

Resource Summary Report

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Functional Annotation of the Mammalian Genome

RRID:SCR_000788

Type: Tool

Proper Citation

Functional Annotation of the Mammalian Genome (RRID:SCR_000788)

Resource Information

URL: <http://fantom.gsc.riken.jp/>

Proper Citation: Functional Annotation of the Mammalian Genome (RRID:SCR_000788)

Description: International collaborative research project and database of annotated mammalian genome. Used to improve estimates of total number of genes and their alternative transcript isoforms in both human and mouse. Consortium to assign functional annotations to full length cDNAs that were collected during Mouse Encyclopedia Project at RIKEN.

Abbreviations: FANTOM

Synonyms: Functional Annotation of the Mammalian Genome, FANTOM, Functional Annotation of the Mammalian Genome (FANTOM)

Resource Type: consortium, data or information resource, database, organization portal, portal

Defining Citation: [PMID:20211142](#), [PMID:33211864](#)

Keywords: mammal, genome, isoform, human, gene, transcriptome, regulatory network, FASEB list

Funding: NIMH MH062261

Resource Name: Functional Annotation of the Mammalian Genome

Resource ID: SCR_000788

Alternate IDs: nif-0000-30552

Old URLs: <http://fantom.gsc.riken.jp>

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Ratings and Alerts

No rating or validation information has been found for Functional Annotation of the Mammalian Genome.

No alerts have been found for Functional Annotation of the Mammalian Genome.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 43 mentions in open access literature.

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

Bardales JA, et al. (2018) Selective Activation of Alternative MYC Core Promoters by Wnt-Responsive Enhancers. *Genes*, 9(6).

Harris G, et al. (2018) Toxicity, recovery, and resilience in a 3D dopaminergic neuronal in vitro model exposed to rotenone. *Archives of toxicology*, 92(8), 2587.

Hait TA, et al. (2018) FOCS: a novel method for analyzing enhancer and gene activity patterns infers an extensive enhancer-promoter map. *Genome biology*, 19(1), 56.

Palmieri V, et al. (2018) IMOTA: an interactive multi-omics tissue atlas for the analysis of human miRNA-target interactions. *Nucleic acids research*, 46(D1), D770.

Sehgal A, et al. (2018) The role of CSF1R-dependent macrophages in control of the intestinal stem-cell niche. *Nature communications*, 9(1), 1272.

Latgé G, et al. (2018) Natural Antisense Transcripts: Molecular Mechanisms and Implications in Breast Cancers. *International journal of molecular sciences*, 19(1).

Luan X, et al. (2018) MicroRNAs and immunity in periodontal health and disease. *International journal of oral science*, 10(3), 24.

Sugiaman-Trapman D, et al. (2018) Characterization of the human RFX transcription factor family by regulatory and target gene analysis. *BMC genomics*, 19(1), 181.

Kopp F, et al. (2018) Functional Classification and Experimental Dissection of Long Noncoding RNAs. *Cell*, 172(3), 393.

Francescatto M, et al. (2017) Transcription start site profiling of 15 anatomical regions of the *Macaca mulatta* central nervous system. *Scientific data*, 4, 170163.

Firmin FF, et al. (2017) The RBM14/CoAA-interacting, long intergenic non-coding RNA Para1 regulates adipogenesis and coactivates the nuclear receptor PPAR γ . Scientific reports, 7(1), 14087.

Tang S, et al. (2017) Biallelic Mutations in CFAP43 and CFAP44 Cause Male Infertility with Multiple Morphological Abnormalities of the Sperm Flagella. American journal of human genetics, 100(6), 854.

Qin XY, et al. (2017) Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. EBioMedicine, 24, 257.

Lizio M, et al. (2017) Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. Nucleic acids research, 45(D1), D737.

Galperin MY, et al. (2017) The 24th annual Nucleic Acids Research database issue: a look back and upcoming changes. Nucleic acids research, 45(D1), D1.

Zahir FR, et al. (2017) Comprehensive whole genome sequence analyses yields novel genetic and structural insights for Intellectual Disability. BMC genomics, 18(1), 403.

Lizio M, et al. (2017) Monitoring transcription initiation activities in rat and dog. Scientific data, 4, 170173.

Rosenbluh J, et al. (2017) Complementary information derived from CRISPR Cas9 mediated gene deletion and suppression. Nature communications, 8, 15403.

Kawaji H, et al. (2017) The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. Scientific data, 4, 170113.

Sehgal A, et al. (2017) c-Rel is dispensable for the differentiation and functional maturation of M cells in the follicle-associated epithelium. Immunobiology, 222(2), 316.