

Sequence Search



Sequence Search



The Sequence Search is based on the Protein Knowledgebase
(UniProt KB) www.uniprot.org

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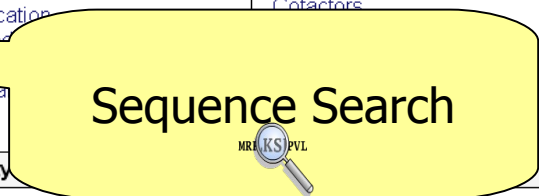
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Latest BRENDA update: June 2008

Nomenclature	Reaction & Specificity	Functional Parameters
Enzyme Names EC Number Common/ Recommended Name Systematic Name Synonyms CAS Registry Number	Pathway Catalysed Reaction Reaction Type Natural Substrates and Products Substrates and Products Substrates Natural Substrate Products Natural Product Inhibitors Cofactors	Km Value Ki Value IC50 Value pI Value Turnover Number Specific Activity pH Optimum pH Range Temperature Optimum Temperature Range
Isolation & Preparation		Organism-related information
Purification Crystallization		Organism Source Tissue Localization Protein-Specific Search
Stability		Disease & References
pH Stability Temperature Stability General Stability Organic Solvent Stability Oxidation Stability Storage Stability	Sequence/ SwissProt link 3D-Structure/ PDB link Molecular Weight Subunits Posttranslational Modification	Disease References
		Application & Engineering
		Engineering Application



Webmaster: **Maurice Scheer**
 m.scheer@tu-bs.de

For access to all features of the website Javascript must be activated, frames enabled and Java (at least version 1.4) has to be installed

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MRKS PVL Sequence Search

Examples:

Example	Search
sequences which contain "ikea"	start search
sequences which begin with "mia"	
sequences which end with "tkg"	
1. sequences which contain "tkr"	
2. followed by "mai" in a not defined distance	
sequences with the consensus PROSITE GDA1/CD39 family of nucleoside phosphatase [LIVM]-x-G-x(2)-E-G-x-[FY]-x-[FW]-[LIVA]	
You have a DNA or RNA sequence and want to know if the translated sequence codes for an enzyme	

The database search is restricted to amino acid sequences

Amino acid Sequence contains

No. of results: 1

Recommended name (or enzyme) contains

EC Number contains

1st Accession Code (UniProt) contains

Organism contains

Number of amino acids =

Molecular weight [Da] =

Transmembrane helices = N-term inside outside

Source SwissProt TrEMBL

reset Search

Search options:

- Amino acid sequence
- Recommended enzyme name
- EC number
- 1st Accession Code (UniProt)
- Organism
- Number of amino acids
- Molecular weight [Da]
- Transmembrane helices (calculated from TMHMM)

http://www.brenda-enzymes.info/sequences/index.php4

Start Enzyme Database - B... Frame-Information Tutorial Short tutorial - Open... DE 16:55

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Examples: Example
sequences which contain "ikea"
sequences which begin with "mia"
sequences which end with "tkg"
1. sequences which contain "tkr"
2. followed by "mai" in a not defined distance
sequences with the consensus PROSITE pat
GDA1/CD39 family of nucleoside phosphatas
[LIVM]-x-G-x(2)-E-G-x-[FY]-x-[FW]-[LVA]-[TA
You have a DNA or RNA sequence and want
if the translated sequence codes for an enzyr

The database search is restricted to amino acid s

Amino acid Sequence
contains
contains
exact
begins with
ends with
use * as joker
as regular expression
as DNA (forward and reverse)
as DNA 1st frame (forward)
as DNA 2nd frame (forward)
as DNA 3rd frame (forward)
as DNA 1st frame (reverse)
as DNA 2nd frame (reverse)
as DNA 3rd frame (reverse)

Molecular weight [Da] =
Transmembrane helices =
Source SwissProt Tr

Search modes for amino acid sequence:

- contains
- exact
- begins with
- ends with
- use * as a joker
- as regular expression
- as DNA (forward and reverse)
- as DNA 1st frame (forward)
- as DNA 2nd frame (forward)
- as DNA 3rd frame (forward)
- as DNA 1st frame (reverse)
- as DNA 2nd frame (reverse)
- as DNA 3rd frame (reverse)

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MARKS PVL Sequence Search

Examples:	Example	Search
	sequences which contain "ikea"	start search
	sequences which begin with "mia"	start search
	sequences which end with "tkg"	start search
	1. sequences which contain "tkr" 2. followed by "mai" in a not defined distance	start search
	sequences with the consensus PROSITE pattern PDOC00952: GDA1/CD39 family of nucleoside phosphatases [LIVM]-x-G-x(2)-E-G-x-[FY]-x-[FW]-[LVA]-[TAG]-x-N-[HY]	start search
	You have a DNA or RNA sequence and want to know if the translated sequence codes for an enzyme	start search

The database search is restricted to amino acid sequences of enzymes!

