

Sequence retrieval system(SRS)



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SRS

The Sequence Retrieval System (SRS) – a network browser for databases in molecular biology.

It is a powerful sequence information indexing, search and retrieval system (<http://srs.ebi.ac.uk/>)

- Developed in 1993, by Thure Etzold.

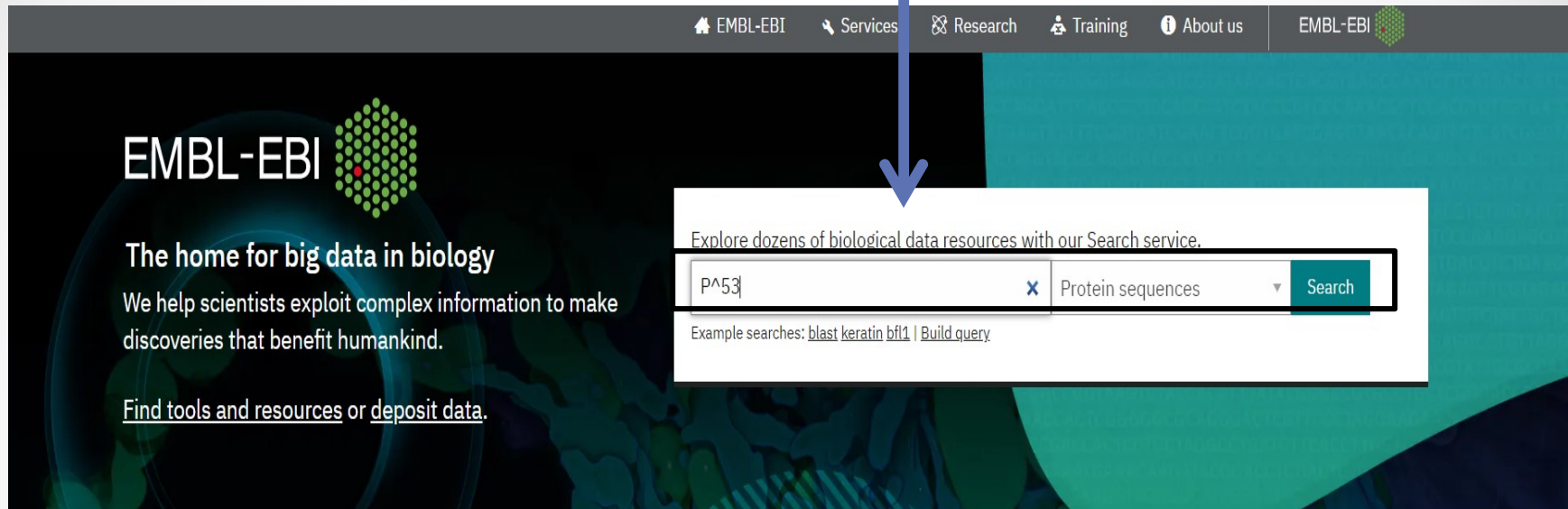
SRS Features:

- SRS databases are **well indexed**, thus reducing the search time for the large number of potential databases
- SRS allows any **flat file database** to be indexed to any other. The advantage being the derived indices may be rapidly searched, allowing users to retrieve, link and access entries from all the interconnected resources
- The system has the particular strength that it can be readily **customized** to use any defined set of databanks.

- SRS is a homogeneous interface to over 80 biological databases that has been developed at the European Bioinformatics Institute (EBI) at Hinxton, UK.
- The types of databases included are sequence and sequence related, metabolic pathways, transcription factors, application results (e.g. BLAST), protein 3-D structure, genome, mapping, mutations and locus-specific mutations. You can access and query their contents and navigate among them.
- The Web page listing all the databases contains a link to a description page about the database and includes the date on which it was last updated.
- You select one or more of the databases to search before entering your query. Over 30 versions of SRS are currently running on the WWW. Each includes a different subset of databases and associated analytical tools.



Procedure



EMBL-EBI

The home for big data in biology

We help scientists exploit complex information to make discoveries that benefit humankind.

