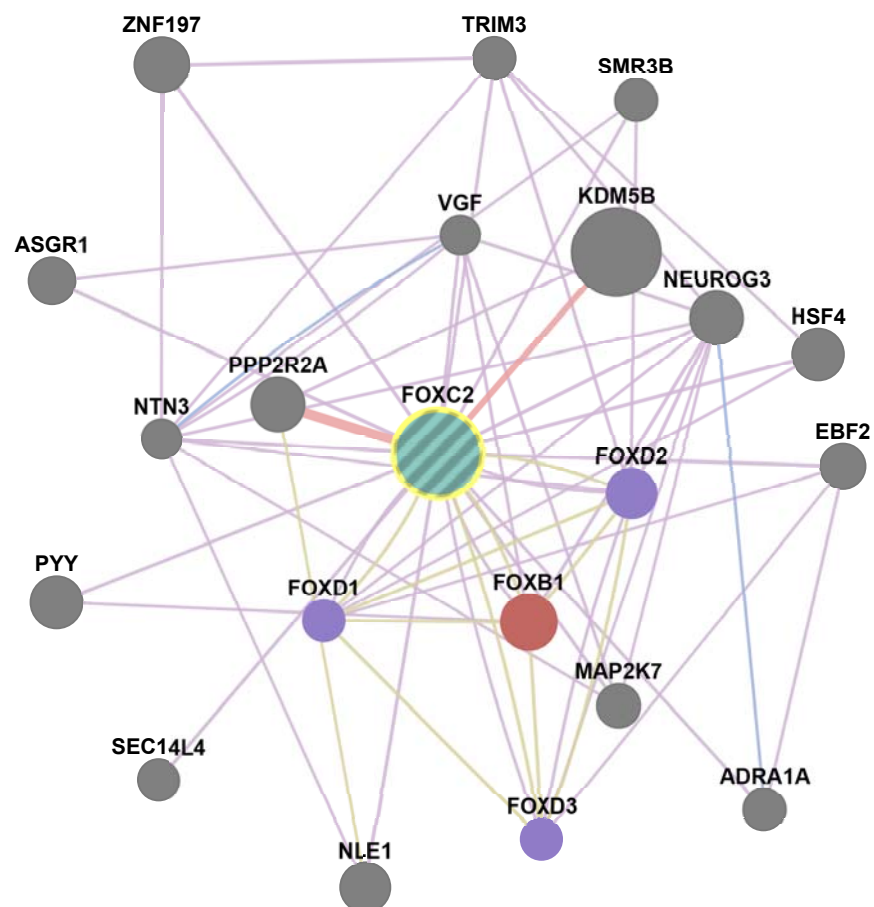


GENEMANIA

Created on: 2 January 2016 00:24:09
Last database update: 1 June 2014 20:00:00
Application version: 3.1.2.8

Report of GeneMANIA search

Network image



Functions legend

- connective tissue development
- tube development
- tube morphogenesis
- epithelial tube morphogenesis
- branching morphogenesis of an epithelial tube
- morphogenesis of a branching structure
- pattern specification process
- query genes

Networks legend

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

Search parameters

Organism: H. sapiens (human)

Genes: FOXC2

Networks:

Attributes:**Co-expression:**

Alizadeh-Staudt-2000 Arijis-Rutgeerts-2009 Bahr-Bowler-2013 Bild-Nevins-2006 B Boldrick-Relman-2002 Burington-Shaughnessy-2008 Chen-Brown-2002
Cheok-Evans-2003 Gysin-McMahon-2012 Innocenti-Brown-2011 Kang-Willman-2010 Mallon-McKay-2013 Perou-Botstein-1999 Ramaswamy-Golub-2001
Rieger-Chu-2004 Roth-Zlotnik-2006 Salaverria-Siebert-2011 Smirnov-Cheung-2009 Wang-Maris-2006 Wu-Garvey-2007

Co-localization:

Johnson-Shoemaker-2003 Satoh-Yamamoto-2013 Schadt-Shoemaker-2004

Genetic interactions:

BIOGRID-SMALL-SCALE-STUDIES IREF-SMALL-SCALE-STUDIES Lin-Boeke-2012 A Lin-Boeke-2012 B Lin-Smith-2010 Toyoshima-Grandori-2012
Willingham-Muchowski-2003

Pathway:

PATHWAYCOMMONS-CELL_MAP PATHWAYCOMMONS-HUMANCYC PATHWAYCOMMONS-IMID PATHWAYCOMMONS-NCI_NATURE
PATHWAYCOMMONS-REACTOME Wu-Stein-2010

Physical interactions:

Abu-Odeh-Aqeilan-2014 Agrawal-Sedivy-2010 Aichem-Groettrup-2012 Albers-Koegl-2005 Alexandru-Deshaies-2008 Altun-Kessler-2011 Andresen-Flores-Morales-2014
Arbuckle-Grant-2010 Arora-Mercola-2008 BIOGRID-SMALL-SCALE-STUDIES 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
Blandin-Richard-2013 Bouwmeester-Superti-Furga-2004 Brajenovic-Drewes-2004 Brehme-Superti-Furga-2009 Bruderer-Hay-2011 Byron-Humphries-2012
Cai-Conaway-2007 Camargo-Brandon-2007 Cannavo-Jiricny-2007 Cao-Chinnaiyan-2014 Chen-Ge-2013 Chen-Naus-2012 Chen-Zhang-2013 Cheng-Chen-2010
Cloutier-Coulombe-2013 Colland-Gauthier-2004 Couzens-Gingras-2013 Cox-Rizzino-2013 Danielsen-Nielsen-2011 Dyer-Sobral-2010 Emanuele-Elledge-2011
Ewing-Figeys-2007 Fenner-Prehn-2010 Foerster-Ritter-2013 Foster-Marshall-2013 Freibaum-Taylor-2010 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
Havrylov-Redowicz-2009 Havugimana-Emili-2012 Hayes-Urbé-2012 Hegele-Stelzl-2012 A Hegele-Stelzl-2012 B Humphries-Humphries-2009 Hutchins-Peters-2010
IREF-BIND IREF-BIOGRID IREF-DIP IREF-HPRD IREF-INNATEDB IREF-INTACT IREF-MATRIXDB IREF-MPPI IREF-OPHID IREF-PUBMED

IREF-SMALL-SCALE-STUDIES Ingham-Pawson-2005 Jeronimo-Coulombe-2007 Jin-Pawson-2004 Jones-MacBeath-2006 Joshi-Cristea-2013 Jäger-Krogan-2012
Kahle-Zoghbi-2011 Kim-Gygi-2011 Kneissl-Grummt-2003 Koch-Hermeking-2007 Kristensen-Foster-2012 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 Liu-Wang-2012 Loch-Strickler-2012
Lopitz-Otsoa-Rodriguez-2012 Lu-Zhang-2013 Mak-Moffat-2010 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
Nakayama-Ohara-2002 Nakayasu-Adkins-2013 Napolitano-Meroni-2011 Nathan-Goldberg-2013 Neganova-Lako-2011 Newman-Keating-2003 Olma-Pintard-2009
Oláh-Ovádi-2011 Oshikawa-Nakayama-2012 Ouyang-Gill-2009 Panigrahi-Pati-2012 Perez-Hernandez-Yáñez-Mó-2013 Persaud-Rotin-2009
Pichlmair-Superti-Furga-2011 Pichlmair-Superti-Furga-2012 Pilot-Storck-Goillot-2010 Povlsen-Choudhary-2012 Ramachandran-LaBaer-2004 Ravasi-Hayashizaki-2010
Reinke-Keating-2013 Richter-Chrzanowska-Lightowlers-2010 Roux-Burke-2012 Rowbotham-Mermoud-2011 Roy-Parent-2013 Rual-Vidal-2005 A Rual-Vidal-2005 B
San-Marina-Minden-2008 Sang-Jackson-2011 Sato-Conaway-2004 Shi-Qin-2011 Singh-Moore-2012 Soler-López-Aloy-2011 Sowa-Harper-2009 Stehling-Lill-2012
Stelzl-Wanker-2005 Suter-Wanker-2013 Taipale-Lindquist-2012 Takahashi-Conaway-2011 Tarallo-Weisz-2011 Tatham-Hay-2011 Teixeira-Gomes-2010
Thalappilly-Dusetti-2008 Tsai-Cristea-2012 Udeshi-Carr-2012 Vandamme-Angrand-2011 Vanderwerf-Bagby-2009 Varjosalo-Gstaiger-2013 A Varjosalo-Gstaiger-2013 B
Varjosalo-Superti-Furga-2013 Venkatesan-Vidal-2009 Vinayagam-Wanker-2011 Wagner-Choudhary-2011 Wallach-Kramer-2013 Wang-Balch-2006 Wang-He-2008
Wang-Yang-2011 Weimann-Stelzl-2013 A Weimann-Stelzl-2013 B Weinmann-Meister-2009 Wilker-Yaffe-2007 Wong-O'Bryan-2012 Woods-Monteiro-2012
Woodsmith-Sanderson-2012 Wu-Li-2007 Wu-Ma-2012 Xiao-Lefkowitz-2007 Xie-Cong-2013 Xu-Jaffrey-2010 Xu-Ye-2012 Yang-Chen-2010 Yatim-Benkirane-2012
Yu-Chow-2013 Yu-Vidal-2011 Zanon-Pichler-2013 Zhang-Zou-2011 Zhao-Krug-2005 Zhao-Yang-2011 Zhou-Conrads-2004 Zhou-Liang-2012 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-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-MGI-Mouse2Human
I2D-MINT-Fly2Human I2D-MINT-Mouse2Human I2D-MINT-Rat2Human I2D-MINT-Worm2Human I2D-MINT-Yeast2Human I2D-Manual-Mouse2Human
I2D-Manual-Rat2Human I2D-Ptacek-Snyder-2005-Yeast2Human I2D-Tarassov-PCA-Yeast2Human I2D-Tewari-Vidal-2004-TGFb-Worm2Human
I2D-Wang-Orkin-2006-EScmplx-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:

INTERPRO PFAM

Network weighting: Automatically selected weighting method (Biological process based)

