Resource Summary Report

Generated by dkNET on Apr 17, 2025

R/ONEMAP

RRID:SCR_009371
Type: Tool

Proper Citation

R/ONEMAP (RRID:SCR_009371)

Resource Information

URL: https://cran.r-project.org/web/packages/onemap/index.html

Proper Citation: R/ONEMAP (RRID:SCR_009371)

Description: Software environment for constructing linkage maps in outcrossing plant species, using full-sib families derived from two outbreed (non-inbreeding) parent plants. (entry from Genetic Analysis Software)

Synonyms: ONEMAP

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, r

Funding:

Resource Name: R/ONEMAP

Resource ID: SCR_009371

Alternate IDs: nlx_154502, SCR_009312, nlx_154593

Old URLs: http://www.ciagri.usp.br/~aafgarci/OneMap/

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063545+0000

Ratings and Alerts

No rating or validation information has been found for R/ONEMAP.

No alerts have been found for R/ONEMAP.

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 dkNET.

Ouellet-Fagg CL, et al. (2025) Complex and Dynamic Gene-by-Age and Gene-by-Environment Interactions Underlie Functional Morphological Variation in Adaptive Divergence in Arctic Charr (Salvelinus alpinus). Evolution & development, 27(1), e70000.

Chen R, et al. (2023) XY sex determination in a cnidarian. BMC biology, 21(1), 32.

Liu T, et al. (2022) Genome-wide identification of quantitative trait loci for morpho-agronomic and yield-related traits in foxtail millet (Setaria italica) across multi-environments. Molecular genetics and genomics : MGG, 297(3), 873.

Smith HM, et al. (2018) Genetic identification of SNP markers linked to a new grape phylloxera resistant locus in Vitis cinerea for marker-assisted selection. BMC plant biology, 18(1), 360.

Smith HM, et al. (2018) SNP markers tightly linked to root knot nematode resistance in grapevine (Vitis cinerea) identified by a genotyping-by-sequencing approach followed by Sequenom MassARRAY validation. PloS one, 13(2), e0193121.

Nunes JR, et al. (2017) Large-scale SNP discovery and construction of a high-density genetic map of Colossoma macropomum through genotyping-by-sequencing. Scientific reports, 7, 46112.

Oral M, et al. (2017) Gene-centromere mapping in meiotic gynogenetic European seabass. BMC genomics, 18(1), 449.

Niedzicka M, et al. (2017) Linkage Map of Lissotriton Newts Provides Insight into the Genetic Basis of Reproductive Isolation. G3 (Bethesda, Md.), 7(7), 2115.

Schiffthaler B, et al. (2017) BatchMap: A parallel implementation of the OneMap R package for fast computation of F1 linkage maps in outcrossing species. PloS one, 12(12), e0189256.

Brown JK, et al. (2016) Mapping the sex determination locus in the h?puku (Polyprion oxygeneios) using ddRAD sequencing. BMC genomics, 17, 448.

Pértille F, et al. (2016) High-throughput and Cost-effective Chicken Genotyping Using Next-Generation Sequencing. Scientific reports, 6, 26929.

Palaiokostas C, et al. (2015) A novel sex-determining QTL in Nile tilapia (Oreochromis niloticus). BMC genomics, 16(1), 171.

Zhou Z, et al. (2015) High-Density Genetic Mapping with Interspecific Hybrids of Two Sea Urchins, Strongylocentrotus nudus and S. intermedius, by RAD Sequencing. PloS one, 10(9), e0138585.

Palaiokostas C, et al. (2013) Mapping and validation of the major sex-determining region in Nile tilapia (Oreochromis niloticus L.) Using RAD sequencing. PloS one, 8(7), e68389.

Palaiokostas C, et al. (2013) Mapping the sex determination locus in the Atlantic halibut (Hippoglossus hippoglossus) using RAD sequencing. BMC genomics, 14, 566.

Hecht BC, et al. (2012) Genetic architecture of migration-related traits in rainbow and steelhead trout, Oncorhynchus mykiss. G3 (Bethesda, Md.), 2(9), 1113.