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

- antigen processing and presentation of peptide antigen
- antigen processing and presentation
- MHC protein complex
- antigen binding
- antigen processing and presentation of exogenous peptide antigen
- antigen processing and presentation of exogenous antigen
- antigen processing and presentation of peptide antigen via MHC class II

Search parameters

Organism Rattus norvegicus (rat)

Genes RT1-CE5 , Cd74 , RT1-DOa , RT1-Bb , RT1-Da

Network weighting Automatically selected weighting method

Networks A

Almon-Jusko-2005

B

Bhatnagar-Attie-2014 , BIOGRID-SMALL-SCALE-STUDIES

C

CELL_MAP , Chan-Miron-2007 , Chen-Naus-2012 , Cirilli-Nerlov-2017 , Costigan-Woolf-2010

D

Devarajan-Ketha-Kumar-2012 , Duan-Li-2015

E

Ehyai-McDermott-2018

I

I2D-Bandyopadhyay-Ideker-2010-MAPK-HIGH-Human2Rat , I2D-Bandyopadhyay-Ideker-2010-MAPK-LOW-Human2Rat , I2D-Behrends-Harper-2010-AUTOPHAGY-HIGH-Human2Rat , I2D-Behrends-Harper-2010-AUTOPHAGY-LOW-Human2Rat , I2D-BIND-Fly2Rat , I2D-BIND-Human2Rat , I2D-BIND-Mouse2Rat , I2D-BIND-Worm2Rat , I2D-BIND-Yeast2Rat , I2D-BioGRID-Fly2Rat , I2D-BioGRID-Human2Rat , I2D-BioGRID-Mouse2Rat , I2D-BioGRID-Worm2Rat , I2D-BioGRID-Yeast2Rat , I2D-Formstecher-Daviet-2005-Embryo-Fly2Rat , I2D-Formstecher-Daviet-2005-Head-Fly2Rat , I2D-Giot-Rothbert-2003-High-Fly2Rat , I2D-Giot-Rothbert-2003-Low-Fly2Rat , I2D-HPRD-Human2Rat , I2D-Ingham-Pawson-2005-Human2Rat , I2D-INNATEDB-Human2Rat , I2D-INNATEDB-Mouse2Rat , I2D-IntAct-Fly2Rat , I2D-IntAct-Human2Rat , I2D-IntAct-Mouse2Rat , I2D-IntAct-Worm2Rat , I2D-IntAct-Yeast2Rat , I2D-Jorgensen-Pawson-2009-Human2Rat , I2D-Krogan-Greenblatt-2006-Core-Yeast2Rat , I2D-Krogan-Greenblatt-2006-NonCore-Yeast2Rat , I2D-Li-Vidal-2004-CE-DATA-Worm2Rat , I2D-Li-Vidal-2004-CORE-1-Worm2Rat , I2D-Li-Vidal-2004-CORE-2-Worm2Rat , I2D-Li-Vidal-2004-interolog-Worm2Rat , I2D-Li-Vidal-2004-literature-Worm2Rat , I2D-Li-Vidal-2004-non-core-Worm2Rat , I2D-ManualRat , I2D-MGI-Mouse2Rat , I2D-Miller-Attisano-2009-Human2Rat , I2D-MINT-Fly2Rat , I2D-MINT-Human2Rat , I2D-MINT-Mouse2Rat , I2D-MINT-Worm2Rat , I2D-MINT-Yeast2Rat , I2D-MIPS-Yeast2Rat , I2D-Ptacek-Snyder-2005-Yeast2Rat , I2D-Rual-Vidal-2004-core-Human2Rat , I2D-Rual-Vidal-2004-non-core-Human2Rat , I2D-Stanyon-Finley-2004-

