]

Synonyms: 22900; CARD8; CARD8\_HUMAN; CARDINAL; DACAR; DAKAR; DKFZp779L0366; ENSG00000105483; ENSP00000350423; ENSP00000351901; ENSP00000375767; ENSP00000391248; ENSP00000427727; ENSP00000427858; ENSP00000427922; ENSP00000428662; ENSP00000428736; ENSP00000428740; ENSP00000428862; ENSP00000428883; ENSP00000428975; ENSP00000429362; ENSP00000429741; ENSP00000429839; ENSP00000430057; ENSP00000430108; ENSP00000430178; ENSP00000430460; ENSP00000430495; ENSP00000430567; ENSP00000430747; ENSP00000430836; FLJ18119; FLJ18121; KIAA0955; MGC57162; NDPP; NM\_001184900; NM\_001184901; NM\_001184902; NM\_001184903; NM\_001184904; NM\_014959; NP\_001171829; NP\_001171830; NP\_001171831; NP\_001171832; NP\_001171833; NP\_055774; NR\_033678; NR\_033679; NR\_033680; Q9Y2G2; TUCAN;

GO annotations: No significantly enriched annotations

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LAIR1 leukocyte-associated immunoglobulin-like receptor 1 [Source:HGNC Symbol;Acc:6477]

Synonyms: 3903; CD305; ENSG00000167613; ENSP00000301193; ENSP00000319204; ENSP00000375621; ENSP00000375622; ENSP00000375623; ENSP00000391003; ENSP00000392058; ENSP00000392722; ENSP00000397226; ENSP00000399710; ENSP00000402727; ENSP00000404124; ENSP00000411632; ENSP00000412796; ENSP00000418998; LAIR-1; LAIR1; LAIR1\_HUMAN; NM\_002287; NM\_021706; NP\_002278; NP\_068352; Q6GTX8;

GO annotations: No significantly enriched annotations

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**OGFR** opioid growth factor receptor [Source:HGNC Symbol;Acc:15768]

Synonyms: 11054; 7-60; ENSG00000060491; ENSP00000290291; ENSP00000349686; ENSP00000359491; ENSP00000359499; ENSP00000359500; ENSP00000395168; NM\_007346; NP\_031372; OGFR; OGFR\_HUMAN; Q9NZT2;

GO annotations: No significantly enriched annotations

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MAP3K1 mitogen-activated protein kinase kinase kinase 1 [Source:HGNC Symbol;Acc:6848]

Synonyms: 4214; ENSG00000095015; ENSP00000382423; M3K1\_HUMAN; MAP3K1; MAPKKK1; MEKK; MEKK1; NM\_005921; NP\_005912; Q13233;

GO annotations: No significantly enriched annotations

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IGHMBP2 immunoglobulin mu binding protein 2 [Source:HGNC Symbol;Acc:5542]

Synonyms: 3508; CATF1; ENSG00000132740; ENSP00000255078; ENSP00000440465; ENSP00000443343; FLJ34220; FLJ41171; HCSA; HMN6; IGHMBP2; NM\_002180; NP\_002171; P38935; SMARD1; SMBP2\_HUMAN; SMUBP2;

GO annotations: | DNA replication

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www.genemania.org/print 9/23

#### OCA2 oculocutaneous albinism II [Source:HGNC Symbol;Acc:8101]

Synonyms: 4948; BEY; BEY1; BEY2; D15S12; ENSG00000104044; ENSP00000261276; ENSP00000346659; ENSP00000372457; ENSP00000414425; ENSP00000415431; EYCL; EYCL2; EYCL3; HCL3; NM\_000275; NP\_000266; OCA2; P\_HUMAN; Q04671;

GO annotations: No significantly enriched annotations

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GCNT4 glucosaminyl (N-acetyl) transferase 4, core 2 [Source:HGNC Symbol;Acc:17973]

Synonyms: 51301; C2GNT3; ENSG00000176928; ENSP00000317027; GCNT4; GCNT4\_HUMAN; NM\_016591; NP\_057675; Q9P109;

GO annotations: No significantly enriched annotations

More at Entrez

APOH apolipoprotein H (beta-2-glycoprotein I) [Source:HGNC Symbol;Acc:616]

Synonyms: 350; APOH; APOH\_HUMAN; B2G1; B2GP1; ENSG00000091583; ENSP00000205948; NM\_000042; NP\_000033; P02749;

GO annotations: No significantly enriched annotations

More at Entrez

ATM ataxia telangiectasia mutated [Source:HGNC Symbol;Acc:795]

Synonyms: 472; 651610; ATA; ATC; ATD; ATE; ATM; ATM\_HUMAN; DKFZp781A0353; ENSG00000149311; ENSP00000278616; ENSP00000374162; ENSP00000388058; ENSP00000431839; ENSP00000432318; ENSP00000432560; ENSP00000433955; ENSP00000434327; ENSP00000435524; ENSP00000435747; LOC651610; MGC74674; NM\_000051; NP\_000042; Q13315; TEL1; TELO1; XM\_940791; XP\_945884;

GO annotations: | positive regulation of cell cycle process

More at Entrez

TTN titin [Source:HGNC Symbol;Acc:12403]

Synonyms: 7273; CMD1G; CMH9; CMPD4; DKFZp451N061; ENSG00000155657; ENSP00000304714; ENSP00000340554; ENSP00000343764; ENSP00000348444; ENSP00000352154; ENSP00000354117; ENSP00000376219; ENSP00000390316; ENSP00000392336; ENSP00000394672; ENSP00000396805; ENSP00000397437; ENSP00000399176; ENSP00000400616; ENSP00000401501; ENSP00000405517; ENSP00000408004; ENSP00000413356; ENSP00000433840; ENSP00000434586; ENSP00000445986; EOMFC; FLJ26020; FLJ26409; FLJ32040; FLJ34413; FLJ39564; FLJ43066; HMERF; LGMD2J; NM\_003319; NM\_133378; NM\_133379; NM\_133432; NM\_133437; NP\_003310; NP\_596869; NP\_596870; NP\_597676; NP\_597681; TMD; TTN;

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TLR4 toll-like receptor 4 [Source:HGNC Symbol;Acc:11850]

Synonyms: 7099; ARMD10; CD284; ENSG00000136869; ENSP00000363089; ENSP00000377997; NM\_138554; NP\_612564; NR\_024168; NR\_024169; O00206; TLR4; TLR4\_HUMAN; TOLL; hToll;

GO annotations: No significantly enriched annotations

More at Entrez

LNPEP leucyl/cystinyl aminopeptidase [Source:HGNC Symbol;Acc:6656]

Synonyms: 4012; ENSG00000113441; ENSP00000231368; ENSP00000379117; LCAP\_HUMAN; LNPEP; NM\_005575; NM\_175920; NP\_005566; NP\_787116; P-LAP; Q9UIQ6;

