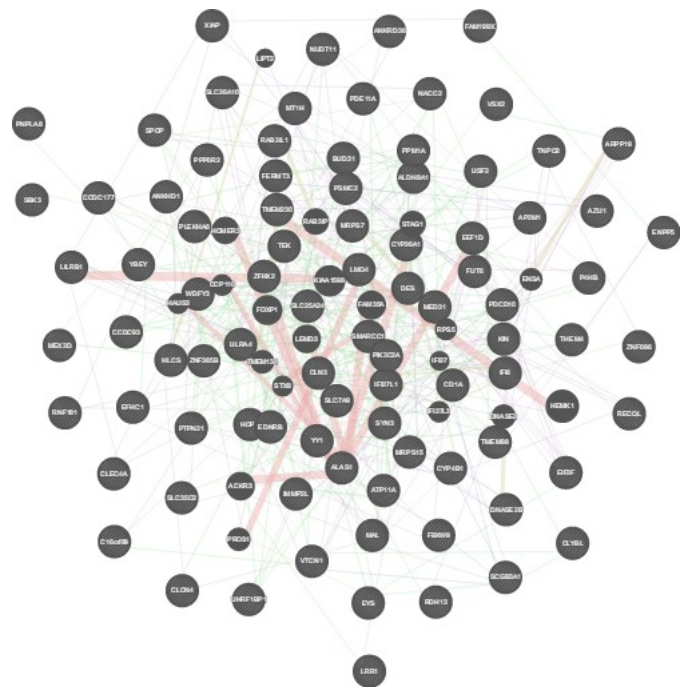


GeneMANIA report

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Last database update : 16 October 2014 00:00:00
Application version : 3.5.0



Networks

- Co-expression
- Physical interactions
- Co-localization
- Genetic interactions
- Shared protein domains

Functions

N/A

Search parameters

Organism Homo sapiens (human)

Genes RECQL , TMEM98 , PIK3C2A , SLC7A9 , ALAS1 , UHRF1BP1 , ATP11A , PTPN21 , CLCN4 , SLC35C2 , SLC25A24 , TMEM230 , CYP26A1 , EFHC1 , PPP6R2 , PPM1A , YY1 , XIAP , EEF1D , LILRB1 , TNPO2 , USF2 , BUD31 , MED31 , CLEC4A , ENPP5 , PDCD10 , MRPS15 , ALDH8A1 , VSX2 , TEK , SPOP , FAM199X , CLYBL , MRPS7 , CCDC93 , IFI6 , PDE11A , ARPP19 , ANKHD1 , FBXW9 , VTCN1 , PNPLA8 , SLC26A10 , ANKRD36 , EDNRB , ZFHX2 , DNASE2B , CYP4B1 , LMO4 , PLEKHA6 , ZNF385B , NACC2 , FERMT3 , KIN , C16orf89 , FUT6 , CD1A , HLCS , THEM4 , RDH13 , SCGB3A1 , PSMC2 , AP2M1 , WDFY3 , LRR1 , IFI27L1 , RAB3IL1 , RNF181 , HOPX , MAL , AZU1 , SMARCC1 , DES , EIF3F , MEX3D , YBEY , IMMP2L , P4HB , SYN3 , ZNF696 , KRTAP19-5 , EYS , CLN3 , ZFP92 , NUDT11 , MT1H , EIF3CL , SBK3 , LILRA4 , CCDC177

Network weighting Automatically selected weighting method

Networks A

Abu-Odeh-Aqeilan-2014 , Agrawal-Sedivy-2010 , Aichem-Groettrup-2012 , Albers-Koegl-2005 , Alexandru-Deshaies-2008 , Alizadeh-Staudt-2000 , Altun-Kessler-2011 , Andresen-Flores-Morales-2014 , Arbuckle-Grant-2010 , Arijs-Rutgeerts-2009 , Arora-Mercola-2008

