

Resource Summary Report

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UniRef

RRID:SCR_010646

Type: Tool

Proper Citation

UniRef (RRID:SCR_010646)

Resource Information

URL: <http://www.uniprot.org/help/uniref>

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Description: Databases which provide clustered sets of sequences from UniProt Knowledgebase and selected UniParc records, in order to obtain complete coverage of sequence space at several resolutions while hiding redundant sequences from view. The UniRef100 database combines identical sequences and sub-fragments with 11 or more residues (from any organism) into a single UniRef entry. The sequence of a representative protein, the accession numbers of all the merged entries, and links to the corresponding UniProtKB and UniParc records are all displayed in the entry. UniRef90 and UniRef50 are built by clustering UniRef100 sequences with 11 or more residues such that each cluster is composed of sequences that have at least 90% (UniRef90) or 50% (UniRef50) sequence identity to the longest sequence (UniRef seed sequence). All the sequences in each cluster are ranked to facilitate the selection of a representative sequence for the cluster.

Synonyms: UniProt Reference Clusters

Resource Type: data or information resource, database

Defining Citation: [PMID:17379688](#)

Keywords: database, protein sequence, sub-fragment, sequence cluster, clustered set

Funding: NHGRI U01 HG02712

Availability: Updated biweekly

Resource Name: UniRef

Resource ID: SCR_010646

Alternate IDs: nlx_66133, r3d100011518

Record Creation Time: 20220129T080259+0000

Record Last Update: 20260804T043432+0000

Ratings and Alerts

No rating or validation information has been found for UniRef.

No alerts have been found for UniRef.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 277 mentions in open access literature.

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

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. *Molecular biology and evolution*, 42(3).

Lev?? M, et al. (2025) Metabolomics and metagenomics in mice reveal the role of the gut microbiota in tryptophan metabolism. *iScience*, 28(11), 113751.

Liu H, et al. (2025) RNA-protein interaction prediction using network-guided deep learning. *Communications biology*, 8(1), 247.

Yue Y, et al. (2025) Protein language model-based prediction for plant miRNA encoded peptides. *PeerJ. Computer science*, 11, e2733.

Bredon M, et al. (2025) Gut microbiota alterations are linked to COVID-19 severity in North African and European populations. *NPJ biofilms and microbiomes*, 11(1), 106.

Harun-Or-Roshid M, et al. (2025) A genetic algorithm-based ensemble model for efficiently identifying interleukin 6 inducing peptides. *Scientific reports*, 15(1), 21213.

Zhong G, et al. (2025) SeekTP: identifying multifunctional therapeutic peptides via graph attention and deep property integration. *Briefings in bioinformatics*, 26(5).

Cho Y, et al. (2025) Stable de novo protein design via joint conformational landscape and sequence optimization. *Nature communications*, 17(1), 8.

Arif S, et al. (2025) Host transcriptional responses to gut microbiome variation arising from urbanism. *bioRxiv : the preprint server for biology*.

Xiao B, et al. (2025) A comprehensive dataset of therapeutic peptides on multi-function property and structure information. *Scientific data*, 12(1), 1213.

Zhang L, et al. (2025) The resident gut microbiome modulates the effect of synbiotics on the immunogenicity after SARS-COV-2 vaccination in elderly and diabetes patients. NPJ biofilms and microbiomes, 11(1), 171.

Nguyen NDH, et al. (2025) xBitterT5: an explainable transformer-based framework with multimodal inputs for identifying bitter-taste peptides. Journal of cheminformatics, 17(1), 127.

Brito Rodrigues P, et al. (2025) Integrative metagenomics and metabolomics reveal age-associated gut microbiota and metabolite alterations in a hamster model of COVID-19. Gut microbes, 17(1), 2486511.

Mu Q, et al. (2025) DRBP-EDP: classification of DNA-binding proteins and RNA-binding proteins using ESM-2 and dual-path neural network. NAR genomics and bioinformatics, 7(2), lqaf058.

Ye A, et al. (2025) Carmna: classification and regression models for nitrogenase activity based on a pretrained large protein language model. Briefings in bioinformatics, 26(2).

Shin D, et al. (2025) Biosynthesis and Physiological Significance of Organ-Specific Flavonol Glycosides in Solanaceae. bioRxiv : the preprint server for biology.

Silva JVD, et al. (2025) Dietary modulation of the rumen microbiome drives the expression of metabolic and methanogenic pathways in Bos indicus. mSphere, 10(10), e0053525.

Gu C, et al. (2025) Proteogenomic Reassessment Provides Novel Insight into the Life Cycle of Tetrahymenathermophila. Molecular & cellular proteomics : MCP, 24(11), 101081.

Wallmann A, et al. (2025) Structural and evolutionary determinants of Argonaute function. Nucleic acids research, 53(18).

Rued BE, et al. (2025) Impact of the RaS-RiPP tryglysin and culturing conditions on ex-vivo oral microbiomes. NPJ biofilms and microbiomes, 11(1), 152.