

Resource Summary Report

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FunDO

RRID:SCR_001725

Type: Tool

Proper Citation

FunDO (RRID:SCR_001725)

Resource Information

URL: <http://django.nubic.northwestern.edu/fundo/>

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Description: Tool that takes a list of genes and finds relevant diseases based on statistical analysis of the Disease Ontology annotation database. It accepts Entrez gene ids or gene symbols, separated by tabs, newlines, or commas. This list of genes can be obtained by microarray, proteomics, sequencing or other high-throughput screening methods.

Abbreviations: FunDO

Synonyms: FunDO - Exploring Genes Using Functional Disease Ontology Annotations

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Keywords: gene, disease, ontology, function

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: FunDO

Resource ID: SCR_001725

Alternate IDs: nif-0000-10225

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260821T042528+0000

Ratings and Alerts

No rating or validation information has been found for FunDO.

No alerts have been found for FunDO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Martinez ME, et al. (2022) DIO3 protects against thyrotoxicosis-derived cranio-encephalic and cardiac congenital abnormalities. JCI insight, 7(21).

Martinez ME, et al. (2020) Thyroid hormone influences brain gene expression programs and behaviors in later generations by altering germ line epigenetic information. Molecular psychiatry, 25(5), 939.

Ling B, et al. (2019) Probing the Antitumor Mechanism of Solanum nigrum L. Aqueous Extract against Human Breast Cancer MCF7 Cells. Bioengineering (Basel, Switzerland), 6(4).

Ghatge M, et al. (2018) Integrative gene ontology and network analysis of coronary artery disease associated genes suggests potential role of ErbB pathway gene EGFR. Molecular medicine reports, 17(3), 4253.

Tayeh Z, et al. (2018) Molecular Mode of Action of Asteriscus graveolens as an Anticancer Agent. International journal of molecular sciences, 19(8).

Sakai A, et al. (2017) Genome-Wide Target Analyses of Otx2 Homeoprotein in Postnatal Cortex. Frontiers in neuroscience, 11, 307.

Jurca G, et al. (2016) Integrating text mining, data mining, and network analysis for identifying genetic breast cancer trends. BMC research notes, 9, 236.

Yu L, et al. (2015) Inferring drug-disease associations based on known protein complexes. BMC medical genomics, 8 Suppl 2(Suppl 2), S2.

Roy S, et al. (2015) Systematic Analysis of Integrated Gene Functional Network of Four Chronic Stress-related Lifestyle Disorders. Genome integrity, 6, 1.

Li X, et al. (2013) N-glycoproteome analysis of the secretome of human metastatic hepatocellular carcinoma cell lines combining hydrazide chemistry, HILIC enrichment and mass spectrometry. PloS one, 8(12), e81921.

Sarajli?? A, et al. (2013) Network topology reveals key cardiovascular disease genes. PloS one, 8(8), e71537.