



EBI services

Jennifer McDowall

EMBL-EBI

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des brevets

enzymeta
GmbH



Overview

- **Introduction**
- **EBI Databases**
- **Searching for sequences**
 - Simple EB-eye search
 - Advanced SRS text search
 - Sequence search tools
- **Accessing Old entries**
 - Sequence archives



Website:

<http://www.ebi.ac.uk/>

EB-eye
Search all main databases in one go

Data Resources & Tools

- EMBL-BANK
- UniProt
- ArrayExpress
- Ensembl
- InterPro
- PDB-EBI

- Genomes
- Nucleotide Sequences
- Protein Sequences
- Macromolecular Structures
- Small Molecules
- Gene Expression
- Molecular Interactions
- Reactions & Pathways
- Protein Families
- Enzymes
- Literature
- Taxonomy
- Ontologies
- Sequence Similarity & Analysis
- Pattern & Motif Searches
- Structure Analysis
- Text Mining
- Downloads

Thematic index



European Bioinformatics Institute

About the EBI

- Research
- Training
- Industry Support
- Group & Team Leaders
- EBI Funders
- User Support
- EBI Mission
- People
- Events at the EBI
- How to Find us

Latest News

RSS

June 07, 2007
EBI consolidates management of sequence data
 Today the European Bioinformatics Institute announces a major reorganisation of its processing of biomolecular sequence information. This will affect EMBL-Bank, UniProt and the EBI team working on Ensembl (which is a joint project with the Wellcome Trust Sanger Institute)... [more](#)



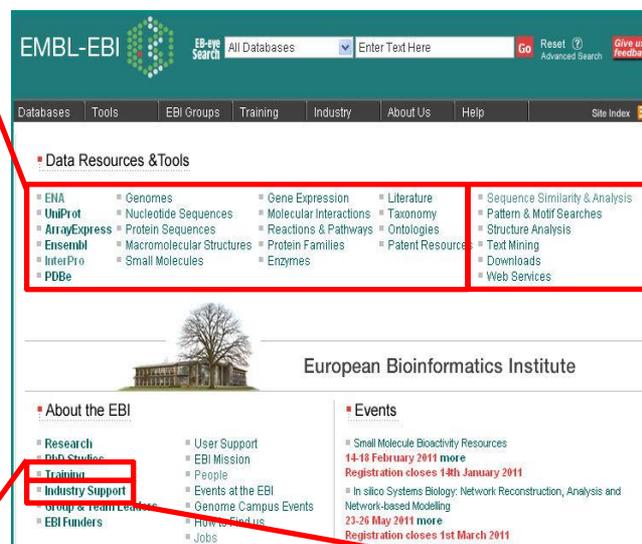
Website:

Databases

- Patent resources
- Sequences
- Genomes
- Chemistry
- Structures
- Gene expression
- Reactions & pathways
- Literature

Tools

- Sequence searching
- Sequence analysis
- Structural analysis
- Functional analysis



Training

- eLearning
- Workshops
- 2Can education resource

Industry programme

- Industry support
- SME Support

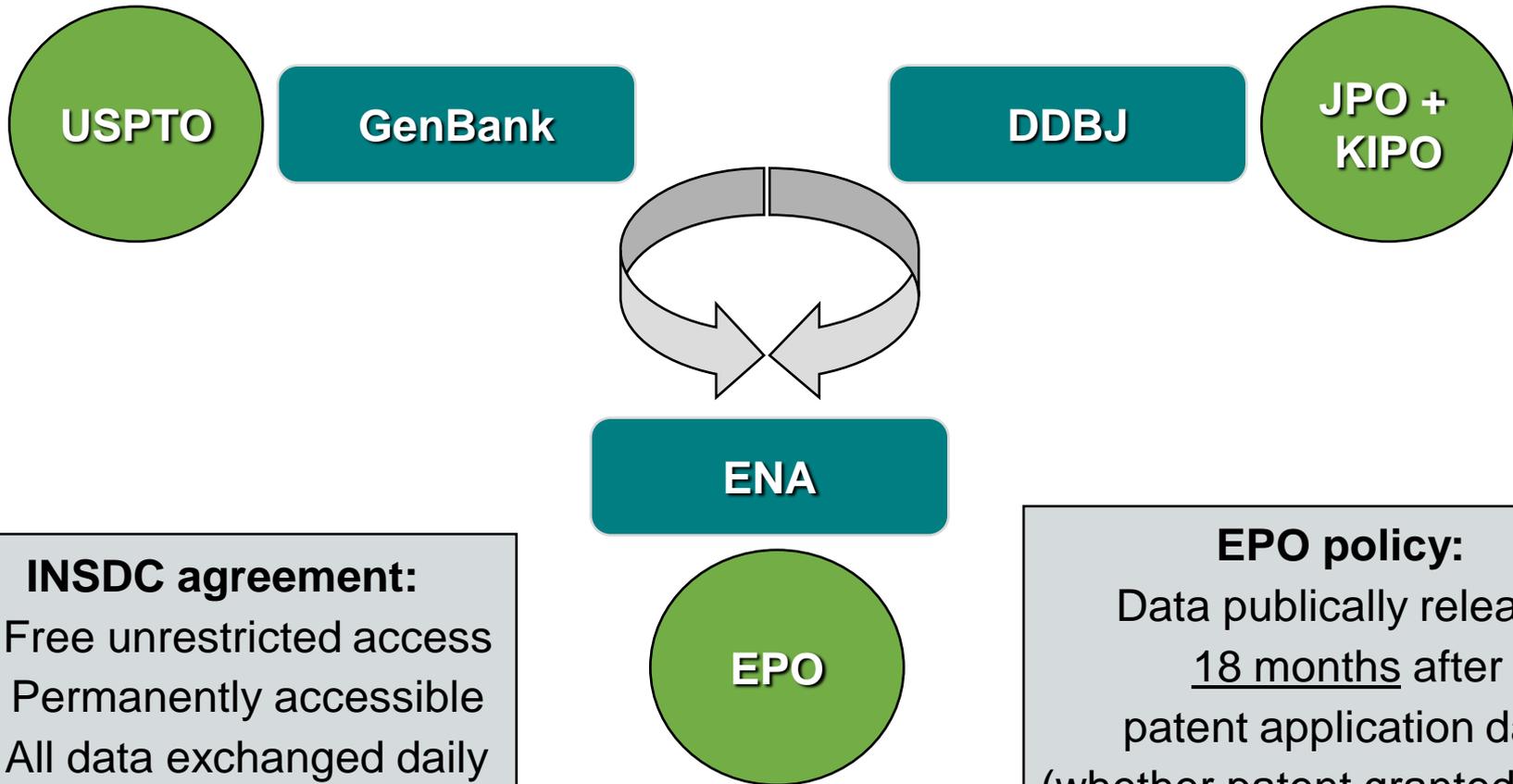


EBI databases

patent-related resources...



Sequence data from patent literature



INSDC agreement:

- Free unrestricted access
- Permanently accessible
- All data exchanged daily

EPO policy:

Data publically released
18 months after
patent application date
(whether patent granted or not)

October 2010

patent nucleotides > 17.5m sequences
patent proteins > 4.9m sequences



Patent resources at EBI

Resources	Description	Access
Patent Abstracts	Patent abstracts contain the biology-related abstracts of patent applications derived from data products of the European Patent Office (EPO). Patent documents from Europe (EP), USA (US) and World (WO) are included. Patent abstracts can be accessed via the SRS, EB-eye and the literature search engine CiteXplore.	CiteXplore EB-eye SRS
Patent Chemical Compounds	Patent chemical compounds are available in the ChEBI database which is a dictionary of molecular entities focused on 'small' chemical compounds. You can search the patent chemical compounds using the ChEBI Advanced Search page by narrowing down your search to the Patent Database.	ChEBI ChEBI Advanced
Patent Sequences	Multiple sets of patent sequences are available at EBI. <ol style="list-style-type: none"> Patent proteins cover sequences of EPO (European Patent Office) proteins, JPO (Japan Patent Office) proteins, KIPO (Korean Intellectual Property Office) proteins and USPTO (United States Patent and Trademark Office) proteins. Patent nucleotides contain the patent class data in the EMBL-Bank. Non-redundant patent sequences consist of 2 levels databases. Level-1 non-redundant patent sequences are 100% identical over the same length; Level-2 non-redundant patent sequences are identical and belong to a same patent family (a same invention). 	Patent proteins Patent nucleotides Non-redundant patent sequences
Patent Equivalent Data	A "patent family" can be defined as all patent equivalents for a single invention. All of the published patent applications from various countries and the subsequent granted patents on an invention are commonly referred to as patent equivalents. They are not "true equivalents" in that each country may have different regulations for filing and different interpretations of the invention. It may include multiple patents in some countries because of differences in patent laws (e.g., how much new technology can be included in a single patent).	SRS



Patent sequence records at EBI

ENA
(formerly EMBL-Bank)

- >124 million sequences
- p

**non-patent sequence
prior art searches**

UniParc
(division of UniProt)

- 74
- patent + non-patent proteins
- non-redundant

**NR patent
sequences**

- p
- ac

**patent sequence
prior art searches**

Sequence submissions

Generate sequence

Step 1

Submit claim to EPO



Step 2

Submit ~~to~~ journal **Not accepted**

Submit to ENA → Submit to journal

Enter data - denotes mandatory fields **vmap axis 1**

Entry number	Organism	Amplification strategy	Strain name	Clone identifier	Isolate name	Isolation source	Culture collection	sequence
1	Escherichia coli, serotype: EPEC, O157:H7, D66/94	<input type="radio"/> Yes <input type="radio"/> No If yes, indicate source, instrument & assembly	EHEC 542, O157:H7	nc211_109, nt_3_3	biochem1_054g14	fast freezing cow reservoir	ATCC 35270	
2		<input type="radio"/> Yes <input type="radio"/> No						
3		<input type="radio"/> Yes <input type="radio"/> No						
4		<input type="radio"/> Yes <input type="radio"/> No						
5		<input type="radio"/> Yes <input type="radio"/> No						

Submission guides at www.ebi.ac.uk





Searching for sequences

simple EB-eye search...



EB-eye – search by patent number

Search for patent
WO0146262

Data Resources & Tools

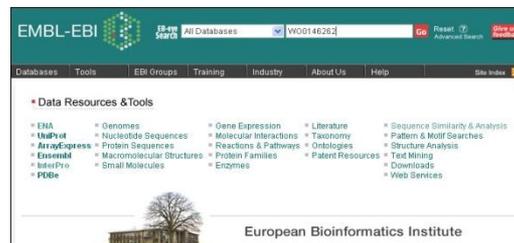
- [ENA](#)
- [UniProt](#)
- [ArrayExpress](#)
- [Ensembl](#)
- [InterPro](#)
- [PDBe](#)
- [Genomes](#)
- [Nucleotide Sequences](#)
- [Protein Sequences](#)
- [Macromolecular Structures](#)
- [Small Molecules](#)
- [Gene Expression](#)
- [Molecular Interactions](#)
- [Reactions & Pathways](#)
- [Protein Families](#)
- [Enzymes](#)
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- [Pattern & Motif Searches](#)
- [Structure Analysis](#)
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European Bioinformatics Institute



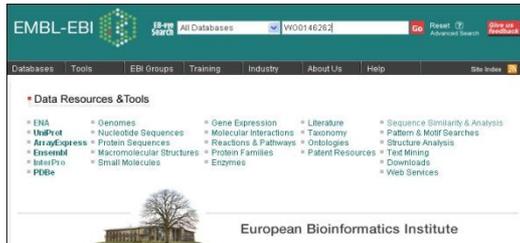
EB-eye – search by patent number



Search for WO0146262



EB-eye – search by patent number



Search for WO0146262

Databases with sequence data for WO0146262

EMBL-EBI EB-eye Search All Databases WO0146262 Go Reset Advanced Search Give us feedback

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Search for *WO0146262* in All the EBI

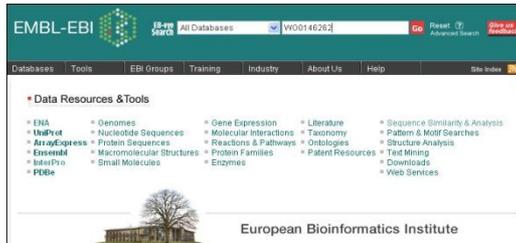
Expand all Collapse all

Genomes	0	Molecular Interactions	0
Nucleotide Sequences	253	Reactions & Pathways	0
INSDC Project <i>INSDC Project records from the European Nucleotide Archive</i>	0	Protein Families	0
ASTD <i>Database of alternative splice events and transcripts of genes from human, mouse and rat.</i>	0	Enzymes	0
EMBL-Bank <i>Europe's primary nucleotide sequence resource</i>	253	Literature	2
EMBL-Bank (Coding Sequence) <i>Coding Sequences in EMBL-Bank</i>	0	Medicine <i>Citations and abstracts from many life-science journals</i>	0
Sequence Read Archive (SRA) <i>Next generation sequencing raw data repository from the European Nucleotide Archive</i>	0	Patents <i>Biology-related abstracts of patent applications</i>	2
Protein Sequences	0	Ontologies	0
Macromolecular Structures	0	EBI Web Site	0
Small molecules	0		
Gene Expression	0		

Literature for WO0146262



EB-eye – search by patent number



Search for WO0146262

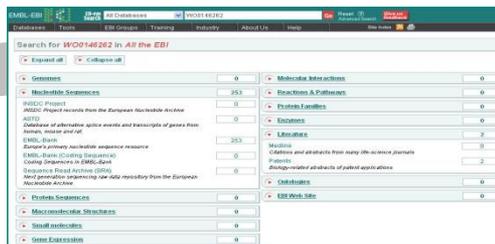


WO0146262 literature and sequence databases

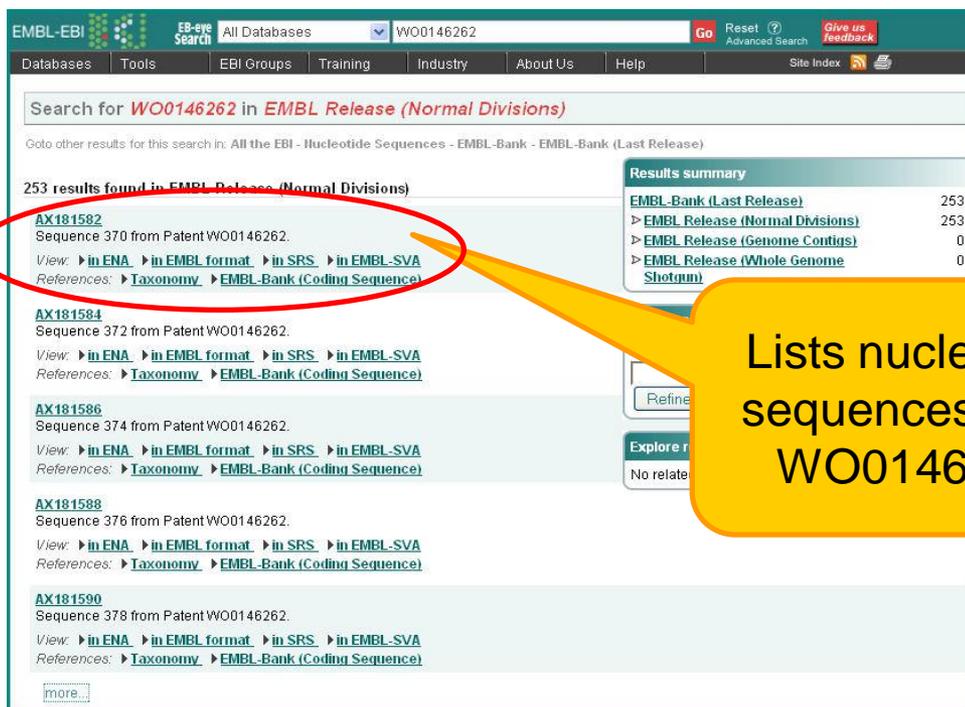
EB-eye – search by patent number



Search for WO0146262



WO0146262 literature and **sequence databases**



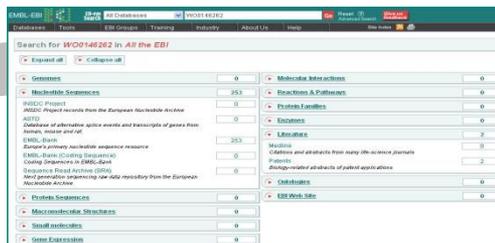
Lists nucleotide sequences from WO0146262



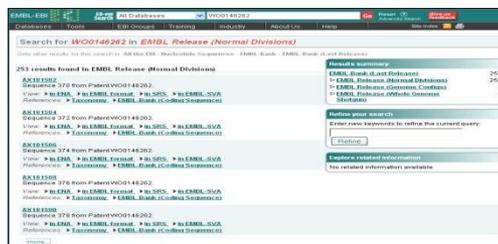
EB-eye – search by patent number



Search for WO0146262



WO0146262 literature and **sequence databases**



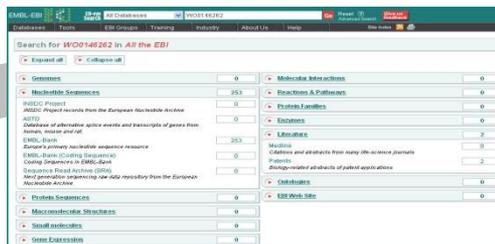
WO0146262 sequences



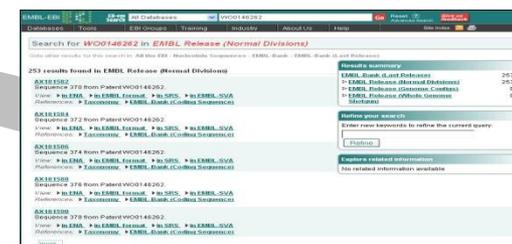
EB-eye – search by patent number



Search for WO0146262



WO0146262 literature and **sequence databases**



WO0146262 sequences

EMBL-Bank : A39349.1 : Sequence 15 from Patent WO9413821.

