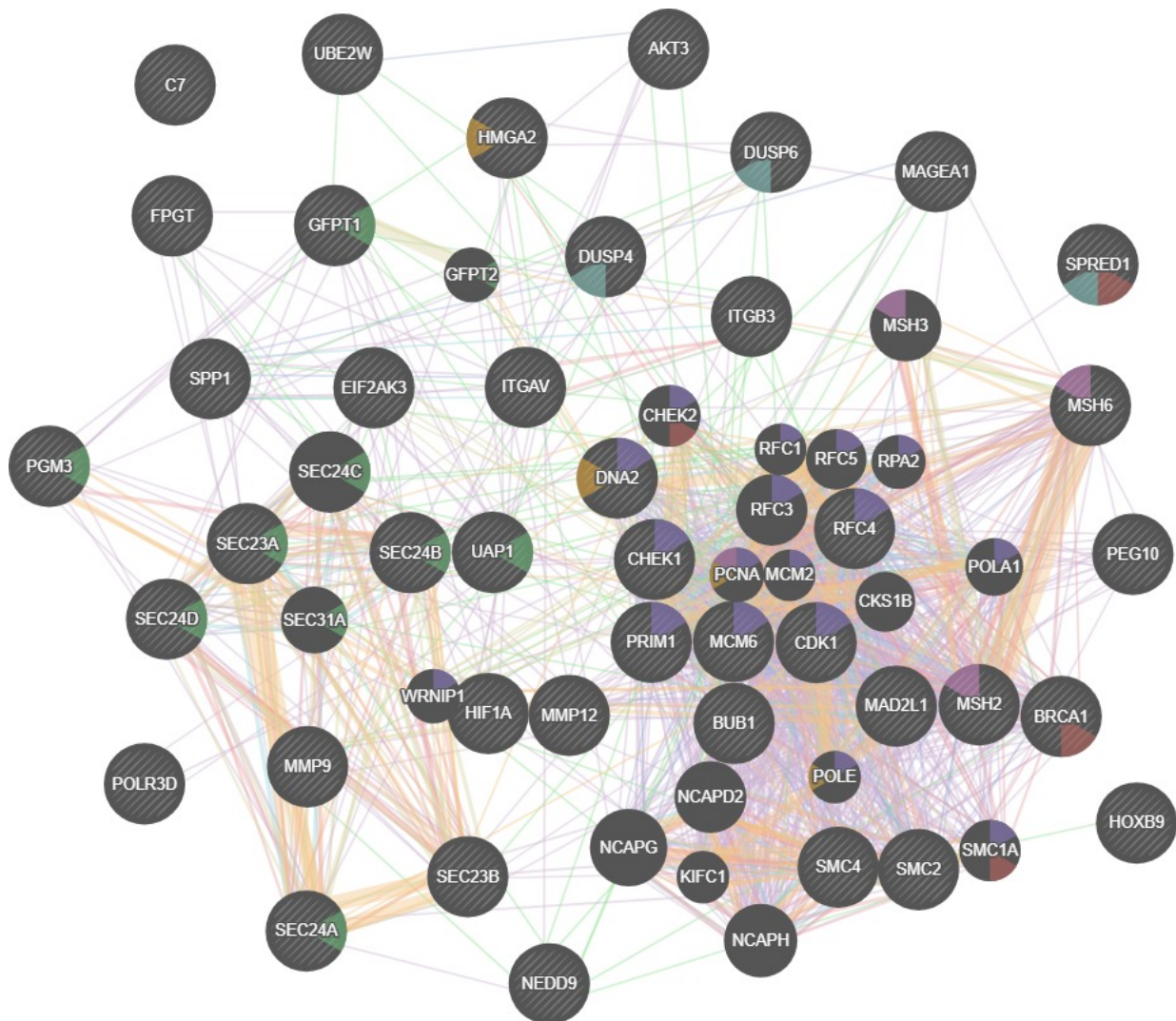


GeneMANIA report

Created on : 12 August 2018 18:05:43
Last database update : 13 March 2017 00:00:00
Application version : 3.6.0



Networks

- Co-expression
- Predicted
- Physical Interactions
- Shared protein domains
- Co-localization
- Pathway
- Genetic Interactions

Functions

- DNA replication
- post-translational protein modification
- signal transduction in response to DNA damage
- inactivation of MAPK activity
- base-excision repair
- mismatch repair

Search parameters

Organism Homo sapiens (human)

