

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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: 20260905T132713+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 [Kravitz](#) .

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.