

# Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

## piCALL

RRID:SCR\_001242

Type: Tool

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### Proper Citation

piCALL (RRID:SCR\_001242)

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### Resource Information

**URL:** <https://sites.google.com/site/vibansal/software/picall>

**Proper Citation:** piCALL (RRID:SCR\_001242)

**Description:** Software to detect short insertion / deletion variants (and SNPs) from population sequence data, i.e. sequence reads generated from a population of individuals. It uses a probabilistic model to utilize sequence reads from a population of individuals to automatically account for context-specific sequencing errors associated with indels. piCALL is implemented in C for use on Linux platforms and can be applied to sequence data from different sequencing platforms. However, the method requires each individual in a dataset to be sequenced using the same platform. The reads for each individual should be aligned to the same reference genome sequence. Note that the program will not be able to call indels from individual sequence datasets or data from a small number of individuals.

**Abbreviations:** piCALL

**Resource Type:** software resource

**Defining Citation:** [PMID:21653520](#)

**Keywords:** c, genotyping, indel, population, high-throughput sequencing, insertion, deletion, variant, single nucleotide polymorphism, linux, bio.tools

**Resource Name:** piCALL

**Resource ID:** SCR\_001242

**Alternate IDs:** OMICS\_02098, biotools:picall

**Alternate URLs:** <https://bio.tools/picall>

**Old URLs:** <http://polymorphism.scripps.edu/~vbansal/software/piCALL/>

**Record Creation Time:** 20220129T080206+0000

**Record Last Update:** 20260801T190144+0000

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## Ratings and Alerts

No rating or validation information has been found for piCALL.

No alerts have been found for piCALL.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Bansal V, et al. (2016) A statistical method for the detection of variants from next-generation resequencing of DNA pools. Bioinformatics (Oxford, England), 32(20), 3213.