

Resource Summary Report

Generated by [T1D](#) on Sep 5, 2026

Classifier for Metagenomic Sequences

RRID:SCR_005519

Type: Tool

Proper Citation

Classifier for Metagenomic Sequences (RRID:SCR_005519)

Resource Information

URL: <http://clams.jgi-psf.org/>

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Description: ClaMS is a sequence composition-based classifier for metagenomic sequences. ClaMS works by capturing signatures of each sequence based on the sequence composition. Each sequence is modeled as a walk in a de Bruijn graph with underlying Markov chain properties. ClaMS captures stationary parameters of the underlying Markov chain as well as structural parameters of the underlying de Bruijn graph to form this signature. In practice, for each sequence to be binned, such a signature is computed and matched to similar signatures computed for the training sets. The best match that also qualifies the normalized distance cut-off wins. In the case that the best match does not qualify this cut-off, the sequence remains un-binned.

Abbreviations: ClaMS

Resource Type: software resource, data analysis software, data processing software, software application

Resource Name: Classifier for Metagenomic Sequences

Resource ID: SCR_005519

Alternate IDs: nlx_144629

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260903T234758+0000

Ratings and Alerts

No rating or validation information has been found for Classifier for Metagenomic Sequences.

No alerts have been found for Classifier for Metagenomic Sequences.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 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.

Santiago-Rodriguez TM, et al. (2017) Gut Microbiome and Putative Resistome of Inca and Italian Nobility Mummies. *Genes*, 8(11).

Mikhailov KV, et al. (2017) Genomic Survey of a Hyperparasitic Microsporidian *Amphiamblys* sp. (Metchnikovellidae). *Genome biology and evolution*, 9(3), 454.

Reddy AP, et al. (2013) Discovery of microorganisms and enzymes involved in high-solids decomposition of rice straw using metagenomic analyses. *PloS one*, 8(10), e77985.

D'haeseleer P, et al. (2013) Proteogenomic analysis of a thermophilic bacterial consortium adapted to deconstruct switchgrass. *PloS one*, 8(7), e68465.

van der Lelie D, et al. (2012) The metagenome of an anaerobic microbial community decomposing poplar wood chips. *PloS one*, 7(5), e36740.

Park JI, et al. (2012) A thermophilic ionic liquid-tolerant cellulase cocktail for the production of cellulosic biofuels. *PloS one*, 7(5), e37010.

Hollister EB, et al. (2012) Mesophilic and thermophilic conditions select for unique but highly parallel microbial communities to perform carboxylate platform biomass conversion. *PloS one*, 7(6), e39689.

Pati A, et al. (2011) ClaMS: A Classifier for Metagenomic Sequences. *Standards in genomic sciences*, 5(2), 248.