

Resource Summary Report

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MfunGD - MIPS Mouse Functional Genome Database

RRID:SCR_007783

Type: Tool

Proper Citation

MfunGD - MIPS Mouse Functional Genome Database (RRID:SCR_007783)

Resource Information

URL: <http://mips.gsf.de/genre/proj/mfungd>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 16, 2019. Database for annotated mouse proteins and their occurrence in protein networks. It contains cDNA and protein sequences, annotation, gene models and mapping, FunCat, UCSC Genome Viewer, SIMAP, pseudogenes (Genome Viewer Track), InterPro, and splice variants. Protein function annotation is performed using the Functional Catalogue (FunCat) annotation scheme, which is a hierarchically structured classification system. To provide up-to-date similarity search results and InterPro domain analyses, the protein entries are interconnected with the SIMAP database. The gene models are based on the RefSeq mouse cDNAs. The work of our group is focussed on the annotation of biological systems. Therefore, results from the Mammalian Protein-Protein Interaction Database and the Comprehensive Resource of Mammalian Protein Complexes are linked to the MfunGD dataset. Links to external resources are also provided. MfunGD is implemented in GenRE, a J2EE based component oriented multi-tier architecture.

Abbreviations: MfunGD

Synonyms: Mouse Functional Genome Database

Resource Type: data or information resource, database

Defining Citation: [PMID:16381934](#)

Keywords: bio.tools

Funding: GSF National Research Center for Environment and Health ; German Federal Ministry of Research and Education

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MfunGD - MIPS Mouse Functional Genome Database

Resource ID: SCR_007783

Alternate IDs: nif-0000-03121, biotools:mfungd

Alternate URLs: <https://bio.tools/mfungd>

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260729T044213+0000

Ratings and Alerts

No rating or validation information has been found for MfunGD - MIPS Mouse Functional Genome Database.

No alerts have been found for MfunGD - MIPS Mouse Functional Genome Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 89 mentions in open access literature.

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

Huang G, et al. (2016) Exploring Mouse Protein Function via Multiple Approaches. PloS one, 11(11), e0166580.

Zhang K, et al. (2014) Comparative proteomic analyses provide new insights into low phosphorus stress responses in maize leaves. PloS one, 9(5), e98215.

da Silva Neto BR, et al. (2014) Transcriptional profile of *Paracoccidioides* spp. in response to itraconazole. BMC genomics, 15, 254.

Hu WJ, et al. (2014) Comparative proteomic analysis of differential responses of *Pinus massoniana* and *Taxus wallichiana* var. *mairei* to simulated acid rain. International journal of molecular sciences, 15(3), 4333.

Liu T, et al. (2014) A combined proteomic and transcriptomic analysis on sulfur metabolism pathways of *Arabidopsis thaliana* under simulated acid rain. PloS one, 9(3), e90120.

Quesada V, et al. (2013) PORPHOBILINOGEN DEAMINASE deficiency alters vegetative and reproductive development and causes lesions in *Arabidopsis*. PloS one, 8(1), e53378.

Bian Y, et al. (2013) Global screening of CK2 kinase substrates by an integrated phosphoproteomics workflow. Scientific reports, 3, 3460.

Pierce EJ, et al. (2013) Assessing Global Transcriptome Changes in Response to South African Cassava Mosaic Virus [ZA-99] Infection in Susceptible *Arabidopsis thaliana*. PloS one, 8(6), e67534.

Han HW, et al. (2013) Yin and Yang of disease genes and death genes between reciprocally scale-free biological networks. Nucleic acids research, 41(20), 9209.

Zhao YH, et al. (2013) Developmental genetics of the perianthless flowers and bracts of a paleoherb species, *Saururus chinensis*. PloS one, 8(1), e53019.

Yu WB, et al. (2012) Prediction of the mechanism of action of fusaricidin on *Bacillus subtilis*. PloS one, 7(11), e50003.

Jansk?? A, et al. (2011) Transcriptional responses of winter barley to cold indicate nucleosome remodelling as a specific feature of crown tissues. Functional & integrative genomics, 11(2), 307.

Kim ED, et al. (2011) Unstable transcripts in *Arabidopsis* allotetraploids are associated with nonadditive gene expression in response to abiotic and biotic stresses. PloS one, 6(8), e24251.

Siebers B, et al. (2011) The complete genome sequence of *Thermoproteus tenax*: a physiologically versatile member of the Crenarchaeota. PloS one, 6(10), e24222.

Ahmed KS, et al. (2011) Improving the prediction of yeast protein function using weighted protein-protein interactions. Theoretical biology & medical modelling, 8, 11.

D'Addabbo P, et al. (2011) Position and sequence conservation in Amniota of polymorphic enhancer HS1.2 within the palindrome of IgH 3'Regulatory Region. BMC evolutionary biology, 11, 71.

Huang H, et al. (2011) Mining and validating grape (*Vitis L.*) ESTs to develop EST-SSR markers for genotyping and mapping. Molecular breeding : new strategies in plant improvement, 28(2), 241.

Rhrissorrakrai K, et al. (2011) MINE: Module Identification in Networks. BMC bioinformatics, 12, 192.

Yu WB, et al. (2011) Comparative transcriptome analysis of *Bacillus subtilis* responding to dissolved oxygen in adenosine fermentation. PloS one, 6(5), e20092.

Medema MH, et al. (2010) The sequence of a 1.8-mb bacterial linear plasmid reveals a rich evolutionary reservoir of secondary metabolic pathways. Genome biology and evolution, 2, 212.