Resource Summary Report

Generated by dkNET on Apr 16, 2025

UniParc

RRID:SCR_005818
Type: Tool

Proper Citation

UniParc (RRID:SCR_005818)

Resource Information

URL: http://www.uniprot.org/uniparc/

Proper Citation: UniParc (RRID:SCR_005818)

Description: Database that contains publicly available protein sequences with stable and unique identifiers (UPI) which are never removed, changed or reassigned. UniParc tracks sequence changes in the source databases and archives the history of all changes. Information other than protein sequence must be retrieved from the UniParc source databases using the database cross-references.

Synonyms: UniProt Archive

Resource Type: database, data or information resource

Keywords: protein sequence, database, public protein sequence, gold standard, upi, unique protein identifier, identifier, bio.tools

Funding:

Availability: Public, Entries are available for download

Resource Name: UniParc

Resource ID: SCR_005818

Alternate IDs: SCR_004769, nif-0000-03610, biotools:uniparc, nlx_76940

Alternate URLs: https://bio.tools/uniparc

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250416T063420+0000

Ratings and Alerts

No rating or validation information has been found for UniParc.

No alerts have been found for UniParc.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 75 mentions in open access literature.

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

Pees B, et al. (2024) The Caenorhabditis elegans proteome response to two protective Pseudomonas symbionts. mBio, 15(4), e0346323.

Windels A, et al. (2024) CANDy: Automated analysis of domain architectures in carbohydrate-active enzymes. PloS one, 19(7), e0306410.

Pudžiuvelyt? I, et al. (2024) TemStaPro: protein thermostability prediction using sequence representations from protein language models. Bioinformatics (Oxford, England), 40(4).

Dickson A, et al. (2024) Fine-tuning protein embeddings for functional similarity evaluation. Bioinformatics (Oxford, England), 40(8).

Podoliak E, et al. (2024) A subgroup of light-driven sodium pumps with an additional Schiff base counterion. Nature communications, 15(1), 3119.

Vazquez JM, et al. (2024) Extensive longevity and DNA virus-driven adaptation in nearctic Myotis bats. bioRxiv : the preprint server for biology.

Spaccasassi A, et al. (2024) Sensoproteomic Characterization of Lactobacillus Johnsonii-Fermented Pea Protein-Based Beverage: A Promising Strategy for Enhancing Umami and Kokumi Sensations while Mitigating Bitterness. Journal of agricultural and food chemistry, 72(28), 15875.

Clark CM, et al. (2024) Creating and leveraging bespoke large-scale knowledge graphs for comparative genomics and multi-omics drug discovery with SocialGene. bioRxiv : the preprint server for biology.

Mia MM, et al. (2024) Characterization of a unique catechol-O-methyltransferase as a molecular drug target in parasitic filarial nematodes. PLoS neglected tropical diseases, 18(8), e0012473.

Jones JA, et al. (2024) Structural basis for peroxidase encapsulation inside the encapsulin from the Gram-negative pathogen Klebsiella pneumoniae. Nature communications, 15(1), 2558.

Al-Nijir M, et al. (2024) Metabolic modelling uncovers the complex interplay between fungal probiotics, poultry microbiomes, and diet. Microbiome, 12(1), 267.

Thompson R, et al. (2024) The amino acid composition of a protein influences its expression. PloS one, 19(10), e0284234.

DiCandia MA, et al. (2024) A conserved switch controls virulence, sporulation, and motility in C. difficile. PLoS pathogens, 20(5), e1012224.

Xie Y, et al. (2023) Unexpected metabolic rewiring of CO2 fixation in H2-mediated materials-biology hybrids. Proceedings of the National Academy of Sciences of the United States of America, 120(42), e2308373120.

Kilinc M, et al. (2023) Improved global protein homolog detection with major gains in function identification. Proceedings of the National Academy of Sciences of the United States of America, 120(9), e2211823120.

Kang Y, et al. (2023) AFTGAN: prediction of multi-type PPI based on attention free transformer and graph attention network. Bioinformatics (Oxford, England), 39(2).

Jones JA, et al. (2023) Structural basis for peroxidase encapsulation in a protein nanocompartment. bioRxiv : the preprint server for biology.

Chen ZZ, et al. (2023) Mitochondria and cytochrome components released into the plasma of severe COVID-19 and ICU acute respiratory distress syndrome patients. Clinical proteomics, 20(1), 17.

Li Y, et al. (2023) AcrNET: predicting anti-CRISPR with deep learning. Bioinformatics (Oxford, England), 39(5).

Gonzales MEM, et al. (2023) Protein embeddings improve phage-host interaction prediction. PloS one, 18(7), e0289030.