

Задание по базам данных

**Список баз данных которые
МОЖНО ИСПОЛЬЗОВАТЬ**

База данных национального института рака NCBI

(<http://www.ncbi.nlm.nih.gov>)

NCBI Resources How To Sign in to NCBI

NCBI National Center for Biotechnology Information

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Chemicals & Bioassays
Data & Software
DNA & RNA
Domains & Structures
Genes & Expression
Genetics & Medicine
Genomes & Maps
Homology
Literature
Proteins
Sequence Analysis
Taxonomy
Training & Tutorials
Variation

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Databases

[Assembly](#)
A database providing information on the structure of assembled genomes, assembly names and other meta-data, statistical reports, and links to genomic sequence data.

[BioProject \(formerly Genome Project\)](#)
A collection of genomics, functional genomics, and genetics studies and links to their resulting datasets. This resource describes project scope, material, and objectives and provides a mechanism to retrieve datasets that are often difficult to find due to inconsistent annotation, multiple independent submissions, and the varied nature of diverse data types which are often stored in different databases.

[BioSample](#)
The BioSample database contains descriptions of biological source materials used in experimental assays.

[BioSystems](#)
Database that groups biomedical literature, small molecules, and sequence data in terms of biological relationships.

[Bookshelf](#)
A collection of biomedical books that can be searched directly or from linked data in other NCBI databases. The collection includes biomedical textbooks, other scientific titles, genetic resources such as *GeneReviews*, and NCBI help manuals.

[ClinVar](#)
A resource to provide a public, tracked record of reported relationships between human variation and observed health status with supporting evidence. Related information in the [NIH Genetic Testing Registry \(GTR\)](#), [MedGen](#), [Gene](#), [OMIM](#), [PubMed](#) and other sources is accessible through hyperlinks on the records.

[ClincialTrials.gov](#)
A registry and results database of publicly- and privately-supported clinical studies of human participants conducted around the world.

[CloneDB \(formerly Clone Registry\)](#)
A database that integrates information about clones and libraries, including sequence data, map positions and distributor information.

[Computational Resources from NCBI's Structure Group](#)
A centralized page providing access and links to resources developed by the Structure Group of the NCBI Computational Biology Branch (CBB). These

Необходимо описать базу данных, структуру, основные вкладки, какую информацию они несут.

Описание вкладок базы данных NSBI

The screenshot displays the NCBI (National Center for Biotechnology Information) homepage. At the top, there is a navigation bar with the NCBI logo, a search bar, and a 'Sign in to NCBI' link. Below the navigation bar, a dropdown menu for 'All Databases' is open, listing various databases such as Assembly, BioProject, BioSample, BioSystems, Books, ClinVar, Clone, Conserved Domains, dbGaP, dbVar, Epigenomics, EST, Gene, Genome, GEO DataSets, GEO Profiles, GSS, GTR, and HomoloGene. The main content area features a central banner with the text 'Enter for Biotechnology Information advances science and health by providing access to genomic information.' Below this banner, there are six service tiles: 'Submit' (for manuscripts and databases), 'Download' (transfer NCBI data to your computer), 'Learn' (find help documents, attend a class or watch a tutorial), 'Develop' (use NCBI APIs and code libraries to build applications), 'Analyze' (identify an NCBI tool for your data analysis task), and 'Research' (explore NCBI research and collaborative projects). On the right side, there are sections for 'Popular Resources' (PubMed, Bookshelf, PubMed Central, PubMed Health, BLAST, Nucleotide, Genome, SNP, Gene, Protein, PubChem) and 'NCBI Announcements' (Search for WGS Sequences using Stand-alone BLAST!, It is now much easier to search WGS (Whole Genome Shotgun) with First of the New Bookshelf NCBI Insights Blog Posts - New Streptococcus pyogenes book, The first of a new series of NCBI Insights, NCBI is phasing out sequence IDs - use Accession Version instead!, As of September 2016, the integer contig identifiers known as "C1" will). A 'More...' link is located at the bottom right of the announcements section.

Всего 43 вкладки, одному человеку достаточно описать одну вкладку с указанием информации этой вкладки и примером работы во вкладке (примеры в виде скриншотов).

COSMIC Catalogue Of Somatic Mutations In Cancer

баз данных соматических мутаций, свойственных различным типам
опухолевых заболеваний человека.

<http://cancer.sanger.ac.uk/cosmic>



Home ▾ About ▾ Resources ▾ Curation ▾ Tools ▾ Data ▾ News ▾ Help ▾ [Login ▾](#)

COSMIC v76

eg: Braf, COLO-829, Carcinoma, V600E, BRCA-UK, Campbell [SEARCH](#)

R Resources

Key COSMIC resources

- [Cell Lines Project](#)
- [COSMIC Whole Genomes](#)
- [Cancer Gene Census](#)
- [Drug Sensitivity](#)
- [Mutational Signatures](#)
- [GRCh37 Cancer Archive](#)

T Tools

Additional tools to explore COSMIC

- [Cancer Browser](#)
- [Genome Browser](#)
- [GA4GH Beacon^{New}](#)
- [COSMIC Mart](#)
- [CONAN](#)

C Expert Curation

High quality curation by expert postdoctoral scientists

- [Cancer Gene Census](#)
- [Curated Genes](#)
- [Gene Fusions](#)
- [Genome-Wide Screens](#)

D Data

Further details on using COSMIC's content

- [Downloads](#)
- [License](#)
- [Submission](#)
- [Genome Annotation](#)
- [Datasheets](#)

Genomic Landscape of Cancer

COSMIC expansion

We welcome two new scientists who will be investigating the curated database and annotating the most interesting target and biomarker opportunities across this enormous database.

