VBRC Base By Base: View gene annotations

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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

Protocol

Step 1.
When opening sequence files from the VOCs database, gene annotations are <u>automatically uploaded to your alignment together with the sequences</u>.

Step 2.
To locate genes, either click on the relevant toolbar buttons to move the display to the last/next gene, or skip directly to the gene of interest by selecting it in the pull-down menu located on the top right of the display.

(**NOTE:** Be sure to select the sequence of interest first, or the wrong group of genes will be displayed.)

Step 3.

Click on the **"Three Frame Translation"** button (located to the right of the Sequence List) to view all three possible translations of the gene sequence.

The annotated open reading frame is highlighted in red.