

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

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

Resource Name: PROGENY

Resource ID: SCR_006647

Alternate IDs: nlx_154553, OMICS_00216

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260728T043236+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 407 mentions in open access literature.

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

Fortunato MC, et al. (2025) Maternal Tryptophan Supplementation Alters Offspring Gut-Brain Axis and Behavior in a Sex-Specific Manner. *Journal of neurochemistry*, 169(7), e70161.

Stier MT, et al. (2025) Metabolic Adaptations Rewire CD4 T Cells in a Subset-Specific Manner in Human Critical Illness with and without Sepsis. *bioRxiv : the preprint server for biology*.

Horn S, et al. (2025) IL-1 protects from fatal systemic candidiasis in mice by inhibiting oxidative phosphorylation and hypoxia. *Nature communications*, 16(1), 2626.

Wang X, et al. (2025) Characterizing resistant cellular states in nasopharyngeal carcinoma during EBV lytic induction. *Oncogene*, 44(23), 1805.

Huang J, et al. (2025) Reliable mass production of *Ganaspis kimorum* (Hymenoptera: Figitidae), a larval parasitoid of *Drosophila suzukii* (Diptera: Drosophilidae). *Journal of insect science (Online)*, 25(2).

Chen X, et al. (2025) Integrative single cell transcriptomic analysis reveals 3p deletion associated tumor microenvironment and chemoresistance in head and neck squamous cell carcinoma. *Scientific reports*, 15(1), 8224.

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).

Leung RWT, et al. (2025) CORN 2.0 - Condition Orientated Regulatory Networks 2.0. *Computational and structural biotechnology journal*, 27, 1518.

Nummelin JR, et al. (2025) The families SHARE project: novel insights on recruiting and engaging Black men in a community-based genomic education program. *BMC public health*, 25(1), 805.

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

Abu-Sultanah M, et al. (2025) TGF β -dependent signaling drives tumor growth and aberrant extracellular matrix dynamics in NF1-associated plexiform neurofibroma. *Science advances*, 11(25), eadu0772.

Mao J, et al. (2025) CA3 bridges dietary restriction to glioblastoma suppression and tumor progression as a key downstream effector. *Scientific reports*, 15(1), 18661.

Xu DM, et al. (2025) Decoding the impact of MMP1+ malignant subsets on tumor-immune interactions: insights from single-cell and spatial transcriptomics. *Cell death discovery*, 11(1), 244.

Cao Z, et al. (2025) Integrated single-cell and bulk RNA sequencing analysis establishes a cancer associated fibroblast-related signature for predicting prognosis and therapeutic responses in neuroblastoma. *Discover oncology*, 16(1), 1235.

Vlachavas EI, et al. (2025) Molecular and functional profiling unravels targetable vulnerabilities in colorectal cancer. *Molecular oncology*, 19(6), 1751.

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

Ma X, et al. (2025) Programmed cell death-related prognostic genes mediate dysregulation of the immune microenvironment in triple-negative breast cancer. *Frontiers in immunology*, 16, 1563630.

Gunter-Rahman F, et al. (2025) Hypoxia in extravillous trophoblasts links maternal obesity and offspring neurobehavior. *iScience*, 28(6), 112636.

Lenartowski R, et al. (2025) Myosin VI is expressed in developing ovarian follicles in *Drosophila* but is not essential for effective oogenesis. *Frontiers in cell and developmental biology*, 13, 1535117.