

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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260919T195219+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 61 mentions in open access literature.

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

Mendes EA, et al. (2025) RUNX2 inhibition disrupts a PAX3::FOXO1-RUNX2 feed-forward loop and dismantles oncogenic gene programs in fusion-positive rhabdomyosarcoma. *bioRxiv : the preprint server for biology*.

Schwarz FM, et al. (2025) MethyStat sensitizes ovarian cancer cells to PARP-inhibition by targeting the histone demethylases JMJD1B/C. *Cancer gene therapy*, 32(3), 286.

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

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

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-Hegedűs 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.

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

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

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

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.