**News and Events**

Join the ViPR User Advisory Group to help us better serve the scientific community

ViPR is a bioinformatics resource built for the virology research community. We are calling for users to join the ViPR User Advisory Group to provide feedback and advise on ViPR development. [Click here for details.](#)

**IRD/ViPR hands-on workshops**

ViPR will be providing a hands-on workshop at Mount Sinai School of Medicine, New York, NY, December 5. Please contact Ryan Camping (ryan.camping@mssm.edu) for workshop registration.

**Sequence Conservation/Variation Analysis tutorial**

The Analyze Sequence Variation (SNP) tool in ViPR provides the ability to quickly quantify the sequence variations present at all homologous positions for user-selected sequences at either the nucleotide or amino acid level and simultaneously calculates the consensus sequence. Check out the [tutorial](#) to see how to use it.

**Improved mature viral protein annotation pipeline**

In addition to integrating virus-related data from multiple public repositories, the ViPR Bioinformatics Resource Center has also developed a variety of custom annotation and computational pipelines. Efforts to improve protein annotations by the ViPR team are exemplified in the recent development of an annotation pipeline designed to predict regions containing mature viral proteins from polypeptide sequence data obtained from GenBank. This pipeline combines multiple sequence alignment with protease cleavage site information from well-annotated Reference Sequence (RefSeq) strains for each virus taxon, to map the homologous mature peptide locations from the RefSeq record to the other genome sequences within the same virus taxon. This pipeline was recently improved by incorporating the ClustaW algorithm for the multiple sequence alignment step in order to improve accuracy, especially for genome sequences with incomplete CDS. Currently, the annotation pipeline has been implemented to predict mature viral proteins for many taxa in the Arenaviridae, Bunyaviridae, Caliciviridae, Coronaviridae, Flaviviridae, and Togaviridae families in ViPR.

**PCR primer design tool enhanced**

ViPR has recently implemented a PCR primer design tool, which uses the Primer3 algorithm to predict the optimal set(s) of PCR primers for a particular sequence. In addition to uploading or pasting your own nucleotide sequence to the PCR Primer Design tool page accessible from the "Analyze & Visualize" tab, you can now launch the PCR Primer Design tool directly from either a Nucleotide Search Results page or from a Working Set Details page within your personalized Workbench. To do so, on the Search Results page or Working Set Details page, select the desired sequence, mouse over the "Run Analysis" menu and click "PCR Primer Design". Your selected sequence will automatically be transferred to the PCR Primer Design tool. At present, primers can only be designed for one target sequence at a time. However, ViPR is working on enhancing the tool to allow primer design for a group of target sequences in the future.

In response to user feedback, we have also added end-of-line position numbers in the primer design sequence input sequence box. This feature will help ensure accurate selection of the desired target region within the displayed sequence.

**Rock your protein structure**

ViPR provides a customized interactive protein structure viewer for virus-related protein structures obtained from the Protein Data Bank. In addition to choosing from a variety of structure display options, including ball & stick, line, space, primary structure, secondary structure, etc., you can now rock a structure back and forth to get a better 3D view of your region of interest. First orient or zoom the structure to your needs, then click the "Rock" button in the Display Options section and adjust the rocking parameters if needed. Take a look at a sample structure here.

**Added support for Rhabdoviridae viruses**

In addition to supporting the Lyssavirus genus in the Rhabdoviridae family, ViPR has added sequence, immune epitope, and protein structure data for Bracorhabdovirus, Cytorhabdovirus, Ephemerovirus, Novirhabdovirus, Nucleorhabdovirus, Vesiculovirus (Vesicular Stomatitis Virus), and unclassified Rhabdoviridae viruses (Bas-Congo virus) in Rhabdoviridae. Come to ViPR to search for the various types of data integrated in the database and take advantage of the suite of analysis and visualization tools provided in ViPR.

**The November 2012 release of ViPR is now available, visit [www.viprbrc.org/brc/](http://www.viprbrc.org/brc/)**