Resource Summary Report

Generated by NIF on Apr 17, 2025

SAMMate

RRID:SCR_013037
Type: Tool

Proper Citation

SAMMate (RRID:SCR_013037)

Resource Information

URL: http://sammate.sourceforge.net/

Proper Citation: SAMMate (RRID:SCR_013037)

Description: An open source GUI software suite to process RNA-Seq data. It is composed of two modules: assemblySAM and SAMMate.

Abbreviations: SAMMate

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: SAMMate

Resource ID: SCR_013037

Alternate IDs: biotools:sammate, OMICS_01264

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

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250410T070326+0000

Ratings and Alerts

No rating or validation information has been found for SAMMate.

No alerts have been found for SAMMate.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Rhodes JW, et al. (2021) Human anogenital monocyte-derived dendritic cells and langerin+cDC2 are major HIV target cells. Nature communications, 12(1), 2147.

Afrasiabi A, et al. (2019) Evidence from genome wide association studies implicates reduced control of Epstein-Barr virus infection in multiple sclerosis susceptibility. Genome medicine, 11(1), 26.

Sun F, et al. (2019) Promoter-Enhancer Communication Occurs Primarily within Insulated Neighborhoods. Molecular cell, 73(2), 250.

Gao B, et al. (2017) Inhibition of lobuloalveolar development by FOXC1 overexpression in the mouse mammary gland. Scientific reports, 7(1), 14017.

Zhang R, et al. (2017) Interaction of Epstein-Barr virus genes with human gastric carcinoma transcriptome. Oncotarget, 8(24), 38399.

Huang C, et al. (2017) Cbx3 maintains lineage specificity during neural differentiation. Genes & development, 31(3), 241.

Sepe S, et al. (2016) Inefficient DNA Repair Is an Aging-Related Modifier of Parkinson's Disease. Cell reports, 15(9), 1866.

Deng N, et al. (2013) Detecting splicing variants in idiopathic pulmonary fibrosis from non-differentially expressed genes. PloS one, 8(7), e68352.

Ferrari R, et al. (2012) Reorganization of the host epigenome by a viral oncogene. Genome research, 22(7), 1212.

Xu G, et al. (2011) SAMMate: a GUI tool for processing short read alignments in SAM/BAM format. Source code for biology and medicine, 6(1), 2.