

Resource Summary Report

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Stacks

RRID:SCR_003184

Type: Tool

Proper Citation

Stacks (RRID:SCR_003184)

Resource Information

URL: <http://creskolab.uoregon.edu/stacks/>

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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.

Abbreviations: Stacks

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

Defining Citation: [PMID:23701397](#), [PMID:22384329](#), [DOI:10.1111/mec.12354](#)

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

Availability: GNU General Public License, v3

Resource Name: Stacks

Resource ID: SCR_003184

Alternate IDs: OMICS_01567, biotools:stacks

Alternate URLs: <https://bio.tools/stacks>, <https://sources.debian.org/src/stacks/>

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 463 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Yildirim Y, et al. (2024) Phylogeography and phenotypic wing shape variation in a damselfly across populations in Europe. *BMC ecology and evolution*, 24(1), 19.

Taichi N, et al. (2024) Habitat diversification associated with urban development has a little effect on genetic structure in the annual native plant *Commelina communis* in an East Asian megacity. *Ecology and evolution*, 14(2), e10975.

Strait JT, et al. (2024) Local environments, not invasive hybridization, influence cardiac performance of native trout under acute thermal stress. *Evolutionary applications*, 17(2), e13663.

Liu Y, et al. (2024) Conservation genetics and potential geographic distribution modeling of *Corybas taliensis*, a small 'sky Island' orchid species in China. *BMC plant biology*, 24(1), 11.

Soares LS, et al. (2024) The phylogeographic journey of a plant species from lowland to highlands during the Pleistocene. *Scientific reports*, 14(1), 3825.

Corrochano-Fraile A, et al. (2024) Estimating blue mussel (*Mytilus edulis*) connectivity and settlement capacity in mid-latitude fjord regions. *Communications biology*, 7(1), 166.

Li B, et al. (2024) Natural selection and genetic diversity maintenance in a parasitic wasp during continuous biological control application. *Nature communications*, 15(1), 1379.

Arpin KE, et al. (2024) Evaluating genotyping-in-thousands by sequencing as a genetic monitoring tool for a climate sentinel mammal using non-invasive and archival samples. *Ecology and evolution*, 14(2), e10934.

Gao Y, et al. (2024) Genomic insights into differentiation and adaptation of *Amorphophallus yunnanensis* in the mountainous region of Southwest China. *Ecology and evolution*, 14(1), e10861.

Reyes-Ardila WL, et al. (2024) Exploring Genomics and Microbial Ecology: Analysis of *Bidens pilosa* L. Genetic Structure and Soil Microbiome Diversity by RAD-Seq and

Metabarcoding. *Plants* (Basel, Switzerland), 13(2).

Cisternas-Fuentes A, et al. (2024) Effective population size mediates the impact of pollination services on pollen limitation. *Proceedings. Biological sciences*, 291(2014), 20231519.

Rengefors K, et al. (2024) Population genomic analyses reveal that salinity and geographic isolation drive diversification in a free-living protist. *Scientific reports*, 14(1), 4986.

Colangelo P, et al. (2024) Genome-wide diversity, population structure and signatures of inbreeding in the African buffalo in Mozambique. *BMC ecology and evolution*, 24(1), 29.

Waizumi R, et al. (2024) A major endogenous glycoside hydrolase mediating quercetin uptake in *Bombyx mori*. *PLoS genetics*, 20(1), e1011118.

Kohli M, et al. (2024) Genome-wide association studies for earliness, MYMIV resistance, and other associated traits in mungbean (*Vigna radiata* L. Wilczek) using genotyping by sequencing approach. *PeerJ*, 12, e16653.

Thakro V, et al. (2023) A superior gene allele involved in abscisic acid signaling enhances drought tolerance and yield in chickpea. *Plant physiology*, 191(3), 1884.

Hanko GR, et al. (2023) High Prevalence of Clonal Reproduction and Low Genetic Diversity in *Scutellaria floridana*, a Federally Threatened Florida-Endemic Mint. *Plants* (Basel, Switzerland), 12(4).

Leiva C, et al. (2023) Exceptional population genomic homogeneity in the black brittle star *Ophiocomina nigra* (Ophiuroidea, Echinodermata) along the Atlantic-Mediterranean coast. *Scientific reports*, 13(1), 12349.

Wang TR, et al. (2023) Adaptive divergence and genetic vulnerability of relict species under climate change: a case study of *Pterocarya macroptera*. *Annals of botany*, 132(2), 241.

Hawlitschek O, et al. (2023) The Genomics of Isolated Populations of *Gampsocleis glabra* (Orthoptera: Tettigoniidae) in Central and Western Europe. *Insects*, 14(12).