

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

PREST

RRID:SCR_009336

Type: Tool

Proper Citation

PREST (RRID:SCR_009336)

Resource Information

URL: <http://fisher.utstat.toronto.edu/sun/Software/Prest> or previously, <http://galton.uchicago.edu/~mcpeek/software/prest>

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Description: Software program that detects pedigree errors in general outbred pedigrees by use of genome-screen data. When a potential pedigree error is detected, our companion program, ALTERTEST, determines which relationships are compatible with the observed genotype data. Both programs are freely available on the web. (entry from Genetic Analysis Software)

Abbreviations: PREST

Synonyms: Pedigree Relationship Statistical Test

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c, linux, unix, solaris

Resource Name: PREST

Resource ID: SCR_009336

Alternate IDs: nlx_154548

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260905T133250+0000

Ratings and Alerts

No rating or validation information has been found for PREST.

No alerts have been found for PREST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Hinkle TB, et al. (2025) Comprehensive Protein Inference Analysis with PyProteinInference Elucidates Biological Understanding of Tandem Mass Spectrometry Data. Journal of proteome research, 24(4), 2135.

Dong Y, et al. (2025) Tree resistance outweighs climatic drivers in governing extreme growth suppression. iScience, 28(8), 113043.

Qian C, et al. (2024) ONECUT2 acts as a lineage plasticity driver in adenocarcinoma as well as neuroendocrine variants of prostate cancer. Nucleic acids research, 52(13), 7740.

Zhu Y, et al. (2023) Exploring Route-Specific Pharmacokinetics of PFAS in Mice by Coupling in Vivo Tests and Physiologically Based Toxicokinetic Models. Environmental health perspectives, 131(12), 127012.

Qian C, et al. (2023) ONECUT2 Activates Diverse Resistance Drivers of Androgen Receptor-Independent Heterogeneity in Prostate Cancer. bioRxiv : the preprint server for biology.

Lopes GS, et al. (2022) Identification of sex-specific genetic associations in response to opioid analgesics in a White, non-Hispanic cohort from Southeast Minnesota. The pharmacogenomics journal, 22(2), 117.

Chou WC, et al. (2022) An Interactive Generic Physiologically Based Pharmacokinetic (igPBPK) Modeling Platform to Predict Drug Withdrawal Intervals in Cattle and Swine: A Case Study on Flunixin, Florfenicol, and Penicillin G. Toxicological sciences : an official journal of the Society of Toxicology, 188(2), 180.

Chou WC, et al. (2021) Development of a Gestational and Lactational Physiologically Based Pharmacokinetic (PBPK) Model for Perfluorooctane Sulfonate (PFOS) in Rats and Humans and Its Implications in the Derivation of Health-Based Toxicity Values. Environmental health perspectives, 129(3), 37004.

Musolf AM, et al. (2018) Myopia in Chinese families shows linkage to 10q26.13. Molecular vision, 24, 29.

Itzhak DN, et al. (2016) Global, quantitative and dynamic mapping of protein subcellular localization. eLife, 5.

Saccone SF, et al. (2007) Genetic linkage to chromosome 22q12 for a heavy-smoking quantitative trait in two independent samples. American journal of human genetics, 80(5), 856.