

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

GCE

RRID:SCR_017332

Type: Tool

Proper Citation

GCE (RRID:SCR_017332)

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 processing software, software application, data analysis software, software resource

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: 20260731T043012+0000

Ratings and Alerts

No rating or validation information has been found for GCE.

No alerts have been found for GCE.

Data and Source Information

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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

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

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.

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.

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.

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

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