Number of gene results: 20

Networks

Physical interactions	64.66 %
Leng-Wang-2014 A proteomics strategy for the identification of FAT10-modified sites by mass spectrometry. Leng et al. (2014). <i>J Proteome Res.</i> Source: Direct interaction with 140 interactions from iRefIndex	< 0.01 %
Zhao-Yang-2011 Interactome study suggests multiple cellular functions of hepatoma-derived growth factor (HDGF). Zhao et al. (2011). <i>J Proteomics.</i> Source: Direct interaction with 161 interactions from iRefIndex	< 0.01 %
Soler-López-Aloy-2011 Interactome mapping suggests new mechanistic details underlying Alzheimer's disease. Soler-López et al. (2011). <i>Genome Res.</i> Source: Direct interaction with 312 interactions from iRefIndex Tags: fibroblasts; cultured cells; cell line; immune system	< 0.01 %
Takahashi-Conaway-2011 Human mediator subunit MED26 functions as a docking site for transcription elongation factors. Takahashi et al. (2011). <i>Cell.</i> Source: Direct interaction with 131 interactions from iRefIndex Tags: cell proliferation; transcription factors; cancer	< 0.01 %
Zhou-Liang-2012 Shotgun proteomics and network analysis of ubiquitin-related proteins from human breast carcinoma epithelial cells. Zhou et al. (2012). <i>Mol Cell Biochem.</i> Source: Direct interaction with 207 interactions from BioGRID Tags: cultured cells; cancer; epithelial cells; cell line; transcription factors; breast cancer	6.59 %
Singh-Moore-2012 The cellular EJC interactome reveals higher-order mRNP structure and an EJC-SR protein nexus. Singh et al. (2012). <i>Cell.</i> Source: Direct interaction with 301 interactions from iRefIndex	4.76 %
Altun-Kessler-2011 Activity-based chemical proteomics accelerates inhibitor development for deubiquitylating enzymes. Altun et al. (2011). <i>Chem Biol.</i> Source: Direct interaction with 287 interactions from BioGRID Tags: cultured cells; cell line	3.63 %
Matsumoto-Nakayama-2005 Large-scale analysis of the human ubiquitin-related proteome. Matsumoto et al. (2005). <i>Proteomics.</i>	2.64 %

Source: [Direct interaction](#) with 648 interactions from [BioGRID](#)

Tags: cultured cells; cell line

Lee-Doedens-2011 2.56 %

[Ubiquitin ligase substrate identification through quantitative proteomics at both the protein and peptide levels.](#) Lee et al. (2011). *J Biol Chem*.

Source: [Direct interaction](#) with 1,320 interactions from [BioGRID](#)

Jones-MacBeath-2006 1.88 %

[A quantitative protein interaction network for the ErbB receptors using protein microarrays.](#) Jones et al. (2006). *Nature*.

Source: [Direct interaction](#) with 172 interactions from [iRefIndex](#)

Tags: cultured cells; cell line

Behzadnia-Lührmann-2007 1.82 %

[Composition and three-dimensional EM structure of double affinity-purified, human prespliceosomal A complexes.](#) Behzadnia et al. (2007). *EMBO J*.

Source: [Direct interaction](#) with 112 interactions from [iRefIndex](#)

Maréchal-Zou-2014 1.65 %

[PRP19 transforms into a sensor of RPA-ssDNA after DNA damage and drives ATR activation via a ubiquitin-mediated circuitry.](#) Maréchal et al. (2014). *Mol Cell*.

Source: [Direct interaction](#) with 996 interactions from [BioGRID](#)

Tags: transcription factors; signal transduction

Shi-Qin-2011 1.60 %

[A data set of human endogenous protein ubiquitination sites.](#) Shi et al. (2011). *Mol Cell Proteomics*.

Source: [Direct interaction](#) with 269 interactions from [BioGRID](#)

Tags: cancer

Berggård-James-2006 1.60 %

[140 mouse brain proteins identified by Ca²⁺-calmodulin affinity chromatography and tandem mass spectrometry.](#) Berggård et al. (2006). *J Proteome Res*.

Source: [Direct interaction](#) with 151 interactions from [iRefIndex](#)

Tags: brain; nervous system

Vanderwerf-Bagby-2009 1.59 %

[TLR8-dependent TNF-\(alpha\) overexpression in Fanconi anemia group C cells.](#) Vanderwerf et al. (2009). *Blood*.

Source: [Direct interaction](#) with 149 interactions from [BioGRID](#)

Tags: knockout; cell signalling; signal transduction

Mak-Moffat-2010 1.42 %

[A lentiviral functional proteomics approach identifies chromatin remodeling complexes important for the induction of pluripotency.](#) Mak et al. (2010). *Mol Cell Proteomics*.

Source: [Direct interaction](#) with 108 interactions from [BioGRID](#)

Tags: transcription factors; cell line; cultured cells; stem cells

McCracken-Blencowe-2005**1.32 %**

[Proteomic analysis of SRm160-containing complexes reveals a conserved association with cohesin.](#) McCracken et al. (2005). *J Biol Chem*.

Source: [Direct interaction](#) with 177 interactions from [iRefIndex](#)

Neganova-Lako-2011**1.31 %**

[An important role for CDK2 in G1 to S checkpoint activation and DNA damage response in human embryonic stem cells.](#) Neganova et al. (2011). *Stem Cells*.

Source: [Direct interaction](#) with 388 interactions from [iRefIndex](#)

Tags: development; cultured cells; cancer; cell proliferation; apoptosis; cell line; stem cells; transcription factors

McFarland-Nussbaum-2008**1.01 %**

[Proteomics analysis identifies phosphorylation-dependent alpha-synuclein protein interactions.](#) McFarland et al. (2008). *Mol Cell Proteomics*.

Source: [Direct interaction](#) with 157 interactions from [iRefIndex](#)

Tags: brain; nervous system

Bett-Hay-2013**0.93 %**

[The P-body component USP52/PAN2 is a novel regulator of HIF1A mRNA stability.](#) Bett et al. (2013). *Biochem J*.

Source: [Direct interaction](#) with 317 interactions from [iRefIndex](#)

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

Udeshi-Carr-2012**0.93 %**

[Methods for quantification of in vivo changes in protein ubiquitination following proteasome and deubiquitinase inhibition.](#) Udeshi et al. (2012). *Mol Cell Proteomics*.

Source: [Direct interaction](#) with 2,481 interactions from [BioGRID](#)

Tags: cultured cells; cell line; cancer; immune system

Oshikawa-Nakayama-2012**0.86 %**

[Proteome-wide identification of ubiquitylation sites by conjugation of engineered lysine-less ubiquitin.](#) Oshikawa et al. (2012). *J Proteome Res*.

Source: [Direct interaction](#) with 895 interactions from [BioGRID](#)

Gloeckner-Ueffing-2007**0.80 %**

[A novel tandem affinity purification strategy for the efficient isolation and characterisation of native protein complexes.](#) Gloeckner et al. (2007). *Proteomics*.

Source: [Direct interaction](#) with 100 interactions from [BioGRID](#)

Tags: cell line; cultured cells; cancer

Jeronimo-Coulombe-2007**0.78 %**

[Systematic analysis of the protein interaction network for the human transcription machinery reveals the identity of the 7SK capping enzyme.](#) Jeronimo et al. (2007). *Mol Cell*.

Source: [Direct interaction](#) with 699 interactions from [BioGRID](#)

Tags: cultured cells; cell line

Xu-Ye-2012	0.76 %
SGTA recognizes a noncanonical ubiquitin-like domain in the Bag6-Ubl4A-Trc35 complex to promote endoplasmic reticulum-associated degradation. Xu et al. (2012). <i>Cell Rep.</i>	
Source: Direct interaction with 224 interactions from iRefIndex	
Tags: cultured cells; cell line	
Zhou-Conrads-2004	0.74 %
An investigation into the human serum "interactome". Zhou et al. (2004). <i>Electrophoresis.</i>	
Source: Direct interaction with 160 interactions from iRefIndex	
Yu-Chow-2013	0.70 %
VCP phosphorylation-dependent interaction partners prevent apoptosis in Helicobacter pylori-infected gastric epithelial cells. Yu et al. (2013). <i>PLoS One.</i>	
Source: Direct interaction with 272 interactions from iRefIndex	
Tags: cultured cells; signal transduction; cancer; cell proliferation; apoptosis; cell line; epithelial cells	
Varjosalo-Gstaiger-2013 B	0.69 %
The protein interaction landscape of the human CMGC kinase group. Varjosalo et al. (2013). <i>Cell Rep.</i>	
Note: One of 2 datasets produced from this publication.	
Source: Direct interaction with 306 interactions from BioGRID	
Tags: cultured cells; cell line	
Freibaum-Taylor-2010	0.69 %
Global analysis of TDP-43 interacting proteins reveals strong association with RNA splicing and translation machinery. Freibaum et al. (2010). <i>J Proteome Res.</i>	
Source: Direct interaction with 222 interactions from BioGRID	
Tags: transcription factors; cultured cells; cell line; immune system	
Hegele-Stelzl-2012 B	0.68 %
Dynamic protein-protein interaction wiring of the human spliceosome. Hegele et al. (2012). <i>Mol Cell.</i>	
Note: One of 2 datasets produced from this publication.	
Source: Direct interaction with 600 interactions from BioGRID	
Brehme-Superti-Furga-2009	0.67 %
Charting the molecular network of the drug target Bcr-Abl. Brehme et al. (2009). <i>Proc Natl Acad Sci U S A.</i>	
Source: Direct interaction with 579 interactions from iRefIndex	
Tags: cultured cells; cancer; cell line	
Weinmann-Meister-2009	0.63 %
Importin 8 is a gene silencing factor that targets argonaute proteins to distinct mRNAs. Weinmann et al. (2009). <i>Cell.</i>	
Source: Direct interaction with 96 interactions from BioGRID	

Tags: cultured cells; cell line

Agrawal-Sedivy-2010**0.61 %**

[Proteomic profiling of Myc-associated proteins.](#) Agrawal et al. (2010). *Cell Cycle*.

