

# Resource Summary Report

Generated by [dkNET](#) on Sep 10, 2026

## BioInfoBank Meta Server

RRID:SCR\_007181

Type: Tool

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### Proper Citation

BioInfoBank Meta Server (RRID:SCR\_007181)

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### Resource Information

**URL:** <http://bioinfo.pl/>

**Proper Citation:** BioInfoBank Meta Server (RRID:SCR\_007181)

**Description:** This service offers a gateway to well-benchmarked protein structure and function prediction methods. Structural models collected from the prediction servers are assessed using the powerful 3D-jury consensus approach. The Structure Prediction Meta Server provides access to various fold recognition, function prediction and local structure prediction methods. The Server takes the amino acid sequence of the query protein, the reference name for the prediction job, and the E-mail address as input. The E-mail address is used only for notification about errors during the execution of the job. The query sequence and the reference name are placed in the process queue. The Meta Server accepts only sequences, which have not been submitted before. In case of duplicate sequences the second user will be notified with a link to the previous submission. Sequences longer than 800 amino acids are not accepted by some services. The internal SQL database offers the possibility to find any previous jobs processed by the Meta Server using regular expressions addressing field like E-mail, Job Name and the host name, from which the job was initiated. Each server has its own process queuing system managed by the Meta Server. All results of fold recognition servers are translated into uniform formats. The information extracted from the raw output of the servers includes the PDB codes of the hits, the alignments and the similarity (reliability) scores specific for every server. Mapping of the hits to the SCOP and FSSP classifications are made either using known PDB representatives or alignment of the template sequence with the databases of proteins in both classifications. The secondary structure assignments for all hits are taken from the mapped FSSP (red for helices and blue for strands). Underscored amino acids indicate the first residue after an insertion in the template sequence. The Meta server provides translation of the alignments in standard formats like FASTA, PDB or CASP. The Meta Server is coupled to consensus servers. They provide jury predictions based on the results collected from other services. Not all fold recognition servers are used by the jury system. The data stored on the meta server is available through <http://meta.bioinfo.pl/data/JOBID/>. Jobs older than 2 months are not shown. The Meta Server is only a set of programs aimed to process and manage biological data, while the

predictive power of the service comes from (mostly) remote prediction providers.  
Sponsors: This resource is supported by The BioInfoBank Institute.

**Abbreviations:** BioInfoBank

**Synonyms:** The BioInfoBank Meta Server, BioInfoBank Meta Server

**Resource Type:** data or information resource, portal, topical portal

**Keywords:** server, meta, biology, function, protein, structure, method, model, prediction, 3-dimentional, amino acid, sequence

**Resource Name:** BioInfoBank Meta Server

**Resource ID:** SCR\_007181

**Alternate IDs:** nif-0000-30180

**Old URLs:** <http://meta.bioinfo.pl>

**Record Creation Time:** 20220129T080240+0000

**Record Last Update:** 20260905T132608+0000

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## Ratings and Alerts

No rating or validation information has been found for BioInfoBank Meta Server.

No alerts have been found for BioInfoBank Meta Server.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Kanto S, et al. (2016) A variant of Runx2 that differs from the bone isoform in its splicing is expressed in spermatogenic cells. PeerJ, 4, e1862.

Liu X, et al. (2015) Reliable cell cycle commitment in budding yeast is ensured by signal integration. eLife, 4.

Szafron LM, et al. (2015) The Novel Gene CRNDE Encodes a Nuclear Peptide (CRNDEP) Which Is Overexpressed in Highly Proliferating Tissues. PloS one, 10(5), e0127475.

Patterson NJ, et al. (2014) Two TIR-like domain containing proteins in a newly emerging zoonotic Staphylococcus aureus strain sequence type 398 are potential virulence factors

by impacting on the host innate immune response. *Frontiers in microbiology*, 5, 662.

Selão TT, et al. (2014) Subcellular localization of monoglucosyldiacylglycerol synthase in *Synechocystis* sp. PCC6803 and its unique regulation by lipid environment. *PloS one*, 9(2), e88153.

Afzal AJ, et al. (2013) Homo-dimerization and ligand binding by the leucine-rich repeat domain at RHG1/RFS2 underlying resistance to two soybean pathogens. *BMC plant biology*, 13, 43.

Yerko V, et al. (2013) Structurally unique interaction of RBD-like and PH domains is crucial for yeast pheromone signaling. *Molecular biology of the cell*, 24(3), 409.

Grada Z, et al. (2013) TanCAR: A Novel Bispecific Chimeric Antigen Receptor for Cancer Immunotherapy. *Molecular therapy. Nucleic acids*, 2(7), e105.

Giacani L, et al. (2012) Footprint of positive selection in *Treponema pallidum* subsp. *pallidum* genome sequences suggests adaptive microevolution of the syphilis pathogen. *PLoS neglected tropical diseases*, 6(6), e1698.

Karkare S, et al. (2012) The role of Ca<sup>2+</sup> in the activity of *Mycobacterium tuberculosis* DNA gyrase. *Nucleic acids research*, 40(19), 9774.

Kumar SP, et al. (2012) Evolutionary and molecular aspects of Indian tomato leaf curl virus coat protein. *International journal of plant genomics*, 2012, 417935.

Nair S, et al. (2011) Identification of B cell epitopes of alcohol dehydrogenase allergen of *Curvularia lunata*. *PloS one*, 6(5), e20020.

Ajjawi I, et al. (2011) A J-like protein influences fatty acid composition of chloroplast lipids in *Arabidopsis*. *PloS one*, 6(10), e25368.

Wlodarski T, et al. (2011) Comprehensive structural and substrate specificity classification of the *Saccharomyces cerevisiae* methyltransferome. *PloS one*, 6(8), e23168.

Krupovic M, et al. (2009) Geminiviruses: a tale of a plasmid becoming a virus. *BMC evolutionary biology*, 9, 112.

Garron ML, et al. (2009) Structural insights into the association between BCAR3 and Cas family members, an atypical complex implicated in anti-oestrogen resistance. *Journal of molecular biology*, 386(1), 190.

Hsiang CY, et al. (2008) Emodin is a novel alkaline nuclease inhibitor that suppresses herpes simplex virus type 1 yields in cell cultures. *British journal of pharmacology*, 155(2), 227.

Zhu X, et al. (2007) High incidence of ubiquitin-like domains in human ubiquitin-specific proteases. *Proteins*, 69(1), 1.

Malagoli D, et al. (2007) A putative helical cytokine functioning in innate immune signalling in *Drosophila melanogaster*. *Biochimica et biophysica acta*, 1770(6), 974.

Hoellerer MK, et al. (2003) Molecular recognition of paxillin LD motifs by the focal adhesion targeting domain. *Structure (London, England : 1993)*, 11(10), 1207.