Resource Summary Report

Generated by dkNET on Apr 16, 2025

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: database, data or information resource

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

Record Creation Time: 20220129T080259+0000

Record Last Update: 20250412T055520+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 220 mentions in open access literature.

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

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.

Ramakrishnan U, et al. (2025) Sequence and biochemical analysis of vaccinia virus A32 protein: Implications for in vitro stability and coiled-coil motif mediated regulation of the DNA-dependent ATPase activity. PloS one, 20(1), e0316818.

Vasiliauskien? D, et al. (2024) Changes in Microbiota Composition during the Anaerobic Digestion of Macroalgae in a Three-Stage Bioreactor. Microorganisms, 12(1).

McLean TC, et al. (2024) LazyAF, a pipeline for accessible medium-scale in silico prediction of protein-protein interactions. Microbiology (Reading, England), 170(7).

Liu Z, et al. (2024) Changes in Rhizosphere Soil Microorganisms and Metabolites during the Cultivation of Fritillaria cirrhosa. Biology, 13(5).

Miao H, et al. (2024) Genomic evolution and insights into agronomic trait innovations of Sesamum species. Plant communications, 5(1), 100729.

Ribeiro-Filho HV, et al. (2024) Exploring the Potential of Structure-Based Deep Learning Approaches for T cell Receptor Design. bioRxiv : the preprint server for biology.

Drago VN, et al. (2024) Neutron diffraction from a microgravity-grown crystal reveals the active site hydrogens of the internal aldimine form of tryptophan synthase. Cell reports. Physical science, 5(2).

Almeida GMdF, et al. (2024) Relevance of the bacteriophage adherence to mucus model for Pseudomonas aeruginosa phages. Microbiology spectrum, 12(8), e0352023.

Ding K, et al. (2024) Machine learning-guided co-optimization of fitness and diversity facilitates combinatorial library design in enzyme engineering. Nature communications, 15(1), 6392.

Heinz JM, et al. (2024) Novel metagenomics analysis of stony coral tissue loss disease. G3 (Bethesda, Md.), 14(8).

Kariapper L, et al. (2024) Setdb1 and Atf7IP form a hetero-trimeric complex that blocks Setdb1 nuclear export. bioRxiv : the preprint server for biology.

Wang H, et al. (2024) A gut aging clock using microbiome multi-view profiles is associated with health and frail risk. Gut microbes, 16(1), 2297852.

Griffiths JA, et al. (2024) Peripheral neuronal activation shapes the microbiome and alters gut physiology. Cell reports, 43(4), 113953.

Soriano-Lerma A, et al. (2024) Comprehensive insight into the alterations in the gut microbiome and the intestinal barrier as a consequence of iron deficiency anaemia. Biomedical journal, 47(6), 100701.

Ji Y, et al. (2024) PlasGO: enhancing GO-based function prediction for plasmid-encoded proteins based on genetic structure. GigaScience, 13.

Liu D, et al. (2024) Anaerostipes hadrus, a butyrate-producing bacterium capable of metabolizing 5-fluorouracil. mSphere, 9(4), e0081623.

Zhang B, et al. (2024) Sustained mucosal colonization and fecal metabolic dysfunction by Bacteroides associates with fecal microbial transplant failure in ulcerative colitis patients. Scientific reports, 14(1), 18558.

Feng Z, et al. (2024) DGCPPISP: a PPI site prediction model based on dynamic graph convolutional network and two-stage transfer learning. BMC bioinformatics, 25(1), 252.

Ding H, et al. (2024) MEG-PPIS: a fast protein-protein interaction site prediction method based on multi-scale graph information and equivariant graph neural network. Bioinformatics (Oxford, England), 40(5).