

EDAM ontology and **Bio.Tools** registry

The ontology and the registry for bioinformatics

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EDAM

The ontology of bioinformatics data and methods



[@edamontology](https://twitter.com/edamontology)



edamontology.org



[/edamontology/edamontology](https://github.com/edamontology/edamontology)



<http://www.ebi.ac.uk/ols/ontologies/edam>



bioportal.bioontology.org/ontologies/EDAM

- **Searching for tools and other resources**
- **Tools & data integration**
- **Data provenance**
- **Text mining**

Topic

Phylogenetics
Protein classification

Data

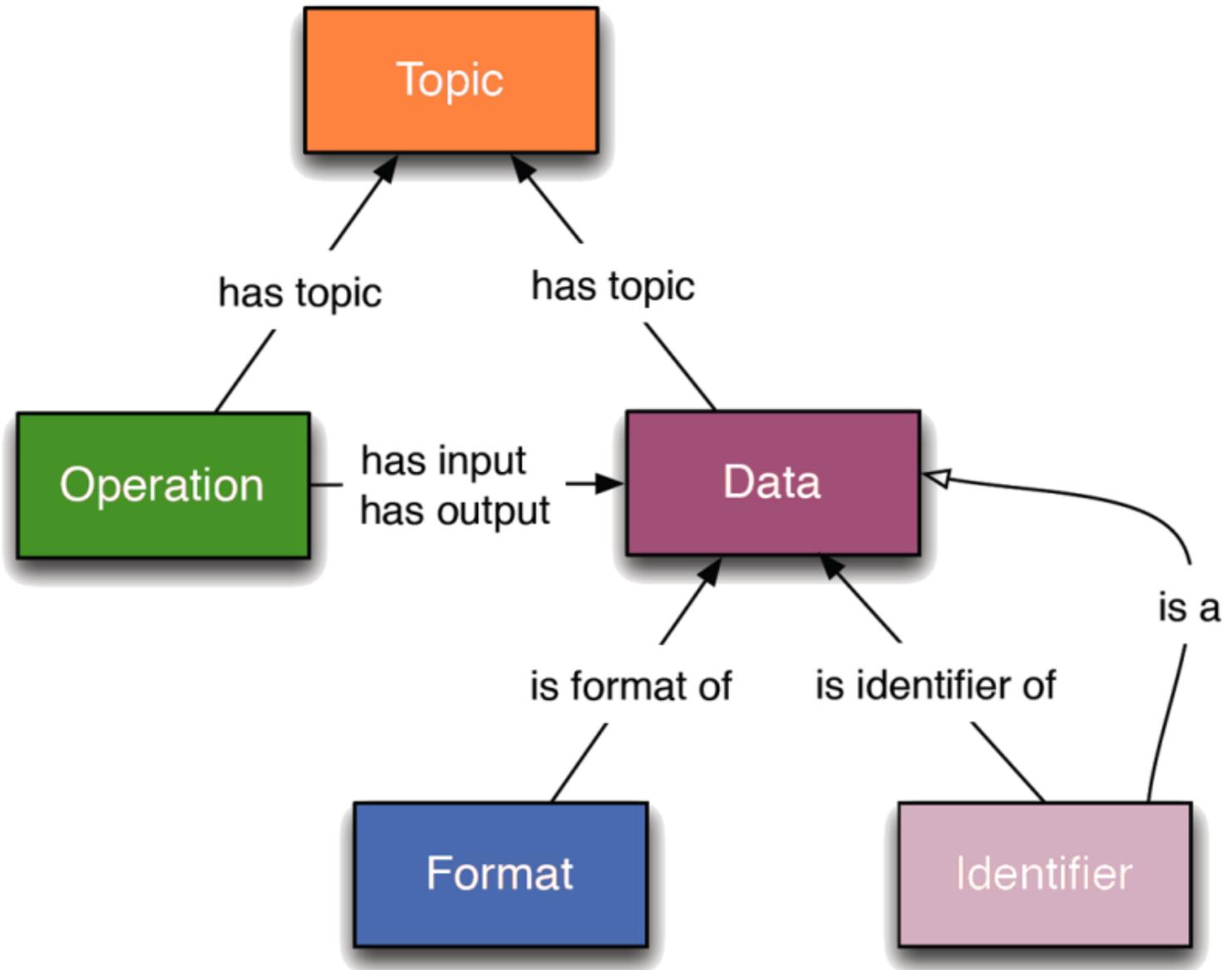
Sequence trace
Position weight matrix

Operation

Sequence alignment construction
Molecular dynamics simulation

Format

FASTQ
SBML



EDAM is used in numerous projects

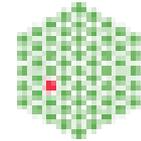
elixir Tools and Data Services Registry

Bio.Tools

1785 entries found

Name	Version	Description	Function	Homepage URL	Resource type
affymetrix	1.44.0	A Command User Interface for analysis of Affymetrix microarray gene expression data using the affy and limma Bioconductor packages	Operations Input: Data (Format) Output: Data (Format)	Topic	- Tool
AggScore	1	The tool to detect structural variations is specifically designed to cluster short-read paired-end data into closely overlapping predictors for deletions and insertions. The method does not make any assumptions on the composition of the data, such as the number of samples, heterogeneity, ploidy, etc. Taking paired ends mapped to a reference genome as input, it iteratively merges mappings to clusters based on a similarity score that takes both the relative location and size of an read into account.	Sequence clustering, Mutation detection - Taking paired ends mapped to a reference genome as input, it iteratively merges mappings to clusters based on a similarity score that takes both the relative location and size of an read into account. Output: Nucleic acid features	Sequence data, Features and motifs	- Tool
