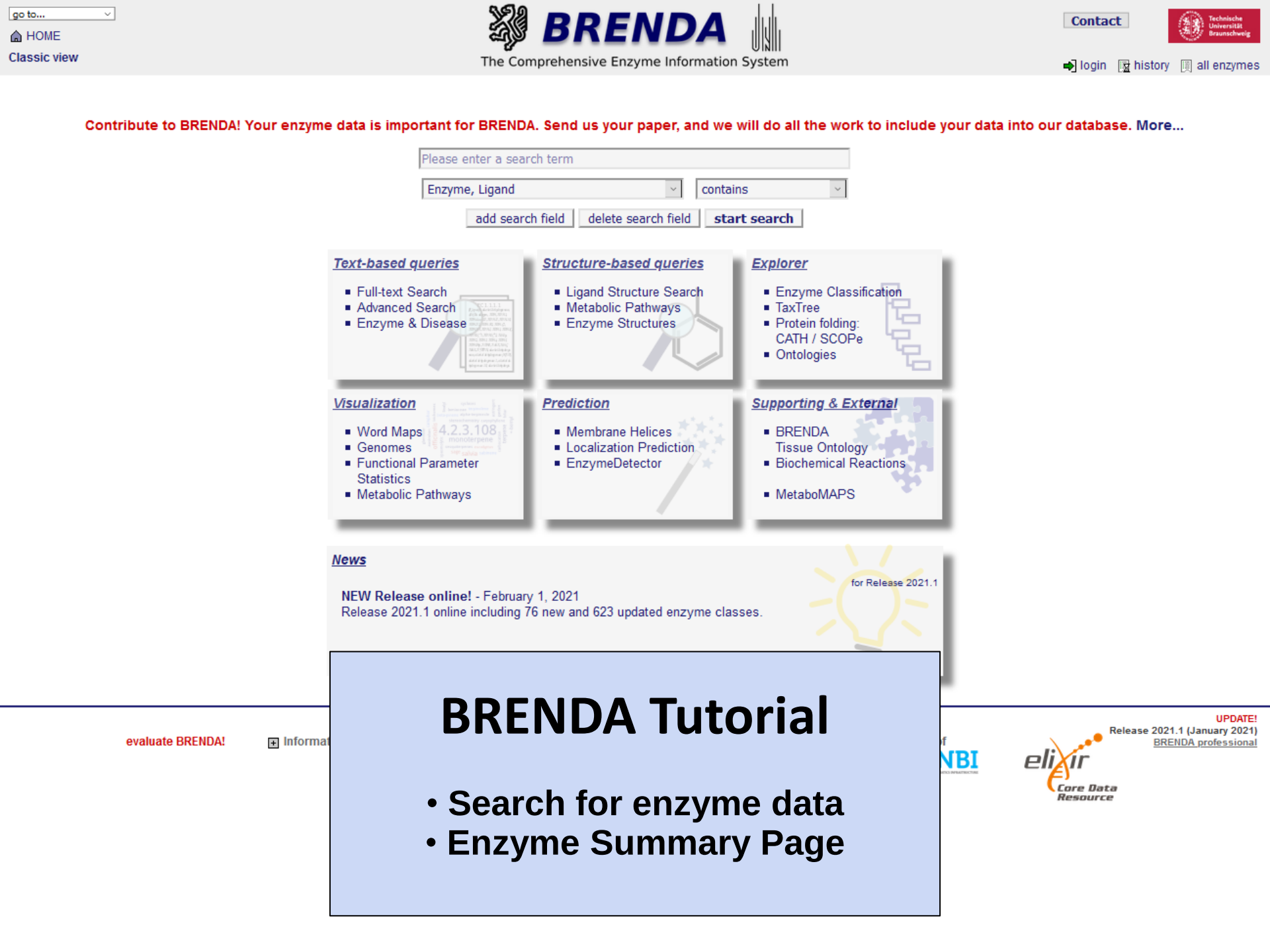
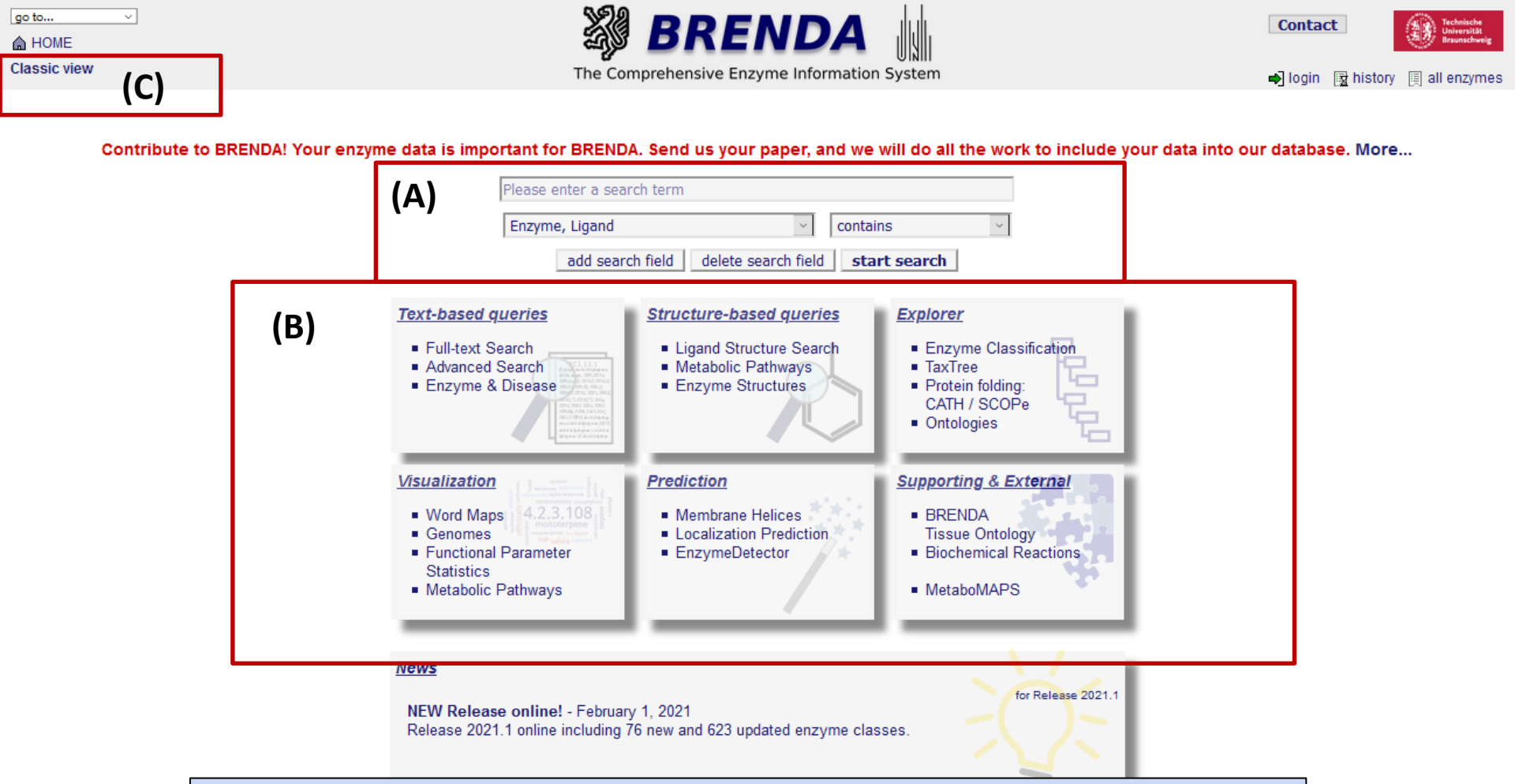
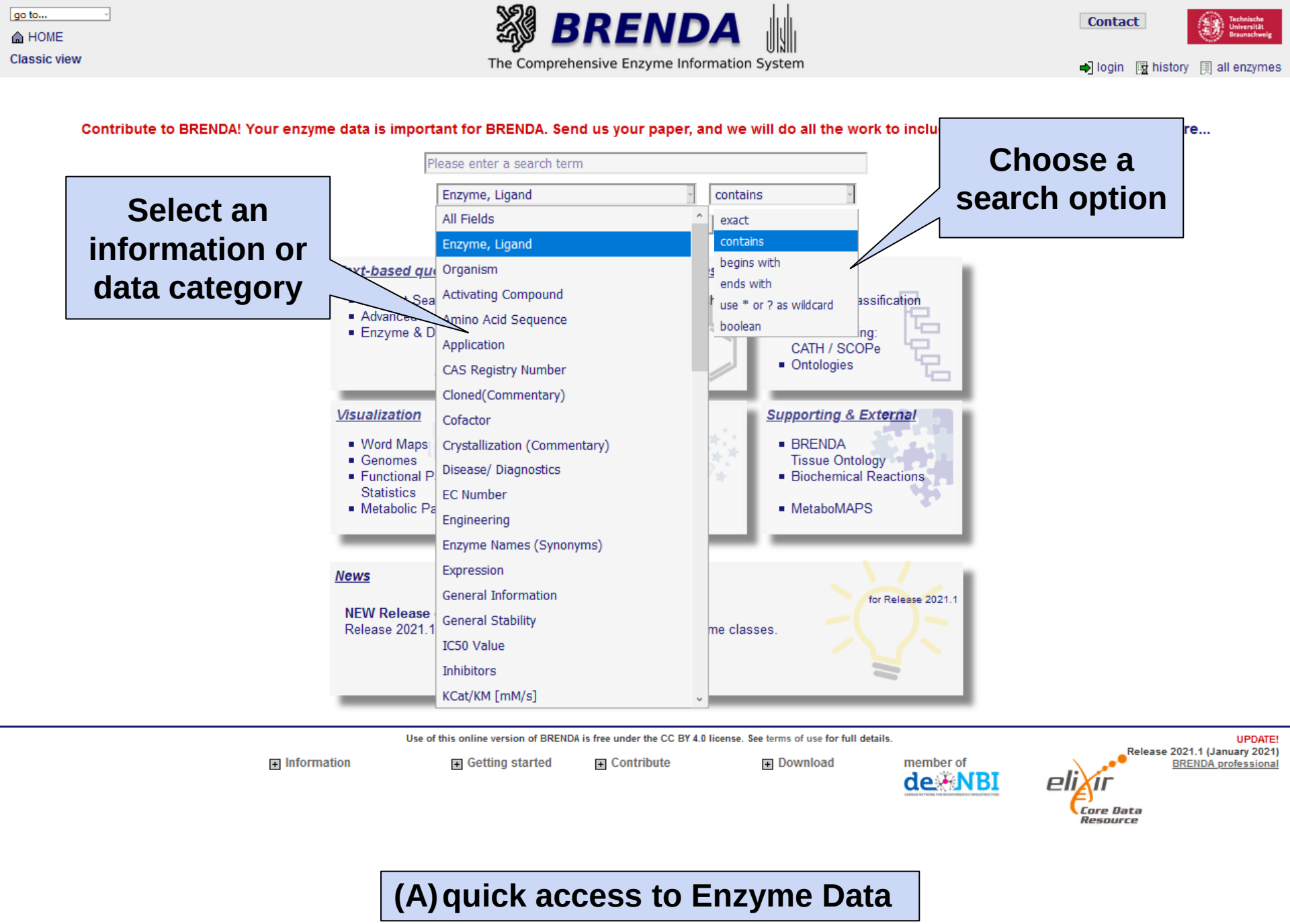

