

Resource Summary Report

Generated by [RRID](#) on Sep 10, 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: 20260905T133132+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 98 mentions in open access literature.

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

Elreify HM, et al. (2026) BiGKbhb: a bi-directional gated recurrent unit model for predicting lysine γ -hydroxybutyrylation sites. BMC genomics, 27(1), 102.

Jasnauskaitė M, et al. (2026) Structure and mechanism of antiphage retron Eco2. Nature structural & molecular biology, 33(2), 330.

Perdigao CC, et al. (2026) Structural insights into target detection by the *S. marcescens* type III CRISPR complex and its deployment in SNP identification. bioRxiv : the preprint server for biology.

Rapala JR, et al. (2026) Deep homology and design of proteasome chaperone proteins in *Candidozyma auris*. Nature communications, 17(1).

Gravel N, et al. (2026) CLASPP: A unified model for predicting post-translational modifications. bioRxiv : the preprint server for biology.

Ray S, et al. (2026) Structural and functional basis of proton-independent transition metal import by a canonical bacterial Nramp transporter. bioRxiv : the preprint server for biology.

Elshemy HM, et al. (2026) Photodynamic larvicidal activity of magnesium chlorophyllin and magnesium chlorophyllin zinc oxide nanocomposite against *Spodoptera frugiperda* with non-target safety assessment. Scientific reports, 16(1).

Dohmen RL, et al. (2026) Functional insights into the photoactive yellow protein family from homologs, multidomain proteins, and inferred pyp operons. Journal of bacteriology, 208(1), e0021625.

Lima AR, et al. (2026) Ancestral Protein Reconstruction Uncovers a Thermotolerant Rieske Oxygenase with Enhanced O-Demethylation Activity toward 3-O-Methylgallate. ACS synthetic biology, 15(6), 2660.

Pal N, et al. (2026) Crystal Structure and Conformational Dynamics of N $\rightarrow$ N Bond-Forming Piperazate Synthase. Chembiochem : a European journal of chemical biology, 27(12), e70430.

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.

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