

Resource Summary Report

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Entrez Utilities

RRID:SCR_013249

Type: Tool

Proper Citation

Entrez Utilities (RRID:SCR_013249)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/books/NBK25500/>

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Description: Entrez Programming Utilities are tools that provide access to Entrez data outside of the regular web query interface and may be helpful for retrieving search results for future use in another environment.

Additional information is available in the NCBI Bookshelf Short Courses Building Customized Data Pipelines Using the Entrez Programming Utilities (eUtils) and the NCBI PowerScripting course.

User Requirements: Please read for important information on scripting NCBI servers.

EInfo: Provides field index term counts, last update, and available links for each database.

ESearch: Searches and retrieves primary IDs (for use in EFetch, ELink, and ESummary) and term translations and optionally retains results for future use in the user's environment.

EPost: Posts a file containing a list of primary IDs for future use in the user's environment to use with subsequent search strategies.

ESummary: Retrieves document summaries from a list of primary IDs or from the user's environment.

EFetch: Retrieves records in the requested format from a list of one or more primary IDs or from the user's environment.

ELink: Checks for the existence of an external or Related Articles link from a list of one or more primary IDs. Retrieves primary IDs and relevancy scores for links to Entrez databases or Related Articles; creates a hyperlink to the primary LinkOut provider for a specific ID and database, or lists LinkOut URLs and Attributes for multiple IDs.

EGQuery: Provides Entrez database counts in XML for a single search using Global Query.

ESpell: Retrieves spelling suggestions.

SOAP Interface for Entrez Utilities

PMID to PMC ID Converter

Entrez DTDs

Demonstration Program

Announcement Mailing List
Leasing Data from the National Library of Medicine
Help Desk
User Requirements

Do not overload NCBI's systems. Users intending to send numerous queries and/or retrieve large numbers of records from Entrez should comply with the following:

Run retrieval scripts on weekends or between 9 pm and 5 am Eastern Time weekdays for any series of more than 100 requests.

Send E-utilities requests to <http://eutils.ncbi.nlm.nih.gov>, not the standard NCBI Web address.

Make no more than 3 requests every 1 second.

Use the URL parameter email, and tool for distributed software, so that we can track your project and contact you if there is a problem.

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Synonyms: Entrez Utilities

Resource Type: software resource

Resource Name: Entrez Utilities

Resource ID: SCR_013249

Alternate IDs: nif-0000-30519

Alternate URLs: http://eutils.ncbi.nlm.nih.gov/entrez/query/static/eutils_help.html

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260903T235231+0000

Ratings and Alerts

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

No alerts have been found for Entrez Utilities.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Bannach-Brown A, et al. (2021) Technological advances in preclinical meta-research. *BMJ open science*, 5(1), e100131.

Liu B, et al. (2018) Rapid Succession of Actively Transcribing Denitrifier Populations in Agricultural Soil During an Anoxic Spell. *Frontiers in microbiology*, 9, 3208.

Shameer K, et al. (2018) Systematic analyses of drugs and disease indications in RepurposeDB reveal pharmacological, biological and epidemiological factors influencing drug repositioning. *Briefings in bioinformatics*, 19(4), 656.

Piazza R, et al. (2017) OncoScore: a novel, Internet-based tool to assess the oncogenic potential of genes. *Scientific reports*, 7, 46290.

Cannon MV, et al. (2016) In silico assessment of primers for eDNA studies using PrimerTree and application to characterize the biodiversity surrounding the Cuyahoga River. *Scientific reports*, 6, 22908.

Finkelstein J, et al. (2016) Automated Summarization of Publications Associated with Adverse Drug Reactions from PubMed. *AMIA Joint Summits on Translational Science proceedings. AMIA Joint Summits on Translational Science*, 2016, 68.

Liu W, et al. (2015) OntoMate: a text-mining tool aiding curation at the Rat Genome Database. *Database : the journal of biological databases and curation*, 2015.

Kim SK, et al. (2015) TM-MC: a database of medicinal materials and chemical compounds in Northeast Asian traditional medicine. *BMC complementary and alternative medicine*, 15, 218.

McGarvey KM, et al. (2015) Mouse genome annotation by the RefSeq project. *Mammalian genome : official journal of the International Mammalian Genome Society*, 26(9-10), 379.

Cameron D, et al. (2015) Context-driven automatic subgraph creation for literature-based discovery. *Journal of biomedical informatics*, 54, 141.

Jimeno Yepes A, et al. (2014) Literature mining of genetic variants for curation: quantifying the importance of supplementary material. *Database : the journal of biological databases and curation*, 2014, bau003.

Zhang J, et al. (2014) Profiling animal toxicants by automatically mining public bioassay data: a big data approach for computational toxicology. *PloS one*, 9(6), e99863.

Tripathy SJ, et al. (2014) NeuroElectro: a window to the world's neuron electrophysiology data. *Frontiers in neuroinformatics*, 8, 40.

Ragusa M, et al. (2014) Highly skewed distribution of miRNAs and proteins between colorectal cancer cells and their exosomes following Cetuximab treatment: biomolecular, genetic and translational implications. *Oncoscience*, 1(2), 132.

Landrum MJ, et al. (2014) ClinVar: public archive of relationships among sequence variation and human phenotype. *Nucleic acids research*, 42(Database issue), D980.

Shamsaddini A, et al. (2014) Census-based rapid and accurate metagenome taxonomic profiling. *BMC genomics*, 15(1), 918.

Jimeno Yepes A, et al. (2014) Mutation extraction tools can be combined for robust recognition of genetic variants in the literature. *F1000Research*, 3, 18.

Wei CH, et al. (2013) PubTator: a web-based text mining tool for assisting biocuration. *Nucleic acids research*, 41(Web Server issue), W518.

Stoltzfus A, et al. (2013) Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. *BMC bioinformatics*, 14, 158.

Anguita A, et al. (2013) NCBI2RDF: enabling full RDF-based access to NCBI databases. *BioMed research international*, 2013, 983805.