Resource Summary Report

Generated by NIF on May 16, 2025

SNPdat

RRID:SCR_005187
Type: Tool

Proper Citation

SNPdat (RRID:SCR_005187)

Resource Information

URL: http://code.google.com/p/snpdat/

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Description: A simple and easy to use high through-put analysis tool which can provide comprehensive annotation of both novel and known single nucleotide polymorphisms (SNPs) for any organism with a draft sequence and annotation. SNPdat makes possible analyses involving non-model organisms that are not supported by the vast majority of SNP annotation tools currently available. It is especially intended for use by researchers with limited bioinformatic experience.

Abbreviations: SNPdat

Synonyms: SNP Data Analysis Tool, SNPdat - A Simple High Throughput Analysis Tool for Annotating SNPs

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

Defining Citation: PMID:23390980

Keywords: high through-put, single nucleotide polymorphism, annotation, gtf, gff, fasta, sequence analysis, genome, command line

Funding:

Availability: GNU General Public License, v2, Acknowledgement requested

Resource Name: SNPdat

Resource ID: SCR_005187

Alternate IDs: OMICS_00184

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250514T061332+0000

Ratings and Alerts

No rating or validation information has been found for SNPdat.

No alerts have been found for SNPdat.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Sánchez-Adriá IE, et al. (2025) Sterol-Targeted Laboratory Evolution Allows the Isolation of Thermotolerant and Respiratory-Competent Clones of the Industrial Yeast Saccharomyces cerevisiae. Microbial biotechnology, 18(1), e70092.

Cardenas M, et al. (2024) Modulation of human-to-swine influenza a virus adaptation by the neuraminidase low-affinity calcium-binding pocket. Communications biology, 7(1), 1230.

Legrand C, et al. (2023) Time-resolved, integrated analysis of clonally evolving genomes. PLoS genetics, 19(12), e1011085.

Rodríguez A, et al. (2020) Being red, blue and green: the genetic basis of coloration differences in the strawberry poison frog (Oophaga pumilio). BMC genomics, 21(1), 301.

Riemersma KK, et al. (2019) Chikungunya Virus Fidelity Variants Exhibit Differential Attenuation and Population Diversity in Cell Culture and Adult Mice. Journal of virology, 93(3).

Riemersma KK, et al. (2019) Chikungunya virus populations experience diversity- dependent attenuation and purifying intra-vector selection in Californian Aedes aegypti mosquitoes. PLoS neglected tropical diseases, 13(11), e0007853.

Rubino F, et al. (2017) Divergent functional isoforms drive niche specialisation for nutrient

acquisition and use in rumen microbiome. The ISME journal, 11(4), 932.

Wang L, et al. (2015) Construction of a high-density linkage map and fine mapping of QTL for growth in Asian seabass. Scientific reports, 5, 16358.