

# Resource Summary Report

Generated by [dkNET](#) on Jul 31, 2026

## Bulked segregation analysis tools for outbreeding species

RRID:SCR\_017009

Type: Tool

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### Proper Citation

Bulked segregation analysis tools for outbreeding species (RRID:SCR\_017009)

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### Resource Information

**URL:** <https://github.com/maypoleflyn/BSATOS>

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**Description:** Software tools for next generation sequencing based bulked segregation analysis for outbreeding species including fruit trees such as apple or citrus. Used to improve gene mapping efficiency of next generation sequencing based segregant analysis in outbreeding species and realize rapid candidate gene mining based on multi-omics data.

**Abbreviations:** BSATOS

**Synonyms:** Bulked segregation analysis tools for outbreeding species, Bulked Segregation Analysis Tools for Outbreeding Species, BSATOS

**Resource Type:** data processing software, time-series analysis software, data analysis software, 1d time-series analysis software, software resource, software application

**Keywords:** next, generation, sequencing, bulked, segregation, analysis, outbreeding, specie, gene, mapping, data

**Availability:** Free, Available for download, Freely available

**Resource Name:** Bulked segregation analysis tools for outbreeding species

**Resource ID:** SCR\_017009

**License:** MIT License

**Record Creation Time:** 20220129T080333+0000

**Record Last Update:** 20260731T043015+0000

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## Ratings and Alerts

No rating or validation information has been found for Bulk segregant analysis tools for outbreeding species.

No alerts have been found for Bulk segregant analysis tools for outbreeding species.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Shen F, et al. (2022) A bulk segregant analysis tool for out-crossing species (BSATOS) and QTL-based genomics-assisted prediction of complex traits in apple. Journal of advanced research, 42, 149.

Wu B, et al. (2021) Role of MdERF3 and MdERF118 natural variations in apple flesh firmness/crispness retainability and development of QTL-based genomics-assisted prediction. Plant biotechnology journal, 19(5), 1022.