

Resource Summary Report

Generated by SPARC SAWG on Sep 18, 2026

Anchored Assembly

RRID:SCR_001188

Type: Tool

Proper Citation

Anchored Assembly (RRID:SCR_001188)

Resource Information

URL: <http://www.spiralgenetics.com/products/>

Proper Citation: Anchored Assembly (RRID:SCR_001188)

Description: Analysis pipeline that accurately detects and maps variations that are often missed by standard analysis algorithms. It uses direct de novo read overlap assembly to accurately detect and characterize SNPs (single nucleotide polymorphisms), indels, and SVs (structural variations). The pipeline uses existing Illumina HiSeq data and does not require additional library preparation. The algorithm is optimized for projects with at least 20x coverage per chromosome set (i.e. 40x for diploid).

Abbreviations: Anchored Assembly

Resource Type: commercial organization, software resource

Keywords: variation, structural variation, single nucleotide polymorphism

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Anchored Assembly

Resource ID: SCR_001188

Alternate IDs: OMICS_02167

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T200311+0000

Ratings and Alerts

No rating or validation information has been found for Anchored Assembly.

No alerts have been found for Anchored Assembly.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.