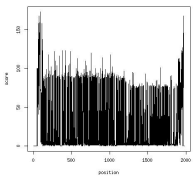
ViPR Virus Pathogen Resource

http://www.viprbrc.org/

Freely available *Integrated datasets* *Bioinformatics tool suite*

Sequence Conservation/Variation Analysis



- Analyze sequence polymorphism at the nucleotide or amino acid level.
- Calculate concensus sequence and polymorphism of ViPR sequences or your own

Sequence Variation Analysis Sample Report

Save SNP result to Workbench for future retrieval

Download consensus sequence in FASTA format

Download raw alignment of all sequences

Score ranges from 0 (no polymorphism) to 232 (highest polymorphism).

At each position, the consensus is the allele with frequency greater than 50%. If no allele exceeds 50%, N (for nucleotide) or Xaa (for amino acid) is used to indicate ambiguity.

Count for different nucleotides at each position

SEARCH DATA | ANALYZE & VISUALIZE | WORKBENCH | SUBMIT DATA | VIRUS FAMILIES | HOME | Dengue

Home ▸ Results

Sequence Variation Analysis Result

Save Analysis | FASTA Format | Download

Position	Score (SOP)	Consensus	A	T	G	C	Deletion	# Sequences
1	0	G	0	0	1	0	0	1
2	0	G	0	0	1	0	0	1
3	0	A	1	0	0	0	0	1
4	0	C	0	0	0	1	0	1
5	0	C	0	0	0	1	0	1
6	0	G	0	0	1	0	0	1
7	0	A	27	0	0	0	0	27
8	0	C	0	0	0	27	0	27
9	0	A	27	0	0	0	0	27
9905	0	G	0	0	32	0	0	32
9906	100	N	0	16	0	16	0	32
9907	0	C	0	0	0	32	0	32
9908	20	A	31	0	1	0	0	32
9909	0	C	0	0	0	32	0	32
9910	0	A	32	0	0	0	0	32
9911	0	T	0	32	0	0	0	32

The analysis report page shows the polymorphism score, consensus, and counts for each different base/amino acid at each position.

Consensus sequence and raw alignment are available for download.

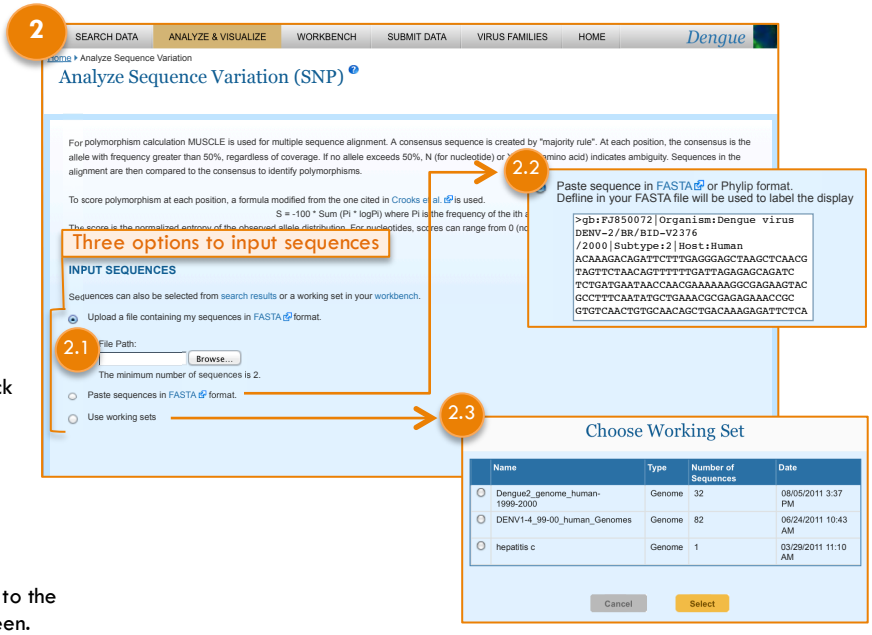
Option 1: Calculate consensus sequence and sequence variation of your own sequences

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

1. Mouse-over the "Analyze & Visualize" tab and click "Analyze Sequence Variation (SNP)".
2. On the SNP landing page, use one of the three options to input sequences:

2.1 Upload a sequence file in FASTA format OR
2.2 Paste sequences in FASTA format OR
2.3 Use a working set from your Workbench.
Then click "Run" to run the analysis.

