

# Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

## FreClu

RRID:SCR\_005524

Type: Tool

### Proper Citation

FreClu (RRID:SCR\_005524)

### Resource Information

**URL:** <http://mlab.cb.k.u-tokyo.ac.jp/~quwei/DeNovoShortReadClustering/>

**Proper Citation:** FreClu (RRID:SCR\_005524)

**Description:** An algorithm for efficient frequency-based de novo short read clustering for error trimming in next-generation sequencing. It organizes erroneous short sequences originating in a single abundant sequence into a tree structure such that each child sequence is considered to be derived stochastically from its more abundant parent sequence because of sequencing errors.

**Abbreviations:** FreClu

**Synonyms:** FreClu - Efficient Frequency-based de Novo Short Read Clustering

**Resource Type:** software resource

**Keywords:** next-generation sequencing

**Resource Name:** FreClu

**Resource ID:** SCR\_005524

**Alternate IDs:** OMICS\_01048

**Record Creation Time:** 20220129T080230+0000

**Record Last Update:** 20260912T195627+0000

### Ratings and Alerts

No rating or validation information has been found for FreClu.

No alerts have been found for FreClu.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.