



ViPR

Virus Pathogen Resource

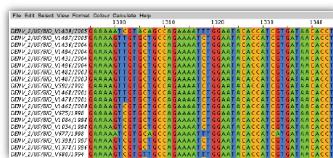
<http://www.viprbrc.org/>

Freely available

Integrated datasets

Bioinformatics tool suite

Multiple Sequence Alignment (MSA)



Choose sequences for alignment

Run the alignment

Customize the alignment based on your needs

Option 1: Search for sequences and then align sequences

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On the ViPR homepage, choose a virus family to start.

- Identify sequences to align: mouse-over the “Search Data” tab and click “Genomes” or “Genes & Proteins”. For this example, we will use genome sequences.
- Select search criteria on the Genome Search page and click the “Search” button to run your query.
- Select sequences from the search result page by clicking the checkboxes. Mouse-over the yellow “Run Analysis” button and click “Align Sequences (MSA)”. If you want to include sequences that are not in this search result or to use the sequences to do further analysis, select the desired sequences and click “Add to Working Set”. Then add other sequences to the same working set later by repeating the process. Click the “Workbench” tab and find the working set you saved. Click *i* next to it to view the details of the working set. Then mouse-over the yellow “Run Analysis” button and click “Align Sequences (MSA)”.

- A “Select Sequence Type” lightbox will pop-up. Select appropriate sequence type and click “Continue”.
- On the next page, select output format and output order. Then click “Run”.
- If you have a large number of long sequences to align, the analysis may take a few minutes to run. While the analysis is running, you can choose to save it (upon completion) to your Workbench by entering a name for the analysis and then clicking the “Save to Workbench” button. Then you can move to other parts of the ViPR site, and retrieve the alignment later from your Workbench.



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Option 2: Align sequences from a working set or your own sequences

The screenshot shows the 'Align Sequences (MSA)' page. Step 1 highlights the 'ANALYZE & VISUALIZE' tab and the 'Align Sequences (MSA)' option. Step 2 shows the input options: 'Upload a file containing my sequences in FASTA' (selected), 'Paste sequence in FASTA format', and 'Use working set'. Step 3 shows the 'Choose Working Set' dialog with three entries: 'Dengue2_genome_human-1999-2000' (selected), 'DENV1-4_99-00_human_Genomes', and 'hepatitis c'. Step 4 shows the processing status with a progress bar and a ticket number 'MS_339739173704'.

1. Mouse-over the “Analyze & Visualize” tab and click “Align Sequences (MSA)”.
2. On the MSA landing page, use one of the three options to input sequences:
 - 2.1 Upload a file containing sequences in FASTA format.
 - 2.2 Paste sequences in FASTA format.
 - 2.3 Use a working set from your Workbench.
 Select output format and output order. Then click “Run”.
3. If you have a large number of long sequences to align, the analysis may take a few minutes to run. While the analysis is running, you can choose to save it (upon completion) to your Workbench by entering a name for the analysis and then clicking the “Save to Workbench” button. Then you can move to other parts of the ViPR site, and retrieve the alignment later from your Workbench.

Customize the look of the alignment

The screenshot shows the 'Visualize Aligned Sequences' customization window and the resulting alignment visualization. Step 1 shows the 'Alignment Report' page with the 'Visualize Aligned Sequences' button highlighted. Step 2 shows the 'Visualize Aligned Sequences Customization' window with the 'Custom' radio button selected. Step 3 shows the 'Analysis Detail - Dengue2-human-1999-2000-MSA' page with a right-click context menu open over the alignment.

1. After the alignment analysis is finished, mouse-over “Run Analysis” and click “Visualize Aligned Sequences”.
2. On the next page, you will have the option to customize the sequence labels by selecting the “Custom” radio button in the “Label sequence by” section. Click “Run” to load the alignment visualization window.
3. In the alignment visualization window, many customization options exist:
 - Rename a sequence label: Right-click a strain name in the alignment, mouse-over the sequence name in pop-up menu, click “Edit Name/Description”, modify the name and click “Accept”.
 - Highlight Sequence Features on the alignment: Click and drag a desired region of sequence alignment, right-click the selected region, mouse-over “Selection” and click “Create Sequence Feature”.
 - Color alignment based on sequence identity cutoff: Click on “Colour” pulldown menu and then the “Above Identity Threshold” option. Using sliding bar to adjust color display.
 - Manually adjust the alignment: Click a sequence and then use ← or → on the keyboard to adjust the alignment.
4. Export the alignment from the “File” menu.