

Resource Summary Report

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PLEK

RRID:SCR_012132

Type: Tool

Proper Citation

PLEK (RRID:SCR_012132)

Resource Information

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

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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

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: 20260801T190434+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 122 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#).

Huang P, et al. (2025) PotatoBSLnc: a curated repository of potato long noncoding RNAs in response to biotic stress. Database : the journal of biological databases and curation, 2025.

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.

Sun Q, et al. (2025) Characterizing hub biomarkers for metabolic-induced endothelial dysfunction and unveiling their regulatory roles in EndMT through RNA sequencing and machine learning approaches. Frontiers in cardiovascular medicine, 12, 1585030.

Bai H, et al. (2025) TetraRNA, a tetra-class machine learning model for deciphering the coding potential derivation of RNA world. Computational and structural biotechnology journal, 27, 1305.

Pei Y, et al. (2025) Transcriptomics data for muscle development in Goats. Scientific data, 12(1), 928.

Qi M, et al. (2025) Hyperoside, a flavonoid, induces lnc187 and lnc999 to enhance pigeon pea pollen tube growth and seed production. Science advances, 11(46), eadz3499.

Hao J, et al. (2025) Whole-transcriptome sequencing reveals the effects of acupuncture on early embryos post-IVF-ET in poor ovarian response. Journal of ovarian research, 18(1), 91.

Chen M, et al. (2025) Drought-induced transposon expression reveals complex drought response mechanisms in Brassica napus. Frontiers in plant science, 16, 1614169.

Sharma E, et al. (2025) RNA sequencing of the lncRNA regulome modulated by Withania somnifera in human neuroblastoma SK-N-SH cells. Molecular biology reports, 52(1), 890.

Li Y, et al. (2025) Skeleton-Forming Responses of Reef-Building Corals under Ocean Acidification. Research (Washington, D.C.), 8, 0736.

Shao Y, et al. (2025) Identification of SDC4 as a potential target for obesity via integrated analysis of the lncRNA-miRNA-mRNA network in visceral adipose tissue. Adipocyte,

14(1), 2583542.

Zhang S, et al. (2025) Comprehensive analysis of lncRNAs and mRNAs revealed potential participants in the process of avian reovirus infection. *Frontiers in microbiology*, 16, 1539903.

Yan Y, et al. (2025) Comprehensive full-Length transcriptomic resource for wing dimorphism in English green aphid, *Sitobion avenae*. *Scientific data*, 12(1), 1034.

Riquier S, et al. (2025) RNA-Seq analysis reveals the long noncoding RNAs associated with immunity in wild *Myotis myotis* bats. *BMC genomics*, 26(1), 345.

Kennedy Ng MM, et al. (2025) Reference-guided Genome Assembly of Long Non-coding RNA Transcripts Reveals Target Genes Associated With Crohn's Disease. *bioRxiv : the preprint server for biology*.

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).

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.

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.