Source: [Direct interaction](#) with 102 interactions from [iRefIndex](#)

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

Varjosalo-Superti-Furga-2013**0.60 %**

[Interlaboratory reproducibility of large-scale human protein-complex analysis by standardized AP-MS.](#) Varjosalo et al. (2013). *Nat Methods*.

Source: [Direct interaction](#) with 4,194 interactions from [BioGRID](#)

Tags: cultured cells; cell line

Danielsen-Nielsen-2011**0.59 %**

[Mass spectrometric analysis of lysine ubiquitylation reveals promiscuity at site level.](#) Danielsen et al. (2011). *Mol Cell Proteomics*.

Source: [Direct interaction](#) with 5,424 interactions from [BioGRID](#)

Tags: cultured cells; cell line

Kristensen-Foster-2012**0.59 %**

[A high-throughput approach for measuring temporal changes in the interactome.](#) Kristensen et al. (2012). *Nat Methods*.

Source: [Direct interaction](#) with 7,104 interactions from [BioGRID](#)

Tags: time series

Cannavo-Jiricny-2007**0.54 %**

[Characterization of the interactome of the human MutL homologues MLH1, PMS1, and PMS2.](#) Cannavo et al. (2007). *J Biol Chem*.

Source: [Direct interaction](#) with 101 interactions from [iRefIndex](#)

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

Rowbotham-Mermoud-2011**0.53 %**

[Maintenance of silent chromatin through replication requires SWI/SNF-like chromatin remodeler SMARCAD1.](#) Rowbotham et al. (2011). *Mol Cell*.

Source: [Direct interaction](#) with 114 interactions from [iRefIndex](#)

Tags: cell proliferation; fibroblasts; cell line; cancer; cultured cells

Barr-Knapp-2009**0.52 %**

[Large-scale structural analysis of the classical human protein tyrosine phosphatome.](#) Barr et al. (2009). *Cell*.

Source: [Direct interaction](#) with 165 interactions from [iRefIndex](#)

Foerster-Ritter-2013**0.52 %**

[Characterization of the EGFR interactome reveals associated protein complex networks and intracellular receptor dynamics.](#) Foerster et al. (2013). *Proteomics*.

Source: [Direct interaction](#) with 161 interactions from [iRefIndex](#)

IREF-DIP	0.51 %
Source: Direct interaction with 3,719 interactions from iRefIndex	
Cox-Rizzino-2013	0.49 %
The SOX2-interactome in brain cancer cells identifies the requirement of MSI2 and USP9X for the growth of brain tumor cells. Cox et al. (2013). <i>PLoS One</i> .	
Source: Direct interaction with 280 interactions from iRefIndex	
Tags: cell proliferation; transcription factors; cell line; cultured cells; cancer	
Havugimana-Emili-2012	0.49 %
A census of human soluble protein complexes. Havugimana et al. (2012). <i>Cell</i> .	
Source: Direct interaction with 13,710 interactions from BioGRID	
Giannone-Liu-2010	0.46 %
The protein network surrounding the human telomere repeat binding factors TRF1, TRF2, and POT1. Giannone et al. (2010). <i>PLoS One</i> .	
Source: Direct interaction with 279 interactions from iRefIndex	
Tags: transcription factors; cultured cells; cell line	
Li-Dorf-2011 A	0.46 %
Mapping a dynamic innate immunity protein interaction network regulating type I interferon production. Li et al. (2011). <i>Immunity</i> .	
Note: One of 2 datasets produced from this publication.	
Source: Direct interaction with 400 interactions from BioGRID	
Tags: cell signalling; cultured cells; cell line; immune system	
Persaud-Rotin-2009	0.44 %
Comparison of substrate specificity of the ubiquitin ligases Nedd4 and Nedd4-2 using proteome arrays. Persaud et al. (2009). <i>Mol Syst Biol</i> .	
Source: Direct interaction with 244 interactions from iRefIndex	
IREF-MATRIXDB	0.44 %
Source: Direct interaction with 179 interactions from iRefIndex	
Wagner-Choudhary-2011	0.41 %
A proteome-wide, quantitative survey of in vivo ubiquitylation sites reveals widespread regulatory roles. Wagner et al. (2011). <i>Mol Cell Proteomics</i> .	
Source: Direct interaction with 4,590 interactions from BioGRID	
Tags: signal transduction	
Varjosalo-Gstaiger-2013 A	0.39 %
The protein interaction landscape of the human CMGC kinase group. Varjosalo et al. (2013). <i>Cell Rep</i> .	
Note: One of 2 datasets produced from this publication.	

Source: [Direct interaction](#) with 686 interactions from [BioGRID](#)

Tags: cultured cells; cell line

Roux-Burke-2012**0.39 %**

[A promiscuous biotin ligase fusion protein identifies proximal and interacting proteins in mammalian cells.](#) Roux et al. (2012). *J Cell Biol.*

Source: [Direct interaction](#) with 113 interactions from [iRefIndex](#)

Tags: transcription factors

BIOGRID-SMALL-SCALE-STUDIES**0.37 %**

Source: [Direct interaction](#) with 51,715 interactions from [BioGRID](#)

Zhao-Krug-2005**0.35 %**

[Human ISG15 conjugation targets both IFN-induced and constitutively expressed proteins functioning in diverse cellular pathways.](#) Zhao et al. (2005). *Proc Natl Acad Sci U S A.*

Source: [Direct interaction](#) with 149 interactions from [iRefIndex](#)

Tags: cell signalling; immune system

Hutchins-Peters-2010**0.35 %**

[Systematic analysis of human protein complexes identifies chromosome segregation proteins.](#) Hutchins et al. (2010). *Science.*

Source: [Direct interaction](#) with 1,770 interactions from [BioGRID](#)

Tags: cell proliferation; nervous system; localization

Loch-Strickler-2012**0.33 %**

[A microarray of ubiquitylated proteins for profiling deubiquitylase activity reveals the critical roles of both chain and substrate.](#) Loch et al. (2012). *Biochim Biophys Acta.*

Source: [Direct interaction](#) with 147 interactions from [iRefIndex](#)

Sowa-Harper-2009**0.33 %**

[Defining the human deubiquitinating enzyme interaction landscape.](#) Sowa et al. (2009). *Cell.*

Source: [Direct interaction](#) with 1,506 interactions from [BioGRID](#)

Roy-Parent-2013**0.33 %**

[Novel, gel-free proteomics approach identifies RNF5 and JAMP as modulators of GPCR stability.](#) Roy et al. (2013). *Mol Endocrinol.*

Source: [Direct interaction](#) with 153 interactions from [iRefIndex](#)

Tags: transcription factors; signal transduction; cell line; cultured cells

IREF-INNATEDB**0.33 %**

Source: [Direct interaction](#) with 3,870 interactions from [iRefIndex](#)

Taipale-Lindquist-2012**0.30 %**

[Quantitative analysis of HSP90-client interactions reveals principles of substrate recognition.](#) Taipale et al. (2012). *Cell.*

Source: [Direct interaction](#) with 726 interactions from [iRefIndex](#)

Tags: transcription factors

Barrios-Rodiles-Wrana-2005**0.28 %**

[High-throughput mapping of a dynamic signaling network in mammalian cells.](#) Barrios-Rodiles et al. (2005). *Science*.

Source: [Direct interaction](#) with 611 interactions from [iRefIndex](#)

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

Wilker-Yaffe-2007**0.28 %**

[14-3-3sigma controls mitotic translation to facilitate cytokinesis.](#) Wilker et al. (2007). *Nature*.

Source: [Direct interaction](#) with 110 interactions from [iRefIndex](#)

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

IREF-MPPI**0.27 %**

Source: [Direct interaction](#) with 384 interactions from [iRefIndex](#)

Malovannaya-Qin-2010**0.27 %**

[Streamlined analysis schema for high-throughput identification of endogenous protein complexes.](#) Malovannaya et al. (2010). *Proc Natl Acad Sci U S A*.

Source: [Direct interaction](#) with 235 interactions from [iRefIndex](#)

Jin-Pawson-2004**0.26 %**

[Proteomic, functional, and domain-based analysis of in vivo 14-3-3 binding proteins involved in cytoskeletal regulation and cellular organization.](#) Jin et al. (2004). *Curr Biol*.

Source: [Direct interaction](#) with 233 interactions from [iRefIndex](#)

Tags: cell proliferation; cultured cells; immune system

Woods-Monteiro-2012**0.25 %**

[Charting the landscape of tandem BRCT domain-mediated protein interactions.](#) Woods et al. (2012). *Sci Signal*.

Source: [Direct interaction](#) with 927 interactions from [iRefIndex](#)

Tags: transcription factors; cancer

Fenner-Prehn-2010**0.24 %**

[Expanding the substantial interactome of NEMO using protein microarrays.](#) Fenner et al. (2010). *PLoS One*.

Source: [Direct interaction](#) with 106 interactions from [iRefIndex](#)

Tags: transcription factors; cultured cells; signal transduction; cell line

Xiao-Lefkowitz-2007**0.23 %**

[Functional specialization of beta-arrestin interactions revealed by proteomic analysis.](#) Xiao et al. (2007). *Proc Natl Acad Sci U S A*.

