

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

Sort-ITEMS

RRID:SCR_004716

Type: Tool

Proper Citation

Sort-ITEMS (RRID:SCR_004716)

Resource Information

URL: <http://metagenomics.atc.tcs.com/binning/Sort-ITEMS/>

Proper Citation: Sort-ITEMS (RRID:SCR_004716)

Description: Sequence orthology based software for improved taxonomic estimation of metagenomic sequences., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: Sort-ITEMS

Synonyms: Sequence orthology based approach for improved taxonomic estimation of metagenomic sequences, Sort-ITEMS: Sequence orthology based approach for improved taxonomic estimation of metagenomic sequences

Resource Type: software resource

Defining Citation: [PMID:19439565](#)

Keywords: metagenome, taxonomy, sequence, orthology, binning

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Sort-ITEMS

Resource ID: SCR_004716

Alternate IDs: OMICS_01465

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260912T195616+0000

Ratings and Alerts

No rating or validation information has been found for SOrt-ITEMS.

No alerts have been found for SOrt-ITEMS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Alvarenga DO, et al. (2017) A Metagenomic Approach to Cyanobacterial Genomics. Frontiers in microbiology, 8, 809.

Escobar-Zepeda A, et al. (2015) The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. Frontiers in genetics, 6, 348.

Dutta A, et al. (2014) Binpairs: utilization of Illumina paired-end information for improving efficiency of taxonomic binning of metagenomic sequences. PloS one, 9(12), e114814.

Sharma VK, et al. (2012) Fast and accurate taxonomic assignments of metagenomic sequences using MetaBin. PloS one, 7(4), e34030.

Rosen GL, et al. (2011) Discovering the unknown: improving detection of novel species and genera from short reads. Journal of biomedicine & biotechnology, 2011, 495849.

Ghosh TS, et al. (2011) ProViDE: A software tool for accurate estimation of viral diversity in metagenomic samples. Bioinformation, 6(2), 91.