The **Search** field offers free text search. The complete word (no fragments) inserted in this field will be searched in the entire database's content, including comments.

The auto completion function makes suggestions and indicates how many results (entries) are in the database for the distinct search terms. Queries can be modified by using the following syntax in the **Search** field:

<table>
<thead>
<tr>
<th>Search</th>
<th>Result</th>
</tr>
</thead>
<tbody>
<tr>
<td>rattus liver</td>
<td>entries containing both terms <em>rattus</em> and <em>liver</em></td>
</tr>
<tr>
<td>rattus AND liver</td>
<td></td>
</tr>
<tr>
<td>Search</td>
<td>Result</td>
</tr>
<tr>
<td>--------</td>
<td>--------</td>
</tr>
<tr>
<td>(rattus OR liver)</td>
<td>entries containing either the term rattus or liver</td>
</tr>
<tr>
<td>(rattus OR human) AND liver</td>
<td>entries containing the term liver and either rattus or human</td>
</tr>
<tr>
<td>&quot;homo sapiens&quot;</td>
<td>entries containing both terms homo and sapiens in the exact order</td>
</tr>
<tr>
<td>ratt*</td>
<td>wildcard search for more than one character</td>
</tr>
<tr>
<td>*kinase</td>
<td>entries containing terms starting with ratt (e.g. Rattus norvegicus) or ending with kinase (e.g. Hexokinase)</td>
</tr>
<tr>
<td>&quot;mammalia (NCBI)&quot; NOT &quot;homo sapiens&quot;</td>
<td>entries for all organisms of class mammalia (based on NCBI taxonomy) but not for homo sapiens</td>
</tr>
<tr>
<td>&quot;liver (BTO)&quot;</td>
<td>entries for tissue liver including all tissue sub-parts and cell lines (based on BRENDA Tissue Ontology)</td>
</tr>
<tr>
<td>Substrate:ATP</td>
<td>entries with reactions containing substrate ATP</td>
</tr>
<tr>
<td>Similar queries for specific attributes can be defined by using all other database attributes (see Advanced Search)</td>
<td></td>
</tr>
<tr>
<td>Substrate:ATP AND Substrate:Pyruvate</td>
<td>entries with reactions containing both ATP and Pyruvate as substrates</td>
</tr>
<tr>
<td>ECNumber:1.*</td>
<td>All entries containing EC numbers starting with 1.</td>
</tr>
<tr>
<td>ECNumber: 1.3.1.?</td>
<td>wildcard search for exactly one character</td>
</tr>
<tr>
<td>Entries containing EC numbers 1.3.1.1 to 1.3.1.9</td>
<td></td>
</tr>
<tr>
<td>Year:[2000 TO 2021]</td>
<td>entries with publication years between 1990 and 2012 (see also Advanced Search)</td>
</tr>
</tbody>
</table>

More specific queries can additionally be defined by the Advanced Search.

**Advanced Search**

To restrict search terms to specific attributes also the Advanced Search can be used. First an attribute from the list must be selected. Then while typing terms a selection list with suggestions will appear containing the number of database entries related to them. Select a term from the list and click the Add & Search button to start the search.
Wildcard search is not possible for the Advanced Search, the exact search term is needed.

Searches with different terms for the same attribute is possible using the OR boolean operator.

For the specific attributes Tissue and Organism an ontology-based search can be defined by selecting terms with additional information (BTO) or (NCBI). By selecting BTO terms the search will include all subclasses of this term based on the BRENDA Tissue Ontology (https://bioportal.bioontology.org/ontologies/BTO) By selecting NCBI terms the search will include all subclasses of this term based on the NCBI Organism Taxonomy (https://www.ncbi.nlm.nih.gov/taxonomy).

Time periods of publications in attribute Year can be defined:

<table>
<thead>
<tr>
<th>Condition</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>&gt;1990</td>
<td>entries with publication years from 1990 until today</td>
</tr>
<tr>
<td>&lt;1990</td>
<td>entries with publication years up to 1990</td>
</tr>
</tbody>
</table>
Filter Options

Queries can be specified additionally by setting different filters using the Filter Options box.

There are filters for the Enzyme (i.e., protein). By default all entries containing wildtype or mutant proteins are displayed. By disabling one of these criteria only Wildtype or only Mutant data will be displayed. Selecting Recombinant will restrict the search output to entries resulting from experiments conducted with recombinantly expressed proteins.

Selecting the Rate Equation filter will display only data entries with a kinetic rate equation. Accordingly, selecting the Transport Reaction filter will restrict the search result to transport reactions.

Environmental conditions (pH value, Temperature) can be specified by moving the slider buttons to select a range. Filtering by temperature and pH values will exclude all entries from search without definition of those values (value = null).

Additionally, the source of the data (Direct Submission, Publication, or BioModel (Model upload via SBML)) and the time of data insertion can be used to restrict the search.

