

Resource Summary Report

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PROGENY

RRID:SCR_006647

Type: Tool

Proper Citation

PROGENY (RRID:SCR_006647)

Resource Information

URL: <http://www.progenygenetics.com/>

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Description: Fully customizable, comprehensive genetic pedigree and clinical data management software including a multi-user relational database with an integrated pedigree drawing component to manage genetic and pedigree data in one database. Manage Pedigrees, Individuals, SNPs, STRs, Samples, Plates, Genotypes and exports to multiple analysis platforms. (entry from Genetic Analysis Software) * LIMS software, providing advanced sample tracking and management (including functionality to generate and record barcodes) and configurable workflows for your specific environment. * Full genotype management gives users the ability to track not only family-based studies, but Whole Genome Association studies containing 1000's of samples with large arrays.

Abbreviations: Progeny

Synonyms: Progeny Software LLC, Progeny Software

Resource Type: data management software, commercial organization, software resource, software application

Keywords: gene, genetic, genomic, c++, active x control, ms-windows, pedigree, clinical, genotype, data management, drawing, family history, questionnaire, sample, lab management, FASEB list

Funding:

Resource Name: PROGENY

Resource ID: SCR_006647

Alternate IDs: nlx_154553, OMICS_00216

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250418T055135+0000

Ratings and Alerts

No rating or validation information has been found for PROGENY.

No alerts have been found for PROGENY.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 350 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Heestand B, et al. (2025) Piwi mutant germ cells transmit a form of heritable stress that promotes longevity. *Aging cell*, 24(1), e14350.

Yang L, et al. (2025) A tunable human intestinal organoid system achieves controlled balance between self-renewal and differentiation. *Nature communications*, 16(1), 315.

Lin W, et al. (2025) Mapping the spatial atlas of the human bone tissue integrating spatial and single-cell transcriptomics. *Nucleic acids research*, 53(2).

Zhang X, et al. (2025) Tumour heterogeneity and personalized treatment screening based on single-cell transcriptomics. *Computational and structural biotechnology journal*, 27, 307.

Cheng Y, et al. (2025) Stromal architecture and fibroblast subpopulations with opposing effects on outcomes in hepatocellular carcinoma. *Cell discovery*, 11(1), 1.

Viswanathan MC, et al. (2025) Dominant myosin storage myopathy mutations disrupt striated muscles in *Drosophila* and the myosin tail-tail interactome of human cardiac thick filaments. *Genetics*, 229(1), 1.

Chen J, et al. (2025) Piwi regulates the usage of alternative transcription start sites in the *Drosophila* ovary. *Nucleic acids research*, 53(1).

Zahid A, et al. (2025) Identifying genetic susceptibility loci associated with human coronary artery disease. *PLoS one*, 20(1), e0315460.

Jenkins BH, et al. (2025) Single cell and spatial analysis of immune-hot and immune-cold tumours identifies fibroblast subtypes associated with distinct immunological niches and positive immunotherapy response. *Molecular cancer*, 24(1), 3.

Yu X, et al. (2025) Integrative bioinformatics and immunohistochemical analysis unravel the prognostic significance and immunological implication of LIMCH1 in breast cancer: a retrospective study. *Scientific reports*, 15(1), 1446.

Xu X, et al. (2025) Gene drive-based population suppression in the malaria vector *Anopheles stephensi*. *Nature communications*, 16(1), 1007.

Zhang D, et al. (2024) Multiomics Data Reveal the Important Role of ANXA2R in T Cell-mediated Rejection After Renal Transplantation. *Transplantation*, 108(2), 430.

Sun W, et al. (2024) Comprehensive analysis of the interaction of antigen presentation during anti-tumour immunity and establishment of AIDPS systems in ovarian cancer. *Journal of cellular and molecular medicine*, 28(8), e18309.

Romashin D, et al. (2024) Exploring the Functions of Mutant p53 through TP53 Knockout in HaCaT Keratinocytes. *Current issues in molecular biology*, 46(2), 1451.

Jiang Y, et al. (2024) Unveiling macrophage diversity in myocardial ischemia-reperfusion injury: identification of a distinct lipid-associated macrophage subset. *Frontiers in immunology*, 15, 1335333.

Buse M, et al. (2024) Lineage tracing reveals transient phenotypic adaptation of tubular cells during acute kidney injury. *iScience*, 27(3), 109255.

Kisakol B, et al. (2024) Identification of unique rectal cancer-specific subtypes. *British journal of cancer*, 130(11), 1809.

Essadik I, et al. (2024) Mutations in *Podospira anserina* MCM1 and VelC Trigger Spontaneous Development of Barren Fruiting Bodies. *Journal of fungi (Basel, Switzerland)*, 10(1).

Broghammer F, et al. (2024) Resistance of HNSCC cell models to pan-FGFR inhibition depends on the EMT phenotype associating with clinical outcome. *Molecular cancer*, 23(1), 39.

Liu J, et al. (2024) Spatial transcriptome and single-cell reveal the role of nucleotide metabolism in colorectal cancer progression and tumor microenvironment. *Journal of translational medicine*, 22(1), 702.