Resource Summary Report

Generated by NIF on Apr 21, 2025

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 set, data or information resource

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

Funding:

Availability: Free, Freely available

Resource Name: UniProt Proteomes

Resource ID: SCR_018666

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250420T020119+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 56 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

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.

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

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

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).

Toma L, et al. (2023) Mass spectrometry-based proteomic strategy for ecchymotic skin examination in forensic pathology. Scientific reports, 13(1), 6116.

Robin AY, et al. (2023) Deciphering Evolutionary Trajectories of Lactate Dehydrogenases Provides New Insights into Allostery. Molecular biology and evolution, 40(10).

Desbois M, et al. (2023) Optimized protocol for in vivo affinity purification proteomics and biochemistry using C. elegans. STAR protocols, 4(2), 102262.

Aristide L, et al. (2023) Genomic Insights into Mollusk Terrestrialization: Parallel and Convergent Gene Family Expansions as Key Facilitators in Out-of-the-Sea Transitions. Genome biology and evolution, 15(10).

Rocha JJ, et al. (2023) Functional unknomics: Systematic screening of conserved genes of unknown function. PLoS biology, 21(8), e3002222.

Mohammadi Y, et al. (2023) In silico design and evaluation of a novel mRNA vaccine against BK virus: a reverse vaccinology approach. Immunologic research, 71(3), 422.

, et al. (2023) UniProt: the Universal Protein Knowledgebase in 2023. Nucleic acids research, 51(D1), D523.

Bowler-Barnett EH, et al. (2023) UniProt and Mass Spectrometry-Based Proteomics-A 2-Way Working Relationship. Molecular & cellular proteomics : MCP, 22(8), 100591.

Goodyear MC, et al. (2023) Quantitative proteomics reveals unique responses to antimicrobial treatments in clinical Pseudomonas aeruginosa isolates. mSystems, 8(5), e0049123.

Bokor BJ, et al. (2023) Network-centric analysis of co-fractionated protein complex profiles using SECAT. STAR protocols, 4(2), 102293.

Reddy PJ, et al. (2023) Borrelia PeptideAtlas: A proteome resource of common Borrelia burgdorferi isolates for Lyme research. bioRxiv : the preprint server for biology.