View: TEXT XML FASTA Download: TEXT XML FASTA

Overview Source Feature Other Features References Comments Sequence Send feedback

Molecule type	Topology	Date class	Sequence length	Sequence Version	First public	Last update
unassigned DNA	linear	PAT	300	1	1997-03-05 (Release 51)	2008-11-14 (Release 89)

Description
Sequence 15 from Patent WO9413821.

Navigation
Taxon: [#511](#) : *Kluyveromyces marxianus*
SVA: Historical versions of this EMBL-Bank record are available here: [#39349](#)
CABRI: [CBS 6556](#)
StrainInfo: [#55008](#)

Visible feature range: 1 300

Overview
Forward strand 300 bp
A39349.1
Features
Forward strand 300 bp
1 bp
Source
Kluyveromyces marxianus
Genes
CDS
TRU1

Source/CO Feature(s)
Source 1..300
Taxon: [#511](#) : *Kluyveromyces marxianus*
Strain CBS 6556
Clone PUR2415

Other Features
Visible feature range: 1 300 Filter: Default Main
CDS 5..295
partial
gene
product TRU1
protein_id [CAA02439](#)
translation [MAEIQITFSLIRFQVYFFFRSRWQDFHSLMYDAKEEDRWLQYVYRPAATIMSTFLYNGHAYSKDLETSTKDYGSLGPPG](#)
[DDAQLFQSHVLDYNNI](#)
EMBL-CDS [CAA02439](#)

References
[1] THE USE OF THE KLUYVEROMYCES MARXIANUS HULINASE GENE PROMOTER FOR PROTEIN PRODUCTION
CHAPMAN John William, MUSTERS Visster, ROUVENHORST Robert Jan, TOSCHKA Helger York, VERBAKEL Johannes Maria A.
QUEST INTERNATIONAL B.V.
(PubMed:W09413821) abstract
CiteSpace

Comments
Other publication [EU 5811194 940704](#)

Sequence
Visible sequence range: 1 1000 Apply
>ENA:A39349.1:A39349.1 Sequence 15 from Patent WO9413821. 1 Location:1..10
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WO0146262
nucleotide sequence
record in ENA

Patent sequence record in ENA

Sequence version

Navigate to related data e.g. Version archive

Accession Number	Seq. version	Release Date	Release	New Date
A39349.1	1	2006-11-14	Release 89	2006-11-14
A39349.1	2	2007-03-05	Release 91	2007-03-05
A39349.1	3	2007-03-05	Release 91	2007-03-05
A39349.1	4	2007-03-05	Release 91	2007-03-05
A39349.1	5	2007-03-05	Release 91	2007-03-05
A39349.1	6	2007-03-05	Release 91	2007-03-05
A39349.1	7	2007-03-05	Release 91	2007-03-05
A39349.1	8	2007-03-05	Release 91	2007-03-05
A39349.1	9	2007-03-05	Release 91	2007-03-05
A39349.1	10	2007-03-05	Release 91	2007-03-05
A39349.1	11	2007-03-05	Release 91	2007-03-05
A39349.1	12	2007-03-05	Release 91	2007-03-05
A39349.1	13	2007-03-05	Release 91	2007-03-05
A39349.1	14	2007-03-05	Release 91	2007-03-05
A39349.1	15	2007-03-05	Release 91	2007-03-05

Patent reference

Sequence

EMBL-Bank : A39349 .1 : Sequence 15 from Patent WO9413821.

View: [TEXT](#) [XML](#) [FASTA](#) Download: [TEXT](#) [XML](#) [FASTA](#)

Overview [Source Feature](#) [Other Features](#) [References](#) [Comments](#) [Sequence](#) [Send feedback](#)

Molecule type	Topology	Data class	Sequence length	Sequence Version	First public	Last updated
unassigned DNA	linear	PAT	300	1	1997-03-05(Release 51)	2006-11-14(Release 89)

Description
Sequence 15 from Patent WO9413821.

Navigation

Taxon : [4911](#) : Kluyveromyces marxianus
 SVA: [Historical versions of this EMBL-Bank record are available here: A39349](#)
 CABRI: [CBS 6556](#)
 StrainInfo: [455608](#)

Overview [Top](#)

Visible feature range: 1 300 [Apply](#)

Overview [Forward strand](#) 300 bp

Features [Forward strand](#) 300 bp

Source: Kluyveromyces marxianus
 Genes: INU1
 CDS: INU1

Source Feature(s) [Top](#)

source	1..300
Taxon:	4911 : Kluyveromyces marxianus
strain	CBS 6556
clone	PUR2415

Other Features [Top](#)

Visible feature range: 1 300 Filter: Default Main [Apply](#)

CDS	8..295
partial	
gene	INU1
product	INULINASE
protein_id	CAA02439
translation	KAITGTTFSLNRFPSVHFTPSHGWNDFPNGLWYDAKEEDWHLYYQYNPRAIINGTPLYWGHAVSKDLTISWTDYGASLPGSDDAGAFSGSMVIDYNN
EMBL-CDS	CAA02439

References [Top](#)

[1] THE USE OF THE KLUYVEROMYCES MARXIANUS INULINASE GENE PROMOTER FOR PROTEIN PRODUCTION
 CHAPMAN John William, MUSTERS Vivouter, ROUVERHORST Robert Jan, TOSCHKA Hoiger York, VERBAUKEL Johannes Maria A.
 QUEST INTERNATIONAL B.V.
 (PubMed:WO9413821) abstract
 CiteXplore

Comments [Top](#)

Other publication AU 5811194 940704

Sequence [Top](#)

Visible sequence range: 1 1000 [Apply](#)

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Download data

Dates (first public and last updated)

Graphical viewer

DNA source

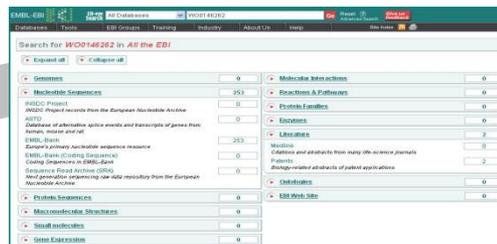
Navigate to external data sources e.g. UniProt

Accession	Entry	Name	Strain
CAA02439	CAA02439.1	INULINASE	

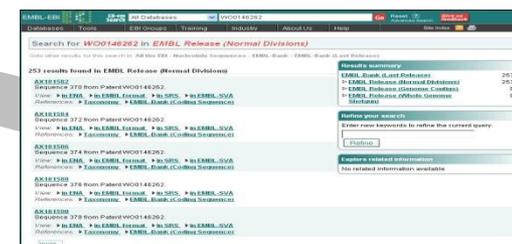
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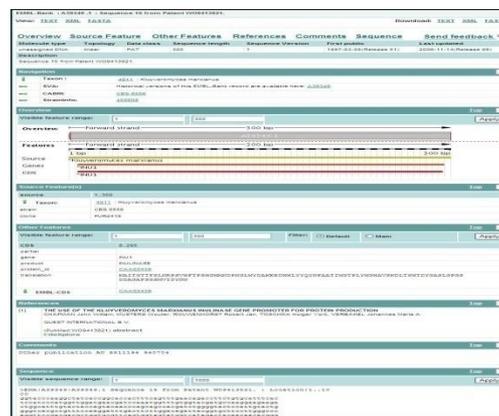
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WO0146262 literature and **sequence databases**



WO0146262 sequences



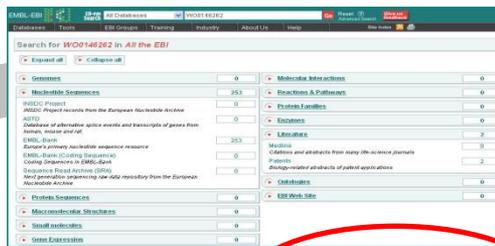
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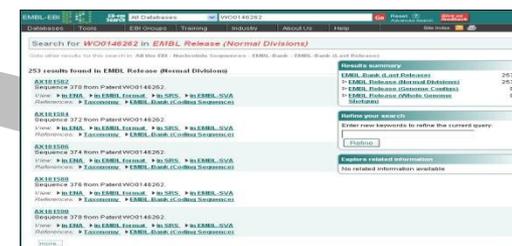
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WO0146262 sequences

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2 results found in Patents

WO0146262
OLFACTORY RECEPTOR GENES AND PSEUDOGENES IN PRIMATES AND MOUSE
 The present invention relates to olfactory receptor genes and pseudogenes of 10 primate species, in addition to mouse. The invention also concerns olfactory receptors encoded by these genes and their utilization.
 View: [in SRS](#) [in CiteXplore](#) [in Esp@cenet](#)

US2002151692
 Novel polypeptides and nucleic acids encoding same
 The present invention provides novel isolated ORX polynucleotides and polypeptides encoded by the ORX polynucleotides. Also provided are the antibodies that immunospecifically bind to an ORX polypeptide or any derivative, variant, mutant or fragment of the ORX polypeptide, polynucleotide or antibody. The invention additionally provides methods in which the ORX polypeptide, polynucleotide and antibody are utilized to assess olfactory acuity.
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 The present invention relates to olfactory receptor genes and pseudogenes of 10 primate species, in addition to mouse. The invention also concerns olfactory receptors encoded by these genes and their utilization.
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US2002151692
 Novel polypeptides and nucleic acids encoding same
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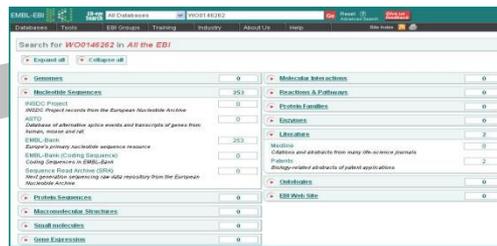
WO0146262 literature

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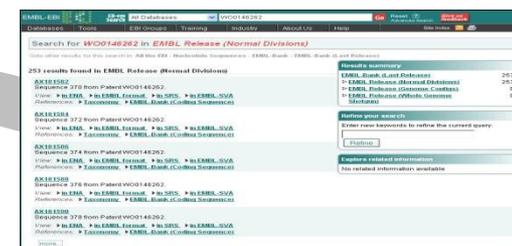
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Search for WO0146262



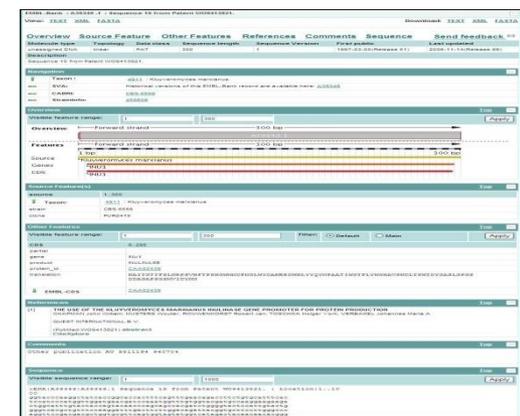
WO0146262 **literature** and sequence databases



WO0146262 sequences



WO0146262 literature

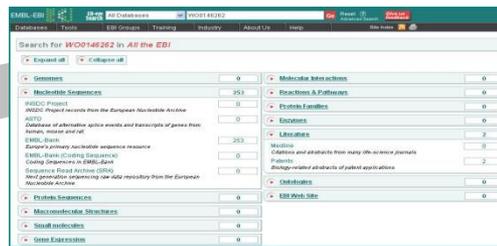


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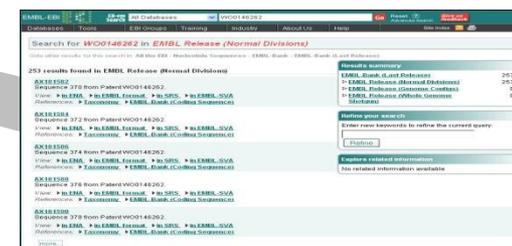
EB-eye – search by patent number



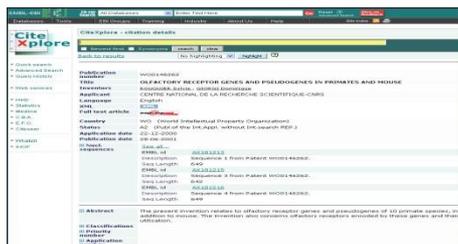
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WO0146262 **literature** and sequence databases



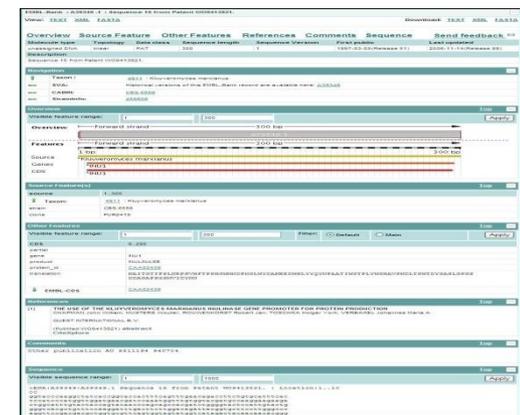
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WO0146262 in CiteXplore



WO0146262 literature



ENA sequence record

EB-eye – search by patent number

EMBL-EBI All Databases WO0146262

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European Bioinformatics Institute

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Genomes	0
Nucleotide Sequences	253
Protein Sequences	0
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PDB	0
Gene Expression	0
Molecular Interactions	0
Reactions & Pathways	0
Protein Families	0
Enzymes	0
Literature	2
Ontologies	0
Text Mining	0
Downloads	0
Web Sites	0

WO0146262 **literature** and sequence databases

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253 results found in EMBL Release (Normal Divisions)

253 results found in EMBL Release (Normal Divisions)

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- EMBL Bank (Archived Releases)
- EMBL Protein (Current Release)
- EMBL Protein (Archived Releases)

WO0146262 sequences

European Patent Office **esp@cenet**

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OLFACTORY RECEPTOR GENES AND PSEUDOGENES IN PRIMATES AND MOUSE

Bibliographic data Description Claims Mosais Original document INPADOC legal status

Publication number: WO0146262 (A2)
Publication date: 2001-06-28
Inventor(s): ROUQUIER SYLVIE [FR]; GIORGI DOMINIQUE [FR] +
Applicant(s): CENTRE NAT RECH SCIENT [FR]; ROUQUIER SYLVIE [FR]; GIORGI DOMINIQUE [FR] +

Classification:
 - international: C07K14/705; A61K38/00; C07K14/435; A61K38/00; (IPC-1-7): C07K14/705
 - European: C07K14/705

Application number: WO20001802017 20001222
Priority number(s): US19990171746P 19991222; US20000747155 20001221

Also published as:
 W00146262 (A3)
 US2002151692 (A1)
 AU2389301 (A)

Cited documents:
 EP0867508 (A2)
 XP002180153 (A)
 XP002180154 (A)
 XP000926681 (A)
 XP004178064 (A)

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Abstract of WO 0146262 (A2)

The present invention relates to olfactory receptor genes and pseudogenes of 10 primate species, in addition to mouse. The invention also concerns olfactory receptors encoded by these genes and their utilization.

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WO0146262 in Esp@cenet

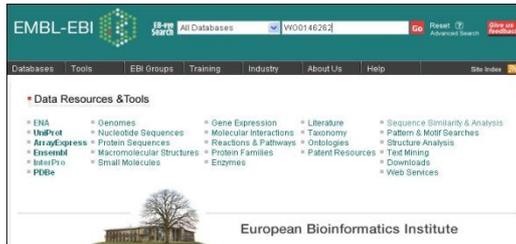
Overview Source Feature Other Features References Comments Sequence Send feedback

Sequence: 1000 bp

Feature: 1000 bp

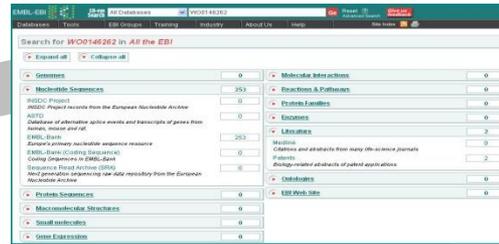
the record

EB-eye – search by patent number



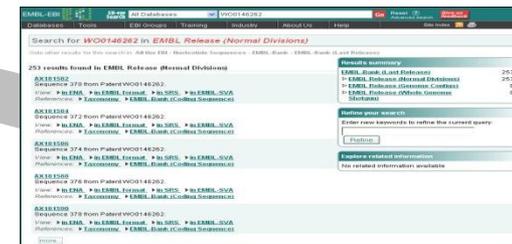
EMBL-EBI search interface showing search results for WO0146262. The interface includes a search bar with the patent number, navigation tabs, and a list of data resources and tools.

Search for WO0146262



EMBL-EBI search results for WO0146262 in the EBI database. The results are categorized into various biological and chemical groups, such as Genomes, Nucleotide Sequences, and Protein Sequences.