go to...
HOME
Classic view
BRENDA
The Comprehensive Enzyme Information System
Contact
login
history
all enzymes
Contribute to BRENDA! Your enzyme data is important for BRENDA. Send us your paper, and we will do all the work to include your data into our database. More...
Please enter a search term
Enzyme, 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
News
for Release 2021.1
NEW Release online! - February 1, 2021
Release 2021.1 online including 76 new and 623 updated enzyme classes.
BRENDA Tutorial
• Search for enzyme data
• Enzyme Summary Page
evaluate BRENDA!
UPDATE!
Release 2021.1 (January 2021)
BRENDA professional
Core Data Resource



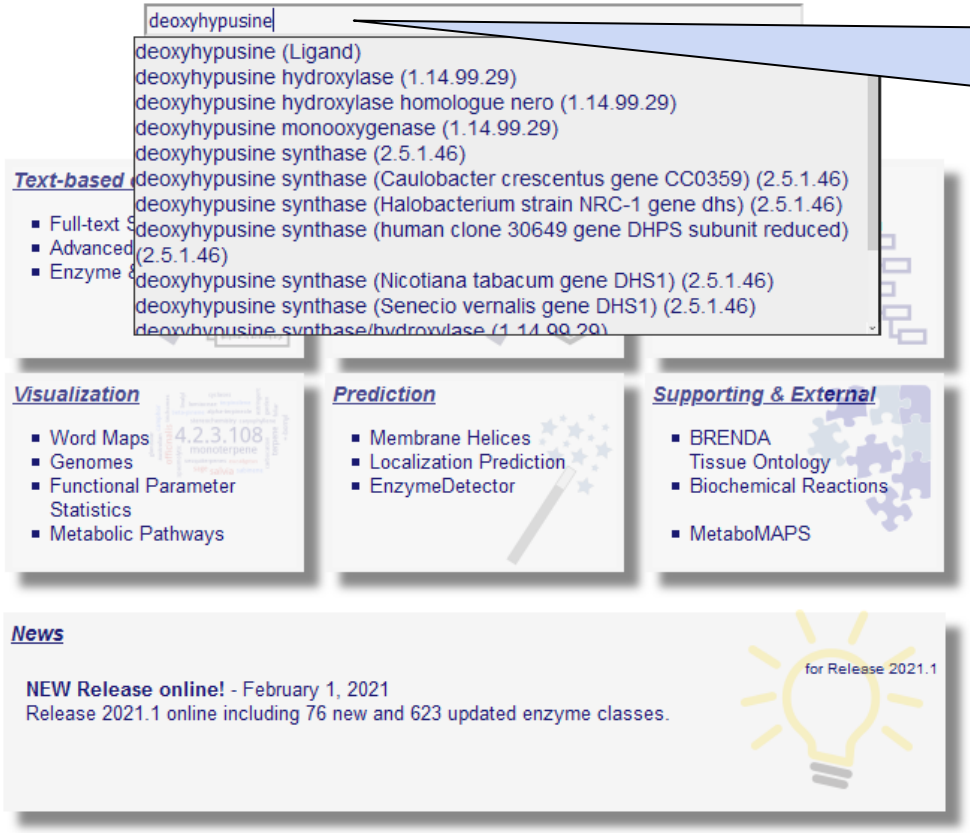
The main search options:

- **Quick access (A)**
- **and more specific queries (B)**
- **Classic View (C)**
- **further details in the corresponding BRENDA tutorials**



(A) quick access to Enzyme Data

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...



Enter a search term and perform the query

(A) quick access to Enzyme Data

Refine search

Field	Hits found
Enzyme Names (Synonyms)	3
Ligands	12

Select the entries you are interested in

Refine search

Search Enzyme Names (Synonyms)

Search term: deoxyhypusine

Results 1 - 3 of 3
download as CSV
download all results as CSV

EC Number	Recommended Name	Synonyms	Commentary
1.1.1.249	[protein eIF-5A]-deoxyhypusine synthase	[protein eIF-5A]-deoxyhypusine synthase	deleted, reinstated as EC 2.5.1.46
1.14.99.29	deoxyhypusine monooxygenase	deoxyhypusine hydroxylase, deoxyhypusine hydroxylase homologue nero, deoxyhypusine monooxygenase, deoxyhypusine synthase/hydroxylase, deoxyhypusine,hydrogen-donor:oxygen oxidoreductase (2-hydroxylating), oxygenase, deoxyhypusine di-	-
2.5.1.46	deoxyhypusine synthase	deoxyhypusine synthase, deoxyhypusine synthase (Caulobacter crescentus gene CC0359), deoxyhypusine synthase (Halobacterium strain NRC-1 gene dhs), deoxyhypusine synthase (human clone 30649 gene DHPS subunit reduced), deoxyhypusine synthase (Nicotiana tabacum gene DHS1), deoxyhypusine synthase (Senecio vernalis gene DHS1), deoxyhypusinesynthase, synthase, deoxyhypusine	-

Results 1 - 3 of 3
download as CSV
download all results as CSV

Result page: Click on the EC number you are interested in

Information on EC 2.5.1.46 - deoxyhypusine synthase

for references in articles please use BRENDA:EC2.5.1.46

Enzyme Summary Page

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 activity. This enzyme catalyses the first reaction of hypusine formation from one specific lysine residue of the eIF5A precursor. The reaction occurs in four steps: NAD+-dependent dehydrogenation of spermidine (1a), formation of an enzyme-imine intermediate by transfer of the 4-aminobutylidene group from dehydrospermidine to the active site lysine residue (Lys329 for the human enzyme; 1b), transfer of the same 4-aminobutylidene group from the enzyme intermediate to the e1F5A precursor (1c), reduction of the e1F5A-imine intermediate to form a 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.

Specify your search results

Mark a special word or phrase in this record: Mark!

Search Reference ID: Search

Search UniProt Accession: Search

Select one or more organisms in this record:

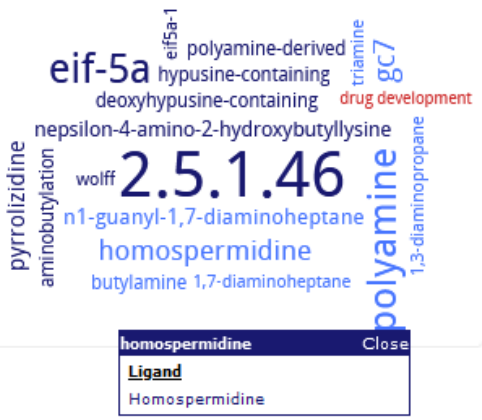
All organisms
Arabidopsis thaliana
Arabidopsis thaliana Col-0
Bos taurus
Brassica napus

Submit

Show additional data

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

Word Map hide



The enzyme appears in viruses and cellular organisms

Reaction Schemes hide (Overall reactions are displayed. Show all >>)

[eIF5A-precursor]-lysine + spermidine = [eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine

Information on EC 2.5.1.46 - deoxyhypusine synthase

for references in articles please use BRENDA:EC2.5.1.46

Enzyme Summary Page

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

Display of the classification of the enzyme within the EC tree

IUBMB Comments

The eukaryotic initiation factor eIF5A contains a hypusine residue that is essential for activity. This enzyme catalyses the first reaction of hypusine formation from one specific lysine residue of the eIF5A precursor. The reaction occurs in four steps: NAD+-dependent dehydrogenation of spermidine (1a), formation of an enzyme-imine intermediate by transfer of the 4-aminobutylidene group from dehydrospermidine to the active site (1b), transfer of the same 4-aminobutylidene group from the enzyme intermediate to the e1F5A precursor (1c), and reduction of the deoxyhypusine residue (1d). Hence the overall reaction is transfer of a 4-aminobutyl group. For the plant enzyme, homospermidine can substitute for the lysine residue of the eIF5A precursor. Hypusine is formed from deoxyhypusine by the action of deoxyhypusine hydroxylase.

