Resource Summary Report

Generated by kravitz2 on Jul 31, 2026

Pash 3.0

RRID:SCR_004078
Type: Tool

Proper Citation

Pash 3.0 (RRID:SCR_004078)

Resource Information

URL: http://www.brl.bcm.tmc.edu/pash/pashDownload.rhtml

Proper Citation: Pash 3.0 (RRID:SCR_004078)

Description: Performs sequence comparison and read mapping and can be employed as a module within diverse configurable analysis pipelines, including ChIP-Seq and methylome mapping by whole-genome bisulfite sequencing.

Abbreviations: Pash 3.0

Resource Type: software resource

Defining Citation: PMID:21092284

Keywords: bio.tools

Resource Name: Pash 3.0

Resource ID: SCR_004078

Alternate IDs: biotools:pash, OMICS_00586

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

Record Creation Time: 20220129T080222+0000

Record Last Update: 20260725T190546+0000

Ratings and Alerts

No rating or validation information has been found for Pash 3.0.

No alerts have been found for Pash 3.0.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Coarfa C, et al. (2010) Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. BMC bioinformatics, 11, 572.