GO annotations: No significantly enriched annotations

More at Entrez

CUBN cubilin (intrinsic factor-cobalamin receptor) [Source:HGNC Symbol;Acc:2548]

Synonyms: 8029; CUBN; CUBN\_HUMAN; ENSG00000107611; ENSP00000367054; ENSP00000367064; ENSP00000391830; ENSP00000415970; ENSP00000437882; FLJ90055; FLJ90747; IFCR; MGA1; NM 001081;

www.genemania.org/print 10/23

NP\_001072; O60494; gp280;

GO annotations: No significantly enriched annotations

More at Entrez

CTSB cathepsin B [Source:HGNC Symbol;Acc:2527]

Synonyms: 1508; APPS; CATB\_HUMAN; CTSB; ENSG00000164733; ENSP00000342070; ENSP00000345672; ENSP00000409917; ENSP00000411254; ENSP00000415889; ENSP00000431143; ENSP00000431518; ENSP00000432077; ENSP00000432244; ENSP00000432408; ENSP00000433215; ENSP00000433379; ENSP00000433929; ENSP00000433995; ENSP00000434217; ENSP00000434725; ENSP00000435074; ENSP00000435105; ENSP00000435260; ENSP00000435367; ENSP00000435650; ENSP00000435886; ENSP00000436074; ENSP00000436122; ENSP00000436159; ENSP00000436456; ENSP00000436627; ENSP00000441700; ENSP00000441827; ENSP00000445490; NM\_001908; NM\_147780; NM\_147781; NM\_147782; NM\_147783; NP\_001899; NP\_680090; NP\_680091; NP\_680092; NP\_680093; P07858;

GO annotations: No significantly enriched annotations

More at Entrez

B3GNT3 UDP-GIcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3 [Source:HGNC Symbol;Acc:13528]

Synonyms: 10331; B3GAL-T8; B3GN-T3; B3GN3\_HUMAN; B3GNT-3; B3GNT3; ENSG00000179913; ENSP00000321874; HP10328; NM\_014256; NP\_055071; Q9Y2A9; TMEM3; beta3Gn-T3;

GO annotations: No significantly enriched annotations

More at Entrez

GTPBP4 GTP binding protein 4 [Source:HGNC Symbol;Acc:21535]

Synonyms: 23560; CRFG; ENSG00000107937; ENSP00000353168; ENSP00000354040; ENSP00000444277; ENSP00000445473; FLJ10686; FLJ10690; FLJ39774; GTPBP4; NM\_012341; NOG1; NOG1\_HUMAN; NP\_036473; Q9BZE4;

GO annotations: | DNA replication | regulation of DNA replication

More at Entrez

PFKFB3 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [Source:HGNC Symbol;Acc:8874]

Synonyms: 5209; ENSG00000170525; ENSP00000351288; ENSP00000353712; ENSP00000369100; ENSP00000369105; ENSP00000369107; ENSP00000369108; ENSP00000369110; ENSP00000369111; ENSP00000369115; ENSP00000390285; ENSP00000402055; ENSP00000404995; ENSP00000416677; ENSP00000432356; ENSP00000433771; ENSP00000434342; ENSP00000434628; ENSP00000436885; ENSP00000443319; ENSP00000446384; F263\_HUMAN; FLJ37326; IPFK2; NM\_001145443; NM\_004566; NP\_001138915; NP\_004557; PFK2; PFKFB3; Q16875;

GO annotations: No significantly enriched annotations

More at Entrez

LILRB1 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 [Source:HGNC Symbol;Acc:6605]

Synonyms: 10859; CD85J; ENSG00000104972; ENSP00000315997; ENSP00000379608; ENSP00000379610; ENSP00000379614; ENSP00000379618; ENSP00000379622; ENSP00000379623; ENSP00000391514; ENSP00000395004; ENSP00000405243; ENSP00000409968; ENSP00000410165; FLJ37515; ILT2; LILRB1; LIR-1; LIRB1\_HUMAN; MIR-7; MIR7; NM\_001081637; NM\_001081638; NM\_001081639; NM\_006669; NP\_001075106; NP\_001075107; NP\_001075108; NP\_006660; Q8NHL6;

GO annotations: No significantly enriched annotations

More at Entrez

SPTA1 spectrin, alpha, erythrocytic 1 (elliptocytosis 2) [Source:HGNC Symbol;Acc:11272]

Synonyms: 6708; EL2; ENSG00000163554; ENSP00000357129; ENSP00000357130; HPP; HS3; NM\_003126; NP\_003117; P02549; SPH3; SPTA; SPTA1 HUMAN;

GO annotations: |actin binding | actin filament organization | cytoskeletal protein binding

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**DMBT1** deleted in malignant brain tumors 1 [Source:HGNC Symbol;Acc:2926]

www.genemania.org/print 11/23

Synonyms: 1755; DMBT1; DMBT1\_HUMAN; ENSG00000187908; ENSP00000327747; ENSP00000331522; ENSP00000339752; ENSP00000342210; ENSP00000342500; ENSP00000342572; ENSP00000343175; ENSP00000343268; ENSP00000345836; ENSP00000352593; ENSP00000357905; ENSP00000357911; ENSP00000357938; ENSP00000357949; ENSP00000357951; ENSP00000357952; FLJ61058; GP340; MGC164738; NM\_004406; NM\_007329; NM\_017579; NP\_004397; NP\_015568; NP\_060049; Q9UGM3; muclin;

GO annotations: No significantly enriched annotations

More at Entrez

UBA1 ubiquitin-like modifier activating enzyme 1 [Source:HGNC Symbol;Acc:12469]

Synonyms: 7317; A1S9; A1S9T; A1ST; AMCX1; ENSG00000130985; ENSP00000338413; ENSP00000366481; ENSP00000366483; ENSP00000366568; ENSP00000389583; ENSP00000397816; ENSP00000401101; ENSP00000404796; ENSP00000405359; ENSP00000415033; GXP1; MGC4781; NM\_003334; NM\_153280; NP\_003325; NP\_695012; P22314; POC20; SMAX2; UBA1; UBA1A; UBA1 HUMAN; UBE1; UBE1X;

GO annotations: No significantly enriched annotations

More at Entrez

RASA1 RAS p21 protein activator (GTPase activating protein) 1 [Source:HGNC Symbol;Acc:9871]

Synonyms: 5921; CM-AVM; CMAVM; DKFZp434N071; ENSG00000145715; ENSP00000274376; ENSP00000411221; ENSP00000420905; ENSP00000422008; ENSP00000423395; ENSP00000433186; NM\_002890; NM\_022650; NP\_002881; NP\_072179; P20936; PKWS; RASA; RASA1; RASA1\_HUMAN; RASGAP; p120GAP; p120RASGAP;

GO annotations: | actin filament organization

More at Entrez

AP1G2 adaptor-related protein complex 1, gamma 2 subunit [Source:HGNC Symbol;Acc:556]