Source: [Direct interaction](#) with 402 interactions from [iRefIndex](#)

Tags: signal transduction

IREF-PUBMED	0.23 %
Source: Direct interaction with 459 interactions from iRefIndex	
Xie-Cong-2013	0.23 %
Deubiquitinase FAM/USP9X interacts with the E3 ubiquitin ligase SMURF1 protein and protects it from ligase activity-dependent self-degradation. Xie et al. (2013). <i>J Biol Chem</i> .	
Source: Direct interaction with 168 interactions from iRefIndex	
Tags: cell line; cultured cells; cancer	
IREF-BIND	0.22 %
Source: Direct interaction with 7,078 interactions from iRefIndex	
Koch-Hermeking-2007	0.22 %
Large-scale identification of c-MYC-associated proteins using a combined TAP/MudPIT approach. Koch et al. (2007). <i>Cell Cycle</i> .	
Source: Direct interaction with 179 interactions from iRefIndex	
Tags: transcription factors; cell line; cultured cells; cancer	
Chen-Zhang-2013	0.21 %
Quantitative study of the interactome of PKC? involved in the EGF-induced tumor cell chemotaxis. Chen et al. (2013). <i>J Proteome Res</i> .	
Source: Direct interaction with 181 interactions from iRefIndex	
Tags: cell line; cultured cells; breast cancer; cancer	
Napolitano-Meroni-2011	0.19 %
Functional interactions between ubiquitin E2 enzymes and TRIM proteins. Napolitano et al. (2011). <i>Biochem J</i> .	
Source: Direct interaction with 81 interactions from BioGRID	
Tags: transcription factors; cultured cells; nervous system	
Lee-Songyang-2011	0.18 %
Genome-wide YFP fluorescence complementation screen identifies new regulators for telomere signaling in human cells. Lee et al. (2011). <i>Mol Cell Proteomics</i> .	
Source: Direct interaction with 603 interactions from iRefIndex	
Tags: transcription factors; signal transduction	
Brajenovic-Drewes-2004	0.17 %
Comprehensive proteomic analysis of human Par protein complexes reveals an interconnected protein network. Brajenovic et al. (2004). <i>J Biol Chem</i> .	
Source: Direct interaction with 125 interactions from iRefIndex	
Tags: cultured cells; cell line	
Yatim-Benkirane-2012	0.17 %
NOTCH1 nuclear interactome reveals key regulators of its transcriptional activity and oncogenic function. Yatim et al. (2012). <i>Mol Cell</i> .	

Source: [Direct interaction](#) with 131 interactions from [iRefIndex](#)

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

Bandyopadhyay-Ideker-2010**0.16 %**

[A human MAP kinase interactome.](#) Bandyopadhyay et al. (2010). *Nat Methods*.

Source: [Direct interaction](#) with 625 interactions from [iRefIndex](#)

Tags: transcription factors; signal transduction; cell line; cultured cells

Bantscheff-Drewes-2011**0.16 %**

[Chemoproteomics profiling of HDAC inhibitors reveals selective targeting of HDAC complexes.](#) Bantscheff et al. (2011). *Nat Biotechnol*.

Source: [Direct interaction](#) with 103 interactions from [BioGRID](#)

Zanon-Pichler-2013**0.16 %**

[Profiling of Parkin-binding partners using tandem affinity purification.](#) Zanon et al. (2013). *PLoS One*.

Source: [Direct interaction](#) with 194 interactions from [BioGRID](#)

Wu-Li-2007**0.16 %**

[Systematic identification of SH3 domain-mediated human protein-protein interactions by peptide array target screening.](#) Wu et al. (2007). *Proteomics*.

Source: [Direct interaction](#) with 923 interactions from [iRefIndex](#)

Tags: cultured cells; signal transduction; cell line

Liu-Wang-2012**0.15 %**

[Proteomic identification of common SCF ubiquitin ligase FBXO6-interacting glycoproteins in three kinds of cells.](#) Liu et al. (2012). *J Proteome Res*.

Source: [Direct interaction](#) with 594 interactions from [BioGRID](#)

Tags: cell line; cultured cells; cancer; immune system

Ewing-Figeys-2007**0.15 %**

[Large-scale mapping of human protein-protein interactions by mass spectrometry.](#) Ewing et al. (2007). *Mol Syst Biol*.

Source: [Direct interaction](#) with 5,673 interactions from [iRefIndex](#)

Oláh-Ovádi-2011**0.15 %**

[Interactions of pathological hallmark proteins: tubulin polymerization promoting protein/p25, beta-amyloid, and alpha-synuclein.](#) Oláh et al. (2011). *J Biol Chem*.

Source: [Direct interaction](#) with 1,851 interactions from [iRefIndex](#)

Tags: epithelial cells; cultured cells; nervous system; cell line

Tsai-Cristea-2012**0.15 %**

[Functional proteomics establishes the interaction of SIRT7 with chromatin remodeling complexes and expands its role in regulation of RNA polymerase I transcription.](#) Tsai et al. (2012). *Mol Cell Proteomics*.

Source: [Direct interaction](#) with 654 interactions from [iRefIndex](#)

Tags: transcription factors; cell line; cultured cells; localization

Chen-Naus-2012**0.15 %**

[Association of connexin43 with E3 ubiquitin ligase TRIM21 reveals a mechanism for gap junction phosphodegron control.](#) Chen et al. (2012). *J Proteome Res.*

Source: [Direct interaction](#) with 106 interactions from [iRefIndex](#)

Tags: cancer

Ingham-Pawson-2005**0.14 %**

[WW domains provide a platform for the assembly of multiprotein networks.](#) Ingham et al. (2005). *Mol Cell Biol.*

Source: [Direct interaction](#) with 297 interactions from [iRefIndex](#)

Tags: cultured cells; cell line; cancer; immune system

van Wijk-Timmers-2009**0.14 %**

[A comprehensive framework of E2-RING E3 interactions of the human ubiquitin-proteasome system.](#) van Wijk et al. (2009). *Mol Syst Biol.*

Source: [Direct interaction](#) with 306 interactions from [iRefIndex](#)

Tags: cell line; cultured cells; cancer

Behrends-Harper-2010**0.12 %**

[Network organization of the human autophagy system.](#) Behrends et al. (2010). *Nature.*

Source: [Direct interaction](#) with 766 interactions from [iRefIndex](#)

Hayes-Urbé-2012**0.11 %**

[Direct and indirect control of mitogen-activated protein kinase pathway-associated components, BRAP/IMP E3 ubiquitin ligase and CRAF/RAF1 kinase, by the deubiquitylating enzyme USP15.](#) Hayes et al. (2012). *J Biol Chem.*

Source: [Direct interaction](#) with 107 interactions from [iRefIndex](#)

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

Couzens-Gingras-2013**0.11 %**

[Protein interaction network of the mammalian Hippo pathway reveals mechanisms of kinase-phosphatase interactions.](#) Couzens et al. (2013). *Sci Signal.*

Source: [Direct interaction](#) with 366 interactions from [BioGRID](#)

IREF-INTACT**0.11 %**

Source: [Direct interaction](#) with 42,475 interactions from [iRefIndex](#)

Kim-Gygi-2011**0.11 %**

[Systematic and quantitative assessment of the ubiquitin-modified proteome.](#) Kim et al. (2011). *Mol Cell.*

Source: [Direct interaction](#) with 4,905 interactions from [BioGRID](#)

Tags: cell line; cultured cells; cancer

Arbuckle-Grant-2010**0.11 %**

[The SH3 domain of postsynaptic density 95 mediates inflammatory pain through phosphatidylinositol-3-kinase recruitment.](#) Arbuckle et al. (2010). *EMBO Rep.*

Source: [Direct interaction](#) with 268 interactions from [iRefIndex](#)

Tags: brain; immune system

Greco-Cristea-2011**0.10 %**

[Nuclear import of histone deacetylase 5 by requisite nuclear localization signal phosphorylation.](#) Greco et al. (2011). *Mol Cell Proteomics.*

Source: [Direct interaction](#) with 240 interactions from [iRefIndex](#)

Tags: cultured cells; cell line; localization

Joshi-Cristea-2013**0.10 %**

[The functional interactome landscape of the human histone deacetylase family.](#) Joshi et al. (2013). *Mol Syst Biol.*

Source: [Direct interaction](#) with 307 interactions from [iRefIndex](#)

Tags: cell proliferation; transcription factors; signal transduction; immune system

Bennett-Harper-2010**0.10 %**

[Dynamics of cullin-RING ubiquitin ligase network revealed by systematic quantitative proteomics.](#) Bennett et al. (2010). *Cell.*

Source: [Direct interaction](#) with 4,386 interactions from [BioGRID](#)

Tags: transcription factors; cultured cells; cell line; hormones

Cai-Conaway-2007**0.09 %**

[YY1 functions with INO80 to activate transcription.](#) Cai et al. (2007). *Nat Struct Mol Biol.*

Source: [Direct interaction](#) with 106 interactions from [BioGRID](#)

Tags: transcription factors; cultured cells; cell line

Thalappilly-Duseti-2008**0.08 %**

[Identification of multi-SH3 domain-containing protein interactome in pancreatic cancer: a yeast two-hybrid approach.](#) Thalappilly et al. (2008). *Proteomics.*

Source: [Direct interaction](#) with 105 interactions from [iRefIndex](#)

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

IREF-HPRD**0.08 %**

Source: [Direct interaction](#) with 34,112 interactions from [iRefIndex](#)

Ouyang-Gill-2009**0.07 %**

[Direct binding of CoREST1 to SUMO-2/3 contributes to gene-specific repression by the LSD1/CoREST1/HDAC complex.](#) Ouyang et al. (2009). *Mol Cell.*

Source: [Direct interaction](#) with 105 interactions from [BioGRID](#)

