

Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

HVRLocator

RRID:SCR_027407

Type: Tool

Proper Citation

HVRLocator (RRID:SCR_027407)

Resource Information

URL: <https://cloud.sylabs.io/library/jsaraiva/repo/hvrlocator>

Proper Citation: HVRLocator (RRID:SCR_027407)

Description: Software application to identify spanning hypervariable region(s) from amplicon sequencing variants or SRA public runs (SRR). Aligns query sequences to reference E. coli full-length 16S rRNA gene and identifies spanning region through alignment. Used for identifying hypervariable regions in 16S rRNA big datasets.

Resource Type: software application, software resource

Defining Citation: [DOI:10.1101/2025.07.24.666487](https://doi.org/10.1101/2025.07.24.666487)

Keywords: Align query sequences, reference E. coli full-length 16S rRNA gene, SRA public runs, 16S rRNA, Amplicon, SRA, identify spanning hypervariable region, amplicon sequencing variants, SRA public runs, identifying hypervariable regions, 16S rRNA big datasets,

Funding: German Centre for Integrative Biodiversity Research (iDiv) sIBTEDS

Availability: Free, Available for download, Freely available

Resource Name: HVRLocator

Resource ID: SCR_027407

Alternate URLs: <https://github.com/fbcorrea/hvrlocator/>

License: CC0-1.0 license

Record Creation Time: 20250909T055154+0000

Record Last Update: 20260810T040942+0000

Ratings and Alerts

No rating or validation information has been found for HVRLocator.

No alerts have been found for HVRLocator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Arboleda-Baena C, et al. (2026) HVRLocator: a computationally efficient tool for identifying hypervariable regions in large 16S rRNA datasets. GigaScience, 15.