Specify your search results

Mark a special word or phrase in this record: Mark!

Search Reference ID: Search

Search UniProt Accession: Search

Select one or more organisms in this record:

- All organisms
- Arabidopsis thaliana
- Arabidopsis thaliana Col-0
- Bos taurus
- Brassica napus

Submit

Show additional data

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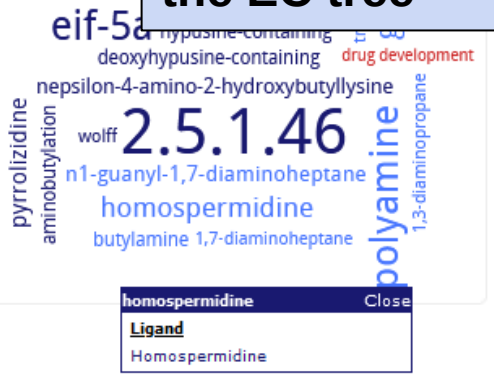
- ( ) Include FRENDA results (AMENDA + additional results, but less precise)

Word Map



The enzyme appears in viruses and cellular organisms

Reaction Schemes hide (Overall reactions are displayed. Show all >>)

[eIF5A-precursor]-lysine + spermidine = [eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine

Information on EC 2.5.1.46 - deoxyhypusine synthase

for references in articles please use BRENDA:EC2.5.1.46

Enzyme Summary Page

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 activity. This enzyme catalyses the first reaction of hypusine formation from one specific lysine residue of the eIF5A precursor. The reaction occurs in four steps: NAD+-dependent dehydrogenation of spermidine (1a), formation of an enzyme-imine intermediate by transfer of the 4-aminobutylidene group from dehydrospermidine to the active site lysine residue (Lys329 for the human enzyme; 1b), transfer of the same 4-aminobutylidene group from the enzyme intermediate to the e1F5A precursor (1c), reduction of the e1F5A-imine intermediate to form a 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.

Specify your search results

Mark a special word or phrase in this record: Mark!

Search Reference ID: Search

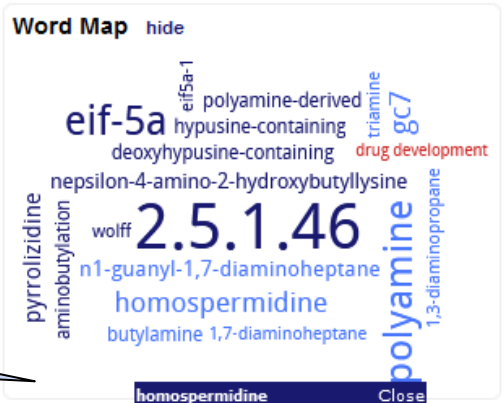
Search UniProt Accession: Search

Submit

Show additional data

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

The display of the Word Map is enlarged



The enzyme appears in viruses and cellular organisms

Reaction Schemes hide (Overall reactions are displayed. Show all >>)

[eIF5A-precursor]-lysine	+	spermidine	=	[eIF5A-precursor]-deoxyhypusine	+	propane-1,3-diamine

IUBMB Comments

The eukaryotic initiation factor eIF5A contains a hypusine residue that is essential for activity. This enzyme catalyses the first reaction of hypusine formation from one specific lysine residue of the eIF5A precursor. The reaction occurs in four steps: NAD+-dependent dehydrogenation of spermidine (1a), formation of an enzyme-imine intermediate by transfer of the 4-aminobutylidene group from dehydrospermidine to the active site lysine residue (Lys329 for the human enzyme; 1b), transfer of the same 4-aminobutylidene group from the enzyme intermediate to the e1F5A precursor (1c), reduction of the e1F5A-imine intermediate to form a 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.

Enzyme Summary Page

Specify your search results

Mark a special word or phrase in this record: Mark!

Search Reference ID: Search

Search UniProt Accession: Search

Select one or more organisms in this record:

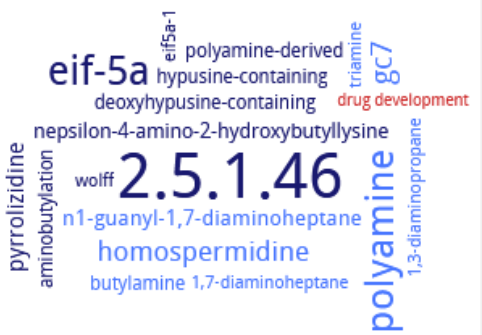
- All organisms
- Arabidopsis thaliana
- Arabidopsis thaliana Col-0
- Bos taurus
- Brassica napus

Submit

Show additional data

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

Word Map hide

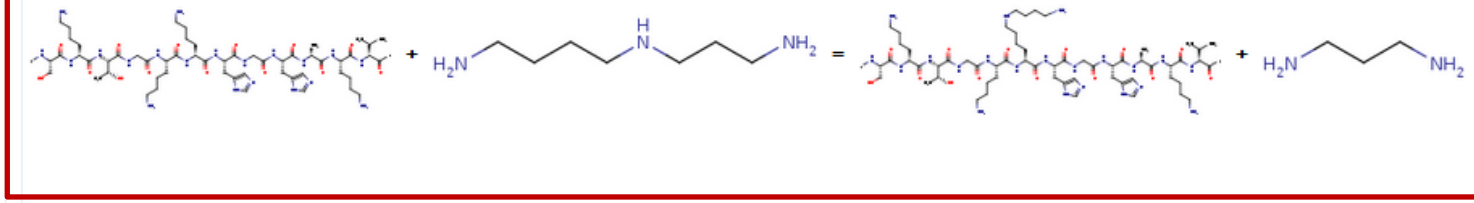


The enzyme appears in viruses and cellular organisms

Display of the reaction scheme

Reaction Schemes hide (Overall reactions are displayed. Show all >>)

[eIF5A-precursor]-lysine + spermidine = [eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine



Information on EC 2.5.1.46 - deoxyhypusine synthase

for references in articles please use BRENDA:EC2.5.1.46

Enzyme Summary Page

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

Navigation bar

IUBMB Comments

The eukaryotic initiation [illegible]hat is essential for activity. This enzyme catalyses the first reaction of hypusine formation from one specific lysine residue o[illegible]n four steps: NAD+-dependent dehydrogenation of spermidine (1a), formation of an enzyme-imine intermediate by transfer[illegible]ospermidine to the active site lysine residue (Lys329 for the human enzyme; 1b), transfer of the same 4-aminobutylidene group from the enzyme intermediate to the e1F5A precursor (1c), reduction of the e1F5A-imine intermediate to form a 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.

Specify your search results

Mark a special word or phrase in this record: Mark!

Search Reference ID: Search

Search UniProt Accession: Search

Select one or more organisms in this record:

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- Arabidopsis thaliana Col-0
- Bos taurus
- Brassica napus

Submit

Show additional data

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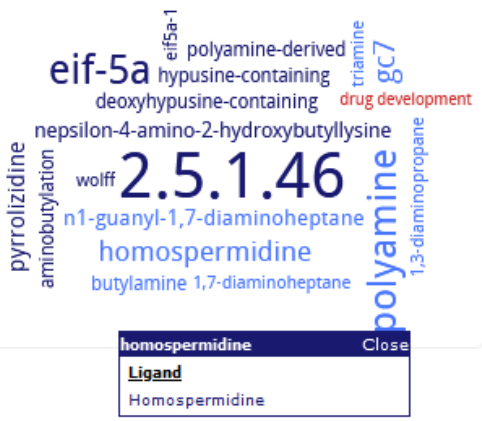
- ( ) Include AMENDA (text mining) results
- ( ) Include FRENDA results (AMENDA + additional results, but less precise)

