# **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

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**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:** database, data or information resource

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:** 20250503T055620+0000

## 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.

#### Data and Source Information

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 14 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

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 IncRNA-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.

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

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.

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.