

# 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:** 20260919T195540+0000

### Ratings and Alerts

No rating or validation information has been found for CodonW.

No alerts have been found for CodonW.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 322 mentions in open access literature.

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

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.

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

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.

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).

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).

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

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

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.

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

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

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.

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).

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).

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.

Huynh TTT, et al. (2026) Complete mitochondrial genome sequence data of *Pterygoplichthys gibbiceps* (Actinopterygii, Loricariidae). *Data in brief*, 67, 112963.

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.