Synonyms: 8906; AP1G2; AP1G2\_HUMAN; ENSG00000213983; ENSP00000312442; ENSP00000380309; ENSP00000442716; ENSP00000445313; G2AD; NM 003917; NP 003908; O75843;

GO annotations: No significantly enriched annotations

More at Entrez

NUP153 nucleoporin 153kDa [Source:HGNC Symbol;Acc:8062]

Synonyms: 9972; ENSG00000124789; ENSP00000262077; ENSP00000402009; ENSP00000444029; HNUP153; N153; NM\_005124; NP\_005115; NU153\_HUMAN; NUP153; P49790;

GO annotations: No significantly enriched annotations

More at Entrez

PSMB5 proteasome (prosome, macropain) subunit, beta type, 5 [Source:HGNC Symbol;Acc:9542]

Synonyms: 5693; ENSG00000100804; ENSP00000334973; ENSP00000355325; ENSP00000395206; LMPX; MB1; MGC104214; NM\_001130725; NM\_001144932; NM\_002797; NP\_001124197; NP\_001138404; NP\_002788; P28074; PSB5 HUMAN; PSMB5; X;

GO annotations: | positive regulation of cell cycle process

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KCNB1 potassium voltage-gated channel, Shab-related subfamily, member 1 [Source:HGNC Symbol;Acc:6231]

Synonyms: 3745; DRK1; ENSG00000158445; ENSP00000360806; ENSP00000438564; KCNB1; KCNB1\_HUMAN; KV2.1; NM\_004975; NP\_004966; Q14721; h-DRK1;

GO annotations: No significantly enriched annotations

More at Entrez

TYROBP TYRO protein tyrosine kinase binding protein [Source:HGNC Symbol;Acc:12449]

Synonyms: 7305; DAP12; ENSG00000011600; ENSP00000262629; ENSP00000402371; ENSP00000445332; KARAP; NM\_001173514; NM\_001173515; NM\_003332; NM\_198125; NP\_001166985; NP\_001166986; NP\_003323; NP\_937758; NR\_033390; O43914; PLO-SL; PLOSL; TYOBP\_HUMAN; TYROBP;

GO annotations: No significantly enriched annotations

www.genemania.org/print 12/23

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AC139494.2 Survival motor neuron protein [Source:UniProtKB/Swiss-Prot;Acc:Q16637] 3.34 Synonyms: AC139494.2; ENSG00000255613; ENSP00000412162; ENSP00000437346; ENSP00000437444; ENSP00000437834; ENSP00000439881; GO annotations: No significantly enriched annotations More at Ensembl 2.85 NAAA N-acylethanolamine acid amidase [Source:HGNC Symbol;Acc:736] Synonyms: 27163; ASAHL; ENSG00000138744; ENSP00000286733; ENSP00000382413; ENSP00000382420; ENSP00000423142; ENSP00000423397; ENSP00000426977; ENSP00000427641; NAAA; NAAA HUMAN; NM\_001042402; NM\_014435; NP\_001035861; NP\_055250; PLT; Q02083; GO annotations: No significantly enriched annotations More at Entrez SMNDC1 survival motor neuron domain containing 1 [Source:HGNC Symbol;Acc:16900] 1.84 Synonyms: 10285; ENSG00000119953; ENSP00000358605; ENSP00000358616; NM 005871; NP 005862; O75940; SMNDC1; SMNR; SPF30; SPF30 HUMAN; GO annotations: No significantly enriched annotations More at Entrez OGFRL1 opioid growth factor receptor-like 1 [Source:HGNC Symbol;Acc:21378] 1.74 Synonyms: 79627; ENSG00000119900; ENSP00000359464; FLJ21079; MGC102783; NM\_024576; NP\_078852; OGFRL1; OGRL1 HUMAN; Q5TC84; dJ331H24.1; GO annotations: No significantly enriched annotations More at Entrez VAPA VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa [Source:HGNC Symbol;Acc:12648] 1.07 Synonyms: 9218; ENSG00000101558; ENSP00000345656; ENSP00000382880; MGC3745; NM 003574; NM 194434; NP 003565; NP 919415; Q9P0L0; VAP-33; VAP-A; VAPA; VAPA; VAPA HUMAN; hVAP-33; GO annotations: membrane lipid metabolic process sphingolipid metabolic process More at Entrez SHROOM1 shroom family member 1 [Source:HGNC Symbol;Acc:24084] 0.99 Synonyms: 134549; APXL2; ENSG00000164403; ENSP00000324245; ENSP00000367947; ENSP00000367950; ENSP00000388049; KIAA1960; NM 001172700; NM 133456; NP 001166171; NP 597713; Q2M3G4; SHRM1 HUMAN; SHROOM1; More at Entrez PYROXD2 pyridine nucleotide-disulphide oxidoreductase domain 2 [Source:HGNC Symbol;Acc:23517] 0.89 Synonyms: 84795; C10orf33; ENSG00000119943; ENSP00000359607; FLJ12197; FLJ23849; FP3420; MGC13047; NM 032709; NP 116098; PYRD2 HUMAN; PYROXD2; Q8N2H3; GO annotations: No significantly enriched annotations More at Entrez MOSPD3 motile sperm domain containing 3 [Source:HGNC Symbol;Acc:25078] 0.89 Synonyms: 64598; CDS3; ENSG00000106330; ENSP00000223054; ENSP00000368842; ENSP00000377522; ENSP00000377525; ENSP00000404626; ENSP00000417276; ENSP00000419535; MOSPD3; MSPD3\_HUMAN; NET30; NM\_001040097; NM\_001040098; NM\_001040099; NM\_023948; NP\_001035186; NP\_001035187; NP\_001035188; NP\_076438; O75425; GO annotations: No significantly enriched annotations More at Entrez

