Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

University of California at Berkeley National Energy Research Scientific Computing Core Facility

RRID:SCR_021318
Type: Tool

Proper Citation

University of California at Berkeley National Energy Research Scientific Computing Core Facility (RRID:SCR_021318)

Resource Information

URL: http://www.nersc.gov

Proper Citation: University of California at Berkeley National Energy Research Scientific Computing Core Facility (RRID:SCR_021318)

Description: Supercomputer user facility operated by Lawrence Berkeley National Laboratory for the United States Department of Energy Office of Science.Houses high performance computing and data systems used by scientists at national laboratories and universities around the country.

Abbreviations: NERSC

Synonyms: National Energy Research Scientific Computing

Resource Type: access service resource, core facility, service resource

Keywords: USEDit, ABRF, supercomputer, United States Department of Energy Office of Science, high performance computing, data systems

Funding: DOE Office of Science

Availability: open

Resource Name: University of California at Berkeley National Energy Research Scientific Computing Core Facility

Resource ID: SCR_021318

Alternate IDs: ABRF_1191

Alternate URLs: https://coremarketplace.org/?FacilityID=1191

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260912T200411+0000

Ratings and Alerts

No rating or validation information has been found for University of California at Berkeley National Energy Research Scientific Computing Core Facility.

No alerts have been found for University of California at Berkeley National Energy Research Scientific Computing Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Zhou Z, et al. (2025) GenomeOcean: An Efficient Genome Foundation Model Trained on Large-Scale Metagenomic Assemblies. bioRxiv : the preprint server for biology.

Yu Q, et al. (2024) Lineage frequency time series reveal elevated levels of genetic drift in SARS-CoV-2 transmission in England. PLoS pathogens, 20(4), e1012090.

Shao R, et al. (2023) Leveraging History to Predict Infrequent Abnormal Transfers in Distributed Workflows. Sensors (Basel, Switzerland), 23(12).

Lui LM, et al. (2021) A method for achieving complete microbial genomes and improving bins from metagenomics data. PLoS computational biology, 17(5), e1008972.