Resource Summary Report

Generated by RRID on Aug 2, 2026

MIPgen

RRID:SCR_003325
Type: Tool

Proper Citation

MIPgen (RRID:SCR_003325)

Resource Information

URL: http://shendurelab.github.io/MIPGEN/

Proper Citation: MIPgen (RRID:SCR_003325)

Description: Software for a fast, simple way to generate designs for MIP assays targeting hundreds or thousands of genomic loci in parallel. Packaged with MIPgen are scripts that aid in visualization of MIP designs and processing of MIP sequence reads to SAM files that can then be passed through any standard variant calling pipeline.

Synonyms: MIPgen - One stop MIP design and analysis

Resource Type: software resource

Defining Citation: PMID:24867941

Keywords: standalone software, c++, python, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: MIPgen

Resource ID: SCR_003325

Alternate IDs: OMICS_04657, biotools:mipgen

Alternate URLs: https://github.com/shendurelab/MIPGEN, https://bio.tools/mipgen

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260801T190208+0000

Ratings and Alerts

No rating or validation information has been found for MIPgen.

No alerts have been found for MIPgen.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 48 mentions in open access literature.

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

Hany U, et al. (2025) Genetic Screening of a Nonsyndromic Amelogenesis Imperfecta Patient Cohort Using a Custom smMIP Reagent for Selective Enrichment of Target Loci. Human mutation, 2025, 8942542.

Sussman JH, et al. (2025) In vivo CRISPR screening reveals epigenetic regulators of hepatobiliary plasticity. Genes & development, 39(9-10), 603.

Ishorst N, et al. (2025) Role of ZFHX4 in orofacial clefting based on human genetic data and zebrafish models. European journal of human genetics : EJHG, 33(5), 595.

Sierant MC, et al. (2025) Genomic analysis of 11,555 probands identifies 60 dominant congenital heart disease genes. Proceedings of the National Academy of Sciences of the United States of America, 122(13), e2420343122.

Lecoquierre F, et al. (2025) Parental germline mosaicism in genome-wide phased de novo variants: Recurrence risk assessment and implications for precision genetic counselling. PLoS genetics, 21(3), e1011651.

Gallon R, et al. (2025) Novel microsatellite instability test of sebaceous tumours to facilitate low-cost universal screening for Lynch syndrome. Clinical and experimental dermatology, 50(6), 1155.

Shin T, et al. (2024) Rare variation in non-coding regions with evolutionary signatures contributes to autism spectrum disorder risk. Cell genomics, 4(8), 100609.

Hany U, et al. (2024) Heterozygous COL17A1 variants are a frequent cause of amelogenesis imperfecta. Journal of medical genetics, 61(4), 347.

Sheth H, et al. (2024) Development, validation and application of single molecule molecular inversion probe based novel integrated genetic screening method for 29 common lysosomal storage disorders in India. Human genomics, 18(1), 46.

Plowman JN, et al. (2024) Targeted sequencing for hereditary breast and ovarian cancer in BRCA1/2-negative families reveals complex genetic architecture and phenocopies. HGG advances, 5(3), 100306.

Van Dijck E, et al. (2024) A Case-Control Study Supports Genetic Contribution of the PON Gene Family in Obesity and Metabolic Dysfunction Associated Steatotic Liver Disease. Antioxidants (Basel, Switzerland), 13(9).

Lecoquierre F, et al. (2024) Assessment of parental mosaicism rates in neurodevelopmental disorders caused by apparent de novo pathogenic variants using deep sequencing. Scientific reports, 14(1), 5289.

Kadam A, et al. (2024) Utilizing insights of DNA repair machinery to discover MMEJ deletions and novel mechanisms. Nucleic acids research, 52(22), e106.

Smits WK, et al. (2023) Elevated enhancer-oncogene contacts and higher oncogene expression levels by recurrent CTCF inactivating mutations in acute T cell leukemia. Cell reports, 42(4), 112373.

Shin T, et al. (2023) Rare variation in noncoding regions with evolutionary signatures contributes to autism spectrum disorder risk. medRxiv : the preprint server for health sciences.

Andralojc KM, et al. (2022) Targeted RNA next generation sequencing analysis of cervical smears can predict the presence of hrHPV-induced cervical lesions. BMC medicine, 20(1), 206.

Webster AK, et al. (2022) Using population selection and sequencing to characterize natural variation of starvation resistance in Caenorhabditis elegans. eLife, 11.

Medeiros JJF, et al. (2022) SmMIP-tools: a computational toolset for processing and analysis of single-molecule molecular inversion probes-derived data. Bioinformatics (Oxford, England), 38(8), 2088.

Girskis KM, et al. (2021) Rewiring of human neurodevelopmental gene regulatory programs by human accelerated regions. Neuron, 109(20), 3239.

B?k A, et al. (2021) Germline mutations among Polish patients with acute myeloid leukemia. Hereditary cancer in clinical practice, 19(1), 42.