

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: data analysis software, data processing software, software application, 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: Free, Available for download, Freely available

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/>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T132459+0000

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 671 mentions in open access literature.

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

Mohanty JK, et al. (2026) Trans-QTL Alliance of HKT1 and PHL7 Modulate Salinity Stress Tolerance and Enhance Crop Yield Endurance. *Plant biotechnology journal*, 24(3), 1166.

Balao F, et al. (2026) Postglacial genetic legacies and climate-driven demography inform conservation of silver fir. *Annals of botany*, 137(7), 2082.

Reutimann O, et al. (2026) The Impact of Pleistocene Glacial Cycles on the Evolutionary Diversification of the Arctic-Alpine *Silene acaulis* Species Complex. *Molecular ecology*, 35(2), e70254.

Salinas NA, et al. (2026) Landscape Genomics and Evolutionary History of *Megamelus scutellaris*, a Biocontrol Agent of the Invasive Water Hyacinth (*Pontederia crassipes*). *Evolutionary applications*, 19(2), e70208.

Adachi AMCL, et al. (2026) Genetic Diversity and Population Structure of *Squalus cf. mitsukurii* (Chondrichthyes: Squalidae) Revealed by ddRAD Sequencing. *Animal genetics*, 57(2), e70096.

Thomas A, et al. (2026) Host genotype and environmental factors differentially shape the black piranha's gill microbiota. *Microbiology spectrum*, 14(6), e0327725.

Starko S, et al. (2026) Environmental Drivers of Genetic Structure and Local Adaptation in a Marine Foundation Species. *Ecology and evolution*, 16(3), e73141.

Fukasawa Y, et al. (2026) Electrical information flows across the sporocarps of two ectomycorrhizal fungi in the field. *Scientific reports*, 16(1).

Herzog KS, et al. (2026) When clades collide: Genomic admixture in blacklegged ticks (*Ixodes scapularis*) from the Great Plains. *bioRxiv : the preprint server for biology*.

Hu Y, et al. (2026) Invasive patterns of *Biomphalaria straminea* revealed by genetic mapping in the Greater Bay Area, China. *Infectious diseases of poverty*, 15(1), 9.

Xie S, et al. (2026) Whole-genome resequencing reveals genetic divergence, local adaptation, and conservation priorities in three helmet catfishes (complex *Cranoglanis boudierius*). *BMC genomics*, 27(1).

Ryder FJ, et al. (2026) Contrasting patterns of population structure in two habitat-forming kelp species in southeastern Australia. *Journal of phycology*, 62(2), 412.

Diaz-Suarez A, et al. (2026) Contrasting population genomic structuring of northern pike (*Esox lucius* L.) in fresh- and brackish water environments: Implications for management and conservation. *Journal of fish biology*, 108(5), 1599.

Choo LQ, et al. (2026) Weak Structure and Environment-Associated Loci Across a Eutrophication Gradient in a Resilient Coral Species. *Ecology and evolution*, 16(7), e73908.

Wang L, et al. (2026) Transposons drove the evolution of a male sex-determining gene from a female gene with deep introgression across cichlids. *Science advances*, 12(23), eaed6242.

Ma B, et al. (2026) Genetic Structure and Historical Dynamics of the Economic Species *Phascolosoma esculenta* in Southeastern China. *Biology*, 15(6).

Wang Z, et al. (2026) Genomic insights into endangerment and conservation of *Euryodendron excelsum*, a critically endangered plant. *BMC plant biology*, 26(1).

Arcila HEI, et al. (2026) Genomic insights into population structure and adaptive variation of *Pimelodus yuma* and *Pimelodus grosskopfii* in the Magdalena-Cauca Basin. *PloS one*, 21(6), e0351301.

Huang J, et al. (2026) GT-Seq Panel Development for Species Identification and Parentage Analysis of Closely Related Hybridising *Scaphirhynchus* Sturgeons. *Molecular ecology resources*, 26(3), e70124.

Cocozza A, et al. (2026) Integrated high-density genetic maps in multi-parent F2 mapping populations provide a framework to unravel the genomic basis of agro-qualitative and metabolic traits in pepper (*Capsicum annuum*). *BMC plant biology*, 26(1).