

# Resource Summary Report

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## Bioinformatics Toolkit

RRID:SCR\_010277

Type: Tool

### Proper Citation

Bioinformatics Toolkit (RRID:SCR\_010277)

### Resource Information

**URL:** <http://toolkit.tuebingen.mpg.de/>

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**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 it 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(Quali), 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.

**Resource Type:** software resource, software toolkit

**Defining Citation:** [DOI:10.1038/NMETH.1818](https://doi.org/10.1038/NMETH.1818)

**Keywords:** bio.tools

**Resource Name:** Bioinformatics Toolkit

**Resource ID:** SCR\_010277

**Alternate IDs:** nlx\_156936, OMICS\_28407, biotools:bioinformatics\_toolkit

**Alternate URLs:** [https://bio.tools/bioinformatics\\_toolkit](https://bio.tools/bioinformatics_toolkit),  
<https://sources.debian.org/src/hhsuite/>

**Record Creation Time:** 20220129T080257+0000

**Record Last Update:** 20260912T200247+0000

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## Ratings and Alerts

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

No alerts have been found for Bioinformatics Toolkit.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 261 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [SPARC SAWG](#) .

Hessami A, et al. (2026) Design of a novel proteome-derived scaffold presenting epitopes of *Pseudomonas aeruginosa* in native conformation. *Scientific reports*, 16(1).

Wang B, et al. (2026) Structural and Spectroscopic Basis for Catalysis by a Class C Radical S-adenosylmethionine Methylase Involved in Nosiheptide/Nocathiacin Biosynthesis. *bioRxiv* : the preprint server for biology.

Candia YG, et al. (2026) Exploring the Virome of *Gyropsylla spegazziniana*: A Major Yerba Mate Pest. *Pathogens* (Basel, Switzerland), 15(6).

Qiu K, et al. (2026) pLM-Repeat: Exploiting the sequence representations of protein language models for sensitive repeat detection. *Protein science* : a publication of the Protein Society, 35(5), e70541.

Shoham S, et al. (2026) Intracellular vesicle-mediated biomineralization of arsenic and barium by a sponge symbiotic bacterium. *ISME communications*, 6(1), ycag039.

Zhou Z, et al. (2026) Stepwise DNA unwinding gates TnpB genome-editing activity. *bioRxiv : the preprint server for biology*.

Zhang Z, et al. (2026) A novel phage preparation capable of simultaneously inhibiting both K1 and K2 serotypes of *Klebsiella pneumoniae*. *Applied and environmental microbiology*, 92(3), e0242325.

Bonardi CM, et al. (2026) Biallelic variants in CELSR1 cause brain malformations, neurodevelopmental disorders and epilepsy in humans. *Nature communications*, 17(1), 862.

Hida S, et al. (2025) Genome analysis of dark-adapted variants identifies the phosphatase gene *phsP* involved in the regulation of photosynthetic and dark-heterotrophic growth in the cyanobacterium *Leptolyngbya boryana*. *Plant & cell physiology*, 66(7), 1102.

Zhou X, et al. (2025) Cas9 senses CRISPR RNA abundance to regulate CRISPR spacer acquisition. *Nature*, 647(8091), 1054.

Benner L, et al. (2025) Programmed meiotic errors facilitate dichotomous sperm production in the silkworm, *Bombyx mori*. *bioRxiv : the preprint server for biology*.

Troshin K, et al. (2025) *Pseudomonas* Phage Lydia and the Evolution of the Mesyanzhinoviridae Family. *Viruses*, 17(3).

Zhang W, et al. (2025) SGBP-B-like bimodular cellulose-binding protein CHU\_1279 is essential for cellulose utilization by *Cytophaga hutchinsonii*. *Applied and environmental microbiology*, 91(4), e0247124.

Kolupaeva NV, et al. (2025) *Acinetobacter baumannii* and *Klebsiella pneumoniae* Isolates Obtained from Intensive Care Unit Patients in 2024: General Characterization, Prophages, Depolymerases and Esterases of Phage Origin. *Viruses*, 17(5).

Zhang HS, et al. (2025) Exploring the recombinant evolution and hosts of crucivirus based on novel oyster-associated viruses. *Frontiers in microbiology*, 16, 1454079.

Russ JE, et al. (2025) Competition between Der1 and ERAD-M substrates controls Hrd1 complex function. *Proceedings of the National Academy of Sciences of the United States of America*, 122(49), e2513595122.

Yefsah K, et al. (2025) Crosstalk between cohesins and axis proteins determines meiotic chromosome architecture in *Sordaria macrospora*. *PLoS genetics*, 21(12), e1012001.

Debat H, et al. (2025) RNA Virus Discovery Sheds Light on the Virome of a Major Vineyard Pest, the European Grapevine Moth (*Lobesia botrana*). *Viruses*, 17(1).

Neuman BW, et al. (2025) Giant RNA genomes: Roles of host, translation elongation, genome architecture, and proteome in nidoviruses. *Proceedings of the National Academy of Sciences of the United States of America*, 122(7), e2413675122.

Diep DTV, et al. (2024) A metabolically controlled contact site between vacuoles and lipid droplets in yeast. *Developmental cell*, 59(6), 740.