

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

FACTA+.

RRID:SCR_001767

Type: Tool

Proper Citation

FACTA+. (RRID:SCR_001767)

Resource Information

URL: <http://www.nactem.ac.uk/facta/>

Proper Citation: FACTA+. (RRID:SCR_001767)

Description: Text mining tool to discover associations between biomedical concepts from MEDLINE articles. Use the service from your browser or via a Web Service. The whole MEDLINE corpus containing more than 20 million articles is indexed with an efficient text search engine, and it allows you to navigate such associations and their textual evidence in a highly interactive manner - the system accepts arbitrary query terms and displays relevant concepts immediately. A broad range of important biomedical concepts are covered by the combination of a machine learning-based term recognizer and large-scale dictionaries for genes, proteins, diseases, and chemical compounds. There is also a FACTA+ visualization service that can be found here: <http://www.nactem.ac.uk/facta-visualizer/>

Abbreviations: FACTA+

Synonyms: Finding Associated Concepts with Text Analysis

Resource Type: data access protocol, service resource, software resource, web service

Defining Citation: [PMID:18772154](#)

Keywords: text mining, gene, protein, disease, symptom, drug, enzyme, compound, biomedical, association, machine learning, chemical, text-mining software, bio.tools

Funding: JISC

Availability: Free, Freely available

Resource Name: FACTA+.

Resource ID: SCR_001767

Alternate IDs: biotools:facta_plus, nif-0000-10272, OMICS_01181

Alternate URLs: <http://refine1-nactem.mc.man.ac.uk/facta/>, https://bio.tools/facta_plus

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260905T132953+0000

Ratings and Alerts

No rating or validation information has been found for FACTA+..

No alerts have been found for FACTA+..

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Cierco Jimenez R, et al. (2022) Machine learning computational tools to assist the performance of systematic reviews: A mapping review. BMC medical research methodology, 22(1), 322.

Ananiadou S, et al. (2015) Event-based text mining for biology and functional genomics. Briefings in functional genomics, 14(3), 213.