www.genemania.org/print 13/23

CARD6 caspase recruitment domain family, member 6 [Source:HGNC Symbol;Acc:16394] 0.89 Synonyms: 84674; CARD6; CARD6 HUMAN; CINCIN1; ENSG00000132357; ENSP00000254691; ENSP00000371093; ENSP00000406763; ENSP00000439680; NM 032587; NP 115976; Q9BX69; GO annotations: No significantly enriched annotations More at Entrez TLR1 toll-like receptor 1 [Source:HGNC Symbol;Acc:11847] 0.88 Synonyms: 7096; CD281; DKFZp547l0610; DKFZp564l0682; ENSG00000174125; ENSP00000354932; ENSP00000421259; ENSP00000421856; ENSP00000423017; ENSP00000423725; ENSP00000424894; KIAA0012; MGC104956; MGC126311; MGC126312; NM 003263; NP 003254; Q15399; TIL; TLR1; TLR1 HUMAN; rsc786: GO annotations: No significantly enriched annotations More at Entrez MOSPD1 motile sperm domain containing 1 [Source:HGNC Symbol;Acc:25235] 0.84 Synonyms: 56180; DJ473B4; ENSG00000101928; ENSP00000359813; ENSP00000359815; ENSP00000359819; MOSPD1; MSPD1\_HUMAN; NM\_019556; NP\_062456; Q9UJG1; GO annotations: No significantly enriched annotations More at Entrez SLC13A5 solute carrier family 13 (sodium-dependent citrate transporter), member 5 [Source:HGNC Symbol;Acc:23089] 0.84 Synonyms: 284111; DKFZp686E17257; ENSG00000141485; ENSP00000293800; ENSP00000370464; ENSP00000406220; MGC138356; NM 001143838; NM 177550; NP 001137310; NP 808218; Q86YT5; S13A5 HUMAN; SLC13A5; GO annotations: No significantly enriched annotations More at Entrez IGF2 insulin-like growth factor 2 (somatomedin A) [Source:HGNC Symbol;Acc:5466] 0.83 Synonyms: 3481; C11orf43; ENSG00000167244; ENSP00000300632; ENSP00000338297; ENSP00000370720; ENSP00000370786; ENSP00000370796; ENSP00000370799; ENSP00000370802; ENSP00000370813; ENSP00000391826; ENSP00000402047; ENSP00000414497; FLJ22066; FLJ44734; IGF-II; IGF2; IGF2 HUMAN; NM\_000612; NM\_001007139; NM\_001127598; NP\_000603; NP\_001007140; NP\_001121070; P01344; PP9974; GO annotations: |insulin receptor binding | positive regulation of cell cycle process | positive regulation of glycogen metabolic process More at Entrez SLC13A3 solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 [Source:HGNC Symbol;Acc:14430] 0.77 Synonyms: 64849; ENSG00000158296; ENSP00000279027; ENSP00000290317; ENSP00000344912; ENSP00000361193; ENSP00000379648; ENSP00000394217; ENSP00000395095; ENSP00000397955; ENSP00000403394; ENSP00000415852; ENSP00000417784; ENSP00000419621; ENSP00000420177; NADC3; NM 001011554; NM 001193339; NM 001193340; NM 001193342; NM 022829; NP 001011554; NP\_001180268; NP\_001180269; NP\_001180271; NP\_073740; Q8WWT9; S13A3\_HUMAN; SDCT2; SLC13A3; GO annotations: No significantly enriched annotations More at Entrez INS insulin [Source: HGNC Symbol: Acc: 6081] 0.75 Synonyms: 3630; ENSG00000254647; ENSP00000250971; ENSP00000370731; ENSP00000380432; ENSP00000408400; ENSP00000424008; IDDM2; ILPR; INS; INS HUMAN; IRDN; MODY10; NM 000207; NM 001185097; NM 001185098; NP 000198; NP 001172026; NP 001172027; P01308; GO annotations: | DNA replication | insulin receptor binding | positive regulation of cell cycle process regulation of glycogen metabolic process | regulation of DNA replication More at Entrez RLN1 relaxin 1 [Source:HGNC Symbol;Acc:10026] 0.73

www.genemania.org/print 14/23

Synonyms: 6013; ENSG00000107018; ENSP00000223858; ENSP00000223862; NM 006911; NP 008842;

P04808; REL1 HUMAN; RLN1; RLXH1; bA12D24.3.1; bA12D24.3.2;

GO annotations: No significantly enriched annotations

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PSAP prosaposin [Source: HGNC Symbol; Acc: 9498]

0.71

Synonyms: 5660; ENSG00000197746; ENSP00000350063; ENSP00000362212; ENSP00000378387; ENSP00000378392; ENSP00000378394; ENSP00000378398; ENSP00000384385; GLBA; MGC110993; NM\_001042465; NM\_001042466; NM\_002778; NP\_001035930; NP\_001035931; NP\_002769; P07602; PSAP; SAP HUMAN;

GO annotations: |membrane lipid metabolic process |sphingolipid metabolic process

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INSL3 insulin-like 3 (Leydig cell) [Source:HGNC Symbol;Acc:6086]

0.70

Synonyms: 3640; ENSG00000248099; ENSP00000321724; ENSP00000369017; INSL3; INSL3\_HUMAN; MGC119818; MGC119819; NM 005543; NP 005534; P51460; RLNL;

GO annotations: |insulin receptor binding

More at Entrez

LIPA lipase A, lysosomal acid, cholesterol esterase [Source:HGNC Symbol;Acc:6617]

0.69

Synonyms: 3988; CESD; ENSG00000107798; ENSP00000282673; ENSP00000337354; ENSP00000360894; ENSP00000360895; ENSP00000360903; ENSP00000388415; ENSP00000392037; ENSP00000413019; ENSP00000437564; ENSP00000438127; ENSP00000439727; LAL; LICH\_HUMAN; LIPA; NM\_000235; NM\_001127605; NP\_000226; NP\_001121077; P38571;

GO annotations: No significantly enriched annotations

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INSL6 insulin-like 6 [Source: HGNC Symbol; Acc: 6089]

0.66

Synonyms: 11172; ENSG00000120210; ENSP00000371054; INSL6; INSL6\_HUMAN; NM\_007179; NP\_009110; Q9Y581;

GO annotations: No significantly enriched annotations

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TMEM171 transmembrane protein 171 [Source:HGNC Symbol;Acc:27031]

Synonyms: 134285; ENSG00000157111; ENSP00000287773; ENSP00000415030; NM\_001161342; NM\_173490; NP\_001154814; NP\_775761; Q8WVE6; TM171\_HUMAN; TMEM171;

GO annotations: No significantly enriched annotations

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www.genemania.org/print 15/23

## **Functions**

GO annotation	FDR	Coverage
query genes	n/a	n/a
insulin receptor binding	1.8E-1	3 / 12
cytoskeletal protein binding	4.26E-1	7 / 286
DNA replication	4.26E-1	6 / 190
regulation of DNA replication	4.82E-1	4 / 68
sphingolipid metabolic process	5.95E-1	4 / 76
membrane lipid metabolic process	6.65E-1	4 / 82
positive regulation of glycogen metabolic process	8.13E-1	2 / 13
actin filament organization	8.13E-1	4 / 117
positive regulation of cell cycle process	8.13E-1	4 / 118
actin binding	8.13E-1	4 / 117