I

CellCycle-Fly2Rat , I2D-Stelzl-Wanker-2005-High-Human2Rat , I2D-Tarassov-PCA-Yeast2Rat , I2D-vonMering-Bork-2002-High-Yeast2Rat , I2D-vonMering-Bork-2002-Low-Yeast2Rat , I2D-vonMering-Bork-2002-Medium-Yeast2Rat , I2D-Wang-Orkin-2006-EScmplxlow-Mouse2Rat , I2D-Wu-Li-2007-Human2Rat , I2D-Yu-Vidal-2008-GoldStd-Yeast2Rat , INTERPRO , IREF-bhf-ucl , IREF-bind , IREF-bind-translation , IREF-biogrid , IREF-corum , IREF-dip , IREF-hpidb , IREF-intact , IREF-intcomplex , IREF-matrixdb , IREF-mbinfo , IREF-mint , IREF-mppi , IREF-quickgo , IREF-SMALL-SCALE-STUDIES , IREF-uniprotpp

J

Jin-Zhang-2007 , Jolly-Estrem-2005

K

Kimpel-McBride-2007

L

López-Boado-Churg-2010

M

Marin-Kuan-Schilter-2006 , Martins-Marques-Girão-2015 , Martins-Rebelo-2018 , Mertz-Peng-2015 , Meyer-Meyer-2004 , Moon-Kim-2014

N

Na-Peng-2012

P

PFAM , Piazzzi-Cocco-2013 , Popiolek-Pausch-2011

R

Rimbault-Galibert-2009 , Roth-Suter-2011 , Römer-Zell-2014 B

S

Stevenson-Butler-2007 , Strøm-Sheikh-2004

T

Thomas-Bowyer-2010

V

von Kriegsheim-Kolch-2009

W

Walker-Bilbe-2004 , Wang-You-2006 , Wilson-Koh-2005 , Wisler-Vonderfecht-2011

Y

Yang-Paschen-2012 , Yang-Salminen-2012 , Young-Tannock-2012

Genes

Gene	Description	Rank
RT1-CE5	RT1 class I, locus CE5 [Source:RGD Symbol;Acc:1595868]	N/A
RT1-Bb	RT1 class II, locus Bb [Source:RGD Symbol;Acc:3469]	N/A
RT1-DOa	RT1 class II, locus DOa [Source:RGD Symbol;Acc:3477]	N/A
Cd74	CD74 molecule [Source:RGD Symbol;Acc:2313]	N/A
RT1-Da	RT1 class II, locus Da [Source:RGD Symbol;Acc:1593283]	N/A
RT1-Ba	RT1 class II, locus Ba [Source:RGD Symbol;Acc:1595867]	1
RT1-Db1	RT1 class II, locus Db1 [Source:RGD Symbol;Acc:1593282]	2
RT1-CE1	RT1 class I, locus1 [Source:RGD Symbol;Acc:1595869]	3
Aif1	allograft inflammatory factor 1 [Source:RGD Symbol;Acc:61924]	4
Ly86	lymphocyte antigen 86 [Source:RGD Symbol;Acc:1309936]	5
RT1-M3-1	RT1 class Ib, locus M3, gene 1 [Source:RGD Symbol;Acc:3494]	6
Ctss	cathepsin S [Source:RGD Symbol;Acc:621513]	7
B2m	beta-2 microglobulin [Source:RGD Symbol;Acc:2189]	8
Lyz2	lysozyme 2 [Source:RGD Symbol;Acc:3026]	9
RT1-DOb	RT1 class II, locus DOb [Source:RGD Symbol;Acc:1595814]	10
C1qb	complement C1q B chain [Source:RGD Symbol;Acc:2229]	11
Irf8	interferon regulatory factor 8 [Source:RGD Symbol;Acc:1312024]	12
RT1-A1	RT1 class Ia, locus A1 [Source:RGD Symbol;Acc:1595924]	13
Cd53	Cd53 molecule [Source:RGD Symbol;Acc:2310]	14
RT1-T24-4	RT1 class I, locus T24, gene 4 [Source:RGD Symbol;Acc:1598233]	15
RT1-S3	RT1 class Ib, locus S3 [Source:RGD Symbol;Acc:735037]	16
Psmb8	proteasome 20S subunit beta 8 [Source:RGD Symbol;Acc:3426]	17
RT1-CE10	RT1 class I, locus CE10 [Source:RGD Symbol;Acc:1359292]	18
Cd37	CD37 molecule [Source:RGD Symbol;Acc:62035]	19
Psmb9	proteasome 20S subunit beta 9 [Source:RGD Symbol;Acc:3427]	20

