Resource Summary Report

Generated by NIF on May 2, 2025

Pecan

RRID:SCR_001909
Type: Tool

Proper Citation

Pecan (RRID:SCR_001909)

Resource Information

URL: https://github.com/benedictpaten/pecan

Proper Citation: Pecan (RRID:SCR_001909)

Description: A Java consistency based multiple sequence alignment software program.

Resource Type: software resource

Defining Citation: PMID:18849524

Keywords: java, sequence, alignment, consistency, bio.tools

Funding:

Availability: MIT License

Resource Name: Pecan

Resource ID: SCR_001909

Alternate IDs: OMICS_03739, biotools:pecan

Alternate URLs: http://hgwdev.cse.ucsc.edu/~benedict/code/Pecan.html, https://bio.tools/pecan

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250420T014044+0000

Ratings and Alerts

No rating or validation information has been found for Pecan.

No alerts have been found for Pecan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Wang X, et al. (2024) WUREN: Whole-modal union representation for epitope prediction. Computational and structural biotechnology journal, 23, 2122.

Ormond C, et al. (2024) Investigating copy number variants in schizophrenia pedigrees using a new consensus pipeline called PECAN. Scientific reports, 14(1), 17518.

Zhang J, et al. (2024) Developing a fair and interpretable representation of the clock drawing test for mitigating low education and racial bias. Scientific reports, 14(1), 17444.

Xiao X, et al. (2024) Beneficial effects of Lactobacillus plantarum on growth performance, immune status, antioxidant function and intestinal microbiota in broilers. Poultry science, 103(12), 104280.

Boer JM, et al. (2024) Oncogenic and immunological targets for matched therapy of pediatric blood cancer patients: Dutch iTHER study experience. HemaSphere, 8(7), e122.

Gahl M, et al. (2024) PECAN Predicts Patterns of Cancer Cell Cytostatic Activity of Natural Products Using Deep Learning. Journal of natural products, 87(3), 567.

Almeida A, et al. (2024) Myb overexpression synergizes with the loss of Pten and is a dependency factor and therapeutic target in T-cell lymphoblastic leukemia. HemaSphere, 8(3), e51.

Demoen L, et al. (2024) A dual role for PSIP1/LEDGF in T cell acute lymphoblastic leukemia. Science advances, 10(44), eado6765.

Wiley RW, et al. (2024) The English Sublexical Toolkit: Methods for indexing sound-spelling consistency. Behavior research methods, 56(7), 6826.

Stoltze UK, et al. (2024) The evolutionary impact of childhood cancer on the human gene pool. Nature communications, 15(1), 1881.

Kalemati M, et al. (2024) ParaAntiProt provides paratope prediction using antibody and

protein language models. Scientific reports, 14(1), 29141.

Zhang J, et al. (2023) FaIRClocks: Fair and Interpretable Representation of the Clock Drawing Test for mitigating classifier bias against lower educational groups. Research square.

Klintwall L, et al. (2023) Perceived Causal Problem Networks: Reliability, Central Problems, and Clinical Utility for Depression. Assessment, 30(1), 73.

Gao Z, et al. (2023) Limited role of generation time changes in driving the evolution of the mutation spectrum in humans. eLife, 12.

Powers SB, et al. (2023) Differential Expression of LLT1, SLAM Receptors CS1 and 2B4 and NCR Receptors NKp46 and NKp30 in Pediatric Acute Lymphoblastic Leukemia (ALL). International journal of molecular sciences, 24(4).

Baumgartner ME, et al. (2023) The PECAn image and statistical analysis pipeline identifies Minute cell competition genes and features. Nature communications, 14(1), 2686.

Meunier F, et al. (2022) Liana optical traits increase tropical forest albedo and reduce ecosystem productivity. Global change biology, 28(1), 227.

Dwarasala A, et al. (2022) ssPINE: Probabilistic Algorithm for Automated Chemical Shift Assignment of Solid-State NMR Data from Complex Protein Systems. Membranes, 12(9).

Hou J, et al. (2022) DIA-MS2pep: a library-free framework for comprehensive peptide identification from data-independent acquisition data. Biophysics reports, 8(5-6), 253.

Euskirchen ES, et al. (2022) Assessing dynamic vegetation model parameter uncertainty across Alaskan arctic tundra plant communities. Ecological applications : a publication of the Ecological Society of America, 32(2), e2499.