Contribute to BRENDA! Your enzyme data is important for BRENDA. Send us your paper, and we will do all the work to include your data into our database. More...

**Text-based queries**
- Full-text Search
- Advanced Search
- Enzyme & Disease

**Structure-based queries**
- Ligand Structure Search
- Metabolic Pathways
- Enzyme Structures

**Explorer**
- Enzyme Classification
- TaxTree
- Protein folding: CATH / SCOPe
- Ontologies

**Visualization**
- Word Maps
- Genomes
- Functional Parameter Statistics
- Metabolic Pathways

**Prediction**
- Membrane Helices
- Localization Prediction
- EnzymeDetector

**Supporting & External**
- BRENDA Tissue Ontology
- Biochemical Reactions
- MetaboMAPS

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**News**

NEW Release online! - February 1, 2021
Release 2021.1 online including 76 new and 623 updated enzyme classes.

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**BRENDA Tutorial**

**EC Explorer**
The EC Explorer provides an easy access to the data of the IUBMB Enzyme Nomenclature list (www.enzyme-database.org/ExplorEnz) directly connected to BRENDA.
BRENDA is the most comprehensive information system on:

- 8149 EC Numbers (Feb. 2021)
- more than 2 Mill. different enzymes
- more than 3 Mill. enzyme data, manually annotated from more than 150,000 literature references

**Enzyme Commission numbers (EC Numbers) are defined according to the catalyzed reaction** by the IUBMB (International Union of Biochemistry and Molecular Biology)

Format: **Four** numbers separated by periods, e.g. 1.2.3.1

Numbers represent from left to right a progressively finer classification scheme

Main Enzyme Classes:
1. Oxidoreductases
2. Transferases
3. Hydrolases
4. Lyases
5. Isomerases
6. Ligases
7. Translocases

**EC 1.2.3.1** an aldehyde + H₂O + O₂ = a carboxylate + H₂O₂

- aldehyde oxidase
- with oxygen as acceptor
- acting on the aldehyde or oxo group of donors
- oxidoreductase (main class)
You can either browse or search the EC Explorer.
You can run a search by entering a complete EC number, or just the main class, the subclass etc....
...and include further search options, i.e. the history and EC subclasses...
On the result page you find a list of the EC numbers...

<table>
<thead>
<tr>
<th>EC number</th>
<th>Common name</th>
<th>Reaction</th>
<th>History</th>
</tr>
</thead>
<tbody>
<tr>
<td>2.5.1.1</td>
<td>dimethylallyltransf erase</td>
<td>dimethylallyl diphosphate + isopentenyl diphosphate = diphosphate + geranyl diphosphate</td>
<td>created 1961</td>
</tr>
<tr>
<td>2.5.1.2</td>
<td>thiamine pyridylase</td>
<td>thiamine + pyridine = 1-[(4-amino-2-methylpyrimidin-5-yl)methyl]pyridinium + 4-methyl-(2-hydroxyethyl)thiazole</td>
<td>created 1991; modified 1978, modified 2001</td>
</tr>
<tr>
<td>2.5.1.3</td>
<td>thiamine phosphate synthase</td>
<td>(1) 4-amino-2-methyl-5-(diphosphoethenyl)pyrimidine + 2-(2R,5Z)-2-carboxy-4-methylthiazol-5(2H)-ylideneethenyl phosphate = diphosphate + thiamine phosphate + CO₂; (2) 4-amino-2-methyl-5-(diphosphoethenyl)pyrimidine + 2-(2-carboxy-4-methylthiazol-5-yl)ethenyl phosphate = diphosphate + thiamine phosphate + CO₂; (3) 4-amino-2-methyl-5-(diphosphoethenyl)pyrimidine + 4-methyl-(2-hydroxyethyl)thiazole = diphosphate + thiamine phosphate</td>
<td>created 1965, modified 2015</td>
</tr>
<tr>
<td>2.5.1.4</td>
<td>adenosylmethionine synthase</td>
<td>S-adenosyl-L-methionine = S-methyl-5'-thioadenosine + 2-amino-6-butan-4-olide</td>
<td>created 1966</td>
</tr>
<tr>
<td>2.5.1.5</td>
<td>galactose-6-sulfatylase</td>
<td>Eliminates sulfate from the D-galactose 6-sulfate residues of porphyrin, producing 3,6-anhydrogalactose residues</td>
<td>created 1965</td>
</tr>
<tr>
<td>2.5.1.6</td>
<td>methionine adenosyltransferase</td>
<td>ATP + L-methionine + H₂O = phosphate + diphosphate + S-adenosyl-L-methionine</td>
<td>created 1961 as EC 2.4.2.13, transferred 1985 to EC 2.5.1.5</td>
</tr>
<tr>
<td>2.5.1.7</td>
<td>UDP-N-acetylgalactosamine-1-carboxyvinyltransferase</td>
<td>phosphoenolpyruvate + UDP-N-acetyl-α-D-glucosamine = phosphate + UDP-N-acetyl-3-O-(1-carboxyvinyl)-α-D-glucosamine</td>
<td>created 1972, modified 1993, modified 2002</td>
</tr>
</tbody>
</table>
According to the information of the IUBMB Enzyme list, including:

