

Resource Summary Report

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Bulked segregation analysis tools for outbreeding species

RRID:SCR_017009

Type: Tool

Proper Citation

Bulked segregation analysis tools for outbreeding species (RRID:SCR_017009)

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

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

Ratings and Alerts

No rating or validation information has been found for BulkEd segregation analysis tools for outbreeding species.

No alerts have been found for BulkEd segregation analysis tools for outbreeding species.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Shen F, et al. (2022) A bulkEd 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.