

Resource Summary Report

Generated by T1D on Aug 1, 2026

GOanna

RRID:SCR_005684

Type: Tool

Proper Citation

GOanna (RRID:SCR_005684)

Resource Information

URL: <http://www.agbase.msstate.edu/cgi-bin/tools/GOanna.cgi>

Proper Citation: GOanna (RRID:SCR_005684)

Description: GOanna is used to find annotations for proteins using a similarity search. The input can be a list of IDs or it can be a list of sequences in FASTA format. GOanna will retrieve the sequences if necessary and conduct the specified BLAST search against a user-specified database of GO annotated proteins. The resulting file contains GO annotations of the top BLAST hits. The sequence alignments are also provided so the user can use these to access the quality of the match. Platform: Online tool

Abbreviations: GOanna

Synonyms: AgBase GOanna

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

Defining Citation: [PMID:17135208](#), [PMID:16961921](#)

Keywords: agriculture, annotation, protein, ontology or annotation search engine, ontology or annotation editor

Funding: USDA ;
Mississippi State University; Mississippi; USA ;
MSU Office of Research ;
MSU Bagley College of Engineering ;
MSU College of College of Veterinary Medicine ;
MSU Life Science and Biotechnology Institute

Availability: Free for academic use

Resource Name: GOanna

Resource ID: SCR_005684

Alternate IDs: nlx_149139

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260801T042601+0000

Ratings and Alerts

No rating or validation information has been found for GOanna.

No alerts have been found for GOanna.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Coates BS, et al. (2023) A draft *Diabrotica virgifera virgifera* genome: insights into control and host plant adaption by a major maize pest insect. *BMC genomics*, 24(1), 19.

Saha S, et al. (2021) Workflows for Rapid Functional Annotation of Diverse Arthropod Genomes. *Insects*, 12(8).

Silva LCF, et al. (2020) Physicochemical characterization of *Pseudomonas stutzeri* UFV5 and analysis of its transcriptome under heterotrophic nitrification/aerobic denitrification pathway induction condition. *Scientific reports*, 10(1), 2215.

Goutham S, et al. (2020) Mutually exclusive locales for N-linked glycans and disorder in human glycoproteins. *Scientific reports*, 10(1), 6040.

Jin X, et al. (2019) An improved protein extraction method applied to cotton leaves is compatible with 2-DE and LC-MS. *BMC genomics*, 20(1), 285.

Zhang Y, et al. (2019) Identification and Functional Analysis of Tomato CIPK Gene Family. *International journal of molecular sciences*, 21(1).

Núñez-Acuña G, et al. (2019) Characterization of the salmon louse *Lepeophtheirus salmonis* miRNome: Sex-biased differences related to the coding and non-coding RNA interplay. *Marine genomics*, 45, 38.

Bitar M, et al. (2019) Genes with human-specific features are primarily involved with brain, immune and metabolic evolution. *BMC bioinformatics*, 20(Suppl 9), 406.

J?kalski M, et al. (2016) Comparative genomic analysis of retrogene repertoire in two green algae *Volvox carteri* and *Chlamydomonas reinhardtii*. *Biology direct*, 11, 35.

Zhang Z, et al. (2016) Transcriptome analyses provide insights into the phylogeny and adaptive evolution of the mangrove fern genus *Acrostichum*. *Scientific reports*, 6, 35634.

Wen M, et al. (2016) Small RNA transcriptomes of mangroves evolve adaptively in extreme environments. *Scientific reports*, 6, 27551.

Johnson SL, et al. (2014) Proteomic analysis of chinook salmon (*Oncorhynchus tshawytscha*) ovarian fluid. *PloS one*, 9(8), e104155.

Sun J, et al. (2014) Comparative proteome analysis of tracheal tissues in response to infectious bronchitis coronavirus, Newcastle disease virus, and avian influenza virus H9 subtype virus infection. *Proteomics*, 14(11), 1403.

Guillén G, et al. (2013) Detailed analysis of putative genes encoding small proteins in legume genomes. *Frontiers in plant science*, 4, 208.

Martyniuk CJ, et al. (2013) Proteome analysis of the fathead minnow (*Pimephales promelas*) reproductive testes. *Journal of proteomics*, 79, 28.

Rebello KM, et al. (2011) Comprehensive proteomic profiling of adult *Angiostrongylus costaricensis*, a human parasitic nematode. *Journal of proteomics*, 74(9), 1545.

Thanthrige-Don N, et al. (2009) Analyses of the spleen proteome of chickens infected with Marek's disease virus. *Virology*, 390(2), 356.