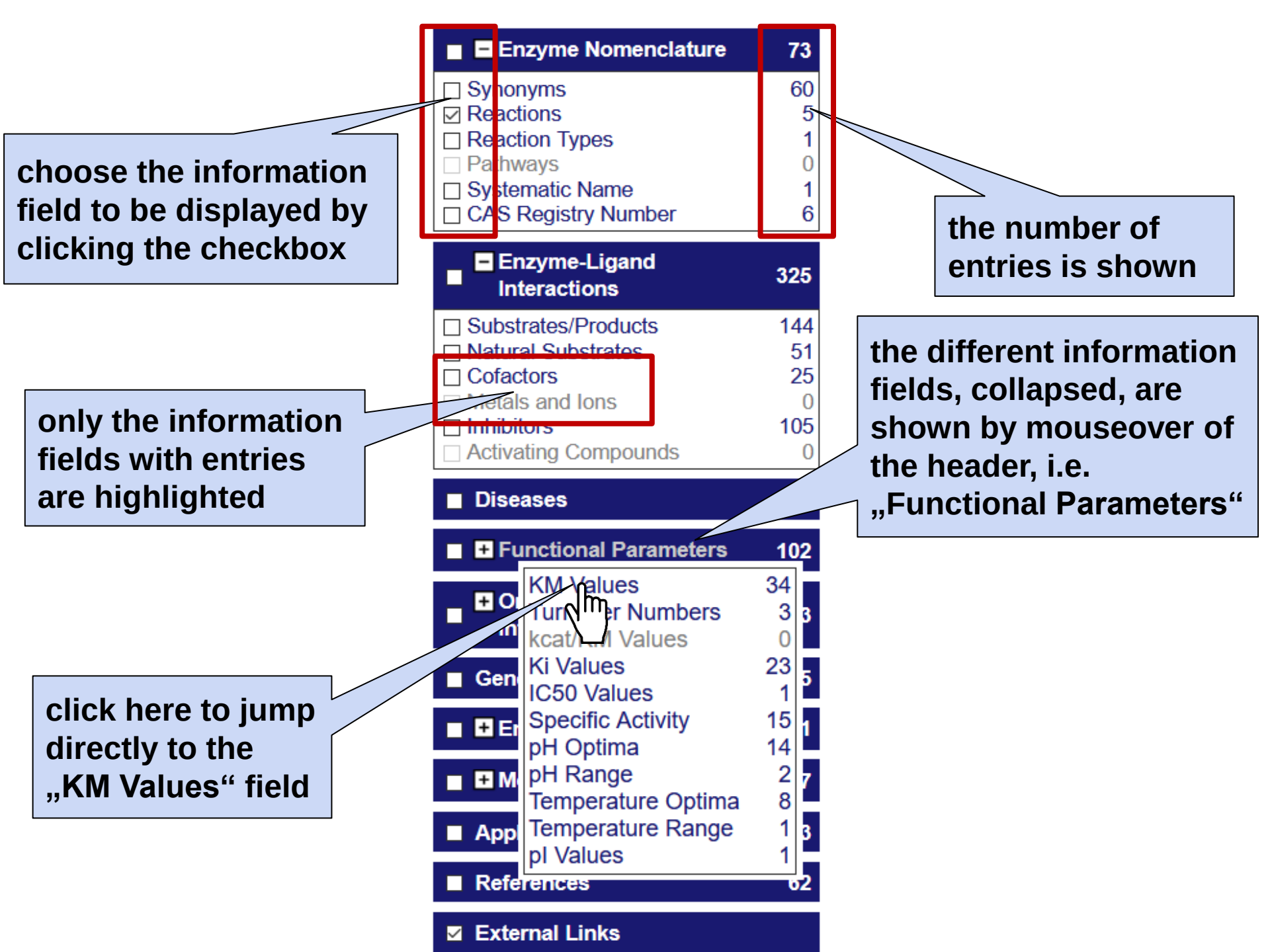
Word Map hide



The enzyme appears in viruses and cellular organisms

Reaction Schemes hide (Overall reactions are displayed. Show all >>)

[eIF5A-precursor]-lysine + spermidine = [eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine


choose the information field to be displayed by clicking the checkbox
Enzyme Nomenclature 73
Synonyms 60
Reactions 5
Reaction Types 1
Pathways 0
Systematic Name 1
CAS Registry Number 6
the number of entries is shown
Enzyme-Ligand Interactions 325
Substrates/Products 144
Natural Substrates 51
Cofactors 25
Metals and Ions 0
Inhibitors 105
Activating Compounds 0
only the information fields with entries are highlighted
Diseases
Functional Parameters 102
the different information fields, collapsed, are shown by mouseover of the header, i.e. „Functional Parameters“
KM Values 34
Turnover Numbers 3
kcat/KM Values 0
Ki Values 23
IC50 Values 1
Specific Activity 15
pH Optima 14
pH Range 2
Temperature Optima 8
Temperature Range 1
pI Values 1
click here to jump directly to the „KM Values“ field
External Links

BRENDA home
History

show all | hide all No of entries

- Enzyme Nomenclature 73
- Enzyme-Ligand Interactions 325
- Diseases 28
- Functional Parameters 102
  - KM Values 34
  - Turnover Numbers 3
  - kcat/KM Values 0
  - Ki Values 23
  - IC50 Values 1
  - Specific Activity 15
  - pH Optima 14
  - pH Range 2
  - Temperature Optima 8
  - Temperature Range 1
  - pI Values 1
- Organism related Information 133
- General Information 65
- Enzyme Structure 1961
- Molecular Properties 47
- Applications 3
- References 62
- External Links

top print hide 34 entries Go to KM Value Search

KM VALUE [mM]	SUBSTRATE	ORGANISM	UNIPROT	COMMENTARY	LITERATURE	IMAGE
0.0954 - 0.1058	1,3-diaminopropane	2 entries				
0.00177	eIF5A	Leishmania donovani	B5APK2	-	704694	-
0.00008 - 1.12	eIF5A-precursor	4 entries				
0.0193	homospermine	Homo sapiens	-	-	638083	
0.0048 - 0.81	NAD+	4 entries				
0.0015 - 0.203	putrescine	2 entries				
0.0006 - 0.37	spermidine	12 entries				
		Homo sapiens	-	pH 9.5, 37°C	658627	
		Homo sapiens	-	pH 9.5, 37°C	658627	
	sine	2 entries				
		3 entries				
		Senecio vernalis	-	-	638080	-

Enzyme Summary Page

Click here to go directly to the specific search to expand or limit the results.

rch

TURNOVER NUMBER [1/s]	SUBST	ORGANISM	UNIPROT	COMMENTARY	LITERATURE	IMAGE
0.0022	eIF5A-prec	Senecio vernalis	-	+ spermidine	638080	
0.015	spermidine	Trypanosoma brucei brucei	Q38BX0, Q4GZD1	pH 7.5, 37°C, heterotetrameric DHS; pH 7.5, 37°C, heterotetrameric DHS	738579	
0.018	[eIF5A-precurso lysine	Trypanosoma brucei brucei	Q38BX0, Q4GZD1	pH 7.5, 37°C, heterotetrameric DHS; pH 7.5, 37°C, heterotetrameric DHS	738579	

top print hide 23 entries Go to Ki Value Search

Ki VALUE [mM]	INHIBITOR	ORGANISM	UNIPR			GE
0.141	(R)-3-methylspermidine	Homo sapiens	-			
0.019	(S)-3-methylspermidine	Homo sapiens	-			
0.0129	1,3-diaminopropane	Saccharomyces cerevisiae	-			
0.0009	1,7-Diaminoheptane	Saccharomyces cerevisiae	-			
0.00191	1,8-diaminooctane	Saccharomyces cerevisiae	-			
0.00752	1,9-diaminononane	Saccharomyces cerevisiae	-			
2.27	FAD	Saccharomyces cerevisiae	-			
1.28	FMN	Saccharomyces cerevisiae	-	-	638077	

BRENDA home
History
show all | hide all
No of entries
Enzyme Nomenclature 73
Enzyme-Ligand Interactions 325
Diseases 28
Functional Parameters 102
KM Values 34
Turnover Numbers 3
kcat/KM Values 0
Ki Values 23
IC50 Values 1
Specific Activity 15
pH Optima 14
pH Range 2
Temperature Optima 8
Temperature Range 1
pI Values 1
Organism related Information 133
General Information 65
Enzyme Structure 1961
Molecular Properties 47
Applications 3
References 62
External Links

top print hide 34 entries Go to KM Value Search

KM VALUE [mM]	SUBSTRATE			COMMENTARY	LITERATURE	IMAGE
0.0954 - 0.1						
0.00177	eIF5A			-	704694	-
0.00008 - 1.12	eIF5A-precu					
0.0193	homosperm			-	638083	
0.0048 - 0.81	NAD+	4 entries				
0.0015 - 0.203	putrescine	2 entries				
0.0006 - 0.37	spermidine	12 entries				
0.0015	[eIF5A-1-precursor]-lysine	Homo sapiens	-	pH 9.5, 37°C	658627	
0.0083	[eIF5A-2-precursor]-lysine	Homo sapiens	-	pH 9.5, 37°C	658627	
0.0066 - 0.0086	[eIF5A-precursor]-deoxyhypusine	2 entries				
0.0007 - 0.00177	[eIF5A-precursor]-lysine	3 entries				
additional information	additional information	Senecio vernalis	-	-	638080	-

Here you can choose to show or to hide all entries

top print hide 3 entries Go to Turnover Number Search

TURNOVER NUMBER [1/s]	SUBSTRATE	ORGANISM	UNIPROT	COMMENTARY	LITERATURE	IMAGE
0.0022	eIF5A-precursor	Senecio vernalis	-	+ spermi		
0.015	spermidine	Trypanosoma brucei brucei	Q38BX0, Q4G	, heter		
0.018	[eIF5A-precursor]-lysine	Trypanosom bru	Q38BX0, Q4GZD1	pH 7.5, 37°C, heterotetrameric DHS; pH 7.5, 37°C, heterotetrameric DHS	738579	

