# Resource Summary Report

Generated by NIF on Apr 8, 2025

## MIPgen

RRID:SCR_003325
Type: Tool

### Proper Citation

MIPgen (RRID:SCR_003325)

### Resource Information

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

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**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

**Funding:**

**Availability:** Non-commercial

**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:** 20250214T183024+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 42 mentions in open access literature.

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


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.

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).

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.

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.

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.

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

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.

Guerrini R, et al. (2021) Is Focal Cortical Dysplasia/Epilepsy Caused by Somatic MTOR Mutations Always a Unilateral Disorder? Neurology. Genetics, 7(1), e540.

Almomani R, et al. (2020) Evaluation of molecular inversion probe versus TruSeq® custom methods for targeted next-generation sequencing. PloS one, 15(9), e0238467.

Qin L, et al. (2020) Genetic analysis of N6-methyladenosine modification genes in Parkinson's disease. Neurobiology of aging, 93, 143.e9.

Kwon YM, et al. (2020) Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. PLoS biology, 18(11), e3000926.

Gallon R, et al. (2020) Sequencing-based microsatellite instability testing using as few as six markers for high-throughput clinical diagnostics. Human mutation, 41(1), 332.

Wada Y, et al. (2020) Peroxisome proliferator-activated receptor ? as a novel therapeutic target for schizophrenia. EBioMedicine, 62, 103130.