Resource Summary Report

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discoSnp

RRID:SCR_002612
Type: Tool

Proper Citation

discoSnp (RRID:SCR_002612)

Resource Information

URL: http://colibread.inria.fr/discosnp/

Proper Citation: discoSnp (RRID:SCR_002612)

Description: Software designed for discovering Single Nucleotide Polymorphism (SNP) from raw sets of reads obtained with Next Generation Sequencers (NGS).

Synonyms: DiscoSnp++, discovering Single Nucleotide Polymorphism, discovering Single Nucleotide Polymorphism (discoSNP)

Resource Type: data processing software, software application, data analysis software, sequence analysis software, software resource

Defining Citation: PMID:25404127

Keywords: single nucleotide polymorphism, snp discovery, discover snp, bio.tools

Funding: SOFIPROTEOL under the FASO project PEAPOL ;
INRIA ANR-12-BS02-0008

Availability: Open source

Resource Name: discoSnp

Resource ID: SCR_002612

Alternate IDs: biotools:discosnp, OMICS_00267

Alternate URLs: https://bio.tools/discosnp, https://sources.debian.org/src/discosnp/

Record Creation Time: 20220129T080214+0000

Record Last Update: 20250418T055001+0000

Ratings and Alerts

No rating or validation information has been found for discoSnp.

No alerts have been found for discoSnp.

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 FDI Lab - SciCrunch.org.

Seah YM, et al. (2023) In Silico Evaluation of Variant Calling Methods for Bacterial Whole-Genome Sequencing Assays. Journal of clinical microbiology, 61(8), e0184222.

Laso-Jadart R, et al. (2023) Holistic view of the seascape dynamics and environment impact on macro-scale genetic connectivity of marine plankton populations. BMC ecology and evolution, 23(1), 46.

Tsui CK, et al. (2018) Beaver Fever: Whole-Genome Characterization of Waterborne Outbreak and Sporadic Isolates To Study the Zoonotic Transmission of Giardiasis. mSphere, 3(2).

Lopez-Maestre H, et al. (2016) SNP calling from RNA-seq data without a reference genome: identification, quantification, differential analysis and impact on the protein sequence. Nucleic acids research, 44(19), e148.

Boutet G, et al. (2016) SNP discovery and genetic mapping using genotyping by sequencing of whole genome genomic DNA from a pea RIL population. BMC genomics, 17, 121.

Uricaru R, et al. (2015) Reference-free detection of isolated SNPs. Nucleic acids research, 43(2), e11.

Leggett RM, et al. (2014) Reference-free SNP detection: dealing with the data deluge. BMC genomics, 15 Suppl 4(Suppl 4), S10.