

Resource Summary Report

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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

Availability: Free

Resource Name: 4Peaks

Resource ID: SCR_000015

Alternate IDs: OMICS_01015

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260727T040241+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 [nidm-terms](#) .

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*.

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.

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.

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

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

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) BRAF Mutations in Canine Cancers. *PloS one*, 10(6), e0129534.

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.

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.