

Resource Summary Report

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UniProt Proteomes

RRID:SCR_018666

Type: Tool

Proper Citation

UniProt Proteomes (RRID:SCR_018666)

Resource Information

URL: <https://www.uniprot.org/proteomes/>

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Description: Protein sets from fully sequenced genomes. Proteomes portal offers protein sequence sets obtained from translation of completely sequenced genomes. Published genomes from NCBI Genome are brought into UniProt if genome is annotated and set of coding sequences is available. Number of predicted coding sequences falls within statistically significant range of published proteomes from neighbouring species.

Resource Type: data or information resource, data set

Keywords: Protein set, fully sequenced genome, proteome, protein sequence set, protein sequence, protein sequence data, annotated genome, published proteome

Availability: Free, Freely available

Resource Name: UniProt Proteomes

Resource ID: SCR_018666

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260728T043548+0000

Ratings and Alerts

No rating or validation information has been found for UniProt Proteomes.

No alerts have been found for UniProt Proteomes.

Data and Source Information

Usage and Citation Metrics

We found 67 mentions in open access literature.

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

Maulana T, et al. (2025) Proteomic analysis of Toraya buffalo seminal plasma and sperm: uncovering insights to optimize reproductive success. *Frontiers in veterinary science*, 12, 1492135.

Gasparotto D, et al. (2025) Mapping cryptic phosphorylation sites in the human proteome. *The EMBO journal*, 44(22), 6704.

Hamaneh MB, et al. (2025) FastSpel: A Method for Fast Spectral Library Generation. *Journal of proteome research*, 24(10), 4952.

Zheng Y, et al. (2025) Deep learning prioritizes cancer mutations that alter protein nucleocytoplasmic shuttling to drive tumorigenesis. *Nature communications*, 16(1), 2511.

Kim EJ, et al. (2025) Bacteriophage cocktail LEC2-LEC10 for broad-spectrum control of pathogenic and uncharacterized *Escherichia coli* in fresh produce. *Frontiers in microbiology*, 16, 1594533.

Qu M, et al. (2025) The RNA binding protein hnRNP A/B controls exosomal miR-27a-5p loading during *Salmonella* infection. *Poultry science*, 104(9), 105482.

Kumabe H, et al. (2025) Proteome profile differences among human, monkey, and mouse brain microvessels and cultured brain microvascular endothelial cells. *Fluids and barriers of the CNS*, 22(1), 53.

Wu S, et al. (2025) Ubiquitin-dependent proteasomal degradation of small hepatitis B virus surface antigen mediated by TRIM21 and antagonized by OTUD4. *Journal of virology*, 99(5), e0230924.

Zuccato JA, et al. (2025) Prediction of brain metastasis development with DNA methylation signatures. *Nature medicine*, 31(1), 116.

Li R, et al. (2025) Phosphoproteomic insights into the regulation of root length in rice (*Oryza sativa* L. cv. KDML 105): uncovering key events and pathways involving phosphorylated proteins. *PeerJ*, 13, e19361.

Iskandar H, et al. (2025) ZPBP and fertility-associated proteomes as novel biomarkers: A shotgun proteomics approach in Murrah buffalo (*Bubalus bubalis*) bulls' seminal plasma and cryopreserved spermatozoa. *PloS one*, 20(10), e0333272.

Raj M, et al. (2025) Cultural dynamics and endogeneity in psychological drivers of adoption of community-based water purification technology in rural India. *iScience*, 28(12), 113857.

Zhang R, et al. (2024) Protocol for mass spectrometric profiling of lysine malonylation by lysine acetyltransferase in CRISPRi K562 cell lines. STAR protocols, 5(2), 103074.

da Silva LL, et al. (2024) What lies behind the large genome of *Colletotrichum lindemuthianum*. Frontiers in fungal biology, 5, 1459229.

Nikolic A, et al. (2024) Chronic stress alters hepatic metabolism and thermodynamic respiratory efficiency affecting epigenetics in C57BL/6 mice. iScience, 27(3), 109276.

Reddy PJ, et al. (2024) Borrelia PeptideAtlas: A proteome resource of common *Borrelia burgdorferi* isolates for Lyme research. Scientific data, 11(1), 1313.

Hamaneh MB, et al. (2024) Systematic Assessment of Deep Learning-Based Predictors of Fragmentation Intensity Profiles. Journal of proteome research, 23(6), 1983.

Naveed M, et al. (2024) Development and immunological evaluation of an mRNA-based vaccine targeting *Naegleria fowleri* for the treatment of primary amoebic meningoencephalitis. Scientific reports, 14(1), 767.

Sganzerla Martinez G, et al. (2024) Multiple Protein Profiler 1.0 (MPP): A Webserver for Predicting and Visualizing Physiochemical Properties of Proteins at the Proteome Level. The protein journal, 43(4), 711.

He S, et al. (2023) Metaproteomic Analysis of an Oral Squamous Cell Carcinoma Dataset Suggests Diagnostic Potential of the Mycobiome. International journal of molecular sciences, 24(2).