Amino acid Sequence

contains

No. of results 10

Recommended name (PFI12)ME contains

EC Number contains

1st Accession Code (U+IP10) exact

Organism begins with

use * as joker ends with

Number of amino acids =

Molecular weight [Da] =

Transmembrane helices = N-term inside outside

Source SwissProt TREMBL

reset Search

Remaining search modes:

- contains
- exact
- begins with
- ends with
- use * as a joker

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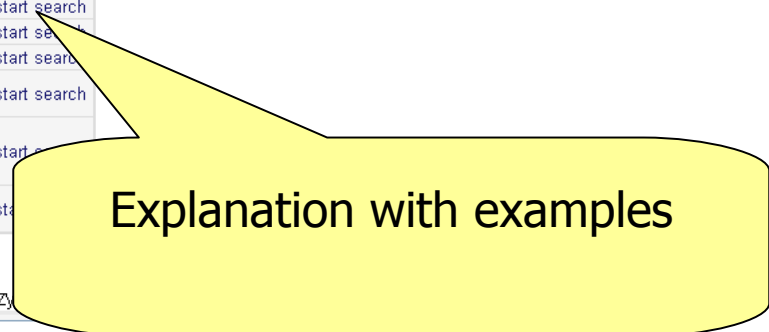
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MRKS PVL Sequence Search

Examples:	Example	Search
	sequences which contain "ikea"	start search
	sequences which begin with "mia"	start se
	sequences which end with "tkg"	start sear
	1. sequences which contain "tkr"	start search
	2. followed by "mai" in a not defined distance	
	sequences with the consensus PROSITE pattern PDOC00952: GDA1/CD39 family of nucleoside phosphatases [LVM]-x-G-x(2)-E-G-x-[FY]-x-[FW]-[LVA]-[TAG]-x-N-[HY]	start
	You have a DNA or RNA sequence and want to know if the translated sequence codes for an enzyme	sta



The database search is restricted to amino acid sequences of enz

Amino acid Sequence

contains

No. of results 10

Recommended name (of enzyme) contains

EC Number contains

1st Accession Code (UIP top) contains

Organism contains

Number of amino acids =

Molecular weight [Da] =

Transmembrane helices = N-term inside outside

Source SwissProt TREMBL

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Amino acid Sequence:

contains

No. of results: 10

Recommended name (of 12 max):

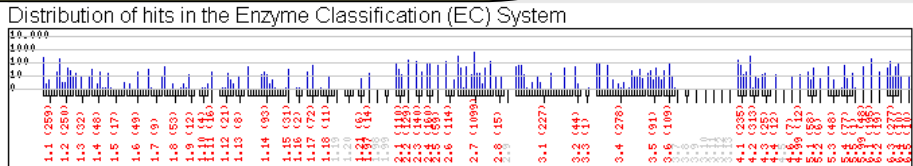
inside outside

reset Search

Choose the search mode:

- contains
- begins with
- ends with

Search a specific amino acid sequence.



1-10 of 4538 results

No.	EC Number	Recommended Name	1st Accession Code	Organism	No of Transm. helices	No aa	MW	Source	Tools/Links
1.	1.1.1.1	alcohol dehydrogenase	P33744	Clostridium acetobutylicum	0	862	95321	Swiss-Prot	
		... EKLKVIKEAQKKFS ...							
		alcohol dehydrogenase							

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MR(KS)PVL Sequence Search

The database search is restricted to amino acid sequences of enzymes!