Click here to hide or display all entries of the information field below

top print hide 23 entries Go to Ki Value Search

Ki VALUE [mM]	INHIBITOR	ORGANISM	UNIPROT	COMMENTARY	LITERATURE	IMAGE
0.141	(R)-3-methylspermidine	Homo sapiens	-	pH and temperature not specified in the publication	737314	
0.019	(S)-3-methylspermidine	Homo sapiens	-	pH and temperature not specified in the publication	737314	
0.0129	1,3-diaminopropane	Saccharomyces cerevisiae	-	-	638077	
0.0009	1,7-Diaminoheptane	Saccharomyces cerevisiae	-	-	638077	
0.00191	1,8-diaminooctane	Saccharomyces cerevisiae	-	-	638077	
0.00752	1,9-diaminononane	Saccharomyces cerevisiae	-	-	638077	
2.27	FAD	Saccharomyces cerevisiae	-	-	638077	
1.28	FMN	Saccharomyces cerevisiae	-	-	638077	

show all | hide all No of entries

- Enzyme Nomenclature 73
- Enzyme-Ligand Interactions 325
- Diseases 77
- Functional Parameters 102
  - KM Values 34
  - Turnover Numbers 3
  - kcat/KM Values 0
  - Ki Values 23
  - IC50 Values 1
  - Specific Activity 15
  - pH Optima 14
  - pH Range 2
  - Temperature Optima 8
  - Temperature Range 1
  - pI Values 1
- Organism related Information 133
- General Information 65
- Enzyme Structure 1185
- Molecular Properties 47
- Applications 3
- References 62
- External Links

top print hide Go to IC50 Value Search

IC50 VALUE [mM]	INHIBITOR	ORGANISM	UNIPROT	COMMENTARY	LITERATURE	IMAGE
0.0015	N1-guanyl-1,7-diaminoheptane	Trypanosoma brucei brucei	Q38BX0, Q4GZD1	pH 7.5, 37°C, heterotetrameric DHS; pH 7.5, 37°C, heterotetrameric DHS	738579	

top print hide 15 entries Go to Specific Activity Search

SPECIFIC ACTIVITY [µmol/min/mg]	ORGANISM	UNIPROT	COMMENTARY	LITERATURE
0.0000096	Leishmania donovani	B5APK2	low specific activity of DHS34 could be due to the fact that one of the NAD+ binding regions in the DHS34 is present in the big long insertion when compared with human deoxyhypusine synthase	704694
0.000137	Rattus norvegicus	-	-	638058
0.00325	Homo sapiens	-	-	638079
0.0034	Nicotiana tabacum	Q9SC80	with donor homospermidine	638061
0.0091	Nicotiana tabacum	Q9SC80	with donor homospermidine	
0.0101	Senecio vernalis	-	with acceptor eIF5A-precursor	
0.0131	Saccharomyces cerevisiae	-	-	
0.015	Homo sapiens	-	-	
0.019	Homo sapiens	-	-	
0.0211	Nicotiana tabacum	Q9SC80	with donor [illegible]	638061
0.0442	Senecio vernalis	-	[illegible]ceptor putrescine	638062
additional information	4 entries			

Click here to hide or display all entries in the table below

top print hide 14 entries Go to pH Optimum Search

pH OPTIMUM	ORGANISM	UNIPROT	COMMENTARY	LITERATURE
7.5	Trypanosoma brucei brucei	Q38BX0, Q4GZD1	assay at; assay at	738579
9 - 9.5	Homo sapiens	-	optimum for spermidine-binding	638069
9	2 entries			
9.2	3 entries			
9.3	Senecio vernalis	-	glycine-NaOH buffer	638080
9.4	Saccharolobus solfataricus	Q97ZF1	assay at	744857
9.5	Homo sapiens	-	assay at	721265
9.5 - 9.6	Rattus norvegicus	-	-	638075
9.5	2 entries			
9.6	Leishmania donovani	B5APK2	assay at; assay at	704694

top print hide 2 entries Go to pH Range Search

pH RANGE	ORGANISM	UNIPROT	COMMENTARY	LITERATURE

show all | hide all No of entries

- Enzyme Nomenclature 73
- Enzyme-Ligand Interactions 325
- Diseases 77
- Functional Parameters 102
  - KM Values 34
  - Turnover Numbers 3
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  - Ki Values 23
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  - Temperature Optima 8
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IC50 VALUE [mM]	INHIBITOR	ORGANISM	UNIPROT	COMMENTARY	LITERATURE	IMAGE
0.0015	N1-guanyl-1,7-diaminoheptane	Trypanosoma brucei brucei	Q38BX0, Q4GZD1	pH 7.5, 37°C, heterotetrameric DHS; pH 7.5, 37°C, heterotetrameric DHS	738579	

top print hide 15 entries Go to Specific Activity Search

SPECIFIC ACTIVITY [µmol/min/mg]	ORGANISM	UNIPROT	COMMENTARY	LITERATURE
0.0000096	Leishmania donovani	B5APK2	low specific activity of DHS34 could be due to the fact that one of the NAD+ binding regions in the DHS34 is present in the big long insertion when compared with human deoxyhypusine synthase	704694
0.000137	Rattus norvegicus	-	-	638058
0.00325	Homo sapiens	-	-	638079
0.0034	Nicotiana tabacum	Q9SC80	with donor homospermidine	638061
0.0091	Nicotiana tabacum	Q9SC80	with donor homospermidine	
0.0101	Senecio vernalis	-	with acceptor eIF5A-precursor	
0.0131	Saccharomyces cerevisiae	-	-	
0.015	Homo sapiens	-	-	
0.019	Homo sapiens	-	-	638065
0.0211	Nicotiana tabacum	Q9SC	with donor spermidine	638061
0.0442	Senecio ver	-	with acceptor putrescine	638062
additional information	4 entries			

Click here to print the information field below

top print hide 14 entries Go to pH Optimum Search

pH OPTIMUM	ORGANISM	UNIPROT	COMMENTARY	LITERATURE
7.5	Trypanosoma brucei brucei	Q38BX0, Q4GZD1	assay at; assay at	738579
9 - 9.5	Homo sapiens	-	optimum for spermidine-binding	638069
9	2 entries			
9.2	3 entries			
9.3	Senecio vernalis	-	glycine-NaOH buffer	638080
9.4	Saccharolobus solfataricus	Q97ZF1	assay at	744857
9.5	Homo sapiens	-	assay at	721265
9.5 - 9.6	Rattus norvegicus	-	-	638075
9.5	2 entries			
9.6	Leishmania donovani	B5APK2	assay at; assay at	704694

