

# Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

## Fulcrum

RRID:SCR\_005523

Type: Tool

### Proper Citation

Fulcrum (RRID:SCR\_005523)

### Resource Information

**URL:** <http://pringlelab.stanford.edu/projects.html>

**Proper Citation:** Fulcrum (RRID:SCR\_005523)

**Description:** Software to collapse identical and near-identical Illumina and 454 reads (such as those from PCR clones) into single error-corrected sequences; it can process paired-end as well as single-end reads. Fulcrum is customizable and can be deployed on a single machine, a local network or a commercially available MapReduce cluster, and it has been optimized to maximize ease-of-use, cross-platform compatibility and future scalability. Sequence datasets have been collapsed by up to 71%, and the reduced number and improved quality of the resulting sequences allow assemblers to produce longer contigs while using less memory.

**Abbreviations:** Fulcrum

**Synonyms:** Fulcrum Read Collapser

**Resource Type:** software resource

**Defining Citation:** [PMID:22419786](#)

**Keywords:** illumina, 454, read, paired-end read, single-end read, high-throughput sequencing, redundant read, genome, transcriptome, ultra high throughput sequencing

**Availability:** BSD-like license

**Resource Name:** Fulcrum

**Resource ID:** SCR\_005523

**Alternate IDs:** OMICS\_01049

**Old URLs:** <http://pringlelab.stanford.edu/protocols.html>

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

**Record Last Update:** 20260815T182315+0000

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## Ratings and Alerts

No rating or validation information has been found for Fulcrum.

No alerts have been found for Fulcrum.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [dkNET](#) .

Di Bernardo M, et al. (2021) easyFulcrum: An R package to process and analyze ecological sampling data generated using the Fulcrum mobile application. PloS one, 16(10), e0254293.

Moran O, et al. (2019) Predictors of mammographic density among women with a strong family history of breast cancer. BMC cancer, 19(1), 631.

Neubauer EF, et al. (2017) A diverse host thrombospondin-type-1 repeat protein repertoire promotes symbiont colonization during establishment of cnidarian-dinoflagellate symbiosis. eLife, 6.

Brand P, et al. (2015) Rapid evolution of chemosensory receptor genes in a pair of sibling species of orchid bees (Apidae: Euglossini). BMC evolutionary biology, 15, 176.