Genes BRCA1 , PGM3 , MCM6 , MSH2 , HIF1A , SEC23A , MMP9 , SEC23B , UBE2W , NEDD9 , C7 , SEC24A , SMC4 , MSH6 , AKT3 , UAP1 , SPP1 , DUSP4 , SMC2 , DNA2 , ITGAV , SEC24B , DUSP6 , CHEK1 , HMGA2 , SEC24D , RFC4 , MAD2L1 , SPRED1 , POLR3D , BUB1 , CDK1 , HOXB9 , EIF2AK3 , PRIM1 , GFPT1 , MAGEA1 , PEG10 , FPGT , ITGB3 , MMP12

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 , Andresen-Flores-Morales-2014 , Arbuckle-Grant-2010 , Arroyo-Aloy-2014 , Arroyo-Aloy-2015

B

Bahr-Bowler-2013 , Bailey-Hieter-2015 , 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 , Bhatnagar-Attie-2014 , Bild-Nevins-2006 B , BIOGRID-SMALL-SCALE-STUDIES , BIOGRID-SMALL-SCALE-STUDIES , Blandin-Richard-2013 , Blomen-Brummelkamp-2015 , Blomen-Brummelkamp-2015 , Bogachek-Weigel-2014 , Boldrick-Relman-2002 , Bonacci-Soubeyran-2014 , Bouwmeester-Superti-Furga-2004 , Brajenovic-Drewes-2004 , Brehme-Superti-Furga-2009 , Bruderer-Hay-2011 , Burington-Shaughnessy-2008 , Butland-Hayden-2014 , Byron-Humphries-2012

C

Cai-Conaway-2007 , Camargo-Brandon-2007 , Campos-Reinberg-2015 , Cao-Chinnaiyan-2014 , Carmon-Liu-2014 , CELL_MAP , Chen-Brown-2002 , Chen-Ge-2013 , Chen-Huang-2014 , Chen-Zhang-2013 , Christianson-Kopito-2011 , Cloutier-Coulombe-2013 , Colland-Gauthier-2004 , Corominas-Iakoucheva-2014 , Couzens-Gingras-2013 , Cox-Rizzino-2013 , Coyaud-Raught-2015

D

Danielsen-Nielsen-2011 , Dart-Wells-2015 , de Hoog-Mann-2004 , Diner-Cristea-2015 , Dobbin-Giordano-2005 , Drissi-Boisvert-2015 , Dyer-Sobral-2010

E

Emanuele-Elledge-2011 , Emdal-Olsen-2015 , Ewing-Figeys-2007

F

Fenner-Prehn-2010 , Floyd-Pagliarini-2016 , Foerster-Ritter-2013 , Fogeron-Lange-2013 , Foster-Marshall-2013 , Freibaum-Taylor-2010

G

Gabriel-Baumgrass-2016 , Galligan-Howley-2015 , Gao-Reinberg-2012 , Gautier-Hall-2009 , Giannone-Liu-2010 , Glatter-Gstaiger-2009 , Gloeckner-Ueffing-2007 , Goehler-Wanker-2004 , Golebiowski-Hay-2009 , Goudreault-Gingras-2009 , Grant-2010 , Greco-Cristea-2011 , Grossmann-Stelzl-2015 , Guarani-Harper-2014 , Gupta-Pelletier-2015

H

Hanson-Clayton-2014 , Hauri-Gstaiger-2013 , Havrylov-Redowicz-2009 , Havugimana-Emili-2012 , Hayes-Urbé-2012 , Hegele-Stelzl-2012 A , Hegele-Stelzl-2012 B , Hein-Mann-2015 , Hill-Livingston-2014 , HUMANCYC , Humphries-Humphries-2009 , Hutchins-Peters-2010 , Huttlin-Gygi-2015

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 , IMID , Ingham-Pawson-2005 , Innocenti-Brown-2011 , INTERPRO , IREF-BIND , IREF-BIOGRID , IREF-DIP , IREF-HPRD , IREF-INTACT , IREF-MATRIXDB , IREF-MPPI , IREF-PUBMED , IREF-SMALL-SCALE-STUDIES , IREF-SMALL-SCALE-STUDIES

J

Jeronimo-Coulombe-2007 , Jin-Pawson-2004 , Johnson-Kerner-Wichterle-2015 , Johnson-Shoemaker-2003 , Jones-MacBeath-2006 , Joshi-Cristea-2013 , Jäger-Krogan-2011