- **the Common Name**
  - dimethylallyl/transferase
  - thiamine pyridinylase
  - thiamine phosphate synthase
  - adenosylmethionine cyclotransferase
  - galactose-6-sulphurylase
  - methionine adenosyltransferase
  - UDP-N-acetylglucosamine 1-carboxymethyltransferase

- **the Reaction**
  - dimethylallyl diphosphate + isopentenyl diphosphate = diphosphate + geranyl diphosphate
  - thiamine + pyridine = 1-(4-amino-2-methylpyrimidin-5-yl) methyl]pyridinium + 4-methyl-5-(2-hydroxyethyl)thiazole
  - (1) 4-amino-2-methyl-5-(diphosphoxygen)pyridine + 2-(2R,5Z)-2-carboxy-4-methylthiazol-5(2H)-ylidenethyphosphate = diphosphate + thiamine phosphate + CO2, (2) 4-amino-2-methyl-5-(diphosphoxygen)pyridine + 2-(2-carboxy-4-methylthiazol-5(2H)-ylidenethyphosphate = diphosphate + thiamine phosphate + CO2: (3) 4-amino-2-methyl-5-(diphosphoxygen)pyridine + 4-methyl-5-(2-hydroxyethyl)thiazole = diphosphate + thiamine phosphate
  - S-adenosyl-L-methionine = S-methyl-5'-thioadenosine + 2-amino-6-hydroxy-4-olide
  - S-adenosyl-L-methionine = S-methyl-5'-thioadenosine + 2-amino-6-hydroxy-4-olide
  - ATP + L-methionine + H2O = phosphate + diphosphate + S-adenosyl-L-methionine
  - phosphoenolpyruvate + UDP-N-acetyl-α-D-glucosamine = phosphate + UDP-N-acetyl-α-D-glucosamine

- **the History**
  - [25.1.1]
  - dimethylallyl/transferase
  - [25.1.2]
  - thiamine pyridinylase
  - [25.1.3]
  - thiamine phosphate synthase
  - [25.1.4]
  - adenosylmethionine cyclotransferase
  - [25.1.5]
  - galactose-6-sulphurylase
  - [25.1.6]
  - methionine adenosyltransferase
  - [25.1.7]
  - UDP-N-acetylglucosamine 1-carboxymethyltransferase
  - [25.1.1]
  - dimethylallyl/transferase
  - [25.1.2]
  - thiamine pyridinylase
  - [25.1.3]
  - thiamine phosphate synthase
  - [25.1.4]
  - adenosylmethionine cyclotransferase
  - [25.1.5]
  - galactose-6-sulphurylase
  - [25.1.6]
  - methionine adenosyltransferase
  - [25.1.7]
  - UDP-N-acetylglucosamine 1-carboxymethyltransferase
The History column provides information on the creation, the modification, the transfer or the deletion of an enzyme.

