

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...](#)

Please enter a search term

Enzyme, Ligand
contains

add search field
delete search field
start search

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

# BRENDa Tutorial

- Search for protein sequences
- Localization prediction
- Search in Genomes
- 3D structures
- Functional parameters

evaluate BRENDa!

Informa

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- Full-text Search
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- Ligand Structure Search
- Metabolic Pathways
- Enzyme Structures



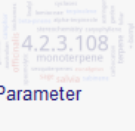
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News

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



evaluate BRENDA!

Information

## There are several options for protein sequence searches:

- Quick Search
- Enzyme Summary Page
- Classic View

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NBI

elixir  
Core Data  
Resource

UPDATE!  
Release 2021.1 (January 2021)  
BRENDA professional

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## Quick Search

Please enter a search term

Enzyme, Ligand

[add search field](#) [delete search field](#) [start search](#)

If you search for sequences using an enzyme name, e.g. of the alcohol dehydrogenase, use the quick search

### Text-based queries

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- Advanced Search
- Enzyme & Disease

### Structure-based queries

- Ligand Structure Search
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[Information](#)

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**elixir**  
Core Data Resource

**UPDATE!**  
Release 2021.1 (January 2021)  
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☐ Refine search

Quick Search

Field	Hits found
Enzyme Names (Synonyms)	<a href="#">44</a>
Ligands	<a href="#">6</a>

Chose „Enzyme Names“  
to continue

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UPDATE!



## Quick Search






























### Search Enzyme Names (Synonyms)

Search term: alcohol dehydrogenase

☐ Refine search

&lt;&lt; Results 1 - 10 of 44 &gt;&gt;

 download as CSV  
 download all results as CSV

EC Number ▼▲	Recommended Name ▼▲	Synonyms ▼▲	Commentary ▼▲
    1.1.1.1	alcohol dehydrogenase	(R)-specific alcohol dehydrogenase, acetaldehyde-alcohol dehydrogenase, alcohol dehydrogenase, alcohol dehydrogenase (NAD), alcohol dehydrogenase 1, alcohol dehydrogenase 10, alcohol dehydrogenase 2, alcohol dehydrogenase 3, alcohol dehydrogenase D, alcohol dehydrogenase GroES domain protein, alcohol dehydrogenase I, alcohol dehydrogenase II, Alcohol dehydrogenase-B2, aldehyde/alcohol dehydrogenase, aliphatic alcohol dehydrogenase, bifunctional acetaldehyde-alcohol dehydrogenase, class III alcohol dehydrogenase, Gastric alcohol dehydrogenase, iron-containing alcohol dehydrogenase, long-chain alkyl alcohol dehydrogenase, medium chain alcohol dehydrogenase, medium-chain secondary alcohol dehydrogenase, NAD(H)-dependent alcohol dehydrogenase, NAD+-dependent (S)-stereospecific alcohol dehydrogenase, NAD+-dependent alcohol dehydrogenase, NAD+-linked alcohol dehydrogenase 1, NAD-dependent alcohol dehydrogenase, NAD-specific aromatic alcohol dehydrogenase, NADH-alcohol dehydrogenase, NADH-dependent alcohol dehydrogenase, primary alcohol dehydrogenase, yeast alcohol dehydrogenase	-
   1.1.1.105	all-trans-retinol dehydrogenase (NAD+)	alcohol dehydrogenase	-
  1.1.1.144	perillyl-alcohol dehydrogenase	perillyl alcohol dehydrogenase, perillyl-alcohol dehydrogenase	-
   1.1.1.192	long-chain-alcohol dehydrogenase	long-chain alcohol dehydrogenase, long-chain alkyl alcohol dehydrogenase, long-chain-alcohol dehydrogenase	-
   1.1.1.194	coniferyl-alcohol dehydrogenase	coniferyl alcohol dehydrogenase, coniferyl-alcohol dehydrogenase	-
   1.1.1.195	cinnamyl-alcohol dehydrogenase	alcohol dehydrogenase, cinnamyl alcohol dehydrogenase, cinnamyl alcohol dehydrogenase 1, cinnamyl alcohol dehydrogenase 12, cinnamyl alcohol dehydrogenase 2, cinnamyl alcohol dehydrogenase 3, cinnamyl alcohol dehydrogenase 4, cinnamyl alcohol dehydrogenase 5, cinnamyl alcohol dehydrogenase 7, cinnamyl alcohol dehydrogenase 9, cinnamyl alcohol dehydrogenase C, cinnamyl alcohol dehydrogenases, cinnamyl-alcohol dehydrogenase	-
   1.1.1.2	alcohol dehydrogenase (NADP+)	alcohol dehydrogenase (NADP+), alcohol dehydrogenase C, alcohol dehydrogenase [NADP(+)], Alcohol dehydrogenase [NADP+], liver alcohol dehydrogenase, NADP(H)-dependent alcohol dehydrogenase, NADP-alcohol dehydrogenase, NADP-linked aryl alcohol dehydrogenase, putative iron alcohol dehydrogenase, short-chain alcohol dehydrogenase, yeast alcohol dehydrogenase	-
   1.1.1.244	methanol dehydrogenase	group III NAD-dependent alcohol dehydrogenase	-
   1.1.1.245	cyclohexanol dehydrogenase	alcohol dehydrogenase	-
  1.1.1.257	4-(hydroxymethyl)benzenesulfonate dehydrogenase	sulfobenzyl alcohol dehydrogenase	-

Click on this icon to display all sequences assigned to the EC number...

Amino acid sequence search

Amino acid Sequence:
contains

No. of results:
10

Recommended name:  
(of enzyme)
contains

EC Number:
exact
1.1.1.1

1st Accession Code:  
(UniProt)
contains

Organism:
contains

Number of amino acids:
=

Molecular weight [Da]:
=

Transmembrane helices:
=

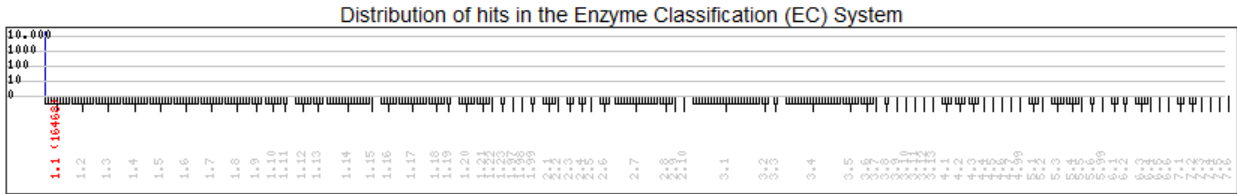
N-terminus:
☐ inside
☐ outside

Source:
☐ SwissProt
☐ TrEMBL

















search
reset

Here, you can perform a search using

- a part of an amino acid sequence
- the enzyme name
- the EC number
- the UniProt accession code
- the organism
- the number of amino acids
- the molecular weight
- the number of transmembrane helices



Results 1 - 10 of 16468

EC Number ▲▼	Recommended Name ▲▼ Organism ▲▼	UNIPROT ▲▼	No of trans. helices ▲▼ No of amino acids ▲▼	MW [Da]▲▼	Source ▲▼	Tools/Links
1.1.1.1	alcohol dehydrogenase <i>Mycobacterium tuberculosis</i> (strain CDC 1551 / Oshkosh)	P9WQC0	0 trans. helices 346 amino acids	36632	Swiss-Prot	   
1.1.1.1	alcohol dehydrogenase <i>Mycobacterium tuberculosis</i> (strain ATCC 25618 / H37Rv)	P9WQC1	0 trans. helices 346 amino acids	36632	Swiss-Prot	   
1.1.1.1	alcohol dehydrogenase <i>Rhizobium meliloti</i> (strain 1021)	O31186	0 trans. helices 340 amino acids	36235	Swiss-Prot	   
1.1.1.1	alcohol dehydrogenase <i>Mycobacterium bovis</i> (strain ATCC BAA-935 / AF2122/97)	Q7U1B9	0 trans. helices 375 amino acids	39748	Swiss-Prot	   

Amino acid sequence search

On the result page you find...