Dr. Sam Thompson is a medical statistician with expertise in clinical trials. In collaboration with Bayer Pharmaceuticals, she will be exploring correlations across the different types of variant annotation in COSMIC, aiming to systematically identify novel markers for disease.

Описание базы данных, описание вкладок, примеры
работы с базой данных. (2 человека)

PFAM - Protein families database of alignments and HMMs

коллекция белковых семейств

<http://pfam.xfam.org/>



[HOME](#) | [SEARCH](#) | [BROWSE](#) | [FTP](#) | [HELP](#) | [ABOUT](#)



Pfam 29.0 (December 2015, 16295 entries)

The Pfam Database is a large collection of protein families, each represented by **multiple sequence alignments** and **hidden Markov models (HMMs)**. [More...](#)

QUICK LINKS	YOU CAN FIND DATA IN PFAM IN VARIOUS WAYS...
SEQUENCE SEARCH	Analyze your protein sequence for Pfam matches
VIEW A PFAM ENTRY	View Pfam annotation and alignments
VIEW A CLAN	See groups of related entries
VIEW A SEQUENCE	Look at the domain organisation of a protein sequence
VIEW A STRUCTURE	Find the domains on a PDB structure
KEYWORD SEARCH	Query Pfam by keywords

JUMP TO

Enter any type of accession or ID to jump to the page for a Pfam entry or clan. Use Prot sequences, PDB structure, etc.

Or view the [help pages](#) for more information

Recent Pfam [blog](#) posts

[Hide this](#)

[Pfam 29.0 is now available](#) Rd (posted 22 December 2015)

Pfam 29.0, our second release of 2015, contains 16295 entries and 559 clans. We have made some major changes to our underlying sequence database and the data that are displayed on the website, which we've outlined below. Full details can be found in our [Nucleic Acids Research](#) paper, which is available [here](#). The growing size of [...]

[Moving to xfam.org](#) Rd (posted 1 May 2014)

Back in November 2012 we announced that the Xfam team in the UK was moving from the Wellcome Trust Sanger Institute to the European Bioinformatics Institute (EMBL EBI), just next door on the Wellcome Trust Genome Campus. On Tuesday we completed that move by switching off the Pfam and Rfam websites inside Sanger and redirecting all traffic [...]

[Short-term Pfam position available](#) Rd (posted 7 February 2014)

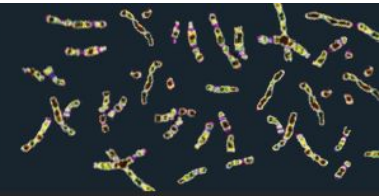
Описание базы данных, описание вкладок, примеры работы с базой данных.

1000 Genomes

<http://www.1000genomes.org/>

IGSR: The International Genome Sample Resource

Providing ongoing support for the 1000 Genomes Project data



Home About Data Analysis Participants Contact Browser FAQ

Search 1000genomes

IGSR and the 1000 Genomes Project



Populations: ● - European; ● - African; ● - American; ● - South Asian; ● - East Asian

The International Genome Sample Resource (IGSR) was established to ensure the ongoing usability of data generated by the 1000 Genomes Project and to extend the data set. More information is available about the IGSR.

Links

- [Announcements](#)
- [IGSR Sample Collection Principles](#)
- [1000 Genomes Project Publications](#)
- [File formats](#)
- [Software tools](#)
- [Download data](#)
- [Twitter](#)

Описание базы данных, описание вкладок, примеры работы с базой данных. (2 человека)

DrugBank

база данных лекарственных веществ с химической, фармакологической и фармацевтической информацией.

<http://www.drugbank.ca/>

The screenshot shows the DrugBank website interface. At the top, there is a navigation bar with the DrugBank logo and menu items: Browse, Search, Downloads, About, Help, and Contact Us. A search bar and a 'Drugs' dropdown menu are also present. The main content area features the DrugBank logo and the text 'Drug & Drug Target Database'. Below this, it states 'DrugBank Version 4.3' and provides a detailed description of the database's scope, including 204 FDA-approved biotech drugs, 93 nutraceuticals, and over 6000 experimental drugs. A 'More about DrugBank' link is provided. A dark grey box contains information about the database's availability and a citation for the original publication. On the right side, there is a 'Tweets' section showing a tweet from David Wishart (@WishartLab) retweeted by Reza Salek (@metabolnright). The 'Drug of the day' section highlights Ezetimibe, showing its chemical structure and a brief description of its use as an anti-hyperlipidemic medication. A 'Learn more about Ezetimibe' button is located below the description.

DrugBank
Drug & Drug Target Database

DrugBank Version 4.3

The DrugBank database is a unique bioinformatics and cheminformatics resource that combines detailed drug (i.e. chemical, pharmacological and pharmaceutical) data with comprehensive drug target (i.e. sequence, structure, and pathway) information. The database contains 8198 drug entries including 1985 FDA-approved small molecule drugs, 204 FDA-approved biotech (protein/peptide) drugs, 93 nutraceuticals and over 6000 experimental drugs. Additionally, 4331 non-redundant protein (i.e. drug target/enzyme/transporter/carrier) sequences are linked to these drug entries. Each DrugCard entry contains more than 200 data fields with half of the information being devoted to drug/chemical data and the other half devoted to drug target or protein data.

