

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: 20260829T183318+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 80 mentions in open access literature.

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

Mrkacek M, et al. (2026) ORMDL Proteins Turnover via Proteasome and Autophagy Is Cell-Type Dependent and Tied to Ceramide Homeostasis. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 40(6), e71655.

Kim TY, et al. (2026) Newly isolated human-derived Lactobacillus fermentum strain stimulates IFN- γ -secreting CD8⁺ T cells for enhanced anti-cancer immunity. iScience, 29(5), 115642.

Lee S, et al. (2026) Peptidoglycan from Bifidobacterium adolescentis enhances IL-10 production in regulatory B cells to alleviate gut inflammation. Gut microbes, 18(1), 2611603.

Raposo P, et al. (2026) A novel method to select Reference Proteomes in UniProt. bioRxiv : the preprint server for biology.

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.

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.

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.

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.

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

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.

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.

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

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