B

Bahr-Bowler-2013 , Bandyopadhyay-Ideker-2010 , Bantscheff-Drewes-2011 , Barr-Knapp-2009 , Barrios-Rodiles-Wrana-2005 , Behrends-Harper-2010 , Behzadnia-Lührmann-2007 , Bennett-Harper-2010 , Benzinger-Hermeking-2005 , Berggård-James-2006 , Bett-Hay-2013 , Bild-Nevins-2006 B , BIOGRID-SMALL-SCALE-STUDIES , BIOGRID-SMALL-SCALE-STUDIES , Blandin-Richard-2013 , Boldrick-Relman-2002 , Bouwmeester-Superti-Furga-2004 , Brajenovic-Drewes-2004 , Brehme-Superti-Furga-2009 , Bruderer-Hay-2011 , Burington-Shaughnessy-2008 , Byron-Humphries-2012

C

Cai-Conaway-2007 , Camargo-Brandon-2007 , Cannavo-Jiricny-2007 , Cao-Chinnaiyan-2014 , Chen-Brown-2002 , Chen-Ge-2013 , Chen-Naus-2012 , Chen-Zhang-2013 , Cheng-Chen-2010 , Cheok-Evans-2003 , Cloutier-Coulombe-2013 , Colland-Gauthier-2004 , Couzens-Gingras-2013 , Cox-Rizzino-2013

D

Danielsen-Nielsen-2011 , de Hoog-Mann-2004 , Dyer-Sobral-2010

E

E

Emanuele-Elledge-2011 , Ewing-Figeys-2007

F

Fenner-Prehn-2010 , Foerster-Ritter-2013 , Foster-Marshall-2013 , Freibaum-Taylor-2010

G

Gao-Reinberg-2012 , Gautier-Hall-2009 , Giannone-Liu-2010 , Glatte-Gstaiger-2009 , Gloeckner-Ueffing-2007 , Goehler-Wanker-2004 , Golebiowski-Hay-2009 , Goudreault-Gingras-2009 , Grant-2010 , Greco-Cristea-2011 , Gysin-McMahon-2012

H

Havrylov-Redowicz-2009 , Havugimana-Emili-2012 , Hayes-Urbé-2012 , Hegele-Stelzl-2012 A , Hegele-Stelzl-2012 B , Humphries-Humphries-2009 , Hutchins-Peters-2010

I

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-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-CORE-1-Worm2Human , I2D-Li-Vidal-2004-non-core-Worm2Human , I2D-Manual-Mouse2Human , I2D-Manual-Rat2Human , I2D-MGI-Mouse2Human , I2D-MINT-Fly2Human , I2D-MINT-Mouse2Human , I2D-MINT-Rat2Human , I2D-MINT-Worm2Human , I2D-MINT-Yeast2Human , I2D-Ptacek-Snyder-2005-Yeast2Human , I2D-Tarassov-PCA-Yeast2Human , I2D-Tewari-Vidal-2004-TGFb-Worm2Human , I2D-vonMering-Bork-2002-High-Yeast2Human , I2D-vonMering-Bork-2002-Low-Yeast2Human , I2D-vonMering-Bork-2002-Medium-Yeast2Human , I2D-Wang-Orkin-2006-EScmplx-Mouse2Human , I2D-Wang-Orkin-2006-EScmplxlow-Mouse2Human , I2D-Yu-Vidal-2008-GoldStd-Yeast2Human , Ingham-Pawson-2005 , Innocenti-Brown-2011 , INTERPRO , IREF-BIND , IREF-BIOGRID , IREF-DIP , IREF-HPRD , IREF-INNATEDB , IREF-INTACT , IREF-MATRIXDB , IREF-MPPI , IREF-OPHID , IREF-PUBMED , IREF-SMALL-SCALE-STUDIES , IREF-SMALL-SCALE-STUDIES

J

Jeronimo-Coulombe-2007 , Jin-Pawson-2004 , Johnson-Shoemaker-2003 , Jones-MacBeath-2006 , Joshi-Cristea-2013 , Jäger-Krogan-2012

K

K

Kahle-Zoghbi-2011 , Kang-Willman-2010 , Kim-Gygi-2011 , Kneissl-Grummt-2003 , Koch-Hermeking-2007 , Kristensen-Foster-2012