[More about DrugBank](#)

DrugBank is offered to the public as a freely available resource. Use and re-distribution of the data, in whole or in part, for commercial purposes requires explicit permission of the authors and explicit acknowledgment of the source material (DrugBank) and the original publication (see below). We ask that users who download significant portions of the database cite the DrugBank paper in any resulting publications.

Citing DrugBank

Wishart DS, Knox C, Guo AC, Shrivastava S, Hassanali M, Stothard P, Chiang Z, Woolsey J. *DrugBank: a comprehensive resource for in silico drug discovery and exploration*. Nucleic Acids Res. 2006 Jan 1;34(Database issue):D668-72. [13381355](#)

Drug of the day: Ezetimibe

Ezetimibe is an anti-hyperlipidemic medication which is used to lower cholesterol levels. Specifically, it appears to bind to a critical mediator of cholesterol absorption, the Niemann-Pick C1-Like 1 (NPC1L1) protein on the gastrointestinal tract epithelial cells as well as in hepatocytes.

For use as adjunctive therapy to diet for the reduction of elevated total-C, LDL-C, and Apo B in patients with primary (heterozygous familial and non-familial) hypercholesterolemia.

[Learn more about Ezetimibe](#)

Tweets by @WishartLab

Wishart Lab @WishartLab
Retweeted **Reza Salek** (@metabolnright):
David Wishart, @WishartLab is giving an overview of #metaboln.c resources fb.me/7NyeqfY7l
15 Feb

Wishart Lab Retweeted
Reza Salek @metabolnright

Entered [View on Twitter](#)

Описание базы данных, описание вкладок, примеры работы с базой данных.

Reactome

База данных о биологических путях у человека

<http://www.reactome.org/>



The image shows a screenshot of the Reactome website. At the top, there is a navigation bar with links for About, Content, Documentation, Tools, Community, Download, and Contact. A search bar contains the text "e.g. O95631, NTN1, signaling by" and a "Search" button. Below the navigation bar are six large buttons: "Browse Pathways", "Analyze Data", "Reactome FIViz app", "User Guide", "Data Download", and "Contact Us". To the right is a "Tweets" section featuring a tweet from EMBL-EBI Training (@EBItraining) about a course on Networks and Pathways. Below the tweets are logos for OICR, NYU Langone Medical Center, CSH Cold Spring Harbor Laboratory, and EMBL-EBI. A footer section contains a list of links for About, Content, Documentation, Tools, and Community, along with social media icons for Facebook, Twitter, and YouTube.

REACTOME
A CURATED PATHWAY DATABASE

About Content Documentation Tools Community Download Contact

Browse Pathways **Analyze Data** **Reactome FIViz app**

User Guide **Data Download** **Contact Us**

About Reactome

Reactome is a free, open-source, curated and peer reviewed pathway database. Our goal is to provide intuitive bioinformatics tools for the visualization, interpretation and analysis of pathway knowledge to support basic research, genome analysis, modeling, systems biology and education. The current version (v55) of Reactome was released on December 15, 2015.

OICR **NYU Langone** **CSH** **Cold Spring Harbor Laboratory** **EMBL-EBI**

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751 and 1U54GM114833-01), Ontario Research Fund, and the European Molecular Biology Laboratory.

About **Content** **Documentation** **Tools** **Community**

About Reactome Table of Contents User Guide Pathway Browser Reactome Outreach
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Описание базы данных, описание вкладок, примеры работы с базой данных. (2 человека)

Пример описания базы данных

База данных STRING - *Search Tool for the Retrieval of Interacting Genes/Proteins* (<http://string-db.org/>)

Это биологическая база данных и web-ресурс описывает и предсказывает белок-белковые взаимодействия. База данных аккумулирует в себя информацию из большого числа источников включающих экспериментальные данные. База содержит в себе информацию о 9,6 млн белков более 2000 организмов.

Home • Download • Help • My Data

STRING 10

STRING - Known and Predicted Protein-Protein Interactions

search by name search protein sequence multiple names multiple sequences

protein name: (examples: #1 #2 #3)

(STRING understands a variety of protein names and accessions; you can also try a [random entry](#))

organism: auto-detect

interactors wanted: COGs Proteins Reset GO!

please enter your protein of interest...

What it does ...

STRING is a database of known and predicted protein interactions. The interactions include direct (physical) and indirect (functional) associations; they are derived from four sources:

- Genomic Context
- High-throughput Experiments
- (Conserved) Coexpression
- Previous Knowledge

STRING quantitatively integrates interaction data from these sources for a large number of organisms, and transfers information between these organisms where applicable. The database currently covers 9'643'763 proteins from 2'031 organisms.

More Info Funding / Support Acknowledgements Use Scenarios

STRING (*Search Tool for the Retrieval of Interacting Genes/Proteins*) is being developed at [CPR](#), [EMBL](#), [SIB](#), [KU](#), [TUD](#) and [UZH](#).
STRING references: [Szklarczyk et al. 2015](#) / [2013](#) / [2011](#) / [2009](#) / [2007](#) / [2005](#) / [2003](#) / [Snel et al. 2000](#).
Miscellaneous: [Access Statistics](#), [Robot Access Guide](#), [Supported Browsers](#).