www.genemania.org/print 16/23

## Interactions

Gene 1	Gene 2	Weight	Network group	Networks
PSAP	CTSB	1.9750595092773438	Co-expression	Arijs-Rutgeerts-2009 Burczynski-Dorner-2006 Gobble-Singer-2011 Hummel-Siebert-2006 Nakayama-Hasegawa-2007 Noble-Diehl-2008 Radtke-Downing-2009
PSAP	TYROBP	0.8363682627677917	Co-expression	Arijs-Rutgeerts-2009 Bild-Nevins-2006 B Burczynski-Dorner-2006 Gobble-Singer-2011 Hummel-Siebert-2006 Nakayama-Hasegawa-2007 Radtke-Downing-2009
TYROBP	LILRB1	0.21906837821006775	Co-expression	Arijs-Rutgeerts-2009 Burczynski-Dorner-2006 Gobble-Singer-2011 Hummel-Siebert-2006 Nakayama-Hasegawa-2007 Radtke-Downing-2009
TYROBP	LAIR1	0.2169637829065323	Co-expression	Arijs-Rutgeerts-2009 Gobble-Singer-2011 Hummel-Siebert-2006 Nakayama-Hasegawa-2007 Noble-Diehl-2008
LILRB1	LAIR1	0.20748436450958252	Co-expression	Arijs-Rutgeerts-2009 Bild-Nevins-2006 B Burczynski-Dorner-2006 Hummel-Siebert-2006 Nakayama-Hasegawa-2007
TLR1	TYROBP	0.1479870080947876	Co-expression	Arijs-Rutgeerts-2009 Bild-Nevins-2006 B Gobble-Singer-2011 Hummel-Siebert-2006 Nakayama-Hasegawa-2007 Noble-Diehl-2008
TYROBP	CTSB	0.07834763824939728	Co-expression	Gobble-Singer-2011 Hummel-Siebert-2006 Nakayama-Hasegawa-2007 Noble-Diehl-2008 Radtke-Downing-2009
LIPA	TYROBP	0.05402440205216408	Co-expression	Gobble-Singer-2011 Hummel-Siebert-2006 Nakayama-Hasegawa-2007 Radtke-Downing-2009
PSAP	LILRB1	0.04877345263957977	Co-expression	Arijs-Rutgeerts-2009 Kang-Willman-2010 Radtke-Downing-2009
TYROBP	TLR4	0.047587428241968155	Co-expression	Gobble-Singer-2011 Nakayama-Hasegawa-2007 Noble-Diehl-2008
MUC4	C1orf116	0.04122453182935715	Co-expression	Burczynski-Dorner-2006 Hummel-Siebert-2006
NUP153	GTPBP4	0.03976823017001152	Co-expression	Burczynski-Dorner-2006 Gobble-Singer-2011

www.genemania.org/print 17/23

LNPEP	MAP3K1	0.037469979375600815	Co-expression	Kang-Willman-2010 Radtke-Downing-2009 Burczynski-Dorner-2006
				Wu-Garvey-2007
TLR1	ASAH1	0.03198153153061867	Co-expression	Hummel-Siebert-2006 Radtke-Downing-2009
PSAP	TLR1	0.02881546877324581	Co-expression	Arijs-Rutgeerts-2009 Gobble-Singer-2011 Radtke-Downing-2009
VAPA	SMNDC1	0.02860933728516102	Co-expression	Radtke-Downing-2009 Rieger-Chu-2004
TLR1	PFKFB3	0.02544470503926277	Co-expression	Burczynski-Dorner-2006 Hummel-Siebert-2006
PYROXD2	FGFRL1	0.024995269253849983	Co-expression	Noble-Diehl-2008
RLN1	GCNT4	0.023670069873332977	Co-expression	Burczynski-Dorner-2006 Kang-Willman-2010
TLR4	LAIR1	0.02352086268365383	Co-expression	Hummel-Siebert-2006 Nakayama-Hasegawa-2007
INSL3	DMBT1	0.02291255258023739	Co-expression	Kang-Willman-2010 Wu-Garvey-2007
RLN1	CUBN	0.022783491760492325	Co-expression	Kang-Willman-2010 Wu-Garvey-2007
SLC13A3	KCNB1	0.021954644471406937	Co-expression	Rieger-Chu-2004
TLR1	TLR4	0.02155771665275097	Co-expression	Arijs-Rutgeerts-2009 Burczynski-Dorner-2006 Gobble-Singer-2011
CGN	ZFYVE28	0.021265214309096336	Co-expression	Arijs-Rutgeerts-2009
RLN1	APOH	0.020553920418024063	Co-expression	Bild-Nevins-2006 B Kang-Willman-2010
KCNB1	OCA2	0.020540980622172356	Co-expression	Wu-Garvey-2007
INS	DMBT1	0.020362209528684616	Co-expression	Bild-Nevins-2006 B
PSMB5	GTPBP4	0.019645893946290016	Co-expression	Gobble-Singer-2011
DMBT1	C1orf116	0.01930554211139679	Co-expression	Nakayama-Hasegawa-2007
INS	OBSCN	0.01909911446273327	Co-expression	Radtke-Downing-2009
SPTA1	APOH	0.018277592957019806	Co-expression	Burczynski-Dorner-2006
SMNDC1	NUP153	0.017863420769572258	Co-expression	Bild-Nevins-2006 B Hummel-Siebert-2006 Kang-Willman-2010 Nakayama-Hasegawa-2007
TLR1	LILRB1	0.017723174765706062	Co-expression	Arijs-Rutgeerts-2009 Nakayama-Hasegawa-2007 Wu-Garvey-2007
PFKFB3	LNPEP	0.017200959846377373	Co-expression	Bild-Nevins-2006 B
TLR1	LAIR1	0.017196685075759888	Co-expression	Arijs-Rutgeerts-2009 Gobble-Singer-2011
INS	SPTA1	0.017033983021974564	Co-expression	Rieger-Chu-2004
ATM	CARD8	0.016996195539832115	Co-expression	Bild-Nevins-2006 B
SLC25A13	VAPB	0.016915813088417053	Co-expression	Noble-Diehl-2008
VAPA	VAPB	0.016738764941692352	Co-expression	Noble-Diehl-2008
TTN	TLR10	0.01673584245145321	Co-expression	Noble-Diehl-2008
AP1G2	UBA1	0.016594836488366127	Co-expression	Burczynski-Dorner-2006 Hummel-Siebert-2006
LIPA	NAAA	0.016133278608322144	Co-expression	Burczynski-Dorner-2006
TLR1	CARD6	0.016094384714961052	Co-expression	Kang-Willman-2010
NAAA	MUC4	0.01590517722070217	Co-expression	Wu-Garvey-2007

