Bioinformatics Toolkit

RRID:SCR_010277
Type: Tool

Proper Citation

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Resource Information

URL: [http://toolkit.tuebingen.mpg.de/](http://toolkit.tuebingen.mpg.de/)

Description: A platform that integrates a great variety of tools for protein sequence analysis. Many tools are developed in-house, and several public tools are offered with extended functionality. Most frequently used tools HHpred Sensitive protein homology detection and structure prediction by HMM-HMM-comparison. Starting from a query sequence, HHpred builds a multiple sequence alignment using HHblits and turns it into a profile HMM. This is then compared with a database of HMMs representing proteins with known structure (e.g. PDB, SCOP) or annotated protein families (e.g. PFAM, SMART, CDD, COGs, KOGs). The output is a list of closest homologs with alignments. HHpred can also build 3d homology models using the identified templates in the PDB database. It can optimize template picking and query-template alignments for homology modeling. The HHblits software is part of the open source package HHsuite. HHblits Remote homology detection method based on iterative HMM-HMM comparison. HHblits can build high-quality MSAs starting from single sequences or from MSAs. It transforms these into a query HMM and iteratively searches through uniprot20 or nr20 databases by adding significantly similar sequences from the previous search to the updated query HMM for the next search iteration. Compared to PSI-BLAST, HHblits is faster, up to twice as sensitive and produces more accurate alignments. The HHblits software is part of the open source package HHsuite. Quick2d Quick2D gives you an overview of secondary structure features like alpha-helices, extended beta-sheets, coiled coils, transmembrane helices and disorder regions. Predictions by PSIPRED, JNET, Prof(Rost), Prof(Ouali), Coils, MEMSAT2, HMMTOP, DISOPRED2 and VSL2. Modeller A Program for Comparative Protein Structure Modelling by Satisfaction of Spatial Restraints. Coils/PCoils This server compares a single sequence (COILS) or a sequence alignment (PCOILS) to a database of known coiled-coils and derives a similarity score. The program then calculates the probability that the sequence will adopt a coiled-coil conformation. PSI-Blast Search with an amino acid sequence against protein databases for locally similar sequences. Similar to ProteinBLAST but more sensitive. PSI-BLAST first performs a BLAST
search and builds an alignment from the best local hits. This alignment is then used as a query for the next round of search. After each successive round the search alignment is updated.

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Resource Type: Resource, software resource, software toolkit

Resource ID: SCR_010277

Website Status: Last checked up

Alternate IDs: nlx_156936

Mentions Count: 155

Ratings and Alerts

No rating or validation information has been found for Bioinformatics Toolkit.

No alerts have been found for Bioinformatics Toolkit.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 155 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


Beltz S, et al. (2016) Regulation by the quorum sensor from Vibrio indicates a receptor function for the membrane anchors of adenylate cyclases. eLife, 5.

Fidler DR, et al. (2016) Using HHsearch to tackle proteins of unknown function: A pilot study with PH domains. Traffic (Copenhagen, Denmark), 17(11), 1214-1226.