

Resource Summary Report

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Protein Clusters

RRID:SCR_003459

Type: Tool

Proper Citation

Protein Clusters (RRID:SCR_003459)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/proteinclusters>

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Description: Database of related protein sequences (clusters) consisting of proteins derived from the annotations of whole genomes, organelles and plasmids. It currently limited to Archaea, Bacteria, Plants, Fungi, Protozoans, and Viruses. It contains annotation information, publications, domains, structures, and external links and analysis tools including multiple alignments, phylogenetic trees, and genomic neighborhoods (ProtMap). Data is available for download via Protein Clusters FTP

Abbreviations: ProtClustDB

Synonyms: Protein Clusters Database, NCBI Protein Clusters, Entrez Protein Clusters

Resource Type: data or information resource, database

Defining Citation: [PMID:18940865](#)

Keywords: bacteriophage, mitochondrial organelle, chloroplast organelle, plasmid, phylogeny, nucleotide sequence, chloroplast, dna, virus, genome, organelle, gold standard

Funding: NIH ;
Intramural Research Program ;
NLM

Availability: Free, Available for download, Freely available

Resource Name: Protein Clusters

Resource ID: SCR_003459

Alternate IDs: nif-0000-03354, r3d100010861

Alternate URLs: <https://doi.org/10.17616/R3TS52>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260729T044043+0000

Ratings and Alerts

No rating or validation information has been found for Protein Clusters.

No alerts have been found for Protein Clusters.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Zhou C, et al. (2014) AST: an automated sequence-sampling method for improving the taxonomic diversity of gene phylogenetic trees. PloS one, 9(6), e98844.

Klitgaard K, et al. (2012) Transcriptional portrait of Actinobacillus pleuropneumoniae during acute disease--potential strategies for survival and persistence in the host. PloS one, 7(4), e35549.

Pruitt KD, et al. (2012) NCBI Reference Sequences (RefSeq): current status, new features and genome annotation policy. Nucleic acids research, 40(Database issue), D130.

Brister JR, et al. (2012) Microbial virus genome annotation-mustering the troops to fight the sequence onslaught. Virology, 434(2), 175.