

Resource Summary Report

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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

Availability: Free, Available for download, Freely available

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: 20260725T190503+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 [kravitz2](#) .

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.

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.

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

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.

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

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

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.