Amino acid Sequence:
contains

No. of results:
10

Recommended name:
contains

EC Number:
exact
1.1.1.1

1st Accession Code:
contains

Organism:
contains

Number of amino acids:
=

Molecular weight [Da]:
=

Transmembrane helices:
=

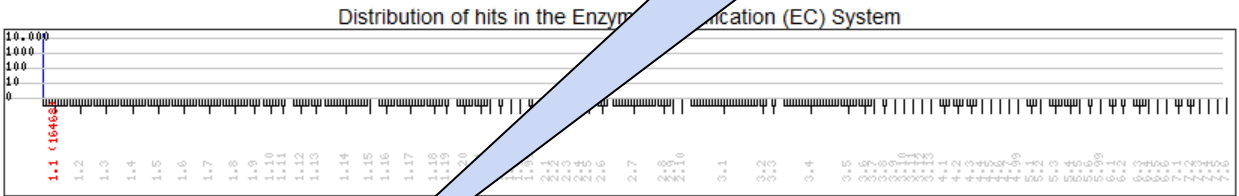
N-terminus:
☐ inside
☐ outside

Source:
☐ SwissProt
☐ TrEMBL

















search

reset

the organism,  
directly linked  
to the TaxTree



Results 1 - 10 of 16468

EC Number	Recommended Name Organism	UNIPROT	No of trans. helices No of amino acids	MW [Da]	Source	Tools/Links
1.1.1.1	alcohol dehydrogenase <i>Mycobacterium tuberculosis</i> (strain CDC 1551 / Oshkosh)	P9WQC0	0 trans. helices 346 amino acids	36632	Swiss-Prot	   
1.1.1.1	alcohol dehydrogenase <i>Mycobacterium tuberculosis</i> (strain ATCC 25618 / H37Rv)	P9WQC1	0 trans. helices 346 amino acids	36632	Swiss-Prot	   
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## Amino acid sequence search

On the result page you find...

 Amino acid Sequence: 

 No. of results: 

 Recommended name: 

 EC Number:  

 1st Accession Code: 

 Organism: 

 Number of amino acids: 

 Molecular weight [Da]: 

 Transmembrane helices: 

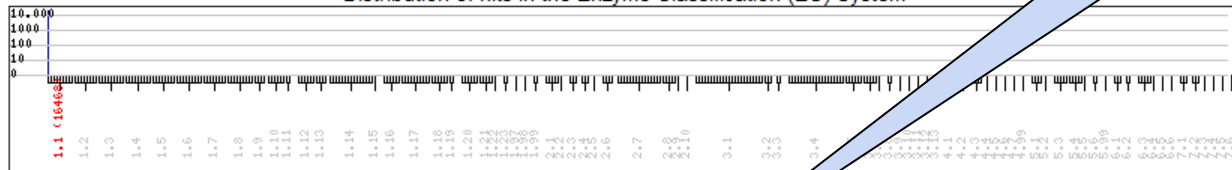
 N-terminus: ☐ inside ☐ outside

 Source: ☐ SwissProt ☐ TrEMBL



















Click on the  
UniProt-ID to  
display ...

Distribution of hits in the Enzyme Classification (EC) System



Results 1 - 10 of 16468

EC Number ▲▼	Recommended Name ▲▼ Organism ▲▼	UNIPROT ▲▼	No. of trans. helices ▲▼ No of amino acids ▲▼	MW [Da]▲▼	Source ▲▼	Tools/Links
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# Sequence of ADHA\_MYCTO

EC Number	Recommended Name	Accession Code	Organism	No of amino acids	Molecular Weight [Da]	Source
1.1.1.1	alcohol dehydrogenas	P9WQC0	Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh)	346	36632	Swiss-Prot

Reaction

a primary alcohol + NAD+ = an aldehyde + NADH + H+

Sequences with same EC No.

Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) (P9WQC0) [Show Sequence](#)

Sequence

show sequence in fasta format
Highlight sequence feature

0 MVSPATTATM SAWQVRPGP MDTGPLERVT TRVPRPAPSE LLVAVHACGV CRTDLHVTEG  
60 DLPVHRERVI PGHEVVGEVI EVGSAVGAAA GGEFDRGDRV GIAWLRHTCG VCKYCRRGSE  
120 NLCPQSRYTG WDADGGYAEF TTVPAAPFAHH LPSGYSDEL APLLCAGIIG YRSLLRTELP  
180 PGGRLGLYGF GGSAHITAQV ALAQGAIEHV MTRGARARKL ALQLGAASAQ DAADRPVPL  
240 DAAILFAPVG DLVLPALAL DRGGILAIAG IHLTDIPDLN YQQLHFERQ IRSVTSNTRA  
300 DARAFEDFAA OHHEVTTP EYPLQADRAL GDLSAGRIAG AAVLLI

...the complete sequence,  
links, download options, and  
detailed enzyme information

Download this sequence

FASTA in fasta format

Download all sequences for 1.1.1.1

FASTA in fasta format

CSV in csv (Excel, OpenOffice) format

Sequence Reference	Authors	Title	Journal	Volume	Pages	Year	PubMed ID
2715	Fleischmann R.D.,Alland D.,Eisen J.A.,Carpenter L.,White O.,Peterson J.D.,DeBoy R.T.,Dodson R.J.,Gwinn M.L.,Haft D.H.,Hickey E.K.,Kolonay J.F.,Nelson W.C.,Umayam L.A.,Ermolaeva M.D.,Salzberg S.L.,Delcher A.,Utterback T.R.,Weidman J.F.,Khoury H.M.,Gill J.,Mikula A.,Bishai W.,Jacobs W.R. Jr.,Venter J.C.,Fraser C.M.	Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.	J. Bacteriol.	184	5479-5490	2002	12218036

Amino acid sequence search

On the result page you find...

Amino acid Sequence:

contains

No. of results:

10

Recommended name:

contains

EC Number:

exact

1.1.1.1

1st Accession Code:

contains

Organism:

con

Number of amino acids:

=

Molecular weight [Da]:

=

Transmembrane helices:

=

N-terminus:

☐ inside ☐ outside

Source:

☐ SwissProt ☐ TrEMBL

search

reset

....an option to perform a BLAST search

....an option to perform a BRENDA localization prediction (more details on the next slide)

....an option to run a *tmhmm* for the prediction of transmembrane helices

Enzyme Classification (EC) System

EC Number	Organism	Accession	Transmembrane helices	Source
1.1.1.1	alcohol dehydrogenase <i>Mycobacterium tuberculosis</i> (strain CDC 1551 / Oshkosh)	P9WQC0	0 trans. helices	Swiss-Prot
1.1.1.1	alcohol dehydrogenase <i>Mycobacterium tuberculosis</i> (strain ATCC 25618 / H37Rv)	P9WQC1	375 amino acids	Prot
1.1.1.1	alcohol dehydrogenase <i>Rhizobium meliloti</i> (strain 1021)	O31186		Prot
1.1.1.1	alcohol dehydrogenase <i>Mycobacterium bovis</i> (strain ATCC BAA-935 / AF2122/97)	Q7U1B9		Prot

Tools/Links

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The „localization prediction“ enables the user to predict the occurrence of an enzyme in organelles

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Release 2021.1 (January 2021)  
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Localization Prediction for Eukaryotes - TargetP-1.1

1st Accession Code:  
(UniProt)

exact

Localization:

☐ Chloroplast

☐ Mitochondrion

☐ Secretory Pathway

☐ other Location

Reliability Class:  
(1 is best)

☐ 1

☐ 2

☐ 3

☐ 4

☐ 5

☒

EC Number:

contains

Recommended name:  
(of enzyme)

contains

Organism:

contains

Number of amino acids:

=

Source:

☒ Swiss-Prot

☒ TrEMBL

No. of results:

10

search

reset

Here you find the search options for the localization prediction

The N-terminal signal peptide sequence is used to predict the localization of the enzyme in chloroplasts, mitochondria, or in the secretory pathways (ER, Golgi)

Localization Prediction for Eukaryotes - TargetP-1.1

1st Accession Code:  
(UniProt)

exact

Localization:

☐ Chloroplast

☐ Mitochondrion

☐ Secretory Pathway

☐ other Location

Reliability Class:

