Resource Summary Report

Generated by dkNET on May 22, 2025

4Peaks

RRID:SCR_000015
Type: Tool

Proper Citation

4Peaks (RRID:SCR_000015)

Resource Information

URL: http://nucleobytes.com/index.php/4peaks

Proper Citation: 4Peaks (RRID:SCR_000015)

Description: Software application for viewing and editing sequence trace files.

Abbreviations: 4Peaks

Resource Type: software application, software resource

Keywords: mac os x, sequence, trace file

Funding:

Availability: Free

Resource Name: 4Peaks

Resource ID: SCR_000015

Alternate IDs: OMICS_01015

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250522T055835+0000

Ratings and Alerts

No rating or validation information has been found for 4Peaks.

No alerts have been found for 4Peaks.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Roberto Rolando Pisano S, et al. (2024) An old unknown: 40 years of crayfish plague monitoring in Switzerland, the water tower of Europe. Journal of invertebrate pathology, 206, 108159.

De Bellis C, et al. (2024) Genomic, epigenomic and transcriptomic inter- and intra-tumor heterogeneity in desmoid tumors. Clinical cancer research : an official journal of the American Association for Cancer Research.

Mosley IA, et al. (2023) Occurrence of Dirofilaria immitis infection in shelter cats in the lower Rio Grande Valley region in South Texas, United States, using integrated diagnostic approaches. Veterinary parasitology, regional studies and reports, 41, 100871.

De León ME, et al. (2023) Genome sequencing and multifaceted taxonomic analysis of novel strains of violacein-producing bacteria and non-violacein-producing close relatives. Microbial genomics, 9(4).

De León ME, et al. (2021) Draft Genome Sequences and Genomic Analysis for Pigment Production in Bacteria Isolated from Blue Discolored Soymilk and Tofu. Journal of genomics, 9, 55.

Mackay A, et al. (2018) Molecular, Pathological, Radiological, and Immune Profiling of Non-brainstem Pediatric High-Grade Glioma from the HERBY Phase II Randomized Trial. Cancer cell, 33(5), 829.

Horrigan SK, et al. (2017) Replication Study: Melanoma genome sequencing reveals frequent PREX2 mutations. eLife, 6.

Mohd Salleh F, et al. (2017) An expanded mammal mitogenome dataset from Southeast Asia. GigaScience, 6(8), 1.

Miranda PJ, et al. (2016) Characterization of Chemosynthetic Microbial Mats Associated with Intertidal Hydrothermal Sulfur Vents in White Point, San Pedro, CA, USA. Frontiers in microbiology, 7, 1163.

Modahl CM, et al. (2016) Full-Length Venom Protein cDNA Sequences from Venom-Derived mRNA: Exploring Compositional Variation and Adaptive Multigene Evolution. PLoS neglected tropical diseases, 10(6), e0004587.

Celerino da Silva R, et al. (2016) DEFB1 gene polymorphisms and tuberculosis in a Northeastern Brazilian population. Brazilian journal of microbiology : [publication of the Brazilian Society for Microbiology], 47(2), 389.

Mochizuki H, et al. (2015) Detection of BRAF Mutation in Urine DNA as a Molecular Diagnostic for Canine Urothelial and Prostatic Carcinoma. PloS one, 10(12), e0144170.

Mochizuki H, et al. (2015) BRAF Mutations in Canine Cancers. PloS one, 10(6), e0129534.

Kondo H, et al. (2014) Transcriptional mapping of the messenger and leader RNAs of orchid fleck virus, a bisegmented negative-strand RNA virus. Virology, 452-453, 166.

Darjany LE, et al. (2014) Lignocellulose-responsive bacteria in a southern California salt marsh identified by stable isotope probing. Frontiers in microbiology, 5, 263.