NEWT

RRID:SCR_004477
Type: Tool

Proper Citation

NEWT (RRID:SCR_004477)

Resource Information

URL: http://www.uniprot.org/taxonomy/

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Description: NEWT is the taxonomy database maintained by the UniProt group. It integrates taxonomy data compiled in the NCBI database and data specific to the UniProt Knowledgebase. Browse by hierarchy, List all, or Complete proteomes. Organisms are classified in a hierarchical tree structure. Our taxonomy database contains every node (taxon) of the tree. UniProtKB taxonomy data is manually curated: next to manually verified organism names, we provide a selection of external links, organism strains and viral host information. Species with protein sequences stored in the UniProt Knowledgebase are named according to UniProt nomenclature. We endeavour to maintain a list of manually curated species names for which protein sequence data is available. In particular, we have adopted a systematic convention for naming viral and bacterial strains and isolates. Links to external sites are chosen by the UniProt taxonomy team and show pictures and various scientific data of interest (taxonomy, biology, physiology,...).

Abbreviations: NEWT

Synonyms: UniProtKB taxonomy database, UniProt Taxonomy Database, UniProt Taxonomy

Resource Type: data or information resource, database

Defining Citation: PMID:12824428

Keywords: archaea, bacteria, eukaryota, viruses, cellular organism, sequence, viroid, gold standard, bio.tools

Funding:

Resource Name: NEWT

Resource ID: SCR_004477

Alternate IDs: nlx_46189, biotools:newt

Alternate URLs: https://bio.tools/newt

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

Record Creation Time: 20220129T080224+0000

Record Last Update: 20250424T064707+0000

Ratings and Alerts

No rating or validation information has been found for NEWT.

No alerts have been found for NEWT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Ginsburg AS, et al. (2023) Newborn weight nomograms in selected low and middle-income countries. Scientific reports, 13(1), 14128.

Ostaszewski M, et al. (2021) COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. Molecular systems biology, 17(10), e10387.

Bergner LM, et al. (2021) Detection of Trypanosoma cruzi in the saliva of diverse neotropical bats. Zoonoses and public health, 68(3), 271.

Pérez SD, et al. (2019) Phylogenetics, patterns of genetic variation and population dynamics of Trypanosoma terrestris support both coevolution and ecological host-fitting as processes driving trypanosome evolution. Parasites & vectors, 12(1), 473.

Tabakmakher VM, et al. (2019) Kalium 2.0, a comprehensive database of polypeptide

ligands of potassium channels. Scientific data, 6(1), 73.

Tsirka T, et al. (2018) Comparative analysis of xenobiotic metabolising N-acetyltransferases from ten non-human primates as in vitro models of human homologues. Scientific reports, 8(1), 9759.

Antonets KS, et al. (2018) Exploring Proteins Containing Amyloidogenic Regions in the Proteomes of Bacteria of the Order Rhizobiales. Evolutionary bioinformatics online, 14, 1176934318768781.

Antonets KS, et al. (2017) Predicting Amyloidogenic Proteins in the Proteomes of Plants. International journal of molecular sciences, 18(10).

Zaragoza J, et al. (2017) Effects of Exogenous Yeast and Bacteria on the Microbial Population Dynamics and Outcomes of Olive Fermentations. mSphere, 2(1).

Álvaro-Blanco J, et al. (2017) MAZ induces MYB expression during the exit from quiescence via the E2F site in the MYB promoter. Nucleic acids research, 45(17), 9960.

Karagianni EP, et al. (2015) Homologues of xenobiotic metabolizing N-acetyltransferases in plant-associated fungi: Novel functions for an old enzyme family. Scientific reports, 5, 12900.

Zhou C, et al. (2015) gPGA: GPU Accelerated Population Genetics Analyses. PloS one, 10(8), e0135028.

Kather R, et al. (2015) Evolution of Cuticular Hydrocarbons in the Hymenoptera: a Meta-Analysis. Journal of chemical ecology, 41(10), 871.

Zhang T, et al. (2015) Novel Trichoderma polysporum Strain for the Biocontrol of Pseudogymnoascus destructans, the Fungal Etiologic Agent of Bat White Nose Syndrome. PloS one, 10(10), e0141316.

Oshita K, et al. (2014) G-Links: a gene-centric link acquisition service. F1000Research, 3, 285.

Aylward FO, et al. (2014) Convergent bacterial microbiotas in the fungal agricultural systems of insects. mBio, 5(6), e02077.

Panjkovich A, et al. (2014) antibacTR: dynamic antibacterial-drug-target ranking integrating comparative genomics, structural analysis and experimental annotation. BMC genomics, 15(1), 36.

Zhang T, et al. (2014) Mycobiome of the bat white nose syndrome affected caves and mines reveals diversity of fungi and local adaptation by the fungal pathogen Pseudogymnoascus (Geomyces) destructans. PloS one, 9(9), e108714.

Ravva SV, et al. (2013) Altered protozoan and bacterial communities and survival of Escherichia coli O157:H7 in monensin-treated wastewater from a dairy lagoon. PloS one, 8(1), e54782.

Muñoz-Mérida A, et al. (2013) De novo assembly and functional annotation of the olive (Olea europaea) transcriptome. DNA research : an international journal for rapid publication of reports on genes and genomes, 20(1), 93.