**ABySS**

RRID:SCR_010709  
Type: Tool

**Proper Citation**

ABySS (RRID:SCR_010709)

**Resource Information**

**URL:** [http://www.bcgsc.ca/platform/bioinfo/software/abyss](http://www.bcgsc.ca/platform/bioinfo/software/abyss)

**Description:** Software providing a de novo, parallel, paired-end sequence assembler that is designed for short reads.

**Resource Name:** ABySS

**Proper Citation:** ABySS (RRID:SCR_010709)

**Resource Type:** Resource, software resource

**Keywords:** mpi

**Resource ID:** SCR_010709

**References:** PMID: 19251739

**Website Status:** Last checked up

**Alternate IDs:** OMICS_00006

**Abbreviations:** ABySS

**Mentions Count:** 387

**Ratings and Alerts**

No rating or validation information has been found for ABySS.

No alerts have been found for ABySS.
Usage and Citation Metrics

We found 387 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch Infrastructure.


Alioto T, et al. (2020) Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. The Plant journal : for cell and molecular biology, 101(2), 455-472.


Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. Cell reports, 29(8), 2338-2354.e7.