[Find tools and resources or deposit data.](#)

EMBL-EBI Services Research Training About us

Explore dozens of biological data resources with our Search service.

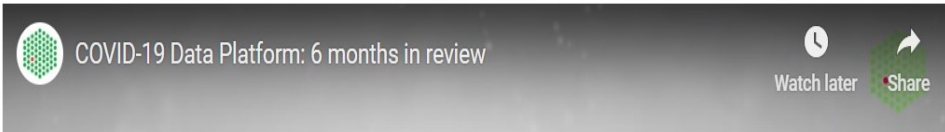
PA53 Protein sequences Search

Example searches: [blast keratin bfl1](#) | [Build query](#)

EMBL-EBI response to COVID-19

To help protect staff and visitors from the coronavirus outbreak, EMBL-EBI closed its premises on 18 March at 17:00. Our data resources and tools will continue to function as normal. [Read more](#) >

Featured topic



COVID-19 Data Platform: 6 months in review

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Search results for **P^A53**

Showing 15 results out of 45,428,598 in All results → Protein sequences

Filter your results

Source

All results (75,404,965)

Protein sequences (45,428,598)

UniProtKB (41,844,121)

UniRef100 (2,162,305)

UniRef90 (1,042,146)

UniRef50 (284,497)

EPO (17,293)

JPO (51,407)

KIPO (1,703)

USPTO (604)

UniParc (24,522)

Organisms

- Salmonella enterica (388,510)
- Human immunodeficiency virus 1 (277,945)
- Gammaproteobacteria bacterium (264,489)
- Arundo donax (259,909)
- Acidobacteria bacterium (256,175)
- Escherichia coli (228,236)
- Clostridiales bacterium (206,589)
- Lachnospiraceae bacterium (196,631)
- Chloroflexi bacterium (175,043)
- Pseudomonas sp. (169,525)

↓ Save result

📡 Create RSS feed

Protein sequences (45,428,598 results)

Q9VHN9(HPS5_DROME) Source: UniProtKB (ID: HPS5_DROME)

Hermansky-Pudlak syndrome 5 protein homolog

Drosophila melanogaster(Reviewed)

Secondary accession number(s): Q8SX11

Cross References: Samples & ontologies (11) Protein families (9) Protein sequences (8) [+ show more](#)

Formats: in FASTA format in Feature Viewer in Interpro Matches [+ show more](#)

Q04671(P_HUMAN) Source: UniProtKB (ID: P_HUMAN)

P protein

Homo sapiens(Reviewed)

Secondary accession number(s): Q15211, Q15212, Q96EN1, Q9UMI5

Cross References: Protein expression data (48) Literature (28) Samples & ontologies (14) [+ show more](#)

Formats: in FASTA format in Feature Viewer in Interpro Matches [+ show more](#)

Q6IPU0(CENPP_HUMAN) Source: UniProtKB (ID: CENPP_HUMAN)

Centromere protein **P** CENP-**P**

Homo sapiens(Reviewed)

Secondary accession number(s): B3KRA5, B3KS17, Q5T9F8, Q5T9F9

Cross References: Protein expression data (115) Nucleotide sequences (9) Samples & ontologies (7) [+ show more](#)



Filter your results

Source

- All results (75,484,965)
- Protein sequences (45,428,598)
- UniProtKB (41,844,121)**

Organisms

- Salmonella enterica (380,544)
- Human immunodeficiency virus 1 (277,923)
- Arundo donax (259,909)
- Acidobacteria bacterium (241,322)
- Gammaproteobacteria bacterium (238,233)
- Clostridiales bacterium (200,671)
- Lachnospiraceae bacterium (188,922)
- Escherichia coli (188,796)
- Pseudomonas sp. (163,475)
- Chloroflexi bacterium (148,221)

