

Resource Summary Report

Generated by [dkNET](#) on Sep 4, 2026

MIPS FunCat

RRID:SCR_008709

Type: Tool

Proper Citation

MIPS FunCat (RRID:SCR_008709)

Resource Information

URL: <http://mips.helmholtz-muenchen.de/funcatDB/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on August 19, 2019. The Functional Catalogue is an annotation scheme for the functional description of proteins of prokaryotic and eukaryotic origin. Taking into account the broad and highly diverse spectrum of known protein functions, the FunCat consists of 28 main functional categories (or branches) that cover general fields like cellular transport, metabolism and cellular communication/signal transduction. The main branches exhibit a hierarchical, tree like structure with up to six levels of increasing specificity. In total, the FunCat version 2.1 includes 1362 functional categories. This general concept was retained since the annotation of the *Saccharomyces cerevisiae* genome with only 4 revisions and later on also proved to be well suited for the annotation of genomes from different domains of life (Ruepp et al. 2004). The present and previous versions as well as a version mapping file of the FunCat and annotation data of our core projects can be downloaded via FTP. The MIPS Functional Catalogue Database provides a search tool to browse and search the Functional Categories including the FunCat Number, description, EC number, GO number or keywords associated with the categories. All FunCat annotated proteins and the amount of Co-annotated-FunCats can be retrieved starting with a specific category in a selected organism. A statistical survey of the functional distribution of a given set of genes/entries, e. g. a set of genes with up-regulated expression under a certain condition can be retrieved.

Abbreviations: MIPS FunCat

Synonyms: FunCat, FunCatDB, Functional Catalogue, MIPS Functional Catalogue

Resource Type: data or information resource, database

Defining Citation: [PMID:15486203](#)

Funding: BMBF ;
European Union BFAM 031U112C;
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European Union Eu-Framework 5 QLRI-CT1999-01333

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MIPS FunCat

Resource ID: SCR_008709

Alternate IDs: nlx_11495

Old URLs: <http://mips.helmholtz-muenchen.de/proj/funcatDB/>

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260904T000248+0000

Ratings and Alerts

No rating or validation information has been found for MIPS FunCat.

No alerts have been found for MIPS FunCat.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 50 mentions in open access literature.

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

Holyavkin C, et al. (2023) Genomic, transcriptomic, and metabolic characterization of 2-Phenylethanol-resistant *Saccharomyces cerevisiae* obtained by evolutionary engineering. *Frontiers in microbiology*, 14, 1148065.

Gao M, et al. (2020) Pyrrocidine, a molecular off switch for fumonisin biosynthesis. *PLoS pathogens*, 16(7), e1008595.

Freitas E Silva KS, et al. (2020) Interaction of Isocitrate Lyase with Proteins Involved in the Energetic Metabolism in *Paracoccidioides lutzii*. *Journal of fungi (Basel, Switzerland)*, 6(4).

Hitzenhammer E, et al. (2019) YPR2 is a regulator of light modulated carbon and secondary metabolism in *Trichoderma reesei*. *BMC genomics*, 20(1), 211.

E Silva KSF, et al. (2019) Interactome of Glyceraldehyde-3-Phosphate Dehydrogenase Points to the Existence of Metabolons in *Paracoccidioides lutzii*. *Frontiers in microbiology*, 10, 1537.

Pinter N, et al. (2019) Signal peptide peptidase activity connects the unfolded protein response to plant defense suppression by *Ustilago maydis*. *PLoS pathogens*, 15(4), e1007734.

Chaves EGA, et al. (2019) Proteomic Analysis of *Paracoccidioides brasiliensis* During Infection of Alveolar Macrophages Primed or Not by Interferon-Gamma. *Frontiers in microbiology*, 10, 96.

Cervantes-Pérez SA, et al. (2018) Transcriptional profiling of the CAM plant *Agave salmiana* reveals conservation of a genetic program for regeneration. *Developmental biology*, 442(1), 28.

Oliveira AS, et al. (2018) A proteomic dataset of secreted proteins by three *Staphylococcus saprophyticus* strains. *Data in brief*, 21, 1472.

Dattenböck C, et al. (2018) Gene regulation associated with sexual development and female fertility in different isolates of *Trichoderma reesei*. *Fungal biology and biotechnology*, 5, 9.

Stappler E, et al. (2017) Analysis of Light- and Carbon-Specific Transcriptomes Implicates a Class of G-Protein-Coupled Receptors in Cellulose Sensing. *mSphere*, 2(3).

Si T, et al. (2017) Automated multiplex genome-scale engineering in yeast. *Nature communications*, 8, 15187.

Henriques SF, et al. (2017) Genome-wide search for candidate genes for yeast robustness improvement against formic acid reveals novel susceptibility (Trk1 and positive regulators) and resistance (Haa1-regulon) determinants. *Biotechnology for biofuels*, 10, 96.

Lacerda Pigosso L, et al. (2017) *Paracoccidioides brasiliensis* presents metabolic reprogramming and secretes a serine proteinase during murine infection. *Virulence*, 8(7), 1417.

Tisch D, et al. (2017) Omics Analyses of *Trichoderma reesei* CBS999.97 and QM6a Indicate the Relevance of Female Fertility to Carbohydrate-Active Enzyme and Transporter Levels. *Applied and environmental microbiology*, 83(22).

Dong Y, et al. (2017) RNA-Seq-based transcriptomic and metabolomic analysis reveal stress responses and programmed cell death induced by acetic acid in *Saccharomyces cerevisiae*. *Scientific reports*, 7, 42659.

Qin L, et al. (2017) Deciphering the Regulatory Network between the SREBP Pathway and Protein Secretion in *Neurospora crassa*. *mBio*, 8(2).

Monroy AA, et al. (2017) A CRE1- regulated cluster is responsible for light dependent production of dihydrotrichotetronin in *Trichoderma reesei*. *PloS one*, 12(8), e0182530.

Guo L, et al. (2016) Conservation and divergence of the cyclic adenosine monophosphate-protein kinase A (cAMP-PKA) pathway in two plant-pathogenic fungi: *Fusarium graminearum* and *F. verticillioides*. *Molecular plant pathology*, 17(2), 196.

Cho H, et al. (2016) Compact Integration of Multi-Network Topology for Functional Analysis of Genes. *Cell systems*, 3(6), 540.