L

Lau-Ronai-2012 , Lee-Doedens-2011 , Lee-Songyang-2011 , Lehner-Sanderson-2004 A , Lehner-Sanderson-2004 B , Leng-Wang-2014 , Li-Dorf-2011 A , Li-Dorf-2011 B , Lim-Zoghbi-2006 , Lin-Boeke-2012 A , Lin-Boeke-2012 B , Lin-Smith-2010 , Liu-Wang-2012 , Loch-Strickler-2012 , Lopitz-Otsoa-Rodriguez-2012 , Lu-Zhang-2013

M

Mak-Moffat-2010 , Mallon-McKay-2013 , Malovannaya-Qin-2010 , Markson-Sanderson-2009 , Maréchal-Zou-2014 , Matafora-Bachi-2009 , Matsumoto-Nakayama-2005 , McCracken-Blencowe-2005 , McFarland-Nussbaum-2008 , Meek-Piwnica-Worms-2004 , Meierhofer-Kaiser-2008 , Miyamoto-Sato-Yanagawa-2010

N

Nakayama-Ohara-2002 , Nakayasu-Adkins-2013 , Napolitano-Meroni-2011 , Nathan-Goldberg-2013 , Neganova-Lako-2011 , Newman-Keating-2003

O

Olma-Pintard-2009 , Oláh-Ovádi-2011 , Oshikawa-Nakayama-2012 , Ouyang-Gill-2009

P

Panigrahi-Pati-2012 , PATHWAYCOMMONS-CELL_MAP , PATHWAYCOMMONS-HUMANCYC , PATHWAYCOMMONS-IMID , PATHWAYCOMMONS-NCI_NATURE , PATHWAYCOMMONS-REACTOME , Perez-Hernandez-Yáñez-Mó-2013 , Perou-Botstein-1999 , Persaud-Rotin-2009 , PFAM , Pichlmair-Superti-Furga-2011 , Pichlmair-Superti-Furga-2012 , Pilot-Storck-Goylot-2010 , Povlsen-Choudhary-2012

R

Ramachandran-LaBaer-2004 , Ramaswamy-Golub-2001 , Ravasi-Hayashizaki-2010 , Reinke-Keating-2013 , Richter-Chrzanowska-Lightowlers-2010 , Rieger-Chu-2004 , Roth-Zlotnik-2006 , Roux-Burke-2012 , Rowbotham-Mermoud-2011 , Roy-Parent-2013 , Rual-Vidal-2005 A , Rual-Vidal-2005 B

S

Salaverria-Siebert-2011 , San-Marina-Minden-2008 , Sang-Jackson-2011 , Sato-Conaway-2004 , Satoh-Yamamoto-2013 , Schadt-Shoemaker-2004 , Shi-Qin-2011 , Singh-Moore-2012 , Smirnov-Cheung-2009 , Soler-López-Aloy-2011 , Sowa-Harper-2009 , Stehling-Lill-2012 , Stelzl-Wanker-2005 , Stuart-Kim-2003 , Suter-Wanker-2013

T

Taipale-Lindquist-2012 , Takahashi-Conaway-2011 , Tarallo-Weisz-2011 , Tatham-

T

Hay-2011 , Teixeira-Gomes-2010 , Thalappilly-Duseti-2008 , Toyoshima-Grandori-2012 , Tsai-Cristea-2012

U

Udeshi-Carr-2012

V

van Wijk-Timmers-2009 , Vandamme-Angrand-2011 , Vanderwerf-Bagby-2009 , Varjosalo-Gstaiger-2013 A , Varjosalo-Gstaiger-2013 B , Varjosalo-Superti-Furga-2013 , Venkatesan-Vidal-2009 , Vinayagam-Wanker-2011

W

Wagner-Choudhary-2011 , Wallach-Kramer-2013 , Wang-Balch-2006 , Wang-He-2008 , Wang-Maris-2006 , Wang-Yang-2011 , Weimann-Stelzl-2013 A , Weimann-Stelzl-2013 B , Weinmann-Meister-2009 , Wilker-Yaffe-2007 , Willingham-Muchowski-2003 , Wong-O'Bryan-2012 , Woods-Monteiro-2012 , Woodsmith-Sanderson-2012 , Wu-Garvey-2007 , Wu-Li-2007 , Wu-Ma-2012 , Wu-Stein-2010