(1 is best)

☐ 1

☐ 2

☐ 3

☐ 4

☐ 5

EC Number:

contains

4.1.1.39

Recommended name:  
(of enzyme)

contains

Organism:

contains

Number of amino acids:

=

Source:

☒ Swiss-Prot

☒ TrEMBL

No. of results:

10

search

reset

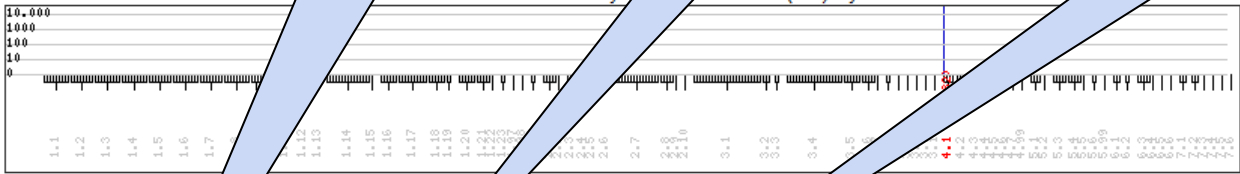
If you search for a specific EC number, you find the predicted information on...

the UniProt-ID

the organisms

the localization

Distribution of hits in the Enzyme Classification (EC) System



Results 1 - 10

46282 (Mitochondrion: 71, Chloroplast: 1262, Secretory Pathway: 608, other Location: 142921)

EC Number	Recommended Name	UNIPROT	Localization	Reliability Class	No of amino acids	Source	Links
4.1.1.39	ribulose-bisphosphate carboxylase <i>Picea sitchensis</i>	A9NXP2	Chloroplast	1	188 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>
4.1.1.39	ribulose-bisphosphate carboxylase <i>Oryza meridionalis</i>	A0A0E0FBG0	Chloroplast	2	175 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>
4.1.1.39	ribulose-bisphosphate carboxylase <i>Brassica cretica</i>	A0A3N6QAI0	Chloroplast	3	188 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>
4.1.1.39	ribulose-bisphosphate carboxylase <i>Arabidopsis suecica</i>	A0A075M996	Chloroplast	3	163 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>
4.1.1.39	ribulose-bisphosphate carboxylase <i>Prunus dulcis</i>	A0A4Y1QRQ3	Chloroplast	1	184 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>
4.1.1.39	ribulose-bisphosphate carboxylase <i>Zostera marina</i>	A0A0K9NJB1	Chloroplast	1	182 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>

## Localization Prediction for Eukaryotes - TargetP-1.1

 1st Accession Code:  

 Localization: ☐ Chloroplast ☐ Mitochondrion  
☐ Secretory Pathway ☐ other Location ☒

 Reliability Class: ☐ 1 ☐ 2 ☐ 3 ☐ 4 ☐ 5 ☒  
 (1 is best)

 EC Number:  

 Recommended name:  

 Organism:  

 Number of amino acids:  

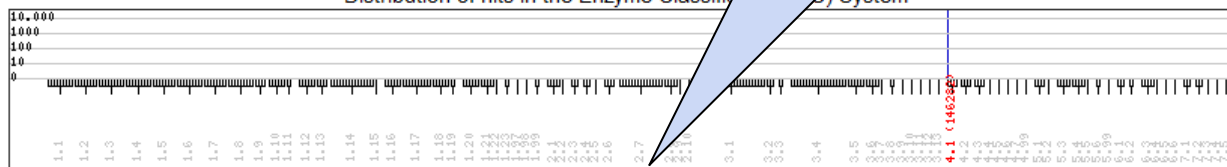
 Source: ☒ Swiss-Prot ☒ TrEMBL

 No. of results: 
 

If you search for a specific EC number, you find..

...an overview of the number of all the predicted localizations

Distribution of hits in the Enzyme Classification (EC) System



Results 1 - 10 of 146282 (Mitochondrion: 1491, Chloroplast: 1262, Secretory Pathway: 608, other Location: 142921) » »

EC Number ▲▼	Recommended Name ▲▼ Organism ▲▼	UNIPROT ▲▼	Localization ▲▼	Reliability Class ▲▼	No of amino acids ▲▼	Source ▲▼	Links
4.1.1.39	ribulose-bisphosphate carboxylase <i>Picea sitchensis</i>	A9NXP2	Chloroplast	1	188 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>
4.1.1.39	ribulose-bisphosphate carboxylase <i>Oryza meridionalis</i>	A0A0E0FBG0	Chloroplast	2	175 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>
4.1.1.39	ribulose-bisphosphate carboxylase <i>Brassica cretica</i>	A0A3N6QAI0	Chloroplast	3	188 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>
4.1.1.39	ribulose-bisphosphate carboxylase <i>Arabidopsis suecica</i>	A0A075M996	Chloroplast	3	163 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>
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4.1.1.39	ribulose-bisphosphate carboxylase <i>Zostera marina</i>	A0A0K9NJB1	Chloroplast	1	182 amino acids	TrEMBL	<a href="#">Check for transm. helices</a>

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Please enter a search term

- UniProt Accession Code
- Posttranslational Modification
- Product
- Purification (Commentary)
- Reaction
- Reaction Type
- Recommended Name
- Reference
- Renatured (Commentary)
- Specific Activity [micromol/min/mg]
- Storage Stability
- Substrate
- Substrates and Products (Substrate)
- Subunits
- Synonyms
- Systematic Name
- Temperature Optimum [°C]
- Temperature Range [°C]
- Temperature Stability [°C]
- Turnover Number [1/s]
- UniProt Accession Code

If you know the UniProt-ID and you would like to get the correlated BRENDA enzyme information, perform a quick search.

### Text-based queries

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**Search term: Q9SC80**

☐ Advanced Search

 download as CSV  
 download all results as CSV







EC Number ▼▲	Recommended Name ▼▲	Accession Code ▼▲
   2.5.1.46	deoxyhypusine synthase	Q9SC80

 [download as CSV](#)

The screenshot shows the BRENDA database interface. At the top, there's a navigation bar with 'HOME', 'Classic view', and a search bar. The main header features the BRENDA logo and the tagline 'The Comprehensive Enzyme Information System'. Below this, the 'Amino acid sequence search' form is displayed. The form includes several input fields and dropdown menus: 'Amino acid Sequence' (set to 'contains'), 'No. of results' (set to '10'), 'Recommended name' (set to 'contains'), 'EC Number' (set to 'exact' with the value '2.5.1.46'), '1st Accession Code' (set to 'contains'), 'Organism' (set to 'contains'), 'Number of amino acids' (set to '='), 'Molecular weight [Da]' (set to '='), and 'Transmembrane helices' (set to '='). There are also checkboxes for 'N-terminus' (inside/outside) and 'Source' (SwissProt/TREMBL). A 'search' button is at the bottom. A blue callout box with a pointer to the search form contains the text: 'display all known sequences via the sequence search form...'.

**display all known  
sequences via the  
sequence search  
form...**



EC Number ▲▼	Recommended Name ▲▼ Organism ▲▼	UNIPROT ▲▼	No of trans. helices No of amino acids ▲▼	MW [Da] ▲▼	Source ▲▼	Tools/Links
2.5.1.46	desoxyhypusine synthase <i>Arabidopsis thaliana</i>	Q9FI94	0 trans. helices 368 amino acids	41064	Swiss-Prot	  
2.5.1.46	desoxyhypusine synthase	Q7SEW4	0 trans. helices	41984	Swiss-Prot	  

## Information on EC 2.5.1.46 - deoxyhypusine synthase

for references in articles please use BRENDA:EC2.5.1.46

EC Tree

### 3 L 2 Transferase:

### 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 sub-subclass identified to date)
  - L 2.5.1.46 deoxyhypusine synthase

100%

**...or go to Enzyme Summary Page**  
(cf. BRENDA tutorial Enzyme Search)

Search UniProt Accession:

Select one or more organisms in this record:

**Al orbivirus**

Adeno-associated virus  
Anabaena  
animal  
Anopheles stephensi

Show additional data

☒ Do not include text mining results

☐ Include AMENDA (text mining) results

☐ Include **AMENDA** results (AMENDA + additional results, but less precise)

