

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

## CoverageCalculator

RRID:SCR\_005352

Type: Tool

### Proper Citation

CoverageCalculator (RRID:SCR\_005352)

### Resource Information

**URL:** <http://covcal.sourceforge.net/>

**Proper Citation:** CoverageCalculator (RRID:SCR\_005352)

**Description:** Small and very fast utility to calculate X-coverage from Next-Generation-Sequencing data.

**Abbreviations:** CoverageCalculator

**Resource Type:** software resource

**Keywords:** next-generation sequencing

**Resource Name:** CoverageCalculator

**Resource ID:** SCR\_005352

**Alternate IDs:** OMICS\_01164

**Record Creation Time:** 20220129T080229+0000

**Record Last Update:** 20260725T190602+0000

### Ratings and Alerts

No rating or validation information has been found for CoverageCalculator.

No alerts have been found for CoverageCalculator.

### Data and Source Information

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

## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Trivedi R, et al. (2019) Amino acid substitution scoring matrices specific to intrinsically disordered regions in proteins. Scientific reports, 9(1), 16380.

Hess M, et al. (2016) Addressing inaccuracies in BLOSUM computation improves homology search performance. BMC bioinformatics, 17, 189.