WO0146262 literature and sequence databases



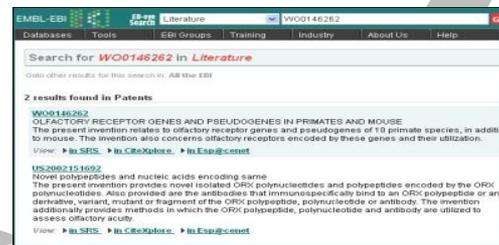
EMBL-EBI search results for WO0146262 in the EMBL Release (Normal Divisions). The results show 253 records found in the EMBL Release, with a detailed list of accession numbers and links to related information.

WO0146262 sequences



CiteXplore search results for WO0146262. The results show a list of publications related to the patent, including titles, authors, and publication dates.

WO0146262 in CiteXplore



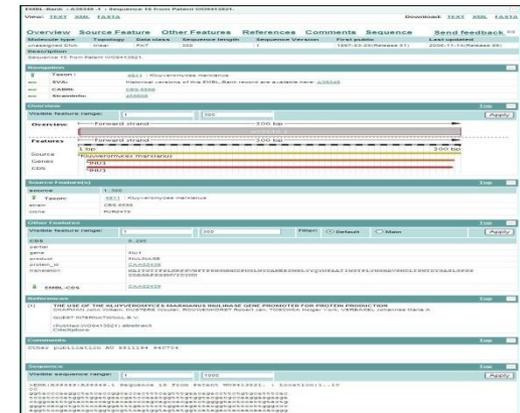
EMBL-EBI search results for WO0146262 in the Literature database. The results show 2 results found in patents, including a detailed abstract of the patent.

WO0146262 literature



Esp@cenet search results for WO0146262. The results show a detailed view of the patent, including bibliographic data, abstract, and classification codes.

WO0146262 in Esp@cenet



EMBL-EBI search results for WO0146262 in the ENA database. The results show a detailed view of the ENA sequence record, including sequence data and associated metadata.

ENA sequence record



Searching for sequences

advanced SRS text search...



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SRS

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Quick Text Search [Search Tips](#)

Find : Nucleotides matching : Enter Text Here

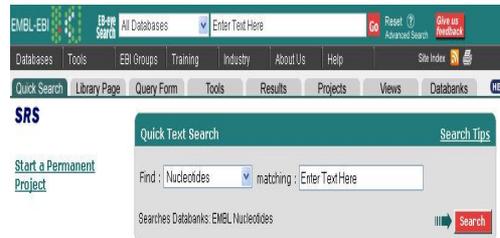
Searches Databanks: EMBL Nucleotides

1st: Select resources to search

2nd: Create query



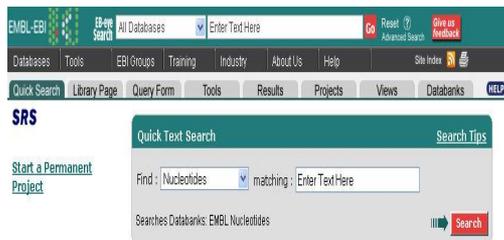
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Select **library** tab

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**Search
>100 databases**



Select library tab

Available Databanks

Expand all Collapse all Show databanks tooltips:

- Literature, Bibliography and Reference Databases
 - MEDLINE Taxonomy OMIM
 - OMIM Morbid Map Patent Abstracts Karyn's Genomes
 - Patent Equivalents
- Literature, Bibliography and Reference Databases - subsections*
 - MEDLINE (Updates) MEDLINE (Main Release 2010) MED2PUB
- Gene Dictionaries and Ontologies
- Nucleotide sequence databases
 - EMBL Patent DNA EMBL (Contig)
 - EMBL (Contig expanded) EMBL (Coding Sequences) EMBL ID/Accession Mapping
 - EMBL MGA IMGTL/IGM-DB IMGTL/HLA
 - IPD-KIR Genome Reviews GR Genes
 - GR Transcripts RefSeq Genome LiveLists
 - Patent DNA NRL1 Patent DNA NRL2
- Nucleotide related databases
- UniProt Universal Protein Resource
- Other protein sequence databases
 - Active protein sequence databases*
 - Patent Proteins EPO Proteins JPO Proteins USPTO Proteins
 - KIPO Proteins IPI IPI History MHCBN
 - RefSeq Proteome RefSeq Proteome (Release) RefSeq Proteome (Updates) Patent Protein NRL1
 - Patent Protein NRL2
 - Deprecated Protein Databases*
 - Swall(SPTR) PIR RemTrEMBL
- Protein function, structure and interaction databases
- Enzymes, reactions and metabolic pathway databases

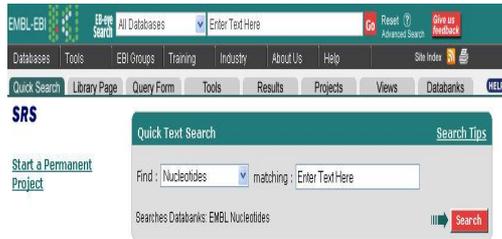
Patent literature

Patent DNA

Patent proteins



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Select library tab



Available Databanks

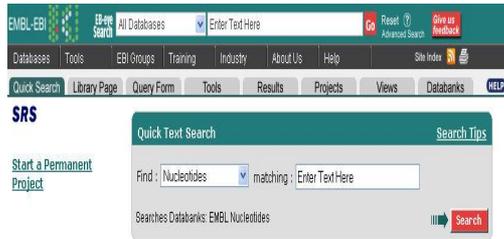
[+ Expand all](#) [- Collapse all](#) Show databanks tooltips:

- Literature, Bibliography and Reference Databases**
 - [MEDLINE](#) [Taxonomy](#) [OMIM](#)
 - [OMIM Morbid Map](#) [Patent Abstracts](#) [Karyn's Genomes](#)
 - [Patent Equivalents](#)
 - Literatures, Bibliography and Reference Databases - subsections**
 - [MEDLINE \(Updates\)](#) [MEDLINE \(Main Release 2010\)](#) [MED2PUB](#)
- Gene Dictionaries and Ontologies**
- Nucleotide sequence databases**
 - [EMBL](#) [Patent DNA](#) [EMBL \(Contig\)](#)
 - [EMBL \(Contigs expanded\)](#) [EMBL \(Coding Sequences\)](#) [EMBL ID/Accession Mapping](#)
 - [EMBL MGA](#) [IMG/TLIGM-DB](#) [IMG/HLA](#)
 - [IPD-KIR](#) [Genome Reviews](#) [GR Genes](#)
 - [GR Transcripts](#) [RefSeq Genome](#) [LiveLists](#)
 - [Patent DNA NRL1](#) [Patent DNA NRL2](#)
- Protein related databases**
- UniProt Universal Protein Resource**
- Other protein sequence databases**
 - Active protein sequence databases**
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 - [KIPO Proteins](#) [IPI](#) [IPI History](#) [MHCBN](#)
 - [RefSeq Proteome](#) [Refseq Proteome \(Release\)](#) [RefSeq Proteome \(Updates\)](#) [Patent Protein NRL1](#)
 - [Patent Protein NRL2](#)
 - Deprecated Protein Databases**
 - [Swal\(SPTR\)](#) [PIR](#) [RemTrEMBL](#)
- Protein function, structure and interaction databases**
- Enzymes, reactions and metabolic pathway databases**

Here, selected NR-level 2 DNA database



SRS – for more search options

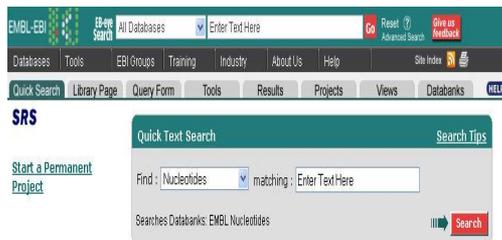


Select library tab



Select resources to search

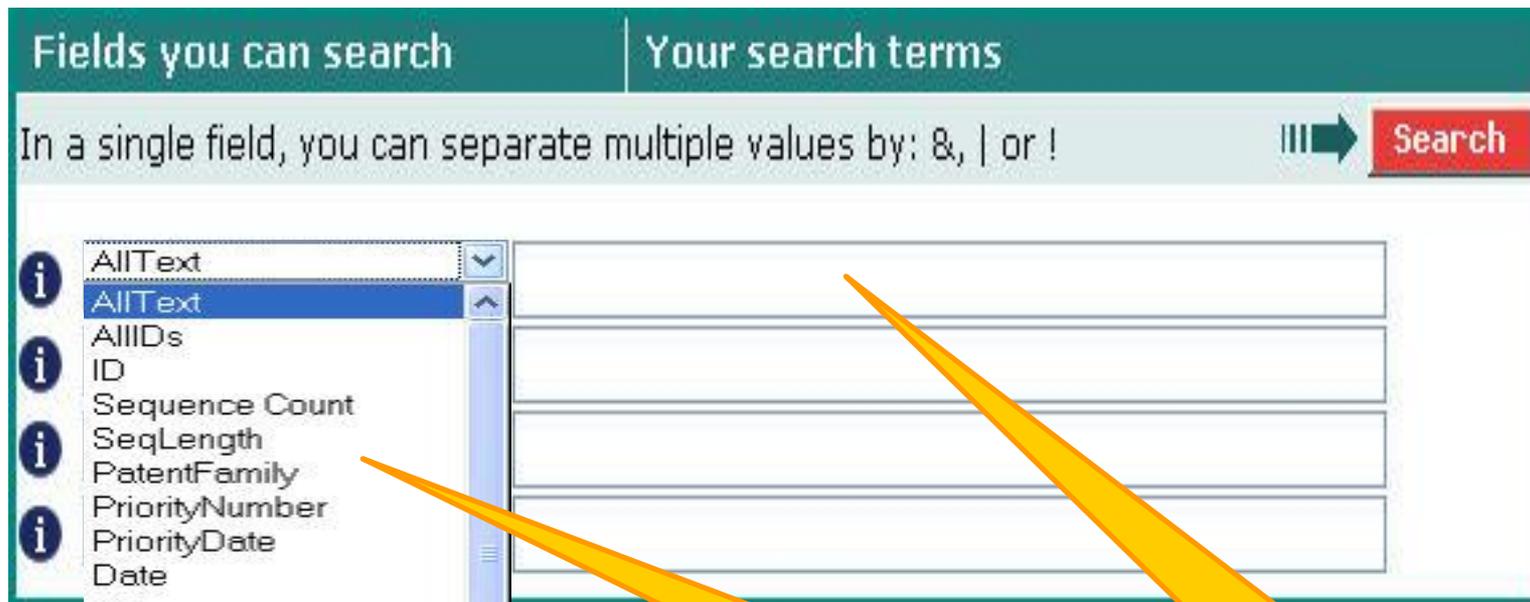
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Select **library** tab



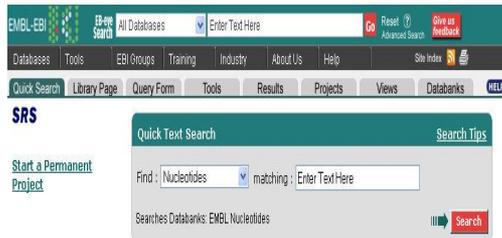
Select resources to search



1) Select field

2) Type in text

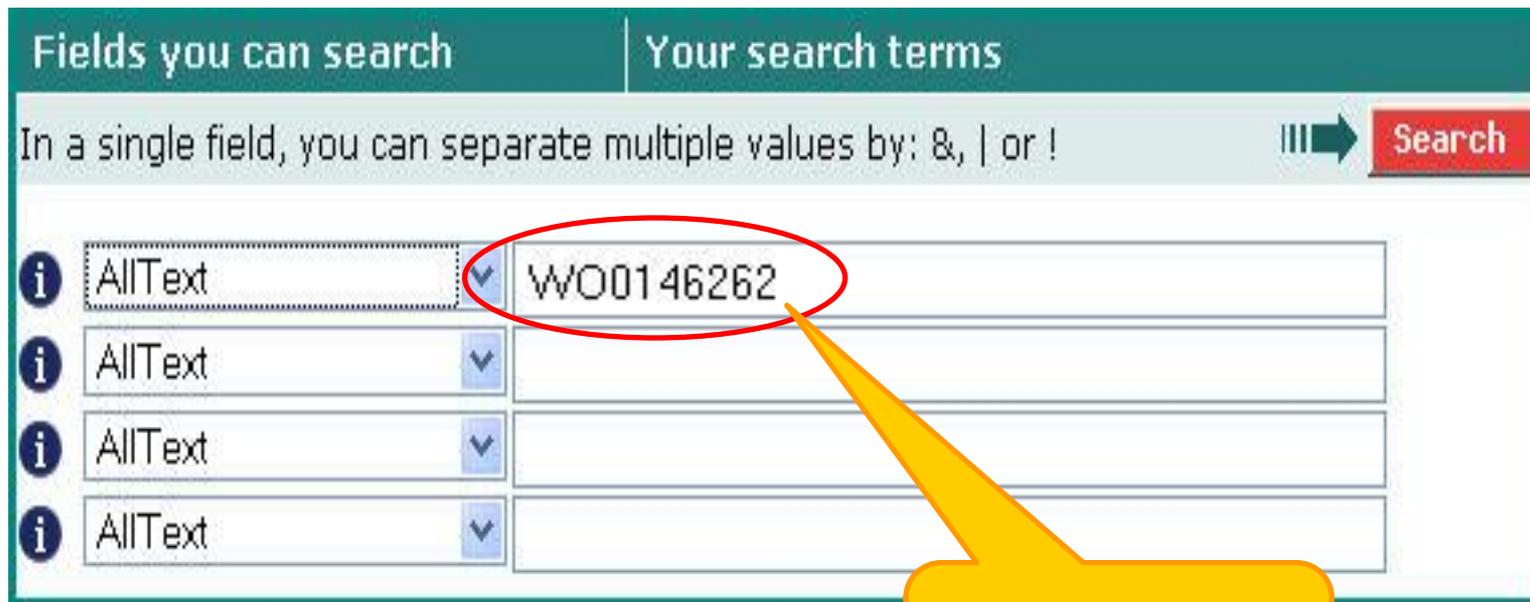
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Select resources to search

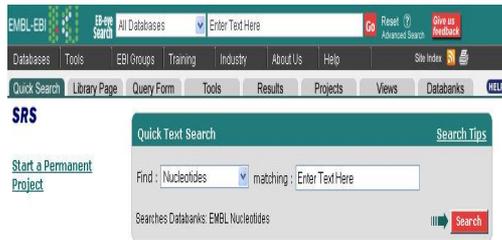


The screenshot shows the 'Fields you can search' and 'Your search terms' section. It features a table with four rows, each with a dropdown menu set to 'AllText' and an input field. The first input field contains the text 'WO0146262', which is circled in red. A yellow callout bubble points to this text with the text 'Here, selected patent number'. To the right of the input fields is a 'Search' button.

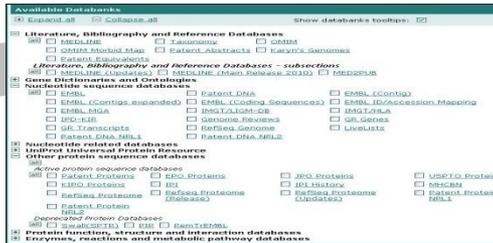
Fields you can search	Your search terms
AllText	WO0146262
AllText	
AllText	
AllText	

Here, selected patent number

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Find: Nucleotides matching: Enter Text Here

Searches Databanks: EMBL, Nucleotides

Select library tab

Available Databases

Literature, Bibliography and Reference Databases

Genes, Databases and Catalogues

Nucleotide sequence databases

Nucleotide related databases

Protein function, structure and interaction databases

Select resources to search

Fields you can search Your search terms

In a single field, you can separate multiple values by: &, | or !