**cartilage** in osteoarthritis neoptope  
hypusine-containing n1-guanyl-1,7-diaminoheptane  
versican metalloproteinase  
aggranalysin  
**disintegrin** 2.5.1.46  
mefis-4 thrombospondin  
brevicain aggrecanase-1  
aminobutylation aggrecan  
pyrrolizidine homoserpermidine  
eif-5a polyamine  
adamts-5  
aggrecan 1.7-diaminoheptane



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

## Sequence/Protein-specific searches using the „Classic View“

### Text-based queries

- Full-text Search
- Advanced Search
- Enzyme & Disease



### Structure-based queries

- Ligand Structure Search
- Metabolic Pathways
- Enzyme Structures



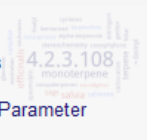
### Explorer

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



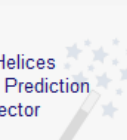
### Visualization

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



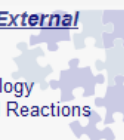
### Prediction

- Membrane Helices
- Localization Prediction
- EnzymeDetector



### Supporting & External

- BRENDA Tissue Ontology
- Biochemical Reactions
- MetaboMAPS



### News

**NEW Release online!** - February 1, 2021

Release 2021.1 online including 76 new and 623 updated enzyme classes.



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EC-Number	Enzyme Name	Organism	Protein	Full text	Ligand	Advanced Search
<div><input type="text"/></div> <div><div>Search</div><div>Display</div><div>10</div><div>▼</div><div>entries</div></div>						
Nomenclature		Reaction & Specificity			Functional Parameters	
<ul style="list-style-type: none"><li>Enzyme Names</li><li>EC Number</li></ul>		<ul style="list-style-type: none"><li>Pathway</li><li>Catalysed Reaction</li><li>Reaction Type</li><li>Natural Substrates &amp; Products</li><li>Substrates &amp; Products</li><li>Inhibitors</li><li>Cofactors</li><li>Metals/Ions</li><li>Activating Compounds</li><li>Ligands</li></ul>			<ul style="list-style-type: none"><li>K<sub>M</sub> Value</li><li>k<sub>cat</sub>/K<sub>M</sub> Value</li><li>K<sub>i</sub> Value</li><li>IC<sub>50</sub> Value</li><li>pI Value</li><li>Turnover Number</li><li>Specific Activity</li><li>pH Optimum</li><li>pH Range</li><li>Temperature Optimum</li><li>Temperature Range</li><li>Kinetic <b>ENzyme DATA</b></li></ul>	
Organism-related information						
<ul style="list-style-type: none"><li>Organism</li><li>Source Tissue</li><li>Localization</li></ul>						
Isolation& Preparation						
<ul style="list-style-type: none"><li>Purification</li><li>Cloned</li><li>Expression</li><li>Renatured</li><li>Crystallization</li></ul>		<ul style="list-style-type: none"><li>Biochemical Reactions</li></ul>				
Stability		Enzyme Structure			Disease, Protein Variants & Application	
<ul style="list-style-type: none"><li>pH Stability</li><li>Temperature Stability</li><li>General Stability</li><li>Organic Solvent Stability</li><li>Oxidation Stability</li><li>Storage Stability</li></ul>		<ul style="list-style-type: none"><li>Sequence</li><li>3D-Structure</li><li>Molecular Weight</li><li>Subunits</li><li>Posttranslational Modification</li><li>Protein-Specific Search</li></ul>			<ul style="list-style-type: none"><li>Disease/ Diagnostics</li><li>Protein Variants</li><li>Application</li></ul>	
		References				
		<ul style="list-style-type: none"><li>References</li></ul>				

Search UniProt Accession

UniProt Accession:
contains
show 10 results

Refine your search

Recommended Name:
EC Number:
UniProt:
Organism:
search

You can perform searches entering:

- the UniProt-ID
- the Enzyme Name
- the EC Number
- the Organism

- ☒ Accession Number or Sequence ID from SwissProt or TrEMBL
- ☒ Please note the following possibilities for searching Accession Numbers:
1. always use 'contains' if you search a part of an accession number  
2. use '.' to choose exact one but any accession number, e.g. 'D\_D' finds 'D5D' and 'D6D' etc.  
    a. If this search string should be a part of the accession number write "D\_D".  
    b. If this should be the beginning of a sequence write "D\_D".  
    c. If this should be the end of a sequence write "D\_D".  
3. use '\*' to choose none or any desired number of accession numbers

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On the result page...

## Search UniProt Accession

UniProt Accession:  contains show  results

Refine your search

Recommended Name: ☒

EC Number:

UniProt: ☒

Organism:

Search



Click on the EC number ...

Search term: **Q9SC80**

Results 1 - 1 of 1 >>>

download as CSV

download all results as CSV

EC Number ▼▲	Recommended Name ▼▲	UniProt ▼▲	Organism ▼▲
  2.5.1.46	deoxyhypusine synthase	Q9SC80	Nicotiana tabacum

<<< Results 1 - 1 of 1 >>>

download as CSV

download all results as CSV

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<input checked="" type="checkbox"/> Enzyme Nomenclature	15
<input checked="" type="checkbox"/> Enzyme-Ligand Interactions	7
<input type="checkbox"/> Diseases	0
<input checked="" type="checkbox"/> Functional Parameters	3
<input checked="" type="checkbox"/> Organism related Information	10
<input type="checkbox"/> General Information	0
<input checked="" type="checkbox"/> Enzyme Structure	3
<input checked="" type="checkbox"/> Molecular Properties	1
<input type="checkbox"/> Applications	0
<input checked="" type="checkbox"/> References	2
<input checked="" type="checkbox"/> External Links	

# Information on EC 2.5.1.46 - deoxyhypusine synthase and Organism(s) *Nicotiana tabacum*

for references in articles please use BRENDA:EC2.5.1.46

## EC Tree

- 2 Transferases
  - 2.5 Transferring alkyl or aryl groups, other than methyl groups
    - 2.5.1 Transferring alkyl or aryl groups, other than methyl groups (only sub-subclass identified to date)
      - 2.5.1.46 deoxyhypusine synthase

## IUBMB Comments

The eukaryotic initiation factor eIF5A contains a hypusine residue that is essential for the function of the eIF5A precursor. The reaction occurs in two steps: 1) formation of a Schiff base intermediate by transfer of the 4-aminobutyridene group from dehydroepiandrosterone to the epsilon-amino group of the same 4-aminobutyridene group from the enzyme intermediate to the epsilon-amino group of the deoxyhypusine residue (1d). Hence the overall reaction is transfer of a 4-aminobutyl group. For the plant enzyme, homospermidine can substitute for spermidine and putrescine can substitute for the lysine residue of the eIF5A precursor. Hypusine is formed from deoxyhypusine by the action of EC 1.14.99.29, deoxyhypusine monooxygenase.

...to display the protein-specific Enzyme Summary Page

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: ☐

Leishmania donovani MHOM/IN/1983/AG83

Mus musculus

Mus musculus C57/BL6J

Neurospora crassa

**Nicotiana tabacum**

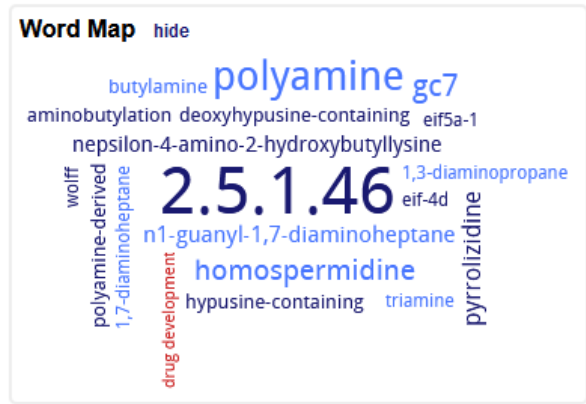
This record set is specific for:  
***Nicotiana tabacum***

Show additional data

☒ Do not include text mining results

☐ Include **AMENDA** (text mining) results

☐ Include **FRENDA** results (AMENDA + additional results, but less precise)



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...](#)

Please enter a search term

Enzyme, Ligand

contains

add search field delete search field start search

Text-based queries

- Full-text Search
- Advanced Search
- Enzyme & Disease

Structure-based queries

- Ligand Structure Search
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for Release 2021.1

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The „Genome Explorer“ enables the user to search for enzymes and/or their comparison with different genomes.

