

Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

ProfCom - Profiling of complex functionality

RRID:SCR_005797

Type: Tool

Proper Citation

ProfCom - Profiling of complex functionality (RRID:SCR_005797)

Resource Information

URL: <http://webclu.bio.wzw.tum.de/profcom/>

Proper Citation: ProfCom - Profiling of complex functionality (RRID:SCR_005797)

Description: Profiling of Complex Functionality (ProfCom) is a web-based tool for the functional interpretation of a gene list that was identified to be related by experiments. A trait which makes ProfCom a unique tool is an ability to profile enrichments of not only available Gene Ontology (GO) terms but also of complex function. A complex function is constructed as Boolean combination of available GO terms. The complex functions inferred by ProfCom are more specific in comparison to single terms and describe more accurately the functional role of genes. Platform: Online tool

Abbreviations: ProfCom

Synonyms: Profiling of Complex Functionality, Profiling of Complex Functionality (ProfCom)

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

Defining Citation: [PMID:16959266](#)

Keywords: gene, function, profile, gene ontology, complex function, statistical analysis, bio.tools

Funding: DFG

Availability: Free for academic use

Resource Name: ProfCom - Profiling of complex functionality

Resource ID: SCR_005797

Alternate IDs: biotools:profcom, nlx_149276

Alternate URLs: <https://bio.tools/profcom>

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260821T193738+0000

Ratings and Alerts

No rating or validation information has been found for ProfCom - Profiling of complex functionality.

No alerts have been found for ProfCom - Profiling of complex functionality.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Schleussner CF, et al. (2016) Clustered marginalization of minorities during social transitions induced by co-evolution of behaviour and network structure. Scientific reports, 6, 30790.

Cartwright R, et al. (2015) Systematic review and metaanalysis of genetic association studies of urinary symptoms and prolapse in women. American journal of obstetrics and gynecology, 212(2), 199.e1.

Darvishi E, et al. (2013) The antifungal eugenol perturbs dual aromatic and branched-chain amino acid permeases in the cytoplasmic membrane of yeast. PloS one, 8(10), e76028.

Ellis J, et al. (2010) Microarray analyses of mouse responses to infection by Neospora caninum identifies disease associated cellular pathways in the host response. Molecular and biochemical parasitology, 174(2), 117.