VBRC Base By Base: Export a text overview of the alignment

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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.
Any BBB alignment can be exported to dense text format.
This is useful if you wish to have a large sequence and wish to be able to scan across it quickly.

Step 2.
To do this, select, **"Export Alignment Overview"**, from the _File_ menu.

Step 3.
This functionality includes difference comparisons and indicates differences by lowering the case of the amino or nucleic acid.

The comparison algorithm is automatically determined based on the current comparison type the user is viewing the sequence with.