X

Xiao-Lefkowitz-2007 , Xie-Cong-2013 , Xu-Jaffrey-2010 , Xu-Ye-2012

Y

Yang-Chen-2010 , Yatim-Benkirane-2012 , Yu-Chow-2013 , Yu-Vidal-2011

Z

Zanon-Pichler-2013 , Zhang-Zou-2011 , Zhao-Krug-2005 , Zhao-Yang-2011 , Zhou-Conrads-2004 , Zhou-Liang-2012

Genes

Gene	Description	Rank
EIF3CL	eukaryotic translation initiation factor 3, subunit C-like [Source:HGNC Symbol;Acc:26347]	N/A
KRTAP19-5	keratin associated protein 19-5 [Source:HGNC Symbol;Acc:18940]	N/A
ZFP92	ZFP92 zinc finger protein [Source:HGNC Symbol;Acc:12865]	N/A
SBK3	SH3 domain binding kinase family, member 3 [Source:HGNC Symbol;Acc:44121]	N/A
PNPLA8	patatin-like phospholipase domain containing 8 [Source:HGNC Symbol;Acc:28900]	N/A
YBEY	ybeY metallopeptidase (putative) [Source:HGNC Symbol;Acc:1299]	N/A
C16orf89	chromosome 16 open reading frame 89 [Source:HGNC Symbol;Acc:28687]	N/A
VSX2	visual system homeobox 2 [Source:HGNC Symbol;Acc:1975]	N/A
UHRF1BP1	UHRF1 binding protein 1 [Source:HGNC Symbol;Acc:21216]	N/A
LRR1	leucine rich repeat protein 1 [Source:HGNC Symbol;Acc:19742]	N/A
RDH13	retinol dehydrogenase 13 (all-trans/9-cis) [Source:HGNC Symbol;Acc:19978]	N/A
IFI27L1	interferon, alpha-inducible protein 27-like 1 [Source:HGNC Symbol;Acc:19754]	N/A
ANKRD36	ankyrin repeat domain 36 [Source:HGNC Symbol;Acc:24079]	N/A
FAM199X	family with sequence similarity 199, X-linked [Source:HGNC Symbol;Acc:25195]	N/A
CCDC177	coiled-coil domain containing 177 [Source:HGNC Symbol;Acc:23243]	N/A
MEX3D	mex-3 RNA binding family member D [Source:HGNC Symbol;Acc:16734]	N/A
THEM4	thioesterase superfamily member 4 [Source:HGNC Symbol;Acc:17947]	N/A
EYS	eyes shut homolog (Drosophila) [Source:HGNC Symbol;Acc:21555]	N/A
CLYBL	citrate lyase beta like [Source:HGNC Symbol;Acc:18355]	N/A
ZNF385B	zinc finger protein 385B [Source:HGNC Symbol;Acc:26332]	N/A
EFHC1	EF-hand domain (C-terminal) containing 1 [Source:HGNC Symbol;Acc:16406]	N/A
RNF181	ring finger protein 181 [Source:HGNC Symbol;Acc:28037]	N/A
SLC35C2	solute carrier family 35 (GDP-fucose transporter), member C2 [Source:HGNC Symbol;Acc:17117]	N/A
TMEM98	transmembrane protein 98 [Source:HGNC Symbol;Acc:24529]	N/A

