Resource Summary Report

Generated by RRID on Apr 12, 2025

PLEK

RRID:SCR_012132
Type: Tool

Proper Citation

PLEK (RRID:SCR_012132)

Resource Information

URL: http://sourceforge.net/projects/plek/

Proper Citation: PLEK (RRID:SCR_012132)

Description: An alignment-free software tool which uses a computational pipeline based on an improved k-mer scheme and a support vector machine (SVM) algorithm to distinguish lncRNAs from messenger RNAs (mRNAs), in the absence of genomic sequences or annotations. It is especially suitable for PacBio or 454 sequencing data and large-scale transcriptome data.

Synonyms: PLEK: predictor of long non-coding RNAs and messenger RNAs based on an improved k-mer scheme

Resource Type: software resource

Defining Citation: PMID:25239089

Keywords: standalone software, roche, pacific biosciences, unix/linux, c, python, bio.tools

Funding:

Availability: GNU General Public License

Resource Name: PLEK

Resource ID: SCR_012132

Alternate IDs: biotools:plek, OMICS_05839

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

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250410T070230+0000

Ratings and Alerts

No rating or validation information has been found for PLEK.

No alerts have been found for PLEK.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 108 mentions in open access literature.

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

Liu L, et al. (2025) Effects of maternal Escherichia coli lipopolysaccharide exposure on offspring: insights from lncRNA analysis in laying hens. Poultry science, 104(1), 104599.

Wu J, et al. (2024) Exploring Gene Expression and Alternative Splicing in Duck Embryonic Myoblasts via Full-Length Transcriptome Sequencing. Veterinary sciences, 11(12).

Qi F, et al. (2024) A multidimensional recommendation framework for identifying biological targets to aid the diagnosis and treatment of liver metastasis in patients with colorectal cancer. Molecular cancer, 23(1), 239.

Zhang S, et al. (2024) Whole-Transcriptome Sequencing Reveals the Global Molecular Responses and NAC Transcription Factors Involved in Drought Stress in Dendrobium catenatum. Antioxidants (Basel, Switzerland), 13(1).

Jiao N, et al. (2024) Genome-wide characterization of post-transcriptional processes related to wood formation in Dalbergia odorifera. BMC genomics, 25(1), 372.

Ding D, et al. (2024) Whole-transcriptome sequencing revealed the role of noncoding RNAs in susceptibility and resistance of Pekin ducks to DHAV-3. Poultry science, 103(3), 103416.

Min Q, et al. (2024) Transcriptomic Profiles of Long Noncoding RNAs and Their Target Protein-Coding Genes Reveals Speciation Adaptation on the Qinghai-Xizang (Tibet) Plateau in Orinus. Biology, 13(5).

Tribhuvan KU, et al. (2024) Identification, genomic localization, and functional validation of salt-stress-related lncRNAs in Indian Mustard (Brassica juncea L.). BMC genomics, 25(1), 1121.

He T, et al. (2024) SINE-Associated LncRNA SAWPA Regulates Porcine Zygotic Genome Activation. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(2), e2307505.

Zhao H, et al. (2024) Transcriptomics and metabolomics of blood, urine and ovarian follicular fluid of yak at induced estrus stage. BMC genomics, 25(1), 201.

Qi X, et al. (2024) The expression profile analysis and functional prediction of lncRNAs in peripheral blood mononuclear cells in maintenance hemodialysis patients developing heart failure. Scientific reports, 14(1), 29577.

Yang J, et al. (2023) Comparative Transcriptomics Identify Key Pituitary Circular RNAs That Participate in Sheep (Ovis aries) Reproduction. Animals : an open access journal from MDPI, 13(17).

Zhang R, et al. (2023) PacBio Full-Length Transcriptome of a Tetraploid Sinocyclocheilus multipunctatus Provides Insights into the Evolution of Cavefish. Animals : an open access journal from MDPI, 13(21).

Zeng Z, et al. (2023) The RNAome landscape of tomato during arbuscular mycorrhizal symbiosis reveals an evolving RNA layer symbiotic regulatory network. Plant communications, 4(1), 100429.

Batista da Silva I, et al. (2023) Discovery of putative long non-coding RNAs expressed in the eyes of Astyanax mexicanus (Actinopterygii: Characidae). Scientific reports, 13(1), 12051.

Shang Y, et al. (2023) Genome-wide analysis of long noncoding RNAs and their association in regulating the metamorphosis of the Sarcophaga peregrina (Diptera: Sarcophagidae). PLoS neglected tropical diseases, 17(6), e0011411.

Wei X, et al. (2023) SMRT Sequencing Technology Was Used to Construct the Batocera horsfieldi (Hope) Transcriptome and Reveal Its Features. Insects, 14(7).

Fang S, et al. (2023) Genome-Wide Analysis of Long Non-Coding RNAs Related to UV-B Radiation in the Antarctic Moss Pohlia nutans. International journal of molecular sciences, 24(6).

Zheng SY, et al. (2023) A Global Survey of the Full-Length Transcriptome of Apis mellifera by Single-Molecule Long-Read Sequencing. International journal of molecular sciences, 24(6).

Dong C, et al. (2023) Identification and validation of crucial lnc-TRIM28-14 and hub genes promoting gastric cancer peritoneal metastasis. BMC cancer, 23(1), 76.