Networks

Co-expression	39.02%
Wang-You-2006	2.67%
Organ-specific expression profiles of rat mammary gland, liver, and lung tissues treated with targretin, 9-cis retinoic acid, and 4-hydroxyphenylretinamide. Wang et al (2006). <i>Mol Cancer Ther</i>	
Co-expression with 138,363 interactions from GEO	
Stevenson-Butler-2007	2.57%
Comprehensive gene expression profiling of rat lung reveals distinct acute and chronic responses to cigarette smoke inhalation. Stevenson et al (2007). <i>Am J Physiol Lung Cell Mol Physiol</i>	
Co-expression with 149,476 interactions from GEO	
Römer-Zell-2014 B	2.32%
Cross-platform toxicogenomics for the prediction of non-genotoxic hepatocarcinogenesis in rat. Römer et al (2014). <i>PLoS One</i>	
Co-expression with 342,316 interactions from GEO	
Rimbault-Galibert-2009	2.14%
RNA profiles of rat olfactory epithelia: individual and age related variations. Rimbault et al (2009). <i>BMC Genomics</i>	
Co-expression with 250,164 interactions from GEO	
Wisler-Vonderfecht-2011	2.05%
Raf inhibition causes extensive multiple tissue hyperplasia and urinary bladder neoplasia in the rat. Wisler et al (2011). <i>Toxicol Pathol</i>	
Co-expression with 362,068 interactions from GEO	
Yang-Salminen-2012	2.02%
Identification of urinary microRNA profiles in rats that may diagnose hepatotoxicity. Yang et al (2012). <i>Toxicol Sci</i>	
Co-expression with 290,575 interactions from GEO	
Chan-Miron-2007	2.01%
Serial transplantation of NMU-induced rat mammary tumors: a model of human breast cancer progression. Chan et al (2007). <i>Int J Cancer</i>	
Co-expression with 239,920 interactions from GEO	
Young-Tannock-2012	2.00%
Changes in bowel microbiota induced by feeding weanlings resistant starch stimulate transcriptomic and physiological responses. Young et al (2012). <i>Appl Environ Microbiol</i>	
Co-expression with 247,577 interactions from GEO	
Duan-Li-2015	1.98%
Transcriptome analyses reveal molecular mechanisms underlying functional recovery after spinal cord injury. Duan et al (2015). <i>Proc Natl Acad Sci U S A</i>	
Co-expression with 406,614 interactions from GEO	
Almon-Jusko-2005	1.94%
Temporal profiling of the transcriptional basis for the development of corticosteroid-induced insulin resistance in rat muscle. Almon et al (2005). <i>J Endocrinol</i>	
Co-expression with 126,978 interactions from GEO	
Strøm-Sheikh-2004	1.91%

Co-expression	39.02%
Strøm-Sheikh-2004	
Identification of a core set of genes that signifies pathways underlying cardiac hypertrophy. Strøm et al (2004). <i>Comp Funct Genomics</i>	
Co-expression with 119,202 interactions from GEO	
López-Boado-Churg-2010	1.88%
Modification of the rat airway explant transcriptome by cigarette smoke. López-Boado et al (2010). <i>Inhal Toxicol</i>	
Co-expression with 328,336 interactions from GEO	
Jolly-Estrem-2005	1.87%
Pooling samples within microarray studies: a comparative analysis of rat liver transcription response to prototypical toxicants. Jolly et al (2005). <i>Physiol Genomics</i>	
Co-expression with 138,955 interactions from GEO	
Costigan-Woolf-2010	1.86%
Multiple chronic pain states are associated with a common amino acid-changing allele in KCNS1. Costigan et al (2010). <i>Brain</i>	
Co-expression with 141,130 interactions from GEO	
Roth-Suter-2011	1.80%
Gene expression-based in vivo and in vitro prediction of liver toxicity allows compound selection at an early stage of drug development. Roth et al (2011). <i>J Biochem Mol Toxicol</i>	
Co-expression with 111,402 interactions from GEO	
Meyer-Meyer-2004	1.69%
Altered mRNA expression of genes related to nerve cell activity in the fracture callus of older rats: A randomized, controlled, microarray study. Meyer et al (2004). <i>BMC Musculoskelet Disord</i>	
Co-expression with 139,512 interactions from GEO	
Wilson-Koh-2005	1.65%
Microarray analysis of postictal transcriptional regulation of neuropeptides. Wilson et al (2005). <i>J Mol Neurosci</i>	
Co-expression with 135,074 interactions from GEO	
Marin-Kuan-Schilter-2006	1.65%
A toxicogenomics approach to identify new plausible epigenetic mechanisms of ochratoxin a carcinogenicity in rat. Marin-Kuan et al (2006). <i>Toxicol Sci</i>	
Co-expression with 136,806 interactions from GEO	
Thomas-Bowyer-2010	1.61%
Endoplasmic reticulum stress responses differ in meninges and associated vasculature, striatum, and parietal cortex after a neurotoxic amphetamine exposure. Thomas et al (2010). <i>Synapse</i>	
Co-expression with 254,504 interactions from GEO	
Kimpel-McBride-2007	1.40%
Functional gene expression differences between inbred alcohol-preferring and -non-preferring rats in five brain regions. Kimpel et al (2007). <i>Alcohol</i>	
Co-expression with 124,453 interactions from GEO	
Physical Interactions	25.61%
von Kriegsheim-Kolch-2009	4.02%
Cell fate decisions are specified by the dynamic ERK interactome. von Kriegsheim et al (2009). <i>Nat Cell Biol</i>	
Physical Interactions with 219 interactions from iRefIndex	

