Sequence Feature Variant Type (SFVT) Analysis

Do you wish to...

- Find regions of virus proteins with specific functional, structural, or immune epitope properties?
- Identify sequence variations that may correlate with phenotypic characteristics, e.g., drug sensitivity/resistance, virulence, transmissibility, fatality in animal models, etc.?

The Sequence Feature Variant Type (SFVT) tool can help!

- Sequence Features (SFs): Specific amino acid residue(s) in virus proteins defined based on functional properties, structural properties, and immune epitope locations. Curated from literature and/or imported from other databases. Validated by domain experts.
- Variant Types (VTs): Polymorphisms in each Sequence Feature are identified as “Variant Types” of the Sequence Feature (SFVT).

Currently, the SFVT analysis is only available for Hepatitis C (subtype 1a), Dengue, and Pox (Vaccinia). From the ViPR homepage, select Dengue, HCV, or Poxviridae to start.

1. Mouse-over “Search Data” and click “Sequence Feature Variant Type”.
2. There are two ways to view Sequence Features:
   - Search by viral mature proteins, SF type, amino acid coordinates, or keyword.
   - Click “Go to Sequence Feature List” to browse all Sequence Features. Click a hyperlinked number to view a specific viral protein’s SFs.
3. From the Sequence Features list, click to view details of an SF.

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Highlight Sequence Features (SFs) on protein 3D structures

1. Mouse over “Search Data” and click “3D Protein Structures”.
2. Search for protein structures of interest.
3. On the search result page, click “View Structure” next to the structure name to load the structure viewing window.
4. To the right of the structure, there are many customization options. Check your desired epitopes in the “Highlight Epitopes” section or enter Sequence Feature positions in the “Highlight by Swiss-Prot Positions” section. Rotate the structure as needed.
5. Click “Save View as Image” under the structure image to save a publication quality structure image with highlighted SFs.