Gene	Description	Rank
ANKHD1	ankyrin repeat and KH domain containing 1 [Source:HGNC Symbol;Acc:24714]	N/A
FBXW9	F-box and WD repeat domain containing 9 [Source:HGNC Symbol;Acc:28136]	N/A
CLEC4A	C-type lectin domain family 4, member A [Source:HGNC Symbol;Acc:13257]	N/A
IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae) [Source:HGNC Symbol;Acc:14598]	N/A
PDE11A	phosphodiesterase 11A [Source:HGNC Symbol;Acc:8773]	N/A
FERMT3	fermitin family member 3 [Source:HGNC Symbol;Acc:23151]	N/A
NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11 [Source:HGNC Symbol;Acc:18011]	N/A
SCGB3A1	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;Acc:18384]	N/A
HOPX	HOP homeobox [Source:HGNC Symbol;Acc:24961]	N/A
ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative) [Source:HGNC Symbol;Acc:13717]	N/A
DNASE2B	deoxyribonuclease II beta [Source:HGNC Symbol;Acc:28875]	N/A
ATP11A	ATPase, class VI, type 11A [Source:HGNC Symbol;Acc:13552]	N/A
ZNF696	zinc finger protein 696 [Source:HGNC Symbol;Acc:25872]	N/A
VTGN1	V-set domain containing T cell activation inhibitor 1 [Source:HGNC Symbol;Acc:28873]	N/A
ALDH8A1	aldehyde dehydrogenase 8 family, member A1 [Source:HGNC Symbol;Acc:15471]	N/A
MRPS15	mitochondrial ribosomal protein S15 [Source:HGNC Symbol;Acc:14504]	N/A
SLC26A10	solute carrier family 26, member 10 [Source:HGNC Symbol;Acc:14470]	N/A
FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase) [Source:HGNC Symbol;Acc:4017]	N/A
MED31	mediator complex subunit 31 [Source:HGNC Symbol;Acc:24260]	N/A
MRPS7	mitochondrial ribosomal protein S7 [Source:HGNC Symbol;Acc:14499]	N/A
NACC2	NACC family member 2, BEN and BTB (POZ) domain containing [Source:HGNC Symbol;Acc:23846]	N/A
SLC7A9	solute carrier family 7 (amino acid transporter light chain, bo,+ system), member 9 [Source:HGNC Symbol;Acc:11067]	N/A
P4HB	prolyl 4-hydroxylase, beta polypeptide [Source:HGNC Symbol;Acc:8548]	N/A
YY1	YY1 transcription factor [Source:HGNC Symbol;Acc:12856]	N/A
SLC25A24	solute carrier family 25 (mitochondrial carrier; phosphate carrier),	N/A

Gene	Description	Rank
	member 24 [Source:HGNC Symbol;Acc:20662]	
CLCN4	chloride channel, voltage-sensitive 4 [Source:HGNC Symbol;Acc:2022]	N/A
TNPO2	transportin 2 [Source:HGNC Symbol;Acc:19998]	N/A
RAB3IL1	RAB3A interacting protein (rabin3)-like 1 [Source:HGNC Symbol;Acc:9780]	N/A
EIF3F	eukaryotic translation initiation factor 3, subunit F [Source:HGNC Symbol;Acc:3275]	N/A
PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1A [Source:HGNC Symbol;Acc:9275]	N/A
HLCS	holocarboxylase synthetase (biotin-(propionyl-CoA-carboxylase (ATP-hydrolysing)) ligase) [Source:HGNC Symbol;Acc:4976]	N/A
SPOP	speckle-type POZ protein [Source:HGNC Symbol;Acc:11254]	N/A
PPP6R2	protein phosphatase 6, regulatory subunit 2 [Source:HGNC Symbol;Acc:19253]	N/A
WDFY3	WD repeat and FYVE domain containing 3 [Source:HGNC Symbol;Acc:20751]	N/A
CCDC93	coiled-coil domain containing 93 [Source:HGNC Symbol;Acc:25611]	N/A
BUD31	BUD31 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:29629]	N/A
PTPN21	protein tyrosine phosphatase, non-receptor type 21 [Source:HGNC Symbol;Acc:9651]	N/A
TMEM230	transmembrane protein 230 [Source:HGNC Symbol;Acc:15876]	N/A
EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) [Source:HGNC Symbol;Acc:3211]	N/A
KIN	KIN, antigenic determinant of recA protein homolog (mouse) [Source:HGNC Symbol;Acc:6327]	N/A
XIAP	X-linked inhibitor of apoptosis [Source:HGNC Symbol;Acc:592]	N/A
CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:2603]	N/A
ZFHX2	zinc finger homeobox 2 [Source:HGNC Symbol;Acc:20152]	N/A
ARPP19	cAMP-regulated phosphoprotein, 19kDa [Source:HGNC Symbol;Acc:16967]	N/A
IFI6	interferon, alpha-inducible protein 6 [Source:HGNC Symbol;Acc:4054]	N/A
RECQL	RecQ protein-like (DNA helicase Q1-like) [Source:HGNC Symbol;Acc:9948]	N/A
PLEKHA6	pleckstrin homology domain containing, family A member 6 [Source:HGNC Symbol;Acc:17053]	N/A

