

Resource Summary Report

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Pedimap

RRID:SCR_010796

Type: Tool

Proper Citation

Pedimap (RRID:SCR_010796)

Resource Information

URL: <http://www.wageningenur.nl/en/show/Pedimap.htm>

Proper Citation: Pedimap (RRID:SCR_010796)

Description: A software tool for visualizing phenotypic and genotypic data for related individuals linked in pedigrees.

Abbreviations: Pedimap

Resource Type: software resource

Defining Citation: [PMID:23087384](#)

Keywords: bio.tools

Resource Name: Pedimap

Resource ID: SCR_010796

Alternate IDs: OMICS_00214, biotools:pedimap

Alternate URLs: <https://bio.tools/pedimap>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260725T190702+0000

Ratings and Alerts

No rating or validation information has been found for Pedimap.

No alerts have been found for Pedimap.

Data and Source Information

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Skytte Af Sättra J, et al. (2025) Genetic Analysis of Apple Autumn Canopy Senescence in a Nordic Climate. *Physiologia plantarum*, 177(6), e70599.

Skytte Af Sättra J, et al. (2024) Why we thrive beneath a northern sky - genomic signals of selection in apple for adaptation to northern Sweden. *Heredity*, 133(2), 67.

Rawandoozi ZJ, et al. (2024) Genetic dissection of stem and leaf rachis prickles in diploid rose using a pedigree-based QTL analysis. *Frontiers in plant science*, 15, 1356750.

Kostick SA, et al. (2021) Fire blight QTL analysis in a multi-family apple population identifies a reduced-susceptibility allele in 'Honeycrisp'. *Horticulture research*, 8(1), 28.

Rathnayake R, et al. (2020) Application of Pedimap: a pedigree visualization tool to facilitate the decisioning of rice breeding in Sri Lanka. *Scientific reports*, 10(1), 14255.

Muranty H, et al. (2020) Using whole-genome SNP data to reconstruct a large multi-generation pedigree in apple germplasm. *BMC plant biology*, 20(1), 2.

Calle A, et al. (2019) Genetic Dissection of Bloom Time in Low Chilling Sweet Cherry (*Prunus avium* L.) Using a Multi-Family QTL Approach. *Frontiers in plant science*, 10, 1647.

Di Guardo M, et al. (2017) Deciphering the genetic control of fruit texture in apple by multiple family-based analysis and genome-wide association. *Journal of experimental botany*, 68(7), 1451.

Verma S, et al. (2017) Clarifying sub-genomic positions of QTLs for flowering habit and fruit quality in U.S. strawberry (*Fragaria×ananassa*) breeding populations using pedigree-based QTL analysis. *Horticulture research*, 4, 17062.

Muranty H, et al. (2015) Accuracy and responses of genomic selection on key traits in apple breeding. *Horticulture research*, 2, 15060.

Tisné S, et al. (2015) Mixed model approach for IBD-based QTL mapping in a complex oil palm pedigree. *BMC genomics*, 16, 798.