Resource Summary Report

Generated by NIF on Sep 3, 2026

Isaac

RRID:SCR_012772
Type: Tool

Proper Citation

Isaac (RRID:SCR_012772)

Resource Information

URL: https://github.com/sequencing

Proper Citation: Isaac (RRID:SCR_012772)

Description: Whole genome secondary analysis on Illumina sequencing platforms.

Abbreviations: Isaac

Resource Type: software resource

Keywords: bio.tools

Resource Name: Isaac

Resource ID: SCR_012772

Alternate IDs: biotools:isaac, OMICS_00289

Alternate URLs: https://bio.tools/isaac

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260903T235219+0000

Ratings and Alerts

No rating or validation information has been found for Isaac.

No alerts have been found for Isaac.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 74 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Wu T, et al. (2026) Therapeutic strategy for cervical gastric-type adenocarcinoma by targeting CLU to relieve CLU-associated stress and sensitize chemotherapy. Precision clinical medicine, 9(1), pbag003.

Kanchan K, et al. (2026) Genetic Determinants of Peanut-Specific IgG4 Levels in the Context of Sustained Oral Peanut Exposure in the LEAP Study. Immunology, 178(2), 280.

Riedhammer C, et al. (2026) The evolution to hepta-refractory myeloma involves sequential loss of CD38, BCMA and GPRC5D. Leukemia, 40(4), 730.

Miwa H, et al. (2026) Polygenic and single-locus selection on BMI during Polynesian expansion. Journal of human genetics, 71(5), 293.

Singh M, et al. (2026) Endogenous retroviral elements LTR8B and MER65 rewire PSG9 regulation to control trophoblast syncytialization and pre-eclampsia risk. Genome biology, 27(1).

Cremer S, et al. (2025) Prognostic significance of somatic mutations in myeloid cells of men with chronic heart failure - interaction between loss of Y chromosome and clonal haematopoiesis. European journal of heart failure, 27(12), 3219.

Menato F, et al. (2025) Rare uniparental lineages reveal external ancestries in the gene pool of the Italian linguistic enclave of Grecìa Salentina. Scientific reports, 16(1), 1528.

Hwang HY, et al. (2025) Engineered Sdd7 cytosine base editors with enhanced specificity. Nature communications, 16(1), 5881.

De la Cruz Sánchez BA, et al. (2025) A hybrid elastic-hyperelastic approach for simulating soft tactile sensors. Frontiers in robotics and AI, 12, 1639524.

Kweon J, et al. (2025) High-efficiency base editing for nuclear and mitochondrial DNA with an optimized DYW-like deaminase. Molecular therapy : the journal of the American Society of Gene Therapy, 33(11), 5611.

Shiozawa AL, et al. (2025) Identification of coexisting Mfrprd6 and Pde6brd10 mutations causing spontaneous retinal detachment in commercially available rd6 mice. PloS one, 20(9), e0332446.

van der Tuin K, et al. (2024) Clinically Relevant Germline Variants in Children With Nonmedullary Thyroid Cancer. The Journal of clinical endocrinology and metabolism, 109(12), e2214.

Shumliakivska M, et al. (2024) DNMT3A clonal hematopoiesis-driver mutations induce cardiac fibrosis by paracrine activation of fibroblasts. Nature communications, 15(1), 606.

Bateman NW, et al. (2024) Proteogenomic analysis of enriched HGSOC tumor epithelium identifies prognostic signatures and therapeutic vulnerabilities. NPJ precision oncology, 8(1), 68.

Dietzen M, et al. (2024) Replication timing alterations are associated with mutation acquisition during breast and lung cancer evolution. Nature communications, 15(1), 6039.

Hwang HY, et al. (2024) Precise editing of pathogenic nucleotide repeat expansions in iPSCs using paired prime editor. Nucleic acids research, 52(10), 5792.

Wang P, et al. (2024) Genome-wide association studies identify novel loci in rapidly progressive Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 20(3), 2034.

Klein K, et al. (2024) A lineage-specific STAT5BN642H mouse model to study NK-cell leukemia. Blood, 143(24), 2474.

Cornish AJ, et al. (2024) The genomic landscape of 2,023 colorectal cancers. Nature, 633(8028), 127.

Ikeda T, et al. (2023) APOBEC3 degradation is the primary function of HIV-1 Vif for virus replication in the myeloid cell line THP-1. bioRxiv : the preprint server for biology.