Tags: transcription factors; nervous system; cancer; cell line; cultured cells

Woodsmith-Sanderson-2012**0.07 %**

Systematic analysis of dimeric E3-RING interactions reveals increased combinatorial complexity in human ubiquitination networks.	Woodsmith et al. (2012). <i>Mol Cell Proteomics</i> .
Source: Direct interaction with 208 interactions from iRefIndex	
IREF-OPHID	0.07 %
Source: Direct interaction with 44,492 interactions from iRefIndex	
Perez-Hernandez-Yáñez-Mó-2013	0.07 %
The intracellular interactome of tetraspanin-enriched microdomains reveals their function as sorting machineries toward exosomes.	Perez-Hernandez et al. (2013). <i>J Biol Chem</i> .
Source: Direct interaction with 452 interactions from iRefIndex	
Tags: knockout; cultured cells; cell line	
Zhang-Zou-2011	0.07 %
A bead-based approach for large-scale identification of in vitro kinase substrates.	Zhang et al. (2011). <i>Proteomics</i> .
Source: Direct interaction with 163 interactions from iRefIndex	
Grant-2010	0.07 %
Identification of SUMOylated proteins in neuroblastoma cells after treatment with hydrogen peroxide or ascorbate.	et al. (2010). <i>BMB Rep</i> .
Source: Direct interaction with 145 interactions from iRefIndex	
Tags: cell line; cultured cells; cancer	
Nakayasu-Adkins-2013	0.06 %
Evaluation of selected binding domains for the analysis of ubiquitinated proteomes.	Nakayasu et al. (2013). <i>J Am Soc Mass Spectrom</i> .
Source: Direct interaction with 881 interactions from iRefIndex	
Tags: cultured cells; signal transduction; cell line; immune system	
Glatte-Gstaiger-2009	0.06 %
An integrated workflow for charting the human interaction proteome: insights into the PP2A system.	Glatte et al. (2009). <i>Mol Syst Biol</i> .
Source: Direct interaction with 244 interactions from BioGRID	
Tags: cultured cells; cell line	
Ravasi-Hayashizaki-2010	0.05 %
An atlas of combinatorial transcriptional regulation in mouse and man.	Ravasi et al. (2010). <i>Cell</i> .
Source: Direct interaction with 635 interactions from iRefIndex	
Tags: cell proliferation; transcription factors	
Golebiowski-Hay-2009	0.04 %
System-wide changes to SUMO modifications in response to heat shock.	Golebiowski et al. (2009). <i>Sci Signal</i> .
Source: Direct interaction with 731 interactions from BioGRID	

Tags: cell proliferation

Cheng-Chen-2010**0.04 %**

[Quantitative nanoproteomics for protein complexes \(QNanoPX\) related to estrogen transcriptional action.](#) Cheng et al. (2010). *Mol Cell Proteomics*.

Source: [Direct interaction](#) with 259 interactions from [iRefIndex](#)

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

Lau-Ronai-2012**0.04 %**

[PKC \$\gamma\$ promotes oncogenic functions of ATF2 in the nucleus while blocking its apoptotic function at mitochondria.](#) Lau et al. (2012). *Cell*.

Source: [Direct interaction](#) with 134 interactions from [iRefIndex](#)

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

Richter-Chrzanowska-Lightowlers-2010**0.03 %**

[A functional peptidyl-tRNA hydrolase, ICT1, has been recruited into the human mitochondrial ribosome.](#) Richter et al. (2010). *EMBO J*.

Source: [Direct interaction](#) with 192 interactions from [iRefIndex](#)

Vinayagam-Wanker-2011**0.03 %**

[A directed protein interaction network for investigating intracellular signal transduction.](#) Vinayagam et al. (2011). *Sci Signal*.

Source: [Direct interaction](#) with 2,526 interactions from [iRefIndex](#)

Tags: transcription factors; signal transduction

Yang-Chen-2010**0.03 %**

[Proteomic dissection of cell type-specific H2AX-interacting protein complex associated with hepatocellular carcinoma.](#) Yang et al. (2010). *J Proteome Res*.

Source: [Direct interaction](#) with 100 interactions from [BioGRID](#)

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

Wong-O'Bryan-2012**0.03 %**

[Intersectin \(ITSN\) family of scaffolds function as molecular hubs in protein interaction networks.](#) Wong et al. (2012). *PLoS One*.

Source: [Direct interaction](#) with 115 interactions from [iRefIndex](#)

Tags: fibroblasts; cultured cells; signal transduction; cell line

Markson-Sanderson-2009**0.02 %**

[Analysis of the human E2 ubiquitin conjugating enzyme protein interaction network.](#) Markson et al. (2009). *Genome Res*.

Source: [Direct interaction](#) with 700 interactions from [iRefIndex](#)

Tags: cell line; cultured cells; cancer

Weimann-Stelzl-2013 A**0.02 %**

[A Y2H-seq approach defines the human protein methyltransferase interactome.](#) Weimann et al. (2013). *Nat Methods*.

Note: One of 2 datasets produced from this publication.

Source: [Direct interaction](#) with 114 interactions from [BioGRID](#)

Wallach-Kramer-2013**0.02 %**

[Dynamic circadian protein-protein interaction networks predict temporal organization of cellular functions.](#) Wallach et al. (2013). *PLoS Genet.*

Source: [Direct interaction](#) with 110 interactions from [iRefIndex](#)

Tags: cell proliferation; transcription factors; signal transduction; biological clocks

Pichlmair-Superti-Furga-2012**0.02 %**

[Viral immune modulators perturb the human molecular network by common and unique strategies.](#) Pichlmair et al. (2012). *Nature.*

Source: [Direct interaction](#) with 14 interactions from [BioGRID](#)

Tags: signal transduction; immune system

Meek-Piwnica-Worms-2004**0.01 %**

[Comprehensive proteomic analysis of interphase and mitotic 14-3-3-binding proteins.](#) Meek et al. (2004). *J Biol Chem.*

Source: [Direct interaction](#) with 351 interactions from [iRefIndex](#)

Tags: cell proliferation

Co-expression**17.38 %****Wang-Maris-2006****1.23 %**

[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). *Cancer Res.*

Source: [Pearson correlation](#) with 264,234 interactions from [GEO](#)

Tags: transcription factors; cancer

Ramaswamy-Golub-2001**1.16 %**

[Multiclass cancer diagnosis using tumor gene expression signatures.](#) Ramaswamy et al. (2001). *Proc Natl Acad Sci U S A.*

Source: [Pearson correlation](#) with 270,142 interactions from supplementary material

Tags: cancer

Bild-Nevins-2006 B**1.11 %**

[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 282,582 interactions from [GEO](#)

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

Salaverria-Siebert-2011**1.10 %**

[Translocations activating IRF4 identify a subtype of germinal center-derived B-cell lymphoma affecting predominantly children and young adults.](#) Salaverria et al. (2011). *Blood.*

Source: [Pearson correlation](#) with 514,070 interactions from [GEO](#)

Tags: transcription factors; cancer

Burington-Shaughnessy-2008**1.00 %**

[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). *Clin Cancer Res*.

Source: [Pearson correlation](#) with 293,587 interactions from [GEO](#)

Tags: transcription factors; time series; cancer; chemotherapy

Bahr-Bowler-2013**1.00 %**

[Peripheral blood mononuclear cell gene expression in chronic obstructive pulmonary disease.](#) Bahr et al. (2013). *Am J Respir Cell Mol Biol*.

Source: [Pearson correlation](#) with 278,447 interactions from [GEO](#)

Mallon-McKay-2013**1.00 %**

[StemCellDB: the human pluripotent stem cell database at the National Institutes of Health.](#) Mallon et al. (2013). *Stem Cell Res*.

Source: [Pearson correlation](#) with 567,140 interactions from [GEO](#)

Tags: cultured cells; stem cells; cell line

Alizadeh-Staudt-2000**0.96 %**

[Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling.](#) Alizadeh et al. (2000). *Nature*.

Source: [Pearson correlation](#) with 88,888 interactions from supplementary material

Tags: cultured cells; cancer

Rieger-Chu-2004**0.86 %**

[Toxicity from radiation therapy associated with abnormal transcriptional responses to DNA damage.](#) Rieger et al. (2004). *Proc Natl Acad Sci U S A*.

Source: [Pearson correlation](#) with 259,055 interactions from [GEO](#)

Tags: cultured cells; cell line

Smirnov-Cheung-2009**0.82 %**

[Genetic analysis of radiation-induced changes in human gene expression.](#) Smirnov et al. (2009). *Nature*.

Source: [Pearson correlation](#) with 463,390 interactions from [GEO](#)

Tags: transcription factors; cultured cells; cell line

Roth-Zlotnik-2006**0.81 %**

[Gene expression analyses reveal molecular relationships among 20 regions of the human CNS.](#) Roth et al. (2006). *Neurogenetics*.

Source: [Pearson correlation](#) with 666,614 interactions from [GEO](#)

Gysin-McMahon-2012**0.80 %**

[Analysis of mRNA profiles after MEK1/2 inhibition in human pancreatic cancer cell lines reveals pathways involved in drug sensitivity.](#) Gysin et al. (2012). *Mol Cancer Res*.

Source: [Pearson correlation](#) with 388,454 interactions from [GEO](#)

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

Innocenti-Brown-2011

0.80 %

[Identification, replication, and functional fine-mapping of expression quantitative trait loci in primary human liver tissue.](#) Innocenti et al. (2011). *PLoS Genet.*

Source: [Pearson correlation](#) with 579,361 interactions from [GEO](#)

Tags: epithelial cells; cultured cells; cell line; liver; cancer

Kang-Willman-2010

0.77 %

[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 656,632 interactions from [GEO](#)

Tags: transcription factors; lymphoma; cancer

Boldrick-Relman-2002

0.74 %

[Stereotyped and specific gene expression programs in human innate immune responses to bacteria.](#) Boldrick et al. (2002). *Proc Natl Acad Sci U S A.*

Source: [Pearson correlation](#) with 108,543 interactions from supplementary material

Tags: immune system

Arijs-Rutgeerts-2009

0.73 %

[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 653,194 interactions from [GEO](#)

Tags: immune system

Wu-Garvey-2007

0.64 %

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

Source: [Pearson correlation](#) with 260,762 interactions from [GEO](#)

Tags: transcription factors; muscle; cultured cells

Chen-Brown-2002

0.62 %

[Gene expression patterns in human liver cancers.](#) Chen et al. (2002). *Mol Biol Cell.*

Source: [Pearson correlation](#) with 275,649 interactions from supplementary material

Tags: cell proliferation; transcription factors; liver; cancer

Cheok-Evans-2003

0.61 %

[Treatment-specific changes in gene expression discriminate in vivo drug response in human leukemia cells.](#) Cheok et al. (2003). *Nat Genet.*

Source: [Pearson correlation](#) with 263,940 interactions from [GEO](#)

Tags: chemotherapy; cultured cells; lymphoma; cancer

Perou-Botstein-1999

0.61 %

[Distinctive gene expression patterns in human mammary epithelial cells and breast cancers.](#) Perou et al. (1999). *Proc Natl Acad Sci U S A*.

