Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 13, 2025

RPG - Ribosomal Protein Gene database

RRID:SCR_007904
Type: Tool

Proper Citation

RPG - Ribosomal Protein Gene database (RRID:SCR_007904)

Resource Information

URL: http://ribosome.med.miyazaki-u.ac.jp/

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Description: It is a database that provides detailed information about ribosomal protein (RP) genes. It contains data from humans and other organisms. Users can search this database by gene name and organism. Each record includes sequences (genomic, cDNA, and amino acid sequences), intron/exon structures, genomic locations, and information about orthologs. In addition, users can view and compare the gene structures from different organisms and make multiple amino acid sequence alignments. RPG also provides information on small nucleolar RNAs (snoRNAs) that are encoded in the introns of RP genes.

Abbreviations: RPG

Synonyms: Ribosomal Protein Gene database

Resource Type: database, data or information resource

Funding:

Resource Name: RPG - Ribosomal Protein Gene database

Resource ID: SCR_007904

Old URLs: http://ribosome.miyazaki-med.ac.jp/

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250412T055220+0000

Ratings and Alerts

No rating or validation information has been found for RPG - Ribosomal Protein Gene database.

No alerts have been found for RPG - Ribosomal Protein Gene database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Liao C, et al. (2025) Single-nucleus transcriptomics reveals time-dependent and cell-type-specific effects of psilocybin on gene expression. bioRxiv : the preprint server for biology.

Maiti S, et al. (2023) Hsf1 and the molecular chaperone Hsp90 support a 'rewiring stress response' leading to an adaptive cell size increase in chronic stress. eLife, 12.

Xiao FH, et al. (2022) ETS1 acts as a regulator of human healthy aging via decreasing ribosomal activity. Science advances, 8(17), eabf2017.

Wang S, et al. (2020) Shared distal regulatory regions may contribute to the coordinated expression of human ribosomal protein genes. Genomics, 112(4), 2886.

Yao Y, et al. (2020) Histone deacetylase 3 controls lung alveolar macrophage development and homeostasis. Nature communications, 11(1), 3822.

Molenaars M, et al. (2020) A Conserved Mito-Cytosolic Translational Balance Links Two Longevity Pathways. Cell metabolism, 31(3), 549.

Hudson AJ, et al. (2019) Patterns of conservation of spliceosomal intron structures and spliceosome divergence in representatives of the diplomonad and parabasalid lineages. BMC evolutionary biology, 19(1), 162.

Garcia V, et al. (2018) Accounting for Programmed Ribosomal Frameshifting in the Computation of Codon Usage Bias Indices. G3 (Bethesda, Md.), 8(10), 3173.

Bräuer KE, et al. (2018) Phylogenetic and genomic analyses of the ribosomal oxygenases Riox1 (No66) and Riox2 (Mina53) provide new insights into their evolution. BMC evolutionary biology, 18(1), 96.

Hiraga SI, et al. (2018) Budding yeast Rif1 binds to replication origins and protects DNA at

blocked replication forks. EMBO reports, 19(9).

Seiler M, et al. (2018) Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell reports, 23(1), 282.

Trotta E, et al. (2016) Selective forces and mutational biases drive stop codon usage in the human genome: a comparison with sense codon usage. BMC genomics, 17, 366.

Takei S, et al. (2016) Evolutionarily conserved autoregulation of alternative pre-mRNA splicing by ribosomal protein L10a. Nucleic acids research, 44(12), 5585.

Simm S, et al. (2015) Identification and Expression Analysis of Ribosome Biogenesis Factor Co-orthologs in Solanum lycopersicum. Bioinformatics and biology insights, 9, 1.

Parker MS, et al. (2015) Homoiterons and expansion in ribosomal RNAs. FEBS open bio, 5, 864.

Gupta V, et al. (2014) Ribosome-omics of the human ribosome. RNA (New York, N.Y.), 20(7), 1004.

Sun L, et al. (2013) Paralogous ribosomal protein l32-1 and l32-2 in fission yeast may function distinctively in cellular proliferation and quiescence by changing the ratio of rpl32 paralogs. PloS one, 8(4), e60689.

Sugihara Y, et al. (2013) Identification and expression of an autosomal paralogue of ribosomal protein S4, X-linked, in mice: potential involvement of testis-specific ribosomal proteins in translation and spermatogenesis. Gene, 521(1), 91.

Gaspin C, et al. (2010) Distribution of short interstitial telomere motifs in two plant genomes: putative origin and function. BMC plant biology, 10, 283.

Rho M, et al. (2009) Independent mammalian genome contractions following the KT boundary. Genome biology and evolution, 1, 2.