What's New? This is version 10 of STRING - now covering more than 2000 organisms, and with improved prediction algorithms!
Sister Projects: check out [STITCH](#) and [eggNOG](#) - two sister projects built on STRING data!
Previous Releases: Trying to reproduce an earlier finding? Confused? Refer to our [old releases](#).

SIB Swiss Institute of Bioinformatics CPR NNF Center for Protein Research EMBL European Molecular Biology Laboratory

STRING - Known and Predicted Protein-Protein Interactions

protein name: (examples: #1 #2 #3)

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organism: auto-detect

Close

- Hirschnia variata
- Hodgkinia cicadicola
- Hoeflea phototrophica
- Holdemania filiformis
- Homo sapiens
- Hordeum vulgare
- Hyaloperonospora arabidopsidis
- Hydra magnipapillata
- Hydrogenobacter thermophilus
- Hydrogenobaculum sp. Y04AAS1
- Hylomanella gracilis

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... covering more than 2000 organisms, and with improved prediction algorithms!
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STRING - Known and Predicted Protein-Protein Interactions

search by name search by protein sequence multiple names multiple sequences

protein name: (examples: #1 #2 #3)
Tp53

(STRING understands a variety of protein names and accessions; you can also try a [random entry](#))

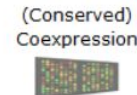
organism:
auto-detect ▼

interactors wanted:
 COGs Proteins

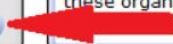


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More Info

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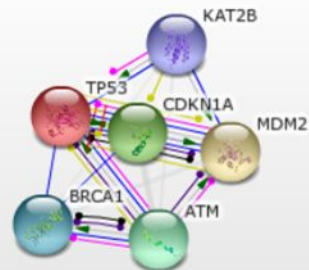
Previous Releases: Trying to reproduce an earlier finding? Confused? Refer to our [old releases](#).

There are several matches for **tp53**.
Please select one from the list below and press Continue to proceed.

[← Back](#) [Continue →](#)

organism	protein
<input checked="" type="radio"/> Homo sapiens	TP53 - tumor protein p53; Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity)
<input type="radio"/> <i>Cavia porcellus</i>	tp53 - Cellular tumor antigen p53 ; Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression. In cooperation with mitochondrial PPIF is involved in [...]
<input type="radio"/> <i>Danio rerio</i>	tp53 - tumor protein p53; Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity)
<input type="radio"/> <i>Oryzias latipes</i>	tp53 - cellular tumor antigen p53 ; Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity)
<input type="radio"/> <i>Rattus norvegicus</i>	tp53 - Cellular tumor antigen p53 ; Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression. In cooperation with mitochondrial PPIF is involved in [...]
<input type="radio"/> <i>Xenopus laurana</i>	tp53 - tumor protein p53; Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity)
<input type="radio"/> <i>Xiphophorus maculatus</i>	tp53 - Cellular tumor antigen p53 ; Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity)
<input type="radio"/> Mus musculus	TP53 - transformation related protein 53; Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression. In cooperation with mitochondrial PPIF is invol [...]
<input type="radio"/> Homo sapiens	ZMAT3 - zinc finger, matrin-type 3; Acts as a bona fide target gene of p53/TP53. May play a role in the TP53 -dependent growth regulatory pathway. May contribute to TP53 -mediated apoptosis by regulation of TP53 expression and translocation to the nucleus and nucleolus
<input type="radio"/> Homo sapiens	CUL7 - cullin 7; Component of a probable SCF-like E3 ubiquitin-protein ligase complex, which mediates the ubiquitination and subsequent proteasomal degradation of target proteins. Probably plays a role in the degradation of proteins involved in endothelial proliferation and/or differentiation (By similarity). Seems not to promote polyubiquitination and proteasomal degradation of TP53 . In vitro, complexes of CUL7 with either CUL9 or FBXW8 or TP53 contain E3 ubiquitin-protein ligase activity. In complex with FBXW8, mediates ubiquitination and consequent degradation of GORASP1, acting as a compo [...]
<input type="radio"/> Homo sapiens	PPP1R13B - protein phosphatase 1, regulatory subunit 13B; Regulator that plays a central role in regulation of apoptosis via its interaction with p53/TP53. Regulates TP53 by enhancing the DNA binding and transactivation function of TP53 on the promoters of proapoptotic genes in vivo
<input type="radio"/> Homo sapiens	FBK - Fb2 binding kinase; Phosphorylates MAP kinase p38. Seems to be active only in mitosis. May also play a role in the activation of lymphoid cells. When phosphorylated, forms a complex with TP53 , leading to TP53 destabilization and attenuation of G2/M checkpoint during doxorubicin-induced DNA damage
<input type="radio"/> Homo sapiens	RYBP - RING1 and YY1 binding protein; Inhibits ubiquitination and subsequent degradation of TP53 , and thereby plays a role in regulating transcription of TP53 target genes. May be implicated in the regulation of the transcription as a repressor of the transcriptional activity of EATF1. May bind to DNA. Promotes apoptosis
<input type="radio"/> Homo sapiens	MDM4 - Mdm4 p53 binding protein homolog (mouse); Inhibits p53/TP53- and TP73/p73-mediated cell cycle arrest and apoptosis by binding its transcriptional activation domain. Inhibits degradation of MDM2. Can reverse MDM2-targeted degradation of TP53 while maintaining suppression of TP53 transactivation and apoptotic functions
<input type="radio"/> Homo sapiens	DFNA5 - deafness, autosomal dominant 5; Involved in apoptosis and cell survival. Plays a role in the TP53 -regulated cellular response to DNA damage probably by cooperating with TP53
<input type="radio"/> Homo sapiens	TP53BP2 - tumor protein p53 binding protein, 2; Regulator that plays a central role in regulation of apoptosis and cell growth via its interactions. Regulates TP53 by enhancing the DNA binding and transactivation function of TP53 on the promoters of proapoptotic genes in vivo. Inhibits the ability of APPBP1 to conjugate NEDD8 to CUL1, and thereby decreases APPBP1 ability to induce apoptosis. Impedes cell cycle progression at G2/M. Its apoptosis-stimulating activity is inhibited by its interaction with DDX42

