Resource Summary Report

Generated by RRID on May 22, 2025

Eddy Lab Software

RRID:SCR_001458
Type: Tool

Proper Citation

Eddy Lab Software (RRID:SCR_001458)

Resource Information

URL: http://eddylab.org/software.html

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Description: Software library containing tools for statistical manipulations of data. Tools include profile hidden Markov models for biological sequence analysis, RNA structure analysis, and a prototype noncoding RNA genefinder.

Synonyms: Eddy Lab: Software, Eddy Lab - Software

Resource Type: software resource

Keywords: software repository, statistics, data, statistical analysis, statistical manipulation, markov model, bio.tools

Funding:

Availability: Available to the research community

Resource Name: Eddy Lab Software

Resource ID: SCR_001458

Alternate IDs: nif-0000-08778, biotools:pknots

Alternate URLs: https://bio.tools/pknots

Old URLs: http://selab.janelia.org/software.html

Record Creation Time: 20220129T080207+0000

Record Last Update: 20250519T203131+0000

Ratings and Alerts

No rating or validation information has been found for Eddy Lab Software.

No alerts have been found for Eddy Lab Software.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Liu G, et al. (2024) Identification of Hammerhead-variant ribozyme sequences in SARS-CoV-2. Nucleic acids research, 52(6), 3262.

Zhang Z, et al. (2024) Minimal twister sister-like self-cleaving ribozymes in the human genome revealed by deep mutational scanning. eLife, 12.

Déjosez M, et al. (2023) Bat pluripotent stem cells reveal unusual entanglement between host and viruses. Cell, 186(5), 957.

Shimwell C, et al. (2023) A first molecular characterization of the scorpion telson microbiota of Hadrurus arizonensis and Smeringurus mesaensis. PloS one, 18(1), e0277303.

Weinberg CE, et al. (2019) Novel ribozymes: discovery, catalytic mechanisms, and the quest to understand biological function. Nucleic acids research, 47(18), 9480.

Boyd JA, et al. (2018) GraftM: a tool for scalable, phylogenetically informed classification of genes within metagenomes. Nucleic acids research, 46(10), e59.

Královicová J, et al. (2018) PUF60-activated exons uncover altered 3' splice-site selection by germline missense mutations in a single RRM. Nucleic acids research, 46(12), 6166.

Dudek NK, et al. (2017) Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. Current biology : CB, 27(24), 3752.

Wang Y, et al. (2015) Genome-wide comparative analysis reveals similar types of NBS genes in hybrid Citrus sinensis genome and original Citrus clementine genome and provides new insights into non-TIR NBS genes. PloS one, 10(3), e0121893.

Rees MA, et al. (2015) Changes in protein abundance are observed in bacterial isolates from a natural host. Frontiers in cellular and infection microbiology, 5, 71.

Tang YT, et al. (2014) Genome of the human hookworm Necator americanus. Nature genetics, 46(3), 261.

Gillett CP, et al. (2014) Bulk de novo mitogenome assembly from pooled total DNA elucidates the phylogeny of weevils (Coleoptera: Curculionoidea). Molecular biology and evolution, 31(8), 2223.

Sangwan N, et al. (2014) Reconstructing an ancestral genotype of two hexachlorocyclohexane-degrading Sphingobium species using metagenomic sequence data. The ISME journal, 8(2), 398.

Sahl JW, et al. (2013) Evolution of a pathogen: a comparative genomics analysis identifies a genetic pathway to pathogenesis in Acinetobacter. PloS one, 8(1), e54287.

Mariotti M, et al. (2013) SECISearch3 and Seblastian: new tools for prediction of SECIS elements and selenoproteins. Nucleic acids research, 41(15), e149.

Sridhar J, et al. (2013) Computational small RNA prediction in bacteria. Bioinformatics and biology insights, 7, 83.

Mitreva M, et al. (2011) The draft genome of the parasitic nematode Trichinella spiralis. Nature genetics, 43(3), 228.

Sievers F, et al. (2011) Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Molecular systems biology, 7, 539.

Li W, et al. (2010) Genomic analysis of codon, sequence and structural conservation with selective biochemical-structure mapping reveals highly conserved and dynamic structures in rotavirus RNAs with potential cis-acting functions. Nucleic acids research, 38(21), 7718.

Copeland CS, et al. (2009) Homology-based annotation of non-coding RNAs in the genomes of Schistosoma mansoni and Schistosoma japonicum. BMC genomics, 10, 464.