

Resource Summary Report

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Strainy

RRID:SCR_026430

Type: Tool

Proper Citation

Strainy (RRID:SCR_026430)

Resource Information

URL: <https://github.com/katerinakazantseva/strainy>

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Description: Software tool for phasing and assembly of bacterial strains from long-read sequencing data (either Oxford Nanopore or PacBio). Given reference (or collapsed de novo assembly) and set of aligned reads as input, tool produces multi-allelic phasing, individual strain haplotypes and strain-specific variant calls. Used for phasing and assembly of strain haplotypes from long-read metagenome sequencing.

Resource Type: software resource, software application, source code

Defining Citation: [PMID:39327484](#)

Keywords: phasing and assembly, strain haplotypes, long-read metagenome sequencing,

Funding: NCI

Availability: Free, Available for download, Freely available

Resource Name: Strainy

Resource ID: SCR_026430

License: Attribution-NonCommercial-ShareAlike 4.0 International

Record Creation Time: 20250219T060352+0000

Record Last Update: 20260731T043216+0000

Ratings and Alerts

No rating or validation information has been found for Strainy .

No alerts have been found for Strainy .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.