Amino acid Sequence *tkr*mai*
use * as a joker

of results 10

contains

Molecular weight [Da] =
Transmembrane helices = N-term inside outside
Source SwissProt TrEMBL

reset Search

Distribution of hits in the Enzyme Classification (EC) System

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No.	EC Number	Recommended Name	1st Accession Code	Organism	No of Transm. helices	No aa	MW	Source	Tools/Links
1.	1.1.1.27	L-lactate dehydrogenase	Q96569	Solanum lycopersicum	0	350	37708	TrEMBL	
2.	1.1.1.27	L-lactate dehydrogenase	A5AJN7	Vitis vinifera	0	350	37627	TrEMBL	
3.	1.1.1.27	L-lactate dehydrogenase	A5B3L3	Vitis vinifera	0	356	38221	TrEMBL	

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Start TOSHIBA (F:) Short tutorial - Open... Enzyme Database - B... LEO Ergebnisse für "s... DE 09:41

Choose the search mode "use * as a joker".

Use * to search for sequences followed by another sequence in a not defined distance.

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MRI KSPVL Sequence Search

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Amino acid Sequence: TACTGTGCGAAATTGATACTCCTATTGGGTTGTTTTGGATTAGTTCGTCGCTTCTGAT
 CCAGTTGATCCGCTGCTAGTGGATCTCCCAATGGCAAGCTACGCGGACGCGATAACGGC
 AACTATTATAGCTACGAATCGCTTCCTACGGCTGAGCCCCAGTCGGAGATCTAAGATTT
 GAAGCCCCGCAACCGTACAAGCAAGCTGGACGGACACTTTCGATGCCACCCAACCAC

as DNA (forward and reverse)

No. of results: 10

Recommended name (or enzyme): contains

transmembrane helices = N-term i

Source SwissProt TREMBL

Frame	Direction	Search mode	No. of results	Translated sequence
1st	forward	contains	0	YCAKLIILLGCFWISSASDPVDPLLVLDLPNGKLRGRDNGNYSYESLPYAEPVGDLE EAPQFYKQWTDTFDATOP
2nd	forward	contains	0	TVRNYSYVWVGLVRLPLLIQLIRCWISPMASYADAITATIIATNRFPTLSPQSEIDL KPRNRTSSSGRTLSPPNH
3rd	forward	contains	0	LCEIDTPIGLFLDFVRFSSSAAGSPQWQATRTROLRLRIASLRAPSRRSKI SPATVQAAVDGHRCHFT
1st	reverse	contains	0	HQPTVAFTRGRRTTCQRPVENLEADPRVASLRASILSTAIAQAHRTVPLGDRRLVLDL VFACLRFLGYPHSVSVS
2nd	reverse	contains	0	TNPFLSQAGDDEHANAPKFRIRLTPESHFPAKHRYVQQRRIERPIVIVALT SSPALGFCWVILIVKACH
3rd	reverse	contains	0	PTHRSFHRQVTTNMPTRPSLESRGPPSRIPSLSIDIINGNSAGASNGNPSRSSPS LRLLLVFWGLSSLKR

No results found

Choose the search mode "as DNA (forward and reverse)".

Check here, if your chosen DNA or RNA sequence converted for an enzyme.

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The database search is restricted to amino acid sequences of enzymes!

Amino acid Sequence [LIVM].G.(2)EG.[FY].[FW][LIVA][TAG].N[HY]
as regular expression

No. of results 10
Recommended name

1-10 of 39 results

No.	EC Number	Recommended Name	1st Accession Code	Organism	No of Transm. helices	No aa	MW	Source	Tools/Links
1.	3.6.1.5	aprase	P49961	Homo sapiens	2	510	57965	Swiss-Prot	
2.	3.6.1.5	aprase	Q9MYU4	Sus scrofa	2	510	57757	Swiss-Prot	
3.	3.6.1.5	aprase	Q8KDL2	Mus musculus	2	497	54650	Swiss-Prot	
4.	3.6.1.5	aprase	P40009	Saccharomyces cerevisiae	1	630	71852	Swiss-Prot	
5.	3.6.1.5	aprase	P55772	Mus musculus	2	510	57205	Swiss-Prot	

Warten auf www.brenda-enzymes.info...

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For example sequences with the consensus PROSITE pattern PDOC00952: GDA1/CD39 family of nucleoside phosphatases. Choose the search mode "as regular expression".

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MRKSPVL Sequence Search

The database search is restricted to amino acid sequences of enzymes!

