

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 2, 2026

AGE

RRID:SCR_005253

Type: Tool

Proper Citation

AGE (RRID:SCR_005253)

Resource Information

URL: <http://sv.gersteinlab.org/age/>

Proper Citation: AGE (RRID:SCR_005253)

Description: A tool that implements an algorithm for optimal alignment of sequences with Structural Variations (SVs).

Abbreviations: AGE

Resource Type: software resource

Keywords: genome

Resource Name: AGE

Resource ID: SCR_005253

Alternate IDs: OMICS_00305

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260801T190251+0000

Ratings and Alerts

No rating or validation information has been found for AGE.

No alerts have been found for AGE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Schall PZ, et al. (2025) Integrative Genotyping and Analysis of Canine Structural Variation Using Long-read and Short-read Data. *Genome biology and evolution*, 17(10).

Zhao M, et al. (2013) Computational tools for copy number variation (CNV) detection using next-generation sequencing data: features and perspectives. *BMC bioinformatics*, 14 Suppl 11(Suppl 11), S1.

Abyzov A, et al. (2011) AGE: defining breakpoints of genomic structural variants at single-nucleotide resolution, through optimal alignments with gap excision. *Bioinformatics* (Oxford, England), 27(5), 595.