www.genemania.org/print 18/23

EHRBPM1	ZFKYB38	0:015898798494343456	60-expression	Reger-eau-2004
LIPA	LILRB1	0.015265876427292824	Co-expression	Nakayama-Hasegawa-2007 Radtke-Downing-2009
VAPA	ASAH1	0.014621475711464882	Co-expression	Burczynski-Dorner-2006
B3GNT3	SHROOM3	0.014604826457798481	Co-expression	Arijs-Rutgeerts-2009
VAPA	SHROOM3	0.014553701505064964	Co-expression	Noble-Diehl-2008
CTSB	ASAH1	0.014438802376389503	Co-expression	Hummel-Siebert-2006
LIPA	CTSB	0.014384537935256958	Co-expression	Hummel-Siebert-2006
RASA1	ASAH1	0.014177893288433552	Co-expression	Arijs-Rutgeerts-2009
TLR1	VAPA	0.014004827477037907	Co-expression	Burczynski-Dorner-2006
PSMB5	VAPB	0.013909447938203812	Co-expression	Hummel-Siebert-2006
OGFRL1	LAIR1	0.013384819030761719	Co-expression	Gobble-Singer-2011
SMNDC1	MAP3K1	0.013103066943585873	Co-expression	Rieger-Chu-2004
LIPA	PSAP	0.012792006134986877	Co-expression	Gobble-Singer-2011 Radtke-Downing-2009
SHROOM1	CGN	0.012728746980428696	Co-expression	Noble-Diehl-2008
LAIR1	CARD8	0.012475715018808842	Co-expression	Kang-Willman-2010
TYROBP	ASAH1	0.012391404248774052	Co-expression	Kang-Willman-2010
ATM	LAIR1	0.012165400199592113	Co-expression	Bild-Nevins-2006 B
APOH	MASP2	0.011839497834444046	Co-expression	Hummel-Siebert-2006
KCNB1	SPTA1	0.010852468200027943	Co-expression	Arijs-Rutgeerts-2009 Rieger-Chu-2004
UBA1	SLC25A13	0.010446776635944843	Co-expression	Hummel-Siebert-2006
NS	USP21	0.010393939912319183	Co-expression	Noble-Diehl-2008
GF2	PFKFB3	0.010373956523835659	Co-expression	Wu-Garvey-2007
B3GNT3	C1orf116	0.010301066562533379	Co-expression	Burczynski-Dorner-2006 Gobble-Singer-2011
DMBT1	IGHMBP2	0.010267690755426884	Co-expression	Kang-Willman-2010
C1orf116	CGN	0.01023324765264988	Co-expression	Noble-Diehl-2008
_IPA	TLR1	0.010077549144625664	Co-expression	Gobble-Singer-2011
OGFRL1	PFKFB3	0.010055581107735634	Co-expression	Gobble-Singer-2011
SMNDC1	GTPBP4	0.009945989586412907	Co-expression	Arijs-Rutgeerts-2009
TLR1	OGFRL1	0.009884342551231384	Co-expression	Arijs-Rutgeerts-2009
NS	MASP2	0.009758291766047478	Co-expression	Burczynski-Dorner-2006
_NPEP	ATM	0.009740314446389675	Co-expression	Rieger-Chu-2004
LIPA	LAIR1	0.00946630910038948	Co-expression	Nakayama-Hasegawa-2007
IGF2	DMBT1	0.009415701031684875	Co-expression	Bild-Nevins-2006 B
VAPA	PFKFB3	0.009388985112309456	Co-expression	Burczynski-Dorner-2006
VAPA NAAA	LILRB1	0.009386985112309438	Co-expression	Gobble-Singer-2011
PYROXD2	KCNB1	0.00890825130045414	Co-expression	Kang-Willman-2010
PFKFB3	CD274	0.008810008876025677	Co-expression	Arijs-Rutgeerts-2009
PSAP	HSPG2	0.008622636087238789	Co-expression	Wu-Garvey-2007
-SAP -NPEP	ASAH1	0.00792365986853838	•	Rieger-Chu-2004
GF2	KCNB1		Co-expression	
NSL6	WRNIP1	0.007863341830670834 0.007706707809120417	Co-expression	Rieger-Chu-2004
			Co-expression	Gobble-Singer-2011
	UBA1 TLR10	0.00743623822927475	Co-expression	Wu-Garvey-2007
	11 K 111	0.007408519275486469	Co-expression	Arijs-Rutgeerts-2009
ATM		0.00707050070507777		
ATM MOSPD3	FGFRL1	0.007278523873537779	Co-expression	Noble-Diehl-2008
ATM MOSPD3 SPTA1	FGFRL1 LILRB1	0.0071728648617863655	Co-expression	Wu-Garvey-2007
PSMB5 ATM MOSPD3 SPTA1 LILRB1 HSPG2	FGFRL1		•	

www.genemania.org/print 19/23

				Radtke-Downing-2009 Arijs-Rutgeerts-2009
SLC13A5	UBA1	0.006961970590054989	Co-expression	
PSAP	UBA1	0.006857689470052719	Co-expression	Wu-Garvey-2007
LNPEP	TLR10	0.0067179943434894085	Co-expression	Arijs-Rutgeerts-2009
PSAP	RASA1	0.006457200273871422	Co-expression	Rieger-Chu-2004
TLR1	LNPEP	0.006248675286769867	Co-expression	Rieger-Chu-2004
NAAA	TYROBP	0.006141790188848972	Co-expression	Radtke-Downing-2009
DMBT1	GCNT4	0.005995009560137987	Co-expression	Kang-Willman-2010
GTPBP4	MCM10	0.00594055000692606	Co-expression	Hummel-Siebert-2006
OGFRL1	TYROBP	0.0058388737961649895	Co-expression	Gobble-Singer-2011
SPTA1	C1orf116	0.005603357683867216	Co-expression	Radtke-Downing-2009
LILRB1	CTSB	0.0054029603488743305	Co-expression	Radtke-Downing-2009
B3GNT3	MASP2	0.005270821508020163	Co-expression	Gobble-Singer-2011
NSL6	INS	0.005069253500550985	Co-expression	Burczynski-Dorner-2006
MAP3K1	TLR10	0.004789678379893303	Co-expression	Arijs-Rutgeerts-2009
RASA1	CARD8	0.004201010335236788	Co-expression	Burczynski-Dorner-2006
AP1G2	CARD8	0.003896249458193779	Co-expression	Burczynski-Dorner-2006 Radtke-Downing-2009
CARD6	SULF1	0.0035814542789012194	Co-expression	Noble-Diehl-2008
PSAP	PSMB5	0.0033620961476117373	Co-expression	Wu-Garvey-2007
B3GNT3	GCNT4	0.0031910899560898542	Co-expression	Gobble-Singer-2011
B3GNT3	OBSCN	0.0029274525586515665	Co-expression	Gobble-Singer-2011
MOSPD1	SPTA1	0.0025666281580924988	Co-expression	Radtke-Downing-2009
NS	KCNB1	0.0025117970071733	Co-expression	Burczynski-Dorner-2006
RLN1	IGHMBP2	0.0019494869047775865	Co-expression	Kang-Willman-2010
RLN1	CD274	0.0016491854330524802	Co-expression	Kang-Willman-2010
RLN1	SULF1	0.001232050359249115	Co-expression	Kang-Willman-2010
RLN1	WRNIP1	0.0010971288429573178	Co-expression	Kang-Willman-2010
GF2	SPTA1	0.016532152891159058	Co-localization	Johnson-Shoemaker-2003
NSL6	IGHMBP2	0.015812981873750687	Co-localization	Johnson-Shoemaker-2003
B3GNT3	MUC4	0.014746345579624176	Co-localization	Johnson-Shoemaker-2003
RLN1	C1orf116	0.012000186368823051	Co-localization	Johnson-Shoemaker-2003
DMBT1	MUC4	0.011158955283463001	Co-localization	Johnson-Shoemaker-2003
CTSB	ASAH1	0.01115229818969965	Co-localization	Johnson-Shoemaker-2003
GF2	APOH	0.009891755878925323	Co-localization	Johnson-Shoemaker-2003
CARD6	CD274	0.009724567644298077	Co-localization	Johnson-Shoemaker-2003
DMBT1	B3GNT3	0.009291338734328747	Co-localization	Johnson-Shoemaker-2003
RASA1	LNPEP	0.009075403213500977	Co-localization	Johnson-Shoemaker-2003
TYROBP	LAIR1	0.008632461540400982	Co-localization	Johnson-Shoemaker-2003
_IPA	INSL3	0.007825628854334354	Co-localization	Johnson-Shoemaker-2003
INSL3	OGFRL1	0.007750046905130148	Co-localization	Johnson-Shoemaker-2003
PFKFB3	TTN	0.007780046903130148	Co-localization	Johnson-Shoemaker-2003
CARD6	NUP153	0.007361927347926266	Genetic interactions	Lin-Smith-2010
ASAH1	CD274	0.003339743721763161	Genetic interactions	Lin-Smith-2010
NAAA	MUC4	0.004345540422946215	Genetic interactions	Lin-Smith-2010
NPEP	C1orf116	0.00430151354521513	Genetic interactions	Lin-Smith-2010
NS II DD4	SHROOM3	0.004259391687810421	Genetic interactions	Lin-Smith-2010
_ILRB1	CTSB	0.0038562011905014515	Genetic interactions	Lin-Smith-2010
NUP153	CROCC	0.0025432317052036524	Genetic interactions	Lin-Smith-2010
SLC25A13	CGN	0.002533102873712778	Genetic interactions	Lin-Smith-2010
PSAP	CTSB	0.0024801704566925764	Genetic interactions	Lin-Smith-2010
PYROXD2	PFKFB3	0.002246732823550701	Genetic interactions	Lin-Smith-2010

