

Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

golang

RRID:SCR_017096

Type: Tool

Proper Citation

golang (RRID:SCR_017096)

Resource Information

URL: <https://golang.org/>

Proper Citation: golang (RRID:SCR_017096)

Description: Software tool as open source programming language to build simple, reliable, and efficient software. Developed by team at Google and many contributors from open source community.

Abbreviations: GO

Synonyms: The Go Programming Language, GO programming language

Resource Type: programming language, software resource

Keywords: programming, language

Availability: Free, Available for download, Freely available

Resource Name: golang

Resource ID: SCR_017096

License: BSD

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260919T195815+0000

Ratings and Alerts

No rating or validation information has been found for golang.

No alerts have been found for golang.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Diener C, et al. (2024) Metagenomic estimation of dietary intake from human stool. bioRxiv : the preprint server for biology.

Chapron K, et al. (2022) LIPSHOK: LIARA Portable Smart Home Kit. Sensors (Basel, Switzerland), 22(8).

Déraspe M, et al. (2022) Flexible protein database based on amino acid k-mers. Scientific reports, 12(1), 9101.

Dieckmann MA, et al. (2021) EDGAR3.0: comparative genomics and phylogenomics on a scalable infrastructure. Nucleic acids research, 49(W1), W185.

Lemoine F, et al. (2021) Gotree/Goalign: toolkit and Go API to facilitate the development of phylogenetic workflows. NAR genomics and bioinformatics, 3(3), lqab075.

Chen B, et al. (2021) Processing single-cell RNA-seq data for dimension reduction-based analyses using open-source tools. STAR protocols, 2(2), 100450.

Wang A, et al. (2020) Single-cell multiomic profiling of human lungs reveals cell-type-specific and age-dynamic control of SARS-CoV2 host genes. eLife, 9.

Wilkey AP, et al. (2020) GCViT: a method for interactive, genome-wide visualization of resequencing and SNP array data. BMC genomics, 21(1), 822.

Zhou H, et al. (2020) Decreased secretoglobin family 2A member 1 expression is associated with poor outcomes in endometrial cancer. Oncology letters, 20(4), 24.

Pont F, et al. (2019) Single-Cell Signature Explorer for comprehensive visualization of single cell signatures across scRNA-seq datasets. Nucleic acids research, 47(21), e133.

Léger S, et al. (2019) Pairwise visual comparison of small RNA secondary structures with base pair probabilities. BMC bioinformatics, 20(1), 293.

Yang X, et al. (2019) Alignment-free filtering for cfNA fusion fragments. Bioinformatics (Oxford, England), 35(14), i225.

Wang K, et al. (2019) MFEprimer-3.0: quality control for PCR primers. Nucleic acids research, 47(W1), W610.