Save Layout Clustering Enrichment Options



This is the **evidence view**. Different line colors represent the types of evidence for the association.



Info & Parameters ...

Network Display - Nodes are either colored (if they are directly linked to the input - as in the table) or white (nodes of a higher iteration/depth). Edges, i.e. predicted functional links, consist of up to eight lines: one color for each type of evidence. Hover or click to reveal more information about the node/edge.

Active Prediction Methods:

- Neighborhood
 Gene Fusion
 Co-occurrence
 Co-expression
 Experiments
 Databases
 Textmining

required confidence (score):

- medium confidence (0.400) ▾
 highest confidence (0.900)
 high confidence (0.700)
 medium confidence (0.400)
 low confidence (0.150)

0

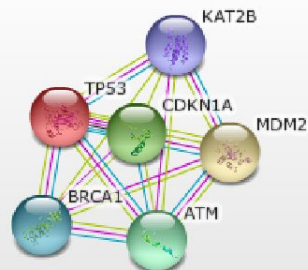
interactors shown:

no more than 10 interactors ▾

or custom limit:

- Disable Structure Previews inside Network Bubbles

Save Layout Clustering Enrichment Options



This is the **evidence view**. Different line colors represent the types of evidence for the association.



ATM

Actions

- [re-center network on this node](#)
- [add this node to input nodes](#)

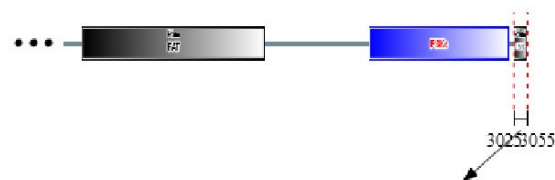
Information

ataxia telangiectasia mutated; Serine/threonine protein kinase which activates checkpoint signaling upon double strand breaks (DSBs), apoptosis and genotoxic stresses such as ionizing ultraviolet A light (UVA), thereby acting as a DNA damage sensor. Recognizes the substrate consensus sequence [ST]-Q. Phosphorylates 'Ser-139' of histone variant H2AX/H2AFX at double strand breaks (DSBs), thereby regulating DNA damage response mechanism. Also plays a role in pre-B cell allelic exclusion, a process leading to expression of a single immunoglobulin heavy chain allele to enforce clonality and [...]

Identifier: ENSP00000278616



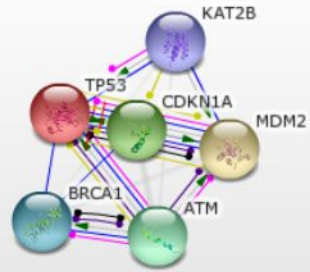
- [show protein sequence](#)
- [homologs among STRING organisms](#)



homology model (**1w1nA**)
identity: 38.7%

[Close](#)

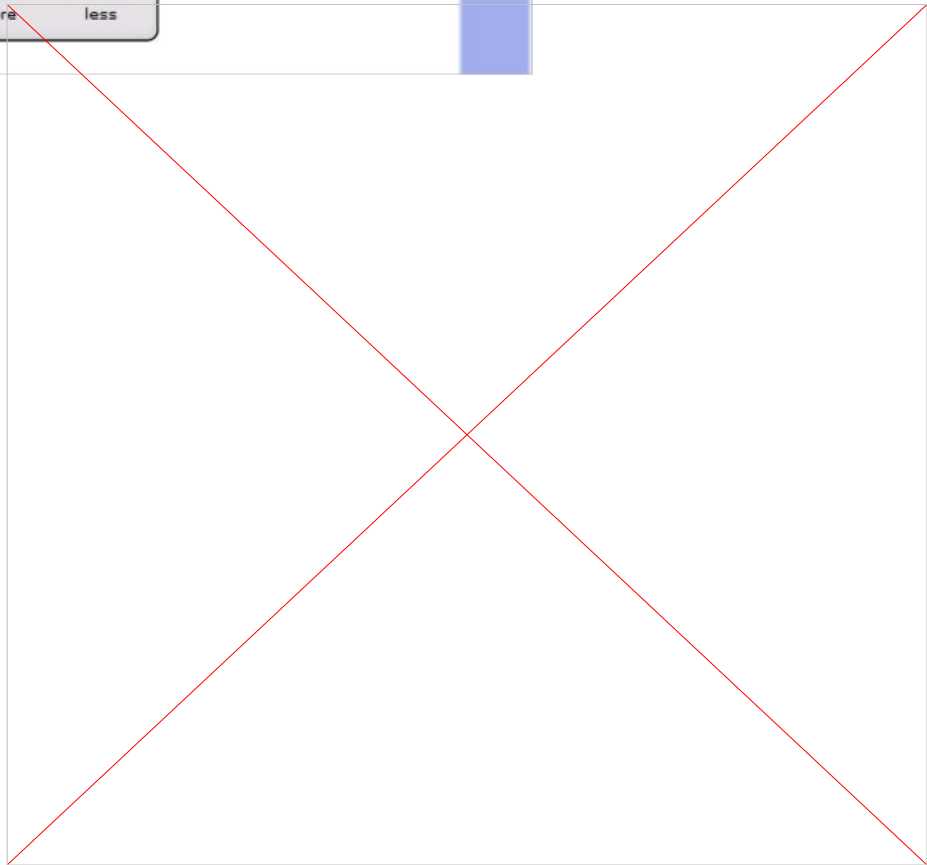
Save Layout Clustering Enrichment Options

