

# Resource Summary Report

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## Gene Reference into Function

RRID:SCR\_003436

Type: Tool

### Proper Citation

Gene Reference into Function (RRID:SCR\_003436)

### Resource Information

**URL:** <http://www.ncbi.nlm.nih.gov/gene/about-generif>

**Proper Citation:** Gene Reference into Function (RRID:SCR\_003436)

**Description:** A database and annotation tool that provides a simple mechanism to allow scientists to add to the functional annotation of genes described in Gene. To be processed, a valid Gene ID must exist for the specific gene, or the Gene staff must have assigned an overall Gene ID to the species. The latter case is implemented via records in Gene with the symbol NEWENTRY.

**Abbreviations:** GeneRIF

**Synonyms:** GeneRIF: Gene Reference into Function

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

**Defining Citation:** [PMID:17094227](#), [PMID:23725347](#)

**Keywords:** functional annotation, gene, function

**Funding:** NIH

**Availability:** The community can contribute to this resource

**Resource Name:** Gene Reference into Function

**Resource ID:** SCR\_003436

**Alternate IDs:** nlx\_157765

**Record Creation Time:** 20220129T080219+0000

**Record Last Update:** 20250424T064623+0000

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## Ratings and Alerts

No rating or validation information has been found for Gene Reference into Function.

No alerts have been found for Gene Reference into Function.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Huang R, et al. (2019) The NCATS BioPlanet - An Integrated Platform for Exploring the Universe of Cellular Signaling Pathways for Toxicology, Systems Biology, and Chemical Genomics. *Frontiers in pharmacology*, 10, 445.

Xuan P, et al. (2019) Graph Convolutional Network and Convolutional Neural Network Based Method for Predicting lncRNA-Disease Associations. *Cells*, 8(9).

Hu Y, et al. (2017) Measuring disease similarity and predicting disease-related ncRNAs by a novel method. *BMC medical genomics*, 10(Suppl 5), 71.

Carson MB, et al. (2017) A disease similarity matrix based on the uniqueness of shared genes. *BMC medical genomics*, 10(Suppl 1), 26.

Hu Y, et al. (2016) Annotating the Function of the Human Genome with Gene Ontology and Disease Ontology. *BioMed research international*, 2016, 4130861.

Venkatesan A, et al. (2016) SciLite: a platform for displaying text-mined annotations as a means to link research articles with biological data. *Wellcome open research*, 1, 25.

Sparrow S, et al. (2016) Epigenomic profiling of preterm infants reveals DNA methylation differences at sites associated with neural function. *Translational psychiatry*, 6(1), e716.

Cheng L, et al. (2016) OAHG: an integrated resource for annotating human genes with multi-level ontologies. *Scientific reports*, 6, 34820.

Huan T, et al. (2015) Integrative network analysis reveals molecular mechanisms of blood

pressure regulation. *Molecular systems biology*, 11(1), 799.

Carson MB, et al. (2015) Network-based prediction and knowledge mining of disease genes. *BMC medical genomics*, 8 Suppl 2(Suppl 2), S9.

Pletscher-Frankild S, et al. (2015) DISEASES: text mining and data integration of disease-gene associations. *Methods (San Diego, Calif.)*, 74, 83.

Dobson JR, et al. (2014) hsa-mir-30c promotes the invasive phenotype of metastatic breast cancer cells by targeting NOV/CCN3. *Cancer cell international*, 14, 73.

Gobeill J, et al. (2014) Closing the loop: from paper to protein annotation using supervised Gene Ontology classification. *Database : the journal of biological databases and curation*, 2014.

Wang V, et al. (2013) GeneTopics--interpretation of gene sets via literature-driven topic models. *BMC systems biology*, 7 Suppl 5(Suppl 5), S10.