

# Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

## Atlas2

RRID:SCR\_010756

Type: Tool

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### Proper Citation

Atlas2 (RRID:SCR\_010756)

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### Resource Information

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

**Proper Citation:** Atlas2 (RRID:SCR\_010756)

**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](https://bio.tools/atlas_suite)

**Record Creation Time:** 20220129T080300+0000

**Record Last Update:** 20260801T190416+0000

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### 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 [RRID](#) .

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

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.

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.