Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 24, 2025

dCAPS Finder

RRID:SCR_008612
Type: Tool

Proper Citation

dCAPS Finder (RRID:SCR_008612)

Resource Information

URL: http://helix.wustl.edu/dcaps/dcaps.html

Proper Citation: dCAPS Finder (RRID:SCR_008612)

Description: A simple program for finding nearly matched primers Sponsor: This material is based upon work supported by the National Science Foundation under Grant No. 0114726.

Synonyms: dCAPS

Resource Type: software resource

Defining Citation: PMID:12446140

Funding:

Resource Name: dCAPS Finder

Resource ID: SCR_008612

Alternate IDs: nif-0000-31957

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250519T203548+0000

Ratings and Alerts

No rating or validation information has been found for dCAPS Finder.

No alerts have been found for dCAPS Finder.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 152 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Fu W, et al. (2024) Whole-genome resequencing identifies candidate genes and allelic variation in the MdNADP-ME promoter that regulate fruit malate and fructose contents in apple. Plant communications, 5(9), 100973.

Wu T, et al. (2024) MutL homolog 1 participates in interference-sensitive meiotic crossover formation in soybean. Plant physiology, 195(4), 2579.

Zhang W, et al. (2024) Genetic analysis and preliminary mapping by BSA-seq of the CmSR gene regulating the spotted rind trait in melon (Cucumis melo L.). Genetics and molecular biology, 47(3), e20240062.

Derrick CJ, et al. (2024) Functional analysis of germline VANGL2 variants using rescue assays of vangl2 knockout zebrafish. Human molecular genetics, 33(2), 150.

Yoo SI, et al. (2024) Genome Sequencing of Lentinula edodes Revealed a Genomic Variant Block Associated with a Thermo-Tolerant Trait in Fruit Body Formation. Journal of fungi (Basel, Switzerland), 10(9).

Kwon SH, et al. (2024) Genetic Insights into the Extremely Dwarf Hibiscus syriacus var. micranthus: Complete Chloroplast Genome Analysis and Development of a Novel dCAPS Marker. Current issues in molecular biology, 46(3), 2757.

Zhang M, et al. (2024) OsGELP77, a QTL for broad-spectrum disease resistance and yield in rice, encodes a GDSL-type lipase. Plant biotechnology journal, 22(5), 1352.

Baral A, et al. (2024) TYPHON proteins are RAB-dependent mediators of the trans-Golgi network secretory pathway. The Plant cell, 37(1).

Maung PP, et al. (2023) Identification and characterization of a novel gene controlling floral organ number in rice (Oryza sativa L.). PloS one, 18(1), e0280022.

Li J, et al. (2023) Characterization of Two AGAMOUS-like Genes and Their Promoters from the Cymbidium faberi (Orchidaceae). Plants (Basel, Switzerland), 12(14).

Hou BH, et al. (2022) Cultivar-specific markers, mutations, and chimerisim of Cavendish banana somaclonal variants resistant to Fusarium oxysporum f. sp. cubense tropical race 4. BMC genomics, 23(1), 470.

Santistevan NJ, et al. (2022) cacna2d3, a voltage-gated calcium channel subunit, functions in vertebrate habituation learning and the startle sensitivity threshold. PloS one, 17(7), e0270903.

Buttress T, et al. (2022) Histone H2B.8 compacts flowering plant sperm through chromatin phase separation. Nature, 611(7936), 614.

Yokoyama R, et al. (2022) Point mutations that boost aromatic amino acid production and CO2 assimilation in plants. Science advances, 8(23), eabo3416.

Tergemina E, et al. (2022) A two-step adaptive walk rewires nutrient transport in a challenging edaphic environment. Science advances, 8(20), eabm9385.

Chustecki JM, et al. (2022) Altered collective mitochondrial dynamics in the Arabidopsis msh1 mutant compromising organelle DNA maintenance. Journal of experimental botany, 73(16), 5428.

Lv Q, et al. (2021) Exploring Natural Allelic Variations of the ?-Triketone Herbicide Resistance Gene HIS1 for Application in indica Rice and Particularly in Two-Line Hybrid Rice. Rice (New York, N.Y.), 14(1), 7.

Liu R, et al. (2021) Association of TaD14-4D, a Gene Involved in Strigolactone Signaling, with Yield Contributing Traits in Wheat. International journal of molecular sciences, 22(7).

Soufflet-Freslon V, et al. (2021) Diversity and selection of the continuous-flowering gene, RoKSN, in rose. Horticulture research, 8(1), 76.

Dash L, et al. (2021) slim shady is a novel allele of PHYTOCHROME B present in the T-DNA line SALK_015201. Plant direct, 5(6), e00326.