

# Resource Summary Report

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

## [Whatizit](#)

RRID:SCR\_005824

Type: Tool

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### Proper Citation

Whatizit (RRID:SCR\_005824)

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### 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:** analysis service resource, data access protocol, data analysis service, production service resource, service resource, software resource, web service

**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:** 20260905T132542+0000

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## Ratings and Alerts

No rating or validation information has been found for Whatizit.

No alerts have been found for Whatizit.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 8 mentions in open access literature.

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

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.