The BRENDA Database

BRENDA has been advanced and is maintained by the Department of Bioinformatics and Biochemistry of the Technical University of Braunschweig, Germany. During the more than 25 years of its existence, it became the most comprehensive information repository on enzymes and enzyme ligand data available.

Applications

Popular applications of BRENDA are its use as encyclopedia of enzymes and their characteristics or its application as controlled vocabulary in the documentation of own research in the area of proteomics. Its content can also be used to train own algorithms or to mine the wealth of information of enzymes. However, if you apply BRENDA you will be surprised by the versatility of this valuable resource.

Further reading

Placzek, S. et al. (2017) BRENDA in 2017: : new perspectives and new tools in BRENDA. Nucleic Acids Res. 45:D380-D388.

Schomburg, I. et al. (2013) BRENDA in 2013: integrated reactions, kinetic data, enzyme function data, improved disease classification: new options and contents in BRENDA. Nucleic Acids Res. 41:764-772

Barthelmes, J. et al. (2007) BRENDA, AMENDA and FRENDA: the enzyme information system in 2007. Nucleic Acids Res. 35:D511-D514

BRENDA

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.
- 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

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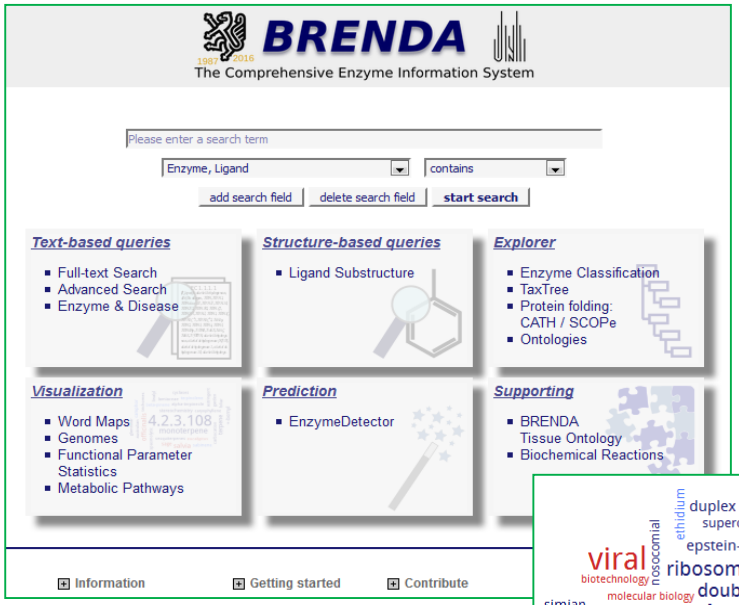
BRENDA

