

Resource Summary Report

Generated by SPARC SAWG on Aug 8, 2026

GOChase

RRID:SCR_005822

Type: Tool

Proper Citation

GOChase (RRID:SCR_005822)

Resource Information

URL: <http://www.snubi.org/software/GOChase/>

Proper Citation: GOChase (RRID:SCR_005822)

Description: GOChase is a set of web-based utilities to detect and correct the errors in GO-based annotations. # GOChase-History resolves the whole modification history of GO IDs. # GOChase-Correct highlights merged GO IDs and redirects to the correct primary term into which the secondary ID was merged. For obsolete GO terms, the nearest non-discarded parent term is recommended by GOChase. This function may be used by GO browsers such as AmiGO and QuickGO to fix broken hyperlinks. # A whole database (such as LocusLink) as a flat file can be loaded into GOChase, reporting the annotation errors and GOChase corrections. # When one inputs a GO ID, GOChase will resolve all gene products annotated with the GO ID across all the major databases. Platform: Online tool

Abbreviations: GOChase

Synonyms: GOChase: correcting errors from gene ontology-based annotations for gene products

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

Defining Citation: [PMID:15513987](#)

Keywords: other analysis, historical views of go, gene ontology, annotation

Funding: Ministry of Health and Welfare - Republic of Korea 0405-BC0206040004

Availability: Free for academic use

Resource Name: GOChase

Resource ID: SCR_005822

Alternate IDs: nlx_149324

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260808T190355+0000

Ratings and Alerts

No rating or validation information has been found for GOChase.

No alerts have been found for GOChase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Park YR, et al. (2011) GOChase-II: correcting semantic inconsistencies from Gene Ontology-based annotations for gene products. BMC bioinformatics, 12 Suppl 1(Suppl 1), S40.