www.genemania.org/print 20/23

NAAA	WRNIP1	0.002160204341635108	Genetic interactions	Lin-Smith-2010
NAAA SMNDC1	WRNIP1 CARD8	0.002160204341635108 0.0020324052311480045	Genetic interactions Genetic interactions	Lin-Smith-2010 Lin-Smith-2010
CTSB	CUBN	0.001953176921233535	Genetic interactions	Lin-Smith-2010
OBSCN	SMN1	0.0019485234515741467	Genetic interactions	Lin-Smith-2010
TTN	FGFRL1	0.0019240512046962976	Genetic interactions	Lin-Smith-2010
MCM10	FGFRL1	0.0019101498182862997	Genetic interactions	Lin-Smith-2010
CD274	CGN	0.0018716314807534218	Genetic interactions	Lin-Smith-2010
PFKFB3	SMN1	0.0018453970551490784	Genetic interactions	Lin-Smith-2010
AP1G2	RASA1	0.0018346235156059265	Genetic interactions	Lin-Smith-2010
LIPA	CUBN	0.0018153605051338673	Genetic interactions	Lin-Smith-2010
LNPEP	CARD8	0.0018107526702806354	Genetic interactions	Lin-Smith-2010
CTSB	OBSCN	0.0017904237611219287	Genetic interactions	Lin-Smith-2010
IGHMBP2	OBSCN	0.0016875338042154908	Genetic interactions	Lin-Smith-2010
AP1G2	IGHMBP2	0.001679399749264121	Genetic interactions	Lin-Smith-2010
APOH	SLC25A13	0.0016727768816053867	Genetic interactions	Lin-Smith-2010
CGN	C15orf42	0.0016658599488437176	Genetic interactions	Lin-Smith-2010
APOH	LAIR1	0.0016527596162632108	Genetic interactions	Lin-Smith-2010
PFKFB3	APOH	0.0016235101502388716	Genetic interactions	Lin-Smith-2010
PSAP	OGFRL1	0.0016193259507417679	Genetic interactions	Lin-Smith-2010
LIPA	LAIR1	0.0016044124495238066	Genetic interactions	Lin-Smith-2010
NUP153	PFKFB3	0.001545567880384624	Genetic interactions	Lin-Smith-2010
VAPA	LAIR1	0.0015337038785219193	Genetic interactions	Lin-Smith-2010
SLC13A3	ZFYVE28	0.001520795514807105	Genetic interactions	Lin-Smith-2010
CTSB	ZFYVE28	0.0014636059058830142	Genetic interactions	Lin-Smith-2010
CELSR1	OBSCN	0.0014518590178340673	Genetic interactions	Lin-Smith-2010
SPTA1	PFKFB3	0.0014382645022124052	Genetic interactions	Lin-Smith-2010
NAAA	LNPEP	0.0014054245548322797	Genetic interactions	Lin-Smith-2010
KCNB1	IGHMBP2	0.0013313754461705685	Genetic interactions	Lin-Smith-2010
DMBT1	ZFYVE28	0.00132117816247046	Genetic interactions	Lin-Smith-2010
MCM10	C15orf42	0.0011586913606151938	Genetic interactions	Lin-Smith-2010
LIPA	SMN1	0.0011170108336955309	Genetic interactions	Lin-Smith-2010
LIPA	RASA1	0.0010568104917183518	Genetic interactions	Lin-Smith-2010
SMNDC1	WRNIP1	0.0010491881985217333	Genetic interactions	Lin-Smith-2010
UBA1	ATM	0.001039548427797854	Genetic interactions	Lin-Smith-2010
DMBT1	C15orf42	0.0010371605167165399	Genetic interactions	Lin-Smith-2010
DMBT1	TTN	0.0010125857079401612	Genetic interactions	Lin-Smith-2010
DMBT1	CTSB	9.968356462195516E-4	Genetic interactions	Lin-Smith-2010
VAPA	TTN	9.966468205675483E-4	Genetic interactions	Lin-Smith-2010
APOH	IGHMBP2	9.965471690520644E-4	Genetic interactions	Lin-Smith-2010
SLC13A3	SMNDC1	9.557590819895267E-4	Genetic interactions	Lin-Smith-2010
DMBT1	IGHMBP2	9.395505767315626E-4	Genetic interactions	Lin-Smith-2010
PYROXD2	ATM	9.314751951023936E-4	Genetic interactions	Lin-Smith-2010
SMNDC1	CTSB	9.198177140206099E-4	Genetic interactions	Lin-Smith-2010
NUP153	DMBT1	9.085976635105908E-4	Genetic interactions	Lin-Smith-2010
PFKFB3	TLR4	8.706679218448699E-4	Genetic interactions	Lin-Smith 2010
SLC13A3	LNPEP	8.515247027389705E-4	Genetic interactions	Lin-Smith-2010
OGFRL1	CD274	8.428365108557045E-4	Genetic interactions	Lin-Smith-2010
VAPA	SPTA1	8.322077919729054E-4	Genetic interactions	Lin-Smith-2010
GCNT4	IGHMBP2	7.745112525299191E-4	Genetic interactions	Lin-Smith-2010
WRNIP1	SHROOM3	7.657340029254556E-4	Genetic interactions	Lin-Smith-2010
SPTA1	CELSR1	7.595451315864921E-4	Genetic interactions	Lin-Smith-2010
CELSR1	VAPB	7.328864885494113E-4	Genetic interactions	Lin-Smith-2010