AMIS	1.2.0	This package contains the AMIS implementation. It contains necessary functions to assign the file intrinsic molecular subtypes (Luminal A, Luminal B, Her2-enriched, Basal-like, Normal-like). Assignments can be done on individual samples as well as on datasets of gene expression data.	Operations Input: Data (Format) Output: Data (Format)	Topic	- Tool
ALDO2	1.2.0	A differential abundance analysis for the comparison of two or more conditions. For example, single-seq and meta-RNA-seq/high-throughput sequencing assays, or of selected and unselected values from in-vitro sequence selections. Uses a Dirichlet-multinomial model to infer abundance from counts, that has been optimized for three or more experimental replicates. Infers sampling variation and calculates the expected false discovery rate given the biological and sampling variation using the Wilcoxon rank test or Wilcoxon t-test (alpha-test) or the glm and crucial Wald tests (alpha-glm). Reports both P and F values calculated by the Benjamini-Hochberg correction.	Operations Input: Data (Format) Output: Data (Format)	Topic	- Tool
ALIGN	2.0	Pairwise alignment	Global sequence alignment: Local sequence alignment-to-profile alignment (pairwise), Sequence-to-profile alignment - Pairwise alignment is a tool designed for performing sequence alignments. Sequence to sequence, sequence to profile and profile alignments with optional support of secondary structure input. Protein sequence (FASTA, FASTA-aln), Protein (msi, PDB) Output: Sequence alignment (pairwise) (FASTA-aln), Sequence alignment (FASTA-aln), Sequence profile alignment (FASTA-aln)	Topic	- Tool
alignTools	16	Read and write alignments	sequence alignment file processing Input: Sequence alignment		

CCISB Software Catalogue



CENTER FOR BIOLOGICAL SEQUENCE ANALYSIS TECHNICAL UNIVERSITY OF DENMARK DTU



Bioinformatics Data Resources

DRCAT Resource Catalogue

Bioinformatics Web-based Data Resources

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

- 2dpage** - 2D PAGE proteome database system for microbial research
- 2dgenomics** - 2D Genomics database of structural annotations for proteomes
- 3dcat** - 3D database of binding sites from self-organizing protein
- 3dmet** - 3D-MET
- 3dgenes** - 3D genes cross species gene expression patterns database
- 3dmsa** - 3D MS/MS database