More... >

Keywords

- Reference proteome (14,293,828)
- Membrane (9,242,280)
- Transmembrane (8,574,365)
- Transmembrane helix (8,473,275)
- Transferase (4,144,435)
- Coiled coil (3,942,576)
- Metal-binding (3,758,536)
- Signal (3,451,235)
- Nucleotide-binding (3,137,425)
- Hydrolase (3,120,711)

Save result | BLAST | Clustal | UniSave | Dbfetch | Create RSS feed

UniProtKB (41,844,121 results)

[Q9VHN9\(HPS5_DROME\)](#) Source: UniProtKB (ID: HPS5_DROME)

Hermansky-Pudlak syndrome 5 protein homolog
Drosophila melanogaster(Reviewed)
Secondary accession number(s): Q8SX11

Cross References: Samples & ontologies (11) Protein families (9) Protein sequences (8) + show more

Formats: in FASTA format in Feature Viewer in Interpro Matches + show more

[Q04671\(P_HUMAN\)](#) Source: UniProtKB (ID: P_HUMAN)

P protein
Homo sapiens(Reviewed)
Secondary accession number(s): Q15211, Q15212, Q96EN1, Q9UMI5

Cross References: Protein expression data (48) Literature (28) Samples & ontologies (14) + show more

Formats: in FASTA format in Feature Viewer in Interpro Matches + show more

[Q6IPU0\(CENPP_HUMAN\)](#) Source: UniProtKB (ID: CENPP_HUMAN)

Centromere protein P CENP-P
Homo sapiens(Reviewed)
Secondary accession number(s): B3KRA5, B3KS17, Q5T9F8, Q5T9F9

Cross References: Protein expression data (115) Nucleotide sequences (9) Samples & ontologies (7) + show more

Formats: in FASTA format in Feature Viewer in Interpro Matches + show more

[P49908\(SEPP1_HUMAN\)](#) Source: UniProtKB (ID: SEPP1_HUMAN)

Selenoprotein P SeP
Homo sapiens(Reviewed)

1. Click on the PDB id to view in UniProt and to download sequence data.
2. Or,
 - Choose desired sequences.
 - Then click on clustal, to download MSA file and phylogenetic tree.



UniProtKB - Q9VHN9 (HPS5_DROME)

[Display](#)
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[Added to basket](#)
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[Add a publication](#)
[Feedback](#)

- Entry
- Publications
- Feature viewer
- Feature table

Protein Herm... **rome 5 protein homolog**
Gene p
Organism *Drosophila melanogaster* (fruit fly)
Status Experimental evidence at transcript levelⁱ

View format ✕
[Text](#)
[FASTA \(canonical\)](#)
[XML](#)
[RDF/XML](#)
[GFF](#)

None

- Function
- Names & Taxonomy
- Subcellular location
- Pathology & Biotech
- PTM / Processing
- Expression
- Interaction
- Structure
- Family & Domains
- Sequences (1+)
- Similar proteins
- Cross-references
- Entry information
- Miscellaneous

Functionⁱ

Has a role in the biogenesis of eye pigment granules. Eye pigment granules are specialized forms of late endosomes or lysosomes. Biogenesis of pigment granules in the eye requires molecular components required for protein delivery to lysosomes. [1 Publication](#)

Miscellaneous

Pink was the second eye color gene identified by Morgan and colleagues, mutant flies were isolated in June 1910 just 2 months after isolation of the first white mutant allele. Another mutant allele of pink, peach, was isolated by Bridges in 1913, and according to a review published by Bridges and Morgan 10 years later, these alleles represented the first case of multiple allelomorphs described for an autosomal gene in *Drosophila*.

GO - Molecular functionⁱ

- pigment binding [Source: UniProtKB-KW](#)

Complete GO annotation on QuickGO ...

GO - Biological processⁱ

- compound eye pigmentation [Source: FlyBase](#)
- eye pigment biosynthetic process [Source: UniProtKB](#)
- negative regulation of gene silencing by RNA [Source: FlyBase](#)
- ommochrome biosynthetic process [Source: FlyBase](#)
- protein targeting to lysosome [Source: UniProtKB](#)
- response to stimulus [Source: UniProtKB-KW](#)
- visual perception [Source: UniProtKB-KW](#)

Complete GO annotation on QuickGO ...