AllText

AllText

AllText

AllText

Search

Create query

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Quick Search Library Page Query Form Tools Results Projects Views Databanks

Text Entry | **NRL2_Entry_View** | Related Data

Reset Previous Entry Entry 44 of 251 from Query 1 Next Entry

Entry Information

Entry from: Patent DNA NRL2

Entry Options

Launch analysis tool: NCBI BLAST Launch

Link to related information: Link

Save entry: Save

View: Printer Friendly

1. NRNL2:NRN00197A41 28-JUN-2001

Patent Family:

Family	Priority Number	Priority date
EM_PAT:AX181616	US19990171746P	22-DEC-1999

Sequence Entries:

Accession	Description	Patent	Date
EM_PAT:AX181616	Sequence 404 from Patent WO0146262.	WO0146262-A2/404	28-JUN-2001
EM_PAT:AX181640	Sequence 428 from Patent WO0146262.	WO0146262-A2/428	28-JUN-2001

Features:

Key	Location	Qualifier	Value
source	1..649	organism	Mus musculus domesticus
		mol_type	unassigned DNA
		note	Taxon = 10092; clone = OR2M; Accession DDBJ/EMBL/GenBank = AF0739
		db_xref	taxon:10092
cds	<2..>649	product	olfactory receptor; region between transmembrane domain s
		protein_id	CAC50154.1
		translation	>CAC50154.1 FTDLCPSSVTPKLLQNMQSQVPSIPYAGCLTQMYFFLFF FPLHYTSIMSPRLCVSLVLLSMLLTMSSMLHTLLLRLS ACSDIHINELVILIGGLVLLPFLLVTVSYARIISSILK VSLFYGTIIGLVLCPSANNLTKDVTMSLYMTVVTPT
		protein_id	CAC50071.1 {AX181640}
		note	AAMTV0.9:AX181640
		note	Taxon = 10092; clone = OR9M; Accession DDBJ/EMBL/GenBank = AF0739

Sequence:

Sequence Length: 649; Checksum: 21041042261dcdce529ca6533d359ff;

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```

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Quick Search Library Page Query Form Tools Results Projects Views Databanks

Text Entry | **NRL2_Entry_View** | Related Data

Reset Previous Entry Entry 44 of 251 from Query 1 Next Entry

Entry Information

Entry from: Patent DNA NRL2

Entry Options

Launch analysis tool: NCBI BLAST Launch

Link to related information: Link

Save entry: Save

View: Printer Friendly

Accession	Description	Patent	Date
EM_PAT:AX181616	Sequence 404 from Patent WO0146262.	WO0146262-A2/404	28-JUN-2001
EM_PAT:AX181640	Sequence 428 from Patent WO0146262.	WO0146262-A2/428	28-JUN-2001

WO0146262 sequences

WO0146262
nucleotide sequence
record in NRNL2

Patent sequence record in NRNL2

PATENT EQUIVALENTS: 26867389

Priority Information:
 P1: US990171746P 22-DEC-1999
 P2: CA2381492 22-DEC-1999

Patent Number	Country	Title
WO0146262	A1	17-OCT-2002 Novel polypeptides and nucleic acids encoding same
WO0146262	A2	28-JUN-2001 OLFACTORY RECEPTOR GENES AND PSEUDOGENES IN PRIMATES AND MOUSE

1. Patent cited by sequence database entry.
 SEQ Classification:
 C027K14/92

Information Classification:
 C07H14/92, A61K 36/00, C07H14/705

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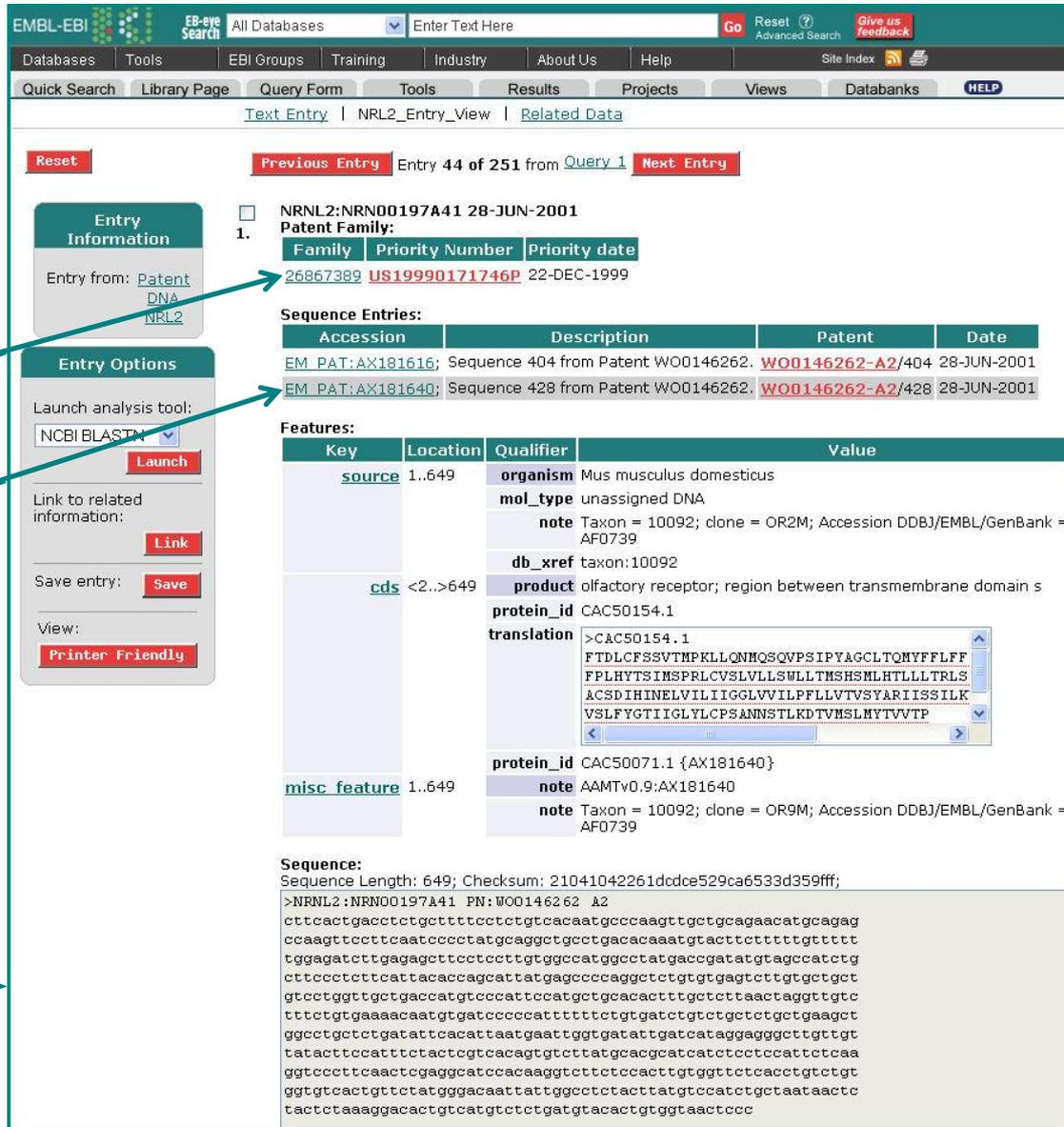
Entry ID	Patent Number	Description
PATENT_SNA_C027K14/92	WO000469991-A2/1	Sequence 1 from Patent WO000469991
PATENT_SNA_C027K14/92	JP2007523601-A/1	OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION.
SEQ_PRT_AA181224	WO0146262-A2/2	Sequence 2 from Patent WO0146262
PATENT_SNA_C027K14/92	WO000469991-A2/2	Sequence 2 from Patent WO000469991
PATENT_SNA_C027K14/92	JP2007523601-A/2	OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION.
PATENT_SNA_C027K14/92	WO000469991-A2/3	Sequence 3 from Patent WO000469991

Patent equivalents

Sequence record in ENA



Sequence



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Quick Search Library Page Query Form Tools Results Projects Views Databanks HELP

Text Entry | **NRL2_Entry_View** | Related Data

Reset Previous Entry Entry 44 of 251 from Query 1 Next Entry

Entry Information

Entry from: Patent DNA NRNL2

Entry Options

Launch analysis tool: NCBI BLASTN Launch

Link to related information: Link

Save entry: Save

View: Printer Friendly

1. **NRNL2:NRN00197A41 28-JUN-2001**

Patent Family:

Family	Priority Number	Priority date
26867389	US19990171746P	22-DEC-1999

Sequence Entries:

Accession	Description	Patent	Date
EM_PAT:AX181616;	Sequence 404 from Patent WO0146262.	WO0146262-A2/404	28-JUN-2001
EM_PAT:AX181640;	Sequence 428 from Patent WO0146262.	WO0146262-A2/428	28-JUN-2001

Features:

Key	Location	Qualifier	Value
source	1..649	organism	Mus musculus domesticus
		mol_type	unassigned DNA
		note	Taxon = 10092; clone = OR2M; Accession DDBJ/EMBL/GenBank = AF0739
		db_xref	taxon:10092
cds	<2..>649	product	olfactory receptor; region between transmembrane domain 5
		protein_id	CAC50154.1
		translation	>CAC50154.1 FTDLCFSSVTMPKLLQNMQSQVPSIPYAGCLTQNYFFLFF FPLHYTSHSPRLCVSLVLLSULLTMSHSLHTLLLRSL ACSDIHINELVILIIIGLVVILPFLLVTVSYARISSILK VSLFYGTIIIGLYLCPANNSTLKDVTMSLHYTVVTP
		protein_id	CAC50071.1 {AX181640}
		note	AAMTv0.9:AX181640
		note	Taxon = 10092; clone = OR9M; Accession DDBJ/EMBL/GenBank = AF0739

Sequence:
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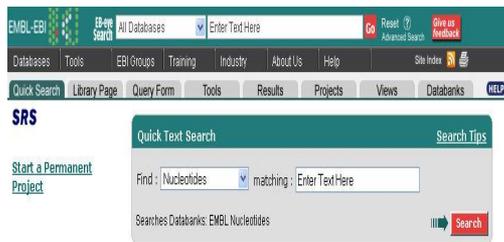
Priority number and date

Patent literature



Translation

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Select **library** tab



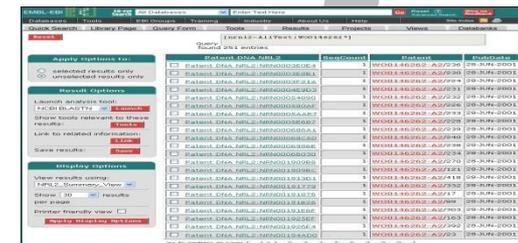
Select resources to search



Create query

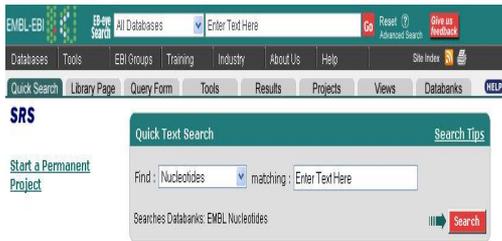


NRNL2 **sequence** record



WO0146262 sequences

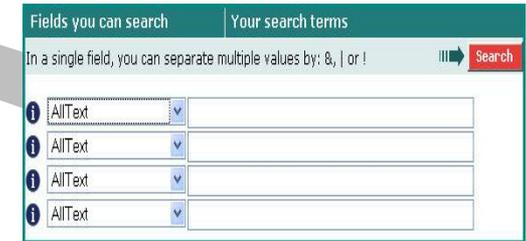
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Select library tab



Select resources to search



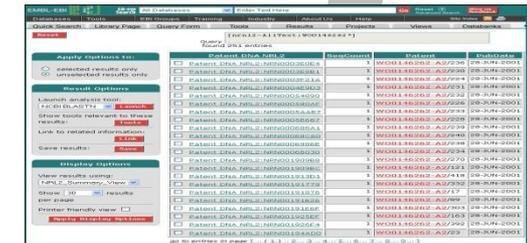
Create query



WO0146262 literature



NRNL2 sequence record



WO0146262 sequences



Searching for sequences

sequence search...



Sequence searching – specialised tools

EMBL-EBI

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Data Resources & Tools

- ENA
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- Protein Sequences
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- Small Molecules
- Gene Expression
- Molecular Interactions
- Reactions & Pathways
- Protein Families
- Enzymes
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- Taxonomy
- Ontologies
- Patent Resources
- **Sequence Similarity & Analysis**
- Pattern & Motif Searches
- Structure Analysis
- Text Mining
- Downloads
- Web Services

European Bioinformatics Institute

About the EBI

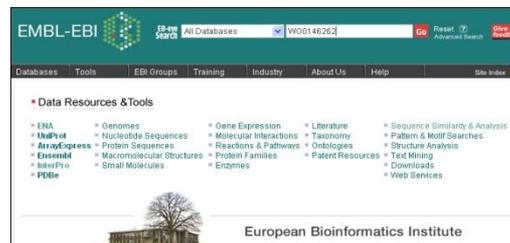
- Research
- PhD Studies
- Training
- Industry Support
- Group & Team Leaders
- EBI Funders
- User Support
- EBI Mission
- People
- Events at the EBI
- Genome Campus Events
- How to Find us
- Jobs

Events

- Small Molecule Bioactivity Resources
14-18 February 2011 more
Registration closes 14th January 2011
- In silico Systems Biology: Network Reconstruction, Analysis and Network-based Modelling
23-26 May 2011 more
Registration closes 1st March 2011



Sequence searching – specialised tools



Navigate to search tools



Sequence searching – specialised tools



Navigate to search tools

The screenshot shows the EMBL-EBI website interface for 'Sequence Similarity & Analysis'. A yellow callout bubble with the text 'Choose NEW INTERFACE' points to a link in a notice box that says 'Please use the new interfaces [here](#).' The link is circled in red.

EMBL-EBI EB-eye Search All Databases Enter Text Here

Databases Tools EBI Groups Training Industry About Us Help Site Index

EBI > Tools > Sequence Similarity & Analysis

Sequence Similarity & Analysis

Sequence Similarity & Homology Tools

Here the user will be able to use various sequence database similarity search tools such as:

- [BLAST](#)
- [FASTA](#)
- [PSI-Search](#)
- [SSEARCH](#)

These old interfaces will be retired on 1st November 2010. Please use the new interfaces [here](#).

→ Go to [Sequence Similarity & Homology Tools](#) page.

Sequence Analysis Tools

Sequence analysis encompasses the use of various bioinformatic methods to determine the biological function and/or structure of genes and the proteins they code for.

→ Go to [Sequence Analysis Tools](#) page.



Sequence searching – specialised tools



Navigate to search tools

BLAST

FASTA

PSI search

Choose Search tool

EMBL-EBI EB-eye Search All Databases Ent

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EBI > Tools > Similarity & Homology

Similarity & Homology

The tools described on this page are provided as part of our **new bioinformatics analysis tools framework**. If you have any feedback or encounter any issues, please let us know via EBI support.

Note: The framework is currently in a beta testing phase.

At present a subset of the sequence similarity search tools available at EBI are available in the new framework. For the complete set see the **old framework**.

BLAST

NCBI BLAST ⓘ NCBI BLAST Sequence Similarity Search using the NCBI BLAST (blastall) program. This tool is available for the following databases:
[Protein](#) [Nucleotide](#) [Vectors](#)

WU-BLAST ⓘ Sequence Similarity Search using the Washington University (WU) BLAST2 program (BLAST 2.0 with gaps). This tool is available for the following databases:
[Protein](#) [Nucleotide](#) [Parasites](#)

PSI-BLAST ⓘ Position Specific Iterative **BLAST (PSI-BLAST)** refers to a feature of BLAST 2.0 in which a profile is automatically constructed from the first set of BLAST alignments.
[Launch PSI-BLAST](#)

FASTA

FASTA ⓘ Sequence Similarity Search using the FASTA program. This tool is available for the following databases:
[Protein](#) [Nucleotide](#) [Proteomes](#) [Genomes](#) [Whole Genome Shotgun](#)
[ASD Protein](#) [ASD Nucleotide](#) [LGIC Protein](#) [LGIC Nucleotide](#)

SSEARCH ⓘ Sequence Similarity Search using the SSEARCH program. This tool is available for the following databases:
[Protein](#) [Nucleotide](#) [Proteomes](#) [Genomes](#) [Whole Genome Shotgun](#)
[ASD Protein](#) [ASD Nucleotide](#) [LGIC Protein](#) [LGIC Nucleotide](#)

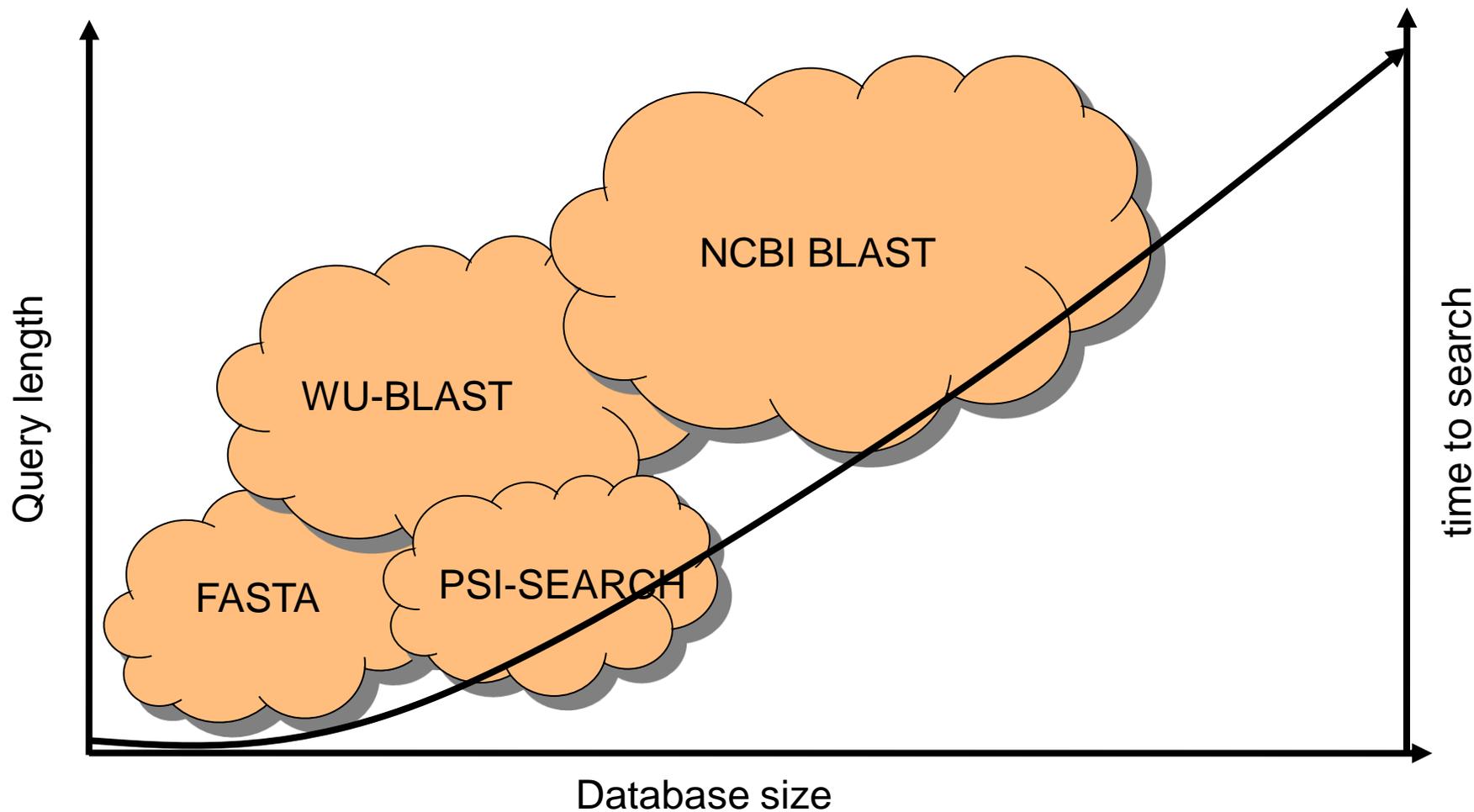
PSI-Search ⓘ PSI-Search combines the sensitivity of the Smith-Waterman search algorithm (SSEARCH) with the PSI-BLAST (blastpgp) iterative profile construction strategy to find distantly related protein sequences.
[Launch PSI-Search](#)

GGSEARCH ⓘ GGSEARCH performs a protein vs. protein search using alignments that are global in the query and global in the database (Needleman-Wunsch).
[Launch GGSEARCH](#)

GLSEARCH ⓘ GLSEARCH performs a protein vs. protein search using alignments that are global in the query and local in the database.
[Launch GLSEARCH](#)



When to use which search?





