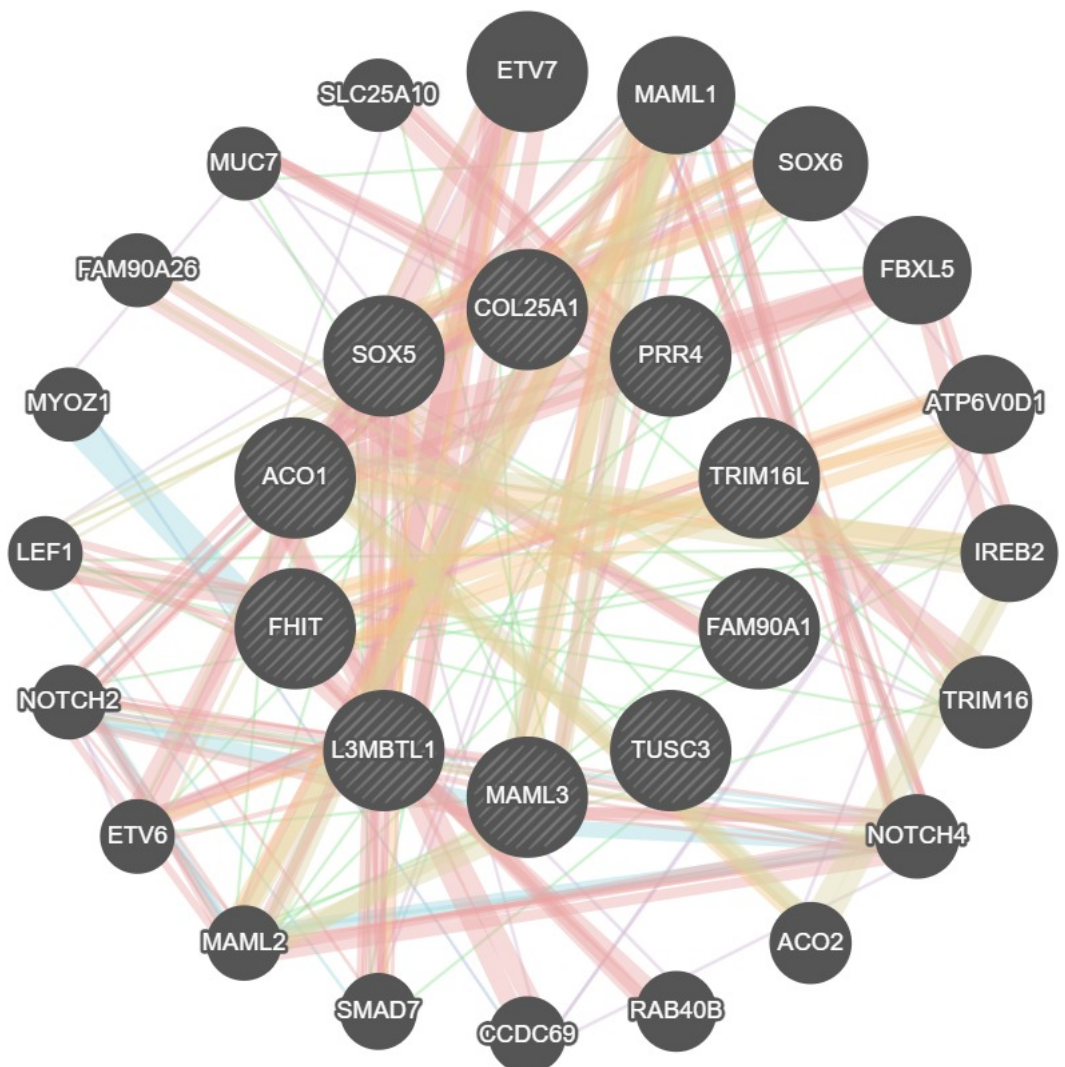


GeneMANIA report

Created on : 25 July 2023 09:58:18
Last database update : 13 August 2021 00:00:00
Application version : 3.6.0



Networks

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

Functions

N/A

Search parameters

Organism Homo sapiens (human)

Genes TUSC3 , TRIM16L , PRR4 , ACO1 , SOX5 , FAM90A1 , L3MBTL1 , COL25A1 , FHIT , MAML3

Network weighting Automatically selected weighting method

Networks A

Abbasi-Schild-Poulter-2019 , Abu-Odeh-Aqeilan-2014 , Achuthankutty-Mailand-2019 , Agrawal-Sedivy-2010 , Ahn-Lee-2008 , Albers-Koegl-2005 , Alexander-Wang-2018 , Alexandru-Deshaies-2008 , Alizadeh-Staudt-2000 , Alsulami-Cagney-2019 , An-Sun-2017 , Andresen-Flores-Morales-2014 , Arbogast-Gros-2019 , Arijs-Rutgeerts-2009 , Arroyo-Aloy-2014 , Arroyo-Aloy-2015 , Asadi-Dhanvantari-2018

B

Bailey-Hieter-2015 , Bandyopadhyay-Ideker-2010 , Banks-Washburn-2016 , Bantscheff-Drewes-2011 , Barr-Knapp-2009 , Barreiro-Alonso-Cerdán-2018 , Barrios-Rodiles-Wrana-2005 , Behrends-Harper-2010 , Behzadnia-Lührmann-2007 , Benleulmi-Chaachoua-Jockers-2016 A , Benleulmi-Chaachoua-Jockers-2016 B , Bennett-Harper-2010 , Benzinger-Hermeking-2005 , Berggård-James-2006 , Bett-Hay-2013 , Beyer-Boldt-2018 , Bhatnagar-Attie-2014 , Bild-Nevins-2006 B , BIOGRID-SMALL-SCALE-STUDIES , BIOGRID-SMALL-SCALE-STUDIES , Bishof-Seyfried-2018 , Blandin-Richard-2013 , Blomen-Brummelkamp-2015 , Blomen-Brummelkamp-2015 , Bogachek-Weigel-2014 , Boldrick-Relman-2002 , Boldt-Roepman-2016 , Botham-Schimmer-2019 , Bouwmeester-Supert-Furga-2004 , Brady-Omary-2018 , Brajenovic-Drewes-2004 , Brehme-Supert-Furga-2009 , Burlington-Shaughnessy-2008 , Butland-Hayden-2014 , Byron-Humphries-2012

C

Cai-Conaway-2007 , Camargo-Brandon-2007 , Campos-Reinberg-2015 , Cao-Chinnaiyan-2014 , Carmon-Liu-2014 , Caron-van Attikum-2019 , CELL_MAP , Chen-Brown-2002 , Chen-Ge-2013 A , Chen-Ge-2013 B , Chen-Guan-2018 , Chen-Huang-2014 , Chen-Krogan-2018 , Chen-Yu-2018 , Chen-Zhang-2013 , Chen-Zhou-2019 , Cheng-DeCaprio-2017 , Chi-Reed-2018 , Chitale-Richly-2017 , Choi-Beutler-2019 , Choi-Busino-2018 , Choudhury-Michlewski-2017 , Christianson-Kopito-2011 , Cloutier-Coulombe-2013 , Cloutier-Coulombe-2017 , Colicelli-2010 , Colland-Gauthier-2004 , Conte-Perez-Oliva-2018 , Cooper-Green-2015 , Corominas-Iakoucheva-2014 , Couzens-Gingras-2013 , Cox-Rizzino-2013 , Coyaoud-Raught-2015 , Crow-Cristea-2017

D

Daakour-Twizere-2016 , Dabbaghizadeh-Tanguay-2018 , Dart-Wells-2015 , Das-Broemer-2019 , Davis-Glaunsinger-2015 , de Hoog-Mann-2004 , Devarajan-Ketha-

D

Kumar-2012 , Diner-Cristea-2015 , Dittmer-Misteli-2014 , Dobbin-Giordano-2005 ,
Douanne-Bidère-2019 , Drissi-Boisvert-2015 , Du-Krogan-2017

E

Elliott-Gyrd-Hansen-2016 , Emdal-Olsen-2015 , Enzo-Dupont-2015 , Ertych-
Bastians-2016 , Ewing-Figeys-2007

F

Fang-Lin-2011 , Faust-Frankel-2018 , Fenner-Prehn-2010 , Floyd-Pagliarini-2016 ,
Foerster-Ritter-2013 , Fogeron-Lange-2013 , Fonseca-Damgaard-2015 , Foster-
Marshall-2013 , Fragoza-Yu-2019 , Freibaum-Taylor-2010

G

Gabriel-Baumgrass-2016 , Gallardo-Vara-Bernabeu-2019 , Galligan-Howley-2015 ,
Gao-Reinberg-2012 , Gao-Vaziri-2016 , Garzia-Sonenberg-2017 , Gautier-Hall-2009 ,
Giannone-Liu-2010 , Gilmore-Washburn-2016 , Giurato-Tarallo-2018 , Glatte-
Gstaiger-2009 , Gloeckner-Ueffing-2007 , Goehler-Wanker-2004 , Gordon-Krogan-
2020 , Goudreault-Gingras-2009 , Greco-Cristea-2011 , Grossmann-Stelzl-2015 ,
Guarani-Harper-2014 , Guard-Old-2019 , Guardia-Laguarta-Przedborski-2019 ,
Guderian-Grimmler-2011 , Gupta-Pelletier-2015

H

Han-Bassik-2017 A , Han-Bassik-2017 B , Hanson-Clayton-2014 , Hauri-Beisel-2016 ,
Hauri-Gstaiger-2013 , Havrylov-Redowicz-2009 , Havugimana-Emili-2012 , Hayes-
Urbé-2012 , Hegele-Stelzl-2012 A , Hegele-Stelzl-2012 B , Heidelberger-Beli-2018 ,
Hein-Mann-2015 , Hermjakob-Apweiler-2004 , Herr-Helleday-2015 , Hoffmeister-
Längst-2017 , Horlbeck-Gilbert-2018 A , Horlbeck-Gilbert-2018 B , Hosp-Selbach-
2015 , Hou-Chen-2018 , Hou-Huang-2017 , Hu-Woods-2019 , Hu-Yin-2019 , Hubel-
Pichlmair-2019 , Huber-Hoelz-2017 , HUMANCYC , Humphries-Humphries-2009 ,
Hussain-Aldaz-2018 , Hutchins-Peters-2010 , Huttlin-Gygi-2015 , Huttlin-Harper-
2017 , Hüttenhain-Krogan-2019

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-
Formstecher-Daviet-2005-Head-Fly2Human , I2D-Giot-Rothbert-2003-High-
Fly2Human , I2D-Giot-Rothbert-2003-Low-Fly2Human , I2D-INNATEDB-
Mouse2Human , I2D-IntAct-Fly2Human , I2D-IntAct-Mouse2Human , I2D-IntAct-
Rat2Human , I2D-IntAct-Worm2Human , I2D-IntAct-Yeast2Human , I2D-Krogan-
Greenblatt-2006-Core-Yeast2Human , I2D-Krogan-Greenblatt-2006-NonCore-
Yeast2Human , I2D-Li-Vidal-2004-CE-DATA-Worm2Human , I2D-Li-Vidal-2004-
CORE-1-Worm2Human , I2D-Li-Vidal-2004-CORE-2-Worm2Human , I2D-Li-Vidal-

I

2004-interolog-Worm2Human , I2D-Li-Vidal-2004-literature-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-MIPS-Yeast2Human , I2D-Ptacek-Snyder-2005-Yeast2Human , I2D-Stanyon-Finley-2004-CellCycle-Fly2Human , 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-EScmplxIP-Mouse2Human , I2D-Wang-Orkin-2006-EScmplxlow-Mouse2Human , I2D-Yu-Vidal-2008-GoldStd-Yeast2Human , IMID , Ingham-Pawson-2005 , Innocenti-Brown-2011 , INTERPRO , Iradi-Borchelt-2018 , IREF-bhf-ucl , IREF-bind , IREF-bind-translation , IREF-biogrid , IREF-corum , IREF-dip , IREF-hpidb , IREF-hprd , IREF-huri , IREF-innatedb , IREF-intact , IREF-intcomplex , IREF-matrixdb , IREF-mbinfo , IREF-mint , IREF-mppi , IREF-quickgo , IREF-reactome , IREF-SMALL-SCALE-STUDIES , IREF-SMALL-SCALE-STUDIES , IREF-spike , IREF-uniprotpp , IREF-virushost , Ivanochko-Arrowsmith-2019

J

Jain-Parker-2016 , Jang-Trono-2018 , Jeronimo-Coulombe-2007 , Jiang-de Kok-2017 , Jin-Pawson-2004 , Jirawatnotai-Sicinski-2011 , Johnson-Kerner-Wichterle-2015 , Johnson-Shoemaker-2003 , Jones-MacBeath-2006 , Joshi-Cristea-2013 , Jozwik-Carroll-2016 , Jäger-Krogan-2011

K

Kahle-Zoghbi-2011 , Kaltenbach-Hughes-2007 , Kang-Shin-2015 , Karras-Soengas-2019 , Kato-Sternberg-2014 , Katsogiannou-Rocchi-2014 , Kawahara-Paes Leme-2017 , Keller-Lee-2014 , Kennedy-Kolch-2020 A , Kennedy-Kolch-2020 B , Khanna-Parnaik-2018 , Kim-Major-2015 , Kneissl-Grummt-2003 , Koch-Hermeking-2007 , Kotlyar-Jurisica-2015 , Kristensen-Foster-2012 , Kumar-Maddika-2017 , Kumar-Vertegaal-2017 , Kupka-Walczak-2016 , Kärblane-Sarmiento-2015 , Kırılı-Görlich-2015

L

Lambert-Gingras-2015 , Lampert-Peter-2018 , Lau-Ronai-2012 , Lee-Choi-2016 , Lee-Choi-2017 , Lee-Jeong-2017 , Lee-Jou-2019 , Lee-Mayr-2019 , Lee-Songyang-2011 , Lehner-Sanderson-2004 A , Lehner-Sanderson-2004 B , Leung-Jones-2014 , Leung-Miller-2017 , Li-Chen-2015 , Li-Dorf-2011 A , Li-Dorf-2011 B , Li-Dorf-2014 , Li-Fu-2017 , Li-Haura-2013 , Li-Hung-2019 , Li-Lu-2018 , Li-Wang-2016 , Li-Zhou-2017 , Liebelt-Vertegaal-2020 , Lim-Zoghbi-2006 , Lin-Smith-2010 , Lipp-Guthrie-2015 , Liu-Chen-2019 , Liu-Sun-2019 , Liu-Takahashi-2017 , Liu-Tan-2018 , Liu-Varjosalo-2018 , Liu-Wang-2012 , Liu-Xu-2018 , Liu-Yang-2019 , Llères-Lamond-2010 , Loch-Strickler-2012 , Low-Heck-2014 , Lu-Bohr-2017 , Lu-Zhang-2013 , Luck-

L

Calderwood-2020 , Lum-Cristea-2018 , Luo-Elledge-2009

M

Mak-Moffat-2010 , Malinová-Verheggen-2017 , Mallon-McKay-2013 , Malovannaya-Qin-2010 , Maly-Babu-2017 , Markson-Sanderson-2009 , Martin-Elledge-2017 , Maréchal-Zou-2014 , Matsumoto-Nakayama-2005 , Matsuoka-Elledge-2007 , McCracken-Blencowe-2005 , McFarland-Nussbaum-2008 , McNamara-D'Orso-2016 , Meek-Piwnica-Worms-2004 , Menon-Litovchick-2019 , Milev-Mouland-2012 , Miyamoto-Sato-Yanagawa-2010 , Mohammed-Carroll-2013 , Moon-Kim-2014 , Moutaoufik-Babu-2019 , Mugabo-Lim-2018 , Muller-Demeret-2012 , Murakawa-Landthaler-2015

N

Nakamura-Groth-2019 , Nakayama-Ohara-2002 , Napolitano-Meroni-2011 , Narayan-Bennett-2012 , Nassa-Weisz-2019 , Nathan-Goldberg-2013 , NCI_NATURE , Neganova-Lako-2011 , Newman-Keating-2003 , Noguchi-Kawahara-2018 , Nowak-Sommer-2019

O

Oliviero-Cagney-2015 , Oliviero-Cagney-2016 , Olma-Pintard-2009 , Oláh-Ovádi-2011 , Ouyang-Gill-2009

P

Panigrahi-Pati-2012 , Pankow-Yates-2015 , Pao-Virdee-2018 , Papp-Lamia-2015 , Pech-Settleman-2019 , Perez-Hernandez-Yáñez-Mó-2013 , Perez-Perri-Espinosa-2016 , Perou-Botstein-1999 , Perou-Botstein-2000 , Persaud-Rotin-2009 A , Persaud-Rotin-2009 B , Petschnigg-Stagljar-2014 , PFAM , Phillips-Corn-2013 , Pichlmair-Supert-Furga-2011 , Pichlmair-Supert-Furga-2012 , Pilling-Cooper-2017 , Pladevall-Morera-Lopez-Contreras-2019 , Ptushkina-Ray-2017

R

Raisner-Gascoigne-2018 , Ramachandran-LaBaer-2004 , Raman-Harper-2015 , Ramaswamy-Golub-2001 , Ravasi-Hayashizaki-2010 , REACTOME , Reinke-Keating-2010 , Reinke-Keating-2013 , Rengasamy-Walsh-2017 , Reyniers-Taymans-2014 , Richter-Chrzanowska-Lightowlers-2010 , Rieger-Chu-2004 , Rivera-Paes Leme-2018 , Rodriguez-von Kriegsheim-2016 , Roewenstrunk-de la Luna-2019 , Rolland-Vidal-2014 , Rosenbluh-Hahn-2016 , Rosenwald-Staudt-2001 , Ross-Perou-2001 , Roth-Zlotnik-2006 , Rowbotham-Mermoud-2011 , Roy-Pardo-2014 , Roy-Parent-2013 , Rual-Vidal-2005

S

Saez-Vilchez-2018 , Sahni-Vidal-2015 , Saito-Kobarg-2017 , Sala-Ampe-2017 , Salvetti-Greco-2016 , Sang-Jackson-2011 , Sato-Conaway-2004 , Savidis-Brass-2016 , Schadt-Shoemaker-2004 , Schiza-Diamandis-2018 , Scholz-Taylor-2016 , Scifo-Lalowski-2015 , Scott-Guy-2017 , Scott-Schulman-2016 , Shami Shah-Baskin-2019 ,

