

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

UCL Bioinformatics Group

RRID:SCR_010248

Type: Tool

Proper Citation

UCL Bioinformatics Group (RRID:SCR_010248)

Resource Information

URL: <http://bioinf.cs.ucl.ac.uk>

Proper Citation: UCL Bioinformatics Group (RRID:SCR_010248)

Description: Group headed by Professor David Jones, and was originally founded as the Joint Research Council funded Bioinformatics Unit within the Department of Computer Science at University College London. Supports the following tools: Protein Structure Prediction Threading (THREADER) Ab initio folding simulations Secondary structure prediction (PSIPRED) Protein disorder prediction (DISOPRED) Protein domain prediction (DomPred) Database of protein disorder (DisoDB) Protein Sequence Analysis Protein function prediction (ffpred) Metsite: Metal binding residue prediction HSPred : Protein-protein interaction characterisation Amino acid substitution matrices Hidden Markov Models (collaboration with N. Goldman, Cambridge, & J. Thorne, NCSU) Genome Analysis Genomic fold recognition (GenTHREADER) Genome annotation using software agents Protein Structure Classification CATH (collaboration with J. Thornton & C. Orengo, UCL Biochemistry) Transmembrane Protein Modelling MEMSAT & MEMSATSV M Folding In Lipid Membranes (FILM) MEMPack Biological Applications of Data-mining and Machine Learning Techniques Information extraction for biological research (BioRat) Microarray Analysis Data integration for microarray analysis Data visualization Systems Biology Systems biology applied to stem cells Legacy Services (to be retired shortly) Comparison of structure classifications (CATH/SCOP/FSSP) Genomic Threading Database (GTD)

Resource Type: data or information resource, organization portal, portal, software repository, software resource

Keywords: FASEB list

Resource Name: UCL Bioinformatics Group

Resource ID: SCR_010248

Alternate IDs: nlx_156885

Record Creation Time: 20220129T080257+0000

Record Last Update: 20260905T132637+0000

Ratings and Alerts

No rating or validation information has been found for UCL Bioinformatics Group.

No alerts have been found for UCL Bioinformatics Group.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 196 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Silva IRM, et al. (2025) Evaluation of binding activities of a putative lipoprotein LIC_13355 of *Leptospira* spp. *FEBS open bio*, 15(3), 447.

Peskett TR, et al. (2025) A network of P-body and Whi3 condensates adjusts cell fate decisions to cellular context. *Molecular cell*, 85(19), 3661.

Li S, et al. (2025) Immunoinformatics method to design universal multi-epitope nanoparticle vaccine for TGEV S protein. *Scientific reports*, 15(1), 10931.

Kumar A, et al. (2025) Novel multi-epitope vaccine candidate for lumpy skin disease: Computational design and recombinant expression. *Veterinary world*, 18(8), 2273.

Wang Y, et al. (2025) Phylogenetics and selective pressure analysis of human papillomavirus types 31 and 33 variants in Eastern China. *BMC infectious diseases*, 25(1), 1124.

Hassani BHM, et al. (2025) A novel homozygous growth differentiation factor 9 variant associated with premature ovarian insufficiency: A case report. *International journal of reproductive biomedicine*, 23(12), 1043.

Zhao D, et al. (2025) The Function of Two *Brassica napus* β -Ketoacyl-CoA Synthases on the Fatty Acid Composition. *Plants (Basel, Switzerland)*, 14(2).

Bottardi S, et al. (2024) MNDA, a PYHIN factor involved in transcriptional regulation and apoptosis control in leukocytes. *Frontiers in immunology*, 15, 1395035.

Kwon SY, et al. (2024) Abrupt-mediated control of ninjurins regulates *Drosophila* sessile haemocyte compartments. *Development (Cambridge, England)*, 151(23).

Mikaeel S, et al. (2024) Putative new combination vaccine candidates identified by reverse vaccinology and genomic approaches to control enteric pathogens. *BMC immunology*, 25(1), 46.

Saleh H, et al. (2024) KH-like Domains in PARP9/DTX3L and PARP14 Coordinate Protein-Protein Interactions to Promote Cancer Cell Survival. *Journal of molecular biology*, 436(4), 168434.

Brown E, et al. (2024) Inhibitors of the small membrane (M) protein viroporin prevent Zika virus infection. *eLife*, 13.

Maryami F, et al. (2023) In silico Analysis of Two Novel Variants in the Pyruvate Carboxylase (PC) Gene Associated with the Severe Form of PC Deficiency. *Iranian biomedical journal*, 27(5), 307.

Li C, et al. (2022) Genome-wide identification and expression profile of YABBY genes in *Averrhoa carambola*. *PeerJ*, 9, e12558.

Philip J, et al. (2022) Cdc6 is sequentially regulated by PP2A-Cdc55, Cdc14, and Sic1 for origin licensing in *S. cerevisiae*. *eLife*, 11.

Namba Y, et al. (2022) Maelstrom functions in the production of Siwi-piRISC capable of regulating transposons in *Bombyx* germ cells. *iScience*, 25(3), 103914.

Hjaltalin VJ, et al. (2022) A novel region within a conserved domain in ATG7 emerged in vertebrates. *Autophagy reports*, 1(1), 393.

Lechuga GC, et al. (2021) Nicastrin-Like, a Novel Transmembrane Protein from *Trypanosoma cruzi* Associated to the Flagellar Pocket. *Microorganisms*, 9(8).

Embarc-Buh A, et al. (2021) The RBS1 domain of Gemin5 is intrinsically unstructured and interacts with RNA through conserved Arg and aromatic residues. *RNA biology*, 18(sup1), 496.

Coelho FS, et al. (2021) A novel receptor for platelet-activating factor and lysophosphatidylcholine in *Trypanosoma cruzi*. *Molecular microbiology*, 116(3), 890.