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## Genome Explorer

Available genomes:  
(Hold down CTRL or SHIFT to select multiple genomes)

**Archaea**

- Acidianus ambivalens plasmid pDL10
- Acidianus hospitalis strain W1 plasmid pAH1
- Acidianus hospitalis W1
- Acidilobus saccharovorans 345-15
- Aciduliprofundum boonei T469
- Aciduliprofundum sp. MAR08-339
- Aeropyrum camini SY1 = JCM 12091 DNA

Organism:   Filter! Reset

Taxonomy:

EC Number:

UniProt Accession:

Protein Name:

Max. number of results:  ☒ Preview all results


Restrict your search: ☒ Search only in selected genomes

Extend your search: ☐ Display homolog proteins with min. ☐ 50% ☐ 90% ☐ 100% sequence identity

search/display

**You can run a search**

- with an organism
- within a taxonomic range
- for an EC number
- for a specific protein
  - UniProt ID
  - protein name

 Click [here](#) for information on the data sources used for the Genome Explorer.

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# Genome Explorer

[\[new search\]](#)  
Please select one or more genomes from below for visualization.

Visualize selected
Visualize all

Results 1 - 19 of 19

Results per page: 20

Organism	Gene	Product	EC Number	Accession
<input type="checkbox"/> Aethionema cordifolium	rbcL	large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase Ribulose bisphosphate carboxylase large chain	4.1.1.39	A4QJC3
<input type="checkbox"/> Aethionema grandiflorum	rbcL	large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase Ribulose bisphosphate carboxylase large chain	4.1.1.39	A4QJK7
<input type="checkbox"/> Arabidopsis thaliana (thale cress)	rbcL	large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase Ribulose bisphosphate carboxylase large chain	4.1.1.39	A4QJG7
<input type="checkbox"/> Arabis alpina (gray rockcress)	rbcL	rbcL protein	4.1.1.39	A4QJH7
<input type="checkbox"/> Arabis hirsuta	rbcL	large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase Ribulose bisphosphate carboxylase large chain	4.1.1.39	A4QJL7
<input type="checkbox"/> Barbarea verna (early winter cress)	rbcL	large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase Ribulose bisphosphate carboxylase large chain	4.1.1.39	A4QJN7
<input type="checkbox"/> Brassica napus (rape)	rbcL	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit Ribulose-1,5-bisphosphate carboxylase large chain	4.1.1.39	A4QJO7
<input type="checkbox"/> Capsella bursa-pastoris (shepherd's purse)	rbcL	large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase Ribulose bisphosphate carboxylase large chain	4.1.1.39	A4QJP7
<input type="checkbox"/> Cardamine impatiens	rbcL	ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit	4.1.1.39	A0A0B4LD24
<input type="checkbox"/> Cardamine resedifolia	rbcL	ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit	4.1.1.39	A0A0B4LD84
<input type="checkbox"/> Crucihimalaya wallichii	rbcL	large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase Ribulose bisphosphate carboxylase large chain	4.1.1.39	A4QKT9
<input type="checkbox"/> Draba nemorosa	rbcL	large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase Ribulose bisphosphate carboxylase large chain	4.1.1.39	A4QL27
<input type="checkbox"/> Lepidium virginicum	rbcL	large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase Ribulose bisphosphate carboxylase large chain	4.1.1.39	A4QLB4

On the result page you find...

- the organism
- the gene and enzyme name
- the EC number
- UniProt accession code





## Genome Explorer

[new search]

Please select one or more genomes from below for visualization.