Search Result

Entry View

The search result is represented by default in the Entry View, which is a table containing overview information of the database entries sorted by SABIO EntryID. The content of the table columns can be re-sorted by clicking on the column headers.

The number of entries per page can be varied.
Detailed information about kinetic data of a specific biochemical reaction determined in one experiment is given in the single database entries which can be displayed by clicking on the blue triangle to open an entry. Alternatively, all entries can be opened at once by selecting “expand all displayed entries”.

<table>
<thead>
<tr>
<th>Kinetic data</th>
<th>Reaction</th>
<th>Enzyme</th>
<th>Tissue</th>
<th>Organism</th>
<th>Parameter (besides concentration)</th>
<th>Cond.</th>
<th>pH</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATP + D-Fructose 6-phosphate → ADP + D-Fructose 1,6-biphosphate</td>
<td>2.7.1.1 Q4E657 wildtype Trypanosoma cruzi</td>
<td></td>
<td></td>
<td></td>
<td>Km, Vmax</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**General information**
- **Organism**: Trypanosoma cruzi
- **EC Number**: 2.7.1.1
- **SABIO reaction id**: 1111
- **Variant**: wildtype
- **Experiment Type**: in vitro

**Pathways**
- Carbon metabolism
- Glycolysis/gluconeogenesis
- Metabolic pathways
- Nitrogen metabolism
- Nucleotide metabolism
- diverse environments
- starch and sucrose metabolism

**Substrates**
- ATP
- D-Fructose 1,6-biphosphate

**Products**
- ADP
- D-Fructose 6-phosphate

**Modifications**
- **pH**: 7.5
- **Concentration**: 23.0

**Reference**
- Urina JA, Herrn Y, Mittaz AS
Furthermore SABIO-RK offers details about the Reaction, Organism, Enzyme, Protein, Pathway and Compound of an entry which are shown in additional pop-up windows after clicking on the appropriate term.

These Details are partially interlinked, and contain additionally links to external databases, e.g., clicking on the Reaction (in the Entry View or in the Reaction View) opens the Reaction Details containing the SABIO ReactionID, Stoichiometric Equation, Substrates, Products, Enzymes known to catalyse this reaction, Pathways and links to external databases.

Reaction Details pop-up window with links to other data resources.
Reaction View

In addition to the Entry View table there is the Reaction View table which groups the entries based on the biochemical reaction and shows the number of entries per reaction. In the Entry and in the Reaction View data can be exported in spreadsheet, SBML or BioPAX format. Entries can be selected either by clicking the checkbox at the end of each entry row in the overview table or by clicking the checkbox in the last column header to select all displayed entries per page (see also Data Export).

To get a quick impression about a certain reaction and to understand the connections between reaction, enzymes, organisms, and tissues a visualization is available.
Bar Chart Search

A visual overview of the frequency distribution of single attributes within a search result is given in the Bar Chart Search. Here the user can confine the search to one specific Organism, Tissue, Cellular location, EC number, Uniprot ID, Parameter type or Kinetic law type by clicking on the corresponding bar.
Visual Search

Visual search is a graphical interface that is customizable and allows interactive navigation of search results. The offered graphs consist of a heat map representing an Overview of the Entry Data, Parallel Coordinates (PC) of the Entry Data and Scatter Plot Matrix of the Entry Data with histograms (SPM). These entry based graphs contain all entry information except the kinetic parameter values of the Search result.

Since each entry can contain several kinetic parameters, the kinetic parameters are represented separately in the KPPC (Parallel Coordinates of the Kinetic Parameters)
and the KPSP (Scatter Plot of the Kinetic Parameter Values) graphs, which allow to explore through the kinetic data space.

By pressing the Help/Information button detailed explanation of all the functionalities in the Visual Search is shown in detail.
Data Export

To export data in SBML, spreadsheet or other formats entries can be selected either in the Entry View or Reaction View by clicking the checkbox at the end of each entry row in the overview table or by clicking the checkbox in the last column header to select all displayed entries per page.
The user can choose which entry information should be exported by selecting the columns to be exported.

As a default choice 8 items are selected (right column) which can easily be removed by clicking on the minus. To include additional columns in the export table the appropriate items on the left side should be included by clicking on the plus.

The order of the columns can easily be changed by shifting them up and down.

After finishing the selection and the order of the favoured columns, which are previewed for the first 3 entries, the Export xls or Export tsv button should be pressed to execute the export.
Write SBML allows to export the selected entries as a model in the Systems Biology Markup Language (SBML)-format or as pdf. Different SBML versions and annotation schema could be selected and a user-defined name could be given to the SBML file.
No Search Result

If the Search did not give any results, a link to a pre-filled request form is given.

User feedback can also be given via the Contact button or within Curation as Request for SABIO-RK curation service. Any feedback is highly appreciated.