

VBRC Base By Base: Export a sequence selection to a different file

Nick Tang

Abstract

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

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Protocol

Step 1.

Suppose that you wish to analyze a subsection of a pre-existing alignment over a reduced number of sequences.

The easiest way to do this is to export your region of interest to a new file.

Step 2.

First, select the desired sequences from the Sequence List to the left (hold down the **CTRL** or **Apple** key to select more than one).

Step 3.

Now switch to the **Select** mouse mode (*from the Toolbar button*) and *click and drag* to select the region of the sequence you wish to export.

Step 4.

NOTE: You **must** switch to **Select** mode first, or you will introduce large gaps into your alignment!

This region will become highlighted on all the selected sequences.

Step 5.

Select “**Export Selection (Marked Sequences)**” from the *File* menu; you can then choose the file format (see previous protocols) and enter a name for your file.