

Resource Summary Report

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Chromaseq

RRID:SCR_005587

Type: Tool

Proper Citation

Chromaseq (RRID:SCR_005587)

Resource Information

URL: <http://mesquiteproject.org/packages/chromaseq/>

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Description: A software package in Mesquite that processes chromatograms, makes contigs, base calls, etc., using in part the programs Phred and Phrap.

Abbreviations: Chromaseq

Synonyms: Chromaseq: a package for processing chromatograms and sequence data in Mesquite

Resource Type: software resource

Keywords: chromatogram, sequence, mesquite

Funding: NSF EF-0531754

Availability: Acknowledgement required

Resource Name: Chromaseq

Resource ID: SCR_005587

Alternate IDs: OMICS_01017

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260801T190255+0000

Ratings and Alerts

No rating or validation information has been found for Chromaseq.

No alerts have been found for Chromaseq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Martinez-Hernandez F, et al. (2023) Genetic Variability of the Internal Transcribed Spacer and Pyruvate:Ferredoxin Oxidoreductase Partial Gene of *Trichomonas vaginalis* from Female Patients. *Microorganisms*, 11(9).

Kavanaugh DH, et al. (2021) Phylogeny of the supertribe Nebriitae (Coleoptera, Carabidae) based on analyses of DNA sequence data. *ZooKeys*, 1044, 41.

Huang YL, et al. (2020) Effect of Host, Environment and Fungal Growth on Fungal Leaf Endophyte Communities in Taiwan. *Journal of fungi* (Basel, Switzerland), 6(4).

Villanueva-Garcia C, et al. (2017) Clarifying the Cryptic Host Specificity of *Blastocystis* spp. Isolates from *Alouatta palliata* and *A. pigra* Howler Monkeys. *PloS one*, 12(1), e0169637.

Brunet T, et al. (2016) The evolutionary origin of bilaterian smooth and striated myocytes. *eLife*, 5.

Maddison WP, et al. (2016) Phylogenetic placement of the unusual jumping spider *Depreissia* Lessert, and a new synapomorphy uniting Hisponinae and Salticinae (Araneae, Salticidae). *ZooKeys*(549), 1.

Kanda K, et al. (2015) Successful Recovery of Nuclear Protein-Coding Genes from Small Insects in Museums Using Illumina Sequencing. *PloS one*, 10(12), e0143929.