

# Resource Summary Report

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## 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 library, software resource, software toolkit

**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:** 20260821T194249+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 13 mentions in open access literature.

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

Rakesh S, et al. (2026) Expanding the landscape of BREX diversity: uncovering multi-layered functional frameworks and identification of novel BREX-related defense systems. *Nucleic acids research*, 54(3).

Hunt M, et al. (2026) Addressing pandemic-wide systematic errors in the SARS-CoV-2 phylogeny. *Nature methods*, 23(3), 653.

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.

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

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.

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.

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

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).

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.

Rubinstein M, et al. (2023) Prolonged survival of a patient with active MDR-TB HIV co-morbidity: insights from a *Mycobacterium tuberculosis* strain with a unique genomic deletion. *Frontiers in medicine*, 10, 1292665.

Summers KM, et al. (2019) Functional Annotation of the Transcriptome of the Pig, *Sus scrofa*, Based Upon Network Analysis of an RNAseq Transcriptional Atlas. *Frontiers in genetics*, 10, 1355.

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.