Keywordsⁱ

Click on Format>>FASTA and download the protein sequence in Fasta format.



>sp|Q9VHN9|HPS5_DROME Hermansky-Pudlak syndrome 5 protein homolog OS=Drosophila melanogaster OX=7227 GN=p PE=2 SV=1
MADAYCLTNFIDFSLSLPLKHHNRIKYTCFDISDSYIIFGASSGSLYLFNRNGKFLLL
IPNKHGAITSLSISANSKYVAFATQRLICVYAVNLSAQATPQVIFTHLDQSVQVTCIHW
TQDEKQFYYGDSRGQVSLVLLSSFIGHSLLFNMTVHPLLYLDSPIVQIDDFEYLLLVSN
TKCILCNTEYEDYKQIGNRPRDGAFGACFFVSPQESLQPSRIYCARPGSRVWEVDFEGEV
IQTHQFKTALATAPARIQRPGSGTDEL DANAELLDYQPQNLQFAKVQRLNDDFLLAFTEL
GLYIFDIRRSVVLWSNQFERIADCRSSGSEIFVFTQSGALYSVQLQTLQSHAVSLIQQS
KLLPCANLLRQHVRVYFADKAREDYELKQLNPLKQLLIERQEYELLNDISVIFDAITQCTG
SALDTHSSGGSSATTERSLSGGSSSRAPPKGVYVLENAFCNLIKQPLKTGHFKDALLTVT
GKFGKNIKYKFNIFAEQQQLVRELIPASERSLPFKDIKARYESGSEDQEEEIVRRCKK
PAPQVPHISPEEKTLYNLYLIAKSAKFSRTQCVDRYRAVFDEYAAGELVNLLKLAQVMV
EHGDTPDQAQRNCYEMYFDYLDPEMIWEVDDATRDHIAAGFVLLNTSQNAEIVKCEHCSF
PLRFDTSCQYHELGAVLLRYFWSRGEQLKCFDVVQSVALLDVLAKFYLAEQNLTKVVAI
VLNYGLPELLADVKGQLSVSAWGRCFEQFVELQRGGRLVCANCECISGVEQEQLGRHFFY
NWNCFLNIALDHMSAGDTLALIFKWSSYIPNDAIDREFYSRCLLKG



Multiple Sequence Alignment

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate alignments between **three or more** sequences. For the alignment of two sequences please instead use our [pairwise sequence alignment tools](#).

Important note: This tool can align up to 4000 sequences or a maximum file size of 4 MB.

STEP 1 - Enter your input sequences

Enter or paste a set of

PROTEIN

sequences in any supported format:

uniprot:HPS5_DROME,uniprot:P_HUMAN,uniprot:PHOSP_SVCV

a →

Or, upload a file: No file chosen

[Use a example sequence](#) | [Clear sequence](#) | [See more example inputs](#)

STEP 2 - Set your parameters

OUTPUT FORMAT

ClustalW with character counts

The default settings will fulfill the needs of most users.

(Click here, if you want to view or change the default settings.)

STEP 3 - Submit your job

Be notified by email (Tick this box if you want to be notified by email when the results are available)

b →

- The code of the sequences that i have choosen.
- Perform MSA by clicking in submit below.



Clustal Omega

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Tools > Multiple Sequence Alignment > Clustal Omega

Results for job clustalo-I20201201063108-0787-32939856-p1m

[Alignment](#)[Result Summary](#)[Guide Tree](#)[Phylogenetic Tree](#)[Results Viewers](#)[Submission Details](#)[Download Alignment File](#)[Show Colors](#)