S

Shen-Chen-2019 , Shen-Mali-2017 , Sherman-Teitell-2010 , Simabuco-Zanchin-2019 , Singh-Moore-2012 , So-Colwill-2015 , Sokolina-Stagljar-2017 , Soler-López-Aloy-2011 , Sowa-Harper-2009 , Srivas-Ideker-2016 , St-Denis-Gingras-2015 , St-Denis-Gingras-2016 , Stehling-Lill-2012 , Stehling-Lill-2013 , Stelzl-Wanker-2005 , Stuart-Kim-2003 , Sundell-Ivarsson-2018 , Suter-Wanker-2013 , Swayampakula-Dedhar-2017

T

Taipale-Lindquist-2012 , Taipale-Lindquist-2014 , Takahashi-Conaway-2011 , Tang-Wang-2019 , Tarallo-Weisz-2011 , Teixeira-Gomes-2010 , Teixeira-Laman-2016 A , Teixeira-Laman-2016 B , Thalappilly-Duseti-2008 , Thompson-Luchansky-2014 , Tiemann-Kani-2019 , Tomkins-Manzoni-2018 , Tong-Moran-2014 , Toyoshima-Grandori-2012 , Trepte-Wanker-2018 A , Trepte-Wanker-2018 B , Tsai-Cristea-2012

U

Ugidos-Vandenbroeck-2019

V

Van Acker-Dewilde-2019 , Van Alstyne-Pellizzoni-2018 , Van Quickelberghe-Gevaert-2018 , van Wijk-Timmers-2009 , Vandamme-Angrand-2011 , Varier-Vermeulen-2016 , Varjosalo-Gstaiger-2013 A , Varjosalo-Gstaiger-2013 B , Varjosalo-Superti-Furga-2013 , Vastrik-Stein-2007 , Venkatesan-Vidal-2009 , Viita-Vartiainen-2019 , Vinayagam-Wanker-2011 , Virok-Fülöp-2011 , Vizeacoumar-Moffat-2013 , von Hundelshausen-Weber-2017

W

Wallach-Kramer-2013 , Wan-Emili-2015 , Wang-Balch-2006 , Wang-Cheung-2015 , Wang-He-2008 , Wang-Huang-2017 , Wang-Liu-2019 , Wang-Maris-2006 , Wang-Xiong-2019 , Wang-Xu-2015 , Wang-Yang-2011 , Watanabe-Fujita-2018 , Weimann-Stelzl-2013 A , Weimann-Stelzl-2013 B , Weinmann-Meister-2009 , Weishäupl-Schmidt-2019 , Weith-Meyer-2018 , Whisenant-Salomon-2015 , Wilkinson-Coba-2019 , Willingham-Muchowski-2003 , Winczura-Jensen-2018 , Wong-O'Bryan-2012 , Woods-Monteiro-2012 A , Woods-Monteiro-2012 B , Woodsmith-Sanderson-2012 , Wu-Garvey-2007 , Wu-Li-2007 , Wu-Ma-2012 , Wu-Stein-2010 , Wu-Stein-2010

X

Xiao-Brown-2018 , Xiao-Lefkowitz-2007 , Xie-Cong-2013 , Xie-Green-2012 , Xie-Zhang-2017 , Xu-Ye-2012 , Xu-Zetter-2016

Y

Yachie-Roth-2016 , Yadav-Varjosalo-2017 , Yamauchi-Maeda-2018 , Yang-Brasier-2015 , Yang-Chen-2010 , Yang-Maurer-2018 , Yang-Vidal-2016 , Yang-Wang-2018 , Yao-Stagljar-2017 A , Yao-Stagljar-2017 B , Yatim-Benkirane-2012 , Yeung-Dougan-2019 , Yu-Chow-2013 , Yu-Engel-2018 , Yu-Vidal-2011 , Yue-Liu-2018

Z

Z

Zanon-Pichler-2013 , Zeller-Wei-2006 , Zhang-Shang-2006 , Zhang-Vermeulen-2017 , Zhang-Wang-2018 , Zhang-Wheeler-2014 , Zhang-Xu-2018 , Zhang-Zou-2011 , Zhao-Krug-2005 , Zhao-Yang-2011 , Zhong-Vidal-2016 , Zhou-Conrads-2004 , Zhou-Hanemann-2016 , Zhu-Liu-2018

Genes

Gene	Description	Rank
COL25A1	collagen type XXV alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:18603]	N/A
PRR4	proline rich 4 [Source:HGNC Symbol;Acc:HGNC:18020]	N/A
TRIM16L	tripartite motif containing 16 like [Source:HGNC Symbol;Acc:HGNC:32670]	N/A
FAM90A1	family with sequence similarity 90 member A1 [Source:HGNC Symbol;Acc:HGNC:25526]	N/A
TUSC3	tumor suppressor candidate 3 [Source:HGNC Symbol;Acc:HGNC:30242]	N/A
MAML3	mastermind like transcriptional coactivator 3 [Source:HGNC Symbol;Acc:HGNC:16272]	N/A
L3MBTL1	L3MBTL histone methyl-lysine binding protein 1 [Source:HGNC Symbol;Acc:HGNC:15905]	N/A
FHIT	fragile histidine triad diadenosine triphosphatase [Source:HGNC Symbol;Acc:HGNC:3701]	N/A
ACO1	aconitase 1 [Source:HGNC Symbol;Acc:HGNC:117]	N/A
SOX5	SRY-box transcription factor 5 [Source:HGNC Symbol;Acc:HGNC:11201]	N/A
ETV7	ETS variant transcription factor 7 [Source:HGNC Symbol;Acc:HGNC:18160]	1
MAML1	mastermind like transcriptional coactivator 1 [Source:HGNC Symbol;Acc:HGNC:13632]	2
SOX6	SRY-box transcription factor 6 [Source:HGNC Symbol;Acc:HGNC:16421]	3
FBXL5	F-box and leucine rich repeat protein 5 [Source:HGNC Symbol;Acc:HGNC:13602]	4
ATP6V0D1	ATPase H ⁺ transporting V0 subunit d1 [Source:HGNC Symbol;Acc:HGNC:13724]	5
IREB2	iron responsive element binding protein 2 [Source:HGNC Symbol;Acc:HGNC:6115]	6
TRIM16	tripartite motif containing 16 [Source:HGNC Symbol;Acc:HGNC:17241]	7
NOTCH4	notch receptor 4 [Source:HGNC Symbol;Acc:HGNC:7884]	8
ACO2	aconitase 2 [Source:HGNC Symbol;Acc:HGNC:118]	9
RAB40B	RAB40B, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:18284]	10
CCDC69	coiled-coil domain containing 69 [Source:HGNC Symbol;Acc:HGNC:24487]	11

Gene	Description	Rank
SMAD7	SMAD family member 7 [Source:HGNC Symbol;Acc:HGNC:6773]	12
MAML2	mastermind like transcriptional coactivator 2 [Source:HGNC Symbol;Acc:HGNC:16259]	13
ETV6	ETS variant transcription factor 6 [Source:HGNC Symbol;Acc:HGNC:3495]	14
NOTCH2	notch receptor 2 [Source:HGNC Symbol;Acc:HGNC:7882]	15
LEF1	lymphoid enhancer binding factor 1 [Source:HGNC Symbol;Acc:HGNC:6551]	16
MYOZ1	myozenin 1 [Source:HGNC Symbol;Acc:HGNC:13752]	17
FAM90A26	family with sequence similarity 90 member A26 [Source:HGNC Symbol;Acc:HGNC:43746]	18
MUC7	mucin 7, secreted [Source:HGNC Symbol;Acc:HGNC:7518]	19
SLC25A10	solute carrier family 25 member 10 [Source:HGNC Symbol;Acc:HGNC:10980]	20

Networks

Physical Interactions	80.30%
Khanna-Parnaik-2018 E3 ubiquitin ligase RNF123 targets lamin B1 and lamin-binding proteins. Khanna et al (2018). <i>FEBS J</i> Physical Interactions with 724 interactions from BioGRID	0.19%
Moutaoufik-Babu-2019 Rewiring of the Human Mitochondrial Interactome during Neuronal Reprogramming Reveals Regulators of the Respirasome and Neurogenesis. Moutaoufik et al (2019). <i>iScience</i> Physical Interactions with 6,357 interactions from BioGRID	0.19%
Pankow-Yates-2015 F508CFTR interactome remodelling promotes rescue of cystic fibrosis. Pankow et al (2015). <i>Nature</i> Physical Interactions with 637 interactions from BioGRID	0.19%
Saez-Vilchez-2018 Insights into the ubiquitin-proteasome system of human embryonic stem cells. Saez et al (2018). <i>Sci Rep</i> Physical Interactions with 304 interactions from BioGRID	0.19%
Lipp-Guthrie-2015 SR protein kinases promote splicing of nonconsensus introns. Lipp et al (2015). <i>Nat Struct Mol Biol</i> Physical Interactions with 388 interactions from BioGRID	0.19%
Cheng-DeCaprio-2017 Merkel cell polyomavirus recruits MYCL to the EP400 complex to promote oncogenesis. Cheng et al (2017). <i>PLoS Pathog</i> Physical Interactions with 95 interactions from BioGRID	0.19%
Douanne-Bidère-2019 CYLD Regulates Centriolar Satellites Proteostasis by Counteracting the E3 Ligase MIB1. Douanne et al (2019). <i>Cell Rep</i> Physical Interactions with 111 interactions from iRefIndex	0.19%
Li-Haura-2013 Perturbation of the mutated EGFR interactome identifies vulnerabilities and resistance mechanisms. Li et al (2013). <i>Mol Syst Biol</i> Physical Interactions with 403 interactions from BioGRID	0.19%
Havrylov-Redowicz-2009 Proteins recruited by SH3 domains of Ruk/CIN85 adaptor identified by LC-MS/MS. Havrylov et al (2009). <i>Proteome Sci</i> Physical Interactions with 106 interactions from BioGRID	0.19%
Banks-Washburn-2016 TNIP2 is a Hub Protein in the NF- BNetwork with Both Protein and RNA Mediated Interactions. Banks et al (2016). <i>Mol Cell Proteomics</i> Physical Interactions with 616 interactions from BioGRID	0.19%
Dart-Wells-2015 PAK4 promotes kinase-independent stabilization of RhoU to modulate cell adhesion. Dart et al (2015). <i>J Cell Biol</i> Physical Interactions with 102 interactions from iRefIndex	0.19%
IREF-reactome	0.19%

Physical Interactions

80.30%

IREF-reactome

Physical Interactions with 111,926 interactions from iRefIndex

Wilkinson-Coba-2019

0.19%

Endogenous Cell Type-Specific Disrupted in Schizophrenia 1 Interactomes Reveal Protein Networks Associated With Neurodevelopmental Disorders. Wilkinson et al (2019). *Biol Psychiatry*

Physical Interactions with 100 interactions from iRefIndex

Yadav-Varjosalo-2017

0.19%

Systematic Analysis of Human Protein Phosphatase Interactions and Dynamics. Yadav et al (2017). *Cell Syst*

Physical Interactions with 928 interactions from BioGRID

Jäger-Krogan-2011

0.19%

Global landscape of HIV-human protein complexes. Jäger et al (2011). *Nature*

Physical Interactions with 35 interactions from BioGRID

Devarajan-Ketha-Kumar-2012

0.19%

The sclerostin-bone protein interactome. Devarajan-Ketha et al (2012). *Biochem Biophys Res Commun*

Physical Interactions with 99 interactions from BioGRID

Luck-Calderwood-2020

0.19%

A reference map of the human binary protein interactome. Luck et al (2020). *Nature*

Physical Interactions with 51,546 interactions from BioGRID

Liu-Varjosalo-2018

0.19%

An AP-MS- and BioID-compatible MAC-tag enables comprehensive mapping of protein interactions and subcellular localizations. Liu et al (2018). *Nat Commun*

Physical Interactions with 825 interactions from BioGRID

Camargo-Brandon-2007

0.19%

Disrupted in Schizophrenia 1 Interactome: evidence for the close connectivity of risk genes and a potential synaptic basis for schizophrenia. Camargo et al (2007). *Mol Psychiatry*

Physical Interactions with 263 interactions from BioGRID

Ingham-Pawson-2005

0.19%

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

Physical Interactions with 298 interactions from BioGRID

IREF-hprd

0.19%

Physical Interactions with 33,375 interactions from iRefIndex

Fragoza-Yu-2019

0.19%

Extensive disruption of protein interactions by genetic variants across the allele frequency spectrum in human populations. Fragoza et al (2019). *Nat Commun*

Physical Interactions with 603 interactions from iRefIndex

Wallach-Kramer-2013

0.19%

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

Physical Interactions with 143 interactions from BioGRID

Choudhury-Michlewski-2017

0.19%

Choudhury-Michlewski-2017

RNA-binding activity of TRIM25 is mediated by its PRY/SPRY domain and is required for ubiquitination. Choudhury et al (2017). *BMC Biol*

Physical Interactions with 250 interactions from BioGRID

Thalappilly-Dusetti-2008

0.19%

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

Physical Interactions with 102 interactions from iRefIndex

Colland-Gauthier-2004

0.19%

Functional proteomics mapping of a human signaling pathway. Colland et al (2004). *Genome Res*

Physical Interactions with 853 interactions from iRefIndex

Heidelberger-Beli-2018

0.19%

Proteomic profiling of VCP substrates links VCP to K6-linked ubiquitylation and c-Myc function. Heidelberger et al (2018). *EMBO Rep*

Physical Interactions with 1,347 interactions from BioGRID

Weinmann-Meister-2009

0.19%

Importin 8 is a gene silencing factor that targets argonaute proteins to distinct mRNAs. Weinmann et al (2009). *Cell*

Physical Interactions with 96 interactions from BioGRID

Kennedy-Kolch-2020 A

0.19%

Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRAS^{G13D}. Kennedy et al (2020). *Nat Commun*

Physical Interactions with 4,232 interactions from BioGRID

Scott-Schulman-2016

0.19%

Two Distinct Types of E3 Ligases Work in Unison to Regulate Substrate Ubiquitylation. Scott et al (2016). *Cell*

Physical Interactions with 111 interactions from BioGRID

Pilling-Cooper-2017

0.19%

SOCS2 Binds to and Regulates EphA2 through Multiple Mechanisms. Pilling et al (2017). *Sci Rep*

Physical Interactions with 126 interactions from BioGRID

Jain-Parker-2016

0.19%

ATPase-Modulated Stress Granules Contain a Diverse Proteome and Substructure. Jain et al (2016). *Cell*

Physical Interactions with 314 interactions from BioGRID

Maréchal-Zou-2014

0.19%

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*

Physical Interactions with 996 interactions from BioGRID

Lee-Mayr-2019

0.19%

Gain of Additional BIRC3 Protein Functions through 3'-UTR-Mediated Protein Complex Formation. Lee et al (2019). *Mol Cell*

Physical Interactions with 1,759 interactions from BioGRID

IREF-matrixdb

0.19%

Physical Interactions with 15,422 interactions from iRefIndex

Physical Interactions	80.30%
Sokolina-Stagljar-2017	0.19%
Systematic protein-protein interaction mapping for clinically relevant human GPCRs. Sokolina et al (2017). <i>Mol Syst Biol</i>	
Physical Interactions with 994 interactions from iRefIndex	
Leung-Jones-2014	0.19%
Enhanced prediction of Src homology 2 (SH2) domain binding potentials using a fluorescence polarization-derived c-Met, c-Kit, ErbB, and androgen receptor interactome. Leung et al (2014). <i>Mol Cell Proteomics</i>	
Physical Interactions with 199 interactions from iRefIndex	
Fenner-Prehn-2010	0.19%
Expanding the substantial interactome of NEMO using protein microarrays. Fenner et al (2010). <i>PLoS One</i>	
Physical Interactions with 103 interactions from iRefIndex	
Wang-Yang-2011	0.19%
Toward an understanding of the protein interaction network of the human liver. Wang et al (2011). <i>Mol Syst Biol</i>	
Physical Interactions with 3,408 interactions from BioGRID	
Persaud-Rotin-2009 B	0.19%
Comparison of substrate specificity of the ubiquitin ligases Nedd4 and Nedd4-2 using proteome arrays. Persaud et al (2009). <i>Mol Syst Biol</i>	
Physical Interactions with 155 interactions from BioGRID	
Lambert-Gingras-2015	0.19%
Proximity biotinylation and affinity purification are complementary approaches for the interactome mapping of chromatin-associated protein complexes. Lambert et al (2015). <i>J Proteomics</i>	
Physical Interactions with 318 interactions from BioGRID	
BIOGRID-SMALL-SCALE-STUDIES	0.19%
Physical Interactions with 79,201 interactions from BioGRID	
Chen-Krogan-2018	0.19%
CRL4 ^{<sup>} AMBRA1 ^{</sup>} targets Elongin C for ubiquitination and degradation to modulate CRL5 signaling. Chen et al (2018). <i>EMBO J</i>	
Physical Interactions with 101 interactions from BioGRID	
Wang-Huang-2017	0.19%
Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome. Wang et al (2017). <i>Mol Cell Proteomics</i>	
Physical Interactions with 73 interactions from BioGRID	
Chen-Yu-2018	0.19%
An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. Chen et al (2018). <i>Nat Genet</i>	
Physical Interactions with 404 interactions from BioGRID	
Schiza-Diamandis-2018	0.19%
Discovery of a Human Testis-specific Protein Complex TEX101-DPEP3 and Selection of Its Disrupting Antibodies. Schiza et al (2018). <i>Mol Cell Proteomics</i>	
Physical Interactions with 247 interactions from BioGRID	
Alexandru-Deshaies-2008	0.19%
UBXD7 binds multiple ubiquitin ligases and implicates p97 in HIF1alpha turnover. Alexandru et al (2008). <i>Cell</i>	

Alexandru-Deshaies-2008

Physical Interactions with 116 interactions from BioGRID

Rual-Vidal-2005

0.19%

Towards a proteome-scale map of the human protein-protein interaction network. Rual et al (2005). *Nature*

Physical Interactions with 4,031 interactions from iRefIndex

Kaltenbach-Hughes-2007

0.19%

Huntingtin interacting proteins are genetic modifiers of neurodegeneration. Kaltenbach et al (2007). *PLoS Genet*

