

# Resource Summary Report

Generated by [dkNET](#) on Aug 4, 2026

## PEDIGRAPH

RRID:SCR\_001938

Type: Tool

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### Proper Citation

PEDIGRAPH (RRID:SCR\_001938)

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### Resource Information

**URL:** <http://animalgene.umn.edu/pedigraph/>

**Proper Citation:** PEDIGRAPH (RRID:SCR\_001938)

**Description:** A pedigree visualization program specifically designed to draw large, complex pedigrees. (entry from Genetic Analysis Software) Options include: \* Full pedigree \* Summarization \* Extraction of individual pedigrees \* Inbreeding calculation \* Coancestry coefficient calculation \* Color control \* Drawing size \* Page size and margins \* Drawing styles

**Abbreviations:** Pedigraph

**Resource Type:** software resource, software application

**Defining Citation:** [PMID:14986440](#)

**Keywords:** gene, genetic, genomic, c, c++, ms-windows, linux, pedigree, java, bio.tools

**Availability:** Acknowledgement required, Copyrighted

**Resource Name:** PEDIGRAPH

**Resource ID:** SCR\_001938

**Alternate IDs:** biotools:pedigraph, OMICS\_00212, nlx\_154519

**Alternate URLs:** <https://bio.tools/pedigraph>

**Record Creation Time:** 20220129T080210+0000

**Record Last Update:** 20260801T191038+0000

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### Ratings and Alerts

No rating or validation information has been found for PEDIGRAPH.

No alerts have been found for PEDIGRAPH.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Javarotti NB, et al. (2025) Genetic monitoring in ex situ populations of the endangered primate *Leontopithecus chrysopygus* and integrative analyses with the wild founder population. *PloS one*, 20(5), e0322817.

Harmoinen J, et al. (2025) Development of a cost-effective, multifunctional SNP panel and analysis workflow for Wolf monitoring in Finland. *Scientific reports*, 15(1), 40816.

Luo J, et al. (2024) Genetic assessment of eight zoo populations of golden snub-nosed monkey (*Rhinopithecus roxellana*) implication to the conservation management of captive populations. *Evolutionary applications*, 17(6), e13726.

Waksmunski AR, et al. (2022) Consequences of a Rare Complement Factor H Variant for Age-Related Macular Degeneration in the Amish. *Investigative ophthalmology & visual science*, 63(9), 8.

Donnelly CG, et al. (2021) Generation of a Biobank From Two Adult Thoroughbred Stallions for the Functional Annotation of Animal Genomes Initiative. *Frontiers in genetics*, 12, 650305.

Miller-Butterworth CM, et al. (2021) Genetic Diversity and Relatedness among Captive African Painted Dogs in North America. *Genes*, 12(10).

Jacinto JGP, et al. (2021) A frameshift insertion in FA2H causes a recessively inherited form of ichthyosis congenita in Chianina cattle. *Molecular genetics and genomics : MGG*, 296(6), 1313.

Lotsander A, et al. (2021) Low Persistence of Genetic Rescue Across Generations in the Arctic Fox (*Vulpes lagopus*). *The Journal of heredity*, 112(3), 276.

Waksmunski AR, et al. (2021) The GGLEAM Study: Understanding Glaucoma in the Ohio Amish. *International journal of environmental research and public health*, 18(4).

Hisey EA, et al. (2020) Whole genome sequencing identified a 16 kilobase deletion on ECA13 associated with distichiasis in Friesian horses. *BMC genomics*, 21(1), 848.

Woolley SA, et al. (2020) Molecular basis of a new ovine model for human 3M syndrome-2. BMC genetics, 21(1), 106.

Krull F, et al. (2020) Frameshift Variant in Novel Adenosine-A1-Receptor Homolog Associated With Bovine Spastic Syndrome/Late-Onset Bovine Spastic Paresis in Holstein Sires. Frontiers in genetics, 11, 591794.

Andrade LR, et al. (2019) Allele Frequency of the C.5G>A Mutation in the PRCD Gene Responsible for Progressive Retinal Atrophy in English Cocker Spaniel Dogs. Animals : an open access journal from MDPI, 9(10).

Finno CJ, et al. (2018) A missense mutation in MYH1 is associated with susceptibility to immune-mediated myositis in Quarter Horses. Skeletal muscle, 8(1), 7.

Hollmann AK, et al. (2017) A genome-wide association study reveals a locus for bilateral iridal hypopigmentation in Holstein Friesian cattle. BMC genetics, 18(1), 30.

Mack M, et al. (2017) Two Variants in SLC24A5 Are Associated with "Tiger-Eye" Iris Pigmentation in Puerto Rican Paso Fino Horses. G3 (Bethesda, Md.), 7(8), 2799.

Bosse M, et al. (2015) Using genome-wide measures of coancestry to maintain diversity and fitness in endangered and domestic pig populations. Genome research, 25(7), 970.