Resource Summary Report

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TRANSPATH

RRID:SCR_005640
Type: Tool

Proper Citation

TRANSPATH (RRID:SCR_005640)

Resource Information

URL: http://www.gene-regulation.com/pub/databases.html#transpath

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Description: Database on eukaryotic transcription factors, their experimentally-proven binding sites, consensus binding sequences (positional weight matrices) and regulated genes. Its broad compilation of binding sites allows the derivation of positional weight matrices. It can either be used as an encyclopedia, for both specific and general information on signal transduction, or can serve as a network analyzer. Cross-references to important sequence and signature databases such as EMBL/GenBank UniProt/Swiss-Prot InterPro or Ensembl EntrezGene RefSeq are provided. The database is equipped with the tools for data visualization and analysis. It has three modules: the first one is the data, which have been manually extracted, mostly from the primary literature; the second is PathwayBuilder, which provides several different types of network visualization and hence facilitates understanding; the third is ArrayAnalyzer, which is particularly suited to gene expression array interpretation, and is able to identify key molecules within signalling networks (potential drug targets). These key molecules could be responsible for the coordinated regulation of downstream events. Manual data extraction focuses on direct reactions between signalling molecules and the experimental evidence for them, including species of genes/proteins used in individual experiments, experimental systems, materials and methods. This combination of materials and methods is used in TRANSPATH to assign a quality value to each experimentally proven reaction, which reflects the probability that this reaction would happen under physiological conditions. Another important feature in TRANSPATH is the inclusion of transcription factor-gene relations, which are transferred from TRANSFAC, a database focused on transcription regulation and transcription factors. Since interactions between molecules are mainly direct, this allows a complete and stepwise pathway reconstruction from ligands to regulated genes.

Abbreviations: TRANSPATH

Resource Type: data or information resource, service resource, data analysis service, analysis service resource, database, production service resource

Defining Citation: PMID:18629064, PMID:16381929, PMID:12519957, PMID:11724734

Keywords: signal transduction, network analyzer, transcriptional regulator, transcription factor, metabolic pathway, signaling pathway, protein-protein interaction, gene-regulatory pathway, signal transduction pathway, complex, signaling molecule, reaction, molecule, gene, pathway, gene expression

Funding: BMBF 031U210B;
BMBF 0313092;
European Union FP6 contract LSHG-CT-2004-503568;
European Union MRTN-CT-2004-512285

Availability: Free for academic use, Free for non-profit use, Account required

Resource Name: TRANSPATH

Resource ID: SCR_005640

Alternate IDs: nif-0000-03580

Old URLs: http://transpath.gbf.de, http://www.gene-regulation.com/pub/databases.html, http://www.biobase.de/pages/products/databases.html

Record Creation Time: 20220129T080231+0000

Record Last Update: 20250421T053512+0000

Ratings and Alerts

No rating or validation information has been found for TRANSPATH.

No alerts have been found for TRANSPATH.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Despotovic V, et al. (2024) Glioma subtype classification from histopathological images using in-domain and out-of-domain transfer learning: An experimental study. Heliyon, 10(5), e27515.

Wlochowitz D, et al. (2016) Computational Identification of Key Regulators in Two Different Colorectal Cancer Cell Lines. Frontiers in genetics, 7, 42.