

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## 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:** data or information resource, database

**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:** 20260905T133147+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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Xiao FH, et al. (2026) Preserved mitochondrial ribosomal protein gene expression marks a youthful transcriptional state in Chinese nonagenarians and centenarians. *Cell reports. Medicine*, 7(5), 102767.

Mitchell RAC, et al. (2025) Identification of universal grass genes and estimates of their monocot-/commelinid-/grass-specificity. *Bioinformatics advances*, 5(1), vbaf079.

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.

Cerulo L, et al. (2023) Single-cell proteo-genomic reveals a comprehensive map of centrosome-associated spliceosome components. *iScience*, 26(5), 106602.

Li W, et al. (2022) Differential Paralog-Specific Expression of Multiple Small Subunit Proteins Cause Variations in Rpl42/eL42 Incorporation in Ribosome in Fission Yeast. *Cells*, 11(15).

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

Bérenger-Currias NM, et al. (2022) A gastruloid model of the interaction between embryonic and extra-embryonic cell types. *Journal of tissue engineering*, 13, 20417314221103042.

Seo SS, et al. (2022) Excess ribosomal protein production unbalances translation in a model of Fragile X Syndrome. *Nature communications*, 13(1), 3236.

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

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

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

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.

Hiraga SI, et al. (2018) Budding yeast Rif1 binds to replication origins and protects DNA at blocked replication forks. *EMBO reports*, 19(9).

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.

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.