- abacus** - A1ATV or A1-antitrypsin database
- abnuc** - Abnuc database - Human keratins by 2D gel proteome database from
- actin** and **clon** databases
- abcdb** - Archaeal and bacterial ABC transporter database (ABCdb)
- abp** - ABC database of binding sites from self-organizing protein
- actinview** - ActinView gene database
- acme** - ACME classification of mobile genetic elements
- adfbdb** - Adfbdb database (Adfbdb) for protein-ligand complexes
- adl** - Assembling the Fungal Tree of Life (AFTOL) database
- adp** - Adipose proteome database (ADP)
- adpms** - Adipose proteome database (ADPMS)
- adpms2** - Adipose proteome protein database (ADPMS2)
- adpms3** - Adipose proteome protein database (ADPMS3)
- adpms4** - Adipose proteome protein database (ADPMS4)
- adpms5** - Adipose proteome protein database (ADPMS5)
- adpms6** - Adipose proteome protein database (ADPMS6)
- adpms7** - Adipose proteome protein database (ADPMS7)
- adpms8** - Adipose proteome protein database (ADPMS8)
- adpms9** - Adipose proteome protein database (ADPMS9)
- adpms10** - Adipose proteome protein database (ADPMS10)

SEQansters

Most popular tools

App	Installs	Downloads
SeqAn	100	1
SeqAn2	100	1
SeqAn3	100	1
SeqAn4	100	1
SeqAn5	100	1
SeqAn6	100	1
SeqAn7	100	1
SeqAn8	100	1
SeqAn9	100	1
SeqAn10	100	1

BioXSD



identifiers

#CommonWL

Bio-jETI.

emboss

The European Molecular Biology Open Software Suite



eSYSBIO

Welcome to eSYSBIO - the adaptable workbench for collaborative life science research

This eSYSBIO workbench allows sharing data with collaborators, synchronizing data, and sharing the results and analysis features. Tools, in form of tool versions or R scripts, can be added to the system on-the-fly, without the need of editing or restarting the server.

The eSYSBIO workbench is now available for testing. If you are interested in learning about eSYSBIO you can either please register for an account (see: www.eSYSBIO.org) or contact us at: support@eSYSBIO.org

Please note that at this stage any data and tools you add to the system may be deleted at any time.

If you have any questions or comments, please contact us at: support@eSYSBIO.org



Bio.Tools

The registry of bioinformatics tools and data services



[@bio_dot_tools](https://twitter.com/bio_dot_tools)



<https://bio.tools>



[/bio-tools](https://github.com/bio-tools)



and other supporting organisations

Tools and data services registry: a community effort to document bioinformatics resources

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WORK IN PROGRESS!

The use cases of the Bio.Tools registry are ...

find

understand

compare

select

attribute

...

... bioinformatics tools and their usage

Bio.Tools should provide answers to various questions

I have this task in mind, what tools are there for it?

I need a tool that reads or writes data in a specific format?

What tools are available in a general area, e.g. proteomics?

What are the interfaces to a given tool?

What are the implementations of a particular algorithm?

What are the parameters of this tool and how do I use it?

What is the last stable version of a tool?

What are the outputs of a particular research institute or infrastructure?

What resources arose from a particular grant?

and many others ...

<https://bio.tools>

Search

Enter search query, e.g. "Proteomics", "Sequence alignment", "BAM".

