Resource Summary Report

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PatMaN

RRID:SCR_011821
Type: Tool

Proper Citation

PatMaN (RRID:SCR_011821)

Resource Information

URL: https://bioinf.eva.mpg.de/patman/

Proper Citation: PatMaN (RRID:SCR_011821)

Description: Software that searches for short patterns in large DNA databases, allowing for approximate matches.

Abbreviations: PatMaN

Synonyms: PatMaN - A DNA pattern matcher for short sequences

Resource Type: software resource

Defining Citation: PMID:18467344, DOI:10.1093/bioinformatics/btn223

Keywords: c++, bio.tools, FASEB list

Funding:

Availability: GNU General Public License, v3

Resource Name: PatMaN

Resource ID: SCR_011821

Alternate IDs: OMICS_00997, biotools:patman

Alternate URLs: https://bio.tools/patman, https://sources.debian.org/src/patman/

Record Creation Time: 20220129T080306+0000

Record Last Update: 20250410T070208+0000

Ratings and Alerts

No rating or validation information has been found for PatMaN.

No alerts have been found for PatMaN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Döring M, et al. (2024) Nucleolar protein TAAP1/C22orf46 confers pro-survival signaling in non-small cell lung cancer. Life science alliance, 7(4).

Sun MS, et al. (2024) Regulatory microRNAs and phasiRNAs of paclitaxel biosynthesis in Taxus chinensis. Frontiers in plant science, 15, 1403060.

Ali M, et al. (2024) Rapid and cost-effective molecular karyotyping in wheat, barley, and their cross-progeny by chromosome-specific multiplex PCR. Plant methods, 20(1), 37.

Moutsopoulos I, et al. (2023) bulkAnalyseR: an accessible, interactive pipeline for analysing and sharing bulk multi-modal sequencing data. Briefings in bioinformatics, 24(1).

Jelicic M, et al. (2023) Discovery and characterization of novel Cre-type tyrosine site-specific recombinases for advanced genome engineering. Nucleic acids research, 51(10), 5285.

Billmeier M, et al. (2022) Mechanistic insights into non-coding Y RNA processing. RNA biology, 19(1), 468.

Ghibaudi M, et al. (2021) miR-7b-3p Exerts a Dual Role After Spinal Cord Injury, by Supporting Plasticity and Neuroprotection at Cortical Level. Frontiers in molecular biosciences, 8, 618869.

Collins DH, et al. (2021) Gene expression during larval caste determination and differentiation in intermediately eusocial bumblebees, and a comparative analysis with advanced eusocial honeybees. Molecular ecology, 30(3), 718.

Lizamore D, et al. (2021) Elevated transcription of transposable elements is accompanied by het-siRNA-driven de novo DNA methylation in grapevine embryogenic callus. BMC

genomics, 22(1), 676.

Sós-Heged?s A, et al. (2020) Suppression of NB-LRR genes by miRNAs promotes nitrogen-fixing nodule development in Medicago truncatula. Plant, cell & environment, 43(5), 1117.

Narjala A, et al. (2020) A conserved sequence signature is essential for robust plant miRNA biogenesis. Nucleic acids research, 48(6), 3103.

Bovolenta LA, et al. (2020) miRTil: An Extensive Repository for Nile Tilapia microRNA Next Generation Sequencing Data. Cells, 9(8).

Thody J, et al. (2020) NATpare: a pipeline for high-throughput prediction and functional analysis of nat-siRNAs. Nucleic acids research, 48(12), 6481.

Parvathaneni RK, et al. (2020) The regulatory landscape of early maize inflorescence development. Genome biology, 21(1), 165.

Hummel G, et al. (2020) Epigenetic silencing of clustered tRNA genes in Arabidopsis. Nucleic acids research, 48(18), 10297.

Sreevalsan S, et al. (2020) MLLT6 maintains PD-L1 expression and mediates tumor immune resistance. EMBO reports, 21(12), e50155.

Singh A, et al. (2019) Artificially induced phased siRNAs promote virus resistance in transgenic plants. Virology, 537, 208.

Shaw B, et al. (2019) Molecular insights into an ancient form of Paget's disease of bone. Proceedings of the National Academy of Sciences of the United States of America, 116(21), 10463.

Neumann P, et al. (2019) Systematic survey of plant LTR-retrotransposons elucidates phylogenetic relationships of their polyprotein domains and provides a reference for element classification. Mobile DNA, 10, 1.

Åsman AKM, et al. (2019) Nucleomorph Small RNAs in Cryptophyte and Chlorarachniophyte Algae. Genome biology and evolution, 11(4), 1117.