Physical Interactions with 101 interactions from iRefIndex

Saito-Kobarg-2017

0.19%

Human Regulatory Protein Ki-1/57 Is a Target of SUMOylation and Affects PML Nuclear Body Formation. Saito et al (2017). *J Proteome Res*

Physical Interactions with 165 interactions from iRefIndex

Kärblane-Sarmiento-2015

0.19%

ABCE1 is a highly conserved RNA silencing suppressor. Kärblane et al (2015). *PLoS One*

Physical Interactions with 140 interactions from iRefIndex

Kennedy-Kolch-2020 B

0.19%

Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRAS^{G13D}. Kennedy et al (2020). *Nat Commun*

Physical Interactions with 197 interactions from BioGRID

Hosp-Selbach-2015

0.19%

Quantitative interaction proteomics of neurodegenerative disease proteins. Hosp et al (2015). *Cell Rep*

Physical Interactions with 365 interactions from BioGRID

Persaud-Rotin-2009 A

0.19%

Comparison of substrate specificity of the ubiquitin ligases Nedd4 and Nedd4-2 using proteome arrays. Persaud et al (2009). *Mol Syst Biol*

Physical Interactions with 139 interactions from BioGRID

Oliviero-Cagney-2015

0.19%

The variant Polycomb Repressor Complex 1 component PCGF1 interacts with a pluripotency sub-network that includes DPPA4, a regulator of embryogenesis. Oliviero et al (2015). *Sci Rep*

Physical Interactions with 677 interactions from BioGRID

Gloeckner-Ueffing-2007

0.19%

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

Physical Interactions with 100 interactions from BioGRID

Hegele-Stelzl-2012 B

0.19%

Dynamic protein-protein interaction wiring of the human spliceosome. Hegele et al (2012). *Mol Cell*

Physical Interactions with 600 interactions from BioGRID

Karras-Soengas-2019

0.19%

p62/SQSTM1 Fuels Melanoma Progression by Opposing mRNA Decay of a Selective Set of Pro-metastatic Factors. Karras et al (2019). *Cancer Cell*

Physical Interactions with 147 interactions from BioGRID

Physical Interactions	80.30%
Cooper-Green-2015	0.19%
A fluorescent bimolecular complementation screen reveals MAF1, RNF7 and SETD3 as PCNA-associated proteins in human cells. Cooper et al (2015). <i>Cell Cycle</i>	
Physical Interactions with 261 interactions from iRefIndex	
Low-Heck-2014	0.19%
A systems-wide screen identifies substrates of the SCF TrCPubiquitin ligase. Low et al (2014). <i>Sci Signal</i>	
Physical Interactions with 221 interactions from BioGRID	
Havugimana-Emili-2012	0.19%
A census of human soluble protein complexes. Havugimana et al (2012). <i>Cell</i>	
Physical Interactions with 13,651 interactions from BioGRID	
Mugabo-Lim-2018	0.19%
Elucidation of the 14-3-3 interactome reveals critical roles of RNA-splicing factors during adipogenesis. Mugabo et al (2018). <i>J Biol Chem</i>	
Physical Interactions with 111 interactions from BioGRID	
Zhao-Krug-2005	0.19%
Human ISG15 conjugation targets both IFN-induced and constitutively expressed proteins functioning in diverse cellular pathways. Zhao et al (2005). <i>Proc Natl Acad Sci U S A</i>	
Physical Interactions with 140 interactions from iRefIndex	
Xu-Ye-2012	0.19%
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>	
Physical Interactions with 189 interactions from iRefIndex	
Freibaum-Taylor-2010	0.19%
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>	
Physical Interactions with 160 interactions from iRefIndex	
Lu-Zhang-2013	0.19%
The HECT type ubiquitin ligase NEDL2 is degraded by anaphase-promoting complex/cyclosome (APC/C)-Cdh1, and its tight regulation maintains the metaphase to anaphase transition. Lu et al (2013). <i>J Biol Chem</i>	
Physical Interactions with 186 interactions from iRefIndex	
Lee-Jou-2019	0.19%
Parkinson's disease-associated LRRK2-G2019S mutant acts through regulation of SERCA activity to control ER stress in astrocytes. Lee et al (2019). <i>Acta Neuropathol Commun</i>	
Physical Interactions with 218 interactions from BioGRID	
Zhang-Wang-2018	0.19%
The intracellular NADH level regulates atrophic nonunion pathogenesis through the CtBP2-p300-Runx2 transcriptional complex. Zhang et al (2018). <i>Int J Biol Sci</i>	
Physical Interactions with 138 interactions from BioGRID	
Woods-Monteiro-2012 A	0.19%
Charting the landscape of tandem BRCT domain-mediated protein interactions. Woods et al (2012). <i>Sci Signal</i>	
Physical Interactions with 602 interactions from BioGRID	
Jeronimo-Coulombe-2007	0.19%

Jeronimo-Coulombe-2007

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*

Physical Interactions with 699 interactions from BioGRID

Bhatnagar-Attie-2014

0.19%

Phosphorylation and degradation of tomosyn-2 de-represses insulin secretion. Bhatnagar et al (2014). *J Biol Chem*

Physical Interactions with 198 interactions from BioGRID

Huttlin-Gygi-2015

0.19%

The BioPlex Network: A Systematic Exploration of the Human Interactome. Huttlin et al (2015). *Cell*

Physical Interactions with 23,384 interactions from BioGRID

Raisner-Gascoigne-2018

0.19%

Enhancer Activity Requires CBP/P300 Bromodomain-Dependent Histone H3K27 Acetylation. Raisner et al (2018). *Cell Rep*

Physical Interactions with 174 interactions from BioGRID

Thompson-Luchansky-2014

0.19%

Quantitative Lys- Gly-Gly (diGly) proteomics coupled with inducible RNAi reveals ubiquitin-mediated proteolysis of DNA damage-inducible transcript 4 (DDIT4) by the E3 ligase HUWE1. Thompson et al (2014). *J Biol Chem*

Physical Interactions with 244 interactions from iRefIndex

Keller-Lee-2014

0.19%

SAICAR induces protein kinase activity of PKM2 that is necessary for sustained proliferative signaling of cancer cells. Keller et al (2014). *Mol Cell*

Physical Interactions with 147 interactions from iRefIndex

Li-Wang-2016

0.19%

Defining the Protein-Protein Interaction Network of the Human Protein Tyrosine Phosphatase Family. Li et al (2016). *Mol Cell Proteomics*

Physical Interactions with 1,476 interactions from BioGRID

Xiao-Lefkowitz-2007

0.19%

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

Physical Interactions with 404 interactions from BioGRID

Soler-López-Aloy-2011

0.19%

Interactome mapping suggests new mechanistic details underlying Alzheimer's disease. Soler-López et al (2011). *Genome Res*

Physical Interactions with 283 interactions from iRefIndex

IREF-mint

0.19%

Physical Interactions with 14,408 interactions from iRefIndex

Yang-Brasier-2015

0.19%

Systematic Determination of Human Cyclin Dependent Kinase (CDK)-9 Interactome Identifies Novel Functions in RNA Splicing Mediated by the DEAD Box (DDX)-5/17 RNA Helicases. Yang et al (2015). *Mol Cell Proteomics*

Physical Interactions with 195 interactions from iRefIndex

Murakawa-Landthaler-2015

0.19%

RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF- κ B pathway. Murakawa et al (2015). *Nat Commun*

Murakawa-Landthaler-2015

Physical Interactions with 155 interactions from BioGRID

Chen-Ge-2013 A

0.19%

Bel2-associated athanogene 3 interactome analysis reveals a new role in modulating proteasome activity. Chen et al (2013). *Mol Cell Proteomics*

Physical Interactions with 277 interactions from BioGRID

Wang-Balch-2006

0.19%

Hsp90 cochaperone Aha1 downregulation rescues misfolding of CFTR in cystic fibrosis. Wang et al (2006). *Cell*

Physical Interactions with 200 interactions from BioGRID

Jirawatnotai-Sicinski-2011

0.19%

A function for cyclin D1 in DNA repair uncovered by protein interactome analyses in human cancers. Jirawatnotai et al (2011). *Nature*

Physical Interactions with 122 interactions from BioGRID

Varjosalo-Gstaiger-2013 B

0.19%

The protein interaction landscape of the human CMGC kinase group. Varjosalo et al (2013). *Cell Rep*

Physical Interactions with 308 interactions from BioGRID

Couzens-Gingras-2013

0.19%

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

Physical Interactions with 365 interactions from BioGRID

Li-Chen-2015

0.19%

Proteomic analyses reveal distinct chromatin-associated and soluble transcription factor complexes. Li et al (2015). *Mol Syst Biol*

Physical Interactions with 1,811 interactions from BioGRID

Gao-Reinberg-2012

0.19%

PCGF homologs, CBX proteins, and RYBP define functionally distinct PRC1 family complexes. Gao et al (2012). *Mol Cell*

Physical Interactions with 171 interactions from BioGRID

Venkatesan-Vidal-2009

0.19%

An empirical framework for binary interactome mapping. Venkatesan et al (2009). *Nat Methods*

Physical Interactions with 160 interactions from iRefIndex

Newman-Keating-2003

0.19%

Comprehensive identification of human bZIP interactions with coiled-coil arrays. Newman et al (2003). *Science*

Physical Interactions with 223 interactions from iRefIndex

von Hundelshausen-Weber-2017

0.19%

Chemokine interactome mapping enables tailored intervention in acute and chronic inflammation. von Hundelshausen et al (2017). *Sci Transl Med*

Physical Interactions with 213 interactions from iRefIndex

Lampert-Peter-2018

0.19%

The multi-subunit GID/CTLH E3 ubiquitin ligase promotes cell proliferation and targets the transcription factor Hbp1 for degradation. Lampert et al (2018). *Elife*

Physical Interactions with 288 interactions from BioGRID

Physical Interactions	80.30%
IREF-dip	0.19%
Physical Interactions with 5,037 interactions from iRefIndex	
IREF-hpidb	0.19%
Physical Interactions with 166 interactions from iRefIndex	
Winczura-Jensen-2018	0.19%
Characterizing ZC3H18, a Multi-domain Protein at the Interface of RNA Production and Destruction Decisions. Winczura et al (2018). <i>Cell Rep</i>	
Physical Interactions with 729 interactions from BioGRID	
Phillips-Corn-2013	0.19%
Conformational dynamics control ubiquitin-deubiquitinase interactions and influence in vivo signaling. Phillips et al (2013). <i>Proc Natl Acad Sci U S A</i>	
Physical Interactions with 142 interactions from BioGRID	
Floyd-Pagliarini-2016	0.19%
Mitochondrial Protein Interaction Mapping Identifies Regulators of Respiratory Chain Function. Floyd et al (2016). <i>Mol Cell</i>	
Physical Interactions with 1,508 interactions from BioGRID	
Whisenant-Salomon-2015	0.19%
The Activation-Induced Assembly of an RNA/Protein Interactome Centered on the Splicing Factor U2AF2 Regulates Gene Expression in Human CD4 T Cells. Whisenant et al (2015). <i>PLoS One</i>	
Physical Interactions with 237 interactions from BioGRID	
Trepte-Wanker-2018 A	0.19%
LuTHy: a double-readout bioluminescence-based two-hybrid technology for quantitative mapping of protein-protein interactions in mammalian cells. Trepte et al (2018). <i>Mol Syst Biol</i>	
Physical Interactions with 70 interactions from BioGRID	
Tarallo-Weisz-2011	0.19%
Identification of proteins associated with ligand-activated estrogen receptor in human breast cancer cell nuclei by tandem affinity purification and nano LC-MS/MS. Tarallo et al (2011). <i>Proteomics</i>	
Physical Interactions with 244 interactions from BioGRID	
Liu-Yang-2019	0.19%
Inflammation-dependent overexpression of c-Myc enhances CRL4 ^{DCAF4} E3 ligase activity and promotes ubiquitination of ST7 in colitis-associated cancer. Liu et al (2019). <i>J Pathol</i>	
Physical Interactions with 279 interactions from BioGRID	
Choi-Beutler-2019	0.19%
LMBR1L regulates lymphopoiesis through Wnt/ β -catenin signaling. Choi et al (2019). <i>Science</i>	
Physical Interactions with 928 interactions from BioGRID	
Drissi-Boisvert-2015	0.19%
Quantitative Proteomics Reveals Dynamic Interactions of the Minichromosome Maintenance Complex (MCM) in the Cellular Response to Etoposide Induced DNA Damage. Drissi et al (2015). <i>Mol Cell Proteomics</i>	
Physical Interactions with 947 interactions from BioGRID	
IREF-biogrid	0.19%
Physical Interactions with 176,314 interactions from iRefIndex	
Bandyopadhyay-Ideker-2010	0.19%

Physical Interactions	80.30%
Bandyopadhyay-Ideker-2010	
A human MAP kinase interactome. Bandyopadhyay et al (2010). <i>Nat Methods</i>	
Physical Interactions with 653 interactions from iRefIndex	
Vinayagam-Wanker-2011	0.19%
A directed protein interaction network for investigating intracellular signal transduction. Vinayagam et al (2011). <i>Sci Signal</i>	
Physical Interactions with 2,585 interactions from iRefIndex	
Nowak-Sommer-2019	0.19%
DCAF8, a novel MuRF1 interaction partner, promotes muscle atrophy. Nowak et al (2019). <i>J Cell Sci</i>	
Physical Interactions with 335 interactions from iRefIndex	
Sundell-Ivarsson-2018	0.19%
Proteome-wide analysis of phospho-regulated PDZ domain interactions. Sundell et al (2018). <i>Mol Syst Biol</i>	
Physical Interactions with 129 interactions from iRefIndex	
Li-Dorf-2011 A	0.19%
Mapping a dynamic innate immunity protein interaction network regulating type I interferon production. Li et al (2011). <i>Immunity</i>	
Physical Interactions with 400 interactions from BioGRID	
Perez-Hernandez-Yáñez-Mó-2013	0.19%
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>	
Physical Interactions with 446 interactions from BioGRID	
Weith-Meyer-2018	0.19%
Ubiquitin-Independent Disassembly by a p97 AAA-ATPase Complex Drives PP1 Holoenzyme Formation. Weith et al (2018). <i>Mol Cell</i>	
Physical Interactions with 355 interactions from BioGRID	
Ivanochko-Arrowsmith-2019	0.19%
Direct interaction between the PRDM3 and PRDM16 tumor suppressors and the NuRD chromatin remodeling complex. Ivanochko et al (2019). <i>Nucleic Acids Res</i>	
Physical Interactions with 311 interactions from BioGRID	
Brady-Omary-2018	0.19%
Nuclear lamina genetic variants, including a truncated LAP2, in twins and siblings with nonalcoholic fatty liver disease. Brady et al (2018). <i>Hepatology</i>	
Physical Interactions with 240 interactions from BioGRID	
Brehme-Superti-Furga-2009	0.19%
Charting the molecular network of the drug target Bcr-Abl. Brehme et al (2009). <i>Proc Natl Acad Sci U S A</i>	
Physical Interactions with 626 interactions from BioGRID	
McNamara-D'Orso-2016	0.19%
KAP1 Recruitment of the 7SK snRNP Complex to Promoters Enables Transcription Elongation by RNA Polymerase II. McNamara et al (2016). <i>Mol Cell</i>	
Physical Interactions with 276 interactions from BioGRID	
Davis-Glaunsinger-2015	0.19%
Global mapping of herpesvirus-host protein complexes reveals a transcription strategy for late genes. Davis et al (2015). <i>Mol Cell</i>	

Physical Interactions	80.30%
Davis-Glaunsinger-2015	
Physical Interactions with 51 interactions from BioGRID	
Sahni-Vidal-2015	0.19%
Widespread macromolecular interaction perturbations in human genetic disorders. Sahni et al (2015). <i>Cell</i>	
Physical Interactions with 591 interactions from BioGRID	
Christianson-Kopito-2011	0.19%
Defining human ERAD networks through an integrative mapping strategy. Christianson et al (2011). <i>Nat Cell Biol</i>	
Physical Interactions with 294 interactions from BioGRID	
Vandamme-Angrand-2011	0.19%
Interaction proteomics analysis of polycomb proteins defines distinct PRC1 complexes in mammalian cells. Vandamme et al (2011). <i>Mol Cell Proteomics</i>	
Physical Interactions with 111 interactions from iRefIndex	
Stelzl-Wanker-2005	0.19%
A human protein-protein interaction network: a resource for annotating the proteome. Stelzl et al (2005). <i>Cell</i>	
Physical Interactions with 3,370 interactions from iRefIndex	
IREF-spike	0.19%
Physical Interactions with 20,971 interactions from iRefIndex	
IREF-SMALL-SCALE-STUDIES	0.19%
Physical Interactions with 75,496 interactions from iRefIndex	
Gautier-Hall-2009	0.19%
In vitro nuclear interactome of the HIV-1 Tat protein. Gautier et al (2009). <i>Retrovirology</i>	
Physical Interactions with 184 interactions from BioGRID	
Xie-Cong-2013	0.19%
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>	
Physical Interactions with 170 interactions from BioGRID	
Grossmann-Stelzl-2015	0.19%
Phospho-tyrosine dependent protein-protein interaction network. Grossmann et al (2015). <i>Mol Syst Biol</i>	
Physical Interactions with 620 interactions from BioGRID	
Moon-Kim-2014	0.19%
Interactome analysis of AMP-activated protein kinase (AMPK)- 1 and - 1 in INS-1 pancreatic beta-cells by affinity purification-mass spectrometry. Moon et al (2014). <i>Sci Rep</i>	
Physical Interactions with 171 interactions from BioGRID	
Oláh-Ovádi-2011	0.19%
Interactions of pathological hallmark proteins: tubulin polymerization promoting protein/p25, beta-amyloid, and alpha-synuclein. Oláh et al (2011). <i>J Biol Chem</i>	
Physical Interactions with 1,854 interactions from BioGRID	
Faust-Frankel-2018	0.19%
The HIV-1 Tat protein recruits a ubiquitin ligase to reorganize the 7SK snRNP for transcriptional activation. Faust et al (2018). <i>Elife</i>	