When to use which search?

Chose the appropriate
search engine for the job

(one search engine won't do everything)

- **BLAST** – initial fast search
- **FASTA** – better general search engine
- **PSI-BLAST** – find remote family members
- **GLSEARCH** – match oligo/peptide to gene/protein
- **GGSEARCH** – force full length matches



Sequence searching – specialised tools



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Here, try FASTA protein

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EBI > Tools > Similarity & Homology

Similarity & Homology

The tools described on this page are provided using our **new bioinformatics analysis tools framework**. If you have any feedback or encounter any issues please let us know via [EBI support](#).

Note: The framework is currently in a beta testing phase.

At present a subset of the sequence similarity search tools available at EBI are available in the new framework. For the complete set see the [Old framework](#).

BLAST

NCBI BLAST NCBI BLAST Sequence Similarity Search using the NCBI BLAST (blastall) program. This tool is available for the following databases:
[Protein](#) [Nucleotide](#) [Vectors](#)

WU-BLAST Sequence Similarity Search using the Washington University (WU) BLAST2 program (BLAST 2.0 with gaps). This tool is available for the following databases:
[Protein](#) [Nucleotide](#) [Parasites](#)

PSI-BLAST Position Specific Iterative **BLAST (PSI-BLAST)** refers to a feature of BLAST 2.0 in which a profile is automatically constructed from the first set of BLAST alignments.
[Launch PSI-BLAST](#)

FASTA

FASTA Sequence Similarity Search using the FASTA program. This tool is available for the following databases:
[Protein](#) [Nucleotide](#) [Proteomes](#) [Genomes](#) [Whole Genome Shotgun](#)
[ASD Protein](#) [ASD Nucleotide](#) [LGIC Protein](#) [LGIC Nucleotide](#)

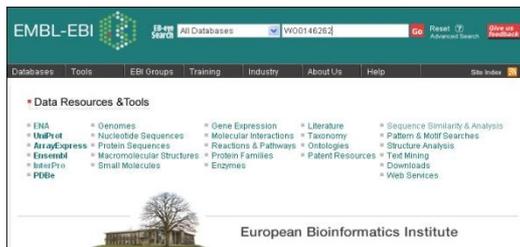
SSEARCH Sequence Similarity Search using the SSEARCH program. This tool is available for the following databases:
[Protein](#) [Nucleotide](#) [Proteomes](#) [Genomes](#) [Whole Genome Shotgun](#)
[ASD Protein](#) [ASD Nucleotide](#) [LGIC Protein](#) [LGIC Nucleotide](#)

PSI-Search PSI-Search combines the sensitivity of the Smith-Waterman search algorithm (SSEARCH) with the PSI-BLAST (blastpgp) iterative profile construction strategy to find distantly related protein sequences.
[Launch PSI-Search](#)

GGSEARCH GGSEARCH performs a protein vs. protein search using alignments that are global in the query and global in the database (Needleman-Wunsch).
[Launch GGSEARCH](#)

GLSEARCH GLSEARCH performs a protein vs. protein search using alignments that are global in the query and local in the database.
[Launch GLSEARCH](#)

Sequence searching – specialised tools



Navigate to search tools

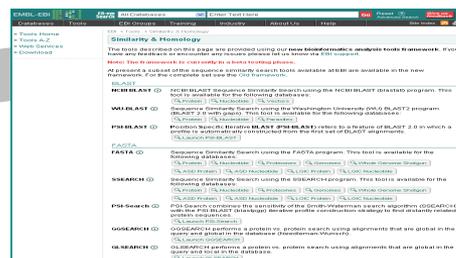


Select search tool

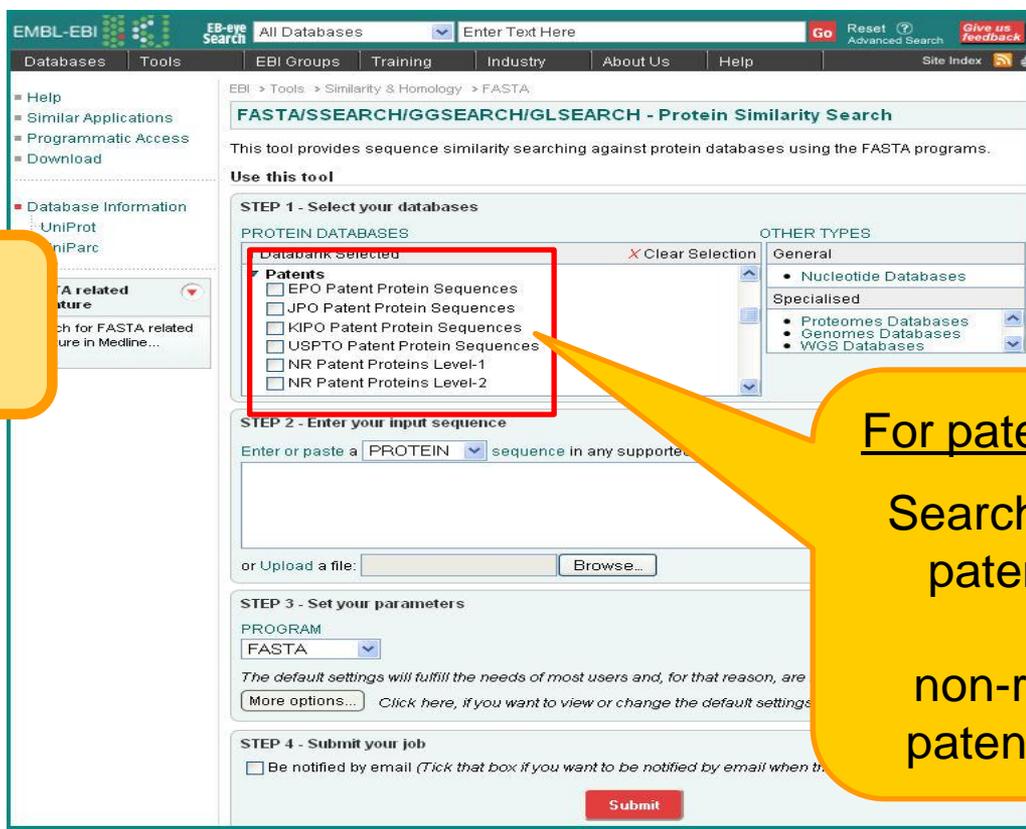
Sequence searching – specialised tools



Navigate to search tools



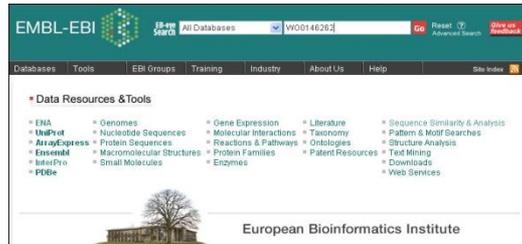
Select search tool



Step 1:
Select database

For patent proteins:
Search individual patent offices or non-redundant patent datasets

