HumanPSD™

The Human Protein Survey Database (HumanPSD) is a rich information resource connecting pathways with targets, drugs and clinical trials.

Historically, it has been created as one of the nine volumes of the PROTEOME databases (Nucleic Acids Res. 30:137-141, 2002). In the beginning, it was designed as a source for comprehensive protein property documentation, displayed as locus reports, with the disease and biomarker annotation as an increasingly important annotation field.

At present, the particular value of HumanPSD lies in its extensive documentation of protein molecules as drug targets and biomarkers. This is enhanced by the TRANSPATH® database on biological pathways and networks.

Applications

By connecting clinical phenotypes (diseases) through drugs with their targets, and further to the pathways they are involved in, HumanPSD™ supports you in making surprising discoveries.

Further reading

Hodges et al. (2002) Annotating the human proteome: the Human Proteome Survey Database (HumanPSD) and an in-depth target database for G protein-coupled receptors (GPCR-PD) from Incyte Genomics. Nucleic Acids Res. 30:137-141.

Michael et al. (2008) Building a knowledge base for systems pathology. Brief. Bioinform. 9:518-531.

HumanPSD™

About geneXplain

GeneXplain's mission is to provide a comprehensive platform for bioinformatic, systems biological and cheminformatic tools. The raison d'être of this platform is to assist translational research in the life sciences, mainly in the context of personalized medicine and pharmacogenomics. We intend to make our expertise available to academic and commercial partners in collaborative research projects.

To achieve this, geneXplain also offers:

- The geneXplain platform providing a large number of bioinformatic and systems biological data analysis workflows. Unique is geneXplain's Upstream Analysis for causal interpretation of expression data
- TRANSFAC®, the gold standard database on transcriptional regulation, containing the most comprehensive library of protein-interacting DNA sequence motifs
- TRANSPATH®, a database of mammalian biological pathways and networks
- PASS and PharmaExpert for predicting biological activities of compounds qualitatively
- GUSAR for QSAR model building and quantitative activity prediction

geneXplain GmbH
Am Exer 10b
D-38302 Wolfenbüttel, Germany

info@genexplain.com
www.genexplain.com
www.facebook.com/genexplain
www.linkedin.com/company/genexplain
www.twitter.com/genexplain

Directors: E. Wingender, A. Kel • Commercial register: HRB 202564, Amtsger. Braunschweig • VAT No.: DE271983408

HumanPSD

The Human Protein Survey Database, the information resource about biomarkers and drug targets

geneXplain

Table of Contents

Introduction
Description
Synonyms

Biomarker Associations
Diseases associated with MYC
Inherited MYC mutations

Pharmacogenomics Variants
Add a subscription to PGMD™ and this report will display detailed information about:

Drug Interactions
Drug(s) targeting MYC

Gene Ontology
Molecular function
Biological process
Cellular component

Expression
Tissue expression
Regulation of MYC expression

Mutant Phenotype
Mutant phenotype of closely related homolog(s)

Pathways & Interactions
Pathways
Protein-protein interactions
Events acting on MYC
Events triggered by MYC

Transcriptional Regulation
Add a subscription to TRANSFAC® and this report will display detailed information about:

RNA Features
Overview of RNA sequence

Protein Features
Overview of protein sequence and structure
Post-translational modifications of MYC protein
View complexes containing MYC protein

Identifiers
Accessions mapped to this record

Annotations
Description
Editor's Notes
Disease related

References

Reports

The basic information unit is a "locus report", which summarizes the existing knowledge about the product(s) of a gene. It is part of a hierarchy, with individual proteins (isoforms such as splice variants) encoded by a gene at a level under the locus report, and summarizing features of the orthologs of human, mouse and rat origin at a higher level.

HumanPSD™: the Human Protein Survey Database on biomarkers, drug targets, and pathways.

Key features

- Reports about more than 53,000 proteins and 5,200 microRNAs (human and model organisms, mostly mouse and rat)
- More than 118,000 gene-disease assignments extracted from original scientific literature and evaluated by experts, referring to about 4000 diseases (human) / disease models (mouse)
- More than 27,000 drug-protein interactions, referring to more than 8,200 drugs
- More than 390,000 clinical trial descriptions, each referring to a defined clinical phenotype and a drug
- More than 580,000 assignments to Gene Ontology (GO), manually annotated and quality-checked
- More than 460,000 gene expression assignments
- More than 949,000 annotation statements given
- More than 377,000 references to peer-reviewed scientific publications provided
- An integrated Ontology Browser supports easy selection of defined sets of gene/molecules
- TRANSPATH included! Comprehensive pathway information allows easy connection between molecules, diseases and pathways affected

Diseases associated with MYC (91 entries)

Show 5 entries Search:

		Type of Association				Indication		
Disease details-all	Significance	Causal 50 associations	Correlative 528 associations	Preventative 26 associations	Negative 6 associations	Disease Mechanism 30 associations	Prognosis 129 associations	Therapeutic Target 27 associations
Breast Neoplasms	39 associations	6 associations	28 associations	5 associations		6 associations	11 associations	3 associations
Prostatic Neoplasms	36 associations	8 associations	24 associations	3 associations	1 associations	5 associations	11 associations	3 associations
Lung Neoplasms	30 associations	2 associations	27 associations	1 associations		1 associations	11 associations	1 associations
Stomach Neoplasms	27 associations	1 associations	26 associations			1 associations	8 associations	
Uterine Cervical Neoplasms	24 associations	1 associations	22 associations		1 associations	1 associations	5 associations	

Showing 1 to 5 of 91 entries First Previous 1 2 3 4 5 Next Last

Benefits

- Quickly access detailed reports for individual genes, proteins, miRNAs, diseases, and drugs without time-consuming literature search.
- Uncover biologically relevant connections between seemingly disparate genes, diseases, and drugs.
- Identify and rank potential therapeutic targets based on known functional characteristics.
- Explore canonical pathways and build custom protein networks, overlaying known disease and drug associations.

Disease / biomarker association

A tabular summary of literature-derived relationships between human genes and gene products with human diseases is given. These associations are clearly sorted according to their type, e.g. whether a gene/protein has a causal relationship with a disease to develop, or whether it is merely correlative, etc.

Availability

Enjoy the easy online access to HumanPSD™ on our high-performance servers