Resource Summary Report

Generated by RRID on Aug 2, 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: 20260801T190440+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 66 mentions in open access literature.

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

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

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

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.

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.

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

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

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

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.

Mas-Peiro S, et al. (2023) Mosaic loss of Y chromosome in monocytes is associated with lower survival after transcatheter aortic valve replacement. European heart journal, 44(21), 1943.

Sturm G, et al. (2023) OxPhos defects cause hypermetabolism and reduce lifespan in cells and in patients with mitochondrial diseases. Communications biology, 6(1), 22.

Pagnamenta AT, et al. (2023) The prevalence and phenotypic range associated with biallelic PKDCC variants. Clinical genetics, 104(1), 121.

Ikeda T, et al. (2023) APOBEC3 degradation is the primary function of HIV-1 Vif determining virion infectivity in the myeloid cell line THP-1. mBio, 14(4), e0078223.

Lenassi E, et al. (2023) EyeG2P: an automated variant filtering approach improves efficiency of diagnostic genomic testing for inherited ophthalmic disorders. Journal of medical genetics, 60(8), 810.

Mauleekoonphairoj J, et al. (2023) A diverse ancestrally-matched reference panel increases genotype imputation accuracy in a underrepresented population. Scientific reports, 13(1), 12360.

Lee H, et al. (2023) Mechanisms of antigen escape from BCMA- or GPRC5D-targeted immunotherapies in multiple myeloma. Nature medicine, 29(9), 2295.

Habib O, et al. (2022) Comprehensive analysis of prime editing outcomes in human embryonic stem cells. Nucleic acids research, 50(2), 1187.