

# Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 29, 2026

## LMAT

RRID:SCR\_004646

Type: Tool

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### Proper Citation

LMAT (RRID:SCR\_004646)

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### Resource Information

**URL:** <https://computation-rnd.llnl.gov/lmat/>

**Proper Citation:** LMAT (RRID:SCR\_004646)

**Description:** Open-source software tool to assign taxonomic labels to as many reads as possible in very large metagenomic datasets and report the taxonomic profile of the input sample. The quick "single pass" analysis of every read allows read binning to support additional more computationally expensive analysis such as metagenomic assembly or sensitive database searches on targeted subsets of reads.

**Abbreviations:** LMAT

**Synonyms:** Livermore Metagenomics Analysis Toolkit

**Resource Type:** software resource

**Defining Citation:** [PMID:23828782](#)

**Keywords:** c++, metagenomic, metagenomic classification, genome, virus, taxonomy, database, reference genome

**Availability:** Open unspecified license

**Resource Name:** LMAT

**Resource ID:** SCR\_004646

**Alternate IDs:** OMICS\_02285

**Record Creation Time:** 20220129T080225+0000

**Record Last Update:** 20260829T182209+0000

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### Ratings and Alerts

No rating or validation information has been found for LMAT.

No alerts have been found for LMAT.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Saettele AL, et al. (2022) Prolonged Dexamethasone Exposure Enhances Zebrafish Lateral-Line Regeneration But Disrupts Mitochondrial Homeostasis and Hair Cell Function. Journal of the Association for Research in Otolaryngology : JARO, 23(6), 683.

Morrison MD, et al. (2021) Investigation of Spaceflight Induced Changes to Astronaut Microbiomes. Frontiers in microbiology, 12, 659179.

Avila-Herrera A, et al. (2020) Crewmember microbiome may influence microbial composition of ISS habitable surfaces. PloS one, 15(4), e0231838.

Mejia R, et al. (2020) Impact of intestinal parasites on microbiota and cobalamin gene sequences: a pilot study. Parasites & vectors, 13(1), 200.

Sichtig H, et al. (2019) FDA-ARGOS is a database with public quality-controlled reference genomes for diagnostic use and regulatory science. Nature communications, 10(1), 3313.

Vijayvargiya P, et al. (2019) Application of metagenomic shotgun sequencing to detect vector-borne pathogens in clinical blood samples. PloS one, 14(10), e0222915.

Namroodi S, et al. (2018) Frequency of exposure of endangered Caspian seals to Canine distemper virus, Leptospira interrogans, and Toxoplasma gondii. PloS one, 13(4), e0196070.

Thissen JB, et al. (2018) A novel variant of torque teno virus 7 identified in patients with Kawasaki disease. PloS one, 13(12), e0209683.

Mart?? JM, et al. (2017) Health and Disease Imprinted in the Time Variability of the Human Microbiome. mSystems, 2(2).

Devault AM, et al. (2017) A molecular portrait of maternal sepsis from Byzantine Troy. eLife, 6.

Treangen TJ, et al. (2016) Identification and Genomic Analysis of a Novel Group C Orthobunyavirus Isolated from a Mosquito Captured near Iquitos, Peru. PLoS neglected tropical diseases, 10(4), e0004440.

Ounit R, et al. (2015) CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. BMC genomics, 16(1), 236.

Ames SK, et al. (2015) Using populations of human and microbial genomes for organism detection in metagenomes. Genome research, 25(7), 1056.

Gardner SN, et al. (2015) Targeted amplification for enhanced detection of biothreat agents by next-generation sequencing. BMC research notes, 8, 682.

Filippidou S, et al. (2015) Under-detection of endospore-forming Firmicutes in metagenomic data. Computational and structural biotechnology journal, 13, 299.