

Resource Summary Report

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Plant DNA C-values Database

RRID:SCR_013434

Type: Tool

Proper Citation

Plant DNA C-values Database (RRID:SCR_013434)

Resource Information

URL: <http://data.kew.org/cvalues/>

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Description: The DNA amount in the unreplicated gametic nucleus of an organism is referred to as its C-value, irrespective of the ploidy level of the taxon. The Plant DNA C-values Database currently contains data for 7058 plant species. It combines data from the Angiosperm DNA C-values Database, Gymnosperm DNA C-values Database, the Pteridophyte DNA C-values Database, the Bryophyte DNA C-values Database, together with the addition of the Algae DNA C-values database.

Resource Type: data or information resource, database

Defining Citation: [PMID:17090588](#)

Keywords: FASEB list

Resource Name: Plant DNA C-values Database

Resource ID: SCR_013434

Alternate IDs: nlx_76473

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260811T043451+0000

Ratings and Alerts

No rating or validation information has been found for Plant DNA C-values Database.

No alerts have been found for Plant DNA C-values Database.

Data and Source Information

Usage and Citation Metrics

We found 76 mentions in open access literature.

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

Motyka S, et al. (2024) Distinction of chia varieties in vivo and in vitro based on the flow cytometry and rosmarinic acid production. *Applied microbiology and biotechnology*, 108(1), 337.

Yuan Y, et al. (2024) *Lilium liangiae*, a new species in the genus *Lilium* (Liliaceae) that reveals parallel evolution within morphology. *Frontiers in plant science*, 15, 1371237.

Hutang GR, et al. (2023) Genome size variation and polyploidy prevalence in the genus *Eragrostis* are associated with the global dispersal in arid area. *Frontiers in plant science*, 14, 1066925.

Bicknell R, et al. (2023) Genetic mapping of the LOSS OF PARTHENOGENESIS locus in *Pilosella piloselloides* and the evolution of apomixis in the Lactuceae. *Frontiers in plant science*, 14, 1239191.

Fujiwara T, et al. (2023) Evolution of genome space occupation in ferns: linking genome diversity and species richness. *Annals of botany*, 131(1), 59.

Zhong Y, et al. (2022) Chromosomal-level genome assembly of the orchid tree *Bauhinia variegata* (Leguminosae; Cercidoideae) supports the allotetraploid origin hypothesis of *Bauhinia*. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 29(2).

Zheng T, et al. (2021) Research advances in and prospects of ornamental plant genomics. *Horticulture research*, 8(1), 65.

Martin GT, et al. (2021) CHH Methylation Islands: A Nonconserved Feature of Grass Genomes That Is Positively Associated with Transposable Elements but Negatively Associated with Gene-Body Methylation. *Genome biology and evolution*, 13(8).

Jiang Y, et al. (2021) Distinct Genetic Structure Reflects Ploidy Level Differentiation in Newly Discovered, Extremely Small Populations of *Xanthocyparis vietnamensis* from Southwestern China. *Frontiers in genetics*, 12, 733576.

Del Valle JC, et al. (2020) Genome skimming and microsatellite analysis reveal contrasting patterns of genetic diversity in a rare sandhill endemic (*Erysimum teretifolium*, Brassicaceae). *PloS one*, 15(5), e0227523.

Franco AL, et al. (2020) Low cytomolecular diversification in the genus *Stylosanthes* Sw. (Papilionoideae, Leguminosae). *Genetics and molecular biology*, 43(1), e20180250.

Ibiapino A, et al. (2020) Intense proliferation of rDNA sites and heterochromatic bands in two distantly related *Cuscuta* species (Convolvulaceae) with very large genomes and

symmetric karyotypes. *Genetics and molecular biology*, 43(3), e20190068.

Jung H, et al. (2020) Twelve quick steps for genome assembly and annotation in the classroom. *PLoS computational biology*, 16(11), e1008325.

Werner O, et al. (2020) A Cost Reduced Variant of Epi-Genotyping by Sequencing for Studying DNA Methylation in Non-model Organisms. *Frontiers in plant science*, 11, 694.

Damasco G, et al. (2019) Leaf Transcriptome Assembly of *Protium copal* (Burseraceae) and Annotation of Terpene Biosynthetic Genes. *Genes*, 10(5).

Fu J, et al. (2019) Identification and characterization of abundant repetitive sequences in *Allium cepa*. *Scientific reports*, 9(1), 16756.

Jin Y, et al. (2019) Genome-Wide Variant Identification and High-Density Genetic Map Construction Using RADseq for *Platycladus orientalis* (Cupressaceae). *G3 (Bethesda, Md.)*, 9(11), 3663.

Lonardi S, et al. (2019) The genome of cowpea (*Vigna unguiculata* [L.] Walp.). *The Plant journal : for cell and molecular biology*, 98(5), 767.

Johnson MG, et al. (2019) A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using k-Medoids Clustering. *Systematic biology*, 68(4), 594.

Barrett CF, et al. (2019) Ancient Polyploidy and Genome Evolution in Palms. *Genome biology and evolution*, 11(5), 1501.