Stacks
RRID:SCR_003184
Type: Tool

Proper Citation

Stacks (RRID:SCR_003184)

Resource Information

URL: [http://creskolab.uoregon.edu/stacks/](http://creskolab.uoregon.edu/stacks/)

Description: A software pipeline for building loci from short-read sequences, such as those generated on the Illumina platform. It was developed to work with restriction enzyme-based data, such as RAD-seq, for the purpose of building genetic maps and conducting population genomics and phylogeography.

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Resource Type: Resource, software resource, software application, data analysis software, data processing software

Keywords: population genomics, genetic map, phylogenetics, genetics, next-generation sequencing, rad-seq, genotype-by-sequencing

Resource ID: SCR_003184

Parent Organization: University of Oregon; Oregon; USA

References: [PMID: 23701397], [PMID: 22384329]

Availability: GNU General Public License, v3

Website Status: Last checked up

Alternate IDs: OMICS_01567
**Abbreviations:** Stacks

**Mentions Count:** 179

### Ratings and Alerts

No rating or validation information has been found for Stacks.

No alerts have been found for Stacks.

### Data and Source Information

**Source:** SciCrunch Registry

### Usage and Citation Metrics

We found 179 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure](http://www.fdi-lab.com).

Adrian-Kalchhauser I, et al. (2020) The round goby genome provides insights into mechanisms that may facilitate biological invasions. BMC biology, 18(1), 11.


Graham CF, et al. (2020) How "simple" methodological decisions affect interpretation of population structure based on reduced representation library DNA sequencing: A case study...
using the lake whitefish. PloS one, 15(1), e0226608.


