

# Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 2026

## 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:** data or information resource, database

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

**Availability:** Public, Entries are available for download

**Resource Name:** UniParc

**Resource ID:** SCR\_005818

**Alternate IDs:** SCR\_004769, nif-0000-03610, r3d100011519, biotools:uniparc, nlx\_76940

**Alternate URLs:** <https://bio.tools/uniparc>, <https://doi.org/10.17616/R3X33B>

**Record Creation Time:** 20220129T080232+0000

**Record Last Update:** 20260801T042618+0000

### Ratings and Alerts

No rating or validation information has been found for UniParc.

No alerts have been found for UniParc.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 87 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Yang S, et al. (2025) PF-AGCN: an adaptive graph convolutional network for protein-protein interaction-based function prediction. *Bioinformatics (Oxford, England)*, 41(9).

Gil-Gomez A, et al. (2025) Proteome remodeling in the zoospore-to-vegetative cell transition of the stramenopile *Aurantiochytrium limacinum* reveals candidate ectoplasmic network proteins. *PloS one*, 20(7), e0326651.

Fong-Zazueta R, et al. (2025) Phylogenetic Signal in Primate Tooth Enamel Proteins and its Relevance for Paleoproteomics. *Genome biology and evolution*, 17(2).

Tijare P, et al. (2025) Prediction and design of thermostable proteins with a desired melting temperature. *Scientific reports*, 15(1), 16683.

Lamm GHU, et al. (2025) CryoRhodopsins: A comprehensive characterization of a group of microbial rhodopsins from cold environments. *Science advances*, 11(27), eadv1015.

Karasikov M, et al. (2025) Efficient and accurate search in petabase-scale sequence repositories. *Nature*, 647(8091), 1036.

Mychack A, et al. (2025) *Staphylococcus aureus* uses a GGDEF protein to recruit diacylglycerol kinase to the membrane for lipid recycling. *Proceedings of the National Academy of Sciences of the United States of America*, 122(12), e2414696122.

Subanovic M, et al. (2025) Proteomic and metabolomic responses of priority bacterial pathogens to subinhibitory concentration of antibiotics. *npj antimicrobials and resistance*, 3(1), 80.

Baars IM, et al. (2025) Exploring the associations between preen oil bacterial, chemical and proteomic profiles of passerines. *Antonie van Leeuwenhoek*, 118(11), 173.

Rao DM, et al. (2025) Systematic identification and characterization of eukaryotic and viral 2A peptide-bond-skipping sequences. *Cell reports*, 44(7), 115822.

Du Z, et al. (2025) PepBERT: Lightweight language models for bioactive peptide representation. *bioRxiv : the preprint server for biology*.

- Levé M, et al. (2025) Metabolomics and metagenomics in mice reveal the role of the gut microbiota in tryptophan metabolism. *iScience*, 28(11), 113751.
- Windels A, et al. (2024) CANDy: Automated analysis of domain architectures in carbohydrate-active enzymes. *PloS one*, 19(7), e0306410.
- Pees B, et al. (2024) The *Caenorhabditis elegans* proteome response to two protective *Pseudomonas* symbionts. *mBio*, 15(4), e0346323.
- Dickson A, et al. (2024) Fine-tuning protein embeddings for functional similarity evaluation. *Bioinformatics (Oxford, England)*, 40(8).
- Pudžiuvėlytė I, et al. (2024) TemStaPro: protein thermostability prediction using sequence representations from protein language models. *Bioinformatics (Oxford, England)*, 40(4).
- 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.
- 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.
- 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*.
- Vazquez JM, et al. (2024) Extensive longevity and DNA virus-driven adaptation in nearctic *Myotis* bats. *bioRxiv : the preprint server for biology*.