

Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

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

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: 20260815T182443+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 134 mentions in open access literature.

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

Gromadziński L, et al. (2026) Unveiling the molecular impact of pulmonary embolism on the right ventricle: a multi-layer transcriptomic study in a porcine model. *Molecular and cellular biochemistry*, 481(1), 509.

Zamora-Ballesteros C, et al. (2026) Dual RNA-seq analysis reveals differences in defensive lncRNA expression in *Pinus* spp. with varying susceptibility to *Fusarium circinatum*. *BMC plant biology*, 26(1), 326.

Zhu X, et al. (2026) Inflammatory arthritis irAE may represent a unique autoimmune disease primarily driven by T cells but likely not autoantibodies. *Science advances*, 12(14), eaea4262.

Ma X, et al. (2026) The role of lncRNA-associated ceRNA networks in yak longissimus dorsi muscle development across feeding systems. *BMC veterinary research*, 22(1).

Wang S, et al. (2026) An Integrated Analysis of circRNA and lncRNA Expression of Bovine Granulosa Cells Induced by Melatonin Reveals the Pathways Potentially Involved in Follicular Development. *Genes*, 17(2).

Zhu Z, et al. (2026) A Multi-Tissue Yak (*Bos grunniens*) ceRNA Atlas with Ribo-Seq-Informed lncRNA Curation and Candidate Prioritization. *Animals : an open access journal from MDPI*, 16(4).

Zhang Y, et al. (2026) Deciphering the Biosynthetic Pathways and Regulatory Networks of the Active Components of *Cibotium barometz* by Transcriptomic Analysis. *International journal of molecular sciences*, 27(4).

Wang YD, et al. (2026) Characterization of the full-length transcriptome of female *Eucolus annulatus* and comparative transcriptomic analysis of its head, middle, and tail body sections. *Parasites & vectors*, 19(1).

Wang J, et al. (2026) Full-length transcriptome sequencing analysis and characterization of MADS-box genes in *Rhododendron fortunei*. *BMC plant biology*, 26(1).

He J, et al. (2026) Pan-tissue transcriptomic profiling of dairy cattle. *Journal of animal science and biotechnology*, 17(1).

- Arza-Apalategi S, et al. (2026) Comprehensive lincRNA Transcriptome in Acute Myeloid Leukemia: Integrating Known and Newly Identified lincRNAs Across Pediatric and Adult Cohorts. *Non-coding RNA*, 12(3).
- Liu L, et al. (2025) Effects of maternal *Escherichia coli* lipopolysaccharide exposure on offspring: insights from lincRNA analysis in laying hens. *Poultry science*, 104(1), 104599.
- 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.
- 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.
- 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.
- 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.
- Pei Y, et al. (2025) Transcriptomics data for muscle development in Goats. *Scientific data*, 12(1), 928.
- Yan Y, et al. (2025) Comprehensive full-Length transcriptomic resource for wing dimorphism in English green aphid, *Sitobion avenae*. *Scientific data*, 12(1), 1034.
- 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.