

# Resource Summary Report

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## GOA

RRID:SCR\_007691

Type: Tool

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### Proper Citation

GOA (RRID:SCR\_007691)

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### Resource Information

**URL:** <http://www.ebi.ac.uk/GOA>

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**Description:** An annotation program which aims to provide high-quality Gene Ontology (GO) annotations to proteins in the UniProt Knowledgebase (UniProtKB) and International Protein Index (IPI). It is a central dataset for other major multi-species databases, such as Ensembl and NCBI. Because of the multi-species nature of the UniProtKB, UniProtKB-GOA assists in the curation of 200,000 species. This involves electronic annotation and the integration of high-quality manual GO annotation from all GO Consortium model organism groups and specialist groups. Gene Association Files can be accessed from the Downloads section of the website.

**Abbreviations:** GOA, GOA REF

**Synonyms:** UniProtKB-GOA, Gene Ontology Annotation (UniProtKB-GOA) Database, GOA - Gene Ontology Annotation, Gene Ontology Annotation, GO Annotation at EBI

**Resource Type:** data or information resource, database

**Keywords:** gene ontology, chicken proteome, cow proteome, human proteome, xref, gene, gene association, gold standard

**Availability:** Public, Available to the research community, All UniProtKB-GOA Gene Association Files are released approximately every four weeks

**Resource Name:** GOA

**Resource ID:** SCR\_007691

**Alternate IDs:** nif-0000-02916

**License URLs:** <http://www.ebi.ac.uk/about/terms-of-use>

**Record Creation Time:** 20220129T080243+0000

**Record Last Update:** 20260729T044210+0000

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## Ratings and Alerts

No rating or validation information has been found for GOA.

No alerts have been found for GOA.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 570 mentions in open access literature.

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

Ma L, et al. (2025) Differential expression of tRNA-derived small RNAs in Juvenile and adult sheep skin: implications for developmental and immune regulation. BMC genomics, 26(1), 144.

Tian L, et al. (2025) Proteomics of stress-induced cardiomyopathy: insights from differential expression, protein interaction networks, and functional pathway enrichment in an isoproterenol-induced TTC mouse model. PeerJ, 13, e18984.

Wang S, et al. (2025) Semaglutide and adenosine alleviate obesity-induced kidney injury, with observed modulation of the Txnip/NLRP3 pathway. Diabetology & metabolic syndrome, 17(1), 164.

Dong C, et al. (2025) CHAC1 Mediates Endoplasmic Reticulum Stress-Dependent Ferroptosis in Calcium Oxalate Kidney Stone Formation. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(10), e2403992.

Xiong T, et al. (2025) BDH1 acetylation at K116 modulates milk fat production in dairy goats. Journal of animal science and biotechnology, 16(1), 177.

Wang Z, et al. (2025) Brucella suis S2 strain inhibits IRE1/caspase-12/caspase-3 pathway-mediated apoptosis of microglia HMC3 by affecting the ubiquitination of CALR. mSphere, 10(3), e0094124.

Yu Y, et al. (2025) Global analysis of protein lysine lactylation profiles in the marine bacterium Photobacterium damsela subsp. damsela. Frontiers in microbiology, 16, 1539893.

Alami NH, et al. (2025) Functional and genomic characterization of polyethylene degrading yeast Meyerozyma carpophila M6.0.2 isolated from marine plastic debris in East Java Indonesia. Scientific reports, 15(1), 40437.

Meng X, et al. (2025) Comprehensive analysis of the succinylome in Vero cells infected with peste des petits ruminants virus Nigeria 75/1 vaccine strain. BMC veterinary research, 21(1), 45.

Schmidt JH, et al. (2025) Membrane curvature association of amphipathic helix 8 drives constitutive endocytosis of GPCRs. Science advances, 11(33), eadv1499.

Zhang Y, et al. (2025) Streptococcus mutans regulates ubiquitin modification of Candida albicans in the bacterial-fungal interaction. PLoS pathogens, 21(2), e1012887.

Wang L, et al. (2025) Serpina3k lactylation protects from cardiac ischemia reperfusion injury. Nature communications, 16(1), 1012.

Li N, et al. (2025) Secretome and Transcriptome Analyses Reveal New Potential Virulence Factors during Cryptosporidium parvum Invasion. Journal of proteome research, 24(11), 5830.

Adim H, et al. (2025) iTRAQ-based quantitative proteomic analysis of herbicide stress in Avena ludoviciana Durieu. Scientific reports, 15(1), 577.

Huo J, et al. (2025) Transcriptome and metabolome analysis of senescent rice (Oryza sativa L.) seeds: insights into the mechanism of germination vigor and seedling morphogenesis. BMC plant biology, 25(1), 591.

Wang S, et al. (2025) Protective Effect of Semaglutide on Obesity-Induced Renal Disease and Obesity-Induced Kidney Renal Clear Cell Carcinoma. Diabetes, metabolic syndrome and obesity : targets and therapy, 18, 805.

Han W, et al. (2025) Ketogenic  $\gamma$ -hydroxybutyrate regulates  $\gamma$ -hydroxybutyrylation of TCA cycle-associated enzymes and attenuates disease-associated pathologies in Alzheimer's mice. Aging cell, 24(1), e14368.

Zhang CL, et al. (2025) CD147-high extracellular vesicles promote gastric cancer metastasis via VEGF/AKT/eNOS and AKT/mTOR pathways. Oncogenesis, 14(1), 21.

Huang Y, et al. (2025) Comprehensive profiling of lysine lactylation in Candida albicans and exploratory analysis of fluconazole tolerance associations. Microbiology spectrum, 13(11), e0081025.

Sun H, et al. (2025) Identification of fecal microbes as potential biomarkers for early diagnosis of fatty liver disease in cattle. Virulence, 16(1), 2530166.