CLUSTAL O(1.2.4) multiple sequence alignment

UNIPROT:P_HUMAN	MHLEGRDGRRRYPGAPAVELLQTSVPSGLAELVAGKRRLPRGAGGADPSHSCPRGAAGQSS	60
UNIPROT:HPS5_DROME	-----	0
UNIPROT:PHOSP_SVCV	-----	0
UNIPROT:P_HUMAN	WAPAGQEFASFLLTKGRSHSLPQMSSSRKSDSCFTENTPLLRNSLQ-----EKGS--	110
UNIPROT:HPS5_DROME	-MADAYCLTNFIDF-SLSLSLPLKHHNRKIKYTCFDISDSYIIFGASSGSLYLFNRNGKFL	58
UNIPROT:PHOSP_SVCV	-----	0
UNIPROT:P_HUMAN	RCIPVYHPEFITAEESWEDSSADW-ERRYLLSREVSGLSASASSEKGDLLDSPHIRLRLS	169
UNIPROT:HPS5_DROME	LLIPNKHGAIISLSISANSKYVAFATQRSLICVYAVNLSAQATP-----QVIFTHLDQS	112
UNIPROT:PHOSP_SVCV	-----	0
UNIPROT:P_HUMAN	KLRRCVQWLKVMGLFAF-----	186
UNIPROT:HPS5_DROME	VQVTCIHWTDQEKQFYGDSRGQVSLVLLSSFIGHSLLFNMTVHPLLYLDSPIVQIDDFE	172
UNIPROT:PHOSP_SVCV	-----MSLHSK-----	6
UNIPROT:P_HUMAN	-----VVLCSILFSLYPDQGK-----LWQLLALSPLNYSV--NLSSHVDSTLL	228
UNIPROT:HPS5_DROME	YLLLVSNCTKICLNTEYEDYKQIGNRPRDGAFGACFFVSPQESLQPSRIYCARPGRVW	232
UNIPROT:PHOSP_SVCV	-----	6
UNIPROT:P_HUMAN	QVDLAGALVA-----SGPS---RPGREEHIV---VELTQADALGSRWRPQQVTHN	273
UNIPROT:HPS5_DROME	EVDFEGEVIQTHQFKTALATAPARIQRPGSGTDELDAEAELLDYQPQNLQFAKVQRLND-	291
UNIPROT:PHOSP_SVCV	-----L-S-	8
	:	
UNIPROT:P_HUMAN	WTVYLNPRRSEHSVMSRTFEVLTRETVISISIRASLQQTQAVPLLMAHQYLRGSVETQVTI	333
UNIPROT:HPS5_DROME	-----DFLLAF-----	297
UNIPROT:PHOSP_SVCV	-----ESLKAY-----	14

1. Click on download alignment file for downloading the MSA file.
2. Or choose phylogenetic tree, for downloading phylogenetic tree.



