Resource Summary Report

Generated by dkNET on Apr 24, 2025

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 resource, software application

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

Funding:

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/

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250423T060117+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 538 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Dufresnes C, et al. (2025) Speciation and historical invasions of the Asian black-spined toad (Duttaphrynus melanostictus). Nature communications, 16(1), 298.

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.

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

Torrado H, et al. (2025) Evolutionary Genomics of Two Co-occurring Congeneric Fore Reef Coral Species on Guam (Mariana Islands). Genome biology and evolution, 17(1).

Paris JR, et al. (2025) The Genomic Signature and Transcriptional Response of Metal Tolerance in Brown Trout Inhabiting Metal-Polluted Rivers. Molecular ecology, 34(1), e17591.

Domínguez M, et al. (2025) Genomics Reveal Population Structure and Intergeneric Hybridization in an Endangered South American Bird: Implications for Management and Conservation. Ecology and evolution, 15(1), e70820.

Kniesz K, et al. (2025) High genomic connectivity within Anatoma at hydrothermal vents along the Central and Southeast Indian Ridge. Scientific reports, 15(1), 1971.

Ho DV, et al. (2024) Post-meiotic mechanism of facultative parthenogenesis in gonochoristic whiptail lizard species. eLife, 13.

Brunharo CACG, et al. (2024) Chromosome-scale genome assembly of Poa trivialis and population genomics reveal widespread gene flow in a cool-season grass seed production system. Plant direct, 8(3), e575.

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.

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.

Raggi L, et al. (2024) Investigating the genetic basis of salt-tolerance in common bean: a genome-wide association study at the early vegetative stage. Scientific reports, 14(1), 5315.

Ramirez-Ramirez AR, et al. (2024) Comparing the performances of SSR and SNP markers for population analysis in Theobroma cacao L., as alternative approach to validate a new ddRADseq protocol for cacao genotyping. PloS one, 19(5), e0304753.

Peralta DM, et al. (2024) A rapid approach for sex assignment by RAD-seq using a reference genome. PloS one, 19(4), e0297987.

Búci M, et al. (2024) Airports for the genetic rescue of a former agricultural pest. Scientific reports, 14(1), 17540.

Çetin C, et al. (2024) Population genetic structure in a self-compatible hermaphroditic snail is driven by drift independently of its contemporary mating system. Ecology and evolution, 14(8), e70162.

Reatini B, et al. (2024) Chromosome-scale Reference Genome and RAD-based Genetic Map of Yellow Starthistle (Centaurea solstitialis) Reveal Putative Structural Variation and QTL Associated With Invader Traits. Genome biology and evolution, 16(12).

Worthington BM, et al. (2024) Serological evidence of sarbecovirus exposure along Sunda pangolin trafficking pathways. BMC biology, 22(1), 274.

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.