

# Resource Summary Report

Generated by [NIF](#) on Sep 17, 2026

## SLOPE

RRID:SCR\_001185

Type: Tool

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### Proper Citation

SLOPE (RRID:SCR\_001185)

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### Resource Information

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

**Proper Citation:** SLOPE (RRID:SCR\_001185)

**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:** 20260912T195521+0000

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### Ratings and Alerts

No rating or validation information has been found for SLOPE.

No alerts have been found for SLOPE.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.