Filter by attribute

Select attributes to display

2227 entries found

Sort by Latest Display as Grid

First Previous 1 2 3 Next Last

Name	Version	Description	Function	Topic	Homepage URL	Resource type
ReMap	1	ReMap is an integrative analysis of transcription factor ChIP-seq experiments publicly available merged with the Encode dataset. We propose an extensive regulatory catalogue of 8 million transcription factor binding sites from 237 transcription factors (TFs). Among those factors 50 TFs are common with Encode, 82 TFs are Public specific and 105 Encode specific. The results of this analysis is available to browse or download either for a given transcription factor or for the entire dataset. Interactive UCSC Genome Browser tracks are also available.	Genome annotation	Functional genomics	2	- Database
MirGeneDB	1.1	A miRBase derived database for microRNA genes that have been validated and annotated. Currently microRNA genes are available for human, mouse, chicken and zebrafish and can be browsed, blasted and downloaded. Data for other species is coming soon!	Data retrieval. Sequence visualisation – Retrieval of curated miRNA Input: Sequence accession (nucleic acid), Organism identifier Output: Gene transcript report (HTML), RNA secondary structure (HTML) Query and retrieval – Retrieve sequence in fasta format Input: Sequence accession (nucleic acid) Output: RNA sequence (FASTA)	Functional, regulatory and non-coding RNA Data deposition, annotation and curation	2	- Database
Prokaryotic Nomenclature up-to-date (PNU)	1	PNU is a compilation of all names of Bacteria and Archaea which have been validly published according to the Bacteriological Code since 1. Jan. 1980, and nomenclatural changes which have been validly published since. It will be updated with the publication of each new issue of the Int. J. Syst. Evol. Microbiol. (IJSEM).	Data retrieval Input: Species name, Genus name, Family name, Taxon, Strain accession, Taxonomic classification Output: Taxonomic classification (XML, HTML, JSON)	Taxonomy Microbiology Biodiversity	2	- Database - Tool
CorNet Arabidopsis	3.0	This tool allows you to do co-expression analysis using either predefined or user-defined groups of micro array experiments	Gene expression profile comparison – This tool allows you to do co-expression analysis using either predefined or user-defined groups of micro array experiments Input: Gene identifier Output: P-value, Pathway or network	Gene regulatory networks Protein interactions	2	- Tool
InterMine	1.6.5	InterMine is an open source data warehouse built specifically for the integration and analysis of complex biological data. Developed by the Micklem lab at the University of Cambridge, InterMine enables the creation of biological databases accessed by sophisticated web query tools. Parsers are provided for integrating data from many common biological data sources, and formats, and there is a framework for adding your own data. InterMine includes an attractive, user friendly web	Database search Input: Sequence features (Textual format) Output: Pathway or network (Textual format)	Molecular biology	2	- Database - Tool

<https://bio.tools>

2227 entries found

Sort by Latest  Display as Cards 

First Previous **1** 2 3 Next Last

ReMap

<http://tagc.univ-mrs.fr/remap/index.php>

ReMap is an integrative analysis of transcription factor ChIP-seq experiments publicly available merged with the Encode dataset. We propose an extensive regulatory catalogue of 8 million transcription factor binding sites from 237 transcription factors (TFs). Among those factors 50 TFs are common with Encode, 82 TFs are Public specific and 105 Encode specific. The results of this analysis is available to browse or download either for a given transcription factor or for the entire dataset. Interactive UCSC Genome Browser tracks are also available.

Genome annotation

Addition date about 21 hours ago
Affiliation inserm.fr
Topic Functional genomics
Resource Type Database
Interface Web UI

Documentation

[Read the docs](#)

[Download](#)

[Citation instructions](#)

MirGeneDB v.1.1 [Edit](#)

<http://mirgenedb.org/>

A miRBase derived database for microRNA genes that have been validated and annotated. Currently microRNA genes are available for human, mouse, chicken and zebrafish and can be browsed, blasted and downloaded. Data for other species is coming soon!

Data retrieval, Sequence visualisation

Retrieval of curated miRNA

Inputs: Sequence accession (nucleic acid)  , Organism Identifier 

Outputs: Gene transcript report (HTML)  , [RNA secondary structure \(HTML\)](#) 

Query and retrieval

Retrieve sequence in fasta format

Inputs: Sequence accession (nucleic acid)

Outputs: RNA sequence (FASTA) 

Addition date a day ago
Affiliation UIO
Topic Functional, regulatory and non-coding RNA, Data deposition, annotation and curation
Resource Type Database
Interface Web UI
Collection UIO tools

Documentation

[Read the docs](#)

Prokaryotic Nomenclature up-to-date (PNU)

<http://bacdive.dsmz.de/api/pnu/>

PNU is a compilation of all names of Bacteria and Archaea which have been validly published according to the Bacteriological Code since 1. Jan. 1980, and nomenclatural changes which have been validly published since. It will be updated with the publication of each new issue of the Int. J. Syst. Evol. Microbiol. (IJSEM).

Addition date 6 days ago
Affiliation bacdive
Topic Taxonomy, Microbiology, Biodiversity
Resource Type Database, Tool
Interface API
Maturity Stable
Cost Free

Documentation

Example record: [MirGeneDB](#)



MirGeneDB v.1.1 [Edit this record](#)



<http://mirgenedb.org/>

A miRBase derived database for microRNA genes that have been validated and annotated. Currently microRNA genes are available for human, mouse, chicken and zebrafish and can be browsed, blasted and downloaded. Data for other species is coming soon!