K

Kahle-Zoghbi-2011 , Kaltenbach-Hughes-2007 , Katsogiannou-Rocchi-2014 , Kim-Gygi-2011 , Kim-Major-2015 , Kneissl-Grummt-2003 , Koch-Hermeking-2007 ,

K

Kotlyar-Jurisica-2015 , Kristensen-Foster-2012 , Kärblane-Sarmiento-2015 , Kırılı-Görlich-2015

L

Lambert-Gingras-2015 , Lamoliatte-Thibault-2014 , Lau-Ronai-2012 , Lee-Songyang-2011 , Lehner-Sanderson-2004 A , Lehner-Sanderson-2004 B , Leng-Wang-2014 , Leung-Jones-2014 , Li-Chen-2015 , Li-Dorf-2011 A , Li-Dorf-2011 B , Li-Dorf-2014 , Li-Haura-2013 , Lim-Zoghbi-2006 , Lin-Smith-2010 , Lipp-Guthrie-2015 , Liu-Wang-2012 , Llères-Lamond-2010 , Loch-Strickler-2012 , Low-Heck-2014 , Lu-Zhang-2013 , Luo-Elledge-2009

M

Mak-Moffat-2010 , Mallon-McKay-2013 , Malovannaya-Qin-2010 , Markson-Sanderson-2009 , Maréchal-Zou-2014 , Matsumoto-Nakayama-2005 , McCracken-Blencowe-2005 , McFarland-Nussbaum-2008 , Meek-Piwnica-Worms-2004 , Milev-Mouland-2012 , Miyamoto-Sato-Yanagawa-2010 , Murakawa-Landthaler-2015

N

Nakayama-Ohara-2002 , Nakayasu-Adkins-2013 , Napolitano-Meroni-2011 , Narayan-Bennett-2012 , Nathan-Goldberg-2013 , NCI_NATURE , Neganova-Lako-2011 , Newman-Keating-2003 , Nicholson-Hupp-2014 , Noble-Diehl-2008

O

Oliviero-Cagney-2015 , Olma-Pintard-2009 , Oláh-Ovádi-2011 , Oshikawa-Nakayama-2012 , Ouyang-Gill-2009

P

Panigrahi-Pati-2012 , Papp-Lamia-2015 , Perez-Hernandez-Yáñez-Mó-2013 , Perou-Botstein-1999 , Perou-Botstein-2000 , Persaud-Rotin-2009 , Petschnigg-Stagljar-2014 , PFAM , Phillips-Corn-2013 , Pichlmair-Superti-Furga-2011 , Pichlmair-Superti-Furga-2012 , Pilot-Storck-Goillot-2010 , Povlsen-Choudhary-2012

R

Ramachandran-LaBaer-2004 , Raman-Harper-2015 , Ramaswamy-Golub-2001 , Ravasi-Hayashizaki-2010 , REACTOME , Reinke-Keating-2013 , Reyniers-Taymans-2014 , Richter-Chrzanowska-Lightowlers-2010 , Rieger-Chu-2004 , Rolland-Vidal-2014 , Rosenwald-Staudt-2001 , Roth-Zlotnik-2006 , Roux-Burke-2012 , Rowbotham-Mermoud-2011 , Roy-Pardo-2014 , Roy-Parent-2013 , Rual-Vidal-2005 A , Rual-Vidal-2005 B

S

Sang-Jackson-2011 , Sato-Conaway-2004 , Schadt-Shoemaker-2004 , Scholz-Taylor-2016 , Singh-Moore-2012 , Smirnov-Cheung-2009 , So-Colwill-2015 , Soler-López-Aloy-2011 , Sowa-Harper-2009 , Stehling-Lill-2012 , Stehling-Lill-2013 , Stelzl-Wanker-2005 , Stes-Gevaert-2014 , Stuart-Kim-2003 , Suter-Wanker-2013

T

Taipale-Lindquist-2012 , Taipale-Lindquist-2014 , Takahashi-Conaway-2011 , Tarallo-Weisz-2011 , Tatham-Hay-2011 , Teixeira-Gomes-2010 , Thalappilly-Duseti-2008 , Thompson-Luchansky-2014 , Tong-Moran-2014 , Toyoshima-Grandori-2012 , Tsai-Cristea-2012

