

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

Pathway Analysis Tool for Integration and Knowledge Acquisition

RRID:SCR_002100

Type: Tool

Proper Citation

Pathway Analysis Tool for Integration and Knowledge Acquisition (RRID:SCR_002100)

Resource Information

URL: <http://www.patika.org/>

Proper Citation: Pathway Analysis Tool for Integration and Knowledge Acquisition (RRID:SCR_002100)

Description: The human pathway database which contains different biological entities and reactions and software tools for analysis. PATIKA Database integrates data from several sources, including Entrez Gene, UniProt, PubChem, GO, IntAct, HPRD, and Reactome. Users can query and access this data using the PATIKAweb query interface. Users can also save their results in XML or export to common picture formats. The BioPAX and SBML exporters can be used as part of this Web service.

Abbreviations: PATIKA

Synonyms: Pathway Analysis Tool for Integration and Knowledge Acquisition (PATIKA), PATIKA - Pathway Analysis Tools for Integration and Knowledge Acquisition

Resource Type: data or information resource, database, pathway analysis software

Defining Citation: [PMID:12117798](#), [PMID:14960461](#)

Keywords: human, pathway, reaction, database, pathway analysis software, web service, biological entity, biological reaction

Availability: THIS RESOURCE IS NO LONGER IS SERVICE.

Resource Name: Pathway Analysis Tool for Integration and Knowledge Acquisition

Resource ID: SCR_002100

Alternate IDs: nif-0000-20882

Alternate URLs: <http://www.cs.bilkent.edu.tr/~patikaweb/>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260903T235749+0000

Ratings and Alerts

No rating or validation information has been found for Pathway Analysis Tool for Integration and Knowledge Acquisition.

No alerts have been found for Pathway Analysis Tool for Integration and Knowledge Acquisition.

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 [kravitz2](#) .

Cifuentes RA, et al. (2012) The autoimmune tautology: an in silico approach. Autoimmune diseases, 2012, 792106.

Dogrusoz U, et al. (2009) Algorithms for effective querying of compound graph-based pathway databases. BMC bioinformatics, 10, 376.