Source: [Pearson correlation](#) with 62,886 interactions from supplementary material

Tags: cultured cells; cancer; epithelial cells; signal transduction; breast; stromal cells; transcription factors; breast cancer

Predicted**7.17 %****I2D-Wang-Orkin-2006-ESmplx-Mouse2Human****< 0.01 %**

[A protein interaction network for pluripotency of embryonic stem cells.](#) Wang et al. (2006). *Nature*.

Note: I2D predictions of protein protein interactions using Wang-Orkin-2006 Mus musculus data

Source: [Direct interaction](#) with 53 interactions from [I2D](#)

Tags: development; transcription factors; stem cells

I2D-vonMering-Bork-2002-High-Yeast2Human**1.06 %**

[Comparative assessment of large-scale data sets of protein-protein interactions.](#) von Mering et al. (2002). *Nature*.

Note: I2D predictions of protein protein interactions using vonMering-Bork-2002 Saccharomyces cerevisiae data

Source: [Direct interaction](#) with 1,184 interactions from [I2D](#)

I2D-vonMering-Bork-2002-Medium-Yeast2Human**0.69 %**

[Comparative assessment of large-scale data sets of protein-protein interactions.](#) von Mering et al. (2002). *Nature*.

Note: I2D predictions of protein protein interactions using vonMering-Bork-2002 Saccharomyces cerevisiae data

Source: [Direct interaction](#) with 3,001 interactions from [I2D](#)

I2D-BioGRID-Yeast2Human**0.60 %**

[BioGRID: a general repository for interaction datasets.](#) Stark et al. (2006). *Nucleic Acids Res*.

Note: I2D predictions of protein protein interactions using BioGRID Saccharomyces cerevisiae data

Source: [Direct interaction](#) with 13,302 interactions from [I2D](#)

I2D-Chen-Pawson-2009-PiwiScreen-Mouse2Human**0.54 %**

[Mouse Piwi interactome identifies binding mechanism of Tdrkh Tudor domain to arginine methylated Miwi.](#) Chen et al. (2009). *Proc Natl Acad Sci U S A*.

Note: I2D predictions of protein protein interactions using Chen-Pawson-2009 Mus musculus data

Source: [Direct interaction](#) with 31 interactions from [I2D](#)

I2D-INNATEDB-Mouse2Human**0.47 %**

[InnateDB: facilitating systems-level analyses of the mammalian innate immune response.](#) Lynn et al. (2008). *Mol Syst Biol*.

Note: I2D predictions of protein protein interactions using INNATEDB Mus musculus data

Source: [Direct interaction](#) with 1,454 interactions from [I2D](#)

Tags: signal transduction; immune system

I2D-Tarassov-PCA-Yeast2Human**0.47 %**

[An in vivo map of the yeast protein interactome.](#) Tarassov et al. (2008). *Science*.

Note: I2D predictions of protein protein interactions using Tarassov-Michnick-2008 *Saccharomyces cerevisiae* data

Source: [Direct interaction](#) with 441 interactions from [I2D](#)

Tags: cell proliferation

I2D-vonMering-Bork-2002-Low-Yeast2Human **0.42 %**

[Comparative assessment of large-scale data sets of protein-protein interactions.](#) von Mering et al. (2002). *Nature*.

Note: I2D predictions of protein protein interactions using vonMering-Bork-2002 *Saccharomyces cerevisiae* data

Source: [Direct interaction](#) with 15,990 interactions from [I2D](#)

I2D-IntAct-Mouse2Human **0.35 %**

[The IntAct molecular interaction database in 2010.](#) Aranda et al. (2010). *Nucleic Acids Res*.

Note: I2D predictions of protein protein interactions using IntAct *Mus musculus* data

Source: [Direct interaction](#) with 3,430 interactions from [I2D](#)

Stuart-Kim-2003 **0.31 %**

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

Source: 24,928 interactions from supplementary material

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

I2D-Yu-Vidal-2008-GoldStd-Yeast2Human **0.28 %**

[High-quality binary protein interaction map of the yeast interactome network.](#) Yu et al. (2008). *Science*.

Note: I2D predictions of protein protein interactions using Yu Gold Standard *Saccharomyces cerevisiae* data

Source: [Direct interaction](#) with 376 interactions from [I2D](#)

Tags: transcription factors; signal transduction

I2D-Krogan-Greenblatt-2006-Core-Yeast2Human **0.25 %**

[Global landscape of protein complexes in the yeast *Saccharomyces cerevisiae*.](#) Krogan et al. (2006). *Nature*.

Note: I2D predictions of protein protein interactions using Krogan-Greenblatt-2006 *Saccharomyces cerevisiae* data

Source: [Direct interaction](#) with 1,822 interactions from [I2D](#)

I2D-BIND-Rat2Human **0.21 %**

[BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways.](#) Bader et al. (2000). *Bioinformatics*.

Note: I2D predictions of protein protein interactions using BIND *Rattus norvegicus* data

Source: [Direct interaction](#) with 548 interactions from [I2D](#)

I2D-MINT-Rat2Human **0.21 %**

[MINT: a Molecular INTERaction database.](#) Zanzoni et al. (2002). *FEBS Lett*.

Note: I2D predictions of protein protein interactions using MINT Rattus norvegicus data

Source: [Direct interaction](#) with 569 interactions from [I2D](#)

I2D-BioGRID-Worm2Human**0.19 %**

[BioGRID: a general repository for interaction datasets.](#) Stark et al. (2006). *Nucleic Acids Res.*

Note: I2D predictions of protein protein interactions using BioGRID Caenorhabditis elegans data

Source: [Direct interaction](#) with 944 interactions from [I2D](#)

I2D-MINT-Mouse2Human**0.19 %**

[MINT: a Molecular INTERaction database.](#) Zanzoni et al. (2002). *FEBS Lett.*

Note: I2D predictions of protein protein interactions using MINT Mus musculus data

Source: [Direct interaction](#) with 977 interactions from [I2D](#)

I2D-BIND-Mouse2Human**0.18 %**

[BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways.](#) Bader et al. (2000). *Bioinformatics.*

Note: I2D predictions of protein protein interactions using BIND Mus musculus data

Source: [Direct interaction](#) with 1,198 interactions from [I2D](#)

I2D-BioGRID-Mouse2Human**0.14 %**

[BioGRID: a general repository for interaction datasets.](#) Stark et al. (2006). *Nucleic Acids Res.*

Note: I2D predictions of protein protein interactions using BioGRID Mus musculus data

Source: [Direct interaction](#) with 284 interactions from [I2D](#)

I2D-BIND-Yeast2Human**0.13 %**

[BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways.](#) Bader et al. (2000). *Bioinformatics.*

Note: I2D predictions of protein protein interactions using BIND Saccharomyces cerevisiae data

Source: [Direct interaction](#) with 1,526 interactions from [I2D](#)

I2D-Krogan-Greenblatt-2006-NonCore-Yeast2Human**0.11 %**

[Global landscape of protein complexes in the yeast Saccharomyces cerevisiae.](#) Krogan et al. (2006). *Nature.*

Note: I2D predictions of protein protein interactions using Krogan-Greenblatt-2006 Saccharomyces cerevisiae data

Source: [Direct interaction](#) with 1,779 interactions from [I2D](#)

I2D-IntAct-Fly2Human**0.11 %**

[The IntAct molecular interaction database in 2010.](#) Aranda et al. (2010). *Nucleic Acids Res.*

Note: I2D predictions of protein protein interactions using IntAct Drosophila melanogaster data

Source: [Direct interaction](#) with 3,934 interactions from [I2D](#)

I2D-Formstecher-Daviet-2005-Embryo-Fly2Human**0.10 %**

[Protein interaction mapping: a Drosophila case study.](#) Formstecher et al. (2005). *Genome Res.*

Note: I2D predictions of protein protein interactions using Formstecher-Daviet-2005 Drosophila melanogaster data

Source: [Direct interaction](#) with 491 interactions from [I2D](#)

Tags: cancer

I2D-MGI-Mouse2Human**0.10 %**

[Ontological visualization of protein-protein interactions.](#) Drabkin et al. (2005). *BMC Bioinformatics.*

Note: I2D predictions of protein protein interactions using MGI Mus musculus data

Source: [Direct interaction](#) with 729 interactions from [I2D](#)

I2D-IntAct-Rat2Human**0.02 %**

[The IntAct molecular interaction database in 2010.](#) Aranda et al. (2010). *Nucleic Acids Res.*

Note: I2D predictions of protein protein interactions using IntAct Rattus norvegicus data

Source: [Direct interaction](#) with 1,055 interactions from [I2D](#)

I2D-MINT-Worm2Human**0.02 %**

[MINT: a Molecular INTERaction database.](#) Zanzoni et al. (2002). *FEBS Lett.*

Note: I2D predictions of protein protein interactions using MINT Caenorhabditis elegans data

Source: [Direct interaction](#) with 1,170 interactions from [I2D](#)

I2D-BIND-Worm2Human**0.01 %**

[BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways.](#) Bader et al. (2000). *Bioinformatics.*

Note: I2D predictions of protein protein interactions using BIND Caenorhabditis elegans data

Source: [Direct interaction](#) with 914 interactions from [I2D](#)

Pathway**5.04 %**

Wu-Stein-2010**1.72 %**

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

Source: 78,183 interactions from supplementary material

Tags: transcription factors; cancer

PATHWAYCOMMONS-REACTOME**1.54 %**

Source: [Direct interaction](#) with 24,930 interactions from [Pathway Commons](#)

PATHWAYCOMMONS-NCI_NATURE**0.68 %**

Source: [Direct interaction](#) with 10,109 interactions from [Pathway Commons](#)

PATHWAYCOMMONS-CELL_MAP**0.56 %**

Source: [Direct interaction](#) with 587 interactions from [Pathway Commons](#)

PATHWAYCOMMONS-IMID**0.51 %**

Source: [Direct interaction](#) with 934 interactions from [Pathway Commons](#)

PATHWAYCOMMONS-HUMANCYC**0.04 %**

Source: [Direct interaction](#) with 685 interactions from [Pathway Commons](#)

Co-localization**3.22 %****Schadt-Shoemaker-2004****1.98 %**

[A comprehensive transcript index of the human genome generated using microarrays and computational approaches.](#) Schadt et al. (2004). *Genome Biol.*

Note: Predicted transcript array

Source: [Pearson correlation](#) with 60,216 interactions from [GEO](#)

Johnson-Shoemaker-2003**1.24 %**

[Genome-wide survey of human alternative pre-mRNA splicing with exon junction microarrays.](#) Johnson et al. (2003). *Science.*

Source: [Pearson correlation](#) with 426,640 interactions from [GEO](#)

Tags: cultured cells; cell line

Genetic interactions**1.68 %****BIOGRID-SMALL-SCALE-STUDIES****0.48 %**

Source: [Direct interaction](#) with 408 interactions from [BioGRID](#)

Lin-Boeke-2012 A**0.42 %**

[Functional dissection of lysine deacetylases reveals that HDAC1 and p300 regulate AMPK.](#) Lin et al. (2012). *Nature.*

Note: One of 2 datasets produced from this publication.

