

# Resource Summary Report

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## NCBI accession download script

RRID:SCR\_024130

Type: Tool

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### Proper Citation

NCBI accession download script (RRID:SCR\_024130)

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### 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 application, software resource

**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:** 20260821T043108+0000

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### 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 1179 mentions in open access literature.

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

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.

Mushtaq A, et al. (2024) Clinical, microbiological and genomic characterization of Gram-negative bacteria with dual carbapenemases as identified by rapid molecular testing. JAC-antimicrobial resistance, 6(1), dlad137.

Kornienko M, et al. (2023) PCR Assay for Rapid Taxonomic Differentiation of Virulent Staphylococcus aureus and Klebsiella pneumoniae Bacteriophages. International journal of molecular sciences, 24(5).

Singh J, et al. (2018) A transcriptome-SNP-derived linkage map of Apios americana (potato bean) provides insights about genome re-organization and syntenic conservation in the phaseoloid legumes. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 131(2), 333.

Rifai EA, et al. (2018) Binding free energy predictions of farnesoid X receptor (FXR) agonists using a linear interaction energy (LIE) approach with reliability estimation: application to the D3R Grand Challenge 2. Journal of computer-aided molecular design, 32(1), 239.

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).

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

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.

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

Mathieson T, et al. (2018) Systematic analysis of protein turnover in primary cells. *Nature communications*, 9(1), 689.

Gao L, et al. (2018) Identifying noncoding risk variants using disease-relevant gene regulatory networks. *Nature communications*, 9(1), 702.

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.

Choi SW, et al. (2018) TERIUS: accurate prediction of lncRNA via high-throughput sequencing data representing RNA-binding protein association. *BMC bioinformatics*, 19(Suppl 1), 41.

Toepfner N, et al. (2018) Detection of human disease conditions by single-cell morpho-rheological phenotyping of blood. *eLife*, 7.

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.

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.