

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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

Defining Citation: [PMID:23390980](#)

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

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: 20260905T132531+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 9 mentions in open access literature.

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

Cardenas M, et al. (2025) Vaccine-induced antigenic drift of a human-origin H3N2 Influenza A virus in swine alters glycan binding and sialic acid avidity. *bioRxiv* : the preprint server for biology.

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.