CLUSTAL O(1.2.4) multiple sequence alignment

```

UNIPROT:P_HUMAN      MHLEGRDGRRYPGAPAVELLQTSVPSGLAELVAGKRRLPRGAGGADPSHSCPRGAAGQSS      60
UNIPROT:HPS5_DROME   -----                                0
UNIPROT:PHOSP_SVCV   -----                                0

UNIPROT:P_HUMAN      WAPAGQEFASFLTKGRSHSSLPQMSSSRKSDSCFTENTPLLRLNSLQ-----EKGS--      110
UNIPROT:HPS5_DROME   -MADAYCLTNFIDF-SLSLSLPLKHHNRIKYTCFDISDSYIIFGASSGSLYLFNRNGKFL      58
UNIPROT:PHOSP_SVCV   -----                                0

UNIPROT:P_HUMAN      RCIPVYHPEFITAEESWEDSSADW-ERRYLLSREVSGLSASASSEKGDLLDSPHIRLRLS      169
UNIPROT:HPS5_DROME   LLIPNKHGAITSLSISANSKYVAFATQRSLICVYAVNLSAQATP-----QVIFTHLDQS      112
UNIPROT:PHOSP_SVCV   -----                                0

UNIPROT:P_HUMAN      KLRRVCVQWLKVMGLFAF-----                                186
UNIPROT:HPS5_DROME   VQVTCIHWQDEKQFYYGDSRGQVSLVLLSSFIGHSLLFNMTVHPLL YLDSPIVQIDDFE      172
UNIPROT:PHOSP_SVCV   -----MSLHSK-----                                6

UNIPROT:P_HUMAN      -----VVLCSILFSLYPDQGK-----LWQLLALSPLENYSV--NLSSHVDSTLL      228
UNIPROT:HPS5_DROME   YLLLVSNCTKCILCNTYEYDKQIGNRPRDGAFGACFFVSPQESLQPSRIYCARPGSRVW      232
UNIPROT:PHOSP_SVCV   -----                                6

UNIPROT:P_HUMAN      QVDLAGALVA-----SGPS---RPGREEHIV---VELTQADALGSRWRRPQQVTHN      273
UNIPROT:HPS5_DROME   EVDFEGEVIQTHQFKTALATAPARIQRPGSGTDEL DANAELLDYQPQLQFAKVQLND-      291
UNIPROT:PHOSP_SVCV   -----L-S-                                8
                                     :

UNIPROT:P_HUMAN      WTVYLNPRRSEHSVMSRTFEVLTRTVSISIRASLQQTQAVPLLMHQYL RGSVETQVTI      333
UNIPROT:HPS5_DROME   -----DFLLAF-----                                297
UNIPROT:PHOSP_SVCV   -----ESLKAY-----                                14
                                     : * .

UNIPROT:P_HUMAN      ATAILAGVYALIFEIVHRTL AAMLGSLAALAALAVIGD-----RPSLT      377
UNIPROT:HPS5_DROME   -----TELGLYIFDIRRSVAVLWSNQFERIADCRSSGSEIFVFTQSGALYSVQLQTLQS      351
UNIPROT:PHOSP_SVCV   -----ADLDKTVKEI-----EE                                26
                                     : :*

UNIPROT:P_HUMAN      HVVEWIDFETLALLFGMMILVAIFSETGFFDY---CAVKAYRLSRGRVWAMIIMLC LIAA      434
UNIPROT:HPS5_DROME   HAVSLIQQSKL---LPCANL--LRQHVRVFA---DKAREDEYELKQL----NPLK----Q-      394
UNIPROT:PHOSP_SVCV   Q-VS-----SMEEP--VPKTVKYVTFEENLSEEEWESDSGDDDEDSID----DS      68
                                     : *.          : . . . : : : . :

UNIPROT:P_HUMAN      VLSAFLDNVTTML-----LFTPVTIRLCEVLNLDPRQVL-IAEIVFTNIGGA      480

```



Clustal Omega

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Tools > Multiple Sequence Alignment > Clustal Omega

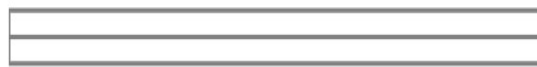
Results for job clustalo-l20201207-063108-0787-32939856-p1m

[Alignments](#)[Result Summary](#)[Guide Tree](#)[Phylogenetic Tree](#)[Results Viewers](#)[Submission Details](#)[Download Phylogenetic Tree Data](#)

Phylogenetic Tree

This is a Neighbour-joining tree without distance corrections.

Branch length: Cladogram Real



UNIPROT_P_HUMAN 0.44742
UNIPROT_HPS5_DROME 0.366
UNIPROT_PHOSP_SVCV 0.434

Tree Data

```
(  
UNIPROT_P_HUMAN:0.44742,  
UNIPROT_HPS5_DROME:0.36600,  
UNIPROT_PHOSP_SVCV:0.43400);
```



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By clicking on download phylogenetic tree data we can download phylogenetic tree

Conclusion

- Although there are many potential databases to search, SRS databases are indexed well, thus reducing the search time. The contents of the data fields in each database are broken down into components, and selected words are extracted and inserted into an index. Each field generally has its own index. The query form allows search terms for a specific field to be entered, or you can search all fields using the option 'All text'. SRS provides an alternative query form that allows more complex Boolean queries to be composed.



Thank You



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