Source: [Direct interaction](#) with 599 interactions from [BioGRID](#)

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

Toyoshima-Grandori-2012**0.34 %**

[Functional genomics identifies therapeutic targets for MYC-driven cancer.](#) Toyoshima et al. (2012). *Proc Natl Acad Sci U S A.*

Source: [Direct interaction](#) with 101 interactions from [BioGRID](#)

Tags: cancer

IREF-SMALL-SCALE-STUDIES**0.32 %**

Source: [Direct interaction](#) with 55 interactions from [iRefIndex](#)

Lin-Boeke-2012 B**0.12 %**

[Functional dissection of lysine deacetylases reveals that HDAC1 and p300 regulate AMPK.](#) Lin et al. (2012). *Nature.*

Note: One of 2 datasets produced from this publication.

Source: [Direct interaction](#) with 266 interactions from [BioGRID](#)

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

Shared protein domains	0.84 %
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INTERPRO	0.48 %
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Source: [Pearson correlation](#) with 562,560 interactions from [InterPro](#)

PFAM	0.36 %
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Source: [Pearson correlation](#) with 543,464 interactions from [Pfam](#)

Attributes

Attribute	Gene
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Genes

FOXC2 forkhead box C2 (MFH-1, mesenchyme forkhead 1) [Source:HGNC Symbol;Acc:3801]

Functions:



Synonyms: ENSG00000176692; ENSP00000326371; 2303; FOXC2; NP_005242; NM_005251; FKHL14; MFH-1; FOXC2_HUMAN; Q99958;

More at [Entrez](#)

KDM5B lysine (K)-specific demethylase 5B [Source:HGNC Symbol;Acc:18039]

Functions:



Synonyms: ENSG00000117139; ENSP00000235790; ENSP00000356233; ENSP00000356234; ENSP00000473481; 10765; KDM5B; NP_006609; NM_006618; CT31; JARID1B; PLU-1; RBBP2H1A; KDM5B_HUMAN; Q9UGL1;

More at [Entrez](#)

FOXB1 forkhead box B1 [Source:HGNC Symbol;Acc:3799]

Functions:



Synonyms: ENSG00000171956; ENSP00000379369; 27023; FOXB1; NP_036314; NM_012182; FKH5; HFKH-5; FOXB1_HUMAN; Q99853;

More at [Entrez](#)

ZNF197 zinc finger protein 197 [Source:HGNC Symbol;Acc:12988]

Functions:



Synonyms: ENSG00000186448; ENSP00000334616; ENSP00000345809; ENSP00000373250; ENSP00000373251; ENSP00000379370; ENSP00000394713; 10168; ZNF197; NP_001020026; NP_008922; NM_001024855; NM_006991; D3S1363E; ZKSCAN9; ZNF166; ZSCAN41; O14709; ZN197_HUMAN;

More at [Entrez](#)

PPP2R2A protein phosphatase 2, regulatory subunit B, alpha [Source:HGNC Symbol;Acc:9304]

Functions:



Synonyms: ENSG00000221914; ENSP00000325074; ENSP00000370113; ENSP00000428164; ENSP00000428165; ENSP00000428542; ENSP00000428705; ENSP00000428800; ENSP00000429279; ENSP00000430320; 5520; PPP2R2A; NP_001171062; NP_002708; NM_001177591; NM_002717; B55A; PR52A; PR55A; 2ABA_HUMAN; P63151;

More at [Entrez](#)

NEUROG3 neurogenin 3 [Source:HGNC Symbol;Acc:13806]

Functions:



Synonyms: ENSG00000122859; ENSP00000242462; 50674; NEUROG3; NP_066279; NM_020999; Atoh5; bHLHa7; Math4B; ngn3; NGN3_HUMAN; Q9Y4Z2;

More at [Entrez](#)

PYY peptide YY [Source:HGNC Symbol;Acc:9748]

Functions:



Synonyms: ENSG00000131096; ENSP00000353198; ENSP00000467310; 5697; PYY; NP_004151; NM_004160; PYY1; P10082; PYY_HUMAN;

More at [Entrez](#)

HSF4 heat shock transcription factor 4 [Source:HGNC Symbol;Acc:5227]

Functions:



Synonyms: ENSG00000102878; ENSP00000264009; ENSP00000403219; ENSP00000408815; ENSP00000427832; ENSP00000427963; ENSP00000428077; ENSP00000428161; ENSP00000428978; ENSP00000429486; ENSP00000429580; ENSP00000430211; ENSP00000430299; ENSP00000430631; ENSP00000430724; ENSP00000430840; ENSP00000430947; ENSP00000463706; 3299; HSF4; NP_001035757; NP_001529; NM_001040667; NM_001538; CTM; HSF4_HUMAN; Q9ULV5;

More at [Entrez](#)

NLE1 notchless homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:19889]

Functions:



Synonyms: ENSG00000073536; ENSP00000354075; ENSP00000413572; ENSP00000465420; ENSP00000466588; ENSP00000466764; ENSP00000468339; 54475; NLE1; NP_001014445; NP_060566; NM_001014445; NM_018096; FLJ10458; NLE1_HUMAN; Q9NVX2;

More at [Entrez](#)

FOXD2 forkhead box D2 [Source:HGNC Symbol;Acc:3803]

Functions:



Synonyms: ENSG00000186564; ENSP00000335493; 2306; FOXD2; NP_004465; NM_004474; FKHL17; FREAC9; FOXD2_HUMAN; O60548;

More at [Entrez](#)

ASGR1 asialoglycoprotein receptor 1 [Source:HGNC Symbol;Acc:742]

Functions:



Synonyms: ENSG00000141505; ENSP00000269299; ENSP00000370307; ENSP00000458530; ENSP00000458803; ENSP00000459169; ENSP00000459896; ENSP00000467511; 432; ASGR1; NP_001184145; NP_001662; NM_001197216; NM_001671; CLEC4H1; ASGR1_HUMAN; P07306;

More at [Entrez](#)

EBF2 early B-cell factor 2 [Source:HGNC Symbol;Acc:19090]

Functions:



Synonyms: ENSG00000221818; ENSP00000386178; ENSP00000430241; ENSP00000437909; 64641; EBF2; NP_073150; NM_022659; COE2; FLJ11500; COE2_HUMAN; Q9HAK2;

More at [Entrez](#)

MAP2K7 mitogen-activated protein kinase kinase 7 [Source:HGNC Symbol;Acc:6847]

Functions:



Synonyms: ENSG00000076984; ENSP00000381066; ENSP00000381068; ENSP00000381070; ENSP00000443946; 5609; MAP2K7; NP_660186; NM_145185; Jnkk2; MKK7; PRKMK7; MP2K7_HUMAN; O14733;

More at [Entrez](#)

TRIM3 tripartite motif containing 3 [Source:HGNC Symbol;Acc:10064]

Functions:



Synonyms: ENSG00000110171; ENSP00000340797; ENSP00000352508; ENSP00000433070; ENSP00000433102; ENSP00000437283; ENSP00000441091; ENSP00000445460; 10612; TRIM3; NP_001234935; NP_001234936; NP_006449; NP_150594; NM_001248006; NM_001248007; NM_006458; NM_033278; BERP; HAC1; RNF22; RNF97; O75382; TRIM3_HUMAN;

More at [Entrez](#)

ADRA1A adrenoceptor alpha 1A [Source:HGNC Symbol;Acc:277]

Functions:



Synonyms: ENSG00000120907; ENSP00000276393; ENSP00000346557; ENSP00000351725; ENSP00000369946; ENSP00000369947; ENSP00000369955; ENSP00000369956; ENSP00000369960; ENSP00000369961; ENSP00000430414; ENSP00000430793; ENSP00000431073; 148; ADRA1A; NP_000671; NP_150645; NP_150646; NP_150647; NM_000680; NM_033302; NM_033303; NM_033304; ADRA1C; ADRA1L1; ADA1A_HUMAN; P35348;

More at [Entrez](#)

SMR3B submaxillary gland androgen regulated protein 3B [Source:HGNC Symbol;Acc:17326]

Functions:



Synonyms: ENSG00000171201; ENSP00000302400; ENSP00000423138; 10879; SMR3B; NP_006676; NM_006685; P-B; PROL3; P02814; SMR3B_HUMAN;

More at [Entrez](#)

FOXD1 forkhead box D1 [Source:HGNC Symbol;Acc:3802]

Functions:



Synonyms: ENSG00000251493; ENSP00000462795; 2297; FOXD1; NP_004463; NM_004472; FKHL8; FREAC4;

More at [Entrez](#)

SEC14L4 SEC14-like 4 (S. cerevisiae) [Source:HGNC Symbol;Acc:20627]

Functions:



Synonyms: ENSG00000133488; ENSP00000255858; ENSP00000314163; ENSP00000317617; ENSP00000371412; ENSP00000376525; ENSP00000440848; 284904; SEC14L4; NP_001154840; NP_777637; NM_001161368; NM_174977; dJ130H16.5; TAP3; Q9UDX3; S14L4_HUMAN;

More at [Entrez](#)

FOXD3 forkhead box D3 [Source:HGNC Symbol;Acc:3804]

