Resource Summary Report

Generated by dkNET on Apr 23, 2025

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

Funding:

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: 20250420T014629+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 13 mentions in open access literature.

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

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.

Kaján 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.

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

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

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.