Gene	Description	Rank
CD1A	CD1a molecule [Source:HGNC Symbol;Acc:1634]	N/A
AZU1	azurocidin 1 [Source:HGNC Symbol;Acc:913]	N/A
TEK	TEK tyrosine kinase, endothelial [Source:HGNC Symbol;Acc:11724]	N/A
LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 [Source:HGNC Symbol;Acc:6605]	N/A
CLN3	ceroid-lipofuscinosis, neuronal 3 [Source:HGNC Symbol;Acc:2074]	N/A
CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1 [Source:HGNC Symbol;Acc:2644]	N/A
SYN3	synapsin III [Source:HGNC Symbol;Acc:11496]	N/A
USF2	upstream transcription factor 2, c-fos interacting [Source:HGNC Symbol;Acc:12594]	N/A
SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 [Source:HGNC Symbol;Acc:11104]	N/A
PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2 [Source:HGNC Symbol;Acc:9548]	N/A
DES	desmin [Source:HGNC Symbol;Acc:2770]	N/A
EDNRB	endothelin receptor type B [Source:HGNC Symbol;Acc:3180]	N/A
MT1H	metallothionein 1H [Source:HGNC Symbol;Acc:7400]	N/A
PIK3C2A	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha [Source:HGNC Symbol;Acc:8971]	N/A
AP2M1	adaptor-related protein complex 2, mu 1 subunit [Source:HGNC Symbol;Acc:564]	N/A
LMO4	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]	N/A
PDCD10	programmed cell death 10 [Source:HGNC Symbol;Acc:8761]	N/A
LILRA4	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4 [Source:HGNC Symbol;Acc:15503]	N/A
MAL	mal, T-cell differentiation protein [Source:HGNC Symbol;Acc:6817]	N/A
ALAS1	aminolevulinate, delta-, synthase 1 [Source:HGNC Symbol;Acc:396]	N/A
HEMK1	HemK methyltransferase family member 1 [Source:HGNC Symbol;Acc:24923]	1
KIAA1598	KIAA1598 [Source:HGNC Symbol;Acc:29319]	2
FOXP1	forkhead box P1 [Source:HGNC Symbol;Acc:3823]	3
FAM35A	family with sequence similarity 35, member A [Source:HGNC Symbol;Acc:28773]	4
ACKR3	atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23692]	5

Gene	Description	Rank
LEMD3	LEM domain containing 3 [Source:HGNC Symbol;Acc:28887]	6
HOMER3	homer homolog 3 (Drosophila) [Source:HGNC Symbol;Acc:17514]	7
RAB3IP	RAB3A interacting protein [Source:HGNC Symbol;Acc:16508]	8
STAG1	stromal antigen 1 [Source:HGNC Symbol;Acc:11354]	9
DNASE2	deoxyribonuclease II, lysosomal [Source:HGNC Symbol;Acc:2960]	10
TMEM134	transmembrane protein 134 [Source:HGNC Symbol;Acc:26142]	11
PROS1	protein S (alpha) [Source:HGNC Symbol;Acc:9456]	12
ENSA	endosulfine alpha [Source:HGNC Symbol;Acc:3360]	13
RPS5	ribosomal protein S5 [Source:HGNC Symbol;Acc:10426]	14
CCP110	centriolar coiled coil protein 110kDa [Source:HGNC Symbol;Acc:24342]	15
IFI27L2	interferon, alpha-inducible protein 27-like 2 [Source:HGNC Symbol;Acc:19753]	16
STX8	syntaxin 8 [Source:HGNC Symbol;Acc:11443]	17
HAUS3	HAUS augmin-like complex, subunit 3 [Source:HGNC Symbol;Acc:28719]	18
IFI27	interferon, alpha-inducible protein 27 [Source:HGNC Symbol;Acc:5397]	19
LIPT2	lipoyl(octanoyl) transferase 2 (putative) [Source:HGNC Symbol;Acc:37216]	20