Amino acid Sequence:

contains

No. of results: 10

Recommended name (of enzyme): contains

amino acids: =

Molecular weight [Da]: =

Transmembrane helices: =

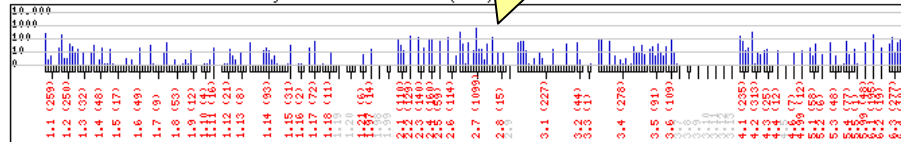
Source: SwissProt TrEMBL

inside outside

reset Search

Scroll down to look at the results.

Distribution of hits in the Enzyme Classification (EC) System



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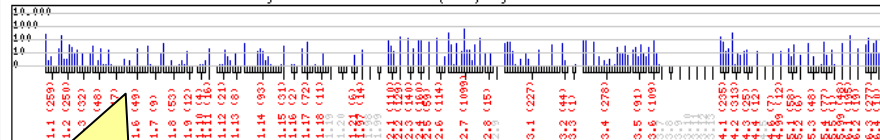
No.	EC Number	Recommended Name	1st Accession Code	Organism	No of Transm. helices	No aa	MW	Source	Tools/Links
1.	1.1.1.1	alcohol dehydrogenase 16 ...EKLKVIKEAQKFS...	P33744	Clostridium acetobutylicum	0	862	95321	Swiss-Prot	

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	Recommended Name	1st Accession Code	Organism	No of Transm. helices	No aa	MW	Source	Tools/Links
				0	862	95321	Swiss-Prot	
				0	185	19674	TrEMBL	
3.	1.1.1.1 ... LHPDR I KEARKFGV ... alcohol dehydrogenase	Q1J919	Streptococcus pyogenes serotype M4 (strain MGAS10270)	0	338	35294	TrEMBL	
4.	1.1.1.1 ... TTYKA I KEAGAAPG ... alcohol dehydrogenase	Q04MG5	Streptococcus pneumoniae serotype 2 (strain D39 / NCTC 7486)	0	339	35750	TrEMBL	
5.	1.1.1.1 ... TTYKA I KEAKVEPG ... alcohol dehydrogenase	Q1J665	Streptococcus pyogenes serotype M2 (strain MGAS10270)	0	338	35380	TrEMBL	
6.	1.1.1.1 ... PTYKA I KEAGAAPG ... alcohol dehydrogenase	Q1JP20	Streptococcus pyogenes serotype M12 (strain MGAS9429)	0	357	37805	TrEMBL	
7.	1.1.1.1 ... RYTRV I YKAOYTVS ... alcohol dehydrogenase	A5HYN9	Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	0	862	94651	TrEMBL	

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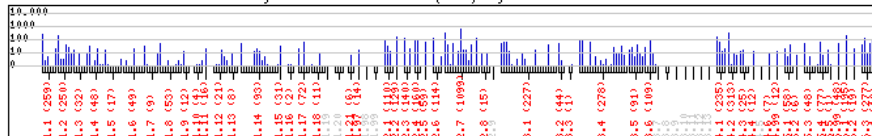
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Listed results

No.	EC Number	Recommended Name	1st Accession Code	Organism	No of Transm. helices	No aa	MW	Source	Tools/Links
1.	1.1.1.1	alcohol dehydrogenase 16 ...EKLKV I KEA Q KKFS...	P33744	Clostridium acetobutylicum	0	862	95321	Swiss-Prot	
2.	1.1.1.1	alcohol dehydrogenase 133 ...LHPDR I KEA R KFGV...	Q9M3S9	Betula verrucosa	0	185	19674	TrEMBL	
3.	1.1.1.1	alcohol dehydrogenase 155 ...TTYKA I KEA G AAPG...	Q1J919	Streptococcus pyogenes serotype M4 (strain MGAS10750)	0	338	35294	TrEMBL	
4.	1.1.1.1	alcohol dehydrogenase 155 ...TTYKA I KEA K VEPG...	Q04MG5	Streptococcus pneumoniae serotype 2 (strain D39 / NCTC 7486)	0	339	35750	TrEMBL	
5.	1.1.1.1	alcohol dehydrogenase 155 ...TTYKA I KEA G AAPG...	Q1J665	Streptococcus pyogenes serotype M2 (strain MGAS10270)	0	338	35380	TrEMBL	
6.	1.1.1.1	alcohol dehydrogenase 174 ...PTYKA I KEA G AAPG...	Q1JP20	Streptococcus pyogenes serotype M12 (strain MGAS9429)	0	357	37805	TrEMBL	
7.	1.1.1.1	alcohol dehydrogenase 16 ...RVLTEV I KEA Q LVLC	A5HYN9	Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	0	862	94651	TrEMBL	

