

Resource Summary Report

Generated by [NIF](#) on Aug 8, 2026

Expression Profiler

RRID:SCR_005821

Type: Tool

Proper Citation

Expression Profiler (RRID:SCR_005821)

Resource Information

URL: <http://www.ebi.ac.uk/expressionprofiler/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented September 2, 2016. The EP:GO browser is built into EBI's Expression Profiler, a set of tools for clustering, analysis and visualization of gene expression and other genomic data. With it, you can search for GO terms and identify gene associations for a node, with or without associated subnodes, for the organism of your choice.

Abbreviations: Expression Profiler

Synonyms: Expression Profiler at the EBI

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:15215431](#)

Keywords: other analysis, cluster, analysis, visualization, gene expression, genomic, gene ontology, gene association, microarray, protein-protein interaction, gene, bio.tools

Funding: European Union ;
Wellcome Trust ;
Estonian Science Foundation 5724;
Estonian Science Foundation 5722

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Expression Profiler

Resource ID: SCR_005821

Alternate IDs: biotools:expression_profiler, nlx_149323

Alternate URLs: https://bio.tools/expression_profiler

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260808T190405+0000

Ratings and Alerts

No rating or validation information has been found for Expression Profiler.

No alerts have been found for Expression Profiler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Pavlopoulos GA, et al. (2015) Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. GigaScience, 4, 38.

Liang XD, et al. (2014) Expression and function analysis of mitotic checkpoint genes identifies TTK as a potential therapeutic target for human hepatocellular carcinoma. PloS one, 9(6), e97739.

InanlooRahatloo K, et al. (2014) Mutation in ST6GALNAC5 identified in family with coronary artery disease. Scientific reports, 4, 3595.

Dezfulian MH, et al. (2012) The SKP1-like gene family of Arabidopsis exhibits a high degree of differential gene expression and gene product interaction during development. PloS one, 7(11), e50984.

Fox JA, et al. (2005) The Bioinformatics Links Directory: a compilation of molecular biology web servers. Nucleic acids research, 33(Web Server issue), W3.

Glatt CM, et al. (2005) Molecular characterization of thyroid toxicity: anchoring gene expression profiles to biochemical and pathologic end points. Environmental health perspectives, 113(10), 1354.