

Resource Summary Report

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VBRC Base By Base: Align entire sequences or subsequence regions

DOI:10.17504/protocols.io.ecybaxw

Type: Protocol

Proper Citation

Nick Tang 2016. VBRC Base By Base: Align entire sequences or subsequence regions. protocols.io dx.doi.org/10.17504/protocols.io.ecybaxw

Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.ecybaxw>

Authors: Nick Tang

Group: VERVE Net, Upton-Lab

Summary: Viral Bioinformatic Resource Centre Provide databases of viral genomic information. Please check the Organisms menu to see which viruses we support: we're now focusing on large DNA viruses The VOCs (Virus Orthologous Clusters) database is at the heart of our system. The database links directly to integrated tools for comparative analyses. VOCs sorts genes into ortholog clusters (e.g. RNA polymerase) to simplify data retrieval. Provide easy access to the genes, gene families, and genomes of the different virus families. via a unique series of powerful Java tools that support multiple computer platforms (see VBRC Tools menu). design and build software to tackle specific bioinformatics/virology problems, often in collaboration with virologists. Rally the research community to provide expert curation of these viral genomes by: Adding value to GenBank sequences through enhancing and updating genome annotations Linking to research reviews/papers for the research community. Collaborate with researchers to help on specific bioinformatics problems, e.g. Custom searches of the databases Building new features into our tools Help with genome annotation

Affiliations: University of Victoria: Department of Biochemistry and Microbiology

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