<table>
<thead>
<tr>
<th>EC</th>
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<th>Created/Modified Dates</th>
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<td>thiamine + pyridine = 1-[(4-amino-2-methylpyrimidin-5-yl)methyl]pyridinium + 4-methyl-5-(2-hydroxyethyl)thiazole</td>
<td>created 1981, modified 2001</td>
</tr>
<tr>
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<td>thiamine phosphate synthase</td>
<td>(1) 4-amino-2-methyl-5-(diphosphoxygenyl)pyrimidine + 2-[(2R,5Z)-2-carboxy-4-methylthiazol-5(2H)-yidene]ethyl phosphate = diphosphate + thiamine phosphate + CO₂;(2) 4-amino-2-methyl-5-(diphosphoxygenyl)pyrimidine + 2-(2-carboxy-4-methylthiazol-5-yl)ethyl phosphate = diphosphate + thiamine phosphate + CO₂;(3) 4-amino-2-methyl-5-(diphosphoxygenyl)pyrimidine + 4-methyl-5-(2-phosphoxygenyl)thiazole = diphosphate + thiamine phosphate</td>
<td>created 1985, modified 2015</td>
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<td>created 1972, deleted 2009</td>
</tr>
<tr>
<td>2.5.1.8</td>
<td>tRNA isopentenyltransferase</td>
<td>isopentenyl diphosphate + tRNA = diphosphate + tRNA containing 6-isopentenyladenosine</td>
<td></td>
</tr>
<tr>
<td>2.5.1.9</td>
<td>riboflavin synthase</td>
<td>2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypteridine</td>
<td></td>
</tr>
<tr>
<td>2.5.1.10</td>
<td>(2E,6E)-farnesyl diphosphate synthase</td>
<td>geranyl diphosphate + isopentenyl diphosphate = diphosphate + (2E,6E)-farnesyl diphosphate</td>
<td></td>
</tr>
</tbody>
</table>
To see more details of a specific enzyme click on the EC number to go to the…
Information on EC 2.5.1.2 - thiamine pyridinylase

for references in articles please use BRENDA:EC2.5.1.2

EC Tree
L 2 Transferases
L 2.5 Transferring alkyl or aryl groups, other than methyl groups
L 2.5.1 Transferring alkyl or aryl groups, other than methyl groups (only substrates identified to date)
L 2.5.1.2 thiamine pyridinylase

IUBMB Comments
Various bases and thiol compounds can act instead of pyridine.

Specify your search results

Mark a special word or phrase in this record:  
Search Reference ID:
Search Uniprot Accession:
Select one or more organisms in this record:

Submit

Show additional data

Do not include text mining results
Include AMENDA (text mining) results
Include BRENDA results (AMENDA + additional results, but less precise)

The expected taxonomic range for this enzyme is: Eukaryota, Bacteria

Word Map

thiaminolyticus
viscera
thiazole
pseudoaerengus
aminine
medicine

Reaction Schemes

thiamine + pyridine = 1-[(4-amino-2-methylpyrimidin-5-yl)methyl]pyridinium + 4-methyl-5-(2-hydroxyethyl)thiazole
You can switch to the EC Tree view by clicking on the icon „Show in EC Tree“.
On this page you see the classification of the enzyme within the EC Tree...
including further information of the number of organisms, the reaction diagram, and the possibility to download known protein sequences in FASTA format or as csv-file, and published PDB-IDs
In the left box you find the complete IUBMB entry of the marked EC Number.

Click on the link to go directly to the BRENDA enzyme summary page.
Starting with the 7 main classes you can navigate along the EC tree through the subclasses, sub-subclasses, and the serial numbers.

You can use the „browse“ function to look for enzymes.
The EC browser with information on the main classes.

All enzymes that catalyse oxido-reductions belong in this class. The substrate oxidized is regarded as a hydrogen or electron donor. The classification is based on donor:acceptor oxidoreductase. The common name is dehydrogenase, wherever this is possible; as an alternative, acceptor reductase can be used. Oxidase is used only where O2 is an acceptor. Classification is difficult in some cases, because of the lack of specificity towards the acceptor.
Click on the (+)-icon to expand a section or on the (-)-icon to collapse a section.
If you find an appropriate EC number click on the entry to open the left box containing the detailed IUBMB information...
...and again the direct link will lead you to the BRENDA enzyme summary page.