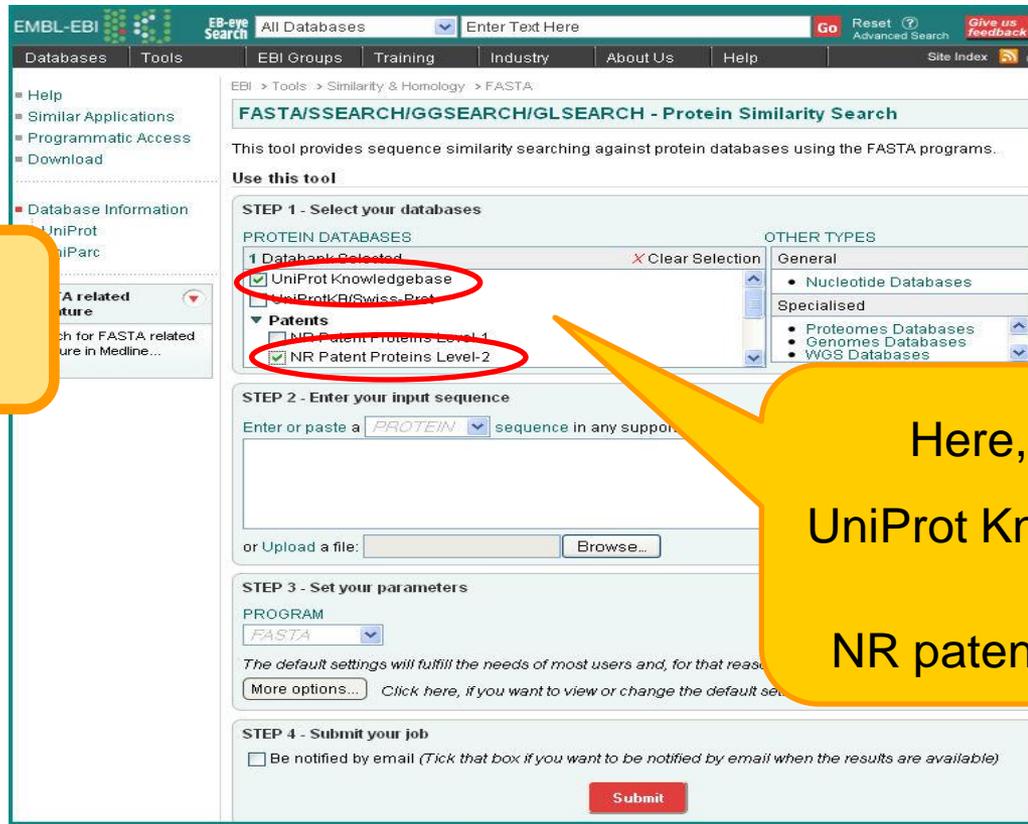
Sequence searching – specialised tools



Navigate to search tools



Select search tool



**Step 1:
Select database**

Here, selected
UniProt Knowledgebase
+
NR patent proteins L2

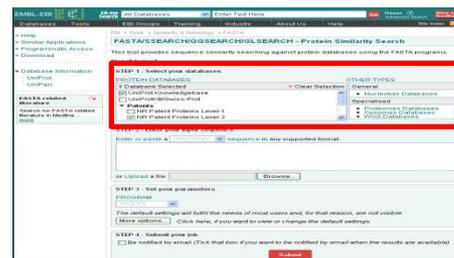
Sequence searching – specialised tools



Navigate to search tools

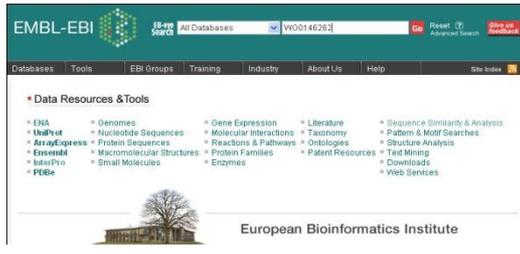


Select search tool



(1) Select database

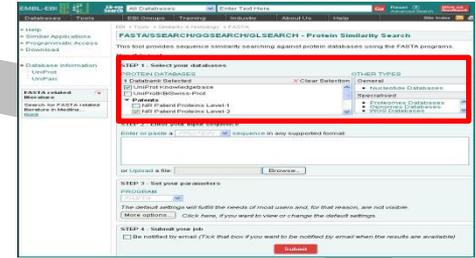
Sequence searching – specialised tools



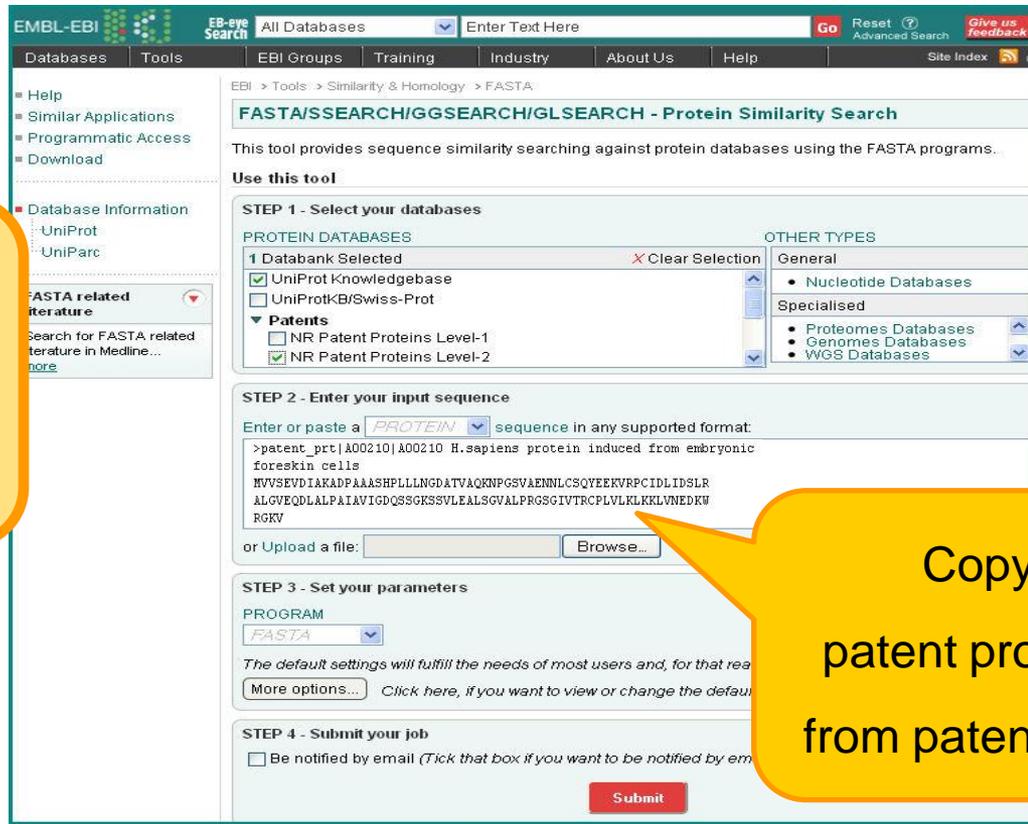
Navigate to search tools



Select search tool



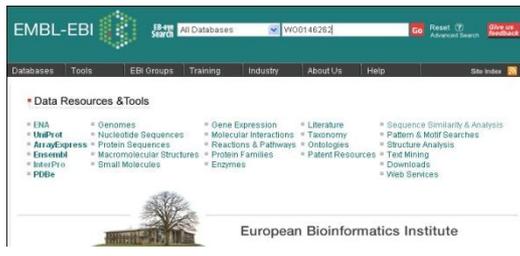
(1) Select database



**Step 2:
Copy/paste
sequence
or
upload file**

**Copy/pasted
patent protein A00210
from patent EP0242329**

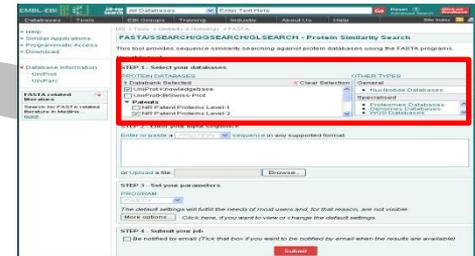
Sequence searching – specialised tools



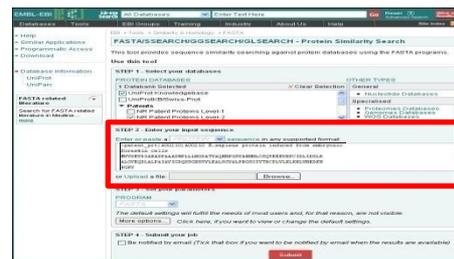
Navigate to search tools



Select search tool



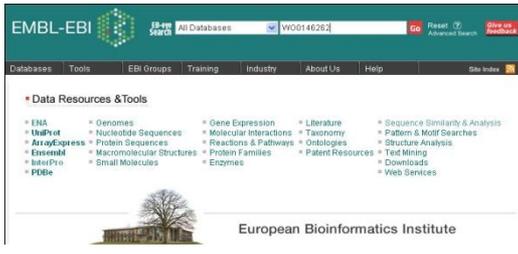
(1) Select database



(2) Copy/paste sequence



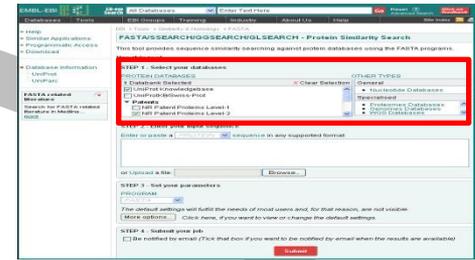
Sequence searching – specialised tools



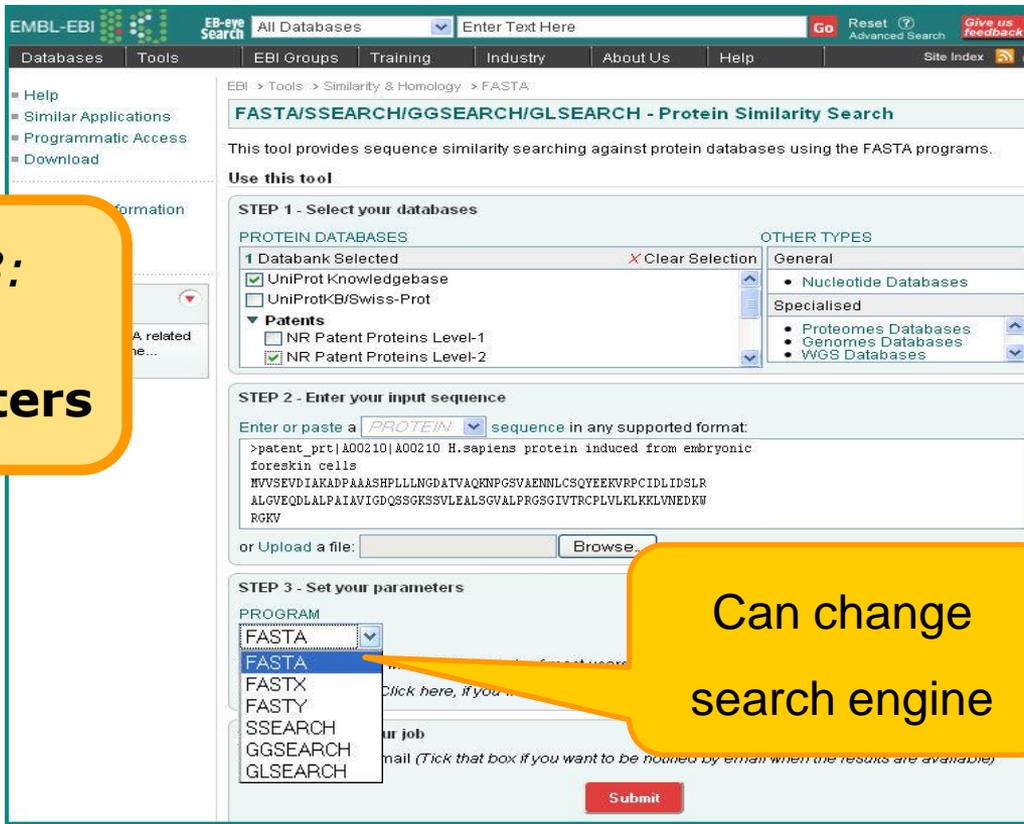
Navigate to search tools



Select search tool

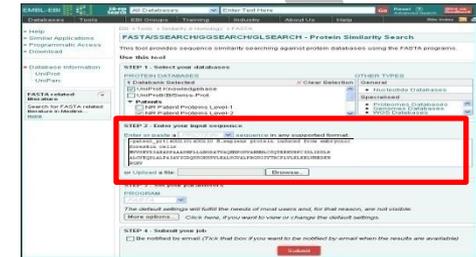


(1) Select database



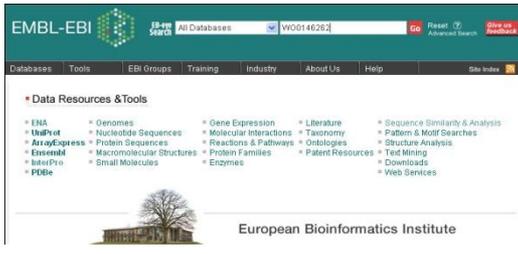
**Step 3:
Set
parameters**

**Can change
search engine**



(2) Copy/paste sequence

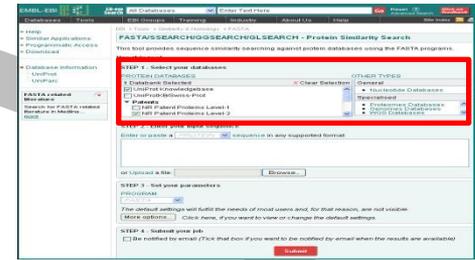
Sequence searching – specialised tools



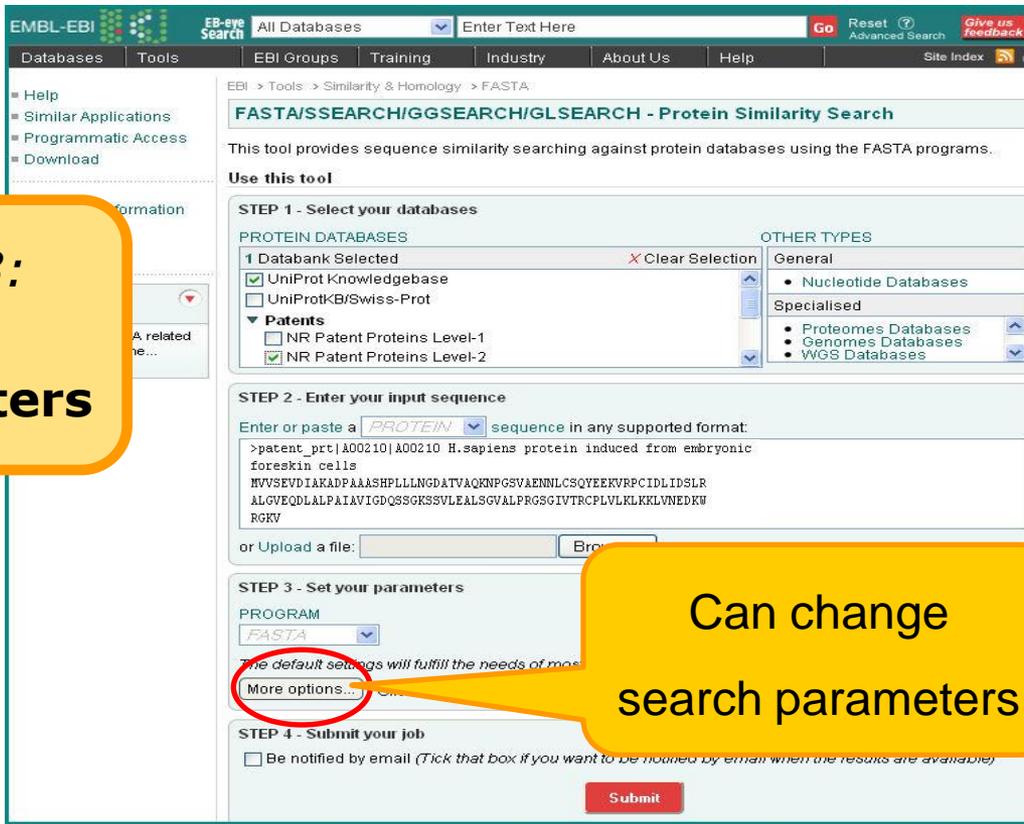
Navigate to search tools



Select search tool

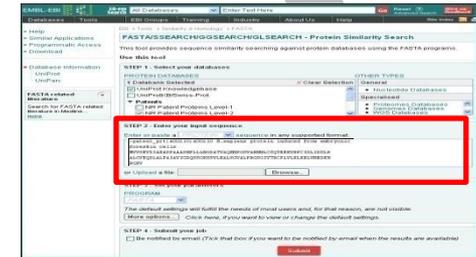


(1) Select database



**Step 3:
Set
parameters**

**Can change
search parameters**



(2) Copy/paste sequence



How to optimise parameters?

STEP 3 - Set your parameters

PROGRAM
FASTA

The default settings will fulfill the needs of most users and

More options... *Click here, if you want to view or change*

EMBL-EBI

Matrix

The comparison matrix to be used to score alignments when searching the database

Matrix Name	Abbreviation
BLOSUM50	BL50
BLOSUM62	BL62
BLASTP62	BP62
BLOSUM80	BL80
PAM120	P120
PAM250	P250
MDM10	M10
MDM20	M20
MDM40	M40

Default value is: BLOSUM50 [BL50]

Additional information

- Read more about matrices



STEP 3 - Set your parameters

PROGRAM
FASTA

MATRIX GAP OPEN GAP EXTEND KTUP EXPECTATION UPPER VALUE EXPECTATION LOWER VALUE

BLOSUM50	-10	-2	2	10	0 (default)
----------	-----	----	---	----	-------------

DNA STRAND HISTOGRAM FILTER STATISTICAL ESTIMATES

N/A	no	none	Regress
-----	----	------	---------

SCORES ALIGNMENTS SEQUENCE RANGE DATABASE RANGE

50	50	START-END	START-END
----	----	-----------	-----------

User manual provides help



How to optimise parameters?

QUERY LENGTH	MATRIX	open	ext
>300	BLOSUM50	-10	-2
85-300	BLOSUM62	-7	-1
50-85	BLOSUM80	-16	-4
>300	PAM250	-10	-2
85-300	PAM120	-16	-4
35-85	MDM40	-12	-2
<=35	MDM20	-22	-4
<=10	MDM10	-23	-4



Choose **MATRIX** and **GAP PENALTIES**
according to the size of the query sequence

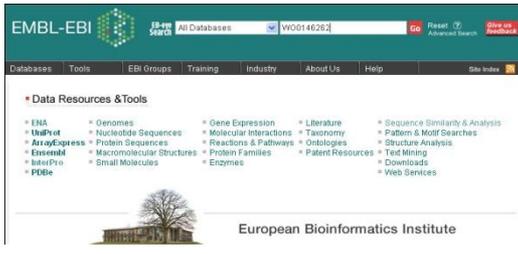


How to optimise parameters?

**What do I use
for short
sequences?**

- use strict matrices
- use high gap penalties
- avoid masking
- allow high e-values

