

Resource Summary Report

Generated by SPARC SAWG on Jul 29, 2026

Entrez Direct

RRID:SCR_024136

Type: Tool

Proper Citation

Entrez Direct (RRID:SCR_024136)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/books/NBK179288/>

Proper Citation: Entrez Direct (RRID:SCR_024136)

Description: Software provides access to NCBI's suite of interconnected databases (publication, sequence, structure, gene, variation, expression, etc.) from Unix terminal window. Search terms are entered as command-line arguments. Individual operations are connected with Unix pipes to construct multi-step queries. Selected records can then be retrieved in variety of formats.

Synonyms: Entrez Direct: E-utilities on the Unix Command Line, EDirect, ncbi-entrez-direct

Resource Type: software resource, software toolkit, software library

Keywords: access to NCBI's suite of interconnected databases, Unix terminal window, construct multi-step queries, retrieve selected records,

Resource Name: Entrez Direct

Resource ID: SCR_024136

Alternate URLs: <https://sources.debian.org/src/ncbi-entrez-direct/>

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260729T044601+0000

Ratings and Alerts

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

No alerts have been found for Entrez Direct.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Soto-Lopez JD, et al. (2025) Taxonomic and functional profiling of bat guano microbiota from hiking trail-associated tunnels: a potential risk for human health? Environmental microbiome, 20(1), 123.

Saraf N, et al. (2025) AlphaFold Database Structure Extractor: a web server and API to download AlphaFold structures using common protein accessions. BMC bioinformatics, 26(1), 305.

Akinyemi MO, et al. (2025) Functional and safety profiles of microbial communities in milk of ranched and nomadic goats and their predictive role in mycotoxin reduction. World journal of microbiology & biotechnology, 41(8), 292.

Tan Y, et al. (2024) Machine learning-based classification reveals distinct clusters of non-coding genomic allelic variations associated with Erm-mediated antibiotic resistance. mSystems, 9(7), e0043024.

Tan Y, et al. (2024) Genomic Underpinnings of Cytoplasmic Incompatibility: CIF Gene-Neighborhood Diversification Through Extensive Lateral Transfers and Recombination in Wolbachia. Genome biology and evolution, 16(8).

Hunt M, et al. (2024) Addressing pandemic-wide systematic errors in the SARS-CoV-2 phylogeny. bioRxiv : the preprint server for biology.

de Almeida FM, et al. (2023) Scalable and versatile container-based pipelines for de novo genome assembly and bacterial annotation. F1000Research, 12, 1205.

Avila Santos AP, et al. (2023) The AnimalAssociatedMetagenomeDB reveals a bias towards livestock and developed countries and blind spots in functional-potential studies of animal-associated microbiomes. Animal microbiome, 5(1), 48.

Arulandhu AJ, et al. (2017) Development and validation of a multi-locus DNA metabarcoding method to identify endangered species in complex samples. GigaScience, 6(10), 1.