Functional, regulatory and non-coding RNA

Data deposition, annotation and curation

Sequence accession (nucleic acid) ⓘ



Data retrieval ⓘ



Gene transcript report (HTML) ⓘ

Organism identifier ⓘ



Sequence visualisation ⓘ



RNA secondary structure (HTML) ⓘ

Sequence accession (nucleic acid)



Query and retrieval ⓘ



RNA sequence (FASTA) ⓘ

DOCUMENTATION

[Read the docs](#)

PUBLICATIONS

- DOI: 10.1146/annurev-genet-120213-092023

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CREDITS

No information

<https://bio.tools/?q=alignment%20visualisation>



alignment visualisation



Enter search query, e.g. "Proteomics", "Sequence alignment", "BAM".

Filter by attribute ▾

Select attributes to display ▾

15 entries found

Sort by

Name ▾



Display as

Grid ▾

First

Previous

1

Next

Last

Name	Description	Function	Topic	Homepage URL	Resource type
Aquaria	Simplifying the generation of insight from protein structures through structure visualisation, annotated with protein features; loads sequence-to-structure alignments from the PSSH2	Structure database search , Sequence database search , Structure visualisation , Sequence alignment visualisation , Sequence visualisation – You can find sequences based on a keyword search. For the identified sequence, Aquaria retrieves sequence-to-structure alignments from the PSSH2 database and	Protein structure prediction Protein sites, features and motifs Protein structure analysis	▶	– Tool – Tool

<https://bio.tools/?q=alignment%20visualisation>

alignment visualisation



Enter search query, e.g. "Proteomics", "Sequence alignment", "BAM".