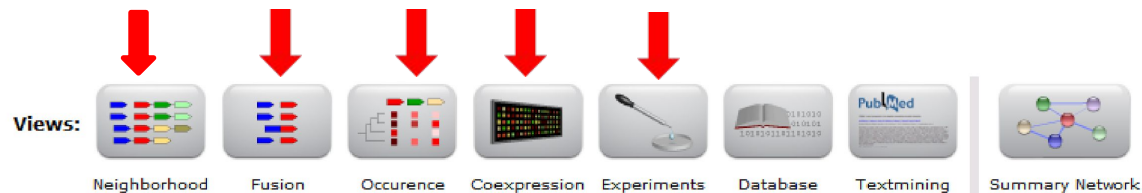


This is the **actions view**. Modes of action are shown in different colors.

 *confidence*  *evidence*  *actions*  *interactive*  *advanced*  *more*  *less*

(requires Flash player 10 or better)





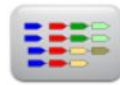
Neighborhood: Подобный геномный контекст у разных видов предполагают аналогичную функцию белков.

Fusion: белки, которые связаны внутри геномов, весьма вероятно, могут быть функционально связаны между.

Occurrence: Белки, которые имеют аналогичную функцию или находятся в том же пути метаболизма, должны быть отображены вместе и имеют схожие филогенетическое профиль.

Coexpression: Прогнозируемая связь между генами на основе наблюдаемых закономерностей одновременной экспрессии генов.

Views:



Neighborhood



Fusion



Occurrence



Coexpression



Experiments



Database



Textmining



Summary Network

Info & Parameters ...

Coexpression Display.

Active Prediction Methods:

- Neighborhood Gene Fusion Co-occurrence
 Co-expression Experiments Databases Textmining

required confidence (score):

medium confidence (0.400) ▾

or custom value:

interactors shown:

no more than 10 interactors ▾

or custom limit:

Update Parameters

Info & Parameters ...

Network Display - Nodes are either colored (if they are directly linked to the input - as in the table) or white (nodes of a higher iteration/depth). Edges, i.e. predicted functional links, consist of up to eight lines: one color for each type of evidence. Hover or click to reveal more information about the node/edge.

Active Prediction Methods:

- Neighborhood Gene Fusion Co-occurrence
 Co-expression Experiments Databases Textmining

required confidence (score):

medium confidence (0.400) ▾

highest confidence (0.900)

high confidence (0.700)

medium confidence (0.400)

low confidence (0.150)

0

interactors shown:

no more than 5 interactors ▾

or custom limit:

Disable Structure Previews inside Network Bubbles

Update Parameters

Info & Parameters ...

Network Display - Nodes are either colored (if they are directly linked to the input - as in the table) or white (nodes of a higher iteration/depth). Edges, i.e. predicted functional links, consist of up to eight lines: one color for each type of evidence. Hover or click to reveal more information about the node/edge.

Active Prediction Methods:

- Neighborhood Gene Fusion Co-occurrence
 Co-expression Experiments Databases Textmining

required confidence (score):

medium confidence (0.400) ▾

or custom value:

interactors shown:

