

Resource Summary Report

Generated by [dkNET](#) on Jul 30, 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: 20260725T190737+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 [dkNET](#) .

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.