

# Resource Summary Report

Generated by [NIF](#) on Aug 14, 2026

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## Functional Annotation

RRID:SCR\_017519

Type: Tool

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### Proper Citation

Functional Annotation (RRID:SCR\_017519)

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### Resource Information

**URL:** <http://www.informatics.jax.org/function.shtml>

**Proper Citation:** Functional Annotation (RRID:SCR\_017519)

**Description:** MGI GO project provides functional annotations for mouse gene products using Gene Ontology. Functional annotation using Gene Ontology (GO).

**Resource Type:** service resource

**Keywords:** MGI, GO, functional, annotation, mouse, gene, product, Gene Ontology

**Availability:** Free, Freely available

**Resource Name:** Functional Annotation

**Resource ID:** SCR\_017519

**Record Creation Time:** 20220129T080335+0000

**Record Last Update:** 20260808T190052+0000

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### Ratings and Alerts

No rating or validation information has been found for Functional Annotation.

No alerts have been found for Functional Annotation.

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### Data and Source Information

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

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### Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Dimond A, et al. (2025) PBK/TOPK mediates Ikaros, Aiolos and CTCF displacement from mitotic chromosomes and alters chromatin accessibility at selected C2H2-zinc finger protein binding sites. Nature communications, 16(1), 8348.

Bujanover N, et al. (2021) Hypersensitivity response has negligible impact on Hematopoietic Stem Cells. Stem cell reports, 16(8), 1884.

Sanavia T, et al. (2021) Temporal Transcriptome Analysis Reveals Dynamic Gene Expression Patterns Driving ??-Cell Maturation. Frontiers in cell and developmental biology, 9, 648791.

Lu T, et al. (2020) Investigating transcriptome-wide sex dimorphism by multi-level analysis of single-cell RNA sequencing data in ten mouse cell types. Biology of sex differences, 11(1), 61.