**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.

**Resource Name:** Stacks  
**Proper Citation:** Stacks (RRID:SCR_003184)  
**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  
**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.

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