U

Udeshi-Carr-2012

V

van Wijk-Timmers-2009 , Vandamme-Angrand-2011 , Varjosalo-Gstaiger-2013 , Varjosalo-Superti-Furga-2013 , Venkatesan-Vidal-2009 , Vermeulen-Mann-2010 , Vinayagam-Wanker-2011 , Virok-Fülöp-2011 , Vizeacoumar-Moffat-2013

W

Wagner-Choudhary-2011 , Wallach-Kramer-2013 , Wan-Emili-2015 , Wang-Balch-2006 , Wang-Cheung-2015 , Wang-He-2008 , Wang-Maris-2006 , Wang-Xu-2015 , Wang-Yang-2011 , Weimann-Stelzl-2013 A , Weimann-Stelzl-2013 B , Weinmann-Meister-2009 , Wen-Wu-2014 , Whisenant-Salomon-2015 , Wilker-Yaffe-2007 , Willingham-Muchowski-2003 , Witt-Labeit-2008 , Wong-O'Bryan-2012 , Woods-Monteiro-2012 , Woodsmith-Sanderson-2012 , Wu-Garvey-2007 , Wu-Li-2007 , Wu-Ma-2012 , Wu-Stein-2010 , Wu-Stein-2010

X

Xiao-Lefkowitz-2007 , Xie-Cong-2013 , Xie-Green-2012 , Xu-Ye-2012

Y

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

Z

Zanon-Pichler-2013 , Zhang-Shang-2006 , Zhang-Zou-2011 , Zhao-Krug-2005 , Zhao-Yang-2011 , Zhou-Conrads-2004 , Zhou-Hanemann-2016

Genes

Gene	Description	Rank
SPRED1	sprouty related EVH1 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:20249]	N/A
HOXB9	homeobox B9 [Source:HGNC Symbol;Acc:HGNC:5120]	N/A
UBE2W	ubiquitin conjugating enzyme E2 W (putative) [Source:HGNC Symbol;Acc:HGNC:25616]	N/A
HMGA2	high mobility group AT-hook 2 [Source:HGNC Symbol;Acc:HGNC:5009]	N/A
SPP1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGNC:11255]	N/A
POLR3D	polymerase (RNA) III subunit D [Source:HGNC Symbol;Acc:HGNC:1080]	N/A
EIF2AK3	eukaryotic translation initiation factor 2 alpha kinase 3 [Source:HGNC Symbol;Acc:HGNC:3255]	N/A
AKT3	AKT serine/threonine kinase 3 [Source:HGNC Symbol;Acc:HGNC:393]	N/A
SEC24D	SEC24 homolog D, COPII coat complex component [Source:HGNC Symbol;Acc:HGNC:10706]	N/A
MAGEA1	MAGE family member A1 [Source:HGNC Symbol;Acc:HGNC:6796]	N/A
ITGB3	integrin subunit beta 3 [Source:HGNC Symbol;Acc:HGNC:6156]	N/A
SEC24A	SEC24 homolog A, COPII coat complex component [Source:HGNC Symbol;Acc:HGNC:10703]	N/A
GFPT1	glutamine--fructose-6-phosphate transaminase 1 [Source:HGNC Symbol;Acc:HGNC:4241]	N/A
PGM3	phosphoglucomutase 3 [Source:HGNC Symbol;Acc:HGNC:8907]	N/A
NEDD9	neural precursor cell expressed, developmentally down-regulated 9 [Source:HGNC Symbol;Acc:HGNC:7733]	N/A
C7	complement component 7 [Source:HGNC Symbol;Acc:HGNC:1346]	N/A
PEG10	paternally expressed 10 [Source:HGNC Symbol;Acc:HGNC:14005]	N/A
FPGT	fucose-1-phosphate guanylyltransferase [Source:HGNC Symbol;Acc:HGNC:3825]	N/A
SEC23B	Sec23 homolog B, coat complex II component [Source:HGNC Symbol;Acc:HGNC:10702]	N/A
DNA2	DNA replication helicase/nuclease 2 [Source:HGNC Symbol;Acc:HGNC:2939]	N/A
MMP12	matrix metalloproteinase 12 [Source:HGNC Symbol;Acc:HGNC:7158]	N/A
DUSP4	dual specificity phosphatase 4 [Source:HGNC Symbol;Acc:HGNC:3070]	N/A
MSH6	mutS homolog 6 [Source:HGNC Symbol;Acc:HGNC:7329]	N/A