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No.	EC Number	Recommended Name	1st Accession Code	Organism	No of Transm. helices	No aa	MW	Source	Tools/Links
1.	1.1.1.1	alcohol dehydrogenase	P337	Escherichia coli	0	362	95321	Swiss-Prot	
		EKTKVTKFAOKKES							
				(strain					
				2 (strain D39 /	0	339	35750	TrEMBL	
				(strain	0	338	35380	TrEMBL	
				2 (strain	0	357	37805	TrEMBL	
				ATCC 3502 / NCTC	0	862	94651	TrEMBL	

Table of results:

- No. of results
- EC number
- Recommended name 1st accession code
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- No. of transmembrane helices
- No. of amino acids
- Molecular weight (MW)
- Source
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Click on the arrows for ascending or descending sort.

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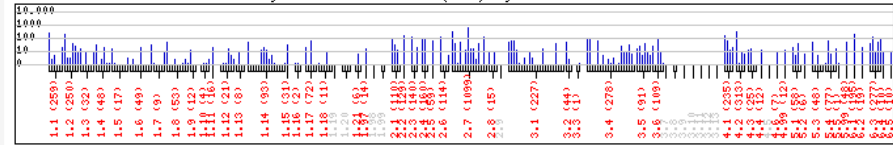
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No.	EC Number	Recommended Name	1st Accession Code	Organism	No of Transm. helices	No aa	MW	Source	Tools/Links
1.	1.1.1.1	alcohol dehydrogenase ... EKLKVIKEAQKKFS ...	P33744	Clostridium acetobutylicum	0	862	95321	Swiss-Prot	
2.	1.1.1.1	alcohol dehydrogenase ... SHPDRIKEARKFGV ...	Q9M3S9	Betula verrucosa	0	185	19674	TrEMBL	
		alcohol dehydrogenase ... EEF ...	Q1J919	Streptococcus pyogenes serotype M4 (strain MGAS10750)	0	338	35294	TrEMBL	
		alcohol dehydrogenase	Q04MG5	Streptococcus pneumoniae serotype 2 (strain D39 / NCTC 7466)	0	339	35750	TrEMBL	
5.	1.1.1.1	alcohol dehydrogenase ... TTYKAIKE ...			0	338	35380	TrEMBL	
6.	1.1.1.1	alcohol dehydrogenase ... PTYKAIKEAGAAPG ...			0	357	37805	TrEMBL	
7.	1.1.1.1	alcohol dehydrogenase ... RYIEYIKFAOKIYS ...	A5HYN9	Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	0	862	94651	TrEMBL	

Click on the EC number for more enzyme data.

Click on the organism to get a link to Tax Tree.

Enzyme Database - BRENDA - Mozilla Firefox

http://www.brenda-enzymes.info/

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BRENDA
The Comprehensive Enzyme Information System

Distribution of hits in the Enzyme Classification (EC) System

1-10 of 4538 results

No.	EC Number	Recommendation	MW	Source	Tools/Links
1.	1.1.1.1	alcohol dehydrogenase			
2.	1.1.1.1	alcohol dehydrogenase		TrEMBL	
3.	1.1.1.1	alcohol dehydrogenase		TrEMBL	
4.	1.1.1.1	alcohol dehydrogenase	750	TrEMBL	
5.	1.1.1.1	alcohol dehydrogenase	338	35380 TrEMBL	
6.	1.1.1.1	alcohol dehydrogenase	357	37805 TrEMBL	
7.	1.1.1.1	alcohol dehydrogenase	862	94651 TrEMBL	

Tools / links:

- Perform a BLAST (Basis Local Alignment) Search.
- Prediction of transmembrane helices in proteins.
- Explore the genomic neighborhood of the protein.

Fertig

Start Short tutorial - Open... Enzyme Database - B... DE 15:43

Ideas for *BRENDA's*
improvement welcome !!!