Faust-Frankel-2018

Physical Interactions with 2,200 interactions from BioGRID

Trepte-Wanker-2018 B

0.19%

LuTHy: a double-readout bioluminescence-based two-hybrid technology for quantitative mapping of protein-protein interactions in mammalian cells. Trepte et al (2018). *Mol Syst Biol*

Physical Interactions with 138 interactions from BioGRID

Glatter-Gstaiger-2009

0.19%

An integrated workflow for charting the human interaction proteome: insights into the PP2A system. Glatter et al (2009). *Mol Syst Biol*

Physical Interactions with 244 interactions from BioGRID

Barrios-Rodiles-Wrana-2005

0.19%

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

Physical Interactions with 596 interactions from iRefIndex

Raman-Harper-2015

0.19%

Systematic proteomics of the VCP-UBXD adaptor network identifies a role for UBXN10 in regulating ciliogenesis. Raman et al (2015). *Nat Cell Biol*

Physical Interactions with 271 interactions from BioGRID

Yang-Maurer-2018

0.19%

rec-YnH enables simultaneous many-by-many detection of direct protein-protein and protein-RNA interactions. Yang et al (2018). *Nat Commun*

Physical Interactions with 325 interactions from BioGRID

Virok-Fülöp-2011

0.19%

Protein array based interactome analysis of amyloid- indicates an inhibition of protein translation. Virok et al (2011). *J Proteome Res*

Physical Interactions with 299 interactions from BioGRID

Taipale-Lindquist-2012

0.19%

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

Physical Interactions with 390 interactions from iRefIndex

Vastrik-Stein-2007

0.19%

Reactome: a knowledge base of biologic pathways and processes. Vastrik et al (2007). *Genome Biol*

Physical Interactions with 111,926 interactions from iRefIndex

Papp-Lamia-2015

0.19%

DNA damage shifts circadian clock time via Hausp-dependent Cry1 stabilization. Papp et al (2015). *Elife*

Physical Interactions with 158 interactions from iRefIndex

Liebelt-Vertegaal-2020

0.19%

Transcription-coupled nucleotide excision repair is coordinated by ubiquitin and SUMO in response to ultraviolet irradiation. Liebelt et al (2020). *Nucleic Acids Res*

Physical Interactions with 100 interactions from BioGRID

Hauri-Gstaiger-2013

0.19%

Interaction proteome of human Hippo signaling: modular control of the co-activator YAP1. Hauri et al (2013). *Mol Syst Biol*

Physical Interactions with 453 interactions from BioGRID

Physical Interactions	80.30%
Corominas-Iakoucheva-2014 Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. Corominas et al (2014). <i>Nat Commun</i> Physical Interactions with 493 interactions from BioGRID	0.19%
Asadi-Dhanvantari-2018 Plasticity in the Glucagon Interactome Reveals Novel Proteins That Regulate Glucagon Secretion in -TC1-6 Cells. Asadi et al (2018). <i>Front Endocrinol (Lausanne)</i> Physical Interactions with 229 interactions from BioGRID	0.19%
Milev-Mouland-2012 Characterization of staufen1 ribonucleoproteins by mass spectrometry and biochemical analyses reveal the presence of diverse host proteins associated with human immunodeficiency virus type 1. Milev et al (2012). <i>Front Microbiol</i> Physical Interactions with 237 interactions from BioGRID	0.19%
Abu-Odeh-Aqeilan-2014 Characterizing WW domain interactions of tumor suppressor WWOX reveals its association with multiprotein networks. Abu-Odeh et al (2014). <i>J Biol Chem</i> Physical Interactions with 216 interactions from BioGRID	0.19%
Ravasi-Hayashizaki-2010 An atlas of combinatorial transcriptional regulation in mouse and man. Ravasi et al (2010). <i>Cell</i> Physical Interactions with 658 interactions from BioGRID	0.19%
Teixeira-Gomes-2010 Identification of FBXO25-interacting proteins using an integrated proteomics approach. Teixeira et al (2010). <i>Proteomics</i> Physical Interactions with 109 interactions from BioGRID	0.19%
Nakayama-Ohara-2002 Protein-protein interactions between large proteins: two-hybrid screening using a functionally classified library composed of long cDNAs. Nakayama et al (2002). <i>Genome Res</i> Physical Interactions with 128 interactions from iRefIndex	0.19%
Taipale-Lindquist-2014 A quantitative chaperone interaction network reveals the architecture of cellular protein homeostasis pathways. Taipale et al (2014). <i>Cell</i> Physical Interactions with 1,227 interactions from iRefIndex	0.19%
Chitale-Richly-2017 Nuclear organization of nucleotide excision repair is mediated by RING1B dependent H2A-ubiquitylation. Chitale et al (2017). <i>Oncotarget</i> Physical Interactions with 103 interactions from BioGRID	0.19%
Garzia-Sonenberg-2017 The E3 ubiquitin ligase and RNA-binding protein ZNF598 orchestrates ribosome quality control of premature polyadenylated mRNAs. Garzia et al (2017). <i>Nat Commun</i> Physical Interactions with 310 interactions from BioGRID	0.19%
Kahle-Zoghbi-2011 Comparison of an expanded ataxia interactome with patient medical records reveals a relationship between macular degeneration and ataxia. Kahle et al (2011). <i>Hum Mol Genet</i> Physical Interactions with 132 interactions from iRefIndex	0.19%

Physical Interactions	80.30%
Swayampakula-Dedhar-2017	0.19%
The interactome of metabolic enzyme carbonic anhydrase IX reveals novel roles in tumor cell migration and invadopodia/MMP14-mediated invasion. Swayampakula et al (2017). <i>Oncogene</i>	
Physical Interactions with 126 interactions from iRefIndex	
Teixeira-Laman-2016 B	0.19%
Gsk3 and Tomm20 are substrates of the SCFFbxo7/PARK15 ubiquitin ligase associated with Parkinson's disease. Teixeira et al (2016). <i>Biochem J</i>	
Physical Interactions with 324 interactions from BioGRID	
Hayes-Urbé-2012	0.19%
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). <i>J Biol Chem</i>	
Physical Interactions with 110 interactions from BioGRID	
Joshi-Cristea-2013	0.19%
The functional interactome landscape of the human histone deacetylase family. Joshi et al (2013). <i>Mol Syst Biol</i>	
Physical Interactions with 375 interactions from BioGRID	
Yu-Chow-2013	0.19%
VCP phosphorylation-dependent interaction partners prevent apoptosis in Helicobacter pylori-infected gastric epithelial cells. Yu et al (2013). <i>PLoS One</i>	
Physical Interactions with 280 interactions from BioGRID	
Greco-Cristea-2011	0.19%
Nuclear import of histone deacetylase 5 by requisite nuclear localization signal phosphorylation. Greco et al (2011). <i>Mol Cell Proteomics</i>	
Physical Interactions with 256 interactions from BioGRID	
Reinke-Keating-2013	0.19%
Networks of bZIP protein-protein interactions diversified over a billion years of evolution. Reinke et al (2013). <i>Science</i>	
Physical Interactions with 143 interactions from BioGRID	
Li-Dorf-2011 B	0.19%
Mapping a dynamic innate immunity protein interaction network regulating type I interferon production. Li et al (2011). <i>Immunity</i>	
Physical Interactions with 125 interactions from BioGRID	
Liu-Tan-2018	0.19%
Proteome-wide analysis of USP14 substrates revealed its role in hepatosteatosis via stabilization of FASN. Liu et al (2018). <i>Nat Commun</i>	
Physical Interactions with 331 interactions from BioGRID	
Llères-Lamond-2010	0.19%
Direct interaction between hnRNP-M and CDC5L/PLRG1 proteins affects alternative splice site choice. Llères et al (2010). <i>EMBO Rep</i>	
Physical Interactions with 848 interactions from BioGRID	
Viita-Vartiainen-2019	0.19%
Nuclear actin interactome analysis links actin to KAT14 histone acetyl transferase and mRNA splicing. Viita et al (2019). <i>J Cell Sci</i>	
Physical Interactions with 213 interactions from BioGRID	

Physical Interactions	80.30%
Blandin-Richard-2013	0.19%
A human skeletal muscle interactome centered on proteins involved in muscular dystrophies: LGMD interactome. Blandin et al (2013). <i>Skelet Muscle</i>	
Physical Interactions with 655 interactions from iRefIndex	
Albers-Koegl-2005	0.19%
Automated yeast two-hybrid screening for nuclear receptor-interacting proteins. Albers et al (2005). <i>Mol Cell Proteomics</i>	
Physical Interactions with 289 interactions from iRefIndex	
Hermjakob-Apweiler-2004	0.19%
IntAct: an open source molecular interaction database. Hermjakob et al (2004). <i>Nucleic Acids Res</i>	
Physical Interactions with 214 interactions from iRefIndex	
Hou-Chen-2018	0.19%
Profiling the interactome of protein kinase C by proteomics and bioinformatics. Hou et al (2018). <i>Proteome Sci</i>	
Physical Interactions with 103 interactions from BioGRID	
Zhou-Conrads-2004	0.19%
"An investigation into the human serum "interactome"." Zhou et al (2004). <i>Electrophoresis</i>	
Physical Interactions with 112 interactions from iRefIndex	
Cloutier-Coulombe-2017	0.19%
R2TP/Prefoldin-like component RUVBL1/RUVBL2 directly interacts with ZNHIT2 to regulate assembly of U5 small nuclear ribonucleoprotein. Cloutier et al (2017). <i>Nat Commun</i>	
Physical Interactions with 506 interactions from BioGRID	
Humphries-Humphries-2009	0.19%
Proteomic analysis of integrin-associated complexes identifies RCC2 as a dual regulator of Rac1 and Arf6. Humphries et al (2009). <i>Sci Signal</i>	
Physical Interactions with 1,060 interactions from BioGRID	
Ptushkina-Ray-2017	0.19%
A non-transcriptional role for the glucocorticoid receptor in mediating the cell stress response. Ptushkina et al (2017). <i>Sci Rep</i>	
Physical Interactions with 142 interactions from BioGRID	
Lehner-Sanderson-2004 B	0.19%
A protein interaction framework for human mRNA degradation. Lehner et al (2004). <i>Genome Res</i>	
Physical Interactions with 427 interactions from BioGRID	
Teixeira-Laman-2016 A	0.19%
Gsk3 and Tomm20 are substrates of the SCFFbxo7/PARK15 ubiquitin ligase associated with Parkinson's disease. Teixeira et al (2016). <i>Biochem J</i>	
Physical Interactions with 130 interactions from BioGRID	
Van Alstyne-Pellizzoni-2018	0.19%
Stasimon/Tmem41b localizes to mitochondria-associated ER membranes and is essential for mouse embryonic development. Van Alstyne et al (2018). <i>Biochem Biophys Res Commun</i>	
Physical Interactions with 110 interactions from BioGRID	
Van Acker-Dewilde-2019	0.19%
Connecting the Dots in the Neuroglobin-Protein Interaction Network of an Unstressed and Ferroptotic Cell Death Neuroblastoma Model. Van Acker et al (2019). <i>Cells</i>	

Van Acker-Dewilde-2019

Physical Interactions with 130 interactions from BioGRID

Chen-Guan-2018

0.19%

SNIP1 Recruits TET2 to Regulate c-MYC Target Genes and Cellular DNA Damage Response. Chen et al (2018). *Cell Rep*

Physical Interactions with 240 interactions from BioGRID

Gabriel-Baumgrass-2016

0.19%

Identification of Novel Nuclear Factor of Activated T Cell (NFAT)-associated Proteins in T Cells. Gabriel et al (2016). *J Biol Chem*

Physical Interactions with 223 interactions from BioGRID

Rivera-Paes Leme-2018

0.19%

Agrin has a pathological role in the progression of oral cancer. Rivera et al (2018). *Br J Cancer*

Physical Interactions with 194 interactions from BioGRID

Behzadnia-Lührmann-2007

0.19%

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

Physical Interactions with 107 interactions from iRefIndex

Cox-Rizzino-2013

0.19%

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). *PLoS One*

Physical Interactions with 190 interactions from iRefIndex

Jones-MacBeath-2006

0.19%

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

Physical Interactions with 158 interactions from iRefIndex

Lee-Songyang-2011

0.19%

Genome-wide YFP fluorescence complementation screen identifies new regulators for telomere signaling in human cells. Lee et al (2011). *Mol Cell Proteomics*

Physical Interactions with 610 interactions from iRefIndex

Zhou-Hanemann-2016

0.19%

The scaffold protein KSR1, a novel therapeutic target for the treatment of Merlin-deficient tumors. Zhou et al (2016). *Oncogene*

Physical Interactions with 378 interactions from BioGRID

Stehling-Lill-2012

0.19%

MMS19 assembles iron-sulfur proteins required for DNA metabolism and genomic integrity. Stehling et al (2012). *Science*

Physical Interactions with 147 interactions from BioGRID

Emdal-Olsen-2015

0.19%

Temporal proteomics of NGF-TrkA signaling identifies an inhibitory role for the E3 ligase Cbl-b in neuroblastoma cell differentiation. Emdal et al (2015). *Sci Signal*

Physical Interactions with 1,917 interactions from BioGRID

An-Sun-2017

0.19%

Interactome Analysis Reveals a Novel Role for RAD6 in the Regulation of Proteasome Activity and Localization in Response to DNA Damage. An et al (2017). *Mol Cell Biol*

Physical Interactions with 129 interactions from BioGRID

Physical Interactions	80.30%
Pladevall-Morera-Lopez-Contreras-2019	0.19%
Proteomic characterization of chromosomal common fragile site (CFS)-associated proteins uncovers ATRX as a regulator of CFS stability. Pladevall-Morera et al (2019). <i>Nucleic Acids Res</i>	
Physical Interactions with 621 interactions from BioGRID	
Hegele-Stelzl-2012 A	0.19%
Dynamic protein-protein interaction wiring of the human spliceosome. Hegele et al (2012). <i>Mol Cell</i>	
Physical Interactions with 103 interactions from BioGRID	
Kato-Sternberg-2014	0.19%
LINKIN, a new transmembrane protein necessary for cell adhesion. Kato et al (2014). <i>Elife</i>	
Physical Interactions with 384 interactions from iRefIndex	
Sang-Jackson-2011	0.19%
Mapping the NPHP-JBTS-MKS protein network reveals ciliopathy disease genes and pathways. Sang et al (2011). <i>Cell</i>	
Physical Interactions with 226 interactions from BioGRID	
Kawahara-Paes Leme-2017	0.19%
Mass spectrometry-based proteomics revealed Glypican-1 as a novel ADAM17 substrate. Kawahara et al (2017). <i>J Proteomics</i>	
Physical Interactions with 114 interactions from BioGRID	
Zeller-Wei-2006	0.19%
Global mapping of c-Myc binding sites and target gene networks in human B cells. Zeller et al (2006). <i>Proc Natl Acad Sci U S A</i>	
Physical Interactions with 634 interactions from iRefIndex	
Suter-Wanker-2013	0.19%
Development and application of a DNA microarray-based yeast two-hybrid system. Suter et al (2013). <i>Nucleic Acids Res</i>	
Physical Interactions with 130 interactions from iRefIndex	
IREF-huri	0.19%
Physical Interactions with 47,604 interactions from iRefIndex	
Tsai-Cristea-2012	0.19%
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). <i>Mol Cell Proteomics</i>	
Physical Interactions with 651 interactions from BioGRID	
Rowbotham-Mermoud-2011	0.19%
Maintenance of silent chromatin through replication requires SWI/SNF-like chromatin remodeler SMARCAD1. Rowbotham et al (2011). <i>Mol Cell</i>	
Physical Interactions with 114 interactions from BioGRID	
Pichlmair-Superti-Furga-2012	0.19%
Viral immune modulators perturb the human molecular network by common and unique strategies. Pichlmair et al (2012). <i>Nature</i>	
Physical Interactions with 14 interactions from BioGRID	
Das-Broemer-2019	0.19%
New roles for the de-ubiquitylating enzyme OTUD4 in an RNA-protein network and RNA granules. Das et al (2019). <i>J Cell Sci</i>	
Physical Interactions with 444 interactions from BioGRID	
Scholz-Taylor-2016	0.19%
FIH Regulates Cellular Metabolism through Hydroxylation of the Deubiquitinase OTUB1. Scholz et al (2016). <i>PLoS Biol</i>	

Physical Interactions	80.30%
Scholz-Taylor-2016	
Physical Interactions with 134 interactions from BioGRID	
Jang-Trono-2018	0.19%
KAP1 facilitates reinstatement of heterochromatin after DNA replication. Jang et al (2018). <i>Nucleic Acids Res</i>	
Physical Interactions with 699 interactions from BioGRID	
Rosenbluh-Hahn-2016	0.19%
Genetic and Proteomic Interrogation of Lower Confidence Candidate Genes Reveals Signaling Networks in -Catenin-Active Cancers. Rosenbluh et al (2016). <i>Cell Syst</i>	
Physical Interactions with 3,482 interactions from BioGRID	
St-Denis-Gingras-2015	0.19%
Myotubularin-related proteins 3 and 4 interact with polo-like kinase 1 and centrosomal protein of 55 kDa to ensure proper abscission. St-Denis et al (2015). <i>Mol Cell Proteomics</i>	
Physical Interactions with 168 interactions from BioGRID	
Kang-Shin-2015	0.19%
Repression of rRNA transcription by PARIS contributes to Parkinson's disease. Kang et al (2015). <i>Neurobiol Dis</i>	
Physical Interactions with 269 interactions from BioGRID	
Bett-Hay-2013	0.19%
The P-body component USP52/PAN2 is a novel regulator of HIF1A mRNA stability. Bett et al (2013). <i>Biochem J</i>	
Physical Interactions with 238 interactions from iRefIndex	
Barr-Knapp-2009	0.19%
Large-scale structural analysis of the classical human protein tyrosine phosphatome. Barr et al (2009). <i>Cell</i>	
Physical Interactions with 173 interactions from iRefIndex	
Hu-Woods-2019	0.19%
CTDP1 regulates breast cancer survival and DNA repair through BRCT-specific interactions with FANCI. Hu et al (2019). <i>Cell Death Discov</i>	
Physical Interactions with 103 interactions from BioGRID	
Zhang-Xu-2018	0.19%
Revealing A-Raf functions through its interactome. Zhang et al (2018). <i>Biochim Biophys Acta Proteins Proteom</i>	
Physical Interactions with 186 interactions from BioGRID	
Arroyo-Aloy-2015	0.19%
Systematic identification of molecular links between core and candidate genes in breast cancer. Arroyo et al (2015). <i>J Mol Biol</i>	
Physical Interactions with 611 interactions from iRefIndex	
Lee-Choi-2017	0.19%
Comparative Interactomes of VRK1 and VRK3 with Their Distinct Roles in the Cell Cycle of Liver Cancer. Lee et al (2017). <i>Mol Cells</i>	
Physical Interactions with 202 interactions from iRefIndex	
Kumar-Vertegaal-2017	0.19%
The STUbL RNF4 regulates protein group SUMOylation by targeting the SUMO conjugation machinery. Kumar et al (2017). <i>Nat Commun</i>	
Physical Interactions with 1,198 interactions from BioGRID	