Physical Interactions	25.61%
Jin-Zhang-2007	3.76%
Identification of novel proteins associated with both alpha-synuclein and DJ-1. Jin et al (2007). <i>Mol Cell Proteomics</i>	
Physical Interactions with 126 interactions from iRefIndex	
Martins-Marques-Girão-2015	2.16%
Interacting Network of the Gap Junction (GJ) Protein Connexin43 (Cx43) is Modulated by Ischemia and Reperfusion in the Heart. Martins-Marques et al (2015). <i>Mol Cell Proteomics</i>	
Physical Interactions with 178 interactions from iRefIndex	
IREF-intcomplex	1.73%
Physical Interactions with 33 interactions from iRefIndex	
Ehyai-McDermott-2018	1.51%
FMRP recruitment of κ -catenin to the translation pre-initiation complex represses translation. Ehyai et al (2018). <i>EMBO Rep</i>	
Physical Interactions with 130 interactions from BioGRID	
IREF-quickgo	1.43%
Physical Interactions with 602 interactions from iRefIndex	
IREF-dip	1.11%
Physical Interactions with 255 interactions from iRefIndex	
Chen-Naus-2012	1.10%
Association of connexin43 with E3 ubiquitin ligase TRIM21 reveals a mechanism for gap junction phosphodegion control. Chen et al (2012). <i>J Proteome Res</i>	
Physical Interactions with 103 interactions from BioGRID	
Moon-Kim-2014	1.06%
Interactome analysis of AMP-activated protein kinase (AMPK)- α 1 and - α 2 in INS-1 pancreatic beta-cells by affinity purification-mass spectrometry. Moon et al (2014). <i>Sci Rep</i>	
Physical Interactions with 435 interactions from BioGRID	
IREF-mbinfo	0.93%
Physical Interactions with 17 interactions from iRefIndex	
BIOGRID-SMALL-SCALE-STUDIES	0.88%
Physical Interactions with 3,299 interactions from BioGRID	
Devarajan-Ketha-Kumar-2012	0.82%
The sclerostin-bone protein interactome. Devarajan-Ketha et al (2012). <i>Biochem Biophys Res Commun</i>	
Physical Interactions with 96 interactions from BioGRID	
IREF-bind-translation	0.78%
Physical Interactions with 549 interactions from iRefIndex	
Piazzzi-Cocco-2013	0.62%
Phosphoinositide-specific phospholipase C α 1b (PI-PLC α 1b) interactome: affinity purification-mass spectrometry analysis of PI-PLC α 1b with nuclear protein. Piazzzi et al (2013). <i>Mol Cell Proteomics</i>	
Physical Interactions with 132 interactions from iRefIndex	
IREF-corum	0.55%
Physical Interactions with 109 interactions from iRefIndex	

