The TRANSPATH® Database

TRANSPATH® is a database of mammalian biological pathways and networks. As one of the earliest pathway databases ever created (Nucleic Acids Res. 27:318-322, 1999), it has grown since to the remarkable volume of nearly 720,000 manually curated reactions.

TRANSPATH® is available as stand-alone solution, either for online access or as downloadable flat files. It can also be obtained as integral part of the HumanPSD database, which provides a rich compendium of additional information on human, mouse or rat genes and proteins.

geneXplain platform, supporting geneXplain's proprietary upstream analysis.

Applications

Whether you use it as encyclopedia of signal transduction or metabolic pathways, for the visualization of pathway connections between any molecules of interest, or for identifying master regulators as potential drug targets: You will be surprised by the versatility of this valuable resource.

Further reading

Krull et al. (2006) TRANSPATH: an information resource for storing and visualizing signaling pathways and their pathological aberrations. Nucleic Acids Res. 34:D546-D551.

Pathway Analysis with geneXplain: http://www.genexplain.com/pathway-analysis

TRANSPATH®

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.

- HumanPSD, a rich information resource connecting pathways with targets, drugs and clinical trials.

- PASS and PharmaExpert for predicting biological activities of compounds qualitatively

- GUSAR for QSAR model building and quantitative activity prediction

geneXplain GmbH
Am Exer 19b
D-38302 Wolfenbüttel, Germany

info@genexplain.com
www.genexplain.com
www.facebook.com/genexplain
www.linkedin.com/company/genexplain
www.gplus.to/geneXplain

TRANSPATH

The database of biological networks

geneXplain

TRANSPATH®: the database on mammalian pathways and networks

Semantic Projection

p38alpha --> p53 (phosphorylation)

A mechanistic Pathway Step reaction being abstracted to a semantic level

Pathway Step

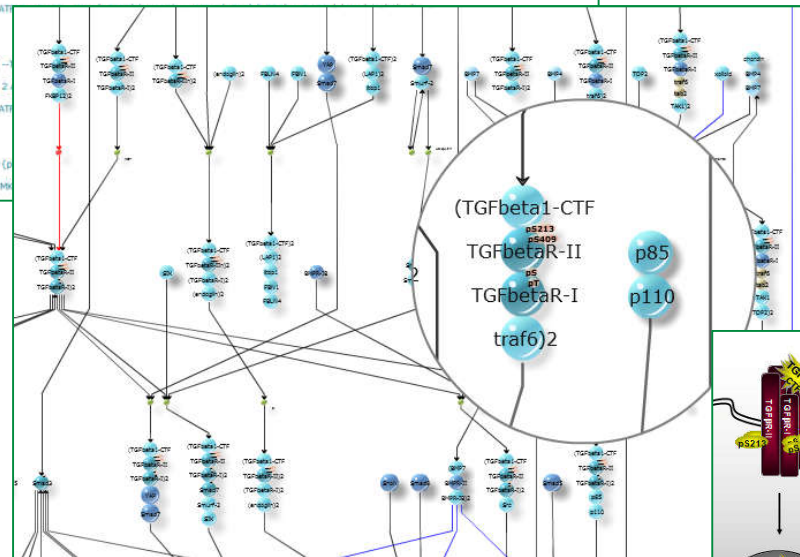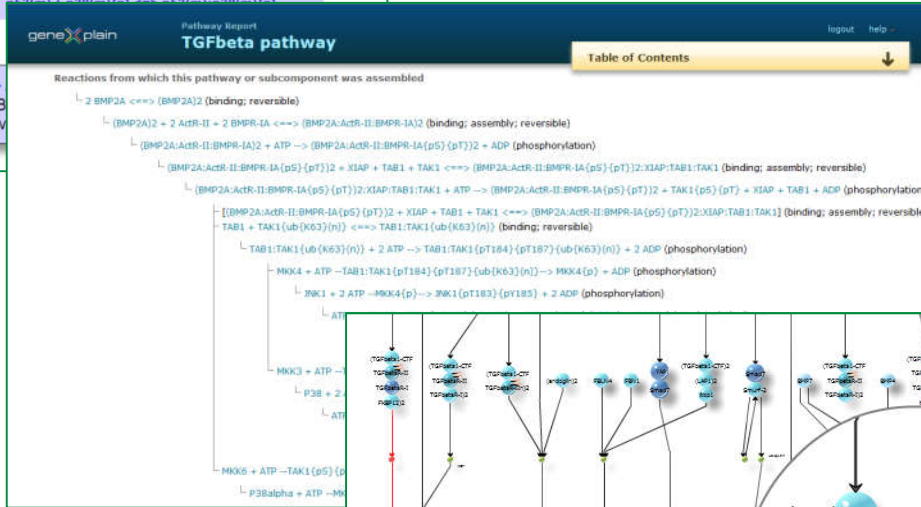p53 + ATP -p38alpha{p}-> p53{pS33} + ADP