Physical Interactions	80.30%
Simabuco-Zanchin-2019 Interactome analysis of the human Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1 (hMTTr1) protein. Simabuco et al (2019). <i>J Cell Biochem</i> Physical Interactions with 135 interactions from BioGRID	0.19%
Behrends-Harper-2010 Network organization of the human autophagy system. Behrends et al (2010). <i>Nature</i> Physical Interactions with 704 interactions from BioGRID	0.19%
Huttlin-Harper-2017 Architecture of the human interactome defines protein communities and disease networks. Huttlin et al (2017). <i>Nature</i> Physical Interactions with 55,868 interactions from BioGRID	0.19%
Galligan-Howley-2015 Proteomic analysis and identification of cellular interactors of the giant ubiquitin ligase HERC2. Galligan et al (2015). <i>J Proteome Res</i> Physical Interactions with 130 interactions from BioGRID	0.19%
Chen-Zhang-2013 Quantitative study of the interactome of PKC involved in the EGF-induced tumor cell chemotaxis. Chen et al (2013). <i>J Proteome Res</i> Physical Interactions with 182 interactions from BioGRID	0.19%
Bennett-Harper-2010 Dynamics of cullin-RING ubiquitin ligase network revealed by systematic quantitative proteomics. Bennett et al (2010). <i>Cell</i> Physical Interactions with 4,362 interactions from BioGRID	0.19%
St-Denis-Gingras-2016 Phenotypic and Interaction Profiling of the Human Phosphatases Identifies Diverse Mitotic Regulators. St-Denis et al (2016). <i>Cell Rep</i> Physical Interactions with 783 interactions from BioGRID	0.19%
Gilmore-Washburn-2016 WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. Gilmore et al (2016). <i>PLoS One</i> Physical Interactions with 944 interactions from BioGRID	0.19%
Noguchi-Kawahara-2018 ZFP36L2 is a cell cycle-regulated CCCH protein necessary for DNA lesion-induced S-phase arrest. Noguchi et al (2018). <i>Biol Open</i> Physical Interactions with 143 interactions from iRefIndex	0.19%
Miyamoto-Sato-Yanagawa-2010 A comprehensive resource of interacting protein regions for refining human transcription factor networks. Miyamoto-Sato et al (2010). <i>PLoS One</i> Physical Interactions with 934 interactions from iRefIndex	0.19%
Ewing-Figeys-2007 Large-scale mapping of human protein-protein interactions by mass spectrometry. Ewing et al (2007). <i>Mol Syst Biol</i> Physical Interactions with 5,759 interactions from iRefIndex	0.19%
Wan-Emili-2015	0.19%

Wan-Emili-2015

Panorama of ancient metazoan macromolecular complexes. Wan et al (2015). *Nature*

Physical Interactions with 16,627 interactions from BioGRID

Neganova-Lako-2011

0.19%

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*

Physical Interactions with 307 interactions from iRefIndex

Gallardo-Vara-Bernabeu-2019

0.19%

Endoglin Protein Interactome Profiling Identifies TRIM21 and Galectin-3 as New Binding Partners. Gallardo-Vara et al (2019). *Cells*

Physical Interactions with 182 interactions from BioGRID

Giurato-Tarallo-2018

0.19%

Quantitative mapping of RNA-mediated nuclear estrogen receptor interactome in human breast cancer cells. Giurato et al (2018). *Sci Data*

Physical Interactions with 2,161 interactions from BioGRID

Lee-Choi-2016

0.19%

Interactomic analysis of REST/NRSF and implications of its functional links with the transcription suppressor TRIM28 during neuronal differentiation. Lee et al (2016). *Sci Rep*

Physical Interactions with 199 interactions from BioGRID

Coyaud-Raught-2015

0.19%

BioID-based Identification of Skp Cullin F-box (SCF) -TrCP1/2 E3 Ligase Substrates. Coyaud et al (2015). *Mol Cell Proteomics*

Physical Interactions with 164 interactions from BioGRID

McCracken-Blencowe-2005

0.19%

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

Physical Interactions with 198 interactions from BioGRID

Hu-Yin-2019

0.19%

Poly(ADP-ribosyl)ation of BRD7 by PARP1 confers resistance to DNA-damaging chemotherapeutic agents. Hu et al (2019). *EMBO Rep*

Physical Interactions with 479 interactions from BioGRID

Pech-Settleman-2019

0.19%

Systematic identification of cancer cell vulnerabilities to natural killer cell-mediated immune surveillance. Pech et al (2019). *Elife*

Physical Interactions with 141 interactions from iRefIndex

Mak-Moffat-2010

0.19%

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

Physical Interactions with 110 interactions from BioGRID

Liu-Wang-2012

0.19%

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

Physical Interactions with 593 interactions from BioGRID

Weimann-Stelzl-2013 A

0.19%

Weimann-Stelzl-2013 A

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

Physical Interactions with 112 interactions from BioGRID

IREF-mppi

0.19%

Physical Interactions with 304 interactions from iRefIndex

IREF-intcomplex

0.19%

Physical Interactions with 212 interactions from iRefIndex

Jin-Pawson-2004

0.19%

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*

Physical Interactions with 247 interactions from iRefIndex

Johnson-Kerner-Wichterle-2015

0.19%

Kelch Domain of Gigaxonin Interacts with Intermediate Filament Proteins Affected in Giant Axonal Neuropathy. Johnson-Kerner et al (2015). *PLoS One*

Physical Interactions with 126 interactions from iRefIndex

Malty-Babu-2017

0.19%

A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- κ B Signaling. Malty et al (2017). *Cell Syst*

Physical Interactions with 1,969 interactions from BioGRID

McFarland-Nussbaum-2008

0.19%

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

Physical Interactions with 159 interactions from BioGRID

Li-Fu-2017

0.19%

The OncoPPi network of cancer-focused protein-protein interactions to inform biological insights and therapeutic strategies. Li et al (2017). *Nat Commun*

Physical Interactions with 749 interactions from BioGRID

Giannone-Liu-2010

0.19%

The protein network surrounding the human telomere repeat binding factors TRF1, TRF2, and POT1. Giannone et al (2010). *PLoS One*

Physical Interactions with 288 interactions from BioGRID

Goudreault-Gingras-2009

0.19%

A PP2A phosphatase high density interaction network identifies a novel striatin-interacting phosphatase and kinase complex linked to the cerebral cavernous malformation 3 (CCM3) protein. Goudreault et al (2009). *Mol Cell Proteomics*

Physical Interactions with 240 interactions from BioGRID

Chen-Ge-2013 B

0.19%

Bcl2-associated athanogene 3 interactome analysis reveals a new role in modulating proteasome activity. Chen et al (2013). *Mol Cell Proteomics*

Physical Interactions with 173 interactions from BioGRID

Ertych-Bastians-2016

0.19%

CHK2-BRCA1 tumor-suppressor axis restrains oncogenic Aurora-A kinase to ensure proper mitotic microtubule assembly. Ertych et al (2016). *Proc Natl Acad Sci U S A*

Ertych-Bastians-2016

Physical Interactions with 486 interactions from BioGRID

Crow-Cristea-2017

0.19%

Human Antiviral Protein IFIX Suppresses Viral Gene Expression during Herpes Simplex Virus 1 (HSV-1) Infection and Is Counteracted by Virus-induced Proteasomal Degradation. Crow et al (2017). *Mol Cell Proteomics*

Physical Interactions with 180 interactions from iRefIndex

Wu-Ma-2012

0.19%

Targeted ubiquitination and degradation of G-protein-coupled receptor kinase 5 by the DDB1-CUL4 ubiquitin ligase complex. Wu et al (2012). *PLoS One*

Physical Interactions with 113 interactions from iRefIndex

Foerster-Ritter-2013

0.19%

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

Physical Interactions with 179 interactions from BioGRID

Ugidos-Vandenbroeck-2019

0.19%

Interactome of the Autoimmune Risk Protein ANKRD55. Ugidos et al (2019). *Front Immunol*

Physical Interactions with 195 interactions from BioGRID

Colicelli-2010

0.19%

ABL tyrosine kinases: evolution of function, regulation, and specificity. Colicelli (2010). *Sci Signal*

Physical Interactions with 147 interactions from iRefIndex

IREF-uniprotpp

0.19%

Physical Interactions with 2,470 interactions from iRefIndex

Wang-He-2008

0.19%

Protein interaction data set highlighted with human Ras-MAPK/PI3K signaling pathways. Wang et al (2008). *J Proteome Res*

Physical Interactions with 213 interactions from iRefIndex

Mohammed-Carroll-2013

0.19%

Endogenous purification reveals GREB1 as a key estrogen receptor regulatory factor. Mohammed et al (2013). *Cell Rep*

Physical Interactions with 112 interactions from BioGRID

Alsulami-Cagney-2019

0.19%

SETD1A Methyltransferase Is Physically and Functionally Linked to the DNA Damage Repair Protein RAD18. Alsulami et al (2019). *Mol Cell Proteomics*

Physical Interactions with 288 interactions from BioGRID

Gordon-Krogan-2020

0.19%

A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Gordon et al (2020). *Nature*

Physical Interactions with 6 interactions from BioGRID

Cao-Chinnaiyan-2014

0.19%

The central role of EED in the orchestration of polycomb group complexes. Cao et al (2014). *Nat Commun*

Physical Interactions with 1,769 interactions from BioGRID

Fonseca-Damgaard-2015

0.19%

La-related Protein 1 (LARP1) Represses Terminal Oligopyrimidine (TOP) mRNA Translation Downstream of mTOR Complex 1

Physical Interactions

80.30%

Fonseca-Damgaard-2015

(mTORC1). Fonseca et al (2015). *J Biol Chem*

Physical Interactions with 105 interactions from BioGRID

Nassa-Weisz-2019

0.19%

The RNA-mediated estrogen receptor interactome of hormone-dependent human breast cancer cell nuclei. Nassa et al (2019). *Sci Data*

Physical Interactions with 1,490 interactions from BioGRID

Van Quickelberghe-Gevaert-2018

0.19%

A protein-protein interaction map of the TNF-induced NF- κ B signal transduction pathway. Van Quickelberghe et al (2018). *Sci Data*

Physical Interactions with 525 interactions from BioGRID

Rodriguez-von Kriegsheim-2016

0.19%

Substrate-Trapped Interactors of PHD3 and FIH Cluster in Distinct Signaling Pathways. Rodriguez et al (2016). *Cell Rep*

Physical Interactions with 2,035 interactions from BioGRID

Pao-Virdee-2018

0.19%

Activity-based E3 ligase profiling uncovers an E3 ligase with esterification activity. Pao et al (2018). *Nature*

Physical Interactions with 134 interactions from BioGRID

Abbasi-Schild-Poulter-2019

0.19%

Mapping the Ku Interactome Using Proximity-Dependent Biotin Identification in Human Cells. Abbasi et al (2019). *J Proteome Res*

Physical Interactions with 166 interactions from iRefIndex

IREF-innatedb

0.19%

Physical Interactions with 2,355 interactions from iRefIndex

Stehling-Lill-2013

0.19%

Human CIA2A-FAM96A and CIA2B-FAM96B integrate iron homeostasis and maturation of different subsets of cytosolic-nuclear iron-sulfur proteins. Stehling et al (2013). *Cell Metab*

Physical Interactions with 121 interactions from BioGRID

Agrawal-Sedivy-2010

0.19%

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

Physical Interactions with 105 interactions from BioGRID

Katsogiannou-Rocchi-2014

0.19%

The functional landscape of Hsp27 reveals new cellular processes such as DNA repair and alternative splicing and proposes novel anticancer targets. Katsogiannou et al (2014). *Mol Cell Proteomics*

Physical Interactions with 221 interactions from iRefIndex

IREF-bind

0.19%

Physical Interactions with 3,524 interactions from iRefIndex

Roy-Pardo-2014

0.19%

hnRNP A1 couples nuclear export and translation of specific mRNAs downstream of FGF-2/S6K2 signalling. Roy et al (2014). *Nucleic Acids Res*

Physical Interactions with 386 interactions from BioGRID

0.19%

Yang-Vidal-2016

Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. Yang et al (2016). *Cell*

Physical Interactions with 741 interactions from BioGRID

Shen-Chen-2019

0.19%

PTEN and PTEN promote carcinogenesis through WDR5 and H3K4 trimethylation. Shen et al (2019). *Nat Cell Biol*

Physical Interactions with 213 interactions from BioGRID

Takahashi-Conaway-2011

0.19%

Human mediator subunit MED26 functions as a docking site for transcription elongation factors. Takahashi et al (2011). *Cell*

Physical Interactions with 151 interactions from BioGRID

Menon-Litovchick-2019

0.19%

DYRK1A regulates the recruitment of 53BP1 to the sites of DNA damage in part through interaction with RNF169. Menon et al (2019). *Cell Cycle*

Physical Interactions with 119 interactions from BioGRID

Blomen-Brummelkamp-2015

0.19%

Gene essentiality and synthetic lethality in haploid human cells. Blomen et al (2015). *Science*

Physical Interactions with 138 interactions from BioGRID

Liu-Chen-2019

0.19%

Oncogenic functions of protein kinase D2 and D3 in regulating multiple cancer-related pathways in breast cancer. Liu et al (2019). *Cancer Med*

Physical Interactions with 106 interactions from BioGRID

Yatim-Benkirane-2012

0.19%

NOTCH1 nuclear interactome reveals key regulators of its transcriptional activity and oncogenic function. Yatim et al (2012). *Mol Cell*

Physical Interactions with 127 interactions from BioGRID

Li-Hung-2019

0.19%

MET Inhibitors Promote Liver Tumor Evasion of the Immune Response by Stabilizing PDL1. Li et al (2019). *Gastroenterology*

Physical Interactions with 179 interactions from BioGRID

Rengasamy-Walsh-2017

0.19%

The PRMT5/WDR77 complex regulates alternative splicing through ZNF326 in breast cancer. Rengasamy et al (2017). *Nucleic Acids Res*

Physical Interactions with 103 interactions from iRefIndex

Lee-Jeong-2017

0.19%

FGF11 induced by hypoxia interacts with HIF-1 and enhances its stability. Lee et al (2017). *FEBS Lett*

Physical Interactions with 100 interactions from iRefIndex

Zhu-Liu-2018

0.19%

Deubiquitinating enzyme PSMD14 promotes tumor metastasis through stabilizing SNAIL in human esophageal squamous cell carcinoma. Zhu et al (2018). *Cancer Lett*

Physical Interactions with 287 interactions from iRefIndex

Olma-Pintard-2009

0.19%

An interaction network of the mammalian COP9 signalosome identifies Dda1 as a core subunit of multiple Cul4-based E3 ligases. Olma et al (2009). *J Cell Sci*

Olma-Pintard-2009

Physical Interactions with 213 interactions from BioGRID

Zhang-Zou-2011

0.19%

A bead-based approach for large-scale identification of in vitro kinase substrates. Zhang et al (2011). *Proteomics*

Physical Interactions with 163 interactions from iRefIndex

Foster-Marshall-2013

0.19%

Proteomic analysis of the NOS2 interactome in human airway epithelial cells. Foster et al (2013). *Nitric Oxide*

Physical Interactions with 111 interactions from iRefIndex

Yang-Wang-2018

0.19%

E3 Ligase Trim21 Ubiquitylates and Stabilizes Keratin 17 to Induce STAT3 Activation in Psoriasis. Yang et al (2018). *J Invest Dermatol*

Physical Interactions with 103 interactions from iRefIndex

Conte-Perez-Oliva-2018

0.19%

USP45 and Spindly are part of the same complex implicated in cell migration. Conte et al (2018). *Sci Rep*

Physical Interactions with 161 interactions from iRefIndex

Weishäupl-Schmidt-2019

0.19%

Physiological and pathophysiological characteristics of ataxin-3 isoforms. Weishäupl et al (2019). *J Biol Chem*

Physical Interactions with 202 interactions from iRefIndex

Dabbaghizadeh-Tanguay-2018

0.19%

Identification of proteins interacting with the mitochondrial small heat shock protein Hsp22 of *Drosophila melanogaster*: Implication in mitochondrial homeostasis. Dabbaghizadeh et al (2018). *PLoS One*

Physical Interactions with 144 interactions from BioGRID

Perez-Perri-Espinosa-2016

0.19%

The TIP60 Complex Is a Conserved Coactivator of HIF1A. Perez-Perri et al (2016). *Cell Rep*

Physical Interactions with 118 interactions from BioGRID

Guderian-Grimmler-2011

0.19%

Riok1, a new interactor of protein arginine methyltransferase 5 (PRMT5), competes with pICln for binding and modulates PRMT5 complex composition and substrate specificity. Guderian et al (2011). *J Biol Chem*

Physical Interactions with 425 interactions from BioGRID

Zhong-Vidal-2016

0.19%

An inter-species protein-protein interaction network across vast evolutionary distance. Zhong et al (2016). *Mol Syst Biol*

Physical Interactions with 472 interactions from BioGRID

Hoffmeister-Längst-2017

0.19%

CHD3 and CHD4 form distinct NuRD complexes with different yet overlapping functionality. Hoffmeister et al (2017). *Nucleic Acids Res*

