

# Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

## 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:** 20260903T235918+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 [kravitz2](#) .

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.