# **Resource Summary Report**

Generated by <u>dkNET</u> on Apr 30, 2025

# **Distributed String Mining Framework**

RRID:SCR\_004736 Type: Tool

#### **Proper Citation**

Distributed String Mining Framework (RRID:SCR\_004736)

#### **Resource Information**

URL: https://github.com/HIITMetagenomics/dsm-framework

Proper Citation: Distributed String Mining Framework (RRID:SCR\_004736)

**Description:** Software package providing distributed string mining for High-Throughput Sequencing data that provides a content-based exploration and retrieval method for whole metagenome sequencing samples.

Abbreviations: dsm-framework

Resource Type: software resource

Defining Citation: PMID:24845653

Keywords: gpu/cuda, bio.tools

Funding:

Availability: GNU General Public License, v2 or greater

**Resource Name:** Distributed String Mining Framework

Resource ID: SCR\_004736

Alternate IDs: biotools:dsm, OMICS\_04171

Alternate URLs: https://bio.tools/dsm

Record Creation Time: 20220129T080226+0000

**Record Last Update:** 20250420T014234+0000

# **Ratings and Alerts**

No rating or validation information has been found for Distributed String Mining Framework.

No alerts have been found for Distributed String Mining Framework.

## 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 <u>dkNET</u>.

Lees JA, et al. (2016) Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. Nature communications, 7, 12797.