# **Resource Summary Report**

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# **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, analysis service resource, data analysis service, service resource, data access protocol, software resource

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

**Funding:** 

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:** 20250507T060333+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 7 mentions in open access literature.

**Listed below are recent publications.** The full list is available at <u>dkNET</u>.

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.

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

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