www.genemania.org/print 21/23

005014	OTOD	7.0400000405007005.4	0 " ' ' "	1: 0 : 0040
OGFRL1 LNPEP	CTSB VAPB	7.210063049569726E-4 6.707063876092434E-4	Genetic interactions Genetic interactions	Lin-Smith-2010 Lin-Smith-2010
LIPA	SHROOM3	6.239469512365758E-4	Genetic interactions	Lin-Smith-2010
TLR4	SMN1	6.170901469886303E-4	Genetic interactions	Lin-Smith-2010
OGFRL1	SMNDC1	6.005573668517172E-4	Genetic interactions	Lin-Smith-2010
OGFRL1	VAPB	5.900936084799469E-4	Genetic interactions	Lin-Smith-2010
SLC13A3	TLR4	5.891766049899161E-4	Genetic interactions	Lin-Smith-2010
RASA1	TLR4	5.838325596414506E-4	Genetic interactions	Lin-Smith-2010
CTSB	TLR4	5.670206155627966E-4	Genetic interactions	Lin-Smith-2010
TTN	OCA2	5.604404723271728E-4	Genetic interactions	Lin-Smith-2010
OCA2	MCM10	5.563912563957274E-4	Genetic interactions	Lin-Smith-2010
CTSB	OCA2	5.51723234821111E-4	Genetic interactions	Lin-Smith-2010
CELSR1	SHROOM3	5.443709087558091E-4	Genetic interactions	Lin-Smith-2010
APOH	OCA2	5.282460479065776E-4	Genetic interactions	Lin-Smith-2010
LIPA	OCA2	5.127936019562185E-4	Genetic interactions	Lin-Smith-2010
DMBT1	TLR4	5.118421977385879E-4	Genetic interactions	Lin-Smith-2010
OGFRL1	SHROOM3	4.3830767390318215E-4	Genetic interactions	Lin-Smith-2010
OCA2	SHROOM3	3.353986539877951E-4	Genetic interactions	Lin-Smith-2010
TLR4	TLR10	0.047011617571115494	Pathway	Wu-Stein-2010
TLR4	MAP3K1	0.014986002817749977	Pathway	Wu-Stein-2010
CARD6	CARD8	0.6985023617744446	Physical interactions	BIOGRID-SMALL-SCALE- STUDIES
TLR1	TLR4	0.32485640048980713	Physical interactions	BIOGRID-SMALL-SCALE- STUDIES
TTN	OBSCN	0.20722170174121857	Physical interactions	BIOGRID-SMALL-SCALE- STUDIES
VAPA	VAPB	0.11406677216291428	Physical interactions	BIOGRID-SMALL-SCALE- STUDIES
SMN1	SMN2	0.052880629897117615	Physical interactions	BIOGRID-SMALL-SCALE- STUDIES
PYROXD2	CTSB	0.8138431906700134	Predicted	Stuart-Kim-2003
LIPA	ASAH1	0.633423388004303	Predicted	Stuart-Kim-2003
TTN	HSPG2	0.11737769842147827	Predicted	Stuart-Kim-2003
NAAA	ASAH1	1.0	Shared protein domains	PFAM
OGFRL1	OGFR	0.6388529539108276	Shared protein domains	PFAM
SMN1	SMN2	0.3004758656024933	Shared protein domains	PFAM
AC139494.2	SMN2	0.3004758656024933	Shared protein domains	PFAM
AC139494.2	SMN1	0.3004758656024933	Shared protein domains	PFAM
SMNDC1	SMN2	0.3004758656024933	Shared protein domains	PFAM
SMNDC1	SMN1	0.3004758656024933	Shared protein domains	PFAM
SMNDC1	AC139494.2	0.3004758656024933	Shared protein domains	PFAM
VAPA	VAPB	0.2827906608581543	Shared protein domains	PFAM
MOSPD3	VAPB	0.2827906608581543	Shared protein domains	PFAM
MOSPD3	VAPA	0.2827906608581543	Shared protein domains	PFAM
MOSPD1	VAPB	0.2827906608581543	Shared protein domains	PFAM
MOSPD1	VAPA	0.2827906608581543	Shared protein domains	PFAM
MOSPD1	MOSPD3	0.2827906608581543	Shared protein domains	PFAM
SLC13A5	OCA2	0.25139105319976807	Shared protein domains	PFAM
SLC13A3	OCA2		•	
		0.25139105319976807	Shared protein domains	PFAM
SLC13A3	SLC13A5	0.24540232121944427	Shared protein domains	PFAM
SHROOM1	SHROOM3	0.2178654819726944	Shared protein domains	PFAM
INS	RP11- 889I17.1	0.14285725355148315	Shared protein domains	PFAM

www.genemania.org/print 22/23

RLN1	RP11- 889l17.1	0.14285725355148315	Shared protein domains	PFAM
RLN1	INS	0.14285725355148315	Shared protein domains	PFAM
INSL3	RP11- 889l17.1	0.14285725355148315	Shared protein domains	PFAM
INSL3	INS	0.14285725355148315	Shared protein domains	PFAM
INSL3	RLN1	0.14285725355148315	Shared protein domains	PFAM
INSL6	RP11- 889I17.1	0.14285725355148315	Shared protein domains	PFAM
INSL6	INS	0.14285725355148315	Shared protein domains	PFAM
INSL6	RLN1	0.14285725355148315	Shared protein domains	PFAM
INSL6	INSL3	0.14285725355148315	Shared protein domains	PFAM
IGF2	RP11- 889I17.1	0.14285679161548615	Shared protein domains	PFAM
INS	IGF2	0.14285679161548615	Shared protein domains	PFAM
RLN1	IGF2	0.14285679161548615	Shared protein domains	PFAM
INSL3	IGF2	0.14285679161548615	Shared protein domains	PFAM
INSL6	IGF2	0.14285679161548615	Shared protein domains	PFAM
CARD6	CARD8	0.04619709029793739	Shared protein domains	PFAM
TLR4	TLR10	0.03398328647017479	Shared protein domains	PFAM
TLR1	TLR4	0.03398328274488449	Shared protein domains	PFAM
TLR1	TLR10	0.03398321941494942	Shared protein domains	PFAM
TTN	OBSCN	0.013619850389659405	Shared protein domains	PFAM
MAP3K1	CGN	0.0134999118745327	Shared protein domains	PFAM
APOH	MASP2	0.012968470342457294	Shared protein domains	PFAM
HSPG2	CELSR1	0.011701952666044235	Shared protein domains	PFAM
DMBT1	MASP2	0.009617800824344158	Shared protein domains	PFAM

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www.genemania.org/print 23/23