

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, software resource, data analysis software, data processing software

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: 20260729T044037+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 623 mentions in open access literature.

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

Gergonne D, et al. (2026) Genomic Evidence for Dual Introductions, Limited Gene Flow and Niche Preferences in the Invasive Wasp *Vespula germanica* in South Africa. *Molecular ecology*, 35(1), e70217.

Didaskalou EA, et al. (2026) Unlocking Demography: Developing an eDNA-Based Toolkit to Measure Sex Ratios From Populations. *Molecular ecology resources*, 26(1), e70089.

Euclide PT, et al. (2025) Human Impacts on Great Lakes Walleye *Sander vitreus* Structure, Diversity and Local Adaptation. *Molecular ecology*, 34(23), e17558.

Amado D, et al. (2025) The genetic architecture of resistance to flubendiamide insecticide in *Helicoverpa armigera* (Hübner). *PloS one*, 20(1), e0318154.

Pollard K, et al. (2025) Genomic Insights From Natural History Collections Reveal Cryptic Speciation in Coral Guard Crabs (Family: Trapeziidae). *Ecology and evolution*, 15(2), e70960.

Ríos N, et al. (2025) Transcriptomic Divergence and Associated Markers Between Genomic Lineages of Silver Catfish (*Rhamdia quelen*). *Ecology and evolution*, 15(3), e71021.

Babaei S, et al. (2025) Genome-wide SNPs reveal novel genetic relationships among Atlantic cod (*Gadus morhua*) from the south coast of Newfoundland, Canada (subdivision 3Ps), Northern cod stock complex, and Gulf of St Lawrence. *PloS one*, 20(3), e0317768.

Rancilhac L, et al. (2025) Introgression across Narrow Contact Zones Shapes the Genomic Landscape of Phylogenetic Variation in an African Bird Clade. *Systematic biology*, 74(6), 935.

Weiss M, et al. (2025) Population Genomics Reveals Small-Scale Metapopulation Structure of Two Strictly Aquatic Keystone Species in a Recently Restored Urban River System (Emscher, Germany). *Ecology and evolution*, 15(4), e71214.

Parajuli S, et al. (2025) Genetic architecture of anthocyanin pigment traits and purple spot (*Stemphylium vesicarium*) resistance in an F1 pseudo-testcross population of asparagus. *The plant genome*, 18(2), e70028.

Lu Y, et al. (2025) Local Adaptation and Climate Change Vulnerability of the Relict Tree Species *Taiwania cryptomerioides* Provide Insights Into Its Conservation and Restoration. *Evolutionary applications*, 18(5), e70113.

Macharia MW, et al. (2025) Cowpea (*Vigna unguiculata* L. Walp.) landraces in Mozambique and neighbouring Southern African countries harbour genetic loci with potential for climate adaptation. *Communications biology*, 8(1), 834.

Gu R, et al. (2025) Reduced representation sequencing reveals genetic diversity and adaptive genetic divergence in *Calamus rhabdocladius*. *Scientific reports*, 15(1), 21848.

Tarusawa Y, et al. (2025) Population genetic structure reveals asymmetric hybridization between *Pinus pumila* and *P. parviflora* var. *Pentaphylla* in the Hakkoda Mountains, Northern Japan. *Scientific reports*, 15(1), 37677.

Suh E, et al. (2025) Hologenomic structure of bacterial and fungal community composition in the West Nile virus vector *Culex tarsalis*. *bioRxiv : the preprint server for biology*.

Urquhart-Cronish M, et al. (2025) An alpine plant shows no decrease in genetic diversity associated with rapid post-glacial range expansion. *American journal of botany*, 112(12), e70128.

Salardi-Jost M, et al. (2025) Genomic characterization of a global *Corylus avellana* L. collection: insights into hazelnut ancestry and genetic determinants of production traits. *BMC plant biology*, 25(1), 1738.

Sampaio S, et al. (2025) Microgeographic genomic variation and connectivity in an endangered semiaquatic mammal. *BMC ecology and evolution*, 25(1), 114.

López A, et al. (2025) Evaluating restriction enzyme selection for reduced representation sequencing in conservation genomics. *Molecular ecology resources*, 25(5), e13865.

Patova A, et al. (2025) Population genomics and connectivity of *Vazella pourtalesii* sponge grounds of the northwest Atlantic with conservation implications of deep sea vulnerable marine ecosystems. *Scientific reports*, 15(1), 1540.