Physical Interactions with 1,015 interactions from BioGRID

Lau-Ronai-2012

0.19%

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

Physical Interactions with 102 interactions from iRefIndex

Physical Interactions	80.30%
Richter-Chrzanowska-Lightowlers-2010	0.19%
A functional peptidyl-tRNA hydrolase, ICT1, has been recruited into the human mitochondrial ribosome. Richter et al (2010). <i>EMBO J</i>	
Physical Interactions with 204 interactions from BioGRID	
Kırlı-Görlich-2015	0.19%
A deep proteomics perspective on CRM1-mediated nuclear export and nucleocytoplasmic partitioning. Kırılı et al (2015). <i>Elife</i>	
Physical Interactions with 1,034 interactions from BioGRID	
Singh-Moore-2012	0.19%
The cellular EJC interactome reveals higher-order mRNP structure and an EJC-SR protein nexus. Singh et al (2012). <i>Cell</i>	
Physical Interactions with 235 interactions from iRefIndex	
Jozwik-Carroll-2016	0.19%
FOXA1 Directs H3K4 Monomethylation at Enhancers via Recruitment of the Methyltransferase MLL3. Jozwik et al (2016). <i>Cell Rep</i>	
Physical Interactions with 179 interactions from iRefIndex	
Arroyo-Aloy-2014	0.19%
Charting the molecular links between driver and susceptibility genes in colorectal cancer. Arroyo et al (2014). <i>Biochem Biophys Res Commun</i>	
Physical Interactions with 621 interactions from iRefIndex	
Woods-Monteiro-2012 B	0.19%
Charting the landscape of tandem BRCT domain-mediated protein interactions. Woods et al (2012). <i>Sci Signal</i>	
Physical Interactions with 325 interactions from BioGRID	
Kristensen-Foster-2012	0.19%
A high-throughput approach for measuring temporal changes in the interactome. Kristensen et al (2012). <i>Nat Methods</i>	
Physical Interactions with 7,044 interactions from BioGRID	
Hüttenhain-Krogan-2019	0.19%
ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. Hüttenhain et al (2019). <i>Cell Host Microbe</i>	
Physical Interactions with 384 interactions from BioGRID	
Tong-Moran-2014	0.19%
Proteomic analysis of the epidermal growth factor receptor (EGFR) interactome and post-translational modifications associated with receptor endocytosis in response to EGF and stress. Tong et al (2014). <i>Mol Cell Proteomics</i>	
Physical Interactions with 321 interactions from BioGRID	
Chi-Reed-2018	0.19%
Interactome analyses revealed that the U1 snRNP machinery overlaps extensively with the RNAP II machinery and contains multiple ALS/SMA-causative proteins. Chi et al (2018). <i>Sci Rep</i>	
Physical Interactions with 456 interactions from BioGRID	
Andresen-Flores-Morales-2014	0.19%
Protein interaction screening for the ankyrin repeats and suppressor of cytokine signaling (SOCS) box (ASB) family identify Asb11 as a novel endoplasmic reticulum resident ubiquitin ligase. Andresen et al (2014). <i>J Biol Chem</i>	
Physical Interactions with 222 interactions from iRefIndex	
IREF-bind-translation	0.19%

IREF-bind-translation

Physical Interactions with 6,056 interactions from iRefIndex

Gao-Vaziri-2016

0.19%

A neomorphic cancer cell-specific role of MAGE-A4 in trans-lesion synthesis. Gao et al (2016). *Nat Commun*

Physical Interactions with 116 interactions from BioGRID

Bantscheff-Drewes-2011

0.19%

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

Physical Interactions with 103 interactions from BioGRID

Goehler-Wanker-2004

0.19%

A protein interaction network links GIT1, an enhancer of huntingtin aggregation, to Huntington's disease. Goehler et al (2004). *Mol Cell*

Physical Interactions with 195 interactions from iRefIndex

Alexander-Wang-2018

0.19%

Ubiquilin 2 modulates ALS/FTD-linked FUS-RNA complex dynamics and stress granule formation. Alexander et al (2018). *Proc Natl Acad Sci U S A*

Physical Interactions with 189 interactions from iRefIndex

Pichlmair-Superti-Furga-2011

0.19%

IFIT1 is an antiviral protein that recognizes 5'-triphosphate RNA. Pichlmair et al (2011). *Nat Immunol*

Physical Interactions with 99 interactions from BioGRID

Byron-Humphries-2012

0.19%

Proteomic analysis of $\alpha 4$ integrin adhesion complexes reveals α -subunit-dependent protein recruitment. Byron et al (2012). *Proteomics*

Physical Interactions with 484 interactions from BioGRID

Rolland-Vidal-2014

0.19%

A proteome-scale map of the human interactome network. Rolland et al (2014). *Cell*

Physical Interactions with 13,057 interactions from BioGRID

Liu-Sun-2019

0.19%

CCT3 acts upstream of YAP and TFCP2 as a potential target and tumour biomarker in liver cancer. Liu et al (2019). *Cell Death Dis*

Physical Interactions with 561 interactions from BioGRID

Sowa-Harper-2009

0.19%

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

Physical Interactions with 1,509 interactions from BioGRID

Shami Shah-Baskin-2019

0.19%

PLEKHA4/kramer Attenuates Dishevelled Ubiquitination to Modulate Wnt and Planar Cell Polarity Signaling. Shami Shah et al (2019). *Cell Rep*

Physical Interactions with 2,927 interactions from BioGRID

Brajenovic-Drewes-2004

0.19%

Comprehensive proteomic analysis of human Par protein complexes reveals an interconnected protein network. Brajenovic et al (2004). *J Biol Chem*

Brajenovic-Drewes-2004

Physical Interactions with 118 interactions from BioGRID

Wang-Liu-2019

0.19%

POH1 contributes to hyperactivation of TGF- signaling and facilitates hepatocellular carcinoma metastasis through deubiquitinating TGF- receptors and caveolin-1. Wang et al (2019). *EBioMedicine*

Physical Interactions with 180 interactions from iRefIndex

Huber-Hoelz-2017

0.19%

Histone-binding of DPF2 mediates its repressive role in myeloid differentiation. Huber et al (2017). *Proc Natl Acad Sci U S A*

Physical Interactions with 217 interactions from iRefIndex

Herr-Helleday-2015

0.19%

A genome-wide IR-induced RAD51 foci RNAi screen identifies CDC73 involved in chromatin remodeling for DNA repair. Herr et al (2015). *Cell Discov*

Physical Interactions with 117 interactions from iRefIndex

Hauri-Beisel-2016

0.19%

A High-Density Map for Navigating the Human Polycomb Complexome. Hauri et al (2016). *Cell Rep*

Physical Interactions with 1,216 interactions from BioGRID

Bouwmeester-Superti-Furga-2004

0.19%

A physical and functional map of the human TNF-alpha/NF-kappa B signal transduction pathway. Bouwmeester et al (2004). *Nat Cell Biol*

Physical Interactions with 1,694 interactions from iRefIndex

Dittmer-Misteli-2014

0.19%

Systematic identification of pathological lamin A interactors. Dittmer et al (2014). *Mol Biol Cell*

Physical Interactions with 332 interactions from BioGRID

Zhang-Vermeulen-2017

0.19%

An Interaction Landscape of Ubiquitin Signaling. Zhang et al (2017). *Mol Cell*

Physical Interactions with 242 interactions from BioGRID

So-Colwill-2015

0.19%

Integrative analysis of kinase networks in TRAIL-induced apoptosis provides a source of potential targets for combination therapy. So et al (2015). *Sci Signal*

Physical Interactions with 652 interactions from BioGRID

Kumar-Maddika-2017

0.19%

A Human Tyrosine Phosphatase Interactome Mapped by Proteomic Profiling. Kumar et al (2017). *J Proteome Res*

Physical Interactions with 1,863 interactions from BioGRID

Malovannaya-Qin-2010

0.19%

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

Physical Interactions with 299 interactions from BioGRID

Malinová-Verheggen-2017

0.19%

Assembly of the U5 snRNP component PRPF8 is controlled by the HSP90/R2TP chaperones. Malinová et al (2017). *J Cell Biol*

Physical Interactions with 2,778 interactions from BioGRID

Physical Interactions	80.30%
Hutchins-Peters-2010	0.19%
Systematic analysis of human protein complexes identifies chromosome segregation proteins. Hutchins et al (2010). <i>Science</i>	
Physical Interactions with 1,783 interactions from BioGRID	
Elliott-Gyrd-Hansen-2016	0.19%
SPATA2 Links CYLD to LUBAC, Activates CYLD, and Controls LUBAC Signaling. Elliott et al (2016). <i>Mol Cell</i>	
Physical Interactions with 543 interactions from BioGRID	
Scott-Guy-2017	0.19%
Blocking an N-terminal acetylation-dependent protein interaction inhibits an E3 ligase. Scott et al (2017). <i>Nat Chem Biol</i>	
Physical Interactions with 488 interactions from BioGRID	
IREF-mbinfo	0.19%
Physical Interactions with 113 interactions from iRefIndex	
Watanabe-Fujita-2018	0.19%
GRWD1 regulates ribosomal protein L23 levels via the ubiquitin-proteasome system. Watanabe et al (2018). <i>J Cell Sci</i>	
Physical Interactions with 158 interactions from iRefIndex	
Benzinger-Hermeking-2005	0.19%
Targeted proteomic analysis of 14-3-3 sigma, a p53 effector commonly silenced in cancer. Benzinger et al (2005). <i>Mol Cell Proteomics</i>	
Physical Interactions with 111 interactions from iRefIndex	
Barreiro-Alonso-Cerdán-2018	0.19%
Delineating the HMGB1 and HMGB2 interactome in prostate and ovary epithelial cells and its relationship with cancer. Barreiro-Alonso et al (2018). <i>Oncotarget</i>	
Physical Interactions with 149 interactions from iRefIndex	
Kupka-Walczak-2016	0.19%
SPATA2-Mediated Binding of CYLD to HOIP Enables CYLD Recruitment to Signaling Complexes. Kupka et al (2016). <i>Cell Rep</i>	
Physical Interactions with 411 interactions from BioGRID	
Tang-Wang-2019	0.19%
The p300/YY1/miR-500a-5p/HDAC2 signalling axis regulates cell proliferation in human colorectal cancer. Tang et al (2019). <i>Nat Commun</i>	
Physical Interactions with 294 interactions from BioGRID	
Yamauchi-Maeda-2018	0.19%
Genome-wide CRISPR-Cas9 Screen Identifies Leukemia-Specific Dependence on a Pre-mRNA Metabolic Pathway Regulated by DCPS. Yamauchi et al (2018). <i>Cancer Cell</i>	
Physical Interactions with 261 interactions from iRefIndex	
Tomkins-Manzoni-2018	0.19%
Comparative Protein Interaction Network Analysis Identifies Shared and Distinct Functions for the Human ROCO Proteins. Tomkins et al (2018). <i>Proteomics</i>	
Physical Interactions with 279 interactions from iRefIndex	
Wu-Li-2007	0.19%
Systematic identification of SH3 domain-mediated human protein-protein interactions by peptide array target screening. Wu et al (2007). <i>Proteomics</i>	
Physical Interactions with 1,105 interactions from iRefIndex	

Physical Interactions	80.30%
Butland-Hayden-2014	0.19%
The palmitoyl acyltransferase HIP14 shares a high proportion of interactors with huntingtin: implications for a role in the pathogenesis of Huntington's disease. Butland et al (2014). <i>Hum Mol Genet</i>	
Physical Interactions with 212 interactions from iRefIndex	
Napolitano-Meroni-2011	0.19%
Functional interactions between ubiquitin E2 enzymes and TRIM proteins. Napolitano et al (2011). <i>Biochem J</i>	
Physical Interactions with 81 interactions from BioGRID	
Berggård-James-2006	0.19%
140 mouse brain proteins identified by Ca ²⁺ -calmodulin affinity chromatography and tandem mass spectrometry. Berggård et al (2006). <i>J Proteome Res</i>	
Physical Interactions with 151 interactions from BioGRID	
Nathan-Goldberg-2013	0.19%
Why do cellular proteins linked to K63-polyubiquitin chains not associate with proteasomes? Nathan et al (2013). <i>EMBO J</i>	
Physical Interactions with 162 interactions from BioGRID	
Matsumoto-Nakayama-2005	0.19%
Large-scale analysis of the human ubiquitin-related proteome. Matsumoto et al (2005). <i>Proteomics</i>	
Physical Interactions with 311 interactions from BioGRID	
Yao-Stagljär-2017 B	0.19%
A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. Yao et al (2017). <i>Mol Cell</i>	
Physical Interactions with 325 interactions from BioGRID	
IREF-intact	0.19%
Physical Interactions with 117,269 interactions from iRefIndex	
Lum-Cristea-2018	0.19%
Interactome and Proteome Dynamics Uncover Immune Modulatory Associations of the Pathogen Sensing Factor cGAS. Lum et al (2018). <i>Cell Syst</i>	
Physical Interactions with 165 interactions from iRefIndex	
Cai-Conaway-2007	0.19%
YY1 functions with INO80 to activate transcription. Cai et al (2007). <i>Nat Struct Mol Biol</i>	
Physical Interactions with 106 interactions from BioGRID	
Li-Lu-2018	0.19%
Heterozygous deletion of chromosome 17p renders prostate cancer vulnerable to inhibition of RNA polymerase II. Li et al (2018). <i>Nat Commun</i>	
Physical Interactions with 176 interactions from iRefIndex	
IREF-corum	0.19%
Physical Interactions with 819 interactions from iRefIndex	
Kim-Major-2015	0.19%
Substrate trapping proteomics reveals targets of the TrCP2/FBXW11 ubiquitin ligase. Kim et al (2015). <i>Mol Cell Biol</i>	
Physical Interactions with 137 interactions from BioGRID	
Savidis-Brass-2016	0.19%
Identification of Zika Virus and Dengue Virus Dependency Factors using Functional Genomics. Savidis et al (2016). <i>Cell Rep</i>	

Savidis-Brass-2016

Physical Interactions with 685 interactions from BioGRID

Iradi-Borchelt-2018

0.19%

Characterization of gene regulation and protein interaction networks for Matrin 3 encoding mutations linked to amyotrophic lateral sclerosis and myopathy. Iradi et al (2018). *Sci Rep*

Physical Interactions with 108 interactions from BioGRID

Fogeron-Lange-2013

0.19%

LGALS3BP regulates centriole biogenesis and centrosome hypertrophy in cancer cells. Fogeron et al (2013). *Nat Commun*

Physical Interactions with 1,492 interactions from BioGRID

Gupta-Pelletier-2015

0.19%

A Dynamic Protein Interaction Landscape of the Human Centrosome-Cilium Interface. Gupta et al (2015). *Cell*

Physical Interactions with 306 interactions from BioGRID

Choi-Busino-2018

0.19%

PTPN14 regulates Roquin2 stability by tyrosine dephosphorylation. Choi et al (2018). *Cell Cycle*

Physical Interactions with 1,087 interactions from BioGRID

Varjosalo-Superti-Furga-2013

0.19%

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

Physical Interactions with 484 interactions from BioGRID

Ramachandran-LaBaer-2004

0.19%

Self-assembling protein microarrays. Ramachandran et al (2004). *Science*

Physical Interactions with 123 interactions from iRefIndex

Yeung-Dougan-2019

0.19%

A Genome-Wide Knockout Screen in Human Macrophages Identified Host Factors Modulating *Salmonella* Infection. Yeung et al (2019). *mBio*

Physical Interactions with 153 interactions from iRefIndex

Roy-Parent-2013

0.19%

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

Physical Interactions with 114 interactions from iRefIndex

Zhang-Wheeler-2014

0.19%

Progesterone receptor membrane component 1 is a functional part of the glucagon-like peptide-1 (GLP-1) receptor complex in pancreatic cells. Zhang et al (2014). *Mol Cell Proteomics*

Physical Interactions with 93 interactions from BioGRID

Markson-Sanderson-2009

0.19%

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

Physical Interactions with 686 interactions from iRefIndex

Hanson-Clayton-2014

0.19%

Identifying biological pathways that underlie primordial short stature using network analysis. Hanson et al (2014). *J Mol Endocrinol*

Physical Interactions with 1,728 interactions from BioGRID

Physical Interactions	80.30%
Xu-Zetter-2016	0.19%
Prohibitin 1 regulates tumor cell apoptosis via the interaction with X-linked inhibitor of apoptosis protein. Xu et al (2016). <i>J Mol Cell Biol</i>	
Physical Interactions with 719 interactions from BioGRID	
Yachie-Roth-2016	0.19%
Pooled-matrix protein interaction screens using Barcode Fusion Genetics. Yachie et al (2016). <i>Mol Syst Biol</i>	
Physical Interactions with 671 interactions from BioGRID	
Leung-Miller-2017	0.19%
ZMYM3 regulates BRCA1 localization at damaged chromatin to promote DNA repair. Leung et al (2017). <i>Genes Dev</i>	
Physical Interactions with 247 interactions from BioGRID	
Sala-Ampe-2017	0.19%
Expanding the Interactome of TES by Exploiting TES Modules with Different Subcellular Localizations. Sala et al (2017). <i>J Proteome Res</i>	
Physical Interactions with 233 interactions from BioGRID	
Zanon-Pichler-2013	0.19%
Profiling of Parkin-binding partners using tandem affinity purification. Zanon et al (2013). <i>PLoS One</i>	
Physical Interactions with 195 interactions from BioGRID	
Tiemann-Kani-2019	0.19%
Loss of ER retention motif of AGR2 can impact mTORC signaling and promote cancer metastasis. Tiemann et al (2019). <i>Oncogene</i>	
Physical Interactions with 339 interactions from BioGRID	
Varjosalo-Gstaiger-2013 A	0.19%
The protein interaction landscape of the human CMGC kinase group. Varjosalo et al (2013). <i>Cell Rep</i>	
Physical Interactions with 690 interactions from BioGRID	
Meek-Piwnica-Worms-2004	0.19%
Comprehensive proteomic analysis of interphase and mitotic 14-3-3-binding proteins. Meek et al (2004). <i>J Biol Chem</i>	
Physical Interactions with 328 interactions from iRefIndex	
Carmon-Liu-2014	0.19%
RSPO-LGR4 functions via IQGAP1 to potentiate Wnt signaling. Carmon et al (2014). <i>Proc Natl Acad Sci U S A</i>	
Physical Interactions with 129 interactions from iRefIndex	
Panigrahi-Pati-2012	0.19%
A cohesin-RAD21 interactome. Panigrahi et al (2012). <i>Biochem J</i>	
Physical Interactions with 137 interactions from iRefIndex	
Muller-Demeret-2012	0.19%
Large scale genotype comparison of human papillomavirus E2-host interaction networks provides new insights for e2 molecular functions. Muller et al (2012). <i>PLoS Pathog</i>	
Physical Interactions with 104 interactions from iRefIndex	
de Hoog-Mann-2004	0.19%
RNA and RNA binding proteins participate in early stages of cell spreading through spreading initiation centers. de Hoog et al (2004). <i>Cell</i>	
Physical Interactions with 214 interactions from iRefIndex	

