Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 16, 2025

Genetic Codes

RRID:SCR_013092
Type: Tool

Proper Citation

Genetic Codes (RRID:SCR_013092)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi

Proper Citation: Genetic Codes (RRID:SCR_013092)

Description: Genetic Codes is a summary resource of the taxonomy of each record and assignment of the correct genetic code for every entry in the GenBank database. GenBank format by historical convention displays mRNA sequences using the DNA alphabet. Thus, for the convenience of people reading GenBank records, the genetic code tables shown here use T instead of U. The following genetic codes are described here: The Standard Code The Vertebrate Mitochondrial Code The Yeast Mitochondrial Code The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code The Invertebrate Mitochondrial Code The Ciliate, Dasycladacean and Hexamita Nuclear Code The Echinoderm and Flatworm Mitochondrial Code The Euplotid Nuclear Code The Bacterial, Archaeal and Plant Plastid Code The Alternative Yeast Nuclear Code The Ascidian Mitochondrial Code The Alternative Flatworm Mitochondrial Code Blepharisma Nuclear Code Chlorophycean Mitochondrial Code Trematode Mitochondrial Code Scenedesmus Obliquus Mitochondrial Code Thraustochytrium Mitochondrial Code

Synonyms: Genetic Codes

Resource Type: database, data or information resource

Keywords: genbank, genetic code, mrna sequences

Funding:

Resource Name: Genetic Codes

Resource ID: SCR_013092

Alternate IDs: nif-0000-02888

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250412T055711+0000

Ratings and Alerts

No rating or validation information has been found for Genetic Codes.

No alerts have been found for Genetic Codes.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 38 mentions in open access literature.

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

Douglas J, et al. (2024) AARS Online: A collaborative database on the structure, function, and evolution of the aminoacyl-tRNA synthetases. IUBMB life, 76(12), 1091.

Schikora-Tamarit MÀ, et al. (2024) Recent gene selection and drug resistance underscore clinical adaptation across Candida species. Nature microbiology, 9(1), 284.

McGowan J, et al. (2024) Multiple independent genetic code reassignments of the UAG stop codon in phyllopharyngean ciliates. PLoS genetics, 20(12), e1011512.

Veeraragavan S, et al. (2024) Evolution and maintenance of mtDNA gene content across eukaryotes. The Biochemical journal, 481(15), 1015.

O'Donnell S, et al. (2023) Telomere-to-telomere assemblies of 142 strains characterize the genome structural landscape in Saccharomyces cerevisiae. Nature genetics, 55(8), 1390.

Emser SV, et al. (2023) Mitochondrial polymorphism m.3017C>T of SHLP6 relates to heterothermy. Frontiers in physiology, 14, 1207620.

Gainor K, et al. (2023) First Report on Detection and Complete Genomic Analysis of a Novel CRESS DNA Virus from Sea Turtles. Pathogens (Basel, Switzerland), 12(4).

Pawlak K, et al. (2023) The Influence of the Selection at the Amino Acid Level on Synonymous Codon Usage from the Viewpoint of Alternative Genetic Codes. International journal of molecular sciences, 24(2).

Jiang S, et al. (2022) CompoDynamics: a comprehensive database for characterizing sequence composition dynamics. Nucleic acids research, 50(D1), D962.

Xu R, et al. (2022) Lack of transcriptional coordination between mitochondrial and nuclear oxidative phosphorylation genes in the presence of two divergent mitochondrial genomes. Zoological research, 43(1), 111.

Parvathy ST, et al. (2022) Codon usage bias. Molecular biology reports, 49(1), 539.

Bucchini F, et al. (2021) TRAPID 2.0: a web application for taxonomic and functional analysis of de novo transcriptomes. Nucleic acids research, 49(17), e101.

Lomsadze A, et al. (2021) GeneMark-HM: improving gene prediction in DNA sequences of human microbiome. NAR genomics and bioinformatics, 3(2), lqab047.

Chen W, et al. (2021) The hidden genomic diversity of ciliated protists revealed by single-cell genome sequencing. BMC biology, 19(1), 264.

Fonseca PLC, et al. (2021) Global Characterization of Fungal Mitogenomes: New Insights on Genomic Diversity and Dynamism of Coding Genes and Accessory Elements. Frontiers in microbiology, 12, 787283.

Pons J, et al. (2021) Aln2tbl: building a mitochondrial features table from a assembly alignment in fasta format. Mitochondrial DNA. Part B, Resources, 6(9), 2732.

Kay C, et al. (2020) Mitochondrial DNAs provide insight into trypanosome phylogeny and molecular evolution. BMC evolutionary biology, 20(1), 161.

Kinkar L, et al. (2020) Marked mitochondrial genetic variation in individuals and populations of the carcinogenic liver fluke Clonorchis sinensis. PLoS neglected tropical diseases, 14(8), e0008480.

Donath A, et al. (2019) Improved annotation of protein-coding genes boundaries in metazoan mitochondrial genomes. Nucleic acids research, 47(20), 10543.

Anwar AM, et al. (2019) vhcub: Virus-host codon usage co-adaptation analysis. F1000Research, 8, 2137.