

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

## SoISNP

RRID:SCR\_013045

Type: Tool

### Proper Citation

SoISNP (RRID:SCR\_013045)

### Resource Information

**URL:** <http://sourceforge.net/projects/solsnp/>

**Proper Citation:** SoISNP (RRID:SCR\_013045)

**Description:** A Java-based DNA variant calling tool for Next-Generation Sequencing alignment data.

**Abbreviations:** SoISNP

**Resource Type:** software resource

**Availability:** MIT License

**Resource Name:** SoISNP

**Resource ID:** SCR\_013045

**Alternate IDs:** OMICS\_00079

**Record Creation Time:** 20220129T080314+0000

**Record Last Update:** 20260905T132731+0000

### Ratings and Alerts

No rating or validation information has been found for SoISNP.

No alerts have been found for SoISNP.

### Data and Source Information

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

## Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Bush SJ, et al. (2021) Generalizable characteristics of false-positive bacterial variant calls. *Microbial genomics*, 7(8).

Driebe EM, et al. (2015) Using Whole Genome Analysis to Examine Recombination across Diverse Sequence Types of *Staphylococcus aureus*. *PloS one*, 10(7), e0130955.

Sahl JW, et al. (2015) Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. *Genome medicine*, 7(1), 52.

Khmaladze E, et al. (2014) Phylogeography of *Bacillus anthracis* in the country of Georgia shows evidence of population structuring and is dissimilar to other regional genotypes. *PloS one*, 9(7), e102651.

Stegger M, et al. (2014) Origin and evolution of European community-acquired methicillin-resistant *Staphylococcus aureus*. *mBio*, 5(5), e01044.

Rawat A, et al. (2014) MetaGeniE: characterizing human clinical samples using deep metagenomic sequencing. *PloS one*, 9(11), e110915.

Scholz HC, et al. (2014) Genotyping of *Burkholderia mallei* from an outbreak of glanders in Bahrain suggests multiple introduction events. *PLoS neglected tropical diseases*, 8(9), e3195.