Resource Summary Report

Generated by dkNET on Apr 23, 2025

proTRAC

RRID:SCR_012078
Type: Tool

Proper Citation

proTRAC (RRID:SCR_012078)

Resource Information

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

Proper Citation: proTRAC (RRID:SCR_012078)

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

Keywords: standalone software, perl

Funding:

Availability: Creative Commons License

Resource Name: proTRAC

Resource ID: SCR_012078

Alternate IDs: OMICS_04874

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250420T014605+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 24 mentions in open access literature.

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

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.

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.

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.

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.

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

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.

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

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

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

Capra E, et al. (2017) Small RNA sequencing of cryopreserved semen from single bull revealed altered miRNAs and piRNAs expression between High- and Low-motile sperm populations. BMC genomics, 18(1), 14.

Bachmayr-Heyda A, et al. (2016) Small RNAs and the competing endogenous RNA network in high grade serous ovarian cancer tumor spread. Oncotarget, 7(26), 39640.