

Resource Summary Report

Generated by [NIF](#) on Aug 11, 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: 20260808T185826+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 [NIF](#) .

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. *Bioinformatics*, 6(2), 91.