Resource Summary Report

Generated by NIF on May 25, 2025

StAMPP

RRID:SCR_022022
Type: Tool

Proper Citation

StAMPP (RRID:SCR_022022)

Resource Information

URL: https://cran.r-project.org/package=StAMPP

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Description: Software R package for statistical analysis of mixed ploidy populations.Used for calculation of population structure and differentiation based on single nucleotide polymorphism genotype data from populations of any ploidy level, and/or mixed ploidy levels.

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

Defining Citation: DOI:10.1111/1755-0998.12129

Keywords: statistical analysis, mixed ploidy populations, single nucleotide polymorphism genotype data

Funding: Victorian Department of Primary Industries ;
Geoffrey Gardiner Foundation ;
Meat and Livestock Australia ;
New Zealand Agriseeds ;
Christchurch ;
New Zealand ;
Australian Postgraduate Award ;
Dairy Futures CRC

Availability: Free, Available for download, Freely available

Resource Name: StAMPP

Resource ID: SCR_022022

Alternate URLs: https://github.com/lpembleton/StAMPP

Record Creation Time: 20220421T050138+0000

Record Last Update: 20250525T031839+0000

Ratings and Alerts

No rating or validation information has been found for StAMPP.

No alerts have been found for StAMPP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Franssen SU, et al. (2022) Geographic Origin and Vertical Transmission of Leishmania infantum Parasites in Hunting Hounds, United States. Emerging infectious diseases, 28(6), 1211.

Pickett BD, et al. (2022) Genome assembly of the roundjaw bonefish (Albula glossodonta), a vulnerable circumtropical sportfish. GigaByte (Hong Kong, China), 2022, gigabyte44.

Qiu Y, et al. (2021) Whole-genome variation of transposable element insertions in a maize diversity panel. G3 (Bethesda, Md.), 11(10).

Franssen SU, et al. (2021) Diversity and Within-Host Evolution of Leishmania donovani from Visceral Leishmaniasis Patients with and without HIV Coinfection in Northern Ethiopia. mBio, 12(3), e0097121.

Rahmatalla SA, et al. (2017) Whole genome population genetics analysis of Sudanese goats identifies regions harboring genes associated with major traits. BMC genetics, 18(1), 92.