

# Resource Summary Report

Generated by [NIF](#) on Sep 9, 2026

## [forqs](#)

RRID:SCR\_000643

Type: Tool

### Proper Citation

forqs (RRID:SCR\_000643)

### Resource Information

**URL:** <https://bitbucket.org/dkessner/forqs>

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**Description:** Software for forward-in-time population genetics simulation that tracks individual haplotype chunks as they recombine each generation. It also also models quantitative traits and selection on those traits.

**Abbreviations:** forqs

**Synonyms:** Forward-in-time simulation of Recombination, and Selection, Quantitative traits

**Resource Type:** simulation software, software application, software resource

**Defining Citation:** [PMID:24336146](#)

**Keywords:** c++, linux, osx, windows, command line, simulation, recombination, quantitative trait, selection, haplotype pattern

**Funding:** NHGRI HG002536;  
NHGRI R01 HG007089;  
NSF EF-0928690

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

**Resource Name:** forqs

**Resource ID:** SCR\_000643

**Alternate IDs:** OMICS\_02196

**License:** BSD License

**Record Creation Time:** 20220129T080202+0000

**Record Last Update:** 20260905T132423+0000

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## Ratings and Alerts

No rating or validation information has been found for forqs.

No alerts have been found for forqs.

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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.