Gene	Description	Rank
UAP1	UDP-N-acetylglucosamine pyrophosphorylase 1 [Source:HGNC Symbol;Acc:HGNC:12457]	N/A
DUSP6	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:HGNC:3072]	N/A
SEC23A	Sec23 homolog A, coat complex II component [Source:HGNC Symbol;Acc:HGNC:10701]	N/A
SMC2	structural maintenance of chromosomes 2 [Source:HGNC Symbol;Acc:HGNC:14011]	N/A
SEC24B	SEC24 homolog B, COPII coat complex component [Source:HGNC Symbol;Acc:HGNC:10704]	N/A
BUB1	BUB1 mitotic checkpoint serine/threonine kinase [Source:HGNC Symbol;Acc:HGNC:1148]	N/A
SMC4	structural maintenance of chromosomes 4 [Source:HGNC Symbol;Acc:HGNC:14013]	N/A
MMP9	matrix metalloproteinase 9 [Source:HGNC Symbol;Acc:HGNC:7176]	N/A
ITGAV	integrin subunit alpha V [Source:HGNC Symbol;Acc:HGNC:6150]	N/A
CHEK1	checkpoint kinase 1 [Source:HGNC Symbol;Acc:HGNC:1925]	N/A
BRCA1	BRCA1, DNA repair associated [Source:HGNC Symbol;Acc:HGNC:1100]	N/A
CDK1	cyclin dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC:1722]	N/A
HIF1A	hypoxia inducible factor 1 alpha subunit [Source:HGNC Symbol;Acc:HGNC:4910]	N/A
MCM6	minichromosome maintenance complex component 6 [Source:HGNC Symbol;Acc:HGNC:6949]	N/A
MSH2	mutS homolog 2 [Source:HGNC Symbol;Acc:HGNC:7325]	N/A
PRIM1	primase (DNA) subunit 1 [Source:HGNC Symbol;Acc:HGNC:9369]	N/A
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast) [Source:HGNC Symbol;Acc:HGNC:6763]	N/A
RFC4	replication factor C subunit 4 [Source:HGNC Symbol;Acc:HGNC:9972]	N/A
SEC24C	SEC24 homolog C, COPII coat complex component [Source:HGNC Symbol;Acc:HGNC:10705]	1
NCAPG	non-SMC condensin I complex subunit G [Source:HGNC Symbol;Acc:HGNC:24304]	2
NCAPH	non-SMC condensin I complex subunit H [Source:HGNC Symbol;Acc:HGNC:1112]	3
NCAPD2	non-SMC condensin I complex subunit D2 [Source:HGNC Symbol;Acc:HGNC:24305]	4
MSH3	mutS homolog 3 [Source:HGNC Symbol;Acc:HGNC:7326]	5

Gene	Description	Rank
RFC3	replication factor C subunit 3 [Source:HGNC Symbol;Acc:HGNC:9971]	6
SEC31A	SEC31 homolog A, COPII coat complex component [Source:HGNC Symbol;Acc:HGNC:17052]	7
CHEK2	checkpoint kinase 2 [Source:HGNC Symbol;Acc:HGNC:16627]	8
SMC1A	structural maintenance of chromosomes 1A [Source:HGNC Symbol;Acc:HGNC:11111]	9
RFC5	replication factor C subunit 5 [Source:HGNC Symbol;Acc:HGNC:9973]	10
CKS1B	CDC28 protein kinase regulatory subunit 1B [Source:HGNC Symbol;Acc:HGNC:19083]	11
POLA1	polymerase (DNA) alpha 1, catalytic subunit [Source:HGNC Symbol;Acc:HGNC:9173]	12
GFPT2	glutamine-fructose-6-phosphate transaminase 2 [Source:HGNC Symbol;Acc:HGNC:4242]	13
PCNA	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:HGNC:8729]	14
WRNIP1	Werner helicase interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:20876]	15
RPA2	replication protein A2 [Source:HGNC Symbol;Acc:HGNC:10290]	16
KIFC1	kinesin family member C1 [Source:HGNC Symbol;Acc:HGNC:6389]	17
POLE	polymerase (DNA) epsilon, catalytic subunit [Source:HGNC Symbol;Acc:HGNC:9177]	18
RFC1	replication factor C subunit 1 [Source:HGNC Symbol;Acc:HGNC:9969]	19
MCM2	minichromosome maintenance complex component 2 [Source:HGNC Symbol;Acc:HGNC:6944]	20

