

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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 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: 20260905T133317+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 1179 mentions in open access literature.

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

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).

Gy??rgy 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.

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.

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

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.

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.

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

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.

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.

Xiong D, et al. (2018) Novel mutational landscapes and expression signatures of lung squamous cell carcinoma. Oncotarget, 9(7), 7424.

Lorentzen A, et al. (2018) Single cell polarity in liquid phase facilitates tumour metastasis. Nature communications, 9(1), 887.

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.