

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

SLOPE

RRID:SCR_001185

Type: Tool

Proper Citation

SLOPE (RRID:SCR_001185)

Resource Information

URL: <http://www-genepi.med.utah.edu/suppl/SLOPE/index.html>

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Description: Software that consists of two command-line utilities, slope_align (which finds the best split-read alignments to the reference genome) and slope_cluster (which clusters and outputs the alignments)., THIS RESOURCE IS NO LONGER IN SERVICE.
Documented on September 16,2025.

Abbreviations: SLOPE

Resource Type: software resource

Defining Citation: [PMID:20876606](#)

Keywords: c++, alignment, cluster, command-line, reference genome, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SLOPE

Resource ID: SCR_001185

Alternate IDs: OMICS_02169, biotools:slope

Alternate URLs: <https://bio.tools/slope>

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260808T185738+0000

Ratings and Alerts

No rating or validation information has been found for SLOPE.

No alerts have been found for SLOPE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.