

Resource Summary Report

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MOLKIN

RRID:SCR_013262

Type: Tool

Proper Citation

MOLKIN (RRID:SCR_013262)

Resource Information

URL: http://pendientedemigracion.ucm.es/info/prodanim/html/JP_Web.htm

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Description: A population genetics computer program that conducts several genetic analyses on multilocus information in a user-friendly environment. Primary functions carried out by MOLKIN are the computation of the between individuals (and populations) molecular coancestry coefficients, the Kinship distance at individual and population levels. Additionally, users can compute with MOLKIN a set of among populations, genetic distances and F statistics from multilocus information. The program will help researchers or those responsible for population management to assess genetic variability and population structure at reduced costs with respect to dataset preparation (entry from Genetic Analysis Software)

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Funding:

Resource Name: MOLKIN

Resource ID: SCR_013262

Alternate IDs: nlx_154041

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250502T060130+0000

Ratings and Alerts

No rating or validation information has been found for MOLKIN.

No alerts have been found for MOLKIN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Ben Sassi-Zaidy Y, et al. (2022) Genetic Characterization and Alternative Preservation Ways of Locally Adapted Sheep Breeds: Cases of Private and Public Sheep Sectors in Tunisia and Italy. *Biology*, 11(11).

Kanyesigye D, et al. (2022) Population Genetic Structure of the Bean Leaf Beetle *Ootheca mutabilis* (Coleoptera: Chrysomelidae) in Uganda. *Insects*, 13(6).

Soglia D, et al. (2021) Genetic Diversity of 17 Autochthonous Italian Chicken Breeds and Their Extinction Risk Status. *Frontiers in genetics*, 12, 715656.

Peixoto MGCD, et al. (2021) Genetic Diversity and Population Genetic Structure of a Guzera (Bos indicus) Meta-Population. *Animals : an open access journal from MDPI*, 11(4).

Abbas A, et al. (2020) A Polyphasic Approach to Compare the Genomic Profiles of Aflatoxigenic and Non-Aflatoxigenic Isolates of *Aspergillus* Section *Flavi*. *Toxins*, 12(1).

Laoun A, et al. (2020) Inference of Breed Structure in Farm Animals: Empirical Comparison between SNP and Microsatellite Performance. *Genes*, 11(1).

Shimma K, et al. (2019) Genetic Differentiation among Commercial Lines of Laying-type Japanese Quail. *The journal of poultry science*, 56(1), 12.

Goszczynski D, et al. (2018) Runs of homozygosity in a selected cattle population with extremely inbred bulls: Descriptive and functional analyses revealed highly variable patterns. *PloS one*, 13(7), e0200069.

Brandies PA, et al. (2018) Disentangling the mechanisms of mate choice in a captive koala population. *PeerJ*, 6, e5438.

Maraci Ö, et al. (2018) Phylogeny and genetic structure in the genus *Secale*. *PloS one*, 13(7), e0200825.

Balao F, et al. (2016) Genetic differentiation and admixture between sibling allopolyploids in

the *Dactylorhiza majalis* complex. *Heredity*, 116(4), 351.

Dos Santos CH, et al. (2016) Genetic differentiation in red-bellied piranha populations (*Pygocentrus nattereri*, Kner, 1858) from the Solimões-Amazonas River. *Ecology and evolution*, 6(12), 4203.

Khalili Samani N, et al. (2016) Phylogenetics and population genetics of *Plotosus canius* (Siluriformes: Plotosidae) from Malaysian coastal waters. *PeerJ*, 4, e1930.

Soto-Cerda BJ, et al. (2014) The potential of pale flax as a source of useful genetic variation for cultivated flax revealed through molecular diversity and association analyses. *Molecular breeding : new strategies in plant improvement*, 34(4), 2091.

Traoré A, et al. (2012) Ascertaining gene flow patterns in livestock populations of developing countries: a case study in Burkina Faso goat. *BMC genetics*, 13, 35.

Johnson PC, et al. (2006) Abundant variation in microsatellites of the parasitic nematode *Trichostrongylus tenuis* and linkage to a tandem repeat. *Molecular and biochemical parasitology*, 148(2), 210.