

Resource Summary Report

Generated by SPARC SAWG on Aug 8, 2026

Whatizit

RRID:SCR_005824

Type: Tool

Proper Citation

Whatizit (RRID:SCR_005824)

Resource Information

URL: <http://www.ebi.ac.uk/webservices/whatizit/info.jsf>

Proper Citation: Whatizit (RRID:SCR_005824)

Description: A text processing system that allows you to do textmining tasks on text. It is great at identifying molecular biology terms and linking them to publicly available databases. Whatizit is also a Medline abstracts retrieval/search engine. Instead of providing the text by Copy&Paste, you can launch a Medline search. The abstracts that match your search criteria are retrieved and processed by a pipeline of your choice. Whatizit is also available as 1) a webservice and as 2) a streamed servlet. The webservice allows you to enrich content within your website in a similar way as in the wikipedia. The streamed servlet allows you to process large amounts of text.

Abbreviations: Whatizit

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

Keywords: textual analysis, protein, gene, gene ontology, text-mining, annotation, literature analysis

Availability: Free for academic use

Resource Name: Whatizit

Resource ID: SCR_005824

Alternate IDs: OMICS_01200, nlx_149329

Alternate URLs: <http://www.ebi.ac.uk/webservices/whatizit>

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260808T185838+0000

Ratings and Alerts

No rating or validation information has been found for Whatizit.

No alerts have been found for Whatizit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Cortolezzis Y, et al. (2025) Post-transcriptional control of KRAS: functional roles of 5'UTR RNA G-quadruplexes, long noncoding RNA, and hnRNPA1. Nucleic acids research, 53(17).

Althubaiti S, et al. (2020) Combining lexical and context features for automatic ontology extension. Journal of biomedical semantics, 11(1), 1.

Kafkas ?, et al. (2019) Ontology based text mining of gene-phenotype associations: application to candidate gene prediction. Database : the journal of biological databases and curation, 2019.

Venkatesan A, et al. (2016) SciLite: a platform for displaying text-mined annotations as a means to link research articles with biological data. Wellcome open research, 1, 25.

Kafkas ?, et al. (2015) Database citation in supplementary data linked to Europe PubMed Central full text biomedical articles. Journal of biomedical semantics, 6, 1.

Nim HT, et al. (2015) CARFMAP: A Curated Pathway Map of Cardiac Fibroblasts. PloS one, 10(12), e0143274.

Li C, et al. (2013) PCorral--interactive mining of protein interactions from MEDLINE. Database : the journal of biological databases and curation, 2013, bat030.

Kafkas ?, et al. (2013) Database citation in full text biomedical articles. PloS one, 8(5), e63184.