

# Resource Summary Report

Generated by [dkNET](#) on Jul 30, 2026

## 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:** 20260729T044257+0000

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## Ratings and Alerts

No rating or validation information has been found for UniRef.

No alerts have been found for UniRef.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 277 mentions in open access literature.

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

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.

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

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.

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.

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.

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

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

Santos PKF, et al. (2025) The genome of the solitary bee *Tetrapedia diversipes* (Hymenoptera, Apidae). *G3 (Bethesda, Md.)*, 15(2).

Do HN, et al. (2025) Dynamics and activation of membrane-bound B cell receptor assembly. *Communications biology*, 8(1), 226.

Plewka J, et al. (2025) Metagenomic analysis of pristine oil sheds new light on the global distribution of microbial genetic repertoire in hydrocarbon-associated ecosystems. *microLife*, 6, uqae027.

Rathore AS, et al. (2025) Prediction of hemolytic peptides and their hemolytic concentration. *Communications biology*, 8(1), 176.

Feng H, et al. (2025) SORFPP: Enhancing rich sequence-driven information to identify SEPs based on fused framework on validation datasets. *PloS one*, 20(4), e0320314.

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

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).

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.

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.

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

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.