Software applications in metagenomics





HOME | SUBMIT | FAQ | BLOG | ALERTS / RSS | RESOURCES | ABOUT | CHANNELS



New Results Previous Next 😜

CAMP: A modular metagenomics analysis system for integrated multistep data exploration

Lauren Mak, Braden Tierney, Cynthia Ronkowski, Rodolfo Brizola Toscan, Berk Turhan, Michael Toomey, Juan Sebastian Andrade Martinez, Chenlian Fu, Alexander G Lucaci, Arthur Henrique Barrios Solano, João Carlos Setubal, James R Henriksen, Sam Zimmerman, Malika Kopbayeva, Anna Noyvert, Zana Iwan, Shraman Kar, Nikita Nakazawa, Dmitry Meleshko, Dmytro Horyslavets, Valeriia Kantsypa, Alina Frolova, Andre Kahles, David Danko, Eran Elhaik, Pawel Labaj, Serghei Mangul, The International MetaSUB Consortium, Christopher E. Mason, Iman Hajirasouliha

doi: https://doi.org/10.1101/2023.04.09.536171

This article is a preprint and has not been certified by peer review [what does this mean?].



Abstract Full Text Info/History Metrics

Posted September 14, 2024.

Download PDF

▼ Print/Save Options

Supplementary Material

Revision Summary

✓ Email

→ Share

Citation Tools

₩ Get QR code



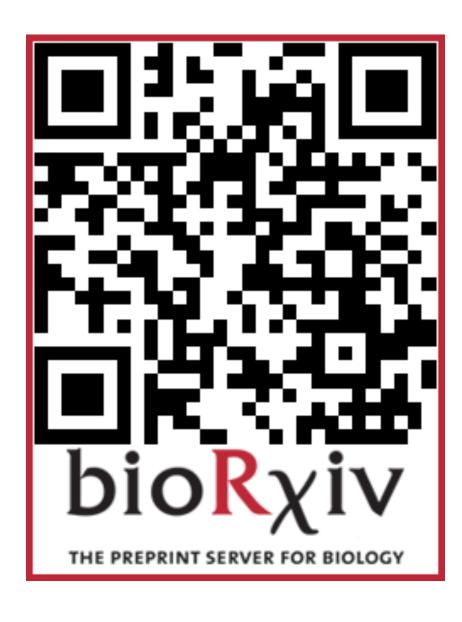


COVID-19 SARS-CoV-2 preprints from medRxiv and bioRxiv

Subject Area

Preview PDF

Bioinformatics



CAMP: The Core Analysis Modular Pipeline

