

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## FunSimMat

RRID:SCR\_002729

Type: Tool

### Proper Citation

FunSimMat (RRID:SCR\_002729)

### Resource Information

**URL:** <http://funsimmat.bioinf.mpi-inf.mpg.de>

**Proper Citation:** FunSimMat (RRID:SCR\_002729)

**Description:** FunSimMat is a comprehensive resource of semantic and functional similarity values. It allows ranking disease candidate proteins for OMIM diseases and searching for functional similarity values for proteins (extracted from UniProt), and protein families (Pfam, SMART). FunSimMat provides several different semantic and functional similarity measures for each protein pair using the Gene Ontology annotation from UniProtKB and the Gene Ontology Annotation project at EBI (GOA). There are several search options available: Disease candidate prioritization: \* Rank candidate proteins using any OMIM disease entry \* Compare a list of proteins to any OMIM disease entry \* Compare all human proteins to any OMIM disease entry Functional similarity: \* Compare one protein / protein family to a list of proteins / protein families \* Compare a list of GO terms to a list of proteins / protein families Semantic similarity: \* For a list of GO terms, FunSimMat performs an all-against-all comparison and displays the semantic similarity values. FunSimMat provides an XML-RPC interface for performing automatic queries and processing of the results as well as a RestLike Interface. Platform: Online tool

**Abbreviations:** FunSimMat

**Synonyms:** FunSimMat - Functional Similarity Matrix

**Resource Type:** service resource, data analysis service, database, web service, analysis service resource, software resource, production service resource, data access protocol, data or information resource

**Defining Citation:** [PMID:19923227](#), [PMID:17932054](#)

**Keywords:** functional similarity value, protein family, protein similarity, semantic similarity value, similarity value, functional similarity, disease gene candidate prioritization, disease, protein, protein family, disease candidate prioritization, semantic similarity, gene ontology, visualization, annotation, database or data warehouse

**Funding:** German National Genome Research Network 01GR0453;  
Klinische Forschergruppe KFO 129/1-1;  
Klinische Forschergruppe KFO 129/1-2;  
European Union LSHG-CT-2003-503265

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** FunSimMat

**Resource ID:** SCR\_002729

**Alternate IDs:** nif-0000-02860

**Record Creation Time:** 20220129T080215+0000

**Record Last Update:** 20260728T043133+0000

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## Ratings and Alerts

No rating or validation information has been found for FunSimMat.

No alerts have been found for FunSimMat.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Dohrmann J, et al. (2015) Global multiple protein-protein interaction network alignment by combining pairwise network alignments. BMC bioinformatics, 16 Suppl 13(Suppl 13), S11.