no more than 5 interactors ▾

no more than 5 interactors

no more than 10 interactors

no more than 20 interactors

no more than 50 interactors

additional (white) nodes

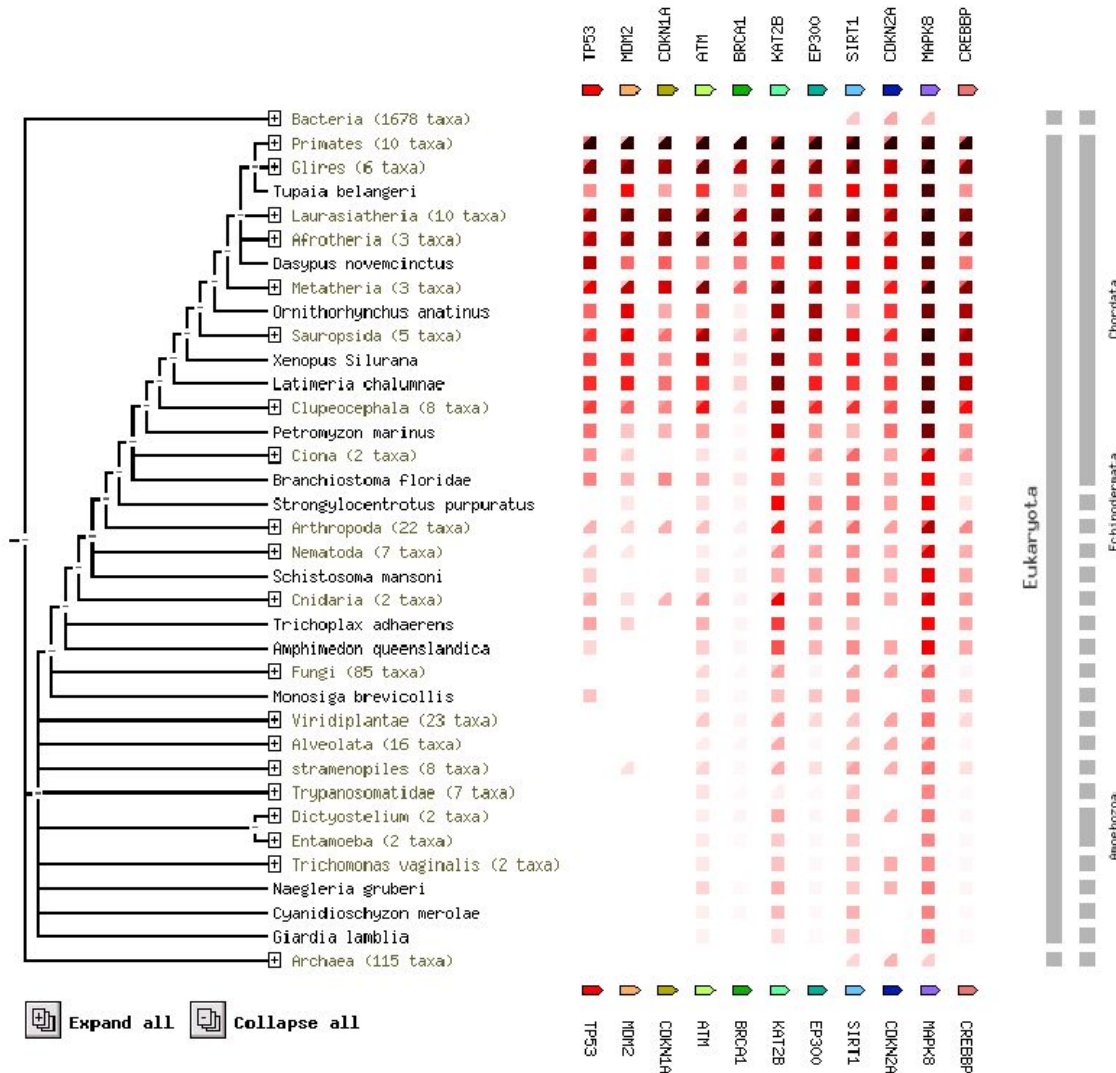
0

Disable Structure Previews inside Network Bubbles

Update Parameters

- Occurrence View -

In which organisms is my protein conserved?
Functional partners often have similar occurrence patterns.

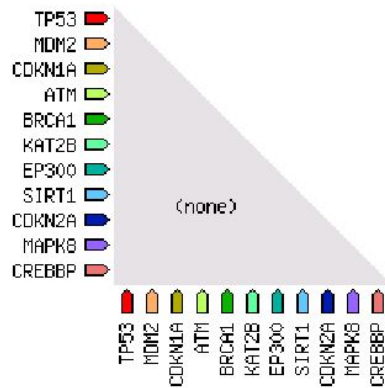


Expand all Collapse all

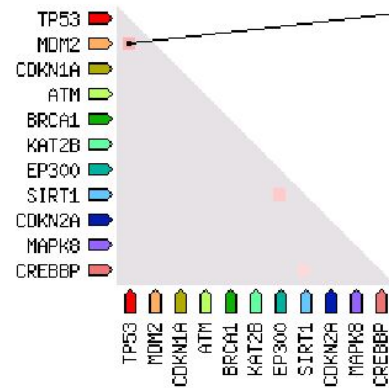
- Coexpression -

association score 

... from Coexpression in
Homo sapiens:



... from Coexpression in
other species (transferred):



from *D. rerio*
[Show](#)

Relevant datasets in Homo sapiens:

- | | |
|---|---|
| <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0676"(tandem affinity purification) assay
 ● CDKN1A ● EP300 ● CREBBP [... and 24 other proteins]</p> | <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0676"(tandem affinity purification) assay
 ● CDKN1A ● EP300 ● CREBBP [... and 24 other proteins]</p> |
| <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0415"(electrophoretic mobility shift assay) assay
 ● TP53 ● MDM2 ● CDKN1A</p> | <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0412"(electrophoretic mobility supershift assay) assay
 ● TP53 ● MDM2 ● CDKN1A</p> |
| <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0402"(chromatin immunoprecipitation assay) assay
 ● TP53 ● MDM2 ● CDKN1A</p> | <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0402"(chromatin immunoprecipitation assay) assay
 ● TP53 ● MDM2 ● CDKN1A</p> |
| <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0402"(chromatin immunoprecipitation assay) assay
 ● TP53 ● MDM2 ● CDKN1A</p> | <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0413"(electrophoretic mobility shift assay) assay
 ● TP53 ● MDM2 ● CDKN1A</p> |
| <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0412"(electrophoretic mobility supershift assay) assay
 ● TP53 ● MDM2 ● CDKN1A</p> | <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0402"(chromatin immunoprecipitation assay) assay
 ● TP53 ● MDM2 ● CDKN1A</p> |

Showing 10 out of 956 sets. [Show All](#)

Relevant Information transferred from other species:

