

Resource Summary Report

Generated by T1D on Aug 3, 2026

proTRAC

RRID:SCR_012078

Type: Tool

Proper Citation

proTRAC (RRID:SCR_012078)

Resource Information

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

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Description: A software which detects and analyses piRNA clusters based on quantifiable deviations from a hypothetical uniform distribution regarding the decisive piRNA cluster characteristics.

Synonyms: probabilistic TRacking and Analysis of Clusters

Resource Type: software resource

Defining Citation: [PMID:22233380](https://pubmed.ncbi.nlm.nih.gov/22233380/)

Keywords: standalone software, perl

Availability: Creative Commons License

Resource Name: proTRAC

Resource ID: SCR_012078

Alternate IDs: OMICS_04874

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260801T190431+0000

Ratings and Alerts

No rating or validation information has been found for proTRAC.

No alerts have been found for proTRAC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Casas E, et al. (2025) Genetic polymorphisms lead to major, locus-specific, variation in piRNA production in mouse. *The EMBO journal*, 44(14), 4104.

Bergman A, et al. (2025) Limited impact of the siRNA pathway on transposable element expression in *Aedes aegypti*. *BMC biology*, 23(1), 130.

Huang S, et al. (2024) Transcriptional landscape of small non-coding RNAs reveals diversity of categories and functions in molluscs. *RNA biology*, 21(1), 1.

Signor S, et al. (2023) Rapid evolutionary diversification of the flamenco locus across simulans clade *Drosophila* species. *PLoS genetics*, 19(8), e1010914.

Wierzbicki F, et al. (2023) The composition of piRNA clusters in *Drosophila melanogaster* deviates from expectations under the trap model. *BMC biology*, 21(1), 224.

Teefy BB, et al. (2023) Dynamic regulation of gonadal transposon control across the lifespan of the naturally short-lived African turquoise killifish. *Genome research*, 33(1), 141.

van Lopik J, et al. (2023) Unistrand piRNA clusters are an evolutionarily conserved mechanism to suppress endogenous retroviruses across the *Drosophila* genus. *Nature communications*, 14(1), 7337.

Bodelón A, et al. (2023) Impact of Heat Stress on Transposable Element Expression and Derived Small RNAs in *Drosophila subobscura*. *Genome biology and evolution*, 15(11).

Martín L, et al. (2021) Altered non-coding RNA expression profile in F1 progeny 1 year after parental irradiation is linked to adverse effects in zebrafish. *Scientific reports*, 11(1), 4142.

Ishino K, et al. (2021) Hamster PIWI proteins bind to piRNAs with stage-specific size variations during oocyte maturation. *Nucleic acids research*, 49(5), 2700.

Waiho K, et al. (2020) Comparative profiling of ovarian and testicular piRNAs in the mud crab *Scylla paramamosain*. *Genomics*, 112(1), 323.

Tan M, et al. (2020) PIWIL3 Forms a Complex with TDRKH in Mammalian Oocytes. *Cells*, 9(6).

Queiroz FR, et al. (2020) Deep sequencing of small RNAs reveals the repertoire of miRNAs and piRNAs in *Biomphalaria glabrata*. *Memorias do Instituto Oswaldo Cruz*, 115,

e190498.

Gòdia M, et al. (2019) A RNA-Seq Analysis to Describe the Boar Sperm Transcriptome and Its Seasonal Changes. *Frontiers in genetics*, 10, 299.

Shamimuzzaman M, et al. (2019) Genome-wide profiling of piRNAs in the whitefly *Bemisia tabaci* reveals cluster distribution and association with begomovirus transmission. *PLoS one*, 14(3), e0213149.

Yang Q, et al. (2019) Single-cell CAS-seq reveals a class of short PIWI-interacting RNAs in human oocytes. *Nature communications*, 10(1), 3389.

Fromm B, et al. (2019) Evolutionary Implications of the microRNA- and piRNA Complement of *Lepidodermella squamata* (Gastrotricha). *Non-coding RNA*, 5(1).

Chang KW, et al. (2018) Stage-dependent piRNAs in chicken implicated roles in modulating male germ cell development. *BMC genomics*, 19(1), 425.

Ray R, et al. (2018) piRNA analysis framework from small RNA-Seq data by a novel cluster prediction tool - PILFER. *Genomics*, 110(6), 355.

Ward NJ, et al. (2018) microRNAs associated with early neural crest development in *Xenopus laevis*. *BMC genomics*, 19(1), 59.