Networks

Co-expression	58.43%
Wang-Maris-2006	6.37%
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 264,023 interactions from GEO	
Burington-Shaughnessy-2008	4.39%
Tumor cell gene expression changes following short-term in vivo exposure to single agent chemotherapeutics are related to survival in multiple myeloma. Burington et al (2008). <i>Clin Cancer Res</i>	
Co-expression with 290,538 interactions from GEO	
Smirnov-Cheung-2009	4.27%
Genetic analysis of radiation-induced changes in human gene expression. Smirnov et al (2009). <i>Nature</i>	
Co-expression with 461,500 interactions from GEO	
Alizadeh-Staudt-2000	3.98%
Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. Alizadeh et al (2000). <i>Nature</i>	
Co-expression with 90,336 interactions from supplementary material	
Innocenti-Brown-2011	3.89%
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 603,765 interactions from GEO	
Bahr-Bowler-2013	3.83%
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 274,949 interactions from GEO	
Rosenwald-Staudt-2001	3.49%
Relation of gene expression phenotype to immunoglobulin mutation genotype in B cell chronic lymphocytic leukemia. Rosenwald et al (2001). <i>J Exp Med</i>	
Co-expression with 114,694 interactions from supplementary material	
Dobbin-Giordano-2005	3.44%
Interlaboratory comparability study of cancer gene expression analysis using oligonucleotide microarrays. Dobbin et al (2005). <i>Clin Cancer Res</i>	
Co-expression with 444,931 interactions from GEO	
Chen-Brown-2002	3.42%
Gene expression patterns in human liver cancers. Chen et al (2002). <i>Mol Biol Cell</i>	
Co-expression with 282,241 interactions from supplementary material	
Bild-Nevins-2006 B	3.12%
Oncogenic pathway signatures in human cancers as a guide to targeted therapies. Bild et al (2006). <i>Nature</i>	
Co-expression with 280,683 interactions from GEO	
Noble-Diehl-2008	3.01%
Regional variation in gene expression in the healthy colon is dysregulated in ulcerative colitis. Noble et al (2008). <i>Gut</i>	

Co-expression	58.43%
<hr/>	
Noble-Diehl-2008	
Co-expression with 661,539 interactions from GEO	
<hr/>	
Boldrick-Relman-2002	2.86%
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 111,707 interactions from supplementary material	
<hr/>	
Wang-Cheung-2015	2.65%
Genetic variation in insulin-induced kinase signaling. Wang et al (2015). <i>Mol Syst Biol</i>	
Co-expression with 411,047 interactions from GEO	
<hr/>	
Roth-Zlotnik-2006	2.21%
Gene expression analyses reveal molecular relationships among 20 regions of the human CNS. Roth et al (2006). <i>Neurogenetics</i>	
Co-expression with 669,062 interactions from GEO	
<hr/>	
Rieger-Chu-2004	2.01%
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 259,974 interactions from GEO	
<hr/>	
Wu-Garvey-2007	1.84%
The effect of insulin on expression of genes and biochemical pathways in human skeletal muscle. Wu et al (2007). <i>Endocrine</i>	
Co-expression with 267,109 interactions from GEO	
<hr/>	
Mallon-McKay-2013	1.64%
StemCellDB: the human pluripotent stem cell database at the National Institutes of Health. Mallon et al (2013). <i>Stem Cell Res</i>	
Co-expression with 585,265 interactions from GEO	
<hr/>	
Perou-Botstein-2000	1.05%
Molecular portraits of human breast tumours. Perou et al (2000). <i>Nature</i>	
Co-expression with 185,068 interactions from supplementary material	
<hr/>	
Perou-Botstein-1999	0.98%
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 65,069 interactions from supplementary material	
<hr/>	
Predicted	17.64%
<hr/>	
I2D-vonMering-Bork-2002-Medium-Yeast2Human	4.66%
Comparative assessment of large-scale data sets of protein-protein interactions. von Mering et al (2002). <i>Nature</i>	
Predicted with 3,009 interactions from I2D	
<hr/>	
I2D-Krogan-Greenblatt-2006-Core-Yeast2Human	3.72%
Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . Krogan et al (2006). <i>Nature</i>	
Predicted with 1,823 interactions from I2D	
<hr/>	
I2D-IntAct-Worm2Human	3.37%
The IntAct molecular interaction database in 2010. Aranda et al (2010). <i>Nucleic Acids Res</i>	
Predicted with 1,409 interactions from I2D	
<hr/>	