3. As soon as the analysis is finished, a report similar to the above sample report will be displayed on the screen.



ViPR is funded by the National Institute of Allergy and Infectious Diseases (NIH / DHHS) under Contract No. HHSN272200900041C and is a collaboration between Northrop Grumman Health IT, J. Craig Venter Institute and Vecna Technologies. Comments, questions, suggestions? Contact us at feedback@virusbrc.org

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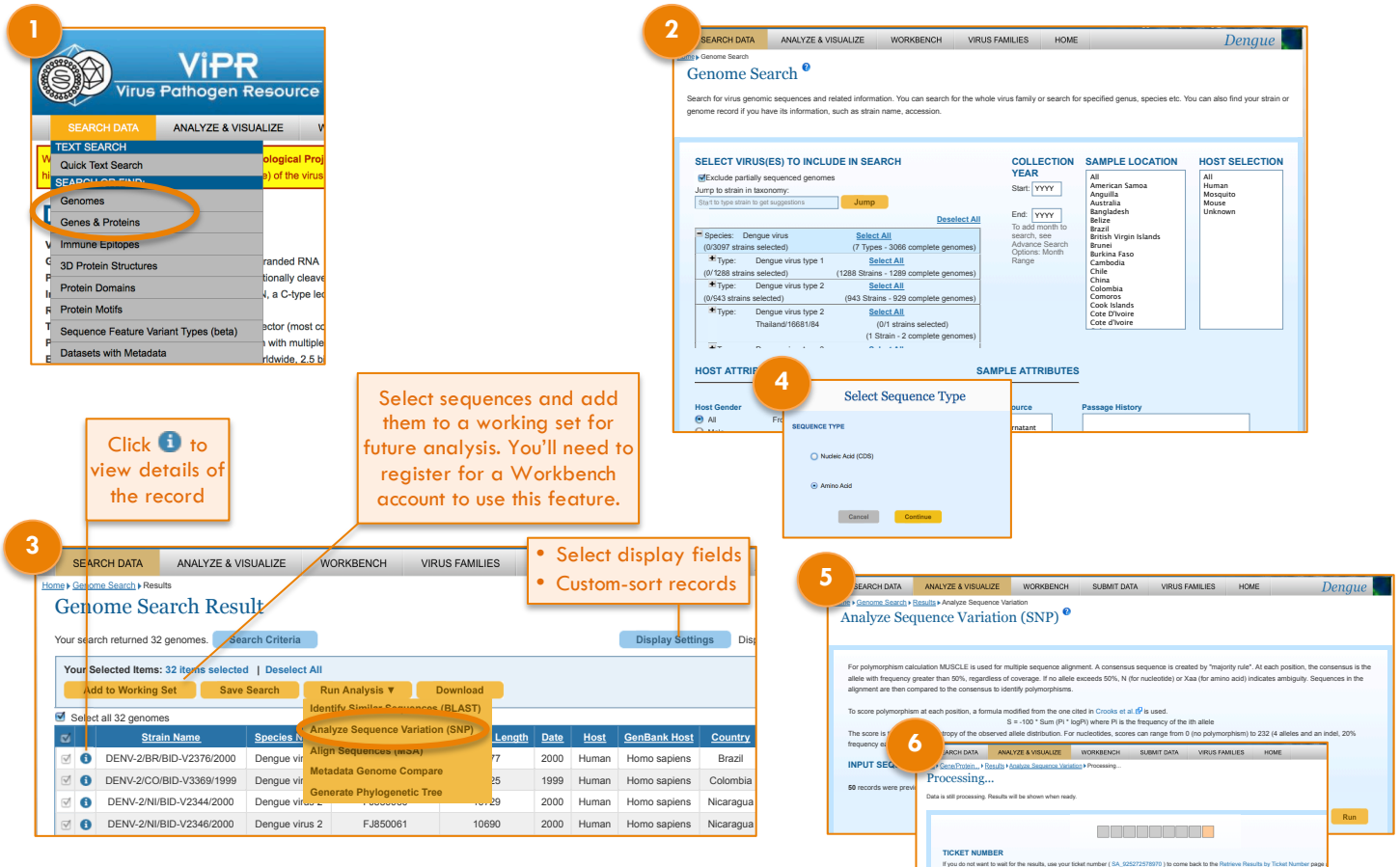
Option 2. Calculate consensus sequence and sequence variation of ViPR sequences



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

1. Search for nucleotide or protein sequences in ViPR by using the "Genomes" or "Genes & Proteins" search option available from the "Search Data" tab. For this example, we will use genome sequences.
2. Select search criteria on the Genome Search page and click the "Search" button to run your query.
3. On the search results page, select the desired sequences by clicking the checkboxes, mouse-over the yellow "Run Analysis" button and click "Analyze Sequence Variation (SNP)".
   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 "Analyze Sequence Variation (SNP)".
4. A "Select Sequence Type" lightbox will pop up. Select the appropriate sequence type and click "Continue".
5. On the next page, you will see a brief description of the SNP tool. Click "Run" to proceed.
6. If you have a large number of long sequences to analyze, it 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 SNP analysis result later from your Workbench.
7. As soon as the analysis is finished, a report similar to the sample report on the reverse page will be displayed on the screen.

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