

# Resource Summary Report

Generated by T1D on Aug 1, 2026

## Sort-ITEMS

RRID:SCR\_004716

Type: Tool

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### Proper Citation

Sort-ITEMS (RRID:SCR\_004716)

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### 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:** 20260801T190244+0000

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### Ratings and Alerts

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

No alerts have been found for SOrt-ITEMS.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

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.