Predicted	17.64%
I2D-BIND-Yeast2Human	1.35%
BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al (2000). <i>Bioinformatics</i> Predicted with 1,541 interactions from I2D	
I2D-vonMering-Bork-2002-Low-Yeast2Human	1.15%
Comparative assessment of large-scale data sets of protein-protein interactions. von Mering et al (2002). <i>Nature</i> Predicted with 16,063 interactions from I2D	
I2D-MINT-Yeast2Human	1.01%
MINT: a Molecular INTeraction database. Zanzoni et al (2002). <i>FEBS Lett</i> Predicted with 5,592 interactions from I2D	
Stuart-Kim-2003	0.98%
A gene-coexpression network for global discovery of conserved genetic modules. Stuart et al (2003). <i>Science</i> Predicted with 24,872 interactions from supplementary material	
I2D-IntAct-Yeast2Human	0.87%
The IntAct molecular interaction database in 2010. Aranda et al (2010). <i>Nucleic Acids Res</i> Predicted with 13,772 interactions from I2D	
I2D-vonMering-Bork-2002-High-Yeast2Human	0.53%
Comparative assessment of large-scale data sets of protein-protein interactions. von Mering et al (2002). <i>Nature</i> Predicted with 1,196 interactions from I2D	
Physical Interactions	10.26%
Wan-Emili-2015	2.14%
Panorama of ancient metazoan macromolecular complexes. Wan et al (2015). <i>Nature</i> Physical Interactions with 16,682 interactions from BioGRID	
Hill-Livingston-2014	1.83%
Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. Hill et al (2014). <i>Genes Dev</i> Physical Interactions with 125 interactions from iRefIndex	
IREF-PUBMED	1.81%
Physical Interactions with 571 interactions from iRefIndex	
IREF-HPRD	1.56%
Physical Interactions with 34,206 interactions from iRefIndex	
Havugimana-Emili-2012	1.49%
A census of human soluble protein complexes. Havugimana et al (2012). <i>Cell</i> Physical Interactions with 13,716 interactions from BioGRID	
Yu-Vidal-2011	1.03%
Next-generation sequencing to generate interactome datasets. Yu et al (2011). <i>Nat Methods</i> Physical Interactions with 1,108 interactions from BioGRID	
Rual-Vidal-2005 B	0.28%
Towards a proteome-scale map of the human protein-protein interaction network. Rual et al (2005). <i>Nature</i>	

Physical Interactions	10.26%
<hr/>	
Rual-Vidal-2005 B	
Physical Interactions with 2,565 interactions from BioGRID	
Hein-Mann-2015	0.09%
A human interactome in three quantitative dimensions organized by stoichiometries and abundances. Hein et al (2015). <i>Cell</i>	
Physical Interactions with 27,044 interactions from BioGRID	
IREF-BIND	0.04%
Physical Interactions with 3,659 interactions from iRefIndex	
Shared protein domains	5.95%
<hr/>	
PFAM	3.63%
Shared protein domains with 457,054 interactions from Pfam	
INTERPRO	2.33%
Shared protein domains with 608,863 interactions from InterPro	
Co-localization	4.85%
<hr/>	
Johnson-Shoemaker-2003	2.32%
Genome-wide survey of human alternative pre-mRNA splicing with exon junction microarrays. Johnson et al (2003). <i>Science</i>	
Co-localization with 426,332 interactions from GEO	
Schadt-Shoemaker-2004	1.64%
A comprehensive transcript index of the human genome generated using microarrays and computational approaches. Schadt et al (2004). <i>Genome Biol</i>	
Co-localization with 60,126 interactions from GEO	
Chen-Huang-2014	0.88%
Using an in situ proximity ligation assay to systematically profile endogenous protein-protein interactions in a pathway network. Chen et al (2014). <i>J Proteome Res</i>	
Co-localization with 559 interactions from BioGRID	
Pathway	2.21%
<hr/>	
Wu-Stein-2010	2.21%
A human functional protein interaction network and its application to cancer data analysis. Wu et al (2010). <i>Genome Biol</i>	
Pathway with 78,010 interactions from supplementary material	
Genetic Interactions	0.66%
<hr/>	
Lin-Smith-2010	0.66%
A genome-wide map of human genetic interactions inferred from radiation hybrid genotypes. Lin et al (2010). <i>Genome Res</i>	
Genetic Interactions with 4,820,370 interactions from supplementary material	