Physical Interactions	80.30%
Beyer-Boldt-2018 CRISPR/Cas9-mediated Genomic Editing of Cluap1/IFT38 Reveals a New Role in Actin Arrangement. Beyer et al (2018). <i>Mol Cell Proteomics</i> Physical Interactions with 213 interactions from BioGRID	0.19%
Yue-Liu-2018 VIRMA mediates preferential m ⁶ A mRNA methylation in 3'UTR and near stop codon and associates with alternative polyadenylation. Yue et al (2018). <i>Cell Discov</i> Physical Interactions with 1,502 interactions from BioGRID	0.19%
Ouyang-Gill-2009 Direct binding of CoREST1 to SUMO-2/3 contributes to gene-specific repression by the LSD1/CoREST1/HDAC complex. Ouyang et al (2009). <i>Mol Cell</i> Physical Interactions with 105 interactions from BioGRID	0.19%
Enzo-Dupont-2015 Aerobic glycolysis tunes YAP/TAZ transcriptional activity. Enzo et al (2015). <i>EMBO J</i> Physical Interactions with 156 interactions from BioGRID	0.19%
Hein-Mann-2015 A human interactome in three quantitative dimensions organized by stoichiometries and abundances. Hein et al (2015). <i>Cell</i> Physical Interactions with 27,015 interactions from BioGRID	0.19%
Wang-Xu-2015 Interaction of amyotrophic lateral sclerosis/frontotemporal lobar degeneration-associated fused-in-sarcoma with proteins involved in metabolic and protein degradation pathways. Wang et al (2015). <i>Neurobiol Aging</i> Physical Interactions with 197 interactions from BioGRID	0.19%
Fang-Lin-2011 Landscape of the SOX2 protein-protein interactome. Fang et al (2011). <i>Proteomics</i> Physical Interactions with 134 interactions from BioGRID	0.19%
Botham-Schimmer-2019 Global Interactome Mapping of Mitochondrial Intermembrane Space Proteases Identifies a Novel Function for HTRA2. Botham et al (2019). <i>Proteomics</i> Physical Interactions with 317 interactions from BioGRID	0.19%
Nakamura-Groth-2019 H4K20me0 recognition by BRCA1-BARD1 directs homologous recombination to sister chromatids. Nakamura et al (2019). <i>Nat Cell Biol</i> Physical Interactions with 1,290 interactions from BioGRID	0.19%
Wang-Xiong-2019 Impaired plasma membrane localization of ubiquitin ligase complex underlies 3-M syndrome development. Wang et al (2019). <i>J Clin Invest</i> Physical Interactions with 609 interactions from BioGRID	0.19%
Guardia-Laguarta-Przedborski-2019 PINK1 Content in Mitochondria is Regulated by ER-Associated Degradation. Guardia-Laguarta et al (2019). <i>J Neurosci</i> Physical Interactions with 468 interactions from BioGRID	0.19%
Guard-Old-2019	0.19%

Physical Interactions	80.30%
Guard-Old-2019	
The nuclear interactome of DYRK1A reveals a functional role in DNA damage repair. Guard et al (2019). <i>Sci Rep</i>	
Physical Interactions with 105 interactions from BioGRID	
IREF-bhf-ucl	0.19%
Physical Interactions with 1,155 interactions from iRefIndex	
Scifo-Lalowski-2015	0.19%
Quantitative analysis of PPT1 interactome in human neuroblastoma cells. Scifo et al (2015). <i>Data Brief</i>	
Physical Interactions with 199 interactions from BioGRID	
Chen-Zhou-2019	0.19%
Identification of a USP9X Substrate NFX1-123 by SILAC-Based Quantitative Proteomics. Chen et al (2019). <i>J Proteome Res</i>	
Physical Interactions with 380 interactions from BioGRID	
Petschnigg-Stagljär-2014	0.19%
The mammalian-membrane two-hybrid assay (MaMTH) for probing membrane-protein interactions in human cells. Petschnigg et al (2014). <i>Nat Methods</i>	
Physical Interactions with 116 interactions from iRefIndex	
Lehner-Sanderson-2004 A	0.19%
Analysis of a high-throughput yeast two-hybrid system and its use to predict the function of intracellular proteins encoded within the human MHC class III region. Lehner et al (2004). <i>Genomics</i>	
Physical Interactions with 127 interactions from iRefIndex	
Woodsmith-Sanderson-2012	0.19%
Systematic analysis of dimeric E3-RING interactions reveals increased combinatorial complexity in human ubiquitination networks. Woodsmith et al (2012). <i>Mol Cell Proteomics</i>	
Physical Interactions with 206 interactions from iRefIndex	
Daakour-Twizere-2016	0.19%
Systematic interactome mapping of acute lymphoblastic leukemia cancer gene products reveals EXT-1 tumor suppressor as a Notch1 and FBWX7 common interactor. Daakour et al (2016). <i>BMC Cancer</i>	
Physical Interactions with 188 interactions from BioGRID	
Salvetti-Greco-2016	0.19%
Nuclear Functions of Nucleolin through Global Proteomics and Interactomic Approaches. Salvetti et al (2016). <i>J Proteome Res</i>	
Physical Interactions with 144 interactions from BioGRID	
Kotlyar-Jurisica-2015	0.19%
In silico prediction of physical protein interactions and characterization of interactome orphans. Kotlyar et al (2015). <i>Nat Methods</i>	
Physical Interactions with 121 interactions from BioGRID	
Hussain-Aldaz-2018	0.19%
Delineating WWOX Protein Interactome by Tandem Affinity Purification-Mass Spectrometry: Identification of Top Interactors and Key Metabolic Pathways Involved. Hussain et al (2018). <i>Front Oncol</i>	
Physical Interactions with 210 interactions from BioGRID	
Ahn-Lee-2008	0.19%
The tumour suppressor PTEN mediates a negative regulation of the E3 ubiquitin-protein ligase Nedd4. Ahn et al (2008). <i>Biochem J</i>	
Physical Interactions with 105 interactions from BioGRID	

Physical Interactions	80.30%
Yao-Stagljär-2017 A A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. Yao et al (2017). <i>Mol Cell</i> Physical Interactions with 312 interactions from BioGRID	0.19%
Oliviero-Cagney-2016 Dynamic Protein Interactions of the Polycomb Repressive Complex 2 during Differentiation of Pluripotent Cells. Oliviero et al (2016). <i>Mol Cell Proteomics</i> Physical Interactions with 638 interactions from BioGRID	0.19%
Bogachek-Weigel-2014 Sumoylation pathway is required to maintain the basal breast cancer subtype. Bogachek et al (2014). <i>Cancer Cell</i> Physical Interactions with 134 interactions from iRefIndex	0.19%
Liu-Takahashi-2017 TTF-1/NKX2-1 binds to DDB1 and confers replication stress resistance to lung adenocarcinomas. Liu et al (2017). <i>Oncogene</i> Physical Interactions with 105 interactions from iRefIndex	0.19%
Yu-Vidal-2011 Next-generation sequencing to generate interactome datasets. Yu et al (2011). <i>Nat Methods</i> Physical Interactions with 1,111 interactions from BioGRID	0.19%
Loch-Strickler-2012 A microarray of ubiquitylated proteins for profiling deubiquitylase activity reveals the critical roles of both chain and substrate. Loch et al (2012). <i>Biochim Biophys Acta</i> Physical Interactions with 145 interactions from BioGRID	0.19%
IREF-virushost Physical Interactions with 145 interactions from iRefIndex	0.19%
IREF-quickgo Physical Interactions with 9,985 interactions from iRefIndex	0.19%
Yu-Engel-2018 BAP1 regulation of the key adaptor protein NCoR1 is critical for γ -globin gene repression. Yu et al (2018). <i>Genes Dev</i> Physical Interactions with 1,308 interactions from BioGRID	0.19%
Caron-van Attikum-2019 WWP2 ubiquitylates RNA polymerase II for DNA-PK-dependent transcription arrest and repair at DNA breaks. Caron et al (2019). <i>Genes Dev</i> Physical Interactions with 609 interactions from BioGRID	0.19%
Sato-Conaway-2004 A set of consensus mammalian mediator subunits identified by multidimensional protein identification technology. Sato et al (2004). <i>Mol Cell</i> Physical Interactions with 229 interactions from BioGRID	0.19%
Hubel-Pichlmair-2019 A protein-interaction network of interferon-stimulated genes extends the innate immune system landscape. Hubel et al (2019). <i>Nat Immunol</i> Physical Interactions with 2,707 interactions from BioGRID	0.19%
Boldt-Roepman-2016	0.19%

Boldt-Roepman-2016

An organelle-specific protein landscape identifies novel diseases and molecular mechanisms. Boldt et al (2016). *Nat Commun*

Physical Interactions with 4,898 interactions from BioGRID

Narayan-Bennett-2012

0.19%

Short-chain 3-hydroxyacyl-coenzyme A dehydrogenase associates with a protein super-complex integrating multiple metabolic pathways. Narayan et al (2012). *PLoS One*

Physical Interactions with 109 interactions from BioGRID

Li-Dorf-2014

0.19%

TRIM65 regulates microRNA activity by ubiquitination of TNRC6. Li et al (2014). *Proc Natl Acad Sci U S A*

Physical Interactions with 495 interactions from BioGRID

Varier-Vermeulen-2016

0.19%

Recruitment of the Mammalian Histone-modifying EMSY Complex to Target Genes Is Regulated by ZNF131. Varier et al (2016). *J Biol Chem*

Physical Interactions with 141 interactions from BioGRID

Li-Zhou-2017

0.19%

Identification of translationally controlled tumor protein in promotion of DNA homologous recombination repair in cancer cells by affinity proteomics. Li et al (2017). *Oncogene*

Physical Interactions with 104 interactions from iRefIndex

Reyniers-Taymans-2014

0.19%

Differential protein-protein interactions of LRRK1 and LRRK2 indicate roles in distinct cellular signaling pathways. Reyniers et al (2014). *J Neurochem*

Physical Interactions with 109 interactions from iRefIndex

van Wijk-Timmers-2009

0.19%

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

Physical Interactions with 322 interactions from iRefIndex

Lim-Zoghbi-2006

0.19%

A protein-protein interaction network for human inherited ataxias and disorders of Purkinje cell degeneration. Lim et al (2006). *Cell*

Physical Interactions with 5,393 interactions from iRefIndex

Xie-Zhang-2017

0.19%

FAF1 phosphorylation by AKT accumulates TGF- type II receptor and drives breast cancer metastasis. Xie et al (2017). *Nat Commun*

Physical Interactions with 227 interactions from BioGRID

Weimann-Stelzl-2013 B

0.19%

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

Physical Interactions with 513 interactions from BioGRID

Diner-Cristea-2015

0.19%

Interactions of the Antiviral Factor Interferon Gamma-Inducible Protein 16 (IFI16) Mediate Immune Signaling and Herpes Simplex Virus-1 Immunosuppression. Diner et al (2015). *Mol Cell Proteomics*

Physical Interactions with 334 interactions from BioGRID

Guarani-Harper-2014

0.19%

Guarani-Harper-2014

TIMMDC1/C3orf1 functions as a membrane-embedded mitochondrial complex I assembly factor through association with the MCIA complex. Guarani et al (2014). *Mol Cell Biol*

Physical Interactions with 323 interactions from BioGRID

Benleulmi-Chaachoua-Jockers-2016 A

0.19%

Protein interactome mining defines melatonin MT1 receptors as integral component of presynaptic protein complexes of neurons. Benleulmi-Chaachoua et al (2016). *J Pineal Res*

Physical Interactions with 126 interactions from BioGRID

Zhao-Yang-2011

0.19%

Interactome study suggests multiple cellular functions of hepatoma-derived growth factor (HDGF). Zhao et al (2011). *J Proteomics*

Physical Interactions with 187 interactions from BioGRID

Roewenstrunk-de la Luna-2019

0.19%

A comprehensive proteomics-based interaction screen that links DYRK1A to RNF169 and to the DNA damage response. Roewenstrunk et al (2019). *Sci Rep*

Physical Interactions with 116 interactions from BioGRID

Yang-Chen-2010

0.19%

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

Physical Interactions with 100 interactions from BioGRID

Lu-Bohr-2017

0.19%

Cell cycle-dependent phosphorylation regulates RECQL4 pathway choice and ubiquitination in DNA double-strand break repair. Lu et al (2017). *Nat Commun*

Physical Interactions with 1,312 interactions from BioGRID

Campos-Reinberg-2015

0.19%

Analysis of the Histone H3.1 Interactome: A Suitable Chaperone for the Right Event. Campos et al (2015). *Mol Cell*

Physical Interactions with 105 interactions from iRefIndex

Liu-Xu-2018

0.19%

The Catalytically Inactive Mutation of the Ubiquitin-Conjugating Enzyme CDC34 Affects its Stability and Cell Proliferation. Liu et al (2018). *Protein J*

Physical Interactions with 184 interactions from iRefIndex

Reinke-Keating-2010

0.19%

Identification of bZIP interaction partners of viral proteins HBZ, MEQ, BZLF1, and K-bZIP using coiled-coil arrays. Reinke et al (2010). *Biochemistry*

Physical Interactions with 118 interactions from iRefIndex

Cloutier-Coulombe-2013

0.19%

A newly uncovered group of distantly related lysine methyltransferases preferentially interact with molecular chaperones to regulate their activity. Cloutier et al (2013). *PLoS Genet*

Physical Interactions with 165 interactions from iRefIndex

Bishof-Seyfried-2018

0.19%

RNA-binding proteins with basic-acidic dipeptide (BAD) domains self-assemble and aggregate in Alzheimer's disease. Bishof et al (2018). *J Biol Chem*

Physical Interactions with 707 interactions from BioGRID

Physical Interactions	80.30%
Koch-Hermeking-2007	0.19%
Large-scale identification of c-MYC-associated proteins using a combined TAP/MudPIT approach. Koch et al (2007). <i>Cell Cycle</i>	
Physical Interactions with 207 interactions from BioGRID	
Wong-O'Bryan-2012	0.19%
Intersectin (ITSN) family of scaffolds function as molecular hubs in protein interaction networks. Wong et al (2012). <i>PLoS One</i>	
Physical Interactions with 114 interactions from BioGRID	
Arbogast-Gros-2019	0.19%
ATG5 is required for B cell polarization and presentation of particulate antigens. Arbogast et al (2019). <i>Autophagy</i>	
Physical Interactions with 649 interactions from BioGRID	
Benleulmi-Chaachoua-Jockers-2016 B	0.19%
Protein interactome mining defines melatonin MT1 receptors as integral component of presynaptic protein complexes of neurons. Benleulmi-Chaachoua et al (2016). <i>J Pineal Res</i>	
Physical Interactions with 271 interactions from BioGRID	
Kneissl-Grummt-2003	0.19%
Interaction and assembly of murine pre-replicative complex proteins in yeast and mouse cells. Kneissl et al (2003). <i>J Mol Biol</i>	
Physical Interactions with 81 interactions from BioGRID	
Predicted	9.48%
I2D-IntAct-Mouse2Human	0.19%
The IntAct molecular interaction database in 2010. Aranda et al (2010). <i>Nucleic Acids Res</i>	
Predicted with 11,478 interactions from I2D	
I2D-IntAct-Yeast2Human	0.19%
The IntAct molecular interaction database in 2010. Aranda et al (2010). <i>Nucleic Acids Res</i>	
Predicted with 7,325 interactions from I2D	
I2D-IntAct-Worm2Human	0.19%
The IntAct molecular interaction database in 2010. Aranda et al (2010). <i>Nucleic Acids Res</i>	
Predicted with 793 interactions from I2D	
I2D-BIND-Fly2Human	0.19%
BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al (2000). <i>Bioinformatics</i>	
Predicted with 1,762 interactions from I2D	
I2D-BioGRID-Mouse2Human	0.19%
BioGRID: a general repository for interaction datasets. Stark et al (2006). <i>Nucleic Acids Res</i>	
Predicted with 10,524 interactions from I2D	
I2D-Stanyon-Finley-2004-CellCycle-Fly2Human	0.19%
A Drosophila protein-interaction map centered on cell-cycle regulators. Stanyon et al (2004). <i>Genome Biol</i>	
Predicted with 176 interactions from I2D	
I2D-Li-Vidal-2004-CORE-1-Worm2Human	0.19%
A map of the interactome network of the metazoan C. elegans. Li et al (2004). <i>Science</i>	
Predicted with 45 interactions from I2D	

