

Resource Summary Report

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CodonW

RRID:SCR_023989

Type: Tool

Proper Citation

CodonW (RRID:SCR_023989)

Resource Information

URL: <http://codonw.sourceforge.net>

Proper Citation: CodonW (RRID:SCR_023989)

Description: Software tool designed to simplify Multivariate analysis (correspondence analysis) of codon and amino acid usage. It also calculates standard indices of codon usage.

Synonyms: codonw

Resource Type: data analysis software, data processing software, software application, software resource

Keywords: Multivariate analysis, correspondence analysis, codon and amino acid usage, calculate standard indices, codon usage,

Availability: Free, Available for download, Freely available

Resource Name: CodonW

Resource ID: SCR_023989

Alternate IDs: OMICS_08756

Alternate URLs: <https://sources.debian.org/src/codonw/>

License: GNU General Public License version 2

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260821T194246+0000

Ratings and Alerts

No rating or validation information has been found for CodonW.

No alerts have been found for CodonW.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 322 mentions in open access literature.

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

Ma D, et al. (2026) The complete mitochondrial genome of *Prinsepia uniflora* (Rosaceae): De novo assembly, characterization, and phylogenetic analysis. *BMC genomics*, 27(1).

Man Y, et al. (2026) Natural selection dominates the codon preference and host adaptability of the novel goose astrovirus related to gout symptoms, with non-structural protein playing a key role. *Poultry science*, 105(3), 106320.

Yu JX, et al. (2026) Newly assembled mitochondrial genomes of *Hypericum* (Hypericaceae) provide insights into phylogenetic relationships and inter-organellar conflict. *Frontiers in plant science*, 17, 1763082.

Naseri M, et al. (2026) A pan-viral map of host dependency factors from multi-omics integration and machine learning across influenza A, SARS-CoV-2, Zika, and dengue viruses. *Journal of translational medicine*, 24(1).

Xu B, et al. (2026) The Mitochondrial Genome of *Curcuma longa*: A Large and Structurally Complex Genome with Extensive Intracellular DNA Transfer. *Genes*, 17(2).

Chew JJ, et al. (2026) Genus- and host-associated codon usage bias patterns in coronavirus spike genes. *PloS one*, 21(6), e0351693.

Zhao J, et al. (2026) Comprehensive analyses of different putative ploidy levels in organelle genomes of an important medicinal plant *Polygonatum kingianum* Collett & Hemsl. *BMC plant biology*, 26(1).

Xu J, et al. (2026) Assembly and comparative analysis of the complete mitochondrial genome of *Holmskioldia sanguinea*. *Frontiers in plant science*, 17, 1867148.

Almerekova S, et al. (2026) Phylogenomics, divergence time estimation, and biogeography of *Iris* species from Kazakhstan using plastome sequence analysis. *Frontiers in plant science*, 17, 1860819.

Zhou Z, et al. (2026) Codon usage bias and molecular evolution of *Dnajc15* across avian lineages. *Frontiers in genetics*, 17, 1841532.

Singh NK, et al. (2026) Chloroplast genome sequencing in winged bean (*Psophocarpus tetragonolobus* L.) and comparative analysis with other legumes. *BMC plant biology*, 26(1), 264.

An KL, et al. (2026) Plastome evolution and phylogenomics of *Glycine* (Leguminosae: Papilionoideae). *BMC plant biology*, 26(1).

Wang J, et al. (2026) The complete mitochondrial genome of *Holothuria atra* (Holothuriida: Holothuriidae: *Holothuria*) and its structural characteristics. *PloS one*, 21(4), e0347494.

Wang Y, et al. (2026) Dissecting the evolutionary forces shaping codon usage bias in SFTSV from eastern China: Insights from a previously underrepresented region. *Virulence*, 17(1), 2621490.

Xie Y, et al. (2026) Mitochondrial genome characterization and new insights on phylogenetic relationship of *Chara* (Charophyceae, Charophyta). *BMC genomics*, 27(1).

Chen JN, et al. (2026) Comparative genomics on chloroplasts of Chinese *Rubus*: genetic structure and phylogenetic relationships with other species of Rosaceae. *Frontiers in plant science*, 17, 1765373.

Hao CL, et al. (2026) Mitochondrial Genome of *Abramis brama orientalis* Reveals Dominant Role of Natural Selection over Mutation Pressure in Shaping Codon Usage Bias in Leuciscinae Fishes. *Animals : an open access journal from MDPI*, 16(7).

Wu ZH, et al. (2026) Comparative analysis of chloroplast genomes reveals molecular evolution and phylogenetic relationships in *Styrax* (Styracaceae). *BMC plant biology*, 26(1).

Alharbi SA, et al. (2026) Conservation Status, Plastome Diversity, and Evolutionary Diversification of Three Arabian *Desmidorchis* Endemics (Apocynaceae). *Biology*, 15(10).

Chen L, et al. (2026) Comparative Analysis of Complete Chloroplast Genomes of *Caltha scaposa* for Identification and Phylogenetic Analysis. *Ecology and evolution*, 16(6), e73728.