Resource Summary Report

Generated by Kravitz on Sep 10, 2026

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: data or information resource, database

Defining Citation: PMID:17094227, PMID:23725347

Keywords: functional annotation, gene, function

Funding: NIH

Availability: Free, Freely available

Resource Name: Gene Reference into Function

Resource ID: SCR_003436

Alternate IDs: nlx_157765

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260905T133121+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 Kravitz .

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

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.

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.

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.

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

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.