Predicted	9.48%
I2D-BIND-Worm2Human	0.19%
BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al (2000). <i>Bioinformatics</i> Predicted with 349 interactions from I2D	
I2D-BIND-Rat2Human	0.19%
BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al (2000). <i>Bioinformatics</i> Predicted with 468 interactions from I2D	
I2D-Tewari-Vidal-2004-TGFb-Worm2Human	0.19%
Systematic interactome mapping and genetic perturbation analysis of a C. elegans TGF-beta signaling network. Tewari et al (2004). <i>Mol Cell</i> Predicted with 2 interactions from I2D	
I2D-IntAct-Rat2Human	0.19%
The IntAct molecular interaction database in 2010. Aranda et al (2010). <i>Nucleic Acids Res</i> Predicted with 1,690 interactions from I2D	
I2D-Li-Vidal-2004-interolog-Worm2Human	0.19%
A map of the interactome network of the metazoan C. elegans. Li et al (2004). <i>Science</i> Predicted with 396 interactions from I2D	
I2D-MINT-Fly2Human	0.19%
MINT: a Molecular INTeraction database. Zanzoni et al (2002). <i>FEBS Lett</i> Predicted with 1,790 interactions from I2D	
I2D-BioGRID-Worm2Human	0.19%
BioGRID: a general repository for interaction datasets. Stark et al (2006). <i>Nucleic Acids Res</i> Predicted with 1,300 interactions from I2D	
I2D-IntAct-Fly2Human	0.19%
The IntAct molecular interaction database in 2010. Aranda et al (2010). <i>Nucleic Acids Res</i> Predicted with 4,830 interactions from I2D	
I2D-Wang-Orkin-2006-EScmplx-Mouse2Human	0.19%
A protein interaction network for pluripotency of embryonic stem cells. Wang et al (2006). <i>Nature</i> Predicted with 53 interactions from I2D	
I2D-Tarassov-PCA-Yeast2Human	0.19%
An in vivo map of the yeast protein interactome. Tarassov et al (2008). <i>Science</i> Predicted with 235 interactions from I2D	
I2D-Li-Vidal-2004-CE-DATA-Worm2Human	0.19%
A map of the interactome network of the metazoan C. elegans. Li et al (2004). <i>Science</i> Predicted with 48 interactions from I2D	
I2D-BioGRID-Rat2Human	0.19%
BioGRID: a general repository for interaction datasets. Stark et al (2006). <i>Nucleic Acids Res</i> Predicted with 2,148 interactions from I2D	
I2D-Wang-Orkin-2006-EScmplxlow-Mouse2Human	0.19%

Predicted	9.48%
I2D-Wang-Orkin-2006-EScmplxlow-Mouse2Human	
A protein interaction network for pluripotency of embryonic stem cells. Wang et al (2006). <i>Nature</i>	
Predicted with 4 interactions from I2D	
I2D-Wang-Orkin-2006-EScmplxIP-Mouse2Human	0.19%
A protein interaction network for pluripotency of embryonic stem cells. Wang et al (2006). <i>Nature</i>	
Predicted with 5 interactions from I2D	
I2D-Ptacek-Snyder-2005-Yeast2Human	0.19%
Global analysis of protein phosphorylation in yeast. Ptacek et al (2005). <i>Nature</i>	
Predicted with 321 interactions from I2D	
I2D-Manual-Mouse2Human	0.19%
Predicted with 18 interactions from I2D	
I2D-Giot-Rothbert-2003-High-Fly2Human	0.19%
A protein interaction map of Drosophila melanogaster. Giot et al (2003). <i>Science</i>	
Predicted with 370 interactions from I2D	
I2D-Formstecher-Daviet-2005-Embryo-Fly2Human	0.19%
Protein interaction mapping: a Drosophila case study. Formstecher et al (2005). <i>Genome Res</i>	
Predicted with 270 interactions from I2D	
I2D-MINT-Rat2Human	0.19%
MINT: a Molecular INTeraction database. Zanzoni et al (2002). <i>FEBS Lett</i>	
Predicted with 540 interactions from I2D	
I2D-MINT-Worm2Human	0.19%
MINT: a Molecular INTeraction database. Zanzoni et al (2002). <i>FEBS Lett</i>	
Predicted with 452 interactions from I2D	
I2D-Li-Vidal-2004-CORE-2-Worm2Human	0.19%
A map of the interactome network of the metazoan C. elegans. Li et al (2004). <i>Science</i>	
Predicted with 58 interactions from I2D	
I2D-MINT-Yeast2Human	0.19%
MINT: a Molecular INTeraction database. Zanzoni et al (2002). <i>FEBS Lett</i>	
Predicted with 2,486 interactions from I2D	
I2D-Chen-Pawson-2009-PiwiScreen-Mouse2Human	0.19%
Mouse Piwi interactome identifies binding mechanism of Tdrkh Tudor domain to arginine methylated Miwi. Chen et al (2009). <i>Proc Natl Acad Sci U S A</i>	
Predicted with 29 interactions from I2D	
I2D-Formstecher-Daviet-2005-Head-Fly2Human	0.19%
Protein interaction mapping: a Drosophila case study. Formstecher et al (2005). <i>Genome Res</i>	
Predicted with 13 interactions from I2D	
I2D-Li-Vidal-2004-non-core-Worm2Human	0.19%
A map of the interactome network of the metazoan C. elegans. Li et al (2004). <i>Science</i>	
Predicted with 62 interactions from I2D	

Predicted	9.48%
I2D-MIPS-Yeast2Human	0.19%
MPact: the MIPS protein interaction resource on yeast. Güldener et al (2006). <i>Nucleic Acids Res</i> Predicted with 475 interactions from I2D	
I2D-Manual-Rat2Human	0.19%
Predicted with 4 interactions from I2D	
I2D-MINT-Mouse2Human	0.19%
MINT: a Molecular INTeraction database. Zanzoni et al (2002). <i>FEBS Lett</i> Predicted with 1,147 interactions from I2D	
I2D-Krogan-Greenblatt-2006-Core-Yeast2Human	0.19%
Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . Krogan et al (2006). <i>Nature</i> Predicted with 860 interactions from I2D	
I2D-vonMering-Bork-2002-Low-Yeast2Human	0.19%
Comparative assessment of large-scale data sets of protein-protein interactions. von Mering et al (2002). <i>Nature</i> Predicted with 7,979 interactions from I2D	
I2D-vonMering-Bork-2002-Medium-Yeast2Human	0.19%
Comparative assessment of large-scale data sets of protein-protein interactions. von Mering et al (2002). <i>Nature</i> Predicted with 1,280 interactions from I2D	
I2D-BIND-Yeast2Human	0.19%
BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al (2000). <i>Bioinformatics</i> Predicted with 599 interactions from I2D	
I2D-vonMering-Bork-2002-High-Yeast2Human	0.19%
Comparative assessment of large-scale data sets of protein-protein interactions. von Mering et al (2002). <i>Nature</i> Predicted with 723 interactions from I2D	
I2D-INNATEDB-Mouse2Human	0.19%
InnateDB: facilitating systems-level analyses of the mammalian innate immune response. Lynn et al (2008). <i>Mol Syst Biol</i> Predicted with 4,049 interactions from I2D	
Stuart-Kim-2003	0.19%
A gene-coexpression network for global discovery of conserved genetic modules. Stuart et al (2003). <i>Science</i> Predicted with 25,001 interactions from supplementary material	
I2D-MGI-Mouse2Human	0.19%
Ontological visualization of protein-protein interactions. Drabkin et al (2005). <i>BMC Bioinformatics</i> Predicted with 595 interactions from I2D	
I2D-Krogan-Greenblatt-2006-NonCore-Yeast2Human	0.19%
Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . Krogan et al (2006). <i>Nature</i> Predicted with 678 interactions from I2D	
I2D-BioGRID-Yeast2Human	0.19%
BioGRID: a general repository for interaction datasets. Stark et al (2006). <i>Nucleic Acids Res</i> Predicted with 17,314 interactions from I2D	

Predicted	9.48%
Wu-Stein-2010	0.19%
A human functional protein interaction network and its application to cancer data analysis. Wu et al (2010). <i>Genome Biol</i>	
Predicted with 89,967 interactions from supplementary material	
I2D-BIND-Mouse2Human	0.19%
BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al (2000). <i>Bioinformatics</i>	
Predicted with 1,007 interactions from I2D	
I2D-Yu-Vidal-2008-GoldStd-Yeast2Human	0.19%
High-quality binary protein interaction map of the yeast interactome network. Yu et al (2008). <i>Science</i>	
Predicted with 173 interactions from I2D	
I2D-BioGRID-Fly2Human	0.19%
BioGRID: a general repository for interaction datasets. Stark et al (2006). <i>Nucleic Acids Res</i>	
Predicted with 8,676 interactions from I2D	
I2D-Giot-Rothbert-2003-Low-Fly2Human	0.19%
A protein interaction map of Drosophila melanogaster. Giot et al (2003). <i>Science</i>	
Predicted with 1,019 interactions from I2D	
I2D-Li-Vidal-2004-literature-Worm2Human	0.19%
A map of the interactome network of the metazoan C. elegans. Li et al (2004). <i>Science</i>	
Predicted with 7 interactions from I2D	
Genetic Interactions	4.28%
Hou-Huang-2017	0.19%
A Genome-Wide CRISPR Screen Identifies Genes Critical for Resistance to FLT3 Inhibitor AC220. Hou et al (2017). <i>Cancer Res</i>	
Genetic Interactions with 105 interactions from BioGRID	
Han-Bassik-2017 A	0.19%
Synergistic drug combinations for cancer identified in a CRISPR screen for pairwise genetic interactions. Han et al (2017). <i>Nat Biotechnol</i>	
Genetic Interactions with 1,042 interactions from BioGRID	
Willingham-Muchowski-2003	0.19%
Yeast genes that enhance the toxicity of a mutant huntingtin fragment or alpha-synuclein. Willingham et al (2003). <i>Science</i>	
Genetic Interactions with 37 interactions from BioGRID	
Xie-Green-2012	0.19%
A synthetic interaction screen identifies factors selectively required for proliferation and TERT transcription in p53-deficient human cancer cells. Xie et al (2012). <i>PLoS Genet</i>	
Genetic Interactions with 100 interactions from BioGRID	
Bailey-Hieter-2015	0.19%
Dependence of Human Colorectal Cells Lacking the FBW7 Tumor Suppressor on the Spindle Assembly Checkpoint. Bailey et al (2015). <i>Genetics</i>	
Genetic Interactions with 114 interactions from BioGRID	
Martin-Elledge-2017	0.19%
A Role for Mitochondrial Translation in Promotion of Viability in K-Ras Mutant Cells. Martin et al (2017). <i>Cell Rep</i>	

Genetic Interactions	4.28%
Martin-Elledge-2017	
Genetic Interactions with 418 interactions from BioGRID	
Du-Krogan-2017	0.19%
Genetic interaction mapping in mammalian cells using CRISPR interference. Du et al (2017). <i>Nat Methods</i>	
Genetic Interactions with 166 interactions from BioGRID	
Blomen-Brummelkamp-2015	0.19%
Gene essentiality and synthetic lethality in haploid human cells. Blomen et al (2015). <i>Science</i>	
Genetic Interactions with 127 interactions from BioGRID	
Xiao-Brown-2018	0.19%
Estrogen-regulated feedback loop limits the efficacy of estrogen receptor-targeted breast cancer therapy. Xiao et al (2018). <i>Proc Natl Acad Sci U S A</i>	
Genetic Interactions with 684 interactions from BioGRID	
Toyoshima-Grandori-2012	0.19%
Functional genomics identifies therapeutic targets for MYC-driven cancer. Toyoshima et al (2012). <i>Proc Natl Acad Sci U S A</i>	
Genetic Interactions with 101 interactions from BioGRID	
Horlbeck-Gilbert-2018 B	0.19%
Mapping the Genetic Landscape of Human Cells. Horlbeck et al (2018). <i>Cell</i>	
Genetic Interactions with 946 interactions from BioGRID	
Luo-Elledge-2009	0.19%
A genome-wide RNAi screen identifies multiple synthetic lethal interactions with the Ras oncogene. Luo et al (2009). <i>Cell</i>	
Genetic Interactions with 316 interactions from BioGRID	
Vizeacoumar-Moffat-2013	0.19%
A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. Vizeacoumar et al (2013). <i>Mol Syst Biol</i>	
Genetic Interactions with 201 interactions from BioGRID	
Srivas-Ideker-2016	0.19%
A Network of Conserved Synthetic Lethal Interactions for Exploration of Precision Cancer Therapy. Srivas et al (2016). <i>Mol Cell</i>	
Genetic Interactions with 173 interactions from BioGRID	
Han-Bassik-2017 B	0.19%
Synergistic drug combinations for cancer identified in a CRISPR screen for pairwise genetic interactions. Han et al (2017). <i>Nat Biotechnol</i>	
Genetic Interactions with 893 interactions from BioGRID	
IREF-SMALL-SCALE-STUDIES	0.19%
Genetic Interactions with 1,159 interactions from iRefIndex	
Achuthankutty-Mailand-2019	0.19%
Regulation of ETAA1-mediated ATR activation couples DNA replication fidelity and genome stability. Achuthankutty et al (2019). <i>J Cell Biol</i>	
Genetic Interactions with 99 interactions from BioGRID	
Shen-Mali-2017	0.19%
Combinatorial CRISPR-Cas9 screens for de novo mapping of genetic interactions. Shen et al (2017). <i>Nat Methods</i>	

Genetic Interactions	4.28%
Shen-Mali-2017	
Genetic Interactions with 152 interactions from BioGRID	
Matsuoka-Elledge-2007	0.19%
ATM and ATR substrate analysis reveals extensive protein networks responsive to DNA damage. Matsuoka et al (2007). <i>Science</i>	
Genetic Interactions with 342 interactions from iRefIndex	
Lin-Smith-2010	0.19%
A genome-wide map of human genetic interactions inferred from radiation hybrid genotypes. Lin et al (2010). <i>Genome Res</i>	
Genetic Interactions with 4,805,334 interactions from supplementary material	
Sherman-Teitell-2010	0.19%
AID-induced genotoxic stress promotes B cell differentiation in the germinal center via ATM and LKB1 signaling. Sherman et al (2010). <i>Mol Cell</i>	
Genetic Interactions with 132 interactions from iRefIndex	
Horlbeck-Gilbert-2018 A	0.19%
Mapping the Genetic Landscape of Human Cells. Horlbeck et al (2018). <i>Cell</i>	
Genetic Interactions with 1,808 interactions from BioGRID	
BIOGRID-SMALL-SCALE-STUDIES	0.19%
Genetic Interactions with 651 interactions from BioGRID	
Co-expression	3.72%
Ramaswamy-Golub-2001	0.19%
Multiclass cancer diagnosis using tumor gene expression signatures. Ramaswamy et al (2001). <i>Proc Natl Acad Sci U S A</i>	
Co-expression with 284,829 interactions from supplementary material	
Dobbin-Giordano-2005	0.19%
Interlaboratory comparability study of cancer gene expression analysis using oligonucleotide microarrays. Dobbin et al (2005). <i>Clin Cancer Res</i>	
Co-expression with 452,322 interactions from GEO	
Alizadeh-Staudt-2000	0.19%
Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. Alizadeh et al (2000). <i>Nature</i>	
Co-expression with 92,360 interactions from supplementary material	
Ross-Perou-2001	0.19%
A comparison of gene expression signatures from breast tumors and breast tissue derived cell lines. Ross et al (2001). <i>Dis Markers</i>	
Co-expression with 146,858 interactions from supplementary material	
Roth-Zlotnik-2006	0.19%
Gene expression analyses reveal molecular relationships among 20 regions of the human CNS. Roth et al (2006). <i>Neurogenetics</i>	
Co-expression with 683,844 interactions from GEO	
Arijs-Rutgeerts-2009	0.19%
Mucosal gene expression of antimicrobial peptides in inflammatory bowel disease before and after first infliximab treatment. Arijs et al (2009). <i>PLoS One</i>	
Co-expression with 676,695 interactions from GEO	
Rosenwald-Staudt-2001	0.19%

Co-expression	3.72%
Rosenwald-Staudt-2001 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 118,097 interactions from supplementary material	
Bild-Nevins-2006 B Oncogenic pathway signatures in human cancers as a guide to targeted therapies. Bild et al (2006). <i>Nature</i> Co-expression with 285,368 interactions from GEO	0.19%
Mallon-McKay-2013 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 602,113 interactions from GEO	0.19%
Perou-Botstein-2000 Molecular portraits of human breast tumours. Perou et al (2000). <i>Nature</i> Co-expression with 189,373 interactions from supplementary material	0.19%
Boldrick-Relman-2002 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 116,197 interactions from supplementary material	0.19%
Wu-Garvey-2007 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 275,155 interactions from GEO	0.19%
Rieger-Chu-2004 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 266,879 interactions from GEO	0.19%
Jiang-de Kok-2017 Omics-based identification of the combined effects of idiosyncratic drugs and inflammatory cytokines on the development of drug-induced liver injury. Jiang et al (2017). <i>Toxicol Appl Pharmacol</i> Co-expression with 444,959 interactions from GEO	0.19%
Chen-Brown-2002 Gene expression patterns in human liver cancers. Chen et al (2002). <i>Mol Biol Cell</i> Co-expression with 291,300 interactions from supplementary material	0.19%
Perou-Botstein-1999 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 68,200 interactions from supplementary material	0.19%
Burington-Shaughnessy-2008 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 295,320 interactions from GEO	0.19%
Wang-Cheung-2015 Genetic variation in insulin-induced kinase signaling. Wang et al (2015). <i>Mol Syst Biol</i>	0.19%

Co-expression	3.72%
Wang-Cheung-2015	
Co-expression with 422,896 interactions from GEO	
Innocenti-Brown-2011	0.19%
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 620,205 interactions from GEO	
Wang-Maris-2006	0.19%
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 270,388 interactions from GEO	
Pathway	1.12%
REACTOME	0.19%
Pathway with 24,890 interactions from Pathway Commons	
Wu-Stein-2010	0.19%
A human functional protein interaction network and its application to cancer data analysis. Wu et al (2010). <i>Genome Biol</i>	
Pathway with 78,117 interactions from supplementary material	
HUMANCYC	0.19%
Pathway with 681 interactions from Pathway Commons	
CELL_MAP	0.19%
Pathway with 397 interactions from Pathway Commons	
IMID	0.19%
Pathway with 1,023 interactions from Pathway Commons	
NCI_NATURE	0.19%
Pathway with 10,118 interactions from Pathway Commons	
Co-localization	0.74%
Chen-Huang-2014	0.19%
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	
Schadt-Shoemaker-2004	0.19%
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 59,920 interactions from GEO	
Zhang-Shang-2006	0.19%
The catalytic subunit of the proteasome is engaged in the entire process of estrogen receptor-regulated transcription. Zhang et al (2006). <i>EMBO J</i>	
Co-localization with 53 interactions from BioGRID	
Johnson-Shoemaker-2003	0.19%
Genome-wide survey of human alternative pre-mRNA splicing with exon junction microarrays. Johnson et al (2003). <i>Science</i>	

Co-localization	0.74%
Johnson-Shoemaker-2003	
Co-localization with 426,464 interactions from GEO	
Shared protein domains	0.37%
INTERPRO	0.19%
Shared protein domains with 621,159 interactions from InterPro	
PFAM	0.19%
Shared protein domains with 471,533 interactions from Pfam	