The Comprehensive Enzyme Information System

The Braunschweig Enzyme Database

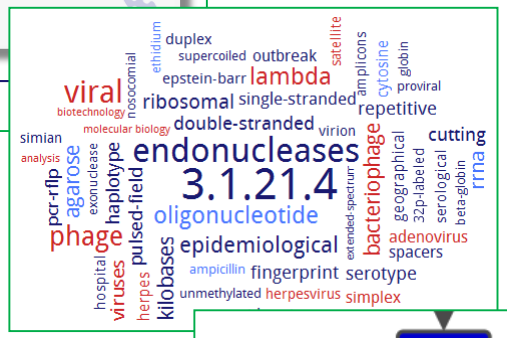
geneXplain

BRENDA®: the comprehensive enzyme information system



Key Features

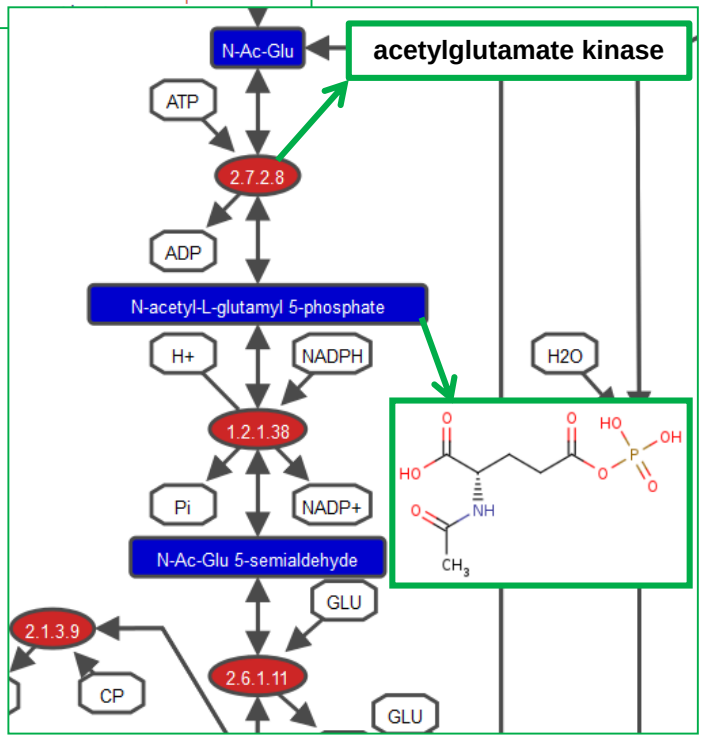
- BRENDA (BRaunschweig ENzyme DAtabase) was created in 1987 at the former German National Center of Biotechnology.
- It contains data relevant for molecular biology, biochemistry, medical research, and biotechnology.
- BRENDA comprises information on more than ➢**7 Mill. different enzymes** and ➢ **7,271 EC classes** classified by the Enzyme Nomenclature (IUBMB).
- Molecular data of more than 30,000 organisms from all kingdoms are stored.
- More than 3 Mill. enzyme data have been annotated manually from more than 136,877 primary literature references.
- Each entry is connected to the literature reference and the source organism.
- Major updates of the data in BRENDA are released twice a year.



Functionalities

BRENDA comes with:

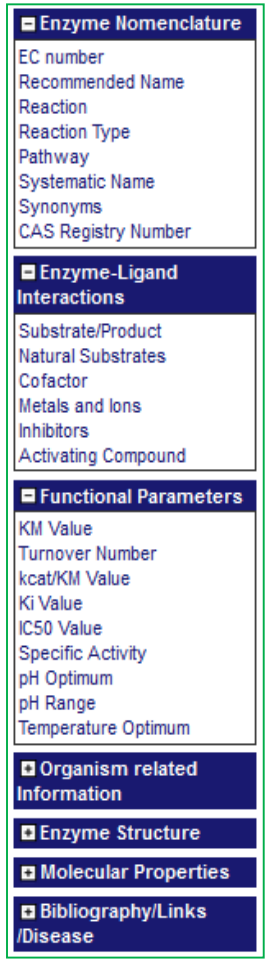
- ➢ Query interfaces for quick access and more specific queries such as search by chemical sub-structure.
- ➢ Word Maps for EC classes. The more frequently a word is specifically associated with an enzyme in a literature text, the more prominent it will be presented in the word map.
- ➢ BRENDA pathway maps. Over 280 pathways can be displayed. They show roughly 2000 enzyme-catalyzed reactions. All metabolites and cofactors are linked to the BRENDA data. Pathways can be selected for an individual organism or for a taxonomic group.
- ➢ Explorers for e.g. Enzyme Class and Taxonomic tree



In BRENDA the information is organized in *Enzyme Summery Pages* and (Metabolite/) *Ligand Summary Views*.

Enzyme-related data encompasses information on:

- Enzyme and ligand nomenclature
- Organism
- Reaction and specificity
- Kinetic properties
- Structure and role of the ligands
- Stability information
- Ligand-enzyme information
- Enzyme sequence and structure
- Mutants and disease
- Occurrence, isolation and properties



Data Sources

The core of BRENDA is created by data annotated manually from primary literature references.

The core is complemented by results from text mining approaches contained in the interconnected proprietary databases

- FRENDA: Enzyme name & organism
- AMENDA: Enzyme name & organism & occurrence
- DRENDA: Disease-related enzyme data
- KENDA: Kinetic data

Cross-linked external databases and ontologies like UniProt, KEGG, MetaCyc, EMBL, NCBI represent yet more sources of information.

UniProt KEGG EMBL PDB PROTEIN DATA BANK

Availability

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

- for downloading* to have the full content locally at your disposal,
- for online use of the familiar look-and-feel provided by a dedicated server, or
- a combination of these options.

*The download version is available for Linux and Windows.