Physical Interactions	25.61%
IREF-intact	0.53%
Physical Interactions with 1,415 interactions from iRefIndex	
Bhatnagar-Attie-2014	0.51%
Phosphorylation and degradation of tomosyn-2 de-represses insulin secretion. Bhatnagar et al (2014). <i>J Biol Chem</i>	
Physical Interactions with 201 interactions from BioGRID	
IREF-bind	0.46%
Physical Interactions with 335 interactions from iRefIndex	
IREF-matrixdb	0.41%
Physical Interactions with 121 interactions from iRefIndex	
IREF-mppi	0.41%
Physical Interactions with 86 interactions from iRefIndex	
IREF-biogrid	0.32%
Physical Interactions with 3,694 interactions from iRefIndex	
IREF-mint	0.27%
Physical Interactions with 796 interactions from iRefIndex	
Cirilli-Nerlov-2017	0.12%
Insights into specificity, redundancy and new cellular functions of C/EBPa and C/EBPb transcription factors through interactome network analysis. Cirilli et al (2017). <i>Biochim Biophys Acta Gen Subj</i>	
Physical Interactions with 106 interactions from BioGRID	
IREF-uniprotp	0.10%
Physical Interactions with 149 interactions from iRefIndex	
Predicted	21.99%
I2D-ManualRat	4.08%
Predicted with 7 interactions from I2D	
I2D-Miller-Attisano-2009-Human2Rat	2.68%
Application of an integrated physical and functional screening approach to identify inhibitors of the Wnt pathway. Miller et al (2009). <i>Mol Syst Biol</i>	
Predicted with 16 interactions from I2D	
I2D-vonMering-Bork-2002-High-Yeast2Rat	1.46%
Comparative assessment of large-scale data sets of protein-protein interactions. von Mering et al (2002). <i>Nature</i>	
Predicted with 81 interactions from I2D	
I2D-Wu-Li-2007-Human2Rat	1.37%
Systematic identification of SH3 domain-mediated human protein-protein interactions by peptide array target screening. Wu et al (2007). <i>Proteomics</i>	
Predicted with 57 interactions from I2D	
I2D-INNATEDB-Mouse2Rat	1.25%
InnateDB: facilitating systems-level analyses of the mammalian innate immune response. Lynn et al (2008). <i>Mol Syst Biol</i>	
Predicted with 268 interactions from I2D	

Predicted	21.99%
I2D-BioGRID-Mouse2Rat	1.07%
BioGRID: a general repository for interaction datasets. Stark et al (2006). <i>Nucleic Acids Res</i> Predicted with 1,003 interactions from I2D	
I2D-Li-Vidal-2004-interolog-Worm2Rat	0.99%
A map of the interactome network of the metazoan <i>C. elegans</i> . Li et al (2004). <i>Science</i> Predicted with 56 interactions from I2D	
I2D-HPRD-Human2Rat	0.87%
Development of human protein reference database as an initial platform for approaching systems biology in humans. Peri et al (2003). <i>Genome Res</i> Predicted with 4,002 interactions from I2D	
I2D-BioGRID-Yeast2Rat	0.83%
BioGRID: a general repository for interaction datasets. Stark et al (2006). <i>Nucleic Acids Res</i> Predicted with 2,556 interactions from I2D	
I2D-INNATEDB-Human2Rat	0.81%
InnateDB: facilitating systems-level analyses of the mammalian innate immune response. Lynn et al (2008). <i>Mol Syst Biol</i> Predicted with 1,411 interactions from I2D	
I2D-BioGRID-Human2Rat	0.69%
BioGRID: a general repository for interaction datasets. Stark et al (2006). <i>Nucleic Acids Res</i> Predicted with 16,098 interactions from I2D	
I2D-IntAct-Mouse2Rat	0.66%
The IntAct molecular interaction database in 2010. Aranda et al (2010). <i>Nucleic Acids Res</i> Predicted with 2,741 interactions from I2D	
I2D-Jorgensen-Pawson-2009-Human2Rat	0.63%
Cell-specific information processing in segregating populations of Eph receptor ephrin-expressing cells. Jørgensen et al (2009). <i>Science</i> Predicted with 127 interactions from I2D	
I2D-vonMering-Bork-2002-Medium-Yeast2Rat	0.48%
Comparative assessment of large-scale data sets of protein-protein interactions. von Mering et al (2002). <i>Nature</i> Predicted with 212 interactions from I2D	
I2D-BioGRID-Worm2Rat	0.47%
BioGRID: a general repository for interaction datasets. Stark et al (2006). <i>Nucleic Acids Res</i> Predicted with 128 interactions from I2D	
I2D-BIND-Human2Rat	0.45%
BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al (2000). <i>Bioinformatics</i> Predicted with 534 interactions from I2D	
I2D-Behrends-Harper-2010-AUTOPHAGY-LOW-Human2Rat	0.44%
Network organization of the human autophagy system. Behrends et al (2010). <i>Nature</i> Predicted with 2,501 interactions from I2D	
I2D-MGI-Mouse2Rat	0.44%

