

# Resource Summary Report

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## Entrez

RRID:SCR\_016640

Type: Tool

### Proper Citation

Entrez (RRID:SCR\_016640)

### Resource Information

**URL:** <https://www.ncbi.nlm.nih.gov/Web/Search/entrezfs.html>

**Proper Citation:** Entrez (RRID:SCR\_016640)

**Description:** Web portal for global query cross database search and retrieval system that provides access to all databases simultaneously with a single query string and user interface. Retrieves nucleotide and protein sequence data, gene centered and genomic mapping information, 3D structures, and references. Covers databases including protein sequence data from PIR-International, PRF, Swiss-Prot, and PDB and nucleotide sequence data from GenBank that includes information from EMBL and DDBJ.

**Resource Type:** data or information resource, web service, portal, software resource, data access protocol

**Keywords:** global, query, cross, database, search, retrieval, system, database, nucleotide, protein, sequence, data, genomic, mapping, structure, reference

**Availability:** Free, Freely available

**Resource Name:** Entrez

**Resource ID:** SCR\_016640

**Record Creation Time:** 20220129T080331+0000

**Record Last Update:** 20260810T040647+0000

### Ratings and Alerts

No rating or validation information has been found for Entrez.

No alerts have been found for Entrez.

### Data and Source Information

## Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Vieira Mourato B, et al. (2025) Fast detection of unique genomic regions. Computational and structural biotechnology journal, 27, 843.

Zhang Y, et al. (2023) Bibliometric Analysis of Global Research on Tumor Dormancy. Cancers, 15(12).

Mei X, et al. (2023) Fail-tests of DNA methylation clocks, and development of a noise barometer for measuring epigenetic pressure of aging and disease. Aging, 15(17), 8552.

Grižan?i? L, et al. (2023) A metabarcode based (species) inventory of the northern Adriatic phytoplankton. Biodiversity data journal, 11, e106947.

Lee CW, et al. (2023) Relationship between drug targets and drug-signature networks: a network-based genome-wide landscape. BMC medical genomics, 16(1), 17.

Jacques F, et al. (2023) Roadmap to the study of gene and protein phylogeny and evolution-A practical guide. PloS one, 18(2), e0279597.

Lifschitz S, et al. (2022) Bio-Strings: A Relational Database Data-Type for Dealing with Large Biosequences. Biotech (Basel (Switzerland)), 11(3).

Holcomb DD, et al. (2022) Protocol to identify host-viral protein interactions between coagulation-related proteins and their genetic variants with SARS-CoV-2 proteins. STAR protocols, 3(3), 101648.

Ben Braiek M, et al. (2021) Identification of homozygous haplotypes carrying putative recessive lethal mutations that compromise fertility traits in French Lacaune dairy sheep. Genetics, selection, evolution : GSE, 53(1), 41.

Saini SK, et al. (2020) Human endogenous retroviruses form a reservoir of T cell targets in hematological cancers. Nature communications, 11(1), 5660.

Freidhoff P, et al. (2019) In silico survey of the central conserved regions in viroids of the Pospiviroidae family for conserved asymmetric loop structures. RNA (New York, N.Y.), 25(8), 985.

Og?uska M, et al. (2017) A porcine gluteus medius muscle genome-wide transcriptome analysis: dietary effects of omega-6 and omega-3 fatty acids on biological mechanisms. Genes & nutrition, 12, 4.

Hou B, et al. (2017) Systemic Identification of Hevea brasiliensis EST-SSR Markers and Primer Screening. Journal of nucleic acids, 2017, 6590902.

Zhang K, et al. (2016) Development and Identification of SSR Markers Associated with Starch Properties and  $\beta$ -Carotene Content in the Storage Root of Sweet Potato (*Ipomoea batatas* L.). *Frontiers in plant science*, 7, 223.

Kubicek CP, et al. (2011) Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of *Trichoderma*. *Genome biology*, 12(4), R40.

Bayer RG, et al. (2011) Mining the soluble chloroplast proteome by affinity chromatography. *Proteomics*, 11(7), 1287.

Qiu L, et al. (2010) Exploiting EST databases for the development and characterization of EST-SSR markers in castor bean (*Ricinus communis* L.). *BMC plant biology*, 10, 278.