top print hide 2 entries Go to pH Range Search

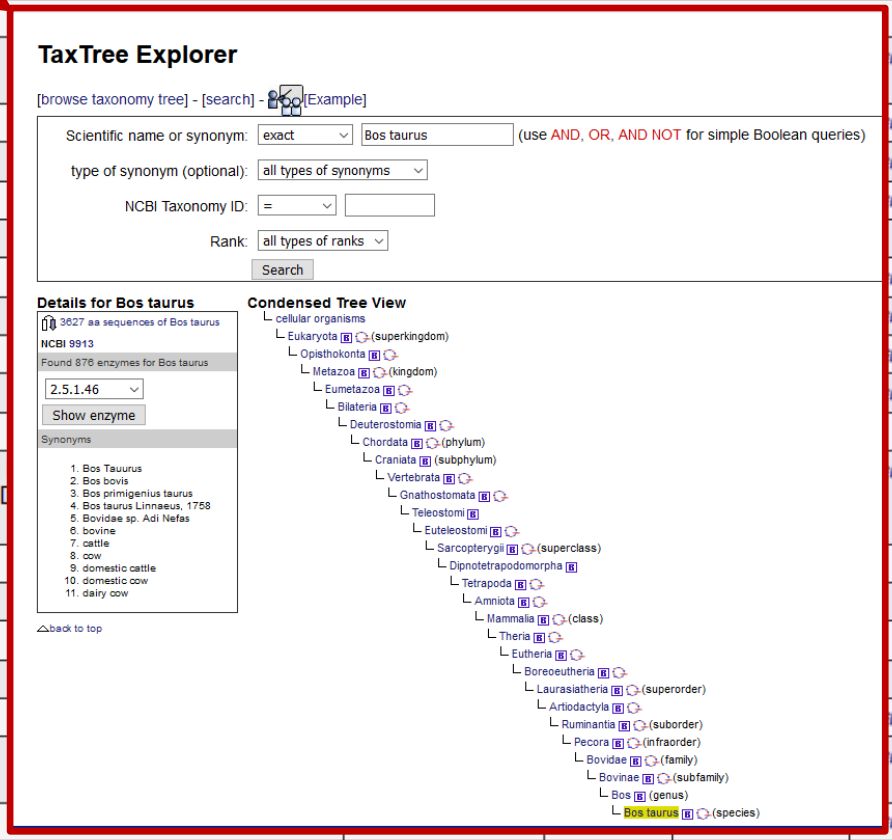
pH RANGE	ORGANISM	UNIPROT	COMMENTARY	LITERATURE

ORGANISM	COMMENTARY	LITERATURE	UNIPROT	SEQUENCE DB	SOURCE
Arabidopsis thaliana	2 entries				
Arabidopsis thaliana Col-0	gene dhs	738298, 738306	Q9FI94	UniProt	BRENDA
Bos taurus	2 entries				
Brassica napus	cv. Westar	660082	-	-	BRENDA
Convolvulus arvensis	gene dhs	739292	-	-	BRENDA
Convolvulus tricolor	gene dhs	739292	-	-	BRENDA
Cricetulus griseus	-	638081	-	-	BRENDA
Crotalaria juncea	-	660106	-	-	BRENDA
Crotalaria scassellatii	-	660106	Q4QZB4	Uniprot	BRENDA
Cryptosporidium parvum	single-copy gene DHS	739026	A3FQA5	UniProt	BRENDA
Distimake quinquefolius	gene dhs	739292	-	-	BRENDA
Fusarium graminearum	2 entries				
Fusarium graminearum FG00323.1	-				BRENDA
Gallus gallus	-				BRENDA
Haloferax volcanii	-				BRENDA
Haloferax volcanii LSP5021	-				BRENDA
Homo sapiens	5 entries				
Ipomoea alba	gene dhs	739292	-	-	BRENDA
Ipomoea hederifolia	gene dhs	739292	-	-	BRENDA
Ipomoea meyeri	gene dhs	739292	-	-	BRENDA
Ipomoea neei	gene dhs	739292	-	-	BRENDA
Leishmania donovani	3 entries				
Leishmania donovani MHOM/IN/1983/AG83	DHS34; DHSL20 is a DHS-like gene from chromosome 20 and DHS34, a DHS gene from chromosome 34	704694	B5APK2	SwissProt	BRENDA
Mus musculus	3 entries				
Mus musculus C57/BL6J	2 entries				
Neurospora crassa	2 entries				
Nicotiana tabacum	2 entries				
Phalaenopsis sp.	-	706133	-	-	BRENDA
Rattus norvegicus	-	638058, 638075, 638076	-	-	BRENDA
Saccharolobus solfataricus	-	744857	Q97ZF1	UniProt	BRENDA
Saccharolobus solfataricus DSM 1617	-	744857	Q97ZF1	UniProt	BRENDA

In the Organism section you will find all organisms expressing the enzyme

ORGANISM	COMMENTARY	LITERATURE	UNIPROT	SEQUENCE DB	SOURCE
Arabidopsis thaliana	2 entries				
Arabidopsis thaliana Col-0	gene dhs	738298, 738306	Q9FI94	UniProt	BRENDA
Bos taurus	2 entries				
Brassica napus	cv.				NDA
Convolvulus arvensis	gene dhs				NDA
Convolvulus tricolor	gene dhs				NDA
Cricetulus griseus	-				NDA
Crotalaria juncea					NDA
Crotalaria scassellatii	-				NDA
Cryptosporidium parvum	single-copy gene DHS	739026	A3FQA5	UniProt	BRENDA
Distimake quinquefolius	gene dhs	739292	-	-	BRENDA
Fusarium graminearum	2 entries				
Fusarium graminearum FG00323.1	-				NDA
Gallus gallus	-				NDA
Haloferax volcanii	-				NDA
Haloferax volcanii LSP5021	-				NDA
Homo sapiens	5 entries				
Ipomoea alba	gene dhs				NDA
Ipomoea hederifolia	gene dhs				NDA
Ipomoea meyeri	gene dhs				NDA
Ipomoea neei	gene dhs				NDA
Leishmania donovani	3 entries				
Leishmania donovani MHOM/IN/1983/AG83	DHS34; DHSL20 is a chromosome 20 and D chromosome 34				NDA
Mus musculus	3 entries				
Mus musculus C57/BL6J	2 entries				
Neurospora crassa	2 entries				
Nicotiana tabacum	2 entries				
Phalaenopsis sp.	-				NDA
Rattus norvegicus	-				NDA
Saccharolobus solfataricus	-				NDA
Saccharolobus solfataricus DSM 1617	-	744857	Q97ZF1	UniProt	BRENDA

Click on the organism to be linked to the TaxTree Explorer (see BRENDA Tutorial TaxTree)



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Cricetulus griseus	-	638081	-	-	BRENDA
Crotalaria juncea	-	660106	-	-	BRENDA
		660106	Q4QZB4	Uniprot	BRENDA
			A3F	UniProt	BRENDA
		739292	-	-	BRENDA
		723229	-	-	BRENDA
		638081	-	-	BRENDA
		737576	-	-	BRENDA
Haloferax volcanii LSP5021	-	737576	-	-	BRENDA
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Nicotiana tabacum	2 entries				
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Rattus norvegicus	-	638058, 638075, 638076	-	-	BRENDA
Saccharolobus solfataricus	-	744857	Q97ZF1	UniProt	BRENDA
Saccharolobus solfataricus DSM 1617	-	744857	Q97ZF1	UniProt	BRENDA

For detailed protein sequence information, click on the UniProt-ID to display the complete sequence

Sequence of Q4QZB4_9FABA

EC Number	Recommended Name	Accession Code	Organism	No of amino acids	Molecular Weight [Da]	Source
2.5.1.46	deoxyhypusine synthase	Q4QZB4	*Crotalaria scassellatii*	373	41278	TrEMBL

Reaction

dehydrospermidine + [enzyme]-lysine = N-(4-aminobutylidene)-[enzyme]-lysine + propane-1,3-diamine

Sequences with same EC No.

Crotalaria scassellatii (Q4QZB4) Show Sequence

Sequence

show sequence in fasta format

```
  0 MSEEVKEAAG GSDDVIASVH STVFKESENL QGKCTPIEGY DFNSGVDYHH LLNSMLTTGF
 60 QASNLGDAIQ LINQMLDWRL ADEPIAEDSS NDERDLNYRN SVTCKVFLGF TSNLISSGVR
120 DIVRFLCQHH MVDVIVTTTG GIEEDLIKCL APTYKGDFSL PGAYLRSKGL NRIGNLLVPN
180 DNYCKFEDWI IPIFDQMLKE QNEENVLWTP SKLIARLGKE INNESSYLYW AYKNNIPVYC
240 PGLTDGSLGD MLYFHSFRSP GLIVDIVQDI RAINGEAVHA SPRKTGMIIL GGGLPKHHIC
300 NANMMRNGAD YAVFINTAQE FDGSDSGARP DEAVSWGKIR GSAKTVKVHC DATIAFPLLV
360 AETFATRVKP CHQ
```

Detailed sequence information including links to the sequence database and download options are shown

Download this sequence

in fasta format

Download all sequences for 2.5.1.46

in fasta format

in csv (Excel, OpenOffice) format

Sequence related references

Sequence Reference	Authors	Title	Journal	Volume	Pages	Year	PubMed ID
56282490	Nurhayati N.,Ober D.	Recruitment of alkaloid-specific homospermidine synthase (HSS) from ubiquitous deoxyhypusine synthase: Does Crotalaria possess a functional HSS that still has DHS activity?	Phytochemistry	66	1346-1357	2005	15935411

BRENDA home
History

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- References 62
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ORGANISM	COMMENTARY	LITERATURE	UNIPROT	SEQUENCE DB	SOURCE
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Convolvulus tricolor	gene dhs	739292	-	-	BRENDA
Cricetulus griseus	-	638081	-	-	BRENDA
Crotalaria juncea	-	660106	-	-	BRENDA
Crotalaria scassellatii	-	660106	Q4QZB4	Uniprot	BRENDA
Cryptosporidium parvum	single-copy gene DHS	739026	A3FQA5	UniProt	BRENDA
Distimake quinquefolius	gene dhs		-	-	BRENDA
Fusarium g					
Fusarium graminearum FG00323.1			-	-	BRENDA
Gallus gallus	-		-	-	BRENDA
Haloferax volcanii	-		-	-	BRENDA
Haloferax volcanii LSP5021	-		-	-	BRENDA
Homo sapiens	5 entr				
Ipomoea alba	gene dhs		-	-	BRENDA
Ipomoea hederifolia	gene dhs	739292	-	-	BRENDA
Ipomoea meyeri	gene dhs	739292	-	-	BRENDA
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Neurospora crassa	2 entries				
Nicotiana tabacum	2 entries				
Phalaenopsis sp.	-	706133	-	-	BRENDA
Rattus norvegicus	-	638058, 638075, 638076	-	-	BRENDA
Saccharolobus solfataricus	-	744857	Q97ZF1	UniProt	BRENDA

Click on „Amino Acid Sequences“ or „Transmembrane Helices“ to get more information on protein sequences

Sequence on EC 2.5.1.46 - deoxyhypusine synthase

print visible entries
print all entries

Please use the AA Sequence and Transmembrane Helices Search for a specific query.

Go back to the **full version** of the Enzyme Summary Page.

