

Resource Summary Report

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CloVR

RRID:SCR_005290

Type: Tool

Proper Citation

CloVR (RRID:SCR_005290)

Resource Information

URL: <http://clovr.org/>

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Description: A desktop application for push-button automated sequence analysis that can utilize cloud computing resources. CloVR is implemented as a single portable virtual machine (VM) that provides several automated analysis pipelines for microbial genomics, including 16S, whole genome and metagenome sequence analysis. The CloVR VM runs on a personal computer, utilizes local computer resources and requires minimal installation, addressing key challenges in deploying bioinformatics workflows. In addition CloVR supports use of remote cloud computing resources to improve performance for large-scale sequence processing.

Abbreviations: CloVR

Synonyms: CloVR - Automated Sequence Analysis from Your Desktop, Cloud Virtual Resource

Resource Type: service resource, software resource

Defining Citation: [PMID:21878105](#)

Keywords: cloud computing, next-generation sequencing

Funding: Amazon Web Services in Education Research Grants program ;
National Human Genome Research Institute ;
NHGRI RC2 HG005597-01;
NSF 0949201

Resource Name: CloVR

Resource ID: SCR_005290

Alternate IDs: OMICS_01216

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260905T133235+0000

Ratings and Alerts

No rating or validation information has been found for CloVR.

No alerts have been found for CloVR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Ooi MC, et al. (2021) Predatory bacteria in the haemolymph of the cultured spiny lobster *Panulirus ornatus*. *Microbiology* (Reading, England), 167(11).

Koppad S, et al. (2021) Cloud Computing Enabled Big Multi-Omics Data Analytics. *Bioinformatics and biology insights*, 15, 11779322211035921.

Muturi SM, et al. (2021) Metagenomics survey unravels diversity of biogas microbiomes with potential to enhance productivity in Kenya. *PloS one*, 16(1), e0244755.

Singh M, et al. (2020) Characterization of Extremely Drug-Resistant and Hypervirulent *Acinetobacter baumannii* AB030. *Antibiotics* (Basel, Switzerland), 9(6).

Ooi MC, et al. (2020) *Aquimarina* sp. Associated With a Cuticular Disease of Cultured Larval Palinurid and Scyllarid Lobsters. *Frontiers in microbiology*, 11, 573588.

Ooi MC, et al. (2019) Haemolymph microbiome of the cultured spiny lobster *Panulirus ornatus* at different temperatures. *Scientific reports*, 9(1), 1677.

Kilian M, et al. (2019) Identification of Virulence-Associated Properties by Comparative Genome Analysis of *Streptococcus pneumoniae*, *S. pseudopneumoniae*, *S. mitis*, Three *S. oralis* Subspecies, and *S. infantis*. *mBio*, 10(5).

Moronta-Barrios F, et al. (2018) Bacterial Microbiota of Rice Roots: 16S-Based Taxonomic Profiling of Endophytic and Rhizospheric Diversity, Endophytes Isolation and Simplified Endophytic Community. *Microorganisms*, 6(1).

Miller CL, et al. (2017) Global transcriptome responses including small RNAs during mixed-species interactions with methicillin-resistant *Staphylococcus aureus* and *Pseudomonas aeruginosa*. *MicrobiologyOpen*, 6(3).

Agrawal S, et al. (2017) CloVR-Comparative: automated, cloud-enabled comparative microbial genome sequence analysis pipeline. *BMC genomics*, 18(1), 332.

Dubovskiy IM, et al. (2016) Immuno-physiological adaptations confer wax moth *Galleria mellonella* resistance to *Bacillus thuringiensis*. *Virulence*, 7(8), 860.

Pathak A, et al. (2016) Comparative Genomics and Metabolic Analysis Reveals Peculiar Characteristics of *Rhodococcus opacus* Strain M213 Particularly for Naphthalene Degradation. *PloS one*, 11(8), e0161032.

Eduok S, et al. (2015) Insights into the effect of mixed engineered nanoparticles on activated sludge performance. *FEMS microbiology ecology*, 91(7).

Bachman MA, et al. (2015) Genome-Wide Identification of *Klebsiella pneumoniae* Fitness Genes during Lung Infection. *mBio*, 6(3), e00775.

Dahl M, et al. (2015) Biolmg.org: A Catalog of Virtual Machine Images for the Life Sciences. *Bioinformatics and biology insights*, 9, 125.

Yue M, et al. (2015) Allelic variation contributes to bacterial host specificity. *Nature communications*, 6, 8754.

Lehmann K, et al. (2015) 16S rRNA assessment of the influence of shading on early-successional biofilms in experimental streams. *FEMS microbiology ecology*, 91(12).

Jackson HT, et al. (2014) Culture-independent evaluation of the appendix and rectum microbiomes in children with and without appendicitis. *PloS one*, 9(4), e95414.

Crabtree J, et al. (2014) Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. *Bioinformatics (Oxford, England)*, 30(21), 3125.

Ottesen AR, et al. (2013) Baseline survey of the anatomical microbial ecology of an important food plant: *Solanum lycopersicum* (tomato). *BMC microbiology*, 13, 114.