Resource Summary Report

Generated by NIF on May 5, 2025

Computational Analysis of gene Family Evolution

RRID:SCR_018924
Type: Tool

Proper Citation

Computational Analysis of gene Family Evolution (RRID:SCR_018924)

Resource Information

URL: https://github.com/hahnlab/CAFExp

Proper Citation: Computational Analysis of gene Family Evolution (RRID:SCR_018924)

Description: Software tool for computational analysis of gene family evolution. Used for statistical analysis of evolution gene family sizes. Models evolution of gene family sizes over phylogeny.

Abbreviations: CAFE

Synonyms: CAFE v2.0, CAFE v4.0, CAFE v3.0, CAFE v5.0, Computational Analysis of gene Family Evolution

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

Defining Citation: PMID:16543274

Keywords: Computational analysis, gene family evolution, evolution statistical analysis, gene family size, gene evolution, phylogeny

Funding: NHGRI R33 HG003070;
NSF MCB 0528465;
METACyt Initiative of Indiana University ;
Lilly Endowment ;
Inc

Resource Name: Computational Analysis of gene Family Evolution

Resource ID: SCR_018924

Record Creation Time: 20220129T080342+0000

Record Last Update: 20250505T054641+0000

Ratings and Alerts

No rating or validation information has been found for Computational Analysis of gene Family Evolution.

No alerts have been found for Computational Analysis of gene Family Evolution.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Weng YM, et al. (2024) Evolutionary genomics of three agricultural pest moths reveals rapid evolution of host adaptation and immune-related genes. GigaScience, 13.

Wang ZF, et al. (2022) Genome assembly of Musa beccarii shows extensive chromosomal rearrangements and genome expansion during evolution of Musaceae genomes. GigaScience, 12.

Wang Z, et al. (2022) A chromosome-level reference genome of Ensete glaucum gives insight into diversity and chromosomal and repetitive sequence evolution in the Musaceae. GigaScience, 11.

Yuan R, et al. (2022) The chromosome-level genome of Chinese praying mantis Tenodera sinensis (Mantodea: Mantidae) reveals its biology as a predator. GigaScience, 12.

Hu Y, et al. (2022) A high-resolution genome of an euryhaline and eurythermal rhinogoby (Rhinogobius similis Gill 1895). G3 (Bethesda, Md.), 12(2).

Kim J, et al. (2022) Comparative Genome and Evolution Analyses of an Endangered Stony Coral Species Dendrophyllia cribrosa Near Dokdo Islands in the East Sea. Genome biology and evolution, 14(9).

Zheng J, et al. (2022) Molecular mechanisms underlying hematophagia revealed by comparative analyses of leech genomes. GigaScience, 12.

Xi H, et al. (2022) Chromosome-level assembly of the common vetch (Vicia sativa) reference genome. GigaByte (Hong Kong, China), 2022, gigabyte38.

Huang R, et al. (2021) De novo screening of disease-resistant genes from the chromosome-level genome of rare minnow using CRISPR-cas9 random mutation. GigaScience, 10(11).

Pardos-Blas JR, et al. (2021) The genome of the venomous snail Lautoconus ventricosus sheds light on the origin of conotoxin diversity. GigaScience, 10(5).

Li Y, et al. (2020) Pacific Biosciences assembly with Hi-C mapping generates an improved, chromosome-level goose genome. GigaScience, 9(10).

Brandies PA, et al. (2020) The first Antechinus reference genome provides a resource for investigating the genetic basis of semelparity and age-related neuropathologies. GigaByte (Hong Kong, China), 2020, gigabyte7.