UNIPROT	ENTRY NAME	ORGANISM	NO. OF AA	NO. OF TRANSM. HELICES	MOLECULAR WEIGHT[Da]	SOURCE	Sequence
Q9FI94 pBLAST	DHYS_ARATH	Arabidopsis thaliana	368	0	41064	Swiss-Prot	Show Sequence
Q75EW4 pBLAST	DHYS_ASHGO	Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056)	382	0	41984	Swiss-Prot	Show Sequence
Q6EWQ6 pBLAST	DHYS_BOVIN	Bos taurus	369	0	41029	Swiss-Prot	Show Sequence
Q6RJS2 pBLAST	DHYS_BRANA	Brassica napus	368	0	41162	Swiss-Prot	Show Sequence
Q9XXJ0 pBLAST	DHYS_CAEEL	Caenorhabditis elegans	371	0	40468	Swiss-Prot	Show Sequence
Q6FRN2 pBLAST	DHYS_CANGA	Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65)	385	0	42442	Swiss-Prot	Show Sequence
Q6BJH5 pBLAST	DHYS_DEBHA	Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / JCM 1990 / NBRC 0083 / IGC 2968)	378	0	41355	Swiss-Prot	Show Sequence
Q9AXQ8 pBLAST	DHYS_DIACA	Dianthus caryophyllus	373	0	41126	Swiss-Prot	Show Sequence
Q54MQ7 pBLAST	DHYS_DICDI	Dictyostelium discoideum	376	0	42544	Swiss-Prot	Show Sequence
Q9VSF4 pBLAST	DHYS_DROME	Drosophila melanogaster	368	0	41080	Swiss-Prot	Show Sequence
Q8SQN2 pBLAST	DHYS_ENCCU	Encephalitozoon cuniculi (strain GB-M1)	334	0	37447	Swiss-Prot	Show Sequence
B0R5L2 pBLAST	DHYS_HALS3			0	36381	Swiss-Prot	Show Sequence
Q9HPX2 pBLAST	DHYS_HALSA			0	36381	Swiss-Prot	Show Sequence
P49366 pBLAST	DHYS_HUMAN			0	40971	Swiss-Prot	Show Sequence
A8AA61 pBLAST	DHYS_IGNH4	Ignicoccus hospitalis (strain KIN4/I / DSM 18386 / JCM 14125)	319	0	35351	Swiss-Prot	Show Sequence
Q6CNG7 pBLAST	DHYS_KLULA	Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37)	379	0	42074	Swiss-Prot	Show Sequence
B5APK2	DHYS_LEIDO	Leishmania donovani	601	0	64440	Swiss-	Show

Here you find all published protein sequences, the number of trans-membrane helices etc.

Thermococcus kodakarensis	-	737576	-	-	BRENDA
Trichomonas vaginalis	gene TvDHS	737787	F1AQF9	UniProt	BRENDA
Trichomonas vaginalis CNCD 147	gene TvDHS	737787	F1AQF9	UniProt	BRENDA
Triticum aestivum	-	723229	-	-	BRENDA
Trypanosoma brucei brucei	2 entries				
Trypanosoma brucei brucei 927 / 4 GUTat10.1 / TREU927	2 entries				
Zea mays	2 entries				

top print hide 14 entries Go to PDB and Structure Links Search

PDB	SCOP	CATH	UNIPROT	ORGANISM
12 entries				Homo sapiens
4p63, download, 3D-view	SCOPe (4p63)	CATH (4p63)	O50105	Pyrococcus horikoshii (strain ATCC 700860 / DSM 12428 / JCM 9974 / NBRC 100139 / OT-3)
6dft, download, 3D-view	SCOPe (6dft)	CATH (6dft)	Q38BX0	Trypanosoma brucei brucei (strain 927/4 GUTat10.1)

Select items on the left to see more con...

top print hide 11 entries

EXTERNAL LINKS (specific for EC-Number 2.5.1.46)
ExplorEnz
ExPASy
KEGG
MetaCyc
SABIO-RK
NCBI: PubMed, Protein, Nucleotide, Structure, Gene, OMIM
IUBMB Enzyme Nomenclature
UniProt
PDB
PROSITE Database of protein families and domains
InterPro (database of protein families, domains and functional sites)

Jump to „PDB and Structure Links“ to get more information on protein structures

Thermococcus kodakarensis	-	737576	-	-	BRENDA
Trichomonas vaginalis	gene TvDHS	737787	F1AQF9	UniProt	BRENDA
Trichomonas vaginalis CNCD 147	gene TvDHS	737787	F1AQF9	UniProt	BRENDA
Triticum aestivum	-	723229	-	-	BRENDA
Trypanosoma brucei brucei	2 entries				
Trypanosoma brucei brucei 927 / 4 GUTat10.1 / TREU927	2 entries				
Zea mays	2 entries				

top print hide 14 entries Go to PDB and Structure Links Search

PDB	SCOP	CATH	UNIPROT	ORGANISM
12 entries				Homo sapiens
4p63, download, 3D-view	SCOPe (4p63)	CATH (4p63		/ JCM 9974 / NBRC
6dft, download, 3D-view	SCOPe (6dft)	C		

CATH Domains Close

Domain	Class	Architecture	Topology	Homologous Superfamily
4p63A00	Alpha Beta	3-Layer(aba) Sandwich	Deoxyhypusine Synthase	Deoxyhypusine synthase
4p63B00	Alpha Beta	3-Layer(aba) Sandwich	Deoxyhypusine Synthase	Deoxyhypusine synthase
4p63C00	Alpha Beta	3-Layer(aba) Sandwich	Deoxyhypusine Synthase	Deoxyhypusine synthase
4p63D00	Alpha Beta	3-Layer(aba) Sandwich	Deoxyhypusine Synthase	Deoxyhypusine synthase

Select items on the left to s

top print hide 11 entries

EXTERNAL LINKS (specific for EC-Number 2.5.1.46)
ExplorEnz
ExPASy
KEGG
MetaCyc
SABIO-RK
NCBI: PubMed, Protein, Nucleotide, Structure, Gene, OMIM
IUBMB Enzyme Nomenclature
UniProt
PDB
PROSITE Database of protein families and domains
InterPro (database of protein families, domains and functional sites)

Detailed information on protein structure classification of SCOPe and CATH are displayed by mouseover

ORGANISM	COMMENTARY	LITERATURE	UNIPROT	SEQUENCE DB	SOURCE
Arabidopsis thaliana	2 entries				
Arabidopsis thaliana Col-0	gene dhs	738298, 738306	Q9FI94	UniProt	BRENDA
Bos taurus	2 entries				
Brassica napus	cv. Westar	660082	-	-	BRENDA
Convolvulus arvensis	gene dhs	739292	-	-	BRENDA
Convolvulus tricolor	gene dhs	739292	-	-	BRENDA
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Distimake quinquefolius	gene dhs	739292	-	-	BRENDA
Fusarium graminearum	2 entries				
Fusarium graminearum FG00323.1	-	723229	-	-	BRENDA
Gallus gallus	-	638081	-	-	BRENDA
Haloferax volcanii	-	737576	-	-	BRENDA
Halofe		737576	-	-	BRENDA
Homo					
Ipomo		739292	-	-	BRENDA
Ipomo		739	-	-	BRENDA
Ipomo		73	-	-	BRENDA
Ipomoea neei	gene dhs	739292	-	-	BRENDA
Leishmania donovani	4 entries				
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Rattus norvegicus	-	638058, 638075, 638076	-	-	BRENDA
Saccharolobus solfataricus	-	744857	Q97ZF1	UniProt	BRENDA

To display the literature information click on the reference-ID…

BRENDA

Evolution of homospermidine synthase in the convolvulaceae: a story of gene duplication, gene loss, and periods of various selection pressures

Kaltenegger, E.; Eich, E.; Ober, D.; *Plant Cell* 25, 1213-1227 (2013) PubMed.gov Europe PMC

Data extracted from this reference:

Cloned(Commentary)

Cloned (Commentary)	Organism
gene dhs, single-copy gene, DNA and amino acid sequence determination and analysis, sequence comparisons and phylogenetic analysis, analysis of gene duplications in Convolvulaceae species	Convolvulus arvensis
gene dhs, single-copy gene, DNA and amino acid sequence determination and analysis, sequence comparisons and phylogenetic analysis, analysis of gene duplications in Convolvulaceae species	Ipomoea neei
gene dhs, single-copy gene, DNA and amino acid sequence determination and analysis, sequence comparisons and phylogen	
gene dhs, single-copy gene, DNA and amino acid sequence determination and analysis, sequence comparisons and phylogen	
gene dhs, single-copy gene, DNA and amino acid sequence determination and analysis, sequence comparisons and phylogen	
gene dhs, single-copy gene, DNA and amino acid sequence determination and analysis, sequence comparisons and phylogen	
gene dhs, single-copy gene, DNA and amino acid sequence determination and analysis, sequence comparisons and phylogen	

…to see the detailed literature information

Molecular Weight [Da]

Molecular Weight [Da]	Molecular Weight Maximum [Da]	Commentary	Organism
42100	-	-	Distimake quinquefolius
42200	-	-	Ipomoea neei
42200	-	-	Ipomoea meyeri
42300	-	-	Ipomoea hederifolia
42300	-	-	Ipomoea alba

Natural Substrates/ Products (Substrates)

Natural Substrates	Organism	Commentary (Nat. Sub.)	Natural Products	Commentary (Nat. Pro.)	Organism (Nat. Pro.)	Reversibility	ID
[eIF5A-precursor]-lysine + spermidine	Convolvulus arvensis	-	[eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine	-	-	?	
[eIF5A-precursor]-lysine + spermidine	Ipomoea neei	-	[eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine	-	-	?	
[eIF5A-precursor]-lysine + spermidine	Ipomoea hederifolia	-	[eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine	-	-	?	
[eIF5A-precursor]-lysine + spermidine	Ipomoea alba	-	[eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine	-	-	?	
[eIF5A-precursor]-lysine + spermidine	Ipomoea meyeri	-	[eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine	-	-	?	
[eIF5A-precursor]-lysine + spermidine	Distimake quinquefolius	-	[eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine	-	-	?	
[eIF5A-precursor]-lysine + spermidine	Convolvulus tricolor	-	[eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine	-	-	?	

