

Resource Summary Report

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Batch Entrez

RRID:SCR_016634

Type: Tool

Proper Citation

Batch Entrez (RRID:SCR_016634)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/sites/batchentrez>

Proper Citation: Batch Entrez (RRID:SCR_016634)

Description: Software program for loading numbers of genome records. Allows the retrieval of a large number of nucleotide sequences or protein sequences, in a batch mode, by importing a file containing a list of the desired GI or accession numbers.

Resource Type: software resource, software application

Keywords: load, number, genome, record, retrieval, nucleotide, sequence, protein, batch, mode

Availability: Public, Free, Freely available

Resource Name: Batch Entrez

Resource ID: SCR_016634

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260801T191107+0000

Ratings and Alerts

No rating or validation information has been found for Batch Entrez.

No alerts have been found for Batch Entrez.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 47 mentions in open access literature.

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

Cui Y, et al. (2025) Bacterial Hachiman complex executes DNA cleavage for antiphage defense. *Nature communications*, 16(1), 2604.

Qiao Y, et al. (2025) Exploring the Mechanism of Qinzhuliangxue Mixture for Treating Skin Lesions in Atopic Dermatitis: Insights from Network Pharmacology and Experimental Validation. *Journal of inflammation research*, 18, 5173.

Wang W, et al. (2025) *Thlaspi arvense* suppresses gut microbiota related TNF inflammatory pathway to alleviates ulcerative colitis. *Frontiers in immunology*, 16, 1537325.

Liu X, et al. (2025) A global perspective on autoinducer-2-mediated cell communication in prokaryotes. *iScience*, 28(7), 112908.

Orel HK, et al. (2025) Genetic Differentiation of Geographically Overlapping Sister Species of *Eucalyptus* in Northern Australia. *Ecology and evolution*, 15(6), e71454.

Reglinski M, et al. (2025) A widely-occurring family of pore-forming effectors broadens the impact of the *Serratia* Type VI secretion system. *The EMBO journal*, 44(23), 6892.

Torosian N, et al. (2025) Characterization of the thermophilic xylanase Fsa02490Xyn from the hyperthermophile *Fervidibacter sacchari* belonging to glycoside hydrolase family 10. *FEBS open bio*, 15(10), 1629.

Beh JQ, et al. (2025) Challenges and considerations for whole-genome-based antimicrobial resistance plasmid investigations. *Antimicrobial agents and chemotherapy*, 69(12), e0109725.

Xu ZM, et al. (2024) Joint host-pathogen genomic analysis identifies hepatitis B virus mutations associated with human NTCP and HLA class I variation. *American journal of human genetics*, 111(6), 1018.

Wang Z, et al. (2024) Genomic and functional divergence of *Staphylococcus aureus* strains from atopic dermatitis patients and healthy individuals: insights from global and local scales. *Microbiology spectrum*, 12(10), e0057124.

Song K, et al. (2024) Decoding the origins, spread, and global risks of *mcr-9* gene. *EBioMedicine*, 108, 105326.

Zhang S, et al. (2024) Conserved untranslated regions of multipartite viruses: Natural markers of novel viral genomic components and tags of viral evolution. *Virus evolution*, 10(1), veae004.

Covington JK, et al. (2024) Biochemical characterization of Fsa16295Glu from "*Fervidibacter sacchari*," the first hyperthermophilic GH50 with ??-1,3-endoglucanase activity and founding member of the subfamily GH50_3. *Frontiers in microbiology*, 15,

1355444.

Susorov D, et al. (2024) mRNA-specific readthrough of nonsense codons by antisense oligonucleotides (R-ASOs). *Nucleic acids research*, 52(15), 8687.

Zuo Y, et al. (2024) MSlocPRED: deep transfer learning-based identification of multi-label mRNA subcellular localization. *Briefings in bioinformatics*, 25(6).

Magar S, et al. (2024) Exploring pangenomic diversity and CRISPR-Cas evasion potential in jumbo phages: a comparative genomics study. *Microbiology spectrum*, 12(10), e0420023.

Li Y, et al. (2023) AcrNET: predicting anti-CRISPR with deep learning. *Bioinformatics (Oxford, England)*, 39(5).

Hurt RC, et al. (2023) Genomically mined acoustic reporter genes for real-time in vivo monitoring of tumors and tumor-homing bacteria. *Nature biotechnology*, 41(7), 919.

Wang Z, et al. (2023) Comparative Functional Genome Analysis Reveals the Habitat Adaptation and Biocontrol Characteristics of Plant Growth-Promoting Bacteria in NCBI Databases. *Microbiology spectrum*, 11(3), e0500722.

Bierman A, et al. (2023) Genome assembly of *Thaumatotibia leucotreta*, a major polyphagous pest of agriculture in sub-Saharan Africa. *G3 (Bethesda, Md.)*, 13(3).