Visualize selected

Visualize all

Results 1 - 19 of 19

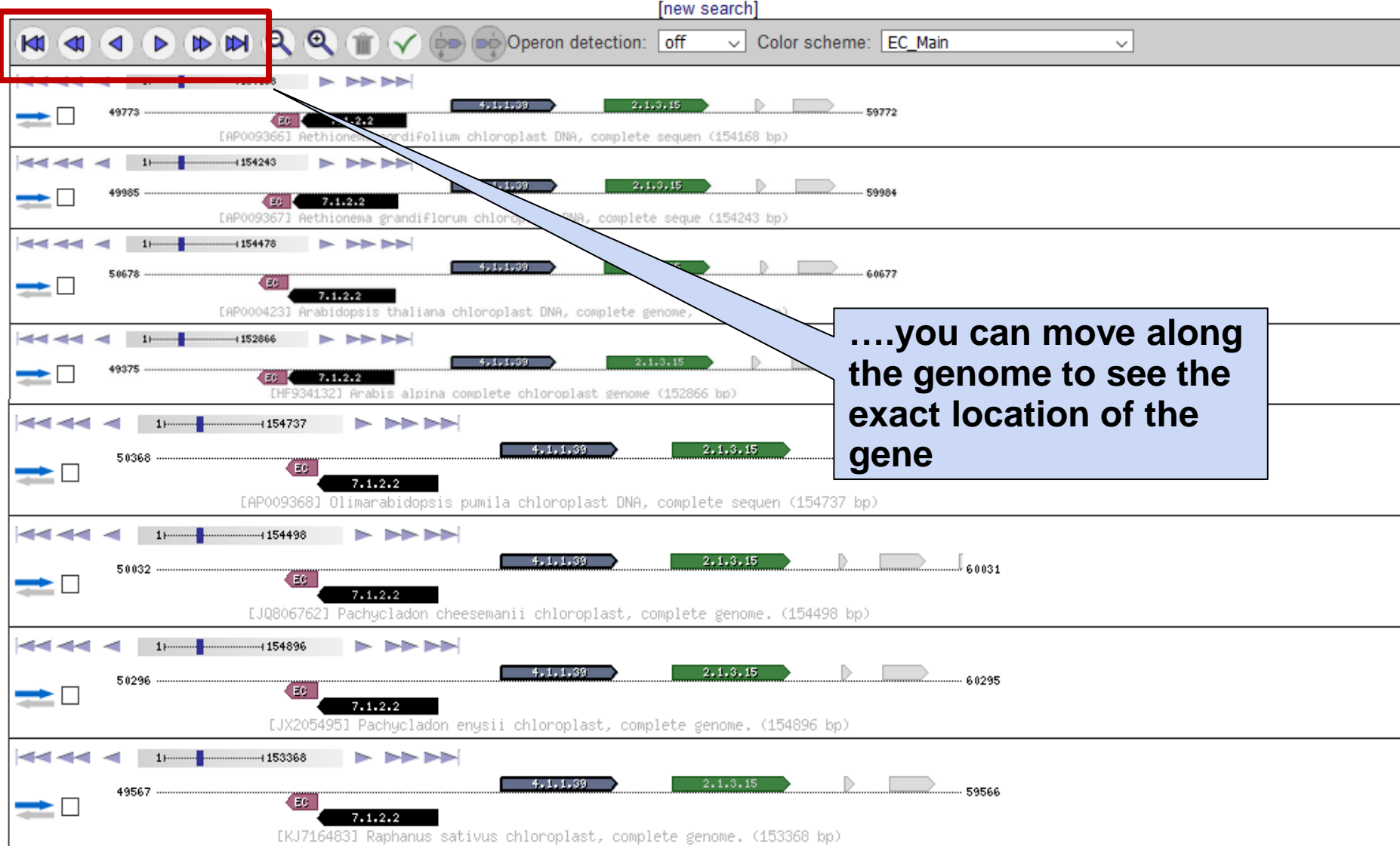
Results per page: 20

<input checked="" type="checkbox"/>	Organism	Gene	Product	EC Number	Accession
<input checked="" type="checkbox"/>	Aethionema cordifolium	rbcL	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase Ribulose biphosphate carboxylase large chain	4.1.1.39	A4QJC3
<input checked="" type="checkbox"/>	Aethionema grandiflorum	rbcL	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase Ribulose biphosphate carboxylase large chain	4.1.1.39	A4QJK7
<input checked="" type="checkbox"/>	Arabidopsis thaliana (thale cress)	rbcL	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase Ribulose biphosphate carboxylase large chain		042
<input checked="" type="checkbox"/>	Arabis alpina (gray rockcress)	rbcL	rbcL protein		UST4
<input checked="" type="checkbox"/>	Arabis hirsuta	rbcL	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase Ribulose biphosphate carboxylase large chain		K26
<input checked="" type="checkbox"/>	Barbarea verna (early winter cress)	rbcL	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase Ribulose biphosphate carboxylase large chain	4.1.1.39	A4QKB3
<input checked="" type="checkbox"/>	Brassica napus (rape)	rbcL	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit Ribulose-1,5-bisphosphate carboxylase/oxygenase	4.1.1.39	Q71SX0
<input checked="" type="checkbox"/>	Capsella bursa-pastoris (shepherd's purse)	rbcL	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase Ribulose biphosphate carboxylase large chain	4.1.1.39	A4QKK0
<input checked="" type="checkbox"/>	Cardamine impatiens	rbcL	ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit	4.1.1.39	A0A0B4LD24
<input checked="" type="checkbox"/>	Cardamine resedifolia	rbcL	ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit	4.1.1.39	A0A0B4LD84
<input checked="" type="checkbox"/>	Crucihimalaya wallichii	rbcL	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase Ribulose biphosphate carboxylase large chain	4.1.1.39	A4QKT9
<input checked="" type="checkbox"/>	Draba nemorosa	rbcL	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase Ribulose biphosphate carboxylase large chain	4.1.1.39	A4QL27
<input checked="" type="checkbox"/>	Lepidium virginicum	rbcL	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase Ribulose biphosphate carboxylase large chain	4.1.1.39	A4QLB4
<input checked="" type="checkbox"/>	Lobularia maritima	rbcL	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase	4.1.1.39	A4QIK2

Here you find further details on the selected genomes

## Genome Explorer

On the result page...



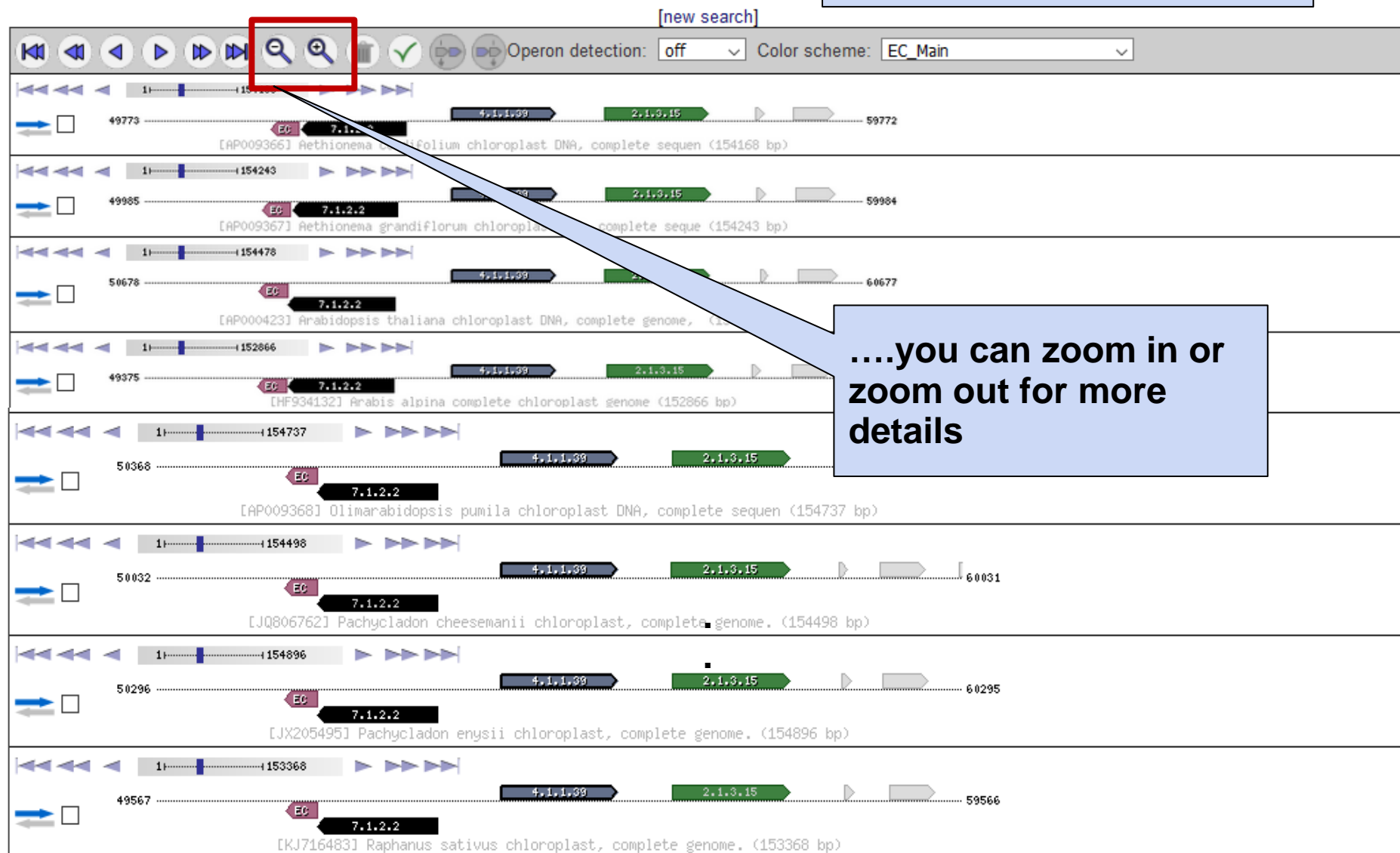
....you can move along the genome to see the exact location of the gene

Key for EC Main palette

Oxidoreductases Transferases Hydrolases Lyases Isomerases Ligases Translocases

## Genome Explorer

On the result page...



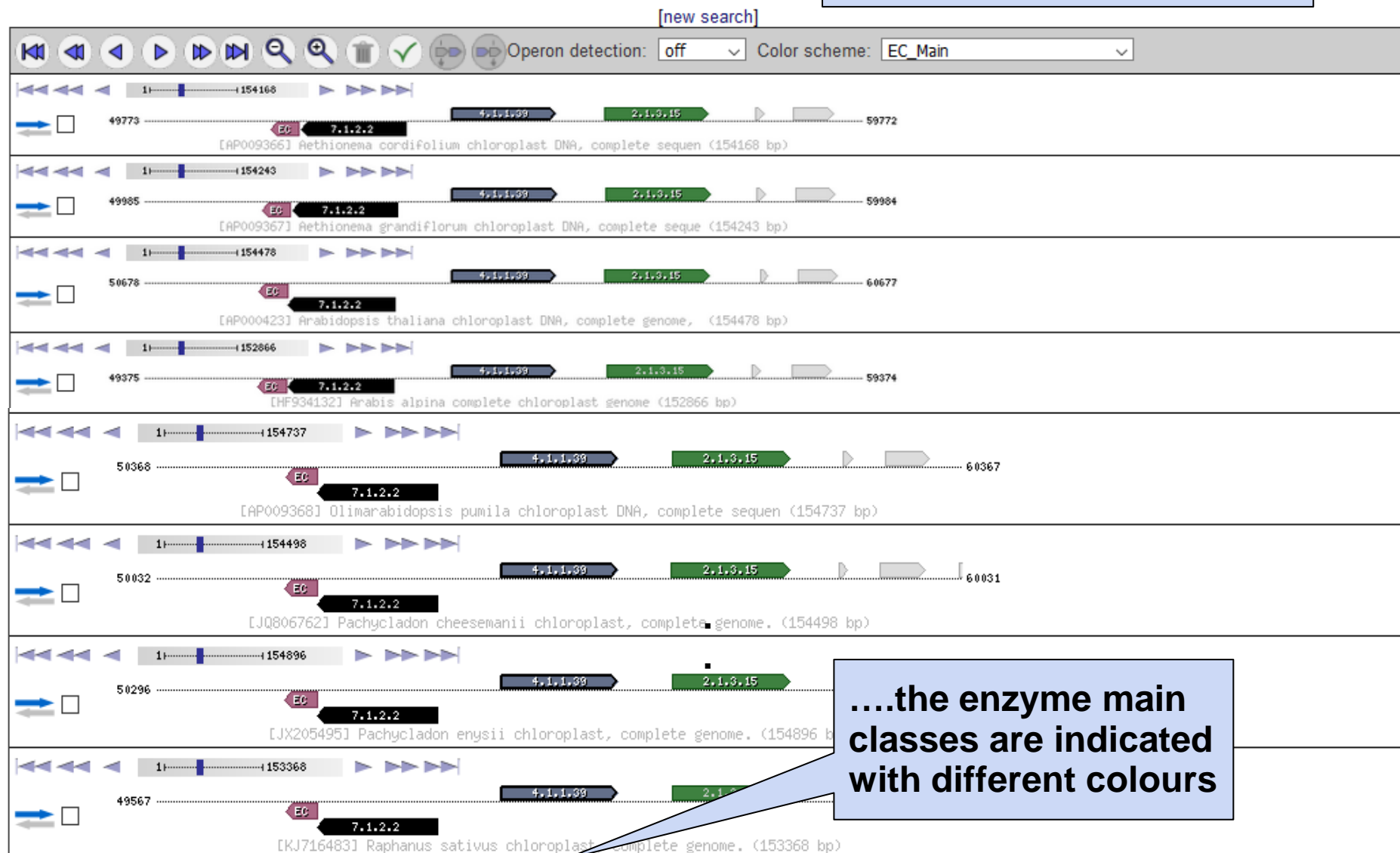
....you can zoom in or zoom out for more details

