

# Resource Summary Report

Generated by [dkNET](#) on Aug 21, 2026

## CEGMA

RRID:SCR\_015055

Type: Tool

### Proper Citation

CEGMA (RRID:SCR\_015055)

### Resource Information

**URL:** <http://korflab.ucdavis.edu/datasets/cegma/>

**Proper Citation:** CEGMA (RRID:SCR\_015055)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE, documented on January 19, 2022. Tool to annotate core genes in eukaryotic genomes (that was replaced by BUSCO). Its resulting core gene dataset can be used to train a gene finder or to assess the completeness of the genome or annotations., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Resource Type:** data set, data or information resource

**Keywords:** gene annotation, eukaryote, benchmark

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** CEGMA

**Resource ID:** SCR\_015055

**Record Creation Time:** 20220129T080323+0000

**Record Last Update:** 20260821T042914+0000

### Ratings and Alerts

No rating or validation information has been found for CEGMA.

No alerts have been found for CEGMA.

### Data and Source Information

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

## Usage and Citation Metrics

We found 755 mentions in open access literature.

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

Li N, et al. (2025) Chromosome-scale genome assembly of three-spotted seahorse (*Hippocampus trimaculatus*) with a unique karyotype. *Scientific data*, 12(1), 49.

Chen C, et al. (2025) Revealing Genomic Traits and Evolutionary Insights of *Oryza officinalis* from Southern China Through Genome Assembly and Transcriptome Analysis. *Rice* (New York, N.Y.), 18(1), 15.

Zheng S, et al. (2025) The origin, evolution, and translocation of sex chromosomes in *Silurus catfish* mediated by transposons. *BMC biology*, 23(1), 54.

Xue Y, et al. (2025) Novel perpetual genetic population development and genome assembly of superior maize inbred lines provide insights into genetic improvement. *BMC biology*, 24(1), 22.

Lodi RS, et al. (2025) Whole genome sequencing and annotations of *Trametes sanguinea* ZHSJ. *Scientific data*, 12(1), 1460.

Wang F, et al. (2025) Analysis of the *Rehmannia chingii* geneome identifies RcCYP72H7 as an epoxidase in iridoid glycoside biosynthesis. *Nature communications*, 16(1), 6035.

Cui J, et al. (2025) Telomere-to-telomere *Phragmites australis* reference genome assembly with a B chromosome provides insights into its evolution and polysaccharide biosynthesis. *Communications biology*, 8(1), 73.

Meng K, et al. (2024) Chromosome-scale genome assembly and annotation of *Cotoneaster glaucophyllus*. *Scientific data*, 11(1), 406.

Lu Y, et al. (2024) Whole-genome sequencing of the invasive golden apple snail *Pomacea canaliculata* from Asia reveals rapid expansion and adaptive evolution. *GigaScience*, 13.

Cheng Y, et al. (2024) A chromosome-level genome assembly of the *Echiura Urechis unicinctus*. *Scientific data*, 11(1), 90.

Huang Z, et al. (2024) High-quality chromosome-level genome assembly of the Northern Pacific sea star *Asterias amurensis*. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 31(2).

Niimura Y, et al. (2024) Synchronized Expansion and Contraction of Olfactory, Vomeronasal, and Taste Receptor Gene Families in Hystricomorph Rodents. *Molecular biology and evolution*, 41(4).

Wang S, et al. (2024) High-quality chromosome-level genomic insights into molecular adaptation to low-temperature stress in *Madhuca longifolia* in southern subtropical China. *BMC genomics*, 25(1), 877.

Zhu S, et al. (2024) The jacktree genome and population genomics provides insights for the mechanisms of the germination obstacle and the conservation of endangered ornamental plants. Horticulture research, 11(8), uhae166.

Wu Q, et al. (2024) Chromosome-scale reference genome of broccoli (*Brassica oleracea* var. *italica* Plenck) provides insights into glucosinolate biosynthesis. Horticulture research, 11(5), uhae063.

Yan S, et al. (2024) Endophytic strategies decoded by genome and transcriptome analysis of *Fusarium nematophilum* strain NQ8GII4. Frontiers in microbiology, 15, 1487022.

Zhang H, et al. (2024) The High-Quality Genome Sequencing and Analysis of Red Raspberry (*Rubus idaeus* L.). International journal of genomics, 2024, 9271183.

Wang J, et al. (2024) A chromosome-level genome assembly of the legume pod borer, *Maruca vitrata* Fabricius (Lepidoptera: Crambidae). Scientific data, 11(1), 1010.

Zhou H, et al. (2024) Chromosome-level genome assembly of *Platycarya strobilacea*. Scientific data, 11(1), 269.

Fang Y, et al. (2024) Pan-genome and phylogenomic analyses highlight *Hevea* species delineation and rubber trait evolution. Nature communications, 15(1), 7232.