Resource Summary Report

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UniRef at the EBI

RRID:SCR_004972
Type: Tool

Proper Citation

UniRef at the EBI (RRID:SCR_004972)

Resource Information

URL: http://www-test.ebi.ac.uk/uniref/

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Description: Various non-redundant databases with different sequence identity cut-offs created by clustering closely similar sequences to yield a representative subset of sequences. In the UniRef90 and UniRef50 databases no pair of sequences in the representative set has >90% or >50% mutual sequence identity. The UniRef100 database presents identical sequences and sub-fragments as a single entry with protein IDs, sequences, bibliography, and links to protein databases. The two major objectives of UniRef are: (i) to facilitate sequence merging in UniProt, and (ii) to allow faster and more informative sequence similarity searches. Although the UniProt Knowledgebase is much less redundant than UniParc, it still contains a certain level of redundancy because it is not possible to use fully automatic merging without risking merging of similar sequences from different proteins. However, such automatic procedures are extremely useful in compiling the UniRef databases to obtain complete coverage of sequence space while hiding redundant sequences (but not their descriptions) from view. A high level of redundancy results in several problems, including slow database searches and long lists of similar or identical alignments that can obscure novel matches in the output. Thus, a more even sampling of sequence space is advantageous. You may access NREF via the FTP server.

Abbreviations: UniRef at the EBI

Synonyms: UniProt Reference Clusters database, UniProt Non-redundant Reference database, UniProt Reference Clusters, UniProt NREF, UniProt Non-redundant Reference

Resource Type: database, data or information resource

Keywords: gold standard

Funding:

Resource Name: UniRef at the EBI

Resource ID: SCR_004972

Alternate IDs: nlx_93434

Old URLs: http://www.ebi.ac.uk/uniref/

Record Creation Time: 20220129T080227+0000

Record Last Update: 20250412T054926+0000

Ratings and Alerts

No rating or validation information has been found for UniRef at the EBI.

No alerts have been found for UniRef at the EBI.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Rodrigues FA, et al. (2012) Subtractive libraries for prospecting differentially expressed genes in the soybean under water deficit. Genetics and molecular biology, 35(1 (suppl)), 304.

Schneider T, et al. (2012) Who is who in litter decomposition? Metaproteomics reveals major microbial players and their biogeochemical functions. The ISME journal, 6(9), 1749.

Chawla B, et al. (2012) A unique modification of the eukaryotic initiation factor 5A shows the presence of the complete hypusine pathway in Leishmania donovani. PloS one, 7(3), e33138.

Xu Q, et al. (2012) Structure of an MmyB-like regulator from C. aurantiacus, member of a new transcription factor family linked to antibiotic metabolism in actinomycetes. PloS one, 7(7), e41359.

Sato S, et al. (2011) Sequence analysis of the genome of an oil-bearing tree, Jatropha curcas L. DNA research : an international journal for rapid publication of reports on genes and genomes, 18(1), 65.

Tyagi N, et al. (2010) A framework for classification of prokaryotic protein kinases. PloS one, 5(5), e10608.

Dvorák J, et al. (2009) SmCL3, a gastrodermal cysteine protease of the human blood fluke Schistosoma mansoni. PLoS neglected tropical diseases, 3(6), e449.

Rosen GL, et al. (2009) Signal processing for metagenomics: extracting information from the soup. Current genomics, 10(7), 493.