Resource Summary Report

Generated by dkNET on Apr 18, 2025

GENECLASS

RRID:SCR_009065
Type: Tool

Proper Citation

GENECLASS (RRID:SCR_009065)

Resource Information

URL: http://www.montpellier.inra.fr/URLB/

Proper Citation: GENECLASS (RRID:SCR_009065)

Description: Software application employing multilocus genotypes to select or exclude populations as origins of individuals (Assignment and Migrants Detection). (entry from Genetic Analysis Software)

Abbreviations: GENECLASS

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, delphi, ms-windos, unix

Funding:

Resource Name: GENECLASS

Resource ID: SCR_009065

Alternate IDs: nlx_154053

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250416T063535+0000

Ratings and Alerts

No rating or validation information has been found for GENECLASS.

No alerts have been found for GENECLASS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 86 mentions in open access literature.

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

Jorde PE, et al. (2024) Genetic analyses verify sexually mature escaped farmed Atlantic cod and farmed cod eggs in the natural environment. Evolutionary applications, 17(4), e13688.

Heddergott M, et al. (2023) Spread of the Zoonotic Nematode Baylisascaris procyonis into a Naive Raccoon Population. EcoHealth, 20(3), 263.

Le Corre V, et al. (2023) Host-associated genetic differentiation and origin of a recent host shift in the generalist parasitic weed Phelipanche ramosa. Ecology and evolution, 13(9), e10529.

Duscher GG, et al. (2021) A potential zoonotic threat: First detection of Baylisascaris procyonis in a wild raccoon from Austria. Transboundary and emerging diseases, 68(6), 3034.

Jia Z, et al. (2021) CAP Analysis of the Distribution of the Introduced Bemisia tabaci (Hemiptera: Aleyrodidae) Species Complex in Xinjiang, China and the Southerly Expansion of the Mediterranean Species. Journal of insect science (Online), 21(2).

Regilme MAF, et al. (2021) The influence of roads on the fine-scale population genetic structure of the dengue vector Aedes aegypti (Linnaeus). PLoS neglected tropical diseases, 15(2), e0009139.

Cejas D, et al. (2021) Spatial and temporal patterns of genetic diversity in Bombus terrestris populations of the Iberian Peninsula and their conservation implications. Scientific reports, 11(1), 22471.

Lee Y, et al. (2021) Complex evolution in Aphis gossypii group (Hemiptera: Aphididae), evidence of primary host shift and hybridization between sympatric species. PloS one, 16(2), e0245604.

Nishio S, et al. (2021) Genetic structure analysis of cultivated and wild chestnut populations reveals gene flow from cultivars to natural stands. Scientific reports, 11(1), 240.

Fazzi-Gomes PF, et al. (2021) Novel Microsatellite Markers Used for Determining Genetic

Diversity and Tracing of Wild and Farmed Populations of the Amazonian Giant Fish Arapaima gigas. Genes, 12(9).

Hauser SS, et al. (2021) Waste not, want not: Microsatellites remain an economical and informative technology for conservation genetics. Ecology and evolution, 11(22), 15800.

Le Cam S, et al. (2020) A genome-wide investigation of the worldwide invader Sargassum muticum shows high success albeit (almost) no genetic diversity. Evolutionary applications, 13(3), 500.

Lewis T, et al. (2020) Unraveling the mystery of the glacier bear: Genetic population structure of black bears (Ursus americanus) within the range of a rare pelage type. Ecology and evolution, 10(14), 7654.

Dalui S, et al. (2020) Fine-scale landscape genetics unveiling contemporary asymmetric movement of red panda (Ailurus fulgens) in Kangchenjunga landscape, India. Scientific reports, 10(1), 15446.

Otterå H, et al. (2020) The pantophysin gene and its relationship with survival in early life stages of Atlantic cod. Royal Society open science, 7(10), 191983.

Gregório I, et al. (2020) Paths for colonization or exodus? New insights from the brown bear (Ursus arctos) population of the Cantabrian Mountains. PloS one, 15(1), e0227302.

Potter S, et al. (2020) Understanding Historical Demographic Processes to Inform Contemporary Conservation of an Arid zone Specialist: The Yellow-Footed Rock-Wallaby. Genes, 11(2).

Zhu Q, et al. (2020) Lack of conspicuous sex-biased dispersal patterns at different spatial scales in an Asian endemic goose species breeding in unpredictable steppe wetlands. Ecology and evolution, 10(14), 7006.

Zhu KX, et al. (2020) Fine-scale genetic structure of the overwintering Chilo suppressalis in the typical bivoltine areas of northern China. PloS one, 15(12), e0243999.

Bhatt S, et al. (2020) Genetic analyses reveal population structure and recent decline in leopards (Panthera pardus fusca) across the Indian subcontinent. PeerJ, 8, e8482.