

Resource Summary Report

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NCBI accession download script

RRID:SCR_024130

Type: Tool

Proper Citation

NCBI accession download script (RRID:SCR_024130)

Resource Information

URL: <https://github.com/kblin/ncbi-acc-download>

Proper Citation: NCBI accession download script (RRID:SCR_024130)

Description: Software tool as partner script to the popular ncbi-genome-download script. Allows to download sequences from GenBank/RefSeq by accession through the NCBI ENTREZ API.

Synonyms: ncbi-acc-download

Resource Type: software resource, software application

Keywords: download sequences, GenBank/RefSeq, accession through NCBI ENTREZ API,

Availability: Free, Available for download, Freely available,

Resource Name: NCBI accession download script

Resource ID: SCR_024130

Alternate URLs: <https://sources.debian.org/src/ncbi-acc-download/>

License: Apache-2.0 license

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260731T043137+0000

Ratings and Alerts

No rating or validation information has been found for NCBI accession download script.

No alerts have been found for NCBI accession download script.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1177 mentions in open access literature.

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

Parvez S, et al. (2025) Tracing the path from conservation to expansion evolutionary insights into NLR genes in oleaceae. BMC plant biology, 25(1), 259.

Kornienko M, et al. (2024) Multiomics analysis of Staphylococcus aureus ST239 strains resistant to virulent Herelleviridae phages. Scientific reports, 14(1), 29375.

Tan CCS, et al. (2024) The evolutionary drivers and correlates of viral host jumps. Nature ecology & evolution, 8(5), 960.

Zaychikova M, et al. (2024) Vic9 mycobacteriophage: the first subcluster B2 phage isolated in Russia. Frontiers in microbiology, 15, 1513081.

Lal MM, et al. (2018) Genome-wide comparisons reveal evidence for a species complex in the black-lip pearl oyster Pinctada margaritifera (Bivalvia: Pteriidae). Scientific reports, 8(1), 191.

Dai W, et al. (2018) Phylogenomic Perspective on the Relationships and Evolutionary History of the Major Otocephalan Lineages. Scientific reports, 8(1), 205.

Hadizadeh Esfahani A, et al. (2018) A systematic atlas of chaperome deregulation topologies across the human cancer landscape. PLoS computational biology, 14(1), e1005890.

Manavalan B, et al. (2018) DHSpred: support-vector-machine-based human DNase I hypersensitive sites prediction using the optimal features selected by random forest. Oncotarget, 9(2), 1944.

Chakraborty M, et al. (2018) Hidden genetic variation shapes the structure of functional elements in Drosophila. Nature genetics, 50(1), 20.

Nowicki EM, et al. (2018) Microbiota and Metatranscriptome Changes Accompanying the Onset of Gingivitis. mBio, 9(2).

Manavalan B, et al. (2018) AIPpred: Sequence-Based Prediction of Anti-inflammatory Peptides Using Random Forest. Frontiers in pharmacology, 9, 276.

Ordinelli A, et al. (2018) Putative human sperm Interactome: a networks study. BMC systems biology, 12(1), 52.

Doud MB, et al. (2018) How single mutations affect viral escape from broad and narrow antibodies to H1 influenza hemagglutinin. Nature communications, 9(1), 1386.

Györfy B, et al. (2018) CRISPR/Cas9 Mediated Disruption of the Swedish APP Allele as a Therapeutic Approach for Early-Onset Alzheimer's Disease. *Molecular therapy. Nucleic acids*, 11, 429.

Liu Q, et al. (2018) Have compensatory mutations facilitated the current epidemic of multidrug-resistant tuberculosis? *Emerging microbes & infections*, 7(1), 98.

Mo Y, et al. (2018) Mapping causal mutations by exome sequencing in a wheat TILLING population: a tall mutant case study. *Molecular genetics and genomics : MGG*, 293(2), 463.

Mars JC, et al. (2018) A Deconvolution Protocol for ChIP-Seq Reveals Analogous Enhancer Structures on the Mouse and Human Ribosomal RNA Genes. *G3 (Bethesda, Md.)*, 8(1), 303.

Jacob Machado D, et al. (2018) A new strategy to infer circularity applied to four new complete frog mitogenomes. *Ecology and evolution*, 8(8), 4011.

Medlar AJ, et al. (2018) AAI-profiler: fast proteome-wide exploratory analysis reveals taxonomic identity, misclassification and contamination. *Nucleic acids research*, 46(W1), W479.

Wang Y, et al. (2018) Comparative Genomics Reveals the Core Gene Toolbox for the Fungus-Insect Symbiosis. *mBio*, 9(3).