Predicted	21.99%
I2D-MGI-Mouse2Rat	
Ontological visualization of protein-protein interactions. Drabkin et al (2005). <i>BMC Bioinformatics</i>	
Predicted with 99 interactions from I2D	
I2D-Yu-Vidal-2008-GoldStd-Yeast2Rat	0.43%
High-quality binary protein interaction map of the yeast interactome network. Yu et al (2008). <i>Science</i>	
Predicted with 33 interactions from I2D	
I2D-BioGRID-Fly2Rat	0.42%
BioGRID: a general repository for interaction datasets. Stark et al (2006). <i>Nucleic Acids Res</i>	
Predicted with 1,327 interactions from I2D	
I2D-Bandyopadhyay-Ideker-2010-MAPK-LOW-Human2Rat	0.28%
A human MAP kinase interactome. Bandyopadhyay et al (2010). <i>Nat Methods</i>	
Predicted with 212 interactions from I2D	
I2D-BIND-Mouse2Rat	0.27%
BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al (2000). <i>Bioinformatics</i>	
Predicted with 138 interactions from I2D	
I2D-Ingham-Pawson-2005-Human2Rat	0.20%
WW domains provide a platform for the assembly of multiprotein networks. Ingham et al (2005). <i>Mol Cell Biol</i>	
Predicted with 17 interactions from I2D	
I2D-Bandyopadhyay-Ideker-2010-MAPK-HIGH-Human2Rat	0.16%
A human MAP kinase interactome. Bandyopadhyay et al (2010). <i>Nat Methods</i>	
Predicted with 83 interactions from I2D	
I2D-MIPS-Yeast2Rat	0.14%
MPact: the MIPS protein interaction resource on yeast. Güldener et al (2006). <i>Nucleic Acids Res</i>	
Predicted with 63 interactions from I2D	
I2D-Krogan-Greenblatt-2006-NonCore-Yeast2Rat	0.14%
Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . Krogan et al (2006). <i>Nature</i>	
Predicted with 79 interactions from I2D	
I2D-MINT-Mouse2Rat	0.11%
MINT: a Molecular INTeraction database. Zanzoni et al (2002). <i>FEBS Lett</i>	
Predicted with 186 interactions from I2D	
I2D-IntAct-Human2Rat	0.10%
The IntAct molecular interaction database in 2010. Aranda et al (2010). <i>Nucleic Acids Res</i>	
Predicted with 8,515 interactions from I2D	
I2D-IntAct-Yeast2Rat	0.10%
The IntAct molecular interaction database in 2010. Aranda et al (2010). <i>Nucleic Acids Res</i>	
Predicted with 955 interactions from I2D	
Pathway	8.15%
CELL_MAP	8.15%

Pathway	8.15%
CELL_MAP	
Pathway with 9 interactions from Pathway Commons	
Co-localization	2.86%
Walker-Bilbe-2004	2.86%
Applications of a rat multiple tissue gene expression data set. Walker et al (2004). <i>Genome Res</i>	
Co-localization with 193,336 interactions from GEO	
Shared protein domains	2.37%
INTERPRO	1.49%
Shared protein domains with 567,125 interactions from InterPro	
PFAM	0.88%
Shared protein domains with 529,507 interactions from Pfam	