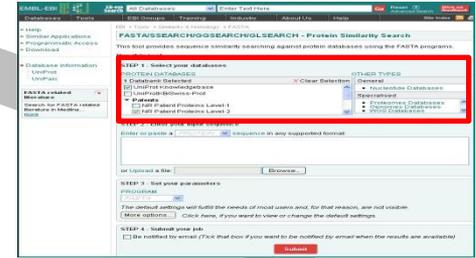
Sequence searching – specialised tools



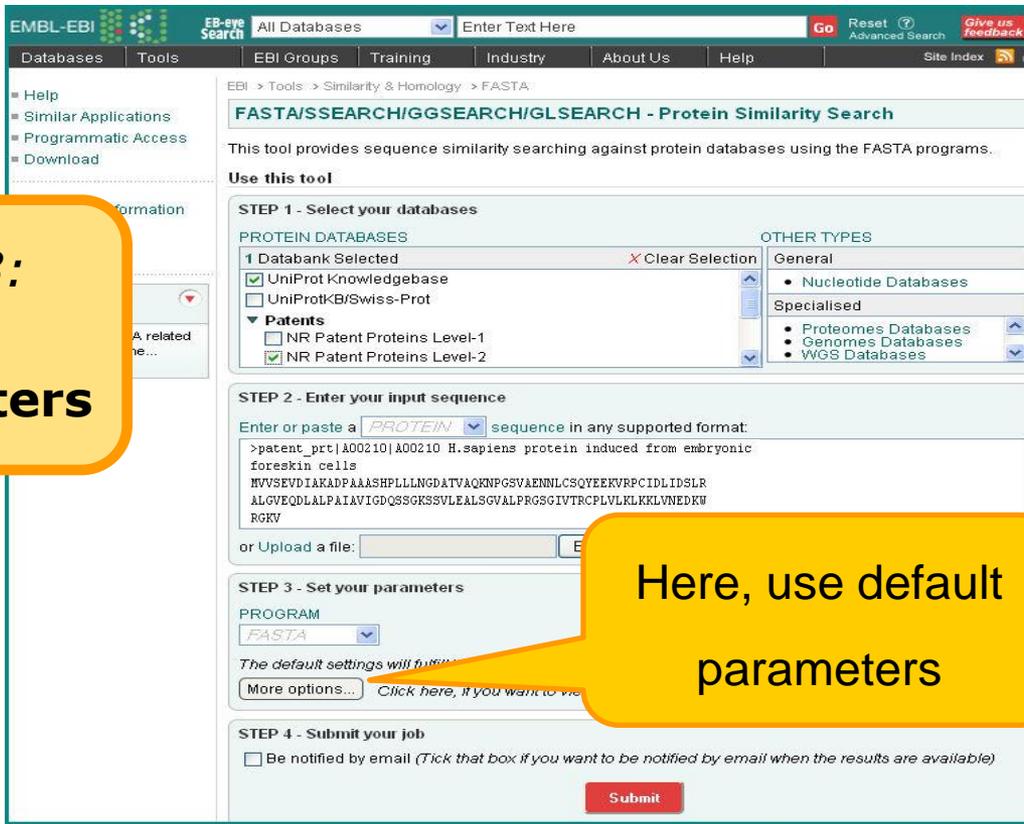
Navigate to search tools



Select search tool

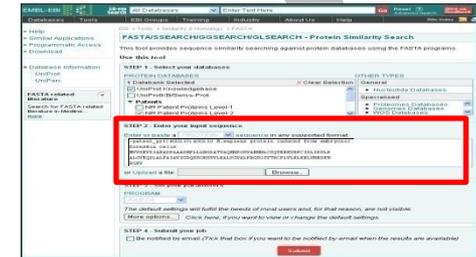


(1) Select database



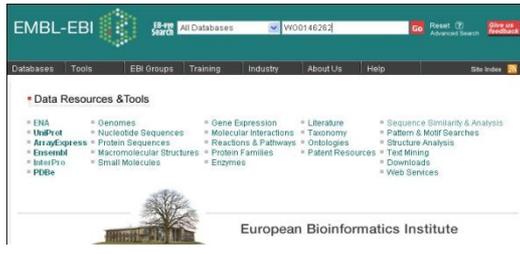
**Step 3:
Set
parameters**

**Here, use default
parameters**



(2) Copy/paste sequence

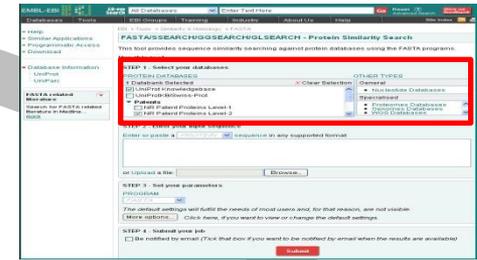
Sequence searching – specialised tools



Navigate to search tools



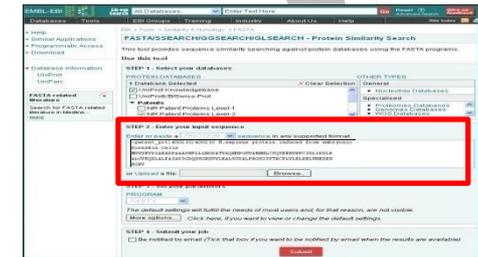
Select search tool



(1) Select database



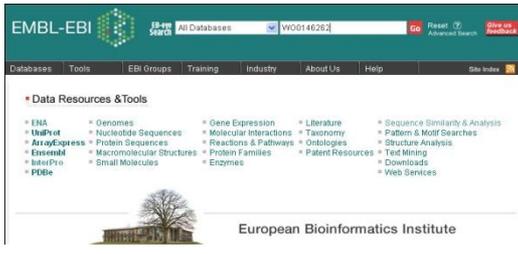
(3) Set parameters



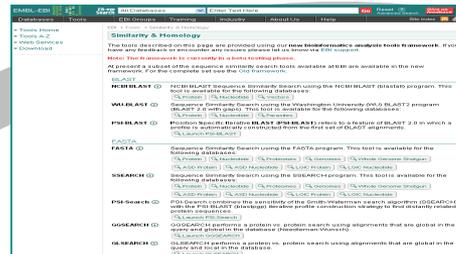
(2) Copy/paste sequence



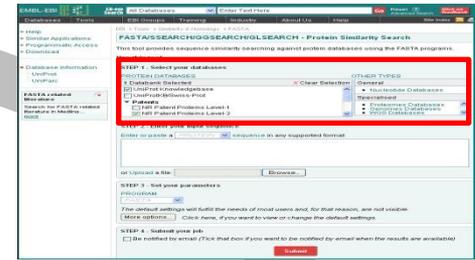
Sequence searching – specialised tools



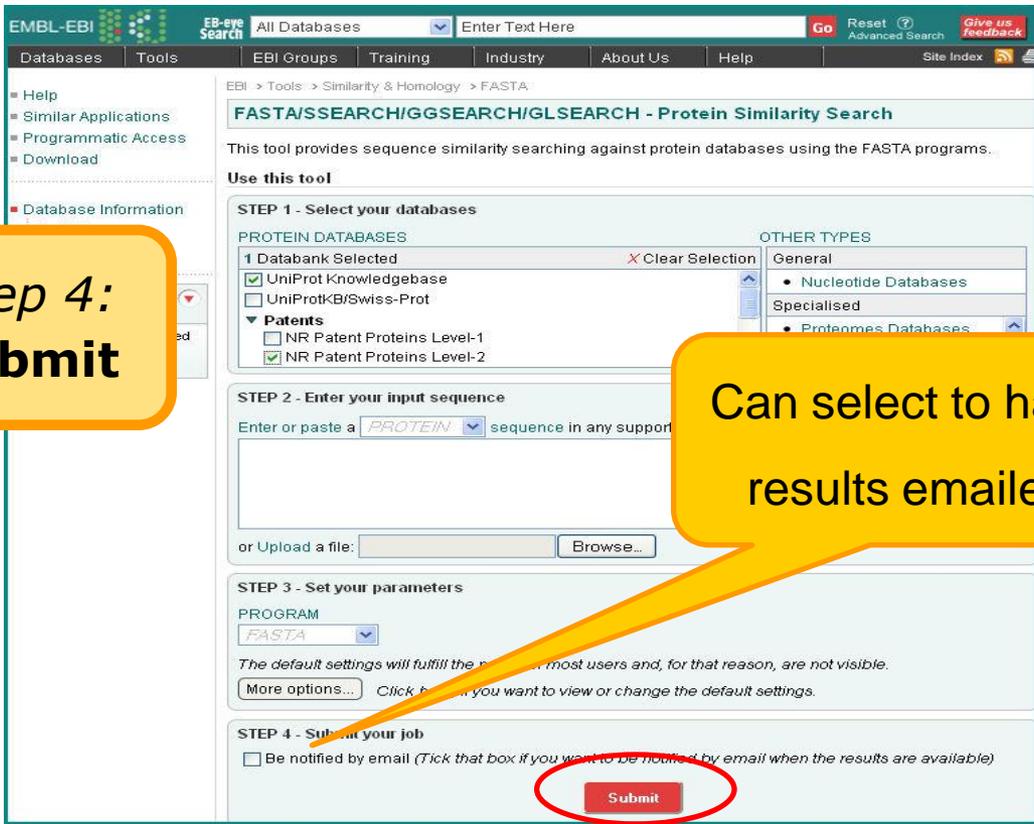
Navigate to search tools



Select search tool

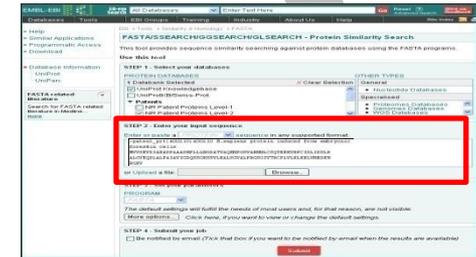


(1) Select database

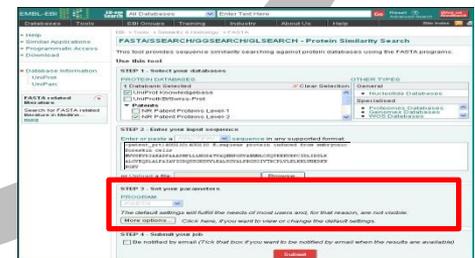


**Step 4:
submit**

Can select to have
results emailed

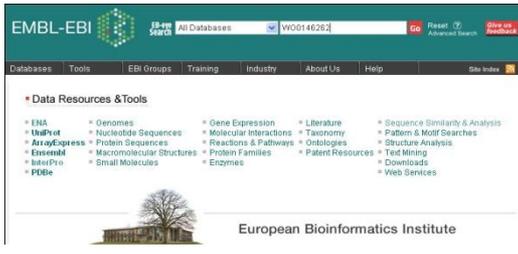


(2) Copy/paste sequence



(3) Set parameters

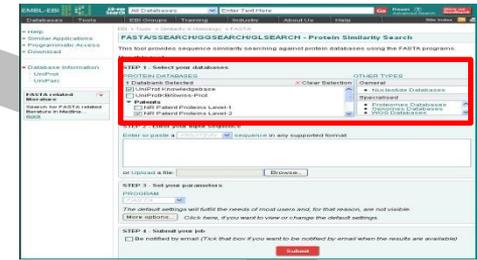
Sequence searching – specialised tools



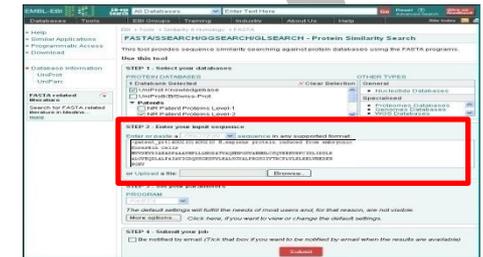
Navigate to search tools



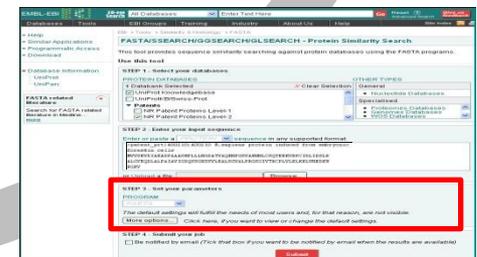
Select search tool



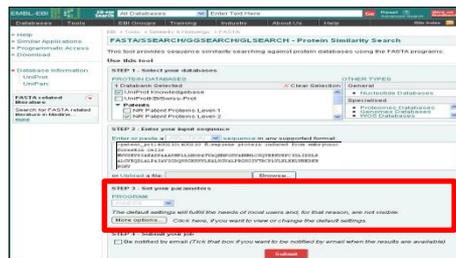
(1) Select database



(2) Copy/paste sequence

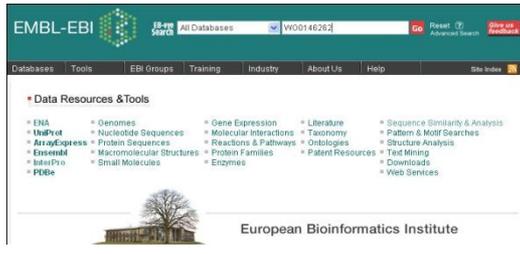


(3) Set parameters



(4) Submit

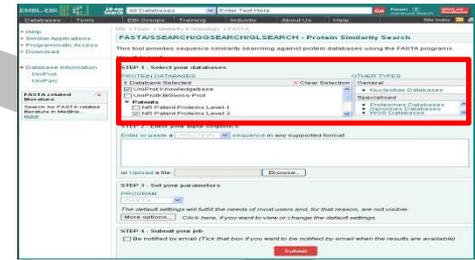
Sequence searching – specialised tools



Navigate to search tools



Select search tool



(1) Select database

FASTA Results

Summary Table | Tool Output | Visual Output | Functional Predictions

Alignments

Selection: Show Annotations | Hide Annotations | Show Alignments

Download in fasta format

Align.	DB:ID	Source	Length
1	NRPL2:NRP001827BA	PN:US6407209 B1	124
2	NRPL2:NRP001827B8	PN:EP0242329 A2	124
3	NRPL2:NRP001827B9	PN:US5466585 A	124
4	TR:C9JUL1_HUMAN	Putative uncharacterized protein MX1 OS=Homo sapiens GN=MX1 PE=3 SV=1	
5	TR:C9JUN19_HUMAN	Putative uncharacterized protein MX1 OS=Homo sapiens GN=MX1 PE=3 SV=1	201
6	NRPL2:NRP00221FC9	PN:US2007218466 A1	508
7	NRPL2:NRP0012C2F5	PN:US2007218466 A1	662

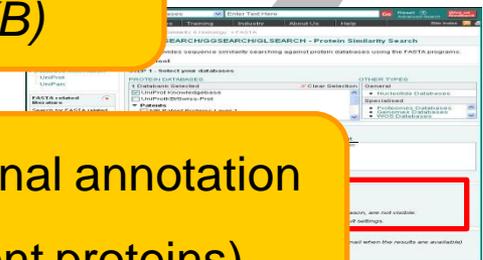
Results include patent proteins (from NRPL2)...

...and non-patent proteins (from UniProtKB)

View additional annotation (non-patent proteins)



Copy/paste sequence



(2) Set parameters

Sequence

Nucleotide Sequences references for entry **C9JUL1_HUMAN** from *UniProtKB*

This entry has other cross references in: [InterPro](#) - [Medline](#) - [Taxonomy](#) - [GO](#) - [Ensembl](#) - [HGNC](#) - [EMBL-Bank](#)

3 results found in EMBL Release (Normal Divisions)

AP001610

Homo sapiens genomic DNA, chromosome 21, clone:CIT2533B8, MX1-D21S171 region.

View: [in ENA](#) [in EMBL format](#) [in SRS](#) [in EMBL-SVA](#)

References: [EMBL-Bank](#) [Taxonomy](#) [InterPro](#) [UniProtKB](#) [PDBe](#) [HGNC](#)

AL773577

Homo sapiens chromosome 21 from cosmid LL21NC02-14C10 map 21q22.2,D21S349-MX1

View: [in ENA](#) [in EMBL format](#) [in SRS](#) [in EMBL-SVA](#)

References: [EMBL-Bank](#) [Taxonomy](#) [UniProtKB](#) [PDBe](#) [InterPro](#) [HGNC](#)

AL773578

Homo sapiens chromosome 21 from PAC RP1-265B9 map 21q22.2,D21S349-MX1

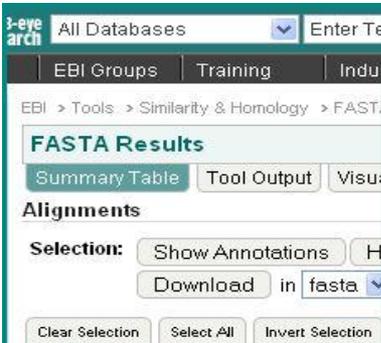
View: [in ENA](#) [in EMBL format](#) [in SRS](#) [in EMBL-SVA](#)

References: [EMBL-Bank](#) [Taxonomy](#) [InterPro](#) [UniProtKB](#) [HGNC](#)

View in the UniProt website: [C9JUL1_HUMAN](#)



Navigate to search



Align.	DB:ID	Source					
<input checked="" type="checkbox"/>	1	NRPL2:NRP001827BA	PN:US64				
<input checked="" type="checkbox"/>	2	NRPL2:NRP001827B8	PN:EP0242329 A2	124	794	100.0	1.6E-46
<input checked="" type="checkbox"/>	3	NRPL2:NRP001827B9	PN:US5466585 A	124	794	100.0	1.6E-46
<input checked="" type="checkbox"/>	4	TR:C9JUL1_HUMAN	Putative uncharacterized protein MX1 OS=Homo sapiens GN=MX1 PE=3 SV=1	197	794	100.0	1.6E-46
<input checked="" type="checkbox"/>	5	TR:C9JUN19_HUMAN	Putative uncharacterized protein MX1 OS=Homo sapiens GN=MX1 PE=3 SV=1	201	794	100.0	1.6E-46
<input checked="" type="checkbox"/>	6	NRPL2:NRP00221FC9	PN:US2007218466 A1	508	794	100.0	5.1E-46
<input checked="" type="checkbox"/>	7	NRPL2:NRP0012C2F5	PN:US2007218466 A1	662	794	100.0	6.3E-46

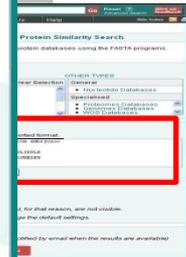
Cross-references and related information in:
[Nucleotide Sequences](#) [Genomes](#) [Ontologies](#)
[Protein Families](#) [Literature](#)

Related EMBL nucleotide entries

(3) Set parameters



base



sequence



Sequences

Genomes references for entry **C9JUL1_HUMAN** from **UniProtKB**

This entry has other cross references in: **InterPro - Medline - Taxonomy - GO - Ensembl - HGNC - EMBL-Bank**

1 result found in HGNC

HGNC:7532

Approved Symbol: MX1
Approved Name: myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
Status: Approved
Aliases: IFI-78K MxA
Locus Type: gene with protein product
Chromosome: 21q22.3
References: [Medline](#) [UniProtKB](#)

1 result found in Ensembl Gene

ENSG00000157601

myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) [Source:HGNC]
Symbol;Acc: 7532
Species: Homo sapiens
References: [Taxonomy](#) [Ensembl Genomes Gene](#) [UniProtKB](#) [Ensembl](#) [GO](#) [HGNC](#) [EMBL-Bank](#)



Navigate to search

FASTA Results

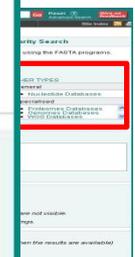
Alignments

Align.	DB:ID	Source					
<input checked="" type="checkbox"/>	1	NRPL2:NRP001827BA	PN:US640				
<input checked="" type="checkbox"/>	2	NRPL2:NRP001827B8	PN:EP0242329 A2	124	794	100.0	1.6E-46
<input checked="" type="checkbox"/>	3	NRPL2:NRP001827B9	PN:US5466585 A	124	794	100.0	1.6E-46
<input checked="" type="checkbox"/>	4	TR:C9JUL1_HUMAN	Putative uncharacterized protein MX1 OS=Homo sapiens GN=MX1 PE=3 SV=1	197	794	100.0	1.6E-46
<input checked="" type="checkbox"/>	5	TR:C9JN19_HUMAN	Putative uncharacterized protein MX1 OS=Homo sapiens GN=MX1 PE=3 SV=1	201	794	100.0	1.6E-46
<input checked="" type="checkbox"/>	6	NRPL2:NRP00221FC9	PN:US2007218466 A1	508	794	100.0	5.1E-46
<input checked="" type="checkbox"/>	7	NRPL2:NRP0012C2F5	PN:US2007218466 A1	662	794	100.0	6.3E-46



Related genomic information

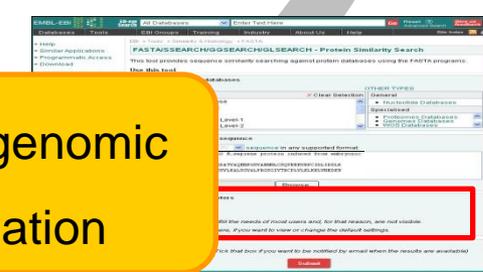
(3) Set parameters



base



sequence



Sequen

Ontologies references for entry **C9JUL1_HUMAN** from **UniProtKB**

This entry has other cross references in: **InterPro - Medline - Taxonomy - GO - Ensembl - HGNC - EMBL-Bank**

2 results found in GO

GO:0003924

GTPase activity

Ontology: molecular function

Catalysis of the reaction: GTP + H₂O = GDP + phosphate.

View: [in SRS](#)

GO:0005525

GTP binding

Ontology: molecular function

Interacting selectively and non-covalently with GTP, guanosine triphosphate.

View: [in SRS](#)

1 result found in Taxonomy

9606

Homo sapiens

Common name: human

View: [in Taxonomy format](#) [in SRS](#) [in ENA](#)

References: [Taxonomy](#) [Other references...](#)

View in the UniProt website: [C9JUL1_HUMAN](#)



Navigate to search



Align.	DB:ID	Source					
<input checked="" type="checkbox"/>	1	NRPL2:NRP001827BA	PN:US6407				
<input checked="" type="checkbox"/>	2	NRPL2:NRP001827B8	PN:EP0242329 A2	124	794	100.0	1.6E-46
<input checked="" type="checkbox"/>	3	NRPL2:NRP001827B9	PN:US5466585 A	124	794	100.0	1.6E-46
<input checked="" type="checkbox"/>	4	TR:C9JUL1_HUMAN	Putative uncharacterized protein MX1 OS=Homo sapiens GN=MX1 PE=3 SV=1 <i>Cross-references and related information in:</i> Nucleotide Sequences Genomes Ontologies Protein Families Literature	127	794	100.0	100.0
<input checked="" type="checkbox"/>	5	TR:C9JN19_HUMAN	Putative uncharacterized protein MX1 OS=Homo sapiens GN=MX1 PE=3 SV=1 <i>Cross-references and related information in:</i> Nucleotide Sequences Genomes Ontologies Protein Families Literature	201	794	100.0	
<input checked="" type="checkbox"/>	6	NRPL2:NRP00221FC9	PN:US2007218466 A1	508	794	100.0	5.1E-46
<input checked="" type="checkbox"/>	7	NRPL2:NRP0012C2F5	PN:US2007218466 A1	662	794	100.0	6.3E-46



Gene ontology (GO) mapping for protein

(3) Set parameters



sequence

Sequen

Protein Families references for entry C9JUL1_HUMAN from UniProtKB

This entry has other cross references in: [InterPro](#) - [Medline](#) - [Taxonomy](#) - [GO](#) - [Ensembl](#) - [HGNC](#) - [EMBL-Bank](#)

4 results found in InterPro

IPR001401

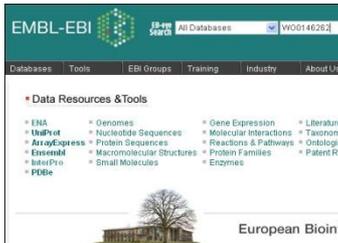
Dynamin, GTPase domain
Membrane transport between compartments in eukaryotic cells requires proteins that allow the budding and scission of nascent cargo vesicles from one compartment and their targeting and fusion with another. Dynamins are large GTPases that belong to a protein superfamily that, in eukaryotic cells, includes classical dynamins, dynamin-like proteins, OPA1, Mx proteins, mitofusins and guanylate-binding proteins/atlastins, and are involved in the scission of a wide range of vesicles and organelles. They play a role in many processes including budding of transport vesicles, division of organelles, cytokinesis and pathogen resistance. The minimal distinguishing architectural features that are common to all dynamins and are distinct from other GTPases are the structure of the large GTPase domain (300 amino acids) and the presence of two additional domains; the middle domain and the GTPase effector domain (GED), which are involved in oligomerization and regulation of the GTPase activity. This entry represents the GTPase domain, containing the GTP-binding motifs that are needed for guanine-nucleotide binding and hydrolysis. The conservation of these motifs is absolute except for the final motif in guanylate-binding proteins. The GTPase catalytic activity can be stimulated by oligomerisation of the protein, which is mediated by interactions between the GTPase domain, the middle domain and the GED.

