

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

Atlas2

RRID:SCR_010756

Type: Tool

Proper Citation

Atlas2 (RRID:SCR_010756)

Resource Information

URL: <https://www.hgsc.bcm.edu/content/atlas2>

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Description: A next-generation sequencing suite of variant analysis tools specializing in the separation of true SNPs and insertions and deletions (indels) from sequencing and mapping errors in WECS data.

Synonyms: Atlas Suite

Resource Type: software resource

Defining Citation: [PMID:22239737](#)

Keywords: bio.tools

Resource Name: Atlas2

Resource ID: SCR_010756

Alternate IDs: biotools:atlas_suite, OMICS_00051

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

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260903T235032+0000

Ratings and Alerts

No rating or validation information has been found for Atlas2.

No alerts have been found for Atlas2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Coban-Akdemir Z, et al. (2024) The impact of the Turkish population variome on the genomic architecture of rare disease traits. *Genetics in medicine open*, 2, 101830.

Leung YY, et al. (2024) Human whole-exome genotype data for Alzheimer's disease. *Nature communications*, 15(1), 684.

Cheng J, et al. (2024) Novel, pathogenic insertion variant of GSDME associates with autosomal dominant hearing loss in a large Chinese pedigree. *Journal of cellular and molecular medicine*, 28(1), e18004.

Rasnic R, et al. (2019) Substantial batch effects in TCGA exome sequences undermine pan-cancer analysis of germline variants. *BMC cancer*, 19(1), 783.

de Haan HG, et al. (2018) Targeted sequencing to identify novel genetic risk factors for deep vein thrombosis: a study of 734 genes. *Journal of thrombosis and haemostasis : JTH*, 16(12), 2432.

Jing D, et al. (2018) Lymphocyte-Specific Chromatin Accessibility Pre-determines Glucocorticoid Resistance in Acute Lymphoblastic Leukemia. *Cancer cell*, 34(6), 906.

Simino J, et al. (2017) Whole exome sequence-based association analyses of plasma amyloid-?? in African and European Americans; the Atherosclerosis Risk in Communities-Neurocognitive Study. *PloS one*, 12(7), e0180046.

Soens ZT, et al. (2016) Hypomorphic mutations identified in the candidate Leber congenital amaurosis gene CLUAP1. *Genetics in medicine : official journal of the American College of Medical Genetics*, 18(10), 1044.

Huang MN, et al. (2015) MSIsq: Software for Assessing Microsatellite Instability from Catalogs of Somatic Mutations. *Scientific reports*, 5, 13321.

Liu X, et al. (2013) Variant callers for next-generation sequencing data: a comparison study. *PloS one*, 8(9), e75619.

Nookaew I, et al. (2012) A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in *Saccharomyces cerevisiae*. *Nucleic acids research*, 40(20), 10084.