Organism

Organism	UniProt	Commentary	Textmining
Convolvulus arvensis	-	gene dhs	-
Convolvulus tricolor	-	gene dhs	-
Distimake quinquefolius	-	gene dhs	-
Ipomoea alba	-	gene dhs	-
Ipomoea hederifolia	-	gene dhs	-
Ipomoea meyeri	-	gene dhs	-
Ipomoea neei	-	gene dhs	-

Source Tissue

Source Tissue	Commentary	Organism	Textmining
additional information	tissue-specific expression of enzyme DSS	Ipomoea neei	-

BRENDA

Evolution of homospermidine synthase in the convolvulaceae: a story of gene duplication, gene loss, and periods of various selection pressures

Kaltenegger, E.; Eich, E.; Ober, D.; *Plant Cell* 25, 1213-1227 (2013) PubMed.gov Europe PMC

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gene dhs, single-copy gene, DNA and amino acid sequence determination and analysis, sequence comparisons and phylogenetic analysis, analysis of gene duplications in Convolvulaceae species	Ipomoea meyeri
gene dhs, single-copy gene, DNA and amino acid sequence determination and analysis, sequence comparisons and phylogenetic analysis, analysis of gene duplications in Convolvulaceae species	Distimake quinquefolius
gene dhs, single-copy gene, DNA and amino acid sequence determination and analysis, sequence comparisons and phylogenetic analysis, analysis of gene duplications in Convolvulaceae species	Convolvulus tricolor

Molecular Weight [Da]

Molecular Weight [Da]	Molecular Weight Maximum [Da]	Commentary	Organism
42100	-	-	Distimake quinquefolius
42200	-	-	Ipomoea neei

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Evolution of homospermidine synthase in the convolvulaceae: a story of gene duplication, gene loss, and periods of various selection pressures

Elisabeth Kaltenegger [1], Eckart Eich, Dietrich Ober

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PMID: 23572540 PMCID: PMC3663263 DOI: 10.1105/tpc.113.109744

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Abstract

Homospermidine synthase (HSS), the first pathway-specific enzyme of pyrrolizidine alkaloid biosynthesis, is known to have its origin in the duplication of a gene encoding deoxyhypusine synthase. To study the processes that followed this gene duplication event and gave rise to HSS, we identified sequences encoding HSS and deoxyhypusine synthase from various species of the Convolvulaceae. We show that HSS evolved only once in this lineage. This duplication event was followed by several losses of a functional gene copy attributable to gene loss or pseudogenization. Statistical analyses of sequence data suggest that, in those lineages in which the gene copy was

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Kaltenegger E[1], Eich E, Ober D

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COFACTOR	ORGANISM	UNIPROT	COMMENTARY	LITERATURE	IMAGE
NAD+	Nicotiana tabacum	Q9SC80	-	638061	
	Senecio vernalis	-	-	638062	
	Homo sapiens	-	the NADH generated in the first step of the reaction remains enzyme-associated during the reaction and the hydride ion generated by the oxidation of spermidine is preserved for the reduction of the eIF5A-imine intermediate	638064	
		-	strict requirement	638065	
	Neurospora crassa	P49365	-	638066	
	Solanum pennellii	Q9AXR0	-	638067	
	Homo sapiens	-	one enzyme tetramer can bind up to four each of NAD+ and spermidine, the binding of spermidine being dependent on NAD+	638068	
		-	induces spermidine binding	638069	
				638070	
	Rattus norvegicus			638075	
		-		638058, 638076	
	Saccharomyces cerevisiae	-		638063, 638066, 638072, 638074, 638077, 638078	
	Homo sapiens	-		638059, 638071, 638073, 638079, 638083	
	Leishmania donovani	B5APK2		704694	
	Homo sapiens	-	required	723106	
	Trypanosoma brucei brucei	Q38BX0, Q4GZD1	required, Km value is 0.082 mM, kcat is 0.018/s for the heterotetrameric DHS; required, Km value is 0.082 mM, kcat is 0.018/s for the heterotetrameric DHS	738579	
	Cryptosporidium parvum	A3FQA5	required	739026	
NADH	8 entries				

Jump to the Enzyme-Ligand Interactions to learn about the substrates, products, inhibitors, cofactors etc., i.e. molecular structures

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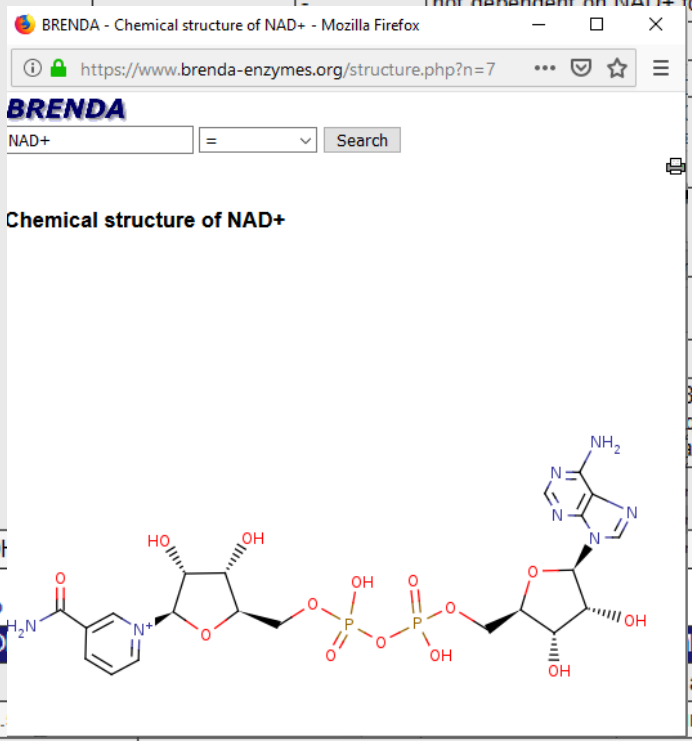
pH OPTIMUM	ORGANISM	UNIPROT	COMMENTARY	LITERATURE
7.5	Trypanosoma brucei brucei	Q38BX0, Q4GZD1	assay at; assay at	738579
9 - 9.5	Homo sapiens	-	optimum for spermidine-binding	638069
9	2 entries			
9.2	3 entries			
9.3	Senecio vernalis	-	glycine-NaOH buffer	638080
9.4	Saccharolobus solfataricus	Q97ZF1	assay at	744857

COFACTOR	ORGANISM	UNIPROT	COMMENTARY	LITERATURE	IMAGE
NAD+	Nicotiana tabacum	Q9SC80	-	638061	
	Senecio vernalis	-	-	638062	
	Homo sapiens	-	the NADH generated in the first step of the reaction remains enzyme-associated during the reaction and the hydride ion generated by the reduction	638064	
				638065	
	Neurospora c			638066	
	Solanum lycopersicum			638067	
	Homo sapiens	-	one enzyme tetramer can bind up to four each of NAD+ and spermidine, the binding of spermidine being dependent on NAD+	638068	
		-	induces spermidine binding	638069	
			not dependent on NAD+ for binding of eIF5A	638070	
				638075	
				638058, 638076	
				638063, 638066, 638072, 638074, 638077, 638078	
				638059, 638071, 638073, 638079, 638083	
				704694	
				723106	
			32 mM, kcat is 0.018/s for the quired, Km value is 0.082 mM, kcat is americ DHS	738579	
				739026	
NADH					

Click on to display the molecular structure



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pH O			ENTARY	LITERATURE
7.5			at; assay at	738579
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9	2 entries			
9.2	3 entries			
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		15377278
	The hypusine cascade prom cell carcinoma.	f RhoA in squamous 27041563
Carcinoma, Squamous Cell	The hypusine cascade prom cell carcinoma.	f RhoA in squamous 27041563
Diabetes Mellitus, Type 1	Deoxyhypusine synthase pr diabetes.	lls in autoimmune 24196968
	Protective effects of polyamine depletion in mouse models of type 1 diabetes: implications for therapy.	23846959
Diabetes Mellitus, Type 2	Inhibition of deoxyhypusine synthase enhances islet {beta} cell function and survival in the setting of endoplasmic reticulum stress and type 2 diabetes.	20956533
Glioblastoma	Expression of Eukaryotic Initiation Factor 5A and Hypusine Forming Enzymes in Glioblastoma Patient Samples: Implications for New Targeted Therapies.	22927971
Hyperglycemia	Protective effects of polyamine depletion in mouse models of type 1 diabetes: implications for therapy.	23846959
Leishmaniasis	Targeting polyamine metabolism for finding new drugs against leishmaniasis: a review.	25769972
Leukemia	Evaluation of deoxyhypusine synthase inhibitors targeting BCR-ABL positive leukemias.	22415796
	[The effect of eIF-5A on the G1-S in cell cycle regulation]	12962555
Leukemia, Erythroblastic, Acute	Effects of inhibitors of deoxyhypusine synthase on the differentiation of mouse neuroblastoma and erythroleukemia cells.	8697449
Malaria	A suggested vital function for eIF-5A and dhs genes during murine malaria blood-stage infection.	27516964
	Cloning, expression and functional activity of deoxyhypusine synthase from Plasmodium vivax.	17042947
	Piperidones with activity against Plasmodium falciparum.	16550432
Neoplasm Metastasis	The hypusine cascade promotes cancer progression and metastasis through the regulation of RhoA in squamous cell carcinoma.	27041563
Neoplasms	Aminohexanoic hydroxamate is a potent inducer of the differentiation of mouse neuroblastoma cells.	11098085
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	diabetes.	
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