Functions:



Synonyms: ENSG00000187140; ENSP00000360157; 27022; FOXD3; NP_036315; NM_012183; Genesis; HFH2; FOXD3_HUMAN; Q9UJU5;

More at [Entrez](#)

NTN3 netrin 3 [Source:HGNC Symbol;Acc:8030]

Functions:



Synonyms: ENSG00000162068; ENSP00000293973; 4917; NTN3; NP_006172; NM_006181; NTN2L; NET3_HUMAN; O00634;

More at [Entrez](#)

VGF VGF nerve growth factor inducible [Source:HGNC Symbol;Acc:12684]

Functions:



Synonyms: ENSG00000128564; ENSP00000249330; ENSP00000400884; 7425; VGF; NP_003369; NM_003378; O15240; VGF_HUMAN;

More at [Entrez](#)

Functions

Function	FDR	Coverage
1 query genes	n/a	1 / 1
2 DNA binding, bending	4.87E-5	5 / 53
3 ureteric bud development	9.83E-4	4 / 41
4 structure-specific DNA binding	2.38E-3	5 / 142
5 RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity	2.43E-3	4 / 66
6 morphogenesis of a branching epithelium	2.43E-3	4 / 67
7 branching morphogenesis of an epithelial tube	2.43E-3	4 / 65
8 morphogenesis of a branching structure	3.12E-3	4 / 74
9 pattern specification process	3.22E-3	5 / 184
10 double-stranded DNA binding	4.04E-3	4 / 84
11 ureteric bud morphogenesis	9.42E-3	3 / 31
12 kidney development	1.24E-2	4 / 117
13 peripheral nervous system development	1.24E-2	3 / 36
14 branching involved in ureteric bud morphogenesis	1.25E-2	3 / 37
15 renal system development	1.27E-2	4 / 125
16 epithelial tube morphogenesis	1.34E-2	4 / 129
17 tube morphogenesis	1.37E-2	4 / 134
18 urogenital system development	1.37E-2	4 / 132
19 transcription factor complex	2.3E-2	4 / 155
20 morphogenesis of an epithelium	2.41E-2	4 / 159
21 tube development	2.91E-2	4 / 169
22 sequence-specific DNA binding RNA polymerase II transcription factor activity	5.24E-2	4 / 199
23 sensory system development	6.2E-2	2 / 12
24 tissue morphogenesis	6.2E-2	4 / 212
25 enteric nervous system development	7.55E-2	2 / 14
26 melanocyte differentiation	7.55E-2	2 / 14
27 somitogenesis	7.55E-2	2 / 14
28 connective tissue development	7.91E-2	3 / 87
29 chromatin DNA binding	8.08E-2	2 / 15
30 sequence-specific DNA binding	9.75E-2	4 / 254

Interactions

Gene 1	Gene 2	Weight	Network group	Networks
NLE1	FOXC2	0.04697827994823456	Co-expression	Bild-Nevins-2006 B Cheok-Evans-2003 Rieger-Chu-2004
HSF4	FOXC2	0.04560056887567043	Co-expression	Salaverria-Siebert-2011 Wang-Maris-2006 Wu-Garvey-2007
EBF2	FOXC2	0.044810318388044834	Co-expression	Roth-Zlotnik-2006 Smirnov-Cheung-2009
ASGR1	FOXC2	0.04471665248274803	Co-expression	Bild-Nevins-2006 B Rieger-Chu-2004 Wu-Garvey-2007
NEUROG3	FOXC2	0.04470365378074348	Co-expression	Bild-Nevins-2006 B Innocenti-Brown-2011 Mallon-McKay-2013
ZNF197	FOXC2	0.04396491311490536	Co-expression	Bild-Nevins-2006 B Burlington-Shaughnessy-2008
FOXD2	NEUROG3	0.043765848502516747	Co-expression	Bild-Nevins-2006 B Wu-Garvey-2007
NEUROG3	FOXB1	0.04204022418707609	Co-expression	Gysin-McMahon-2012 Innocenti-Brown-2011 Mallon-McKay-2013 Roth-Zlotnik-2006
SEC14L4	FOXC2	0.04025964066386223	Co-expression	Arijs-Rutgeerts-2009 Salaverria-Siebert-2011
PYY	FOXC2	0.0373309226706624	Co-expression	Ramaswamy-Golub-2001 Wang-Maris-2006
VGF	NEUROG3	0.03609842713922262	Co-expression	Arijs-Rutgeerts-2009 Wu-Garvey-2007
MAP2K7	FOXC2	0.03571854345500469	Co-expression	Burlington-Shaughnessy-2008 Salaverria-Siebert-2011
VGF	FOXC2	0.03545065503567457	Co-expression	Burlington-Shaughnessy-2008 Rieger-Chu-2004
TRIM3	FOXC2	0.0341287674382329	Co-expression	Burlington-Shaughnessy-2008 Salaverria-Siebert-2011
FOXD2	FOXC2	0.032562218606472015	Co-expression	Cheok-Evans-2003 Roth-Zlotnik-2006
ADRA1A	FOXC2	0.03058313112705946	Co-expression	Ramaswamy-Golub-2001 Salaverria-Siebert-2011
SMR3B	FOXC2	0.029843716882169247	Co-expression	Ramaswamy-Golub-2001 Wang-Maris-2006

Gene 1	Gene 2	Weight	Network group	Networks
NTN3	FOXC2	0.029810241423547268	Co-expression	Bild-Nevins-2006 B Ramaswamy-Golub-2001
FOXB1	FOXC2	0.02945294650271535	Co-expression	Innocenti-Brown-2011 Mallon-McKay-2013
TRIM3	FOXD2	0.02635238878428936	Co-expression	Kang-Willman-2010
VGF	MAP2K7	0.02525254338979721	Co-expression	Burington-Shaughnessy-2008
SMR3B	FOXD2	0.025134509429335594	Co-expression	Rieger-Chu-2004
TRIM3	ZNF197	0.025032274425029755	Co-expression	Rieger-Chu-2004
FOXD3	FOXD2	0.02435959503054619	Co-expression	Roth-Zlotnik-2006
TRIM3	NEUROG3	0.024228164926171303	Co-expression	Salaverria-Siebert-2011
VGF	FOXB1	0.022132189944386482	Co-expression	Salaverria-Siebert-2011
FOXD1	FOXC2	0.020198279060423374	Co-expression	Innocenti-Brown-2011 Roth-Zlotnik-2006
ADRA1A	EBF2	0.01946168951690197	Co-expression	Mallon-McKay-2013
PPP2R2A	KDM5B	0.016437049955129623	Co-expression	Bild-Nevins-2006 B
NTN3	ZNF197	0.016006695572286844	Co-expression	Bild-Nevins-2006 B Burington-Shaughnessy-2008
VGF	ASGR1	0.01595144346356392	Co-expression	Rieger-Chu-2004
FOXD3	FOXC2	0.014324173564091325	Co-expression	Innocenti-Brown-2011 Salaverria-Siebert-2011
NTN3	NEUROG3	0.014171199407428503	Co-expression	Roth-Zlotnik-2006 Salaverria-Siebert-2011
TRIM3	HSF4	0.012714199721813202	Co-expression	Gysin-McMahon-2012
NTN3	FOXD2	0.011717014014720917	Co-expression	Rieger-Chu-2004
PYY	FOXB1	0.010225965641438961	Co-expression	Roth-Zlotnik-2006
FOXD1	NEUROG3	0.008395100012421608	Co-expression	Innocenti-Brown-2011
FOXD1	EBF2	0.008089721202850342	Co-expression	Roth-Zlotnik-2006
VGF	NTN3	0.0072554415091872215	Co-expression	Gysin-McMahon-2012
FOXD1	HSF4	0.007187672425061464	Co-expression	Mallon-McKay-2013
MAP2K7	NEUROG3	0.005269447807222605	Co-expression	Wang-Maris-2006
NTN3	TRIM3	0.004407675936818123	Co-expression	Wu-Garvey-2007
NTN3	MAP2K7	0.004374683368951082	Co-expression	Bild-Nevins-2006 B
NTN3	SMR3B	0.004280054941773415	Co-expression	Bild-Nevins-2006 B
FOXD3	EBF2	0.004173415247350931	Co-expression	Innocenti-Brown-2011
NTN3	NLE1	0.0035729873925447464	Co-expression	Bild-Nevins-2006 B
FOXD3	NEUROG3	0.0028187583666294813	Co-expression	Innocenti-Brown-2011
ADRA1A	NEUROG3	0.015332119539380074	Co-localization	Johnson-Shoemaker-2003
VGF	NTN3	0.011137884110212326	Co-localization	Johnson-Shoemaker-2003
PPP2R2A	FOXC2	0.44884273409843445	Physical interactions	IREF-INTACT
KDM5B	FOXC2	0.21458150446414948	Physical interactions	BIOGRID-SMALL-SCALE-STUDIES

Gene 1	Gene 2	Weight	Network group	Networks
FOXD2	FOXC2	0.04254680685698986	Shared protein domains	INTERPRO PFAM
FOXD1	FOXC2	0.042508743703365326	Shared protein domains	INTERPRO PFAM
FOXD1	FOXD2	0.042508743703365326	Shared protein domains	INTERPRO PFAM
FOXD3	FOXC2	0.042505837976932526	Shared protein domains	INTERPRO PFAM
FOXD3	FOXD2	0.042505837976932526	Shared protein domains	INTERPRO PFAM
FOXD3	FOXD1	0.04246784932911396	Shared protein domains	INTERPRO PFAM
FOXB1	FOXC2	0.04205899313092232	Shared protein domains	INTERPRO PFAM
FOXD2	FOXB1	0.04205899313092232	Shared protein domains	INTERPRO PFAM
FOXD1	FOXB1	0.04202092997729778	Shared protein domains	INTERPRO PFAM
FOXD3	FOXB1	0.04201802425086498	Shared protein domains	INTERPRO PFAM
NLE1	PPP2R2A	0.005774375982582569	Shared protein domains	PFAM

Search results generated by the GeneMANIA algorithm (genemania.org)