Networks

Co-expression	54.61%
Cheok-Evans-2003	8.83%
Treatment-specific changes in gene expression discriminate in vivo drug response in human leukemia cells. Cheok et al (2003). <i>Nat Genet</i>	
Co-expression with 263,940 interactions from GEO	
Wang-Maris-2006	8.16%
Integrative genomics identifies distinct molecular classes of neuroblastoma and shows that multiple genes are targeted by regional alterations in DNA copy number. Wang et al (2006). <i>Cancer Res</i>	
Co-expression with 264,234 interactions from GEO	
Gysin-McMahon-2012	6.81%
Analysis of mRNA profiles after MEK1/2 inhibition in human pancreatic cancer cell lines reveals pathways involved in drug sensitivity. Gysin et al (2012). <i>Mol Cancer Res</i>	
Co-expression with 388,454 interactions from GEO	
Bild-Nevins-2006 B	6.44%
Oncogenic pathway signatures in human cancers as a guide to targeted therapies. Bild et al (2006). <i>Nature</i>	
Co-expression with 282,582 interactions from GEO	
Rieger-Chu-2004	5.34%
Toxicity from radiation therapy associated with abnormal transcriptional responses to DNA damage. Rieger et al (2004). <i>Proc Natl Acad Sci U S A</i>	
Co-expression with 259,055 interactions from GEO	
Chen-Brown-2002	4.49%
Gene expression patterns in human liver cancers. Chen et al (2002). <i>Mol Biol Cell</i>	
Co-expression with 275,649 interactions from supplementary material	
Alizadeh-Staudt-2000	3.99%
Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. Alizadeh et al (2000). <i>Nature</i>	
Co-expression with 88,888 interactions from supplementary material	
Boldrick-Relman-2002	2.92%
Stereotyped and specific gene expression programs in human innate immune responses to bacteria. Boldrick et al (2002). <i>Proc Natl Acad Sci U S A</i>	
Co-expression with 108,543 interactions from supplementary material	
Smirnov-Cheung-2009	2.67%
Genetic analysis of radiation-induced changes in human gene expression. Smirnov et al (2009). <i>Nature</i>	
Co-expression with 463,390 interactions from GEO	
Innocenti-Brown-2011	2.26%
Identification, replication, and functional fine-mapping of expression quantitative trait loci in primary human liver tissue. Innocenti et al (2011). <i>PLoS Genet</i>	
Co-expression with 579,361 interactions from GEO	
Mallon-McKay-2013	1.29%
StemCellDB: the human pluripotent stem cell database at the National Institutes of Health. Mallon et al (2013). <i>Stem Cell Res</i>	

Co-expression	54.61%
<hr/>	
Mallon-McKay-2013	
Co-expression with 567,140 interactions from GEO	
<hr/>	
Kang-Willman-2010	0.60%
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). <i>Blood</i>	
Co-expression with 656,632 interactions from GEO	
<hr/>	
Bahr-Bowler-2013	0.56%
Peripheral blood mononuclear cell gene expression in chronic obstructive pulmonary disease. Bahr et al (2013). <i>Am J Respir Cell Mol Biol</i>	
Co-expression with 278,447 interactions from GEO	
<hr/>	
Perou-Botstein-1999	0.25%
Distinctive gene expression patterns in human mammary epithelial cells and breast cancers. Perou et al (1999). <i>Proc Natl Acad Sci U S A</i>	
Co-expression with 62,886 interactions from supplementary material	
Physical interactions	23.13%
<hr/>	
Dyer-Sobral-2010	23.13%
The human-bacterial pathogen protein interaction networks of <i>Bacillus anthracis</i> , <i>Francisella tularensis</i> , and <i>Yersinia pestis</i> . Dyer et al (2010). <i>PLoS One</i>	
Physical interactions with 583 interactions from iRefIndex	
Co-localization	12.83%
<hr/>	
Johnson-Shoemaker-2003	12.83%
Genome-wide survey of human alternative pre-mRNA splicing with exon junction microarrays. Johnson et al (2003). <i>Science</i>	
Co-localization with 426,640 interactions from GEO	
Genetic interactions	5.96%
<hr/>	
Lin-Smith-2010	5.96%
A genome-wide map of human genetic interactions inferred from radiation hybrid genotypes. Lin et al (2010). <i>Genome Res</i>	
Genetic interactions with 4,836,794 interactions from supplementary material	
Shared protein domains	3.47%
<hr/>	
INTERPRO	3.47%
Shared protein domains with 562,560 interactions from InterPro	