New sequence alignment viewer

Previously, the JalView Java Applet was used as the software tool for the visualization and analysis of multiple sequence alignments (MSAs). Because Java Applets are no longer supported in most modern web-browsers, we have replaced JalView with a custom modified version of the interactive multiple sequence alignments visualization tool MSAViewer (Yachdav et al., 2016), which is written in JavaScript and thus supported in modern browsers. The modified MSAViewer (publicly available at https://github.com/cmzmasek/msa) used in IRD/ViPR has all the basic features of JalView, including display and colorization of alignments, pan and zoom, download in a variety of formats, and selection and deletion of sequences and alignment columns based on various criteria. More advanced features will be implemented in future revisions.

An alignment of influenza virus H1 segment sequences visualized in the new alignment viewer in IRD. A consensus sequence has been added to the top of the alignment (Extras > Add consensus seq). Input sequences are sorted by sequence label (Sorting > Seq ▲). Above the top of the alignment, sequence logos are shown to indicate the sequence conservation at the corresponding positions (Vis.elements > Show sequence logo). More visualization and export options are available through the dropdown menus above the alignment.

New plasmid data

The Orfeome Project is a collaboration of immunology and RNA/DNA virus pathogenesis experts working together to address the hypothesis that RNA and DNA viruses encode common and unique mechanisms to manipulate virus replication efficiency and host responses to determine severe disease outcomes. To address this hypothesis, the project takes advantage of novel expression vector platforms to identify and characterize the role of uncharacterized viral genes.

The project has generated hundreds of plasmids harboring uncharacterized viral open reading frames (ORFs) from Chikungunya virus, Ebola virus, Kaposi’s sarcoma-associated herpesvirus (KSHV), Influenza virus, MERS-Coronavirus, SARS-Coronavirus, Vaccinia virus and Zika virus. Now the plasmid and annotation data are available through the IRD/ViPR sites.

The new Plasmid Data component in IRD/ViPR. This page can be accessed from Search Data > Plasmid Data > View a specific plasmid. Users can download the insert sequence, plasmid vector, plasmid map, plasmid-associated metadata and gene/protein annotations from this page. The source strain is also linked from this page.

Sequence search API supports more viruses

The sequence search API now supports retrieval of sequence data and associated metadata from all families in the Bunyavirales order, including: Feraviridae, Filoviridae, Jonviridae, Phasmaviridae and Tospoviridae.

The November 2018 release of ViPR is now available, visit www.viprbrc.org