Resource Summary Report

Generated by PRECISE-TBI on Sep 19, 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: 20260912T195722+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 PRECISE-TBI .

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) MSIseq: 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.