Related Molecular Evidence reactions being summarized into one pathway step

p53(m) + ATP -p38alpha{p}-> p53{pS33}(m) + ADP
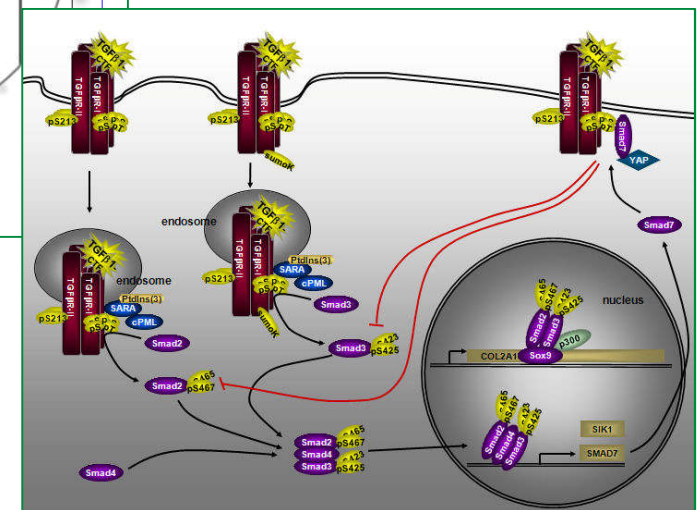
p53(h) + ATP -p38alpha(m)-> p53{pS33}(h) + ADP

Molecular Evidence

p53(m) +
mouse JB
quality lev

Key features

- Information about more than 500,000 signaling or metabolic molecules of human, mouse or rat cells
- More than 700,000 signaling or metabolic reactions extracted from original scientific literature and evaluated by experts
- 1720 experimentally verified pathways and chains
- More than 69,000 peer-reviewed scientific publications evaluated

The structure

TRANSPATH organizes the information about genes/molecules and reactions according to multiple hierarchies. Its sophisticated structure makes it one of the scientifically best conceptualized pathway resources, suitable for multi-purpose uses. It is complemented by one of the richest corpora of pathway data available among all public domain and commercial sources, all manually curated by experts.

Reactions

Individual reactions are documented with all experimental details, in a strictly mechanistic way that includes all reaction partners and the taxonomic origin of each molecule as reported in the published experiment ("molecular evidence level").

All evidences for a certain pathway step are accumulated to provide a more comprehensive and complete picture ("pathway step level"). On top, a semantic view is provided, which focuses on the key components only and omits mechanistic details as well as small abundant molecules ("semantic projection").

Networks & pathways

Complete networks and pathways are built from molecules and their reactions. To consider the heterogeneity of information given in the original publications, TRANSPATH transparently but precisely differentiates protein molecules according to:

- their relatedness within one genome (isoforms/paralogs)
- their relatedness between different genomes (orthologs)
- their association and modification status (complexes, phosphorylations, etc.)

Availability

The most up-to-date version of TRANSPATH® can be obtained either

- for downloading as textual flat files, to have the full content locally at your disposal;
- for online use of the familiar look-and-feel provided by a dedicated server;
- for online access through the geneXplain platform, making full use of the rich functionality of this unique toolbox, or
- any combination of these options.

Predrawn pathway maps

Many "canoncical" pathways have been manually composed and are provided as clickable maps for easy overview and access of the components.