

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

TraceTuner

RRID:SCR_013019

Type: Tool

Proper Citation

TraceTuner (RRID:SCR_013019)

Resource Information

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

Proper Citation: TraceTuner (RRID:SCR_013019)

Description: Software tool for base and quality calling of trace files from DNA sequencing instruments.

Abbreviations: TraceTuner

Synonyms: TraceTuner - DNA sequencing quality values base calling and trace processing

Resource Type: software resource

Availability: Free

Resource Name: TraceTuner

Resource ID: SCR_013019

Alternate IDs: OMICS_01158

Alternate URLs: <https://sources.debian.org/src/tracetuner/>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260912T195757+0000

Ratings and Alerts

No rating or validation information has been found for TraceTuner.

No alerts have been found for TraceTuner.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Cullen LBL, et al. (2026) Exploring molecular mechanisms of aminoglycoside resistance in *Escherichia coli* MG1655 using the antibiotic resistance growth plate. *Scientific reports*, 16(1).

Mishina K, et al. (2023) Wheat Ym2 originated from *Aegilops sharonensis* and confers resistance to soil-borne Wheat yellow mosaic virus infection to the roots. *Proceedings of the National Academy of Sciences of the United States of America*, 120(11), e2214968120.

Takayama J, et al. (2021) Construction and integration of three de novo Japanese human genome assemblies toward a population-specific reference. *Nature communications*, 12(1), 226.

Kaj??n GL, et al. (2018) A multigene typing system for human adenoviruses reveals a new genotype in a collection of Swedish clinical isolates. *PloS one*, 13(12), e0209038.

Hansen TA, et al. (2016) High diversity of picornaviruses in rats from different continents revealed by deep sequencing. *Emerging microbes & infections*, 5(8), e90.

Ng KP, et al. (2016) Identification and characterization of *Daldinia eschscholtzii* isolated from skin scrapings, nails, and blood. *PeerJ*, 4, e2637.

Tee MK, et al. (2016) Alternative splicing of *DENND1A*, a PCOS candidate gene, generates variant 2. *Molecular and cellular endocrinology*, 434, 25.

Liu J, et al. (2015) Natural yeast promoter variants reveal epistasis in the generation of transcriptional-mediated noise and its potential benefit in stressful conditions. *Genome biology and evolution*, 7(4), 969.

Taft AS, et al. (2015) Identification of mammalian-adapting mutations in the polymerase complex of an avian H5N1 influenza virus. *Nature communications*, 6, 7491.

McLaughlin RL, et al. (2014) *UBQLN2* mutations are not a frequent cause of amyotrophic lateral sclerosis in Ireland. *Neurobiology of aging*, 35(1), 267.e9.

Michaud L, et al. (2014) Snow surface microbiome on the High Antarctic Plateau (DOME C). *PloS one*, 9(8), e104505.

Torgerson DG, et al. (2012) Resequencing candidate genes implicates rare variants in asthma susceptibility. *American journal of human genetics*, 90(2), 273.

Valles SM, et al. (2008) Expressed sequence tags from the red imported fire ant, *Solenopsis invicta*: annotation and utilization for discovery of viruses. *Journal of invertebrate pathology*, 99(1), 74.

Lowe JK, et al. (2003) Linkage mapping of the primary disease locus for collie eye anomaly. *Genomics*, 82(1), 86.