

# Resource Summary Report

Generated by T1D on Aug 10, 2026

## GCE

RRID:SCR\_017332

Type: Tool

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### Proper Citation

GCE (RRID:SCR\_017332)

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### Resource Information

**URL:** <https://arxiv.org/abs/1308.2012>

**Proper Citation:** GCE (RRID:SCR\_017332)

**Description:** Software tool for estimation of genomic characteristics by analyzing k-mer frequency in de novo genome projects. Used as general and assembly independent method for estimating genomic characteristics.

**Synonyms:** Genomic Characteristics Estimation

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

**Keywords:** estimation, genomic, characteristic, analysis, k-mer, frequency, de novo

**Resource Name:** GCE

**Resource ID:** SCR\_017332

**Alternate URLs:** <ftp://ftp.genomics.org.cn/pub/gce>

**Record Creation Time:** 20220129T080334+0000

**Record Last Update:** 20260810T040703+0000

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### Ratings and Alerts

No rating or validation information has been found for GCE.

No alerts have been found for GCE.

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### Data and Source Information

## Usage and Citation Metrics

We found 15 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. *GigaScience*, 15.

Liu H, et al. (2025) A telomere-to-telomere gapless genome reveals SIPRR1 control of circadian rhythm and photoperiodic flowering in tomato. *GigaScience*, 14.

Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. *GigaScience*, 14.

Liu R, et al. (2025) A special short-wing petal faba genome and genetic dissection of floral and yield-related traits accelerate breeding and improvement of faba bean. *Genome biology*, 26(1), 62.

Yang H, et al. (2024) High-quality assembly of the T2T genome for *Isodon rubescens* f. *lushanensis* reveals genomic structure variations between 2 typical forms of *Isodon rubescens*. *GigaScience*, 13.

Li WG, et al. (2024) Chromosome-level genome assembly of a cliff plant *Taihangia rupestris* var. *ciliata* provides insights into its adaptation and demographic history. *BMC plant biology*, 24(1), 596.

Wang H, et al. (2024) The genomes of *Dahlia pinnata*, *Cosmos bipinnatus*, and *Bidens alba* in tribe Coreopsideae provide insights into polyploid evolution and inulin biosynthesis. *GigaScience*, 13.

Wang X, et al. (2023) Genome assembly and annotation of the Sharp-nosed Pit Viper *Deinagkistrodon acutus* based on next-generation sequencing data. *GigaByte* (Hong Kong, China), 2023, gigabyte88.

??ilingir FG, et al. (2022) Chromosome-level genome assembly for the Aldabra giant tortoise enables insights into the genetic health of a threatened population. *GigaScience*, 11.

Li X, et al. (2022) The Manchurian Walnut Genome: Insights into Juglone and Lipid Biosynthesis. *GigaScience*, 11.

Liu P, et al. (2022) The assembled and annotated genome of the masked palm civet (*Paguma larvata*). *GigaScience*, 11.

Bodrug-Schepers A, et al. (2021) Quinoa genome assembly employing genomic variation for guided scaffolding. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 134(11), 3577.

Mu W, et al. (2020) The draft genome assembly of the critically endangered *Nyssa yunnanensis*, a plant species with extremely small populations endemic to Yunnan Province, China. GigaByte (Hong Kong, China), 2020, gigabyte4.

Guo Y, et al. (2019) A chromosomal-level genome assembly for the giant African snail *Achatina fulica*. GigaScience, 8(10).

Wang L, et al. (2019) A draft genome assembly of halophyte *Suaeda aralocaspica*, a plant that performs C4 photosynthesis within individual cells. GigaScience, 8(9).