- | | |
|--|--|
| <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0676"(tandem affinity purification) assay
 <i>Saccharomyces cerevisiae</i>: ● SIR2 ● GCN5 ● HST1 ● RSC1 ● BDF1 RSC1 RSC2 [... and 181 other proteins]</p> | <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0676"(tandem affinity purification) assay
 <i>Saccharomyces cerevisiae</i>: ● HST1 ● GCN5 ● SIR2 ● RSC1 ● BDF1 RSC2 RSC1 [... and 181 other proteins]</p> |
| <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0676"(tandem affinity purification) assay
 <i>Saccharomyces cerevisiae</i>: ● SIR2 ● GCN5 ● HST1 ● RSC1 ● BDF1 RSC1 RSC2 [... and 181 other proteins]</p> | <p>protein-protein interaction (intact) info
 Detected by psi-mi:"MI:0676"(tandem affinity purification) assay
 <i>Saccharomyces cerevisiae</i>: ● HST1 ● GCN5 ● SIR2 ● RSC1 ● BDF1 RSC2 RSC1 [... and 181 other proteins]</p> |

- Text Mining View -

Is my protein mentioned with other proteins in publications?
STRING automatically reads abstracts and other text files for
this type of association (but see here for possible mistakes).



VarWalker: personalized mutation network analysis of putative cancer genes from next-generation sequencing data.



Tu P, Phan Z

PLoS Comput Biol. 10(2):e1003460 (2014).

Abstract:

A major challenge in interpreting the large volume of mutation data identified by next-generation sequencing (NGS) is to distinguish driver mutations from neutral passenger mutations to facilitate the identification of targetable genes and new drugs. Current approaches are primarily based on mutation frequencies of single-genes, which lack the power to detect infrequently mutated driver genes and ignore functional interconnection and regulation among cancer genes. We propose a novel mutation network method, VarWalker, to prioritize driver genes in large scale cancer mutation data. VarWalker fits generalized additive models for each sample based on sample specific mutation profiles and builds on the joint frequency of both mutation genes and their close interactors. These interactors are selected and optimized using the Random Walk with Restart algorithm in a protein-protein interaction network. We applied the method in >300 tumor genomes in two large-scale NGS benchmark datasets: 183 lung adenocarcinoma samples and 121 melanoma samples. In each cancer, we derived a consensus mutation subnetwork containing significantly enriched consensus cancer genes and cancer related functional pathways. These cancer specific mutation networks were then validated using independent datasets for each cancer. Importantly, VarWalker prioritizes well known, infrequently mutated genes, which are shown to interact with highly recurrently mutated genes yet have been ignored by conventional single gene based approaches. Utilizing VarWalker, we demonstrated that network-assisted approaches can be effectively adapted to facilitate the detection of cancer driver genes in NGS data.

Excerpts from full text:

... important interactor. For example, TP53 is inhibited by the protein MDM2, but it is activated by **ATM** (●), both of which have a direct interaction with **TP53** (●) [36]. In such cases, consideration of only the most accessible interactor would [...] that function in the regulation of nuclear SMAD2/3 signaling pathways (SMAD2, SMAD4, MYO11, **CREBBP** (●), JUN, SNIP1, NCOA1, NCOR1, CDK2, AKT1, CDK4, and **KAT2B** (●), p16^{INK4} (●), and NTRK3 (11). These genes could also be rarely frequently mutated (e.g., in **CDKN2A** (●) (9), SMAD4 (●), NTRK1 (●), RR1 (4), AKT1 (1), HRA5 (1), and MDM2 (1). Functional [...] mutated gene (n Table 57). These interactions were among 28 infrequently mutated genes (in **BRCA1** (●) (- CGC gene) interacts with TP53 (- high-frequency gene, known I IAD gene, and CGC ...

Mechanisms of radiation toxicity in transformed and non-transformed cells.



Panganiban RA, Snow AL, Day RM

Int J Mol Sci. 14(8):15931-38 (2013).

● SIRT1, Sirtuin-1 ● CIP1, Cip1, Sli1, WAF1, Waf1, waf1 ● p300 ● PCAF, pcaf ● P53, TP53, T53, glioblastoma, p53 ● ATM ● JNK ● INK4a, ink4a ● Hdm2, Mdm2 ● BRCA1 ...

Mitochondrial dysfunction in cancer.



Bolani ML, Chaturvedi AH, Mackool KF

Front Oncol. 3:292 (2013).

● SIRT1, Sirt1, Sirt1n, Sirtuin ● GCN5 ● glioblastoma, p53 ● ATM, Atm ● JNK ● ARF, CDKN2A, INK4A, p16 ● BRCA1 ...

p53 (●)-Based cytotoxic therapy: exploiting the 'guardian of the genome' to protect normal cells from cytotoxic therapy.



Rao B, Lahn S, Thompson AM

Br J Cancer. 109(12):2951-8 (2013).

● Cip1, Waf1, p21, p21Cip1 ● p53 ● ATM ● Arf, p14^{ARF}, p15^{ARF} ● MDM2, Mdm2, mdm2 ● BRCA1 ...

Suppressed expression of T-box transcription factors is involved in senescence in chronic obstructive pulmonary disease.



Accuaah-Mensah GK, Malhotra D, Vulimiri M, McDermott JS, Biswal S

PLoS Comput Biol. 8(7):e1002597 (2012).

● SIRT1 ● p21 ● EP300 ● TP53, p53 ● MAPK0 ● ARF, CDKN2A, p16INK4A ● MDM2 ...