Key for EC Main palette

Oxidoreductases Transferases Hydrolases Lyases Isomerases Ligases Translocases

## Genome Explorer

On the result page...



....the enzyme main classes are indicated with different colours

Key for EC Main palette

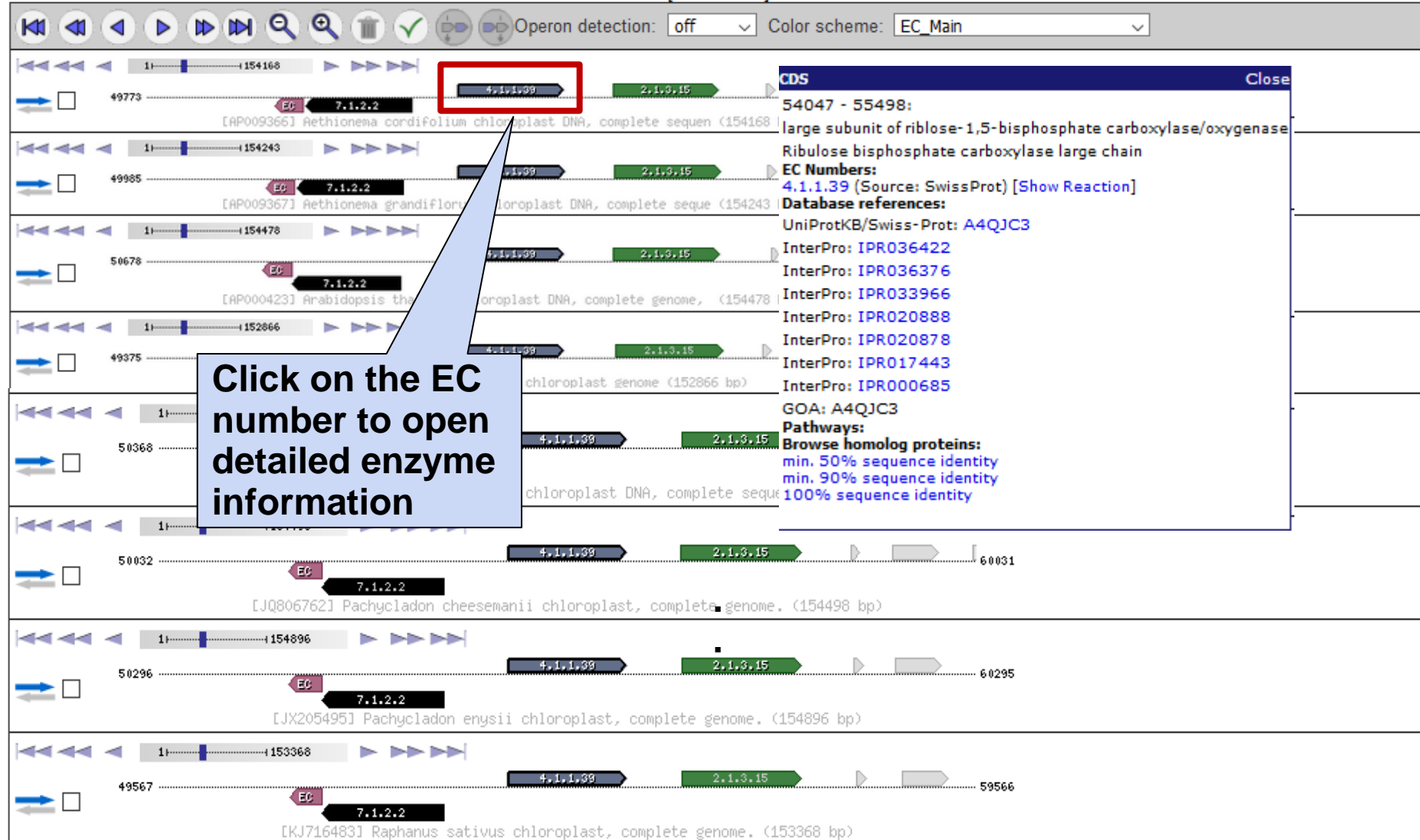
Oxidoreductases Transferases Hydrolases Lyases Isomerases Ligases Translocases

## Genome Explorer

On the result page...

[new search]

Operon detection: ☐ off Color scheme:



**Click on the EC number to open detailed enzyme information**

**CDS** Close

54047 - 55498:  
large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase  
Ribulose biphosphate carboxylase large chain  
**EC Numbers:**  
4.1.1.39 (Source: SwissProt) [\[Show Reaction\]](#)  
**Database references:**  
UniProtKB/Swiss-Prot: [A4QJC3](#)  
InterPro: [IPR036422](#)  
InterPro: [IPR036376](#)  
InterPro: [IPR033966](#)  
InterPro: [IPR020888](#)  
InterPro: [IPR020878](#)  
InterPro: [IPR017443](#)  
InterPro: [IPR000685](#)  
GOA: [A4QJC3](#)  
**Pathways:**  
**Browse homolog proteins:**  
min. 50% sequence identity  
min. 90% sequence identity  
100% sequence identity

Key for EC Main palette  
Oxidoreductases Transferases Hydrolases Lyases Isomerases Ligases Translocases

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...](#)

Please enter a search term

Enzyme, Ligand

contains

add search field

delete search field

start search

#### Text-based queries

- Full-text Search
- Advanced Search
- Enzyme & Disease



#### Structure-based queries

- Ligand Structure Search
- Metabolic Pathways
- Enzyme Structures



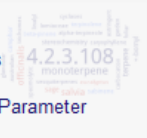
#### Explorer

- Enzyme Classification
- TaxTree
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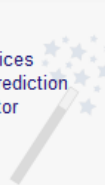
#### Visualization

- Word Maps
- Genomes
- Functional Parameter Statistics
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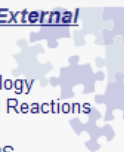
#### Prediction