View: [in InterPro format](#) [in SRS](#) [in Interpro Matches](#)
References: [InterPro](#) [UniProtKB](#) [GO](#) [PDBe](#) [Medline](#)

IPR015577

Interferon-induced Mx protein
The dynamin superfamily consists of large GTPases that play important roles in endocytosis, intracellular membrane trafficking, and are thought to generate force in order to constrict membranes. Interferon-induced Mx proteins are able to assemble into oligomers, such as rings and spirals, and are thought to generate force in order to constrict membranes required for clathrin-mediated endocytosis, which in turn appears to require GTP hydrolysis. Interferon-induced Mx proteins are unique from other members of the dynamin superfamily. Also, Mx proteins are expressed in the cell. In general, they appear to detect viral structures and cause these structures to get sorted into new viral particles. Mx proteins generally consist of a N-terminal GTPase domain and a C-terminal effector domain.

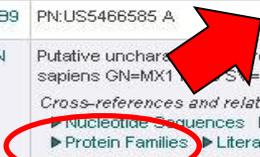
View: [in InterPro format](#) [in SRS](#) [in Interpro Matches](#)
References: [InterPro](#) [Medline](#) [UniProtKB](#)



Navigate to search



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<input checked="" type="checkbox"/>	NRPL2:NRP001827BA	PN:US6407	124	794	100.0	100.0	1.6E-46
<input checked="" type="checkbox"/>	NRPL2:NRP001827B8	PN:EP0242329 A2	124	794	100.0	100.0	1.6E-46
<input checked="" type="checkbox"/>	NRPL2:NRP001827B9	PN:US5466585 A	124	794	100.0	100.0	1.6E-46
<input checked="" type="checkbox"/>	TR:C9JUL1_HUMAN	Putative uncharacterized protein MX1 OS=Homo sapiens GN=MX1 PE=3 SV=1	197	794	100.0	100.0	1.6E-46
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<input checked="" type="checkbox"/>	NRPL2:NRP0012C2F5	PN:US2007218466 A1	662	794	100.0	100.0	6.3E-46



InterPro family/domain classification

(3) Set parameters



sequence

Sequen

Literature references for entry **C9JUL1_HUMAN** from **UniProtKB**

This entry has other cross references in: **InterPro - Medline - Taxonomy - GO - Ensembl - HGHC - EMBL-Bank**

2 results found in Medline

20289799

ALBANESE AA, SAUR B, IRBY V

The microcolorimetric estimation of plasma proteins.

(Mar-1947) *The Journal of laboratory and clinical medicine*, 32 (3) :296-9

View: [in Medline format](#) [in SRS](#)

References: [References in All the EBI](#)

10830953

Hattori M, Fujiyama A, Taylor TD, Watanabe H, Yada T, Park HS, Toyoda A, Ishii K, Totoki Y, Choi DK, Groner Y, Soeda E, Ohki M, Takagi T, Sakaki Y, Taudien S, Blechschmidt K, Polley A, Menzel U, Delabar J, Kumpf K, Lehmann R, Patterson D, Reichwald K, Rump A, Schillhabel M, Schudy A, Zimmermann W, Rosenthal A, Kudoh J, Schibuya K, Kawasaki K, Asakawa S, Shintani A, Sasaki T, Nagamine K, Mitsuyama S, Antonarakis SE, Minoshima S, Shimizu N, Nordsiek G, Hornischer K, Brant P, Scharfe M, Schon O, Desario A, Reichelt J, Kauer G, Blocker H, Ramser J, Beck A, Klages S, Hennig S, Riesselmann L, Dagand E, Haaf T, Wehrmeyer S, Borzym K, Gardiner K, Nizetic D, Francis F, Lehrach H, Reinhardt R, Yaspo ML, Chromosome 21 mapping and sequencing consortium

The DNA sequence of human chromosome 21.

(18-May-2000) *Nature*, 405 (6784) :311-9

View: [in Medline format](#) [in SRS](#)

References: [References in All the EBI](#)

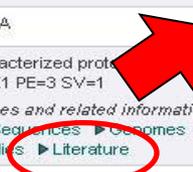
View in the UniProt website: [C9JUL1_HUMAN](#)



Navigate to sea

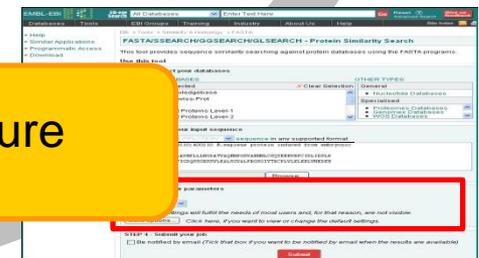


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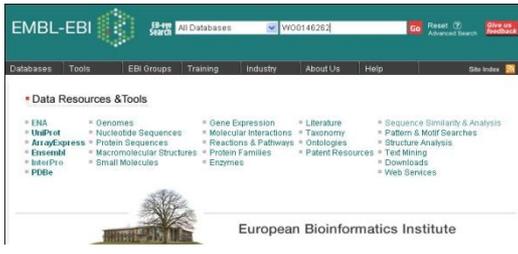
base

sequence

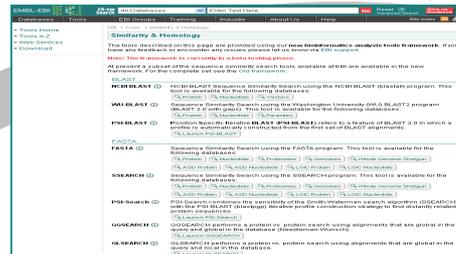


(3) Set parameters

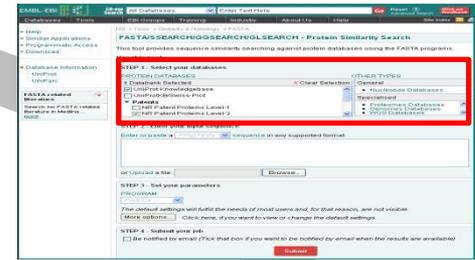
Sequence searching – specialised tools



Navigate to search tools



Select search tool



(1) Select database

FASTA Results

Summary Table | Tool Output | Visual Output | **Functional Predictions** | Submission Details | Submit Another Job

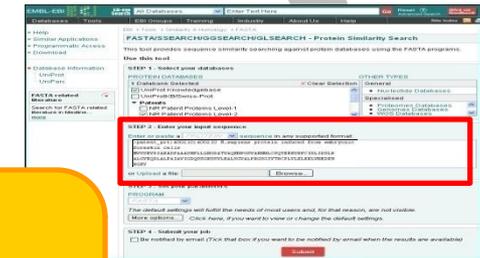
Alignments

Selection: Show Annotations | Hide Annotations | Show Alignments | Hide Annotations

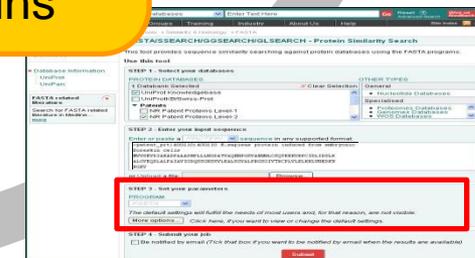
Download in fasta format

Align.	DB:ID	Source	Length	Score	Ident		
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2	NRPL2:NRP001827B8	PN:EP0242329 A2	124	794	100.0		
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4	TR:C9JUL1_HUMAN	Putative uncharacterized protein MX1 OS=Homo sapiens GN=MX1 PE=3 SV=1 <i>Cross-references and related information in:</i> ▶ Nucleotide Sequences ▶ Genomes ▶ Ontologies ▶ Protein Families ▶ Literature	197	794	100.0		
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Functional predictions on ALL proteins

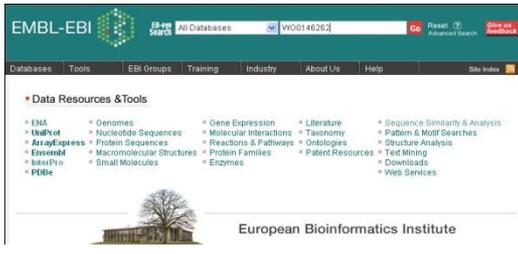


Copy/paste sequence



(3) Set parameters

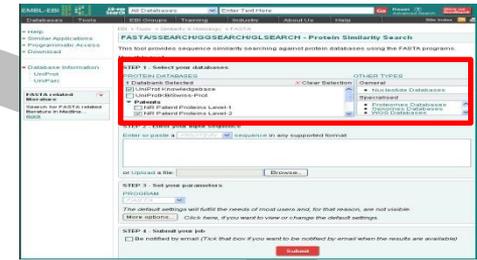
Sequence searching – specialised tools



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Select search tool



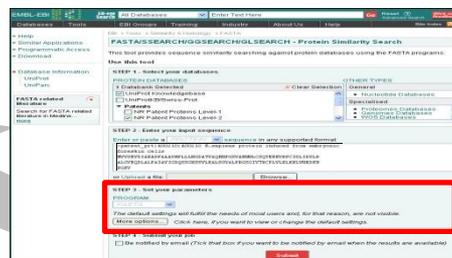
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FASTA Results

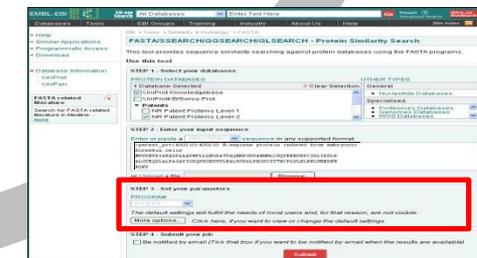
Alignments: [Show Annotations](#) | [Hide Annotations](#) | [Show Alignments](#) | [Hide Alignments](#) | [Download](#) | [in fasta](#) | [format](#)

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[5]	TR104411_HUMAN	Putative uncharacterized protein M01 OS=Homo sapiens (Homo sapiens)	201	794	100.0	100.0	3.46-45
[6]	NP121499.1[2789]	PNUS647200.A1	509	794	100.0	100.0	6.16-80
[7]	NP121499.1[2789]	PNUS647200.A1	662	794	100.0	100.0	6.36-46

Result summary + annotation



(4) Submit



(3) Set parameters

Sequence searching – specialised tools

The screenshot displays the SLING FASTA search interface. At the top, there's a search bar with 'All Databases' selected and a 'Go' button. Below the search bar, navigation links for 'EBI Groups', 'Training', 'Industry', 'About Us', and 'Help' are visible. The main content area is titled 'FASTA Results' and includes tabs for 'Summary Table', 'Tool Output', 'Visual Output', 'Functional Predictions', 'Submission Details', and 'Submit Another Job'. The 'Functional Predictions' tab is active, showing 'Fast Family and Domain Prediction' results. The results are organized into four sections, each corresponding to a different query sequence: C9JUL1_HUMAN, C9JIN19_HUMAN, D3DS18_HUMAN, and B2RDA5_HUMAN. Each section contains a 'MATCH' bar chart where the query sequence is shown at the top, and various domain matches are represented by colored bars below it. A legend on the right side of each chart identifies the databases used for the search: PANTHER, PFAM, SMART, PRINTS, and PROSITE. The results also include 'Putative uncharacterized' proteins and 'Unclassified' entries.

Extract information

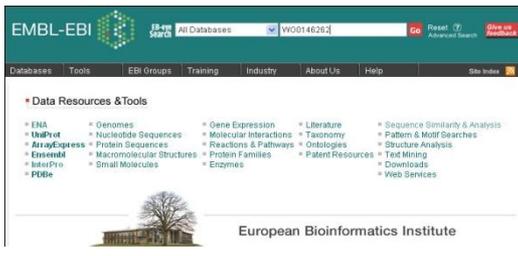
Functional predictions:
InterPro family/domain classifications

Visual comparison →
find mis- or partial matches

Prioritize results

(3) Set parameters

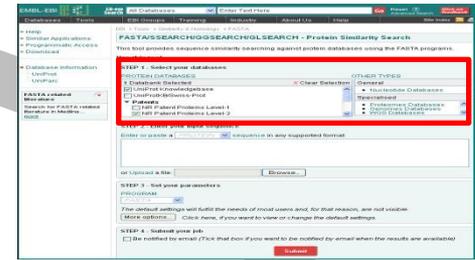
Sequence searching – specialised tools



Navigate to search tools



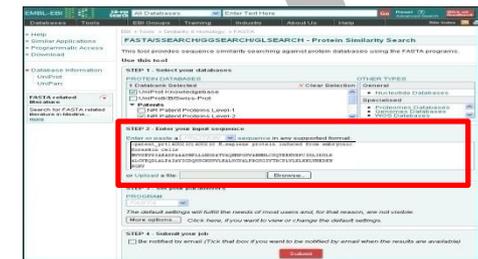
Select search tool



(1) Select database



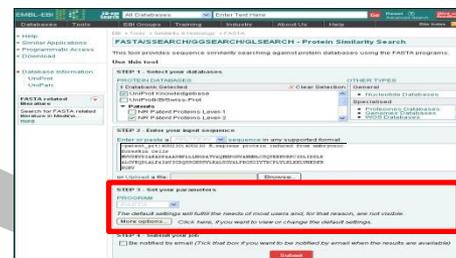
Functional predictions



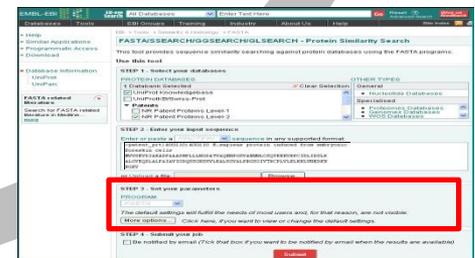
(2) Copy/paste sequence



Result summary + annotation



(4) Submit



(3) Set parameters



Accessing old entries

sequence archives...



Sequence archives

- ENA nucleotide sequence version archive (SVA)
www.ebi.ac.uk/embl/sva

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Search by date →
get specific record

Search by accession only →
get all records

- UniProtKB

UniProtKB Sequence/Annotation Version (UniSave) is a repository of UniProtKB/Swiss-Prot and UniProtKB/TrEMBL entry versions.

Primary accession number or entry name:

Date: day-month-year (e.g. 30-11-1998 or 30-NOV-1998) or year-month-day.

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Snapshot at day-month-year (e.g. 30-11-1998 or 30-NOV-1998) [Current version](#)

8 matches

	Accession Number	Entry Version	Sequence Version	Release	Issue Date	
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<input type="checkbox"/>	All					

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Snapshot at day-month-year (e.g. 30-11-1998 or 30-NOV-1998) [Current version](#)

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AC  AX429748;
XX
SV  AX429748.1
XX
DT  21-JUN-2002 (Rel. 72, Created)
DT  21-JUN-2002 (Rel. 72, Last updated, Version 1)
XX
DE  Sequence 13 from Patent EP1203827.
XX
KW  .
XX
OS  Homo sapiens (human)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC  Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN  [1]
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RT  "Polymorphisms in the human kdr gene";
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[F.A.Q.](#)

Accession Number or Sequence Version: case sensitive

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Differences for AX429748 30-MAY-2002 / 28-NOV-2008 [Back to List](#)

Lines unchanged **Lines removed** Lines inserted

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SV AX429748.1
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DE Sequence 13 from Patent EP1203827.
XX
KW .
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
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OC Homo.
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RL Patent number EP1203827-A2/13, 08-MAY-2002.
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RL AstraZeneca AB (SE).
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cagcgtcct ggtgatgctc cccaaatttc ggggaccggc 100
//

```



Summary

Broad patent sequence coverage

- Protein/nucleotides: EPO, USTPO, JPO, KIPO

Comprehensive sequence databases

- ENA & UniParc (PAT / PRT class data)
- Non-redundant patent sequences → **enriched**

Sequence archives

- ENA SVA & UniSave → **track changes**

Multiple search engines

- EB-eye text search → fetch patent literature and sequences
- SRS → advanced text searching >100 databases (including patents)
- Sequence searching → specialised tools; **annotation-enhanced**



User support

- 2Can bioinformatics user support – www.ebi.ac.uk/2Can
- Online help pages – www.ebi.ac.uk/help
- E-mail support – www.ebi.ac.uk/support



Any questions?

Contacts:

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