Filter by attribute



Select attributes to display



15 entries found

Sort by Name  Display as Grid 

First Previous 1 Next Last

Name	Description	Function	Topic	Homepage URL	Resource type
Aquaria	Simplifying the generation of insight from protein structures through structure visualisation, annotated with protein features; loads sequence-to-structure alignments from the PSSM2 database, sequence features from UniProt and Interpro and user defined features on demand from JSON files; there is also a WebAPI (see...)	Structure database search, Sequence database search, Structure visualisation, Sequence alignment visualisation, Sequence visualisation - You can find sequences based on a keyword search. For the identified sequence, Aquaria retrieves sequence-to-structure alignments from the PSSM2 database and visualises those on the web page. At the same time, a selected alignment is visualised in the 3D viewer (by default the one with most identical residues between sequence and structure). Input: Sequence Identifier (Textual format), Organism Identifier (Textual format)	Protein structure prediction Protein sites, features and motifs Protein structure analysis	<input checked="" type="checkbox"/>	- Tool
BeVu	Calculate trees from multiple alignments	Sequence alignment visualisation Input: Sequence alignment Output: Sequence alignment	Proteins	<input checked="" type="checkbox"/>	- Tool
boxshade	printouts from multiple-aligned protein or DNA sequences	Sequence alignment visualisation Input: Sequence alignment (ClustalW format) alignment Output: Report htmlFile, Report rtfFile, Report stdout, Report stddr	Data visualisation	<input checked="" type="checkbox"/>	- Tool
CG-CAT	With current sequencing technologies, it is feasible to generate a lot of reads for a given genome. However, the assembly usually ends up in a set of contigs with gaps between them. If the sequences of one (or several) related genomes are already known, this information can be used to estimate the order and orientation of the contigs towards each other. This helps in the finishing phase of a sequencing project since it eases the design of specific primer sequences to fill the gaps.	Scaffolding, Dotplot plotting, Sequence alignment visualisation - Match a set of contigs to a related reference genome to order and orient the contigs based on that reference. The mapping is visualized in an interactive synteny plot. Input: Nucleic acid sequence (raw) (Pearson format) Output: Dotplot, Sequence assembly report Scaffolding, Sequence alignment visualisation - The program treecat can be used to estimate an ordering for a set of contigs. A so called layout graph shows the unique order where possible and gives alternatives where necessary. The layout graph is calculated based on the matches to several related genomes as well as the information given by a phylogenetic tree of the involved species. Input: Nucleic acid sequence (raw) (Pearson format), Phylogenetic tree (newick) Output: Sequence assembly report	Sequence assembly	<input checked="" type="checkbox"/>	- Tool
ConSurf	The ConSurf server for the identification of functional regions in proteins	Sequence alignment visualisation - The ConSurf server is a bioinformatics tool for estimating the evolutionary conservation of amino/nucleic acid positions in a protein/DNA/RNA molecule based on the phylogenetic relations between homologous sequences. The degree to which an amino (or nucleic) acid position is evolutionarily conserved is strongly dependent on its structural and functional importance, rapidly evolving positions are variable while slowly evolving positions are conserved. Thus, conservation analysis of positions among members from the same family can often reveal the importance of each position for the protein (or nucleic acid)'s structure or function. In ConSurf, the evolutionary rate is estimated based on the evolutionary relatedness between the protein (DNA/RNA) and its homologues and considering the similarity between amino (nucleic) acids as reflected in the substitutions matrix. One of the advantages of ConSurf in comparison to other methods is the accurate computation of the evolutionary rate by using	Structural biology Molecular modelling	<input checked="" type="checkbox"/>	- Tool
ConSurf	The ConSurf is a tool used for estimation of the evolutionary conservation of amino/nucleic acid positions in a protein/DNA/RNA molecule based on the phylogenetic relations between homologous sequences.	Sequence alignment visualisation - Estimation of the evolutionary conservation	Protein structural motifs and surfaces	<input checked="" type="checkbox"/>	- Tool
html4blast	HTML blast results formatter	Sequence alignment visualisation Input: Report input Output: Report output, Report stdout, Report stddr	Data visualisation	<input checked="" type="checkbox"/>	- Tool
mse	Display multiple-sequence alignment	Sequence alignment visualisation - Visualizes multiple sequence alignment, calculates conservation, shows sequence logo, applies multiple color schemes Input: Sequence alignment (ClustalW format, FASTA-aln) Output: Sequence alignment (FASTA-aln), Sequence alignment image (image format), Sequence set (FASTA), Feature table (GFF)	Sequence analysis Sequence sites, features and motifs	<input checked="" type="checkbox"/>	- Library
MultiDisp	A tool for analysing and visualising multiple sequence alignments (MSAs)	Sequence alignment visualisation Input: Sequence alignment Output: Sequence profile	Data visualisation	<input checked="" type="checkbox"/>	- Tool
mview_alignment	Reformats the results of a Multiple alignment	Sequence alignment formatting, Sequence alignment visualisation, Sequence alignment formatting, Sequence alignment visualisation Input: Sequence alignment (ClustalW format) align Output: Sequence alignment align_file, Report html_file, Report rdb_file, Report stddr	File management Data visualisation	<input checked="" type="checkbox"/>	- Tool
mview_blast	Reformats the results of a sequence database search BLAST	Sequence alignment formatting, Sequence alignment visualisation, Sequence alignment formatting, Sequence alignment visualisation Input: Report blast Output: Sequence alignment align_file, Report html_file, Report rdb_file, Report stddr	File management Data visualisation	<input checked="" type="checkbox"/>	- Tool
PredictProtein Open	Prediction of various aspects of protein structure and function. A user may submit a query to the server without registration	Sequence alignment, Sequence annotation, Protein property calculation, Sequence composition calculation, Taxonomic classification, Variant classification, Heat map generation, Sequence profile generation, Protein SNP mapping, Protein secondary structure prediction, Transmembrane protein prediction, Protein sequence alignment analysis, Protein subcellular localization prediction, Protein-protein interaction prediction (from protein sequence), Protein binding site prediction (from sequence), Protein-protein interaction prediction (from protein sequence), Protein property calculation (from sequence), Protein hydrophathy calculation, Residue interaction prediction, Protein sequence alignment analysis, Protein sequence feature detection, Article analysis, Data retrieval	Proteins Sequence analysis Structure analysis Data mining	<input checked="" type="checkbox"/>	- Tool

Thank you for your attention!

Bio.Tools



[@bio_dot_tools](https://twitter.com/bio_dot_tools)



<https://bio.tools>



[/bio-tools](https://github.com/bio-tools)

EDAM



[@edamontology](https://twitter.com/edamontology)



edamontology.org



[/edamontology/edamontology](https://github.com/edamontology/edamontology)



www.ebi.ac.uk/ols/ontologies/edam



bioportal.bioontology.org/ontologies/EDAM