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#### News

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 Information

To use the 3D-view of protein structures, first switch to „Classic view“

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EC-Number	Enzyme Name	Organism	Protein	Full text	Ligand	Advanced Search
<input type="text"/> <input type="button" value="Search"/> Display <input type="text" value="10"/> entries						
Nomenclature		Reaction & Specificity			Functional Parameters	
<ul style="list-style-type: none"> <li>Enzyme Names</li> <li>EC Number</li> </ul>		<ul style="list-style-type: none"> <li>Pathway</li> <li>Catalysed Reaction</li> <li>Reaction Type</li> <li>Natural Substrates &amp; Products</li> <li>Substrates &amp; Products</li> <li>Inhibitors</li> <li>Cofactors</li> <li>Metals/Ions</li> <li>Activating Compounds</li> <li>Ligands</li> </ul>			<ul style="list-style-type: none"> <li>K<sub>M</sub> Value</li> <li>k<sub>cat</sub>/K<sub>M</sub> Value</li> <li>K<sub>i</sub> Value</li> <li>IC<sub>50</sub> Value</li> <li>pI Value</li> <li>Turnover Number</li> <li>Specific Activity</li> <li>pH Optimum</li> <li>pH Range</li> <li>Temperature Optimum</li> <li>Temperature Range</li> <li>Kinetic <b>ENzyme DATA</b></li> </ul>	
Organism-related information						
<ul style="list-style-type: none"> <li>Organism</li> <li>Source Tissue</li> <li>Localization</li> </ul>						
Isolation& Preparation						
<ul style="list-style-type: none"> <li>Purification</li> <li>Cloned</li> <li>Expression</li> <li>Renatured</li> <li>Crystallization</li> </ul>		<ul style="list-style-type: none"> <li>Biochemical Reactions</li> </ul>				
Stability		Enzyme Structure			Disease, Protein Variants & Application	
<ul style="list-style-type: none"> <li>pH Stability</li> <li>Temperature Stability</li> <li>General Stability</li> <li>Organic Solvent Stability</li> <li>Oxidation Stability</li> <li>Storage Stability</li> </ul>		<ul style="list-style-type: none"> <li>Sequence</li> <li>3D-Structure</li> <li>Molecular Weight</li> <li>Subunits</li> <li>Posttranslational Modification</li> <li>Protein-Specific Search</li> </ul>			<ul style="list-style-type: none"> <li>Disease/ Diagnostics</li> <li>Protein Variants</li> <li>Application</li> </ul>	
					References	
					<ul style="list-style-type: none"> <li>References</li> </ul>	

Click on „3D-structure“

## Search PDB ID

PDB ID:  contains  show  results

### Refine your search

Recommended Name: ☒  contains

EC Number:  contains

Chain: ☐  contains

UniProt: ☒  contains

Organism:  contains

☒ PDB identification code directly linked to the PDB database

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**Enzyme 3D structures  
(PDB) can be searched  
with**

- the PDB-ID
- the enzyme name
- the EC number
- the UniProt-ID



Search PDB ID

PDB ID:  contains show 10

Refine your search

Recommended Name: ☒  contains

EC Number: 2.5.1.46 contains

Chain: ☐  contains

UniProt: ☒  contains

Organism:  contains

Search

Search term:

On the result page you find direct links to

- the Enzyme Summary Page (EC number)
- the Word Map
- the reaction catalyzed
- sequence information
- the PDB ID 1roz
- the 3D structure view
- ProteinsPlus – Protoss protonated enzyme
- ProteinsPlus – DoGSiteScorer enzyme pockets
- the TaxTree

EC Number ▼▲	Recommended Name ▼▲	PDB ID ▼▲	UniProt ▼▲	Organism ▼▲
2.5.1.46	deoxyhypusine synthase	1dhs 3D-view protonated enzyme enzyme pockets	P49366	Homo sapiens
2.5.1.46	deoxyhypusine synthase	1rlz 3D-view protonated enzyme enzyme pockets	P49366	Homo sapiens
2.5.1.46	deoxyhypusine synthase	1roz 3D-view protonated enzyme enzyme pockets	P49366	Homo sapiens
2.5.1.46	deoxyhypusine synthase	1rqd 3D-view protonated enzyme enzyme pockets	P49366	Homo sapiens

# Search PDB ID

PDB ID:
contains
show 10 results

Refine your search

Recommended Name:
contains

EC Number: 2.5.1.46
contains

Chain:
contains

UniProt:
contains

Organism:
contains

Search

Search term:

Results 1 - 10 of 14
download as CSV
download all results as CSV

EC Number ▼▲	Recommended Name ▼▲	PDB ID ▼▲	UniProt ▼▲	Organism ▼
2.5.1.46	deoxyhypusine synthase	1dhs 3D-view protonated enzyme enzyme pockets	P49366	Homo sapiens
2.5.1.46	deoxyhypusine synthase	1rlz 3D-view protonated enzyme enzyme pockets	P49366	Homo sapiens
2.5.1.46	deoxyhypusine synthase	1rpz 3D-view protonated enzyme enzyme pockets	P49366	Homo sapiens
2.5.1.46	deoxyhypusine synthase	1rqd 3D-view protonated enzyme enzyme pockets	P49366	Homo sapiens

Clicking on 3D-view opens an interactive picture of the structure

**3D Structure View**

## Highlight

☒ - Off -

- ☐ active site (Nucleophile)
- ☐ binding site (NAD)
- ☐ binding site (NAD; via amide nitrogen)
- ☐ binding site (Spermidine)
- ☐ nucleotide phosphate-binding region (NAD)

Colour:  

1.

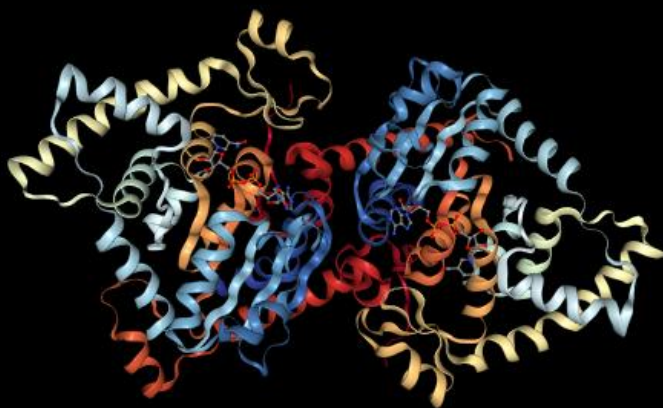
2.

EC Number: 2.5.1.46 

PDB ID: 1roz (Download)

**The 3D Structure View provides**

1. different options to display the structure depending on the chosen
  - color scheme
  - selected binding sites
2. the EC number with a direct link to the Enzyme Summary Page and a download option
3. Different styles, colours, backgrounds to display the structure



Colour by

Residue Index

Protein Style

Cartoon

Ligand Style

Ball &amp; Stick



Background

Black

Screenshot 

- Resolution -

Spin

☐ Water ☒ Hydrogens ☒ Ions 

3.

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include your data into our database. More...

Please enter a search term

Enzyme, Ligand

contains

add search field

delete search field

start search

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

News

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

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The tool „Functional Enzyme Statistics“ provides the graphical display of the parameters

- in a taxonomic group or organism
- of one specific EC number or an EC subclass



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## Functional Enzyme Parameters

Specify the chart of interest:

Functional parameter:

Taxonomic group or organism:

Please enter the beginning of a valid taxonomic term!

EC-Number or beginning of  
EC-Number:  Use "\*" as wildcard!

Search

Chose a functional  
parameter of interest

Enter a taxonomic group  
or an organism

You can limit your search  
to an EC number or EC  
subclass

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## Functional Enzyme Parameters

Specify the chart of interest:

Functional parameter:

Taxonomic group or organism:

- Viridiplantae (kingdom)
- Viridiplantae environmental sample (species)
- Viridiplantae sp. AZH1 (species)
- Viridiplantae sp. AZS1 (species)
- Viridiplantae sp. DHK-2018 (species)
- Viridiplantae sp. ZAA2 (species)

EC-Number or beginning of  
EC-Number:  Use '\*' as wildcard!

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If you interested, for example in an overview of temperature optima within the plant kingdom, choose the corresponding taxonomic group and the functional parameter...

## Functional Enzyme Parameters

Specify the chart of interest:

Functional parameter: 

Temperature\_Optimum

Taxonomic group or organism: 

Viridiplantae (kingdom)

Viridiplantae (kingdom)

EC-Number or beginning of EC-Number:

Use "\*" as wildcard!

Search

On the result page the diagram with the chosen options is displayed

