

Resource Summary Report

Generated by [nidm-terms](#) on Jul 30, 2026

Parliament2

RRID:SCR_019187

Type: Tool

Proper Citation

Parliament2 (RRID:SCR_019187)

Resource Information

URL: <https://github.com/slzarate/parliament2>

Proper Citation: Parliament2 (RRID:SCR_019187)

Description: Software tool to identify structural variants in given sample relative to reference genome. Runs combination of tools to generate structural variant calls on whole genome sequencing data.

Resource Type: software application, data analysis software, software resource, data processing software, software toolkit

Keywords: structural variants identification, reference genome, structural variant calls generation, whole genome sequencing data, sequencing data, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: Parliament2

Resource ID: SCR_019187

Alternate IDs: biotools:parliament2

Alternate URLs: <https://bio.tools/parliament2>

License: Apache 2.0

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260729T044454+0000

Ratings and Alerts

No rating or validation information has been found for Parliament2.

No alerts have been found for Parliament2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Garcia GL, et al. (2025) Aged and BRCA-Mutated Stromal Cells Drive Epithelial Cell Transformation. Cancer discovery, 15(6), 1203.

Jun G, et al. (2023) Structural variation across 138,134 samples in the TOPMed consortium. Research square.

Jun G, et al. (2023) Structural variation across 138,134 samples in the TOPMed consortium. bioRxiv : the preprint server for biology.

Walker K, et al. (2022